

TESTING THE ROLE OF ESCALATION ON JURASSIC MACROEVOLUTIONARY PATTERNS

by

PEDRO MANUEL MONARREZ

(Under the Direction of Steven M. Holland)

ABSTRACT

Ecological escalation (enemy-species driven selection) is thought to have played a primary role in the macroevolutionary patterns of marine invertebrates during the Mesozoic. The escalation hypothesis posits that taxonomic groups that can adapt to intense predation and bioturbation proliferate, whereas groups unable to adapt are reduced in diversity and abundance or driven to extinction. This dissertation tests the role of escalation on global diversity by testing for evidence of escalation during the Jurassic at different geographic scales and different environments. Using a combination of field-collected data and global data from the Paleobiology Database, the proportions of taxa with traits sensitive to escalation are tracked across Jurassic stages and compared between regions to test 1) the global extent of Jurassic escalation, 2) the role of environmental factors on escalation by comparing data among regions, and 3) test for variation of escalation within a single region. The first test tracks the proportional trajectory of taxonomic occurrences with nine ecological traits throughout the Jurassic in five difference regions parsed from global data (Europe, North America, South America, New Zealand, and Middle East). The second test focuses on the role of environmental

factors, by comparing field data from the Middle Jurassic Carmel Formation in Utah, U.S.A., which was prone to poor environmental conditions (i.e., sluggish circulation, low-oxygen, hypersaline) with European data from conditions that were optimal to promote escalation. The third test attempts to find an escalation gradient that parallels a taxonomic diversity and environmental gradient within the Middle Jurassic Sundance Seaway in the western interior U.S. Results reveal that evidence of escalation is strongest in Europe and driven largely by optimal environmental conditions. Environmental conditions in the Carmel Formation hindered escalatory interactions, and despite a taxonomic diversity and environmental gradient in the Sundance Seaway, evidence of escalation is not present. The results of this dissertation underline the fact that while biotic factors may drive some macroevolutionary patterns, the development of these factors may depend on particular physical environmental conditions. Furthermore, these results reveal the importance of comparing paleoecological data across different geographic scales to understand the driving factors of macroevolutionary patterns.

INDEX WORDS: Escalation, Jurassic, Macroevolutionary Patterns, Biotic Interactions, Paleoecology

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DEDICATION

This is for my parents, Manuel and Maria Soledad Monarrez, my family, and all of my academic mentors.

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CHAPTER 1

INTRODUCTION AND LITERATURE REVIEW

Phanerozoic Marine Diversity

Phanerozoic global marine diversity is characterized by plateaus punctuated by mass extinctions and subsequent rapid diversity increases (Sepkoski 1978, 1979, 1981; Sepkoski et al. 1981; Sepkoski 1984). In detail, diversity increases rapidly during the early Cambrian, followed by a minor plateau, a rapid diversification during the Ordovician and a plateau through the Paleozoic, followed by a significant increase through the Mesozoic with a peak during the Cenozoic and with each plateau punctuated by a mass extinction (Fig. 1.1; Sepkoski 1978, 1979, 1981, 1984, 1996). Recent Phanerozoic diversity curves with sampling-based standardization show similar long-term patterns although with reduced diversity increases and only a single plateau during the Paleozoic (Fig. 1.2; Alroy et al. 2008; Alroy 2010). The question remains as to what drives Phanerozoic diversity patterns.

Two major camps of thought in paleobiology have formed over the driver of Phanerozoic diversity patterns. Some argue that physical or extrinsic factors have been the primary driver (Gould 1985; Benton 2009). Others argue that Phanerozoic diversity plateaus reveal diversity saturation, which is controlled by extinction and immigration driven by intrinsic factors such as biotic interactions, primarily competition and predation (MacArthur 1969; Walker and Valentine 1984).

Commonly invoked physical drivers of diversity include fluctuations in climate, tectonics, and sea level, as well as extraterrestrial perturbations such as bolide impacts (Alvarez et al. 1980; Hallam 1989; Benton and Emerson 2007; Stanley 2007; Mayhew et al. 2008; Peters 2008; Benton 2009; Erwin 2009; Mayhew et al. 2012). Plateaus in diversity curves (i.e. Sepkoski 1981; Alroy et al. 2008) are argued by proponents of physical drivers as artifacts of higher classification groups, because plateaus are not present in diversity curves at the genus level (Benton and Emerson 2007; Stanley 2007; Benton 2009). Some argue that diversity is not constrained by plateaus and can increase virtually without limit (Stanley 2007; Benton 2009). Furthermore, there appears to be three tiers (time scales) of macroevolution: species interactions at the community level in the first tier, differences in tempo and mode of selection of clades over geologic time in the second tier, and mass extinctions in the third tier (Gould 1985). Proponents of physical drivers argue that innovations resulting from biotic interactions in the first tier are negated at higher tiers and fail to drive macroevolutionary patterns (Gould 1985; Benton 2009).

Those favoring biotic factors as the driver argue that Phanerozoic diversity patterns, particularly diversity equilibrium or plateaus, result from a global carrying capacity controlled by biotic interactions such as predation and competition (Walker and Valentine 1984; Alroy 2008; Alroy et al. 2008; Alroy 2010). They also argue that adaptive radiations resulting from biotic interactions have driven diversity patterns during some intervals of the Phanerozoic, such as the Ordovician and Mesozoic (Vermeij 2008). Furthermore, proponents of biotic factors note that Phanerozoic diversity patterns are closely correlated with predation traces and niche specialization among marine groups

(Huntley and Kowalewski 2007; Nürnberg and Aberhan 2015). It is clear that biotic interactions increase diversity at the scale of local communities (Paine 1966, 1974; Menge and Sutherland 1976; Holt 1977; Freestone et al. 2010). What remains unclear is whether changes in diversity resulting from biotic interactions at local scales are reflected at the global scale.

Mesozoic Marine Revolution

Perhaps no other time interval in the Phanerozoic has more claims that biotic interactions drove macroevolutionary patterns than the Mesozoic (e.g. Vermeij 1977, 1987). Following the end-Permian mass extinction, the Mesozoic is characterized by the rise in prominence in diversity and ecology of Sepkoski's Modern evolutionary fauna (Figs. 1.1 and 1.2; Sepkoski 1984). Sepkoski's Modern fauna is dominated by bivalves, gastropods, echinoids, scleractinian corals, and decapods (Sepkoski 1984).

This rise in dominance of these groups has been attributed to an increase in marine nutrient availability (Bambach 1993; Martin 1996; Martin et al. 2008; Finnegan et al. 2011; Martin and Quigg 2012; Allmon and Martin 2014), which facilitated an increase in ecospace utilization (Bambach 1983; Bambach et al. 2007; Bush et al. 2007). Increased nutrient availability allowed molluscs to become larger and fleshier, becoming attractive prey items (Bambach 1993). An increase in fleshier prey led to an increase in predators and predation pressure (Vermeij 1977, 1987; Walker and Brett 2002). Prey species adapted to this predatory pressure by developing escape and defensive mechanisms including deep burrowing, increased motility, increased cementation to hard substrates, and defensive shell structuring and ornamentation such as increasing shell thickness,

narrowing apertures, and increased spines (Vermeij 1977, 1987; Harper and Skelton 1993).

The Mesozoic also marks the rise of benthic bioturbators including echinoids, malacostracan arthropods, and deposit-feeding bivalves, and this increase coincided with major changes in benthic community structure (Thayer 1979, 1983). For example, bioturbators displaced sessile and bysally-attached epifauna on soft substrates, which often resulted in mortality in sessile organisms because they are not able to reattach or reorient once disturbed (Thayer 1979). Bioturbation also re-suspends sediment into the water column, which can bury epifaunal organisms and hamper suspension feeding (Thayer 1979). Affected epifaunal groups, which include sessile and bysally-attached bivalves, brachiopods, crinoids, corals, and sponges, became increasingly limited to hard substrates, where the effects of bioturbation are reduced (Thayer, 1979). Increased bioturbation during the Mesozoic also likely contributed to the increase in nutrient availability, as sediment reworking caused nutrients to be released into the water column (Thayer 1979).

Collectively, the increase in predators and bioturbators along with the adaptive response of prey and competitors is known as the Mesozoic marine revolution (Vermeij 1977; Harper 2003). The Mesozoic marine revolution coincides with increased rates of origination of marine groups (Alroy 2008) as well as a rapid increase in diversity that continued largely unabated through the Cenozoic, excepting the end-Cretaceous mass extinction (Alroy 2010). The parallel timing of the Mesozoic marine revolution and the diversification during the Mesozoic has led to the argument that biotic interactions drove marine diversity (Vermeij 2008; Alroy 2010). In particular, regional adaptive radiations

resulting from biotic interactions are argued to have driven global diversity patterns beginning in the Middle to Late Jurassic (Vermeij 2008). Whether biotic interactions drove regional diversity patterns during the Jurassic has not been tested.

Testing the Role of Biotic Interactions

The lack of studies testing the role of biotic interactions on regional diversity patterns during the Jurassic is partly reflects the difficulty of testing how biotic interactions affect diversity over geologic time. Whereas evidence of predatory interactions such as drill holes and bite/crush marks have been found throughout the fossil record (Kelley et al. 2003), such data only record an instance of predation and not the effect of biotic interactions on diversity.

One way to infer the role of biotic interactions on diversity is to measure the predicted consequences of such interactions. For example, the evolutionary trajectories of interacting groups can be compared to indirectly determine if the predicted results of biotic interactions occurred (e.g. Kelley 1992; Kelley and Hansen 1993). One such biotic interaction is escalation, the unidirectional selection driven by interspecific interactions between competing individuals for the same limited resources and by predator-prey interactions (Vermeij 1987, 1994; Dietl and Kelley 2002; Dietl 2003; Vermeij 2004, 2013). Such unidirectional selective pressure exerted by one species to force another species to adapt can result in speciation (Vermeij 1987). Escalation can occur in species competing for limited resources, and between predators and their prey (Vermeij 1987). Escalation is difficult to test directly, owing to the difficulty of observing interactions in the fossil record, but the potential evolutionary consequences of escalation can be detected (Vermeij 1987; Kelley 1992; Kelley and Hansen 1993).

Previous attempts to test the role of escalation on global macroevolutionary patterns have shown no statistical correlations between diversity trajectories of interacting groups (Madin et al. 2006a) or inconclusive results of escalatory trends (Aberhan et al. 2006). However, these studies were criticized for being conducted on a scale too broad and for focusing primarily on diversity as an indicator of escalation (Dietl and Vermeij 2006; Roopnarine et al. 2006; Vermeij 2008). To test for escalation, Vermeij (2004, 2008) argued that studies must compare 1) *specific adaptive traits* at 2) *local to regional scales* in 3) *similar depositional environments*, and 4) *preferably in the tropics*, where abundant resources and warm waters that are well-oxygenated can sustain such interactions. Specific adaptive traits need to be compared to determine if these traits changed as predicted by escalatory pressure (Vermeij 2008). If escalation is argued to occur at the local and regional scale, it needs to be tested at these scales (Vermeij 2008). Similar depositional environments are required so that oceanographic conditions with similar levels of resource availability, oxygenation, and other environmental factors are compared (Vermeij 2008). Tropical regions are preferred for testing escalation because the characteristic environmental conditions of these regions (biologically productive, warm waters that are well-oxygenated) have been argued as necessary for sustaining escalatory interactions (Vermeij 2004, 2008).

Purpose of Study

The purpose of this dissertation is to test if the predicted consequences of escalation in marine benthic invertebrates can be detected during the Jurassic by focusing on two main components of the escalation hypothesis: environmental conditions and geographic scale. This dissertation will take a database and fieldwork approach to test

whether escalation is observed during the Jurassic at regional scales and only in areas with environmental conditions suitable for escalation, as argued by Vermeij (2008). The goal of this dissertation is to determine if escalation did indeed play a role on Jurassic macroevolutionary patterns by testing for regional and local evidence of escalation (Vermeij 2008). Before escalation can continue to be evoked as a driver of marine macroevolutionary patterns during the Jurassic, it is important to test for evidence of escalation. Furthermore, the goal of this dissertation is to contribute to the long-standing debate on whether biotic or abiotic factors are the primary driver of macroevolutionary patterns.

In the first chapter of this dissertation, I test whether escalatory trends can be detected at the regional scale, if any evidence of escalation was strictly a regional phenomenon, or if it was synchronous in regions around the world during the Jurassic. Since escalation at the regional scale is argued to have driven global diversity patterns during the Jurassic (Vermeij 2008), it is important to test whether escalation occurred at all and if it occurred in different regions at the same time. If escalation at the regional scale drove diversity patterns, it is predicted that escalatory trends should be observed only in regions where escalation is expected to occur (i.e. tropics) and that it occurred relatively synchronously, since diversity increased rapidly during the Middle and Late Jurassic (Fig. 1.2; Alroy et al. 2008; Alroy 2010). This chapter uses occurrence data from the Paleobiology Database (PBDB, paleobiodb.org) to compare regional ecological life habit trends that are posited to be sensitive to escalation. These life habit trends include shallow infaunal, deep infaunal, sessile (including pedunculate) and free-lying epifauna, cementers, mobile, and facultatively mobile taxa through the Jurassic. The data and R

code used for this chapter are included in Appendix A as well as the Dryad Digital Repository: <http://dx.doi.org/10.5061/dryad.ds4gd>.

The second chapter of this dissertation takes a field approach to test the environmental component of the escalation hypothesis at the local scale in the southern portion of the Sundance Seaway in east-central Utah. The Sundance Seaway was prone to poor ocean circulation, low oxygen conditions, and hypersalinity (di Gibert and Ekdale 1999). As such, it is expected that evidence of escalation would be weak or lacking. To test for the absence of escalation, changes in the proportions of occurrences and abundances of life habit groups in the Middle Jurassic Carmel Formation are compared from the Bajocian to Bathonian. These temporal comparisons test if they change in the opposite direction predicted by escalation and across an interval of rapid global diversification (Alroy et al. 2008, Alroy 2010). The proportions from Utah are compared with European occurrence and abundance data from the Paleobiology Database. The datasets from Utah and Europe were collected in different settings (restricted epicontinental sea in Utah versus a series of open shelves in western Tethys) because these settings are characterized by contrasting environmental conditions, which is used as a control to test the role of environmental factors. These spatial comparisons determine if the same changes in proportions observed in Utah are also observed at Europe where environmental conditions are generally more conducive for escalation, with the expectation that evidence of escalation is observed in Europe but not in Utah. The data and R code used for this chapter are in Appendix B.

Finally, the third chapter uses field-collected data to test if there is evidence of an escalation gradient in the Sundance Seaway during the Bajocian and Bathonian.

Specifically, two datasets from the Sundance Seaway are used, one that I collected for in Chapter 2 and a previously collected dataset farther north in the Sundance Seaway in Wyoming and southern Montana (Danise and Holland 2017). There are two potential gradients south to north in the seaway: 1) taxonomic richness in the Sundance Seaway is higher to the north and 2) environmental analysis of the seaway suggests that seawater temperature and salinity decreases to the north (Stanley 2010, Danise and Holland 2017). If these gradients exist, then it is expected that the strength of escalation would parallel these gradients such that evidence of escalation would increase to the north. The link to the data as well as the R code used for this chapter are in Appendix C.

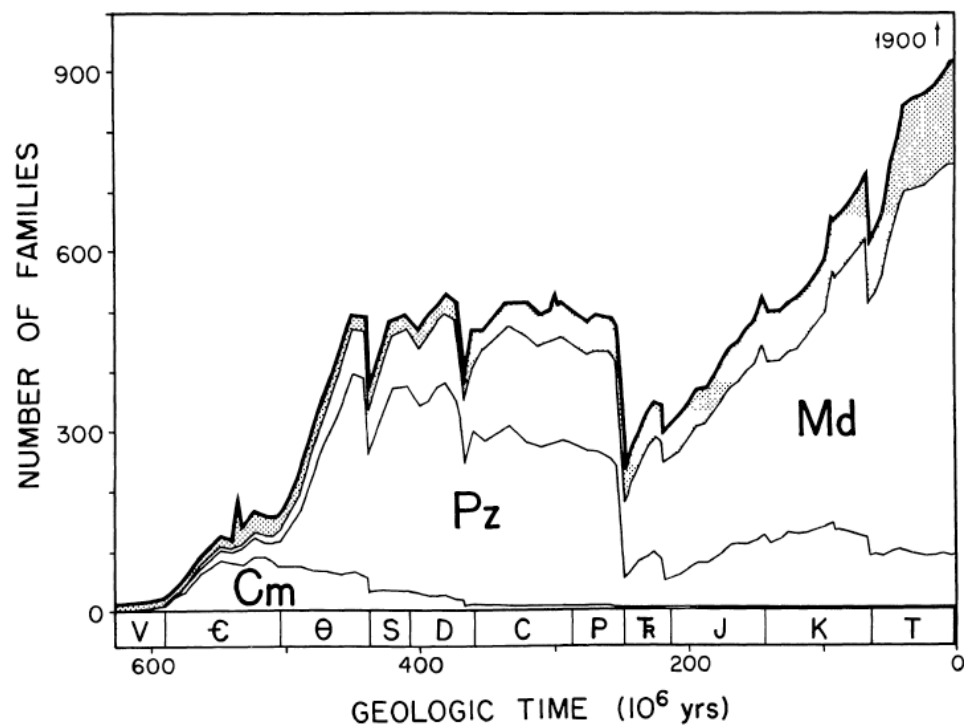


Figure 1.1. Phanerozoic marine family diversity with the three evolutionary faunas labeled (Cm = Cambrian, Pz = Paleozoic, Md = Modern). Overall diversity has increased through the Phanerozoic, with a prominent plateau during the Paleozoic punctuated by the end-Permian mass extinction and a generally sustained increase in the Mesozoic and Cenozoic. From Sepkoski (1981).

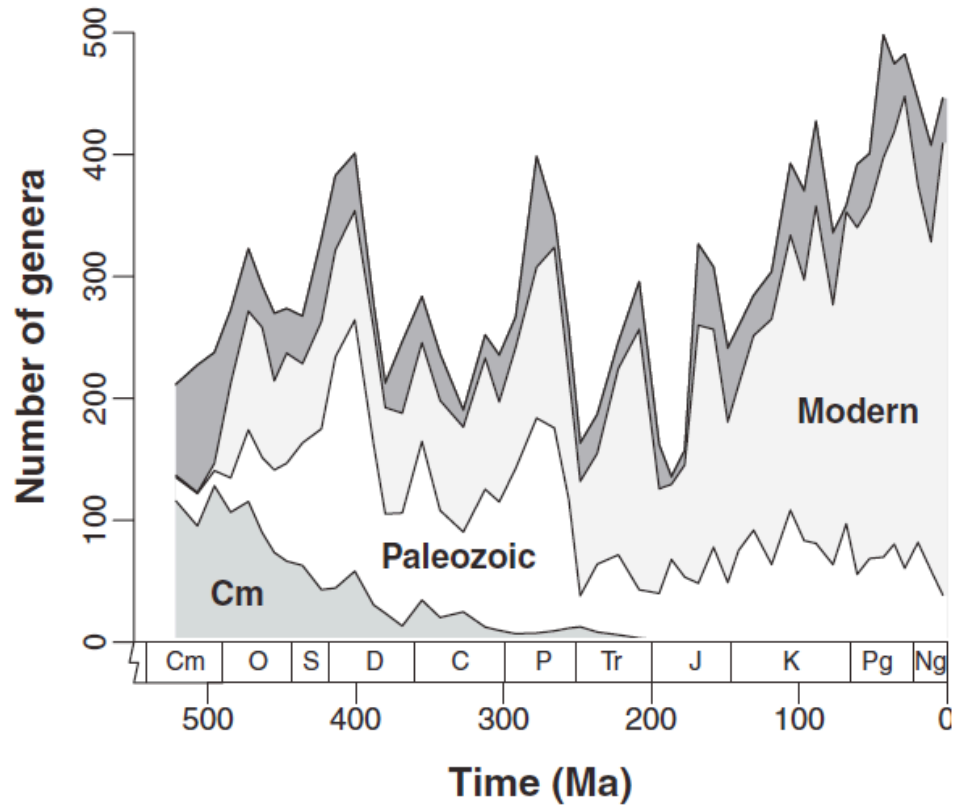


Figure 1.2. Standardized Phanerozoic diversity of marine genera, with Sepkoski's evolutionary faunas labeled. Diversity shows an overall increase through the Phanerozoic with a less defined plateau during the Paleozoic and less increase during the Cenozoic relative to Sepkoski (1981). Although Fig. 1.1 depicts Phanerozoic families, Sepkoski's generic diversity curve delineates a similar trend (Sepkoski 1996) and allows for a fair comparison. From Alroy (2010).

CHAPTER 2

REGIONAL AND ENVIRONMENTAL VARIATION IN ESCALATORY
ECOLOGICAL TRENDS DURING THE JURASSIC: A WESTERN TETHYS HOT
SPOT FOR ESCALATION?¹

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Abstract

Understanding the drivers of macroevolutionary trends through the Phanerozoic has been a central question in paleobiology. Increasingly important is understanding the regional and environmental variation of macroevolutionary patterns and how they are reflected at the global scale. Here we test the role of biotic interactions on regional ecological patterns during the Mesozoic Marine Revolution. We test for escalatory trends in Jurassic marine benthic macroinvertebrate ecosystems using occurrence data from the Paleobiology Database parsed by region and environment. The escalation hypothesis posits that taxonomic groups that can adapt to intense predation and bioturbation proliferated, whereas groups unable to adapt were reduced in diversity and abundance or driven to extinction. We tested these hypotheses in five regions during Jurassic stages as well as among four depositional environments in Europe. Few escalatory trends were detected, although at least one escalatory trend was observed in every region, with the most and strongest trends observed in Europe. These trends include increases in shallow infauna, cementing epifauna, and facultative mobile occurrences and decreases in pedunculate, free-lying, and sessile epifauna. Within Europe, escalatory trends occur in shallow water environments, but also in deeper-water environments, where they are predicted not to occur. When regional trends are aggregated, trends in Europe drive the global signal. The results of this study suggest that while evidence of escalation is rare globally, it is plausible that escalation drove macroevolutionary patterns in Europe. Furthermore, these results underline the need to dissect global fossil data at the regional scale to understand global macroevolutionary dynamics.

Introduction

A persistent debate in paleobiology concerns the mechanisms that drive macroevolutionary patterns. Some argue that physical or extrinsic factors have been the primary driver of macroevolution (e.g., Gould 1985; Benton 2009). Others argue that Phanerozoic diversity patterns, particularly diversity equilibrium and radiations are controlled by extinction and origination driven by biotic interactions such as competition and predation (Walker and Valentine 1984; Alroy 2008, 2010). Previous work also shows that Phanerozoic diversity patterns are closely correlated with occurrences of predation traces and niche specialization among marine groups (Huntley and Kowalewski 2007; Nürnberg and Aberhan 2015). Furthermore, adaptive radiations resulting from biotic interactions have been argued to have driven diversity patterns during some intervals of the Phanerozoic, such as the early-to-mid Paleozoic and Mesozoic (Vermeij 1987, 2004, 2008).

During the Mesozoic in particular, major ecological innovations spurred by the rise of durophagous predators and bioturbators changed the ecological structure of benthic marine macroinvertebrate communities, and thus this transition has been called the Mesozoic Marine Revolution (Vermeij 1977; Thayer 1979, 1983). A previous attempt to test the role of biotic interactions on the structure of Jurassic marine benthic invertebrate communities using global fossil occurrence data yielded mixed results, but it largely supported a role for biotic interactions in structuring benthic communities (Aberhan et al. 2006). However, the study was criticized in part because of its global scope (Vermeij 2008). Building on the approach of Aberhan et al. (2006), we revisit the role of biotic interactions in structuring Jurassic marine benthic ecosystems, using

additional global fossil occurrence data entered over the past eleven years, and by tracking changes in groups with escalation-sensitive traits within geographic regions and within depositional environments.

Mesozoic Marine Revolution

Perhaps no other time interval in the Phanerozoic is more closely associated with biotic interactions driving macroevolutionary patterns than the Mesozoic (e.g., Vermeij 1977, 1987). Following the end-Permian mass extinction, the Mesozoic is characterized by the rise in prominence, in both taxonomic and ecologic diversity, of the Modern Evolutionary Fauna, composed primarily of bivalves, gastropods, echinoids, scleractinian corals, and decapods (Sepkoski 1981, 1984).

This rise in dominance of the Modern Evolutionary Fauna has been attributed to an increase in marine nutrient availability (Bambach 1993; Martin 1996; Martin et al. 2008; Cárdenas and Harries 2010; Martin and Quigg 2012; Allmon and Martin 2014). Increased nutrient availability is thought to have allowed benthic groups, particularly molluscs, to become larger and fleshier, becoming attractive prey items (Bambach 1993). An increase in fleshier prey led to an increase in predators and predation pressure (Vermeij 1977, 1987; Walker and Brett 2002). Prey species adapted to this predatory pressure by developing escape and defensive mechanisms including burrowing, increased motility, stronger cementation to hard substrates, increased shell thickness, narrowed apertures, stronger ornamentation with ribs or spines, or by inhabiting marginal environments, (Vermeij 1977, 1987; Harper 1991; Harper and Skelton 1993; Oji 1996; Harper 2003).

The Mesozoic also marks an increase in benthic bioturbators including echinoids, malacostracan arthropods, and deposit-feeding bivalves, and this increase coincided with major changes in benthic community structure (Thayer 1983). For example, bioturbators displaced sessile and byssally-attached epifauna on soft substrates, which often resulted in mortality of sessile organisms because of their inability to reattach or reorient once disturbed (Thayer 1983). Bioturbation also re-suspends sediment into the water column, which can hamper suspension feeding or result in burial of epifaunal organisms (Thayer 1983). Displaced epifaunal groups, which include stationary unattached and byssally-attached bivalves, brachiopods, crinoids, corals, and sponges, became increasingly limited to hard substrates where the effects of bioturbation are reduced (Thayer 1983). Increased bioturbation during the Mesozoic also likely contributed to the increase in nutrient availability, as sediment reworking releases nutrients into the water column (Thayer 1983).

The Mesozoic rise of predators and bioturbators led to the formulation of the escalation hypothesis, unidirectional selection that was driven by antagonistic interactions between species, such as predator-prey interactions (Vermeij 1987, 1994, 2004, 2013; Dietl and Kelley 2002; Dietl 2003). Such unidirectional selective pressure exerted by one species onto another forces the species under selective pressure to adapt, which can result in speciation (Vermeij 1987). Those groups that were not able to adapt to these increased biotic pressures became extinct or were marginalized and forced to inhabit less productive habitats (Vermeij 1987). Although escalation is difficult to test directly owing to the difficulty of observing interactions in the fossil record, the potential evolutionary

consequences of escalation can be detected (Vermeij 1987; Kelley and Hansen 1993, 1996).

Reevaluating Tests of Escalation

Previous attempts to test the role of escalation on global macroevolutionary patterns have shown no statistically significant correlations between diversity trajectories of interacting groups (Madin et al. 2006) or mixed results, with some trends supporting escalation and others failing to (Aberhan et al. 2006). These studies have been criticized for being conducted on a scale too broad to detect escalation or for their focus on diversity as an indicator of escalation (Dietl and Vermeij 2006; Roopnarine et al. 2006; Vermeij 2008). To test for escalation, Vermeij (2004, 2008) argued that studies must compare (1) *specific adaptive traits* at (2) *local to regional scales* in (3) *similar depositional environments*, and (4) *preferably in the tropics* where abundant resources and well-oxygenated warm waters can sustain the interactions that lead to escalation. Specific adaptive traits need to be compared to determine if these traits changed as predicted by escalatory pressure (Vermeij 2008). If escalation is argued to occur at the local and regional scale, it needs to be tested at these scales (Vermeij 2008). Similar depositional environments are required so that oceanographic conditions with similar levels of resource availability, oxygenation, and other environmental factors are compared (Vermeij 2008). Tropical regions are preferred for testing escalation because the characteristic environmental conditions of these regions (productive, well-oxygenated warm waters) is necessary for sustaining escalatory interactions (Vermeij 2004), although not always (Vermeij, 2008).

The Jurassic represents a crucial interval of the Mesozoic Marine Revolution when adaptive radiations resulting from escalation apparently caused the diversification of many marine benthic invertebrate groups (Vermeij 2008). If escalation drove diversity and abundance patterns in the Jurassic, it is important to constrain when and where escalation took place. Before the role of biotic interactions in shaping global diversity and abundance patterns can be evaluated, it is important to test whether escalation occurred in particular regions or environments.

The goal of this study is to determine whether any specific regions and environments experienced ecological trends consistent with escalation during the Jurassic, when these trends occurred, and if these trends occurred synchronously among regions and environments. This study builds on the approach used by Aberhan et al. (2006) in four ways. First, twice as much data is available now than was previously. Second, the spatial distribution of occurrences has increased. Third, this study focuses on patterns of occurrences at the regional scale rather than the global scale or low versus high latitudes. Fourth, this study compares patterns of occurrences among four depositional environments. Following Vermeij (1987), we predict that the proportion of occurrences of infauna, mobile, and cementing epifauna should increase during the Jurassic, while free-lying (unattached to substrate) sessile epifauna is expected to decrease if escalation occurred (Table 2.1).

Data and Methods

The Jurassic occurrence dataset for this study was downloaded from the Paleobiology Database (<https://paleobiodb.org>) on 20 February 2016 and consists of non-reef benthic macroinvertebrate species of bivalves, gastropods, brachiopods,

echinoderms, corals, sponges, and arthropods body fossil occurrences. Ichnological data were not included in this study because these data are sparse in the Paleobiology Database and no other database exists for the Jurassic that can be analyzed quantitatively. The inclusion of arthropods and other non-echinoid echinoderms expands on the taxonomic groups considered by Aberhan et al. (2006). The data also include information on tiering, feeding strategy, motility, lithology, depositional environment, as well as paleolatitude and paleolongitude coordinates determined from a GPlates paleogeographic rotation model (Wright et al. 2013). Senior synonyms were used where available, and the synonyms as well as ecological data for bivalves were updated using ecological data collected by one of the authors (Aberhan).

A total of 47,340 occurrences were downloaded. After removing occurrences that lack Jurassic stage designations, the data analyzed consist of 43,961 occurrences from 9864 collections. This dataset is almost twice as large as that analyzed by Aberhan et al. (2006), which contained over 22,000 occurrences from over 2800 collections (Table 2.2). The global distribution of occurrences has also increased, lessening the European dominance of occurrences in Aberhan et al. (2006). For example, in their 2006 study, European occurrences represented 41% of Middle Jurassic and 90% of Late Jurassic occurrences (Table 2.2). In contrast, European occurrences in this study constitute 32% of Middle Jurassic and 62% of Late Jurassic global occurrences (Table 2.2). This improved geographic coverage allows occurrence patterns from multiple regions to be analyzed with greater reliability.

Five regional clusters of occurrences were manually selected based on paleocoordinates of each occurrence (Fig. 2.1). Occurrences lying within each region

were determined with the `pnt.in.poly` function in the `SDMTools` R package (VanDerWal et al. 2014; R Core Team 2016). Occurrences from these five regions represent 89% of the downloaded global occurrences and are named based on the continents where the occurrences are concentrated: North America, Europe, South America, Middle East (including parts of Africa and India), and New Zealand. Data are available for every stage for most regions, except the Middle East region, which lacks occurrences for the first three Jurassic stages, and New Zealand, which lacks occurrences for the Bathonian and Oxfordian stages.

As outlined by Vermeij (2008), ecological traits need to be compared by environment to test for escalation. Reliable environmental data are consistently available only for Europe. Within Europe, 29 different depositional environments are reported, and these were grouped into five categories (nearshore, inner shelf, middle shelf, outer shelf, and slope and deep basin) following the time-environment framework of Bottjer and Jablonski (1988).

Species occurrences are used here as proxy for relative abundance, as abundance data in the Paleobiology Database are not standardized. In addition, occurrences have been shown to be suitable for assessing abundances (Buzas et al. 1982; Aberhan et al. 2006; Liow and Stenseth 2007; Hayek and Buzas 2010; Payne et al. 2011; McGhee et al. 2013; Clapham 2015). Proportions of groups with specific traits selected on by escalation were calculated for every Jurassic stage and for every environmental category for every stage within Europe.

Escalation-sensitive ecological traits are grouped to three categories: tiering, epifaunal modes of life, and motility (Table 2.1). Confidence intervals (95%) for all proportions

were calculated based on the method of Raup (1991). Spearman's rank correlation tests were conducted on all time series to determine statistically significant trends in escalation-sensitive traits (Tables 3–5). All calculations were performed in R (R Core Team 2016). Source code and occurrence files used for this study are deposited at Dryad.

Results

Our regional analyses reveal that ecological trends consistent with escalation are generally lacking, although, at least one trend consistent with escalation occurs in every region.

Regional Variation

Tiering.—For all regions, epifaunal is the most common tier, (Fig. 2.2a–e); deep infaunal occurrences are generally static through the Jurassic. Only Europe exhibits statistically significant (i.e. non-zero) trends in tiering (Table 2.3). In Europe, epifaunal occurrences begin a monotonic decrease during the Bajocian driven by a decline in rhynchonelliform brachiopods, with a concomitant increase of shallow infaunal occurrences that continues through the end of the Jurassic (Fig. 2.2a).

Most tiering trends are not consistent with escalation, however shallow infaunal and epifaunal trends in Europe are consistent with Vermeij (1987)'s escalation hypothesis. Additionally, deep infaunal occurrences show no net trend in most regions, and they provide no evidence for or against escalation. Furthermore, insufficient data for New Zealand and wide confidence intervals in the latest Jurassic in South America make it difficult to identify trends.

Epifaunal Modes of Life.—Pedunculate brachiopods (rhynchonelliforms) constitute the largest proportion of epifauna, and they generally decrease during the latter

half of the Jurassic (Fig. 2.3a–e). This decrease in pedunculate occurrences can be observed in every region except North America, but, only in South America is their decrease statistically significant. In general, the proportion of free-lying epifaunal occurrences fluctuates in all regions in the early half of the Jurassic followed by a general decrease. This trend of decreasing free-lying occurrences during the latter half of the Jurassic is most pronounced in North America where the trend is statistically significant (Table 2.3). Cementing epifauna appears to increase in Europe and the Middle East (Fig. 2.3a, b), but this trend is only statistically significant in the Middle East.

Epifaunal modes of life trends overall are not consistent with escalation, however, the observed decrease in pedunculate and free-lying epifauna occurrences and the increase in cementing bivalves are all consistent with escalation.

Motility.—Overall, sessile groups decrease throughout the Jurassic, while facultative mobile groups increase throughout (Fig. 2.4a–e). In Europe, the increase in facultative mobile and decrease in sessile occurrences are statistically significant (Table 2.3). The proportion of fully mobile groups shows no net trend throughout the Jurassic, except for an increase in New Zealand, where the trend is statistically significant.

As with tiering and epifaunal life mode trends, motility trends overall are not consistent with escalation, except for the observed decreases in sessile occurrences and increases in facultative mobile occurrences. The increase in facultative mobile occurrences is primarily driven by the increase in shallow infaunal occurrences. Epifaunal occurrences that are facultative mobile consist primarily of swimming pectinid and entoliid bivalves. The relatively static patterns in actively mobile species neither support nor refute escalation.

Environmental Variation

The abundance of data from a range of environments in Europe allows escalatory trends there to be compared among environments, however, data are missing for deep slope and basin environments and therefore could not be analyzed. Escalatory trends in Europe are most strongly developed in nearshore and middle shelf environments but are also present in outer shelf environments.

Tiering.—Occurrence patterns by tiering are similar in most depositional environments, with epifaunal occurrences dominating throughout (Fig. 2.5a–d). In nearshore and inner shelf environments, tiers generally display little or no net change through the Jurassic except for deep infauna, which shows a statistically significant increase in nearshore environments (Fig. 2.5a, b; Table 2.4), although they represent a minor portion of occurrences. This trend is driven primarily by pholadomyid, thraciid, and lucinid bivalves. In middle and outer shelf environments, epifauna declines in the latter half of the Jurassic as shallow infauna increases (Fig. 2.5c, d); however, the only statistically significant trends are the shallow infaunal increases in middle shelf environments and the deep infauna increase in outer shelf environments (Table 2.4).

Overall, tiering trends consistent with escalation are scarce, however, trends consistent with escalation occur in nearshore as well as middle to outer shelf environments, which is surprising considering that escalation is thought to be restricted to shallower-water environments (see Discussion). Furthermore, the decline of epifauna and increase of shallow infauna in the latter half of the Jurassic in Europe (Fig. 2.2a) are likely driven by the trends in middle and outer shelf environments.

Epifaunal Modes of Life.— Pedunculate forms make up much of the epifaunal occurrences in all environmental categories and dominate the first half of the Jurassic. Although they appear to decline during the latter half of the Jurassic, none of these trends are statistically significant. (Fig. 2.6a–d; Table 2.4). Additionally, although cementing epifauna appears to increase steadily through the latter half of the Jurassic in the nearshore and inner shelf (Fig. 2.6a, b), with a net increase in the middle shelf as well (Fig. 2.6c), only in the nearshore is this trend statistically significant (Table 2.4). Overall, free-lying occurrences show no net trend through the Jurassic except a decline in the inner shelf (statistically significant) and the outer shelf throughout the latter half of the Jurassic.

Overall, epifaunal modes of life trends are not consistent with escalation, but the increase in cementing forms in nearshore settings is consistent with escalation. Cementing bivalves in the nearshore are dominated by species of Gryphaeidae (*Nanogyra* and *Liostrea*) and Ostreidae. Additionally, the general decrease in pedunculate forms is also consistent with escalation, however, they were predicted to increase in deeper water environments to avoid predation (Vörös 2005), which is not observed.

Motility.— In general, mobile species decrease or are static in every environment following a sharp increase during the Middle Jurassic (Fig. 2.7a–d). Facultative mobile occurrences increase in nearshore, middle shelf (statistically significant), and outer shelf environments throughout the Jurassic, particularly through the latter half of the Jurassic (Fig. 2.7a, c, d). Sessile occurrences dominate during the Early and Late Jurassic, except in nearshore settings, where sessile occurrences are low during much of the Early Jurassic (Fig. 2.7a).

Motility trends in general do not support the escalation hypothesis. Sessile occurrences are expected to decrease through time in shallow environments while increasing in deeper environments (Vermeij 1987), but that is not the case in middle and outer shelf environments, in which motility instead increased. The sharp increase of mobile occurrences during the Bajocian in outer shelf environments is driven primarily by several families of grazing gastropods. Furthermore, the increase of facultative mobile occurrences through the Jurassic in the middle and outer shelf is driven by eighteen shallow infaunal bivalve families, especially the Arcticidae and Mactromyidae.

Discussion

The Role of Regional Biotic Interactions on Global Ecological Trends

This analysis reveals heterogeneous ecological signals among regions during the Jurassic, with weak evidence of escalation overall. Directional trends consistent with escalation are most pronounced in Europe, where tiering (epifaunal and shallow infaunal) and motility (sessile and facultative mobile), change as predicted with the escalation hypothesis. Similar patterns consistent with escalation are also observed in the Middle East and New Zealand (albeit mostly not statistically significant). The only observed trends consistent with escalation in North and South America are the decrease in free-living forms, as well as the decrease in pedunculate occurrences in South America, as most trends in these two regions contradict or are neutral with regards to the escalation hypothesis.

The ecological trends in Europe are largely consistent with the global results of Aberhan et al. (2006), particularly trends in motility, epifaunal guilds, and tiering. In their study, Aberhan et al. (2006) noted that most of the occurrences they analyzed were culled

from Europe as a result of the uneven distribution of Jurassic strata around the world. This dominance of European occurrences suggests that their global patterns were likely driven by European patterns. Even with improved global coverage in this study, over 55% of occurrences are from Europe. To determine the importance of European occurrences to global ecological trends, we compared trends globally with and without Europe (Fig. 2.8; Table 2.5). Our global occurrence trends are consistent with the results of Aberhan et al. (2006), and they show directional trends consistent with escalation, particularly in tiering, epifaunal guilds (free-lying), and motility (facultative mobile and sessile; Fig. 2.8a). Excluding Europe from the global aggregate weakens the directional trends consistent with escalation, such that only free-lying forms exhibit escalatory trends (Fig. 2.8b; Table 2.5). These results suggest that global ecological patterns are indeed driven largely by patterns in Europe.

European occurrence data broken down by depositional environment reveal patterns that were unexpected, as the ecological trends consistent with escalation occur in nearshore as well as middle to outer shelf environments (Figs. 2.5–2.7). Although the presence of escalatory trends supports Vermeij's (1987) hypothesis, the observation that they are also apparent in deeper-water environments does not. Vermeij (1987) postulated that deeper environments would become refugia for benthic organisms that are unable to cope with the increased predation and bioturbation pressure in shallower environments. In his later analysis of escalation during the Jurassic, Vermeij (2008) conceded that escalation might occur in any environment at any time, as long as the productive conditions required to sustain escalatory interactions were present, suggesting that escalation is not exclusive to shallow tropical environments. Regardless, these results

suggest the trends observed in Europe are driven by patterns in nearshore and middle to outer shelf environments.

The results of this study underline the importance of dissecting global data regionally and environmentally to understand underlying drivers of global biotic patterns (e.g., Miller 1997a, b, 2000, 2003). Our finding that escalatory trends are prevalent in Europe raises the question of why do strong escalatory trends occur in this region and not others?

Western Tethys Focal Point for Escalation?

During the Jurassic, Europe was located in the tropical to subtropical western Tethys realm (Fig. 2.1). The occurrences in Europe span a paleolatitudinal range of 8°N to 52°N, with the bulk of occurrences clustered around 30°N (Fig. 2.1). This region is dominated by species from carbonate deposits, which constitute approximately 70% of European occurrences and the Middle East also primarily consists of carbonate occurrences with 65%. These two regions are much more carbonate-dominated than the other regions: New Zealand (2% carbonate deposits), North America (32% carbonate deposits), and South America (33% carbonate deposits). This pattern reveals a lithologic underpinning to regions that demonstrate some trends consistent with escalation that likely represent warmer, more biologically productive regions, which is argued to be conducive of escalation (Vermeij 1987, 2004, 2008).

The dominance of occurrences from carbonate deposits in Europe is consistent with the escalatory trends observed in this region, but it still does not fully explain the presence of escalatory trends in deeper-water environments that are generally less productive and nutrient-rich than shallow-water environments (Vermeij 1987).

Geochemical analyses and studies on the Jurassic microfauna of the western Tethys suggest that increased nutrient availability and biological productivity was spurred by changes in ocean circulation and increased continental runoff (Bill et al. 2001; Aguado et al. 2008; Reolid et al. 2008; Baumgartner 2013). Increased nutrient availability in the western Tethys during the Middle Jurassic would have coincided with changes in ecological signals that are consistent with escalation, suggesting a causal link. If increased nutrient availability did indeed drive the escalatory patterns observed in Europe and the Middle East regions, it would support Vermeij's (1987, 2004) hypothesis that high productivity is required for escalation to occur.

Alternative Explanations

Aberhan et al. (2006) correlated observed ecological trends with other possible abiotic and biotic explanations for escalatory patterns. Of abiotic controls beyond nutrients and temperature, they also examined sea-level change and seawater chemistry. Although sea level did increase through the latter half of the Jurassic (Hallam 2001), models suggest that sea-level change may or may not drive changes in habitat area and, therefore, biotic changes (Holland 2012). Whether sea-level change drives changes in habitable space in a region depends on the starting sea-level position as well as shelf geometry (Holland 2012). Since these parameters are difficult to establish for any basin, we did not compare sea-level changes with our results.

With regards to seawater chemistry, Aberhan et al. (2006) tracked shell mineralogy to test if the ecological trends were overprinted by the geochemical state of Jurassic seas. During the latter half of the Jurassic, the oceans switched from an "aragonite" sea to a "calcite" sea, as a result of declining seawater Mg/Ca ratio (Hardie

1996, Lowenstein et al. 2003, Müller et al. 2013). Because the percentage of aragonitic shells increased during the Middle to Late Jurassic, seawater chemistry was inferred to not play a role in the observed ecological trends (Aberhan et al. 2006). Following this approach, we tested whether the observed ecological trends could have been driven by a switch to a calcite sea. As in Aberhan et al. (2006), the percentage of fossil occurrences with aragonitic shells in this study increases after the Middle Jurassic at the global scale (see Appendix A, Part 3), but also within Europe, suggesting that the trends observed in this study were not driven by changing seawater chemistry. Whether changes in seawater chemistry muted an even larger-than-observed increase in the percentage of aragonitic shells cannot be tested with the present dataset.

Aberhan et al. (2006) also explored whether intrinsic biotic factors may have caused the perceived escalatory trends, particularly infaunalization. The reasoning for this analysis is that adaptation for burrowing that occurs within just a single clade might indicate adaptation independent of predation pressure. If several clades that share a specific trait show similar increases in relative abundance, then it is likely that some external factor might have promoted that trait and led to its proliferation, such as an increased escalatory pressure. In this study, several bivalve taxa show similar increases in infaunal occurrences (Cardiida, Carditida, Pholadida, Trigoniida, Nuculida, and Nuculanida among others; Aberhan et al. 2006), and therefore it is unlikely that ecological trends observed are a result of intrinsic biotic factors.

Relatively few statistically significant trends consistent with escalation were recognized here, raising the question of how many trends would be developed by chance alone? To test this, we simulated 10,000 iterations of a null model by conducting a

random permutation of time stages followed by Spearman's rank correlation tests. This analysis allows us to determine if the number of observed statistically significant trends is more or less than ought to occur by chance. The results of this analysis for all regions aggregated, and for Europe separately, suggest that more significant trends were observed than would be expected by chance (global $p = 0.03$, Europe $p = 0.03$; Figs. 2.9 and 2.10), suggesting weak but statistically significant patterns of ecological signals associated with escalation.

Statistical power may also play a role in the number of significant trends observed in this study. The few time bins available for this study ($N = 11$) reduces the statistical power and favors statistical insignificance, because the probability of rejecting a null hypothesis decreases with small sample size. Although statistical significance is used here to establish which directional trends are consistent with escalation, many other ecological trends are also directional and consistent with escalation but are not statistically significant, particularly during the latter half of the Jurassic. It is possible that statistical testing may fail to detect true biological signals, owing to low sample size and low power.

Although, the decrease in epifaunal occurrences in Europe is consistent with the escalation hypothesis, at least four other factors could contribute to this pattern. First, because Europe has the highest amount of epifaunal occurrences during the Jurassic, it has great potential for experiencing a detectable drop in epifauna. It is possible that it is simply easier to detect the epifaunal decline in Europe than in regions that began the Jurassic with a comparatively lower number of epifauna.

Second, a decline in hard substrates may have driven the Jurassic decline in attached epifauna. Although it is possible that the frequency of hardgrounds declined during the Jurassic, quantitative data to test this is not available. Because attached epifaunal species could have colonized to secondary hardgrounds consisting of shells and skeletal debris (Kidwell and Jablonski 1983) and because many other epifaunal species were free-lying on soft substrates, it seems unlikely that the decline in epifauna solely reflects a decline in hardgrounds.

Third, the decrease in epifauna, driven largely by the decline in pedunculate rhynchonelliform brachiopods, might also be explained by competitive exclusion with bivalves (Tomasovych 2006). The data presented here do indicate a modest (but not statistically significant) rise in epifaunal and shallow infaunal bivalves during the Late Jurassic (Fig. 2.11 and Appendix A, Part 3), consistent with the idea that brachiopods were replaced by bivalves. Although the replacement of brachiopods with bivalves has been attributed to the more efficient metabolism of bivalves (Tomasovych 2006), this difference in metabolism was present long before the replacement took place, casting doubt on the role of competition between brachiopods and bivalves (Payne et al. 2014). The decline in brachiopods is mirrored by an increase in non-bivalve and non-brachiopod epifauna, some of which include predators such as asteroids and gastropods (Fig. 2.11). This pattern is consistent with previous arguments that biotic interactions such as predation were responsible for the decimation of Jurassic brachiopods in Europe as well as the observed increase in cementing bivalves (Donovan and Gale 1990; Harper 1991; Harper and Wharton 2000; Vörös 2010; Tyler et al. 2013).

Fourth, because Europe accounts for 55% of all occurrences in this study, it is possible that the greater number of statistically significant trends there merely reflects the larger available sample size. To test this, we randomized occurrences among regions while preserving the age of occurrences and the number of occurrences in each region. For each of the 10,000 randomization trials, we calculated the number of statistically significant escalation trends in Europe, against which we can compare the actual number of significant European trends. If the observed number of trends in Europe is a consequence of sample size, randomization should produce a similar number of significant European trends, but if the observed number of European trends truly reflects a difference in Europe compared with the rest of the world, then the observed number of European trends should be greater than that seen in the randomization. The randomization confirms that the number of trends in Europe is not driven by sample size (Fig. 2.12).

Role of Escalation on Macroevolutionary Patterns

A central question in paleobiology concerns the driver of Phanerozoic diversity patterns (Sepkoski 1978, 1979, 1981, 1984; Alroy et al. 2008). Evidence exists for both abiotic and biotic drivers, with multiple studies outlining the role of physical, abiotic factors (Hallam 1989; Benton and Emerson 2007; Mayhew et al. 2008; Peters 2008; Benton 2009; Erwin 2009; Mayhew et al. 2012) and others attributing macroevolutionary patterns to biotic factors (Walker and Valentine 1984; Huntley and Kowalewski 2007; Alroy 2008; Alroy et al. 2008; Nürnberg and Aberhan 2015).

The escalation hypothesis presupposes certain physical conditions, including warm, productive, well-oxygenated environments (Vermeij 1987, 2004, 2008). If these

conditions are met in a given region, it is argued that escalation would occur and adaptations that arise in these regions will eventually spread to other regions and drive global diversity patterns (Vermeij 2008). Therefore, both physical and biotic factors would synergistically drive macroevolutionary patterns if escalation is sustained over long periods of time. Furthermore, although escalation might occur at any given time and location, only during certain intervals of the Phanerozoic are macroevolutionary patterns attributed to escalation, particularly during the early-to-mid Paleozoic and the mid-to-late Mesozoic (Vermeij 1987, 2004, 2008). This suggests that only during some intervals of the Phanerozoic were optimum conditions established on a wide enough and long enough scale to facilitate a role for escalation in macroevolutionary patterns.

Our results suggest that overall evidence for escalation is weak during the Jurassic, but escalation may be a plausible factor in driving regional macroevolutionary patterns through the latter half of the Jurassic in the western Tethys. A combined phylogenetic-biogeographic study is needed to test when and if the western Tethyan realm acted as a center of dispersal to other regions during the Cretaceous, leading to escalation on a global scale during the height of the Mesozoic Marine Revolution (Vermeij 1977). Nevertheless, the results of this study underline the importance of dissecting global data regionally and environmentally to understand the dynamics of macroevolutionary patterns, be it driven by abiotic or biotic factors.

Conclusions

1. Regional Jurassic ecological trends related to escalation are rare. Some patterns, such as deep infaunal and fully mobile occurrences in most regions, exhibit little to no net

- trends through the Jurassic and some trends even contradict the escalation hypothesis, particularly in North and South America.
2. Ecological trends are geographically heterogeneous. Most of the observed trends consistent with escalation occur in Europe, where the paleolatitudinal positions and carbonate-dominated environments of the western Tethys suggest tropical to subtropical, biologically productive regions. These physical conditions support Vermeij's (2004, 2008) argument that regions with warm, productive, well-oxygenated environments are more likely to sustain escalatory interactions. These results underline the importance of dissecting global patterns regionally to understand the dynamics of global macroevolutionary patterns.
 3. Within Europe, ecological trends are heterogeneous among depositional environments and overall exhibit weak evidence for escalation. Trends that are consistent with escalation such as an increase in infauna, cementing epifauna, and decrease in pedunculate forms occur primarily in nearshore and middle shelf environments but are also present to a lesser extent in inner shelf and outer shelf environments. Evidence of escalation in middle to outer shelf environments is unexpected as escalation has been argued to be restricted to shallower water environments. These results also highlight the need to dissect global and regional data into environments to understand the dynamics of macroevolutionary patterns.
 4. Other factors might contribute to the observed decrease in epifaunal occurrences in Europe, which dominates the global signal of Jurassic escalation. These factors include intrinsic mechanisms such as competitive displacement, extrinsic mechanisms such as availability of hard substrates, and statistical artifacts. None of these is

sufficient to fully explain the observed ecological patterns in Europe, leaving escalation as the most plausible explanation.

Tables

Table 2.1. Expected escalatory pressure and predicted effects during the Jurassic based on Vermeij (1987).

	Escalation Pressure	Escalation Prediction
Tiering		
Epifaunal	Predation/Bioturbation	Decrease
Shallow Infaunal	Predation/Bioturbation	Increase
Deep Infaunal	Predation	Increase
Epifaunal Modes of Life		
Free-lying	Predation/Bioturbation	Decrease
Pedunculate	Predation/Bioturbation	Decrease
Cementing	Predation	Increase
Motility		
Sessile	Predation/Bioturbation	Decrease
Facultative Mobile	Predation/Bioturbation	Increase
Mobile	Predation	Increase

Table 2.2. Geographic distribution of Jurassic occurrences of non-reef bivalves, gastropods, brachiopods, echinoids, corals, and sponges downloaded from the Paleobiology Database in this study, compared with that of Aberhan et al. (2006). The dataset used by Aberhan et al. (2006) consists of over 22,000 occurrences and over 2,800 collections compared with occurrences used in this study consisting of 43,961 occurrences and 9,864 collections and also includes arthropods and other groups of echinoderms. Data used by Aberhan et al. (2006) were downloaded on 19 December 2004 and the data used for this study were downloaded on 20 February 2016.

	Europe	North America	South America	Africa and India	Asia including Russia	Oceania
Aberhan et al. (2006)						
Early Jurassic	57%	2%	38%	2%	2%	0%
Middle Jurassic	41%	2%	2%	33%	23%	0%
Late Jurassic	90%	< 1%	< 1%	7%	3%	0%
This study						
Early Jurassic	65%	13%	16%	< 1%	3%	3%
Middle Jurassic	32%	12%	< 1%	6%	47%	2%
Late Jurassic	62%	14%	< 1%	13%	9%	3%

Table 2.3. Spearman's rank correlation test of changes in ecological traits over time by region through the Jurassic. Bold font indicates trends that are in the expected direction, with the sign of the correlation coefficient indicating direction of predicted escalatory pattern. Value of Spearman's ρ is shown, with significance codes for p -values: ***: $p < 0.001$; **: $p < 0.01$; *: $p < 0.05$; •: $p < 0.1$

	Europe	Middle East	New Zealand	North America	South America
Tiering					
shallow infaunal	0.63*	0.62	0.61•	0.34	0.19
deep infaunal	0.59•	0.19	0.41	-0.15	-0.37
epifaunal	-0.64*	-0.62	-0.61•	-0.23	-0.09
Epifaunal Modes of Life					
pedunculate	-0.59•	-0.51	-0.60•	0.47	-0.82**
cementing	0.45	0.74*	0.42	0.12	-0.16
free-lying	-0.35	-0.31	0.45	-0.75**	-0.57•
Motility					
mobile	0.07	0.12	0.67*	-0.53•	-0.20
facultative mobile	0.65*	0.57	0.59•	0.23	0.28
sessile	-0.69*	-0.52	-0.61•	-0.05	-0.24

Table 2.4. Spearman's rank correlation test of changes in ecological traits over time by environment in the European region through the Jurassic. Environmental categories follow the five-zone classification of Bottjer and Jablonski (1988). Bold font indicates trends that are in the expected direction, with the sign of the correlation coefficient indicating direction of predicted escalatory pattern. Value of Spearman's ρ shown, with significance codes for p -values: ***: $p < 0.001$; **: $p < 0.01$; *: $p < 0.05$; •: $p < 0.1$

	Nearshore	Inner shelf	Middle shelf	Outer shelf
Tiering				
shallow infaunal	-0.04	-0.08	0.61*	0.50
deep infaunal	0.74**	-0.23	0.44	0.63*
epifaunal	-0.18	-0.02	-0.59•	-0.38
Epifaunal Modes of Life				
pedunculate	0.11	-0.08	-0.47	-0.35
cementing	0.66*	0.36	0.38	-0.01
free-lying	0.08	-0.54*	0.20	-0.41
Motility				
mobile	-0.27	0.02	0.34	0.16
facultative mobile	0.24	0.05	0.64*	0.52
sessile	0.47	-0.12	-0.53•	-0.41

Table 2.5. Spearman's rank correlation test of changes in ecological traits over time during the Jurassic at the global scale and global scale without Europe. Bold font indicates trends that are in the expected direction, with the sign of the correlation coefficient indicating direction of predicted escalatory pattern. Values of Spearman's ρ shown with significance codes for p -values: ***: $p < 0.001$; **: $p < 0.01$; *: $p < 0.05$; •: $p < 0.1$

Ecologic Metric/Region	Global aggregate	Global excluding Europe
Tiering		
shallow infaunal	0.79**	0.34
deep infaunal	0.73*	-0.09
epifaunal	-0.75*	-0.15
Epifaunal Modes of Life		
pedunculate	-0.55•	0.11
cementing	0.42	0.44
free-lying	-0.69*	-0.76**
Motility		
mobile	-0.02	-0.17
facultative mobile	0.75*	0.10
sessile	-0.77*	0.06

Figures

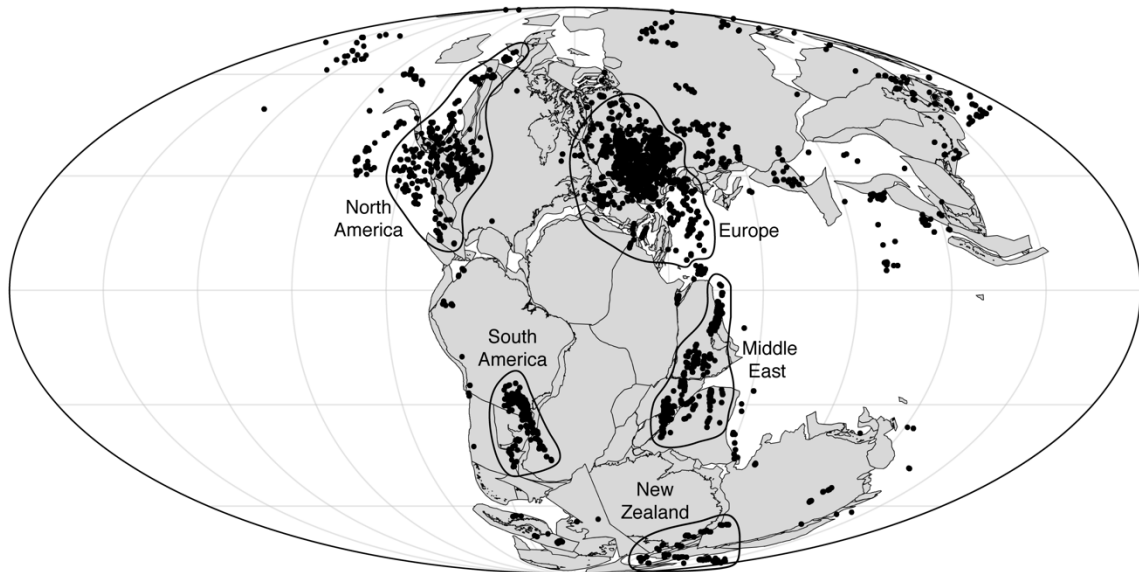


Figure 2.1. Jurassic (173 Ma) global paleogeographic reconstruction based on GPlates software using the rotation model from Seton et al. (2012) showing Paleobiology Database occurrences. Occurrences are plotted approximately, as they span the entire Jurassic and are plotted here in a single time slice. Occurrences plotted using ArcMap (ESRI 2016).

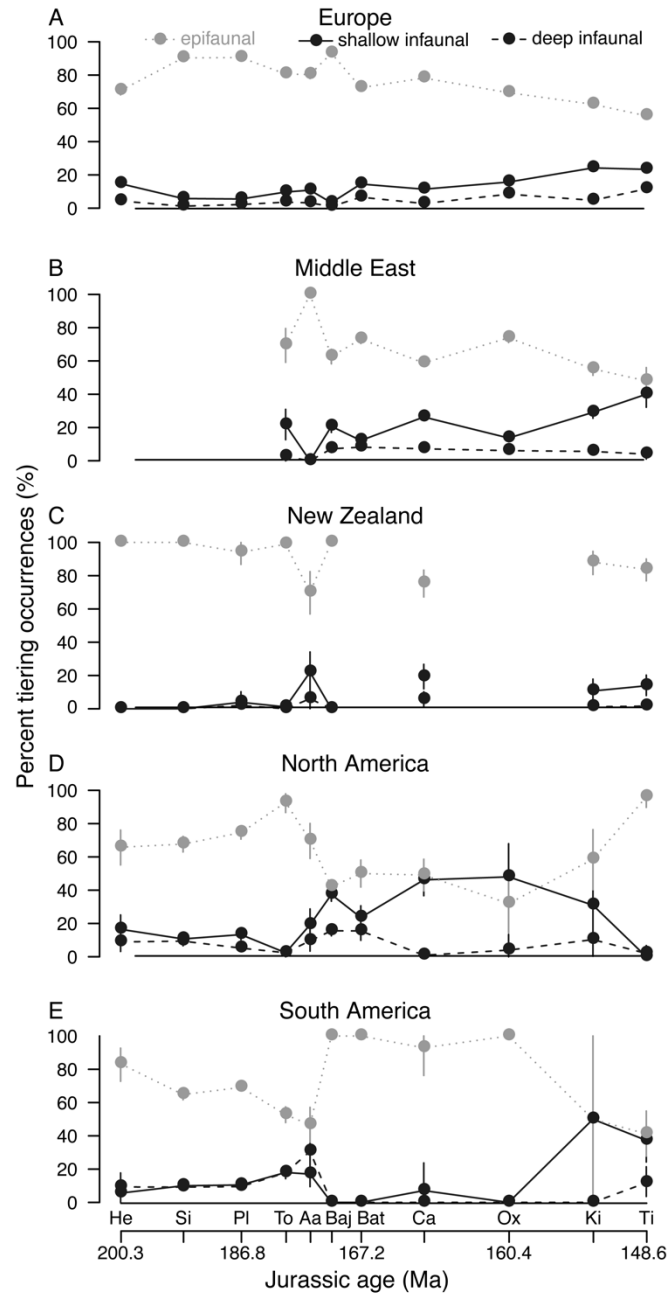


Figure 2.2. Percent occurrences by tiering for each Jurassic stage for a) Europe, b) Middle East, c) New Zealand, d) North America, and e) South America. Escalatory trends predicted to increase through the Jurassic are shown in black; trends predicted to decrease are shown in gray. 95% confidence intervals are indicated; where confidence intervals are absent, they are too narrow to be shown. Time series correlations are summarized in Table 2.3. Geologic ages are the midpoint of stages based on the 2015 International Commission of Stratigraphy chronostratigraphy chart (Cohen et al. 2013; He: Hettangian; Si: Sinemurian, Pl: Pliensbachian, To: Toarcian, Aa: Aalenian, Baj: Bajocian, Bat: Bathonian, Ca: Callovian, Ox: Oxfordian, Ki: Kimmeridgian, Ti: Tithonian).

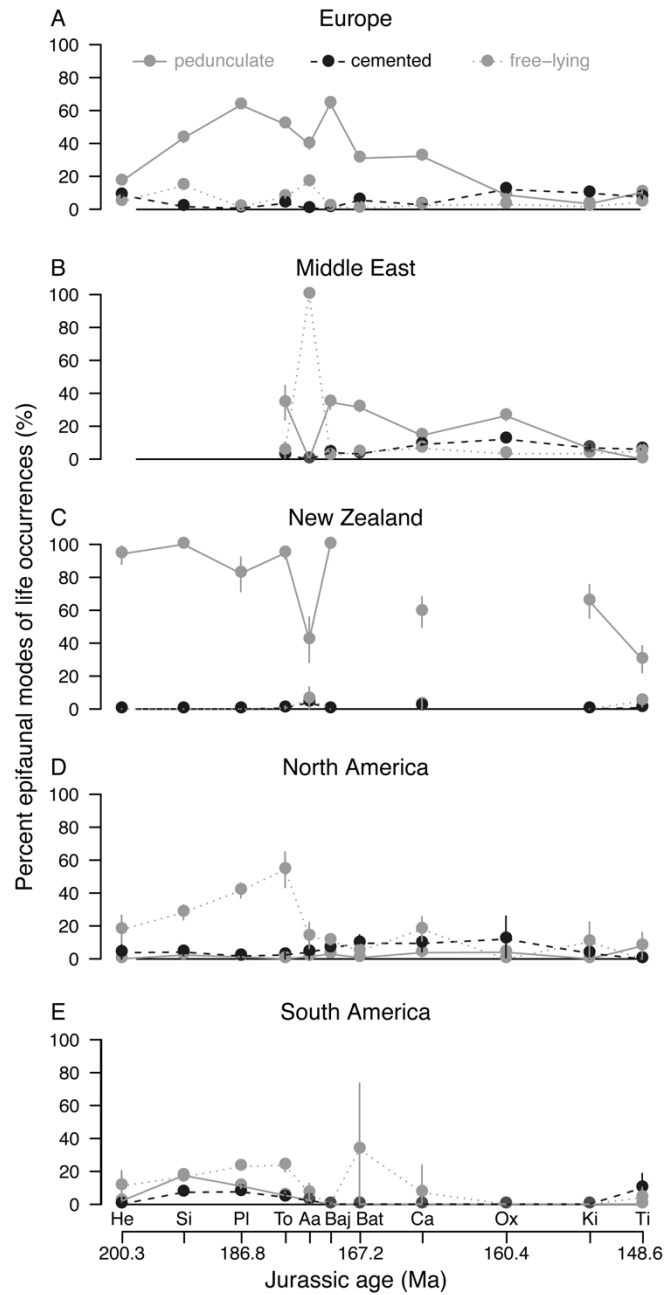


Figure 2.3. Percent occurrences of epifaunal modes of life for each Jurassic stage by region. Time series correlations summarized in Table 2.3.

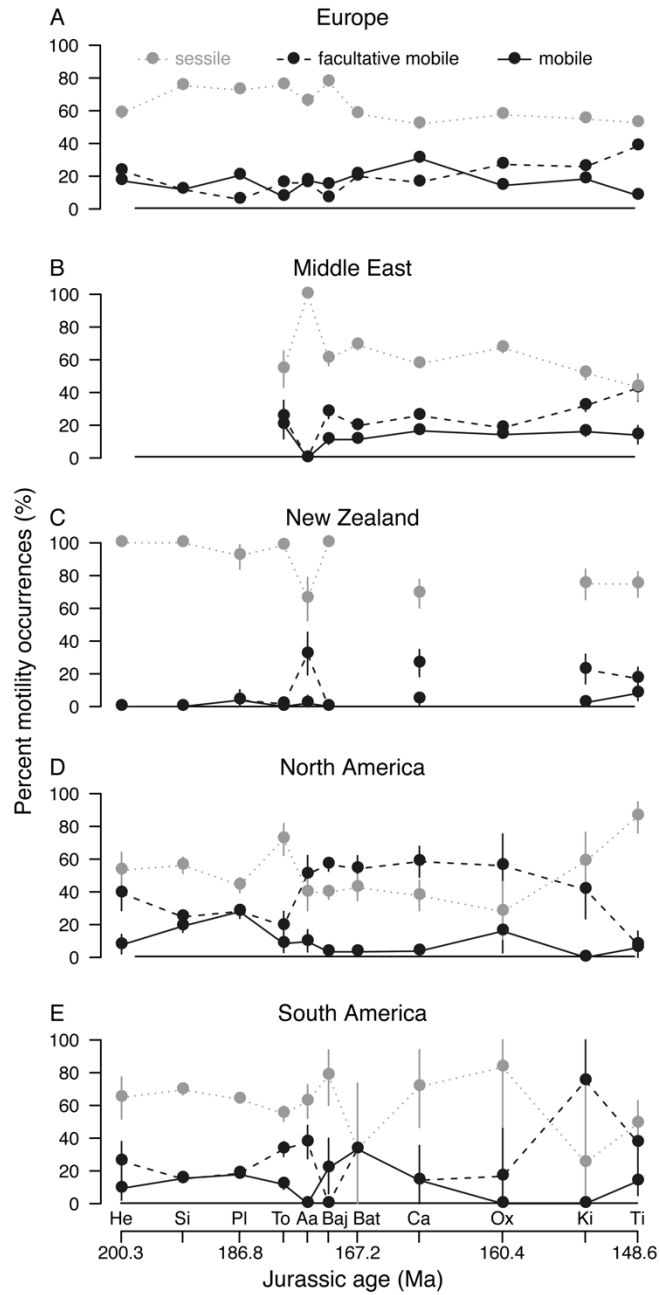


Figure 2.4. Percent occurrences by motility for each Jurassic stage by region. Time series correlations summarized in Table 2.3.

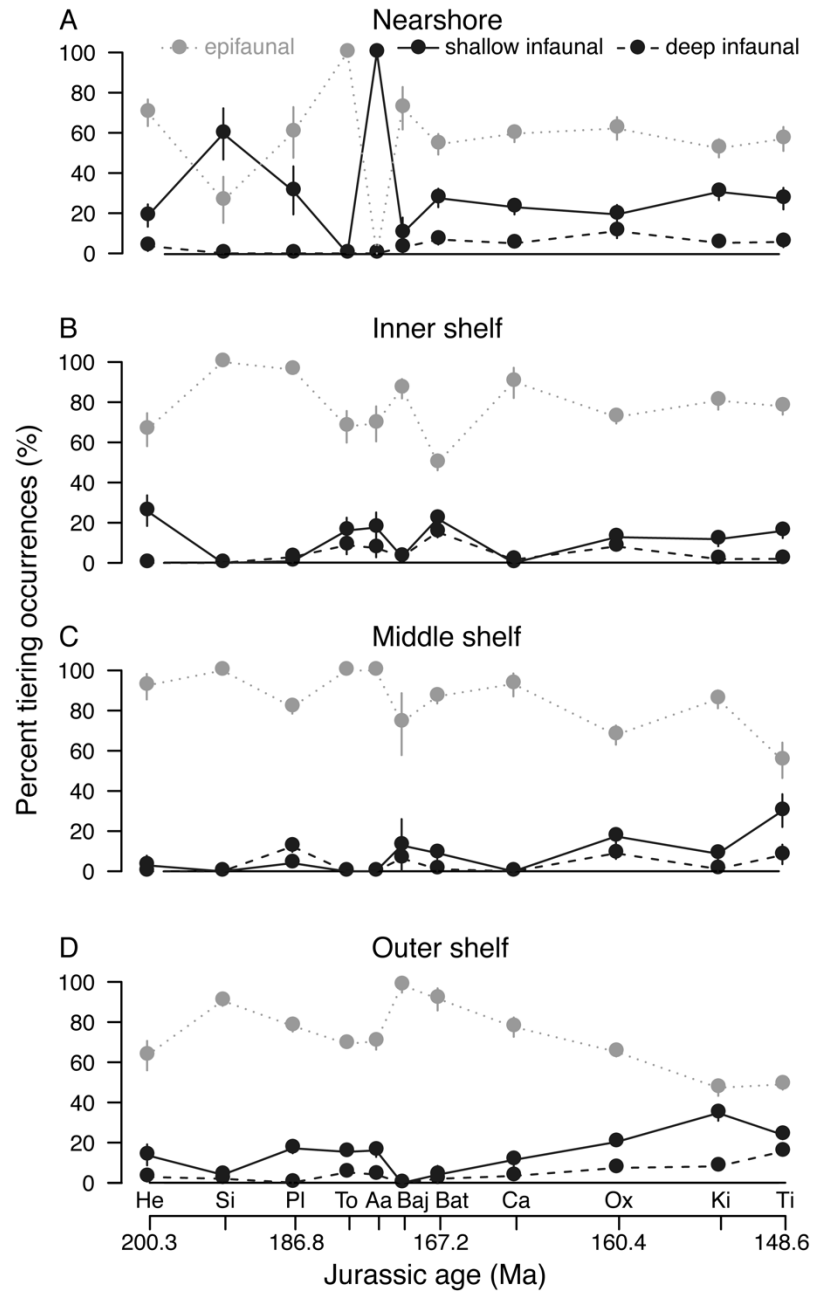


Figure 2.5. Percent occurrences by tiering in the Europe region by Jurassic stage in four depositional environments. Time series correlations summarized in Table 2.4.

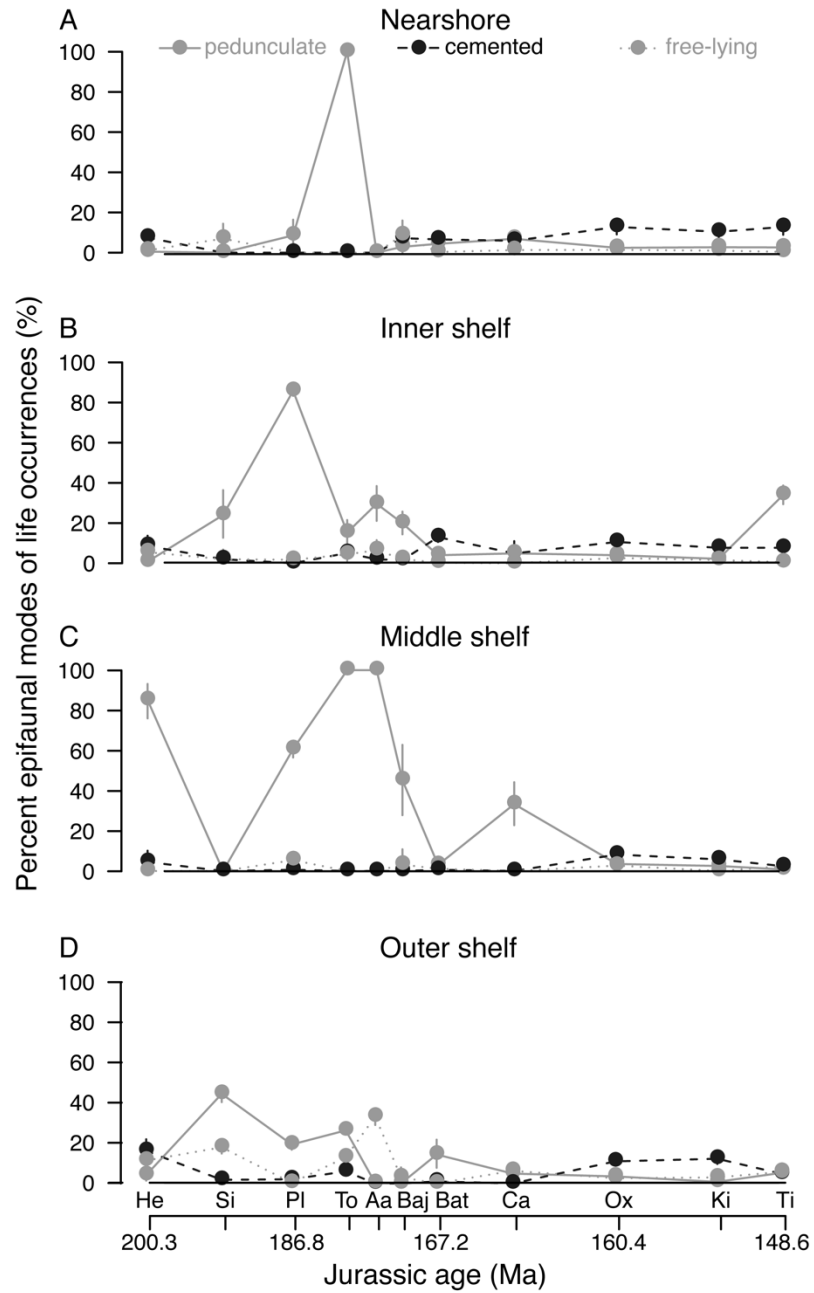


Figure 2.6. Percent occurrences of epifaunal modes of life in Europe by Jurassic stage in four depositional environments. Time series correlations summarized in Table 2.4.

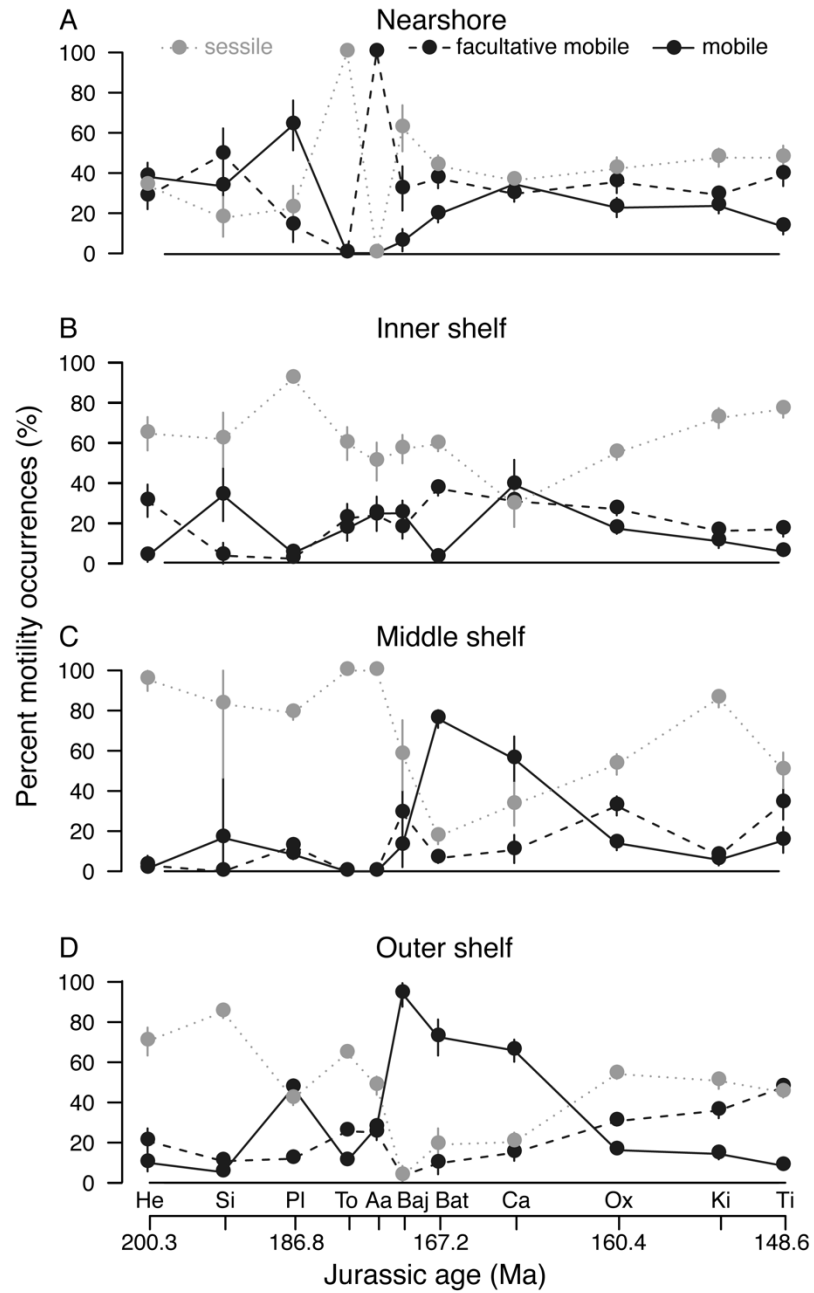


Figure 2.7. Percent occurrences by motility in the Europe region by Jurassic stage in four depositional environments. Time series correlations summarized in Table 2.4.

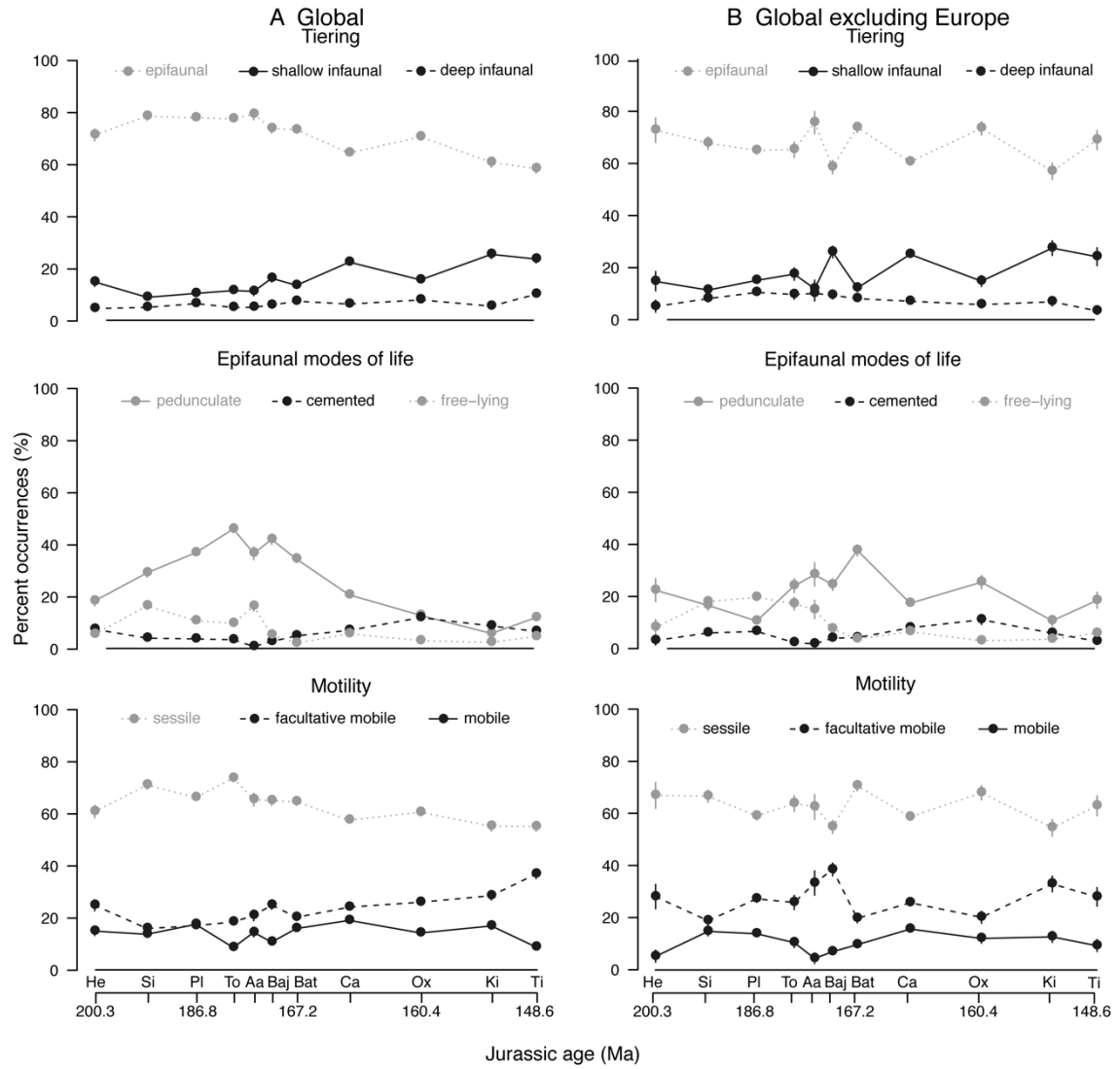


Figure 2.8. Comparison of global ecological trait trends with and without Europe for each Jurassic stage. The global data consists of 43,961 occurrences compared with 19,401 non-European occurrences; the number of non-European occurrences is almost equal to the global amount of occurrences used by Aberhan et al. (2006). Time series correlations summarized in Table 2.5.

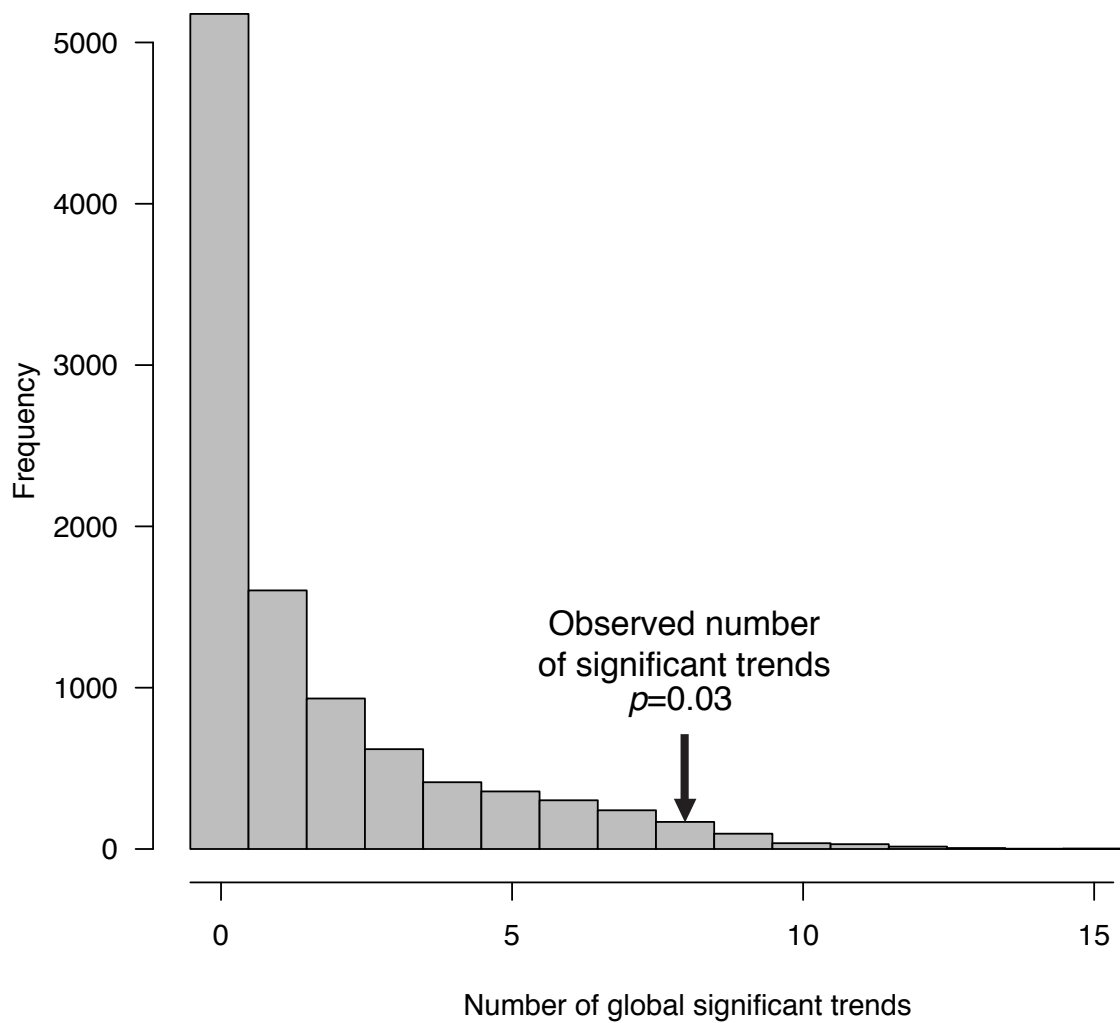


Figure 2.9. Random permutation of time stages followed by Spearman's rank correlation tests using 10,000 iterations for all 45 tests conducted in all regions. The observed number of statistically significant trends is eight (Table 2.3) and only 355 of 10,000 permutations equal or exceed this, for a p -value of 0.03.

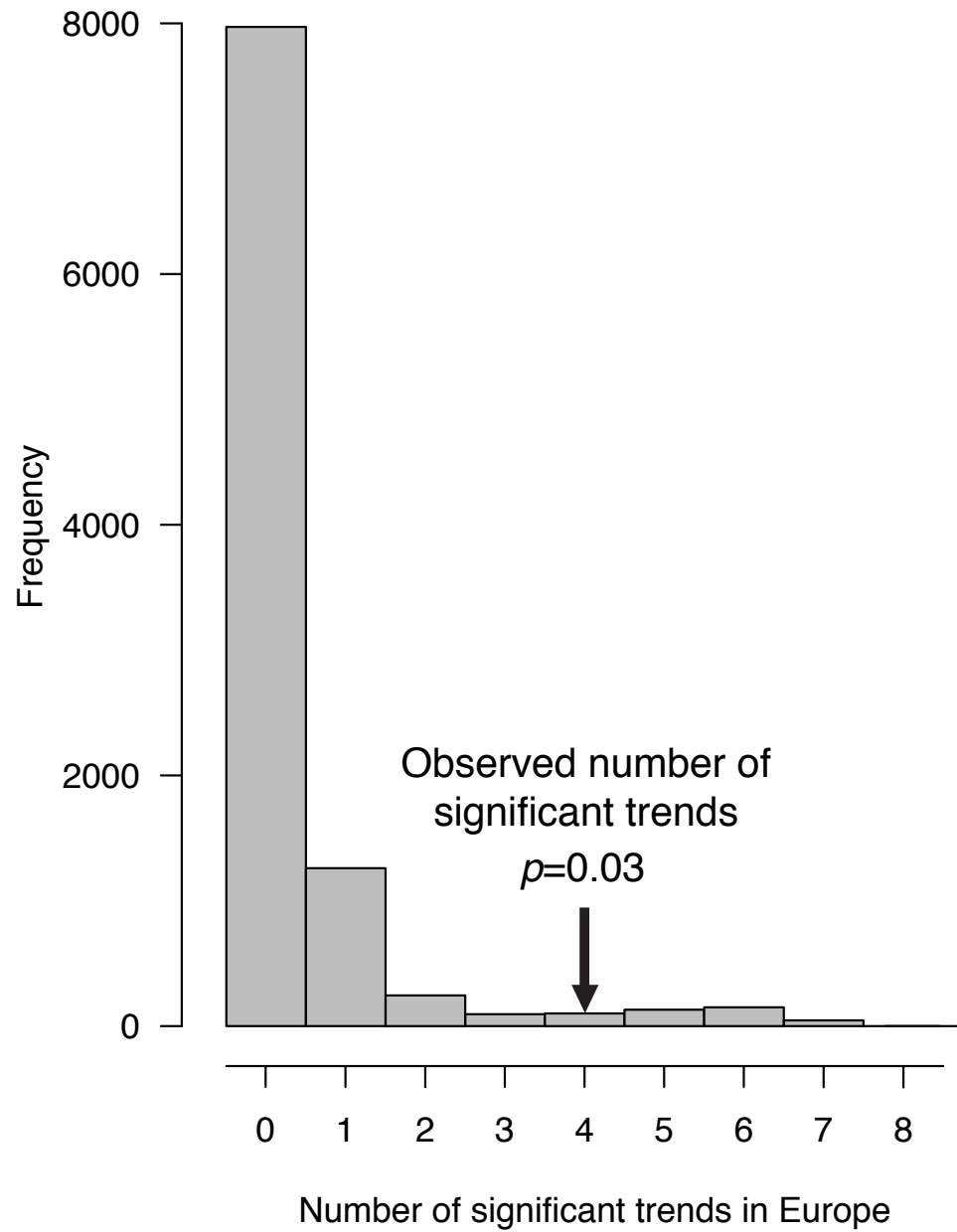


Figure 2.10. Random permutation of time stages followed by Spearman's rank correlation tests using 10,000 iterations for all nine tests conducted in Europe. The observed number of statistically significant trends is four and only 327 of 10,000 permutations equal or exceed this, for a p -value of 0.03.

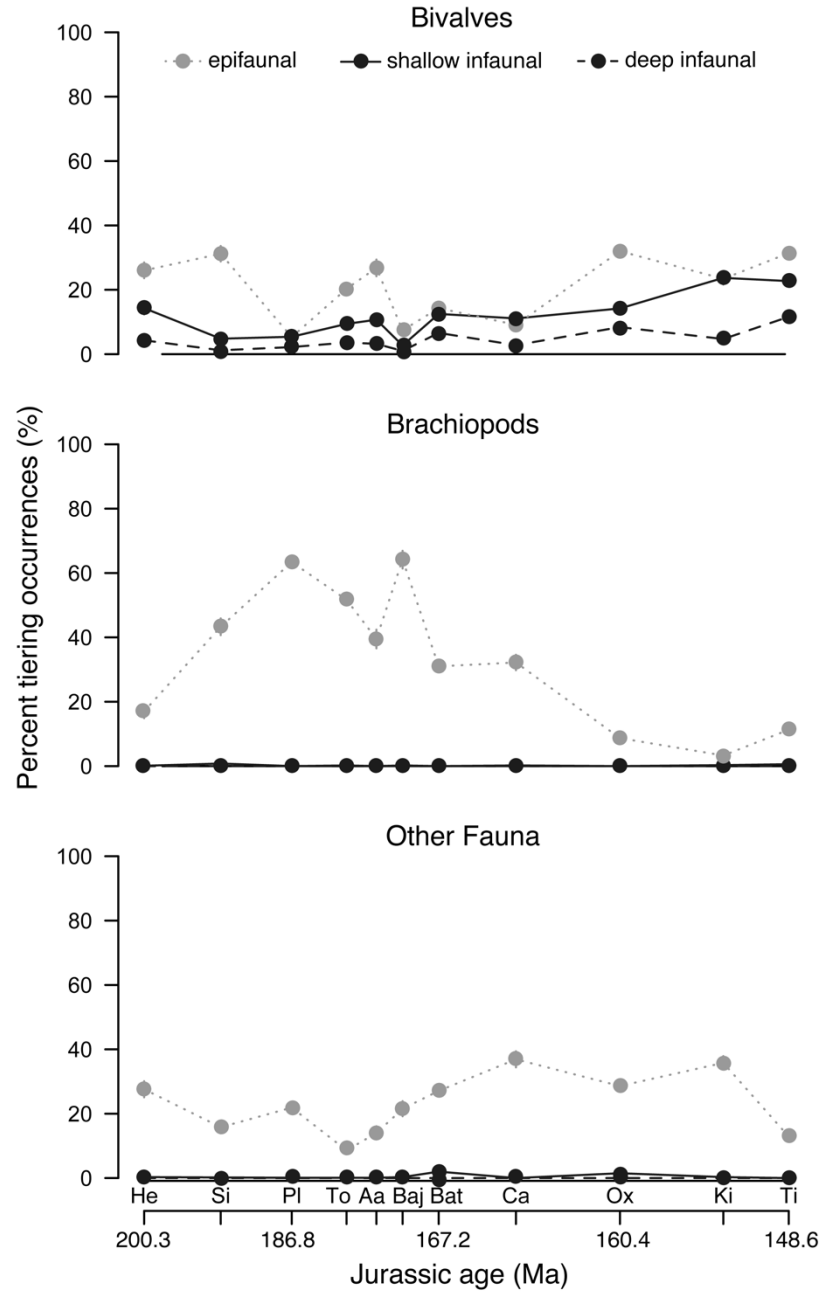


Figure 2.11. Percent occurrences of European taxonomic groups by tiering. Bivalves show a modest rise at the end of the Jurassic while brachiopod occurrences sharply decrease. Rise of epifaunal non-bivalves and non-brachiopods is primarily driven by gastropods. Time series are summarized in Supplementary Table 1.

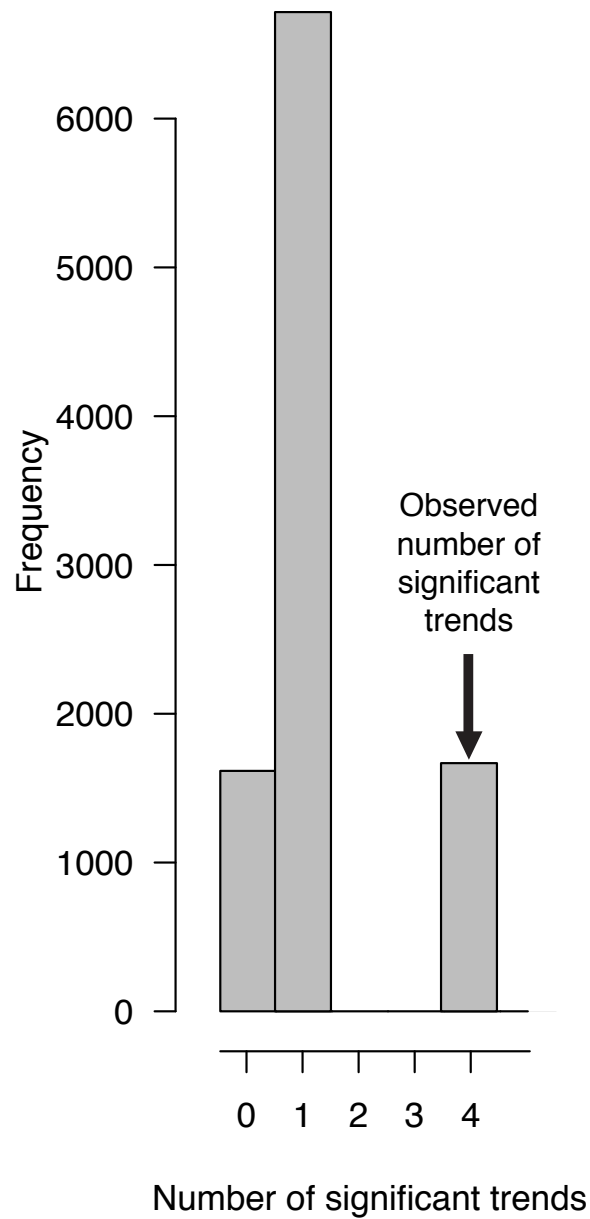


Figure 2.12. Frequency distribution of statistically significant trends in Europe using a random permutation of occurrences by region followed by Spearman's rank correlation tests using 10,000 iterations for all 9 tests conducted. The observed number of statistically significant trends in Europe is 4 (Table 2.3) and only 1,668 of 10,000 permutations equal or exceed this, for a p -value of 0.17.

CHAPTER 3

TESTING THE ROLE OF ENVIRONMENTAL CONDITIONS ON PROMOTING ESCALATION: MIDDLE JURASSIC CARMEL FORMATION, CENTRAL UTAH, U.S.A. ²

² Monarrez, P.M. Submitted to Paleobiology.

Abstract

The escalation hypothesis is posited to have played an important role in structuring Mesozoic marine ecosystems and driving macroevolutionary patterns. For escalation to be sustained, specific environmental conditions are required (i.e. warm, productive, well-oxygenated waters), and it is thought that the global effects of escalation are the sum of ecological patterns from regions with environmental conditions conducive to escalation. Here, the absence of escalation is tested during the Middle Jurassic in the southern Sundance Seaway of the western United States, where the environmental conditions were not conducive to escalation, to determine the extent of regional escalation and its role on macroevolutionary patterns. Using occurrence and abundance proportional data of ecological groups with escalation-sensitive traits, field data from the Bajocian and Bathonian Carmel Formation in Utah are compared with European data from the Paleobiology Database that have previously yielded evidence of escalation. The results reveal that overall evidence of escalation is rare or lacking as predicted in Utah, with evidence of temporal escalation observed in Europe, which was expected. Evidence of escalation in Europe is supported by decreases in non-cementing epifauna, and increases in facultatively mobile, shallow infaunal, and cementing fauna. The results of this study reveal the importance of comparing ecological data across different regions to ultimately determine if global patterns are reflected locally, to understand the driving factors of macroevolutionary patterns. Furthermore, this study underlines the fact that while biotic factors may drive some macroevolutionary patterns, the development of these factors may depend on particular physical environmental conditions.

Introduction

Escalatory ecological interactions (enemy-species driven selection) are thought to have played an important role on Mesozoic global macroevolutionary patterns (Vermeij 1987, 2004, 2008, 2013). The mid-to-late Mesozoic marks a sharp increase in global benthic macroinvertebrate diversity-driven largely by the appearance and radiation of predators and bioturbators (Vermeij 1977, Thayer 1979, 1983, Vermeij 1987). Ecological innovations and the proliferation of previously established ecological groups, spurred by the appearance of predators and bioturbators, led to an increase in ecospace utilization in benthic ecosystems (Bambach 1983, Bambach et al. 2007, Bush et al. 2007).

Collectively, the increase in predators and bioturbators, and adaptive response of prey and competitors during the Mesozoic is known as the Mesozoic marine revolution (Vermeij 1977, Harper 2003). The Mesozoic marine revolution coincides with increased rates of origination of marine groups (Alroy 2008) as well as a rapid increase in diversity that continued largely unabated (excepting the end-Cretaceous mass extinction) through the Cenozoic (Alroy et al. 2008, Alroy 2010). The parallel timing of the Mesozoic marine revolution and Mesozoic diversification suggests that biotic interactions may have driven marine diversity patterns (Vermeij 2008, Alroy 2010).

The first attempts to test the role of escalation on global macroevolutionary patterns found no statistically significant correlations between diversity trajectories of interacting groups (Madin et al. 2006) or mixed results, with some trends supporting escalation and others not (Aberhan et al. 2006). These studies were criticized for being conducted on a scale too broad to detect escalation or for their focus on diversity as an indicator of escalation (Dietl and Vermeij 2006; Roopnarine et al. 2006; Vermeij 2008).

Vermeij (2004, 2008) argued that to test for escalation, specific traits that are selected on by escalation need to be compared through time at local to regional scales and in similar depositional environments. Following these guidelines for testing for escalation, global Jurassic occurrence data from the Paleobiology Database was parsed into five regions (North America, South America, Europe, Middle East, and New Zealand) and tested for escalation using a similar approach as Aberhan et al. (2006; Monarrez et al. 2017). Ecological patterns consistent with escalation are generally rare except in the western Tethys realm (Europe), where escalation likely occurred, after ruling out other possible factors (Monarrez et al. 2017).

An important facet of the escalation hypothesis is the role of environmental conditions in promoting escalation. For escalatory interactions to be sustained, it has been hypothesized that regions need to consist of warm, productive, well-oxygenated environmental conditions (Vermeij 1987, 2004, 2008). These conditions are required because they can sustain the high metabolic rates and high diversity that characterize escalatory biotic interactions (Vermeij, 2004, 2008). The results of Monarrez et al. (2017) suggest that escalation in the western Tethys drove macroevolutionary patterns because this region contained the habitats with the environmental conditions needed to promote escalation.

Demonstrating that escalation occurred in a region characterized by habitats with the posited environmental conditions confirms both the escalation hypothesis and the necessary physical parameters to sustain escalation. Conversely, Vermeij's (1987, 2004, 2008) hypothesis also suggests that escalation does not occur in regions that lack the environmental conditions required to promote and sustain escalation. Because escalation

has been posited to have played an important role on global macroevolutionary patterns, it is important to counter test the escalation hypothesis to determine if escalation is indeed restricted to areas with conducive environmental conditions.

Here I evaluate the escalation hypothesis during the Middle Jurassic using local, field-based data to: 1) test for the absence of escalation during the Bajocian and Bathonian in a local area with environmental conditions that should not have promoted escalation and 2) test whether this area had lower proportions of ecological groups with escalation-sensitive traits during the Bajocian and Bathonian than areas where escalation was previously observed. The Bajocian and Bathonian are chosen to test for escalation specifically because there is a sharp increase in global taxonomic diversity (Alroy et al. 2008, Alroy 2010). If escalation drove macroevolutionary patterns during the Jurassic and Cretaceous (Vermeij 1987, 2008), then evidence of escalation should be observed during intervals of rapid diversification. Furthermore, this study compares spatial data collected from the same facies to ensure a fair ecological comparison to avoid ecological differences based entirely on water depth alone.

This study analyzes ecological patterns from the southern Sundance Seaway in the western interior of North America, which was characterized by restricted water circulation, hypersaline conditions, and low-oxygen levels (Tang and Bottjer 1996, 1997, de Gibert and Ekdale 1999). As such, it is expected that there should be little or no evidence of escalatory-related changes in ecological composition of faunal assemblages in the southern Sundance Seaway and that overall abundance of taxa with escalation-sensitive traits is lower (or higher depending on the trait) in the Sundance Seaway than in Europe during the Middle Jurassic (Aberhan et al. 2006, Monarrez et al. 2017).

Geologic Setting

The Carmel Formation is exposed across much of central and southern Utah (Imlay 1964, Cashion 1967, Imlay 1980, Nielson 1990, Brenner and Peterson 1994, Peterson 1994, Tang and Bottjer 1997, de Gibert and Ekdale 1999, Doelling et al. 2013), where it was deposited in a narrow southern lobe of the Sundance Seaway known as the Utah–Idaho or Twin Creek trough (also Twin Creek–Carmel seaway; Brenner and Peterson 1994, Bjerrum and Dorsey 1995, Doelling et al. 2013; Fig. 3.1A). The Sundance Seaway occupied a retroarc foreland basin in the western interior of North America during the Middle to Late Jurassic (Brenner and Peterson 1994, Bjerrum and Dorsey 1995, Doelling et al. 2013). Based on its molluscan fauna, the Carmel Formation is assigned a late Bajocian to Callovian age (Imlay 1964). This age is corroborated by $^{40}\text{Ar}/^{39}\text{Ar}$ dating of ash beds in the lower Carmel in southwestern Utah, which indicates that the basal age of the unit is 167–168 Ma, and that the youngest ashbed age at 166 Ma coincides with the Bajocian-Bathonian boundary (Kowallis et al. 2001).

The Carmel Formation consists of interbedded fossiliferous limestone, siltstone, mudstone, and gypsum in its lower half, with dolostone and red beds in some areas (Imlay 1964, Thompson and Stokes 1970, Nielson 1990, Peterson 1994). The upper half of the Carmel Formation consists of interbedded claystone, mudstone, and gypsum (Imlay 1964, Thompson and Stokes 1970, Nielson 1990, Peterson 1994). In sum, the lower half of the Carmel Formation contains the majority of the carbonate facies, the most fossiliferous part of the formation.

Depositional environments in the Carmel Formation include open shallow subtidal, oolitic sandy shoal, restricted shallow subtidal to intertidal flats, and sabkhas,

indicating a sea ranging from fully open marine to shallow and restricted (Nielson 1990, Peterson 1994, de Gibert and Ekdale 1999). The evaporites, shallow water depths, geographic restriction of the seaway, and arid regional climate suggest that the seaway was hypersaline and poorly circulated (Imlay 1964, 1967, 1980, Nielson 1990, di Gibert and Ekdale 1999). Furthermore, the trace fossils of the Carmel Formation are a low diversity generalist association, are much smaller than similar trace fossils elsewhere in the Jurassic, and consist of shallow sub-horizontal burrows, collectively indicating low-oxygen conditions (di Gibert and Ekdale, 1999).

The carbonate units of the lower Carmel Formation contain mostly bivalves, but also echinoderms, gastropods, bryozoans, corals, brachiopods, ammonites, serpulid worm tubes, and various ichnofossils (Imlay 1964, Sohl 1965, Cuffey and Ehleiter 1984, Blake 1986, Wilson and Palmer 1994, Wilson et al. 1998, Baker and Wilson 1999, Taylor and Wilson 1999, de Gibert and Ekdale 1999, Tang et al. 2000). The fossiliferous portions of the Carmel Formation are limited to the Bajocian to Bathonian (Imlay 1964, Tang and Bottjer 1997, Doelling, 2013). The Carmel fauna is depauperate, with taxonomic richness half that of Jurassic faunas of Europe (Imlay 1964, 1967, Hallam 1976, Tang and Bottjer 1996, Tang and Bottjer 1997), consistent with it having suboptimal environmental conditions for escalation (Tang and Bottjer 1997, de Gibert and Ekdale 1999).

Methods

This study tests for escalation in two ways. First, it compares the proportions of ecological groups with escalation-sensitive traits from the Bajocian to the Bathonian in the Carmel Formation to determine if there is directional change in the means of these proportions consistent with escalation (Table 3.1). Second, these proportions are

compared with European data from the Bajocian and Bathonian to determine if the ecological proportions from Utah are lower than the European average, as would be expected in an area where escalation should not have occurred. This follows the approach proposed by Geerat Vermeij: “Spatially replicated data on changes in the functional composition of local assemblages through time are needed to track the comings and goings of potentially escalation-related adaptations and patterns of habitat occupation” (Vermeij 2008, p. 7).

Bulk samples were collected from the Carmel Formation in Buckhorn Draw and near the Wedge in the San Rafael Swell in east-central Utah (Fig. 3.1A, B). I measured six stratigraphic sections in the area to create a single composite section (Fig. 3.2). Samples were collected from open shallow subtidal facies (i.e., above storm wave base), which was consistently the most fossiliferous facies in the Carmel Formation. These data were compared with ecological patterns from European data from the Paleobiology Database (<https://paleobiodb.org>).

A total of 46 bulk samples were collected from the Carmel Formation, 23 each from the Bajocian and the Bathonian (Fig. 3.1B). Each bulk sample contains a minimum of 25 individuals for a total of 2,971 individuals from 18 genera and 24 species. Fossils were identified to the species level where possible and counted using the minimum number of individuals method by taking the greater number of left or right valves for bivalves or the apex of gastropods (Gilinsky and Bennington 1994). Ecological tiering, epifaunal mode of life, and motility of identified bivalves was determined from an ecological dataset of Jurassic bivalves assembled by Martin Aberhan (see Aberhan et al. 2006, Monarrez et al. 2017).

Global macroevolutionary patterns are often measured using taxonomic richness over time; however, ecological data are also needed to understand macroevolutionary dynamics (McKinney et al. 1998, Lupia et al. 1999, Droser et al. 2000, Bottjer et al. 2001, McGhee et al. 2004, 2012, Christie et al. 2013, McGhee et al. 2013). Previous quantitative tests of the escalation hypothesis using global and regional data from the Paleobiology Database (i.e., Madin et al. 2006, Aberhan et al. 2006, Monarrez et al. 2017) have been conducted using only taxonomic diversity and occurrence data (the number of times a species is present among all collections), but not ecological abundance data (the number of individuals of a species in each collection). The use of taxonomic richness as a proxy for escalatory interactions has been criticized as a misleading metric of escalation, in that taxonomic richness is a byproduct of escalation that can also be explained by other factors (Vermeij 2008). Furthermore, if escalation is driving ecological patterns, it is expected that escalation will be reflected in abundance data as abundance data reflects adaptation (Vermeij 2008).

For each collection, the proportion of occurrences and abundance of ecological groups with traits sensitive to escalation was calculated. Specifically, these traits are shallow infaunal, epifaunal (free-living, sessile, and cementing), and motility (mobile, facultatively mobile, and sessile). The epibyssate trait was not considered despite its abundance in the Carmel Formation because of the uncertainty of the effect escalation has on this trait, as they are thought to decrease in abundance relative to cementing forms (Aberhan et al. 2006), but they are also known to strengthen their byssus in the presence of a predator (Reimer and Tedengren 1997, Caro et al. 2008).

Global data for the Bajocian and Bathonian was downloaded from the Paleobiology Database on 11 September 2018 and consists of occurrences of non-reef benthic macroinvertebrates, specifically of bivalves, gastropods, brachiopods, and echinoderms. The downloaded data also include ecological tiering, feeding strategy, motility, lithology, depositional environment, as well as paleolatitude and paleolongitude coordinates determined from a GPlates paleogeographic rotation model (Wright et al. 2013). Only occurrence and abundance data collected from “open shallow subtidal” environments were used from the Paleobiology Database dataset. Senior synonyms were used where available, and ecological data for bivalves was updated using data provided by Martin Aberhan (see Monarrez et al. 2017).

The downloaded data includes 10,780 occurrences, but after removing occurrences lacking stage designations, the data consist of 7,798 occurrences from 1,782 collections. The European dataset was manually extracted from the global dataset based on paleocoordinates and environment of deposition. The final occurrence count for the European data is 669 occurrences from 66 collections from open shallow subtidal environments. The proportions of tiering, epifaunal modes of life, and motility were estimated for the Paleobiology Database data as they were for the field data (Table 3.1). These proportions were compared between the Bajocian and Bathonian, and among Utah, and European data for occurrences and abundance.

Confidence intervals (95%) for proportions are based on the method of Raup (1991), and all calculations were performed in R (R Core Team 2019). Source code and occurrence files used for this study are deposited at Dryad [Note to editors and reviewers: the repository will be created upon acceptance of the manuscript].

Results

Comparisons of escalation-sensitive traits are possible only for tiering (shallow infaunal and epifaunal), epifaunal-mode-of-life (cementing), and motility (mobile, facultatively mobile, and sessile), because deep infaunal, pedunculate, and free-lying groups are not present in the Utah field data.

Temporal Comparison of Ecological Traits from Utah

Most traits from the Carmel Formation do not change in a direction consistent with escalation (e.g., shallow infaunal, epifaunal, and facultative mobile species) or they change in a direction opposite that predicted by escalation (e.g., cementing species).

Proportions for each ecological group are summarized in Tables 3.2 and 3.3.

Life habits by occurrences— In general, the proportions of shallow infaunal and epifaunal species occurrences from Utah show little or no directional change from the Bajocian to the Bathonian that is consistent with escalation (Fig. 3.3). Non-cementing epifaunal and sessile occurrences increased from the Bajocian to Bathonian, contrary to the escalation hypothesis. Additionally, cementing occurrences decreased, also inconsistent with escalation. Conversely, only fully mobile life taxa exhibit a pronounced increase that is consistent with escalation. Furthermore, shallow infaunal occurrences also increased, consistent with escalation, but the increase is negligible.

Life habits by abundance— Abundance data from Utah show changes similar to occurrence data, with most life habits changing in the direction opposite that predicted by escalation (Fig. 3.4). The proportional abundance of non-cementing epifaunal and sessile taxa increases, inconsistent with escalation. Similarly, the decrease in the proportional abundance of cementing taxa is inconsistent with escalation. Conversely, the only change

that is pronounced and consistent with escalation is the increase in mobile taxa.

Furthermore, as with the occurrence data, the proportional abundance of shallow infaunal and facultatively mobile taxa increase, and though this is consistent with escalation, these increases are negligible.

Temporal Comparison of Ecological Traits from Europe

In general, most European ecological groups change in proportions consistent with escalation from the Bajocian to the Bathonian. Despite the presence of occurrence data, abundance data are lacking for European Bajocian shallow infaunal species and Bathonian mobile and cementing species. Proportions for each ecological group are summarized in Tables 3.2 and 3.3.

Life habits by occurrences.— In general, most proportions of ecological groups in Europe change in a direction consistent with escalation (Fig. 3.5). In particular, there is a pronounced decrease in non-cementing epifaunal occurrences from the Bajocian to Bathonian, whereas there are increases in shallow infaunal, facultatively mobile, and cementing occurrences. Conversely, mobile occurrences strongly decrease from the Bajocian to Bathonian, inconsistent with escalation. Furthermore, non-cementing sessile occurrences increased from the Bajocian to Bathonian, also inconsistent with escalation.

Life habits by abundance— Where available, abundance data from Europe show changes generally similar to occurrence data (Fig. 3.6). The proportional abundance of non-cementing epifaunal taxa strongly decreases from the Bajocian to Bathonian, and facultatively mobile taxa increase from the Bajocian to Bathonian, which are both consistent with escalation. Conversely, proportional abundance of non-cementing sessile taxa increases, which is inconsistent with escalation. Abundance data is unavailable for

European Bajocian shallow infaunal species and Bathonian cementing and mobile species, which prohibits a temporal change comparison.

Comparison of Utah and European Ecological Proportions

In general, the results are striking from the Bajocian and Bathonian, with proportional differences between Utah and Europe driven by the temporal changes in Europe. Overall, relative differences in proportions yield mixed results, with some trait proportion differences consistent with escalation (motility), but not others (cementing).

Traits by occurrences— Proportional differences between Utah and European occurrence data yield mixed results, with half of the proportional changes being inconsistent with escalation being stronger in Europe (Fig. 3.7). Proportions of shallow infaunal, epifaunal, and cementing taxa are inconsistent with escalation being stronger in Europe, with more shallow infaunal and cementing occurrences in Utah, and more epifaunal occurrences in Europe during the Bajocian. Conversely, fully mobile and facultatively mobile occurrences are greater in Europe, whereas sessile occurrences are greater in Utah, all of which is consistent with escalation being stronger in Europe. Temporal changes in proportions that occurred from the Bajocian to Bathonian in Europe, affect the proportional differences with Utah. Shallow infaunal and facultatively mobile occurrences are greater in Europe during the Bathonian, while epifaunal occurrences are greater in Utah, again consistent with escalation being stronger in Europe. Additionally, whereas the difference in cementing occurrences is greater in Utah, it is only negligibly so. Conversely however, mobile and non-cementing sessile occurrences are greater in Europe, and this is inconsistent with stronger escalation in Europe.

Traits by abundance— Differences in proportional abundance between Europe and Utah are similar to the patterns in occurrence data for the Bajocian but differ substantially during the Bathonian (Fig. 3.8). During the Bajocian, the proportional abundance of mobile and facultatively mobile species are much greater in Europe than in Utah, and the proportional abundance of non-cementing species are much greater in Utah than in Europe, consistent with stronger escalation in Europe. As with occurrence data, the proportional abundance of cementing species is much greater in Utah, and the proportional abundance of non-cementing epifauna are much greater in Europe, both of which are not consistent with there being greater escalation in Europe. Furthermore, the only significant difference from the occurrence patterns is that the shallow infaunal abundance data is negligibly different between Europe and Utah, resulting from the lack of abundance data from Europe and the low number of shallow infaunal taxa in Utah. During the Bathonian, most differences in proportions are smaller between Europe and Utah, with most being inconsistent with more escalation in Europe. Proportional abundance of non-cementing epifaunal and non-cementing sessile species are greater in Europe than in Utah. Proportional abundance of cementing and fully mobile species are greater in Utah relative to Europe, reflecting the lack of abundance data in the Paleobiology Database. Furthermore, the proportion of shallow infaunal species is greater in Utah, but only negligibly so.

Discussion

Did escalation increase in Utah from the Bajocian to Bathonian?

Changes in ecological traits from the Bajocian to Bathonian in Utah data weak support for the escalation hypothesis. Of the 12 ecological proportional changes

(combining occurrence and abundance data), 9 changes are either negligible or are strong in the opposite direction that is consistent with escalation. The only strong changes that are consistent with escalation are the increases in the occurrence and abundance of mobile taxa and the decrease in the occurrences of sessile taxa. During the Bajocian and Bathonian, escalation did not play a major role in the community structure in the southeastern Sundance Seaway, as expected.

The decrease in cementing occurrences observed in Utah could potentially be explained by a change in lithology, as the open shallow subtidal facies in the Bajocian was less muddy than in the Bathonian (Fig. 3.2). This difference in lithology suggests that the softer substrate likely resulted in fewer cementers inhabiting this environment, and it likely also explains the increase in the occurrences and abundance of shallow infaunal species. The increase in mobile species in Utah is primarily driven by gastropods, particularly from the families Nerineoidea and Cylindrobullinidae. Although gastropods increase in numbers over time in Utah, these gastropod families are not carnivorous (Kollman 2014), and likely were not associated with escalatory interactions with species at lower trophic levels. Whether these gastropods were prey to higher trophic-level predators is uncertain, but their occurrence alone does not support escalation. Finally, the decrease in sessile species is consistent with escalation, however, only negligibly and likely not driven by biotic interactions.

Is There Temporal Evidence of Escalation in Europe from the Bajocian to Bathonian?

Despite the lack of abundance data for a few ecological groups, there appears to be some evidence of escalation from the Bajocian to Bathonian in Europe. The strongest changes in proportions consistent with escalation are observed in the decrease of both

occurrences and abundance of non-cementing epifauna, increase of shallow infauna occurrences, increase in cementing occurrences, and increase in facultatively mobile groups. There is also a notable increase in non-cementing sessile epifauna and a decrease in fully mobile taxa, which are both not consistent with escalation. Nevertheless, overall results are consistent with previous ecological trends from Europe, where trends do not appear to be sustained in a manner consistent with escalation in Europe until the Bajocian and Bathonian and increase in strength in the direction predicted by escalation through the latter third of the Jurassic (Monarrez et al. 2017).

Given the short time interval of analysis between the Bajocian and Bathonian, it is possible that there is insufficient time allotted to see significant changes in the ecological composition of faunal assemblages. Despite the short time interval (~4 m.y.), there are notable shifts in the mean ecological composition of each collection from the Bajocian to Bathonian that is in sharp contrast to the Utah data. Since there is a sharp increase in overall global diversity from the Bajocian to Bathonian (driven in large part by European data), it is possible that escalation could have played a role in that increase. Whereas the Mesozoic marine revolution might have been in its infancy during the Jurassic, it is a time of post-consolidation of acquired traits that occurred during the Late Triassic and first half of the Jurassic that lead to the increase of numerous groups during the latter half of the Jurassic (Vermeij, 2008). Furthermore, because there are notable changes in mean ecological composition over a relatively short amount of time that is consistent with previously calculated ecological trends over a longer time span, it is possible that this short time window is capturing the beginning phase of the fundamental ecological restructuring that is better known from and more striking later in the Mesozoic.

Utah Proportions vs. European Proportions

It has been previously shown that North American occurrence data show weak evidence of escalation (Monarrez et al. 2017), as such, it was expected that Utah proportional data would parallel those at the regional scale. Furthermore, the environmental conditions of the Sundance Seaway are thought to hinder enough escalatory interaction to change the ecological composition of faunal assemblages. Indeed, comparison of proportional changes in ecological groups between Utah and European data suggest evidence of escalation is present in Europe but not in Utah, with some exceptions. In particular, the proportion of non-cementing epifauna is greater in Europe than in Utah and the proportions of cementing epifauna and mobile taxa are greater in Utah than it is in Europe. The larger proportion of cementers in Utah can potentially be explained by the prevalence of shellier substrates that promotes taphonomic feedback leading to increased proportions of cementing species. The larger proportion of non-cementing epifauna in Europe relative to Utah is driven by the occurrence of brachiopods, which make up approximately 19% of all European occurrences during the Bajocian. Escalatory trends in Europe are largely driven by the decline in brachiopods (Monarrez et al. 2017, Vörös 2010), which is also the case in this study, as brachiopods decrease to 1% of Bathonian occurrences in Europe and is reflected by a higher proportion of non-cementing epifaunal taxa in Utah relative to Europe (Figs. 7 and 8). Furthermore, the highest proportion of mobile occurrences are found in Utah, which was not expected. This increase in mobile occurrences in Utah relative to Europe is driven by the appearance of several families of gastropods, but none of these are carnivorous, as mentioned above.

The Role of Environmental Conditions on Ecological Patterns

An important component of the escalation hypothesis is the required environmental conditions that are conducive to escalatory interactions (Vermeij 1987, 2004, 2008). Because the Sundance Seaway is characterized by environmental conditions that are not conducive to escalation, it was expected that evidence of escalation would be weak or lacking. The results of this analysis support this prediction, as the Utah data offer weak evidence of escalation and support a key pillar of the escalation hypothesis. Furthermore, this same aspect of the escalation hypothesis is also likely the reason why evidence of escalation is stronger in Europe than it is in Utah.

Evidence of escalation is observed in the western Tethys where the conditions appear to meet the requirements to sustain escalatory interactions: warm, biologically productive environments with sufficient nutrient availability, and high enough diversity to promote antagonistic interactions among species (Monarrez et al. 2017). There has been a long-standing debate in paleobiology regarding the primary driver of macroevolutionary patterns (biotic vs. abiotic), but regarding escalation, it is clear that there is synergistic relationship between biotic and abiotic factors (Monarrez et al. 2017). Biotic factors may drive some macroevolutionary patterns, but the development of these factors may depend on particular physical environmental conditions.

Dissecting Global Fossil Data

A key aspect of a recent test of escalation during the Jurassic is that the western Tethys is the dominant source of perceived global ecological patterns (Monarrez et al. 2017). Patterns of ecological groups in the western Tethys realm, particularly shallow infaunal and epifaunal groups, drive global patterns, as global patterns resemble the

patterns in the western Tethys but not from other regions (Monarrez et al. 2017). The results of that study provide insight into the regional variation that is omitted when macroevolutionary patterns are evaluated only globally. Those findings resonate with previous studies that called for global data to be dissected at regional and local levels because of the possibility of global data obscuring local and regional patterns (Miller 1997a, b, 2000, 2003, Vermeij and Leighton 2003).

This study takes local data and compares them with regional European data to test local scale changes against previously observed trends. Using larger scale macroevolutionary patterns to predict local scale patterns can potentially bias how workers approach their analyses, because global data can be a poor predictor of local patterns as evident by data in this study. Examples from the literature includes the Late Mississippian (Serpukhovian) mass extinction event that is observed in global data (e.g. Sepkoski 1996, McGhee et al. 2013), despite North American regional data revealing no evidence of a mass extinction (Bonelli and Patzkowsky 2008, 2009, Heim 2009). Similarly, for the Early Triassic workers argue for a global protracted recovery phase of the Permian-Triassic mass extinction (e.g. Woods et al. 1999, Payne et al. 2004, Bottjer et al. 2008), yet others argue for a short recovery phase based on local data (e.g. Hofmann et al. 2013, Hautman et al. 2014). Macroevolutionary patterns are the sum of local and regional patterns, and therefore will not be reflected uniformly at local scales. To understand how global macroevolutionary patterns are built, there needs to be more data collected at the local scale that tests for global scale patterns to determine what drives the variation in macroevolutionary patterns, allowing for a better understanding of biological processes and what affects them in the fossil record.

Occurrence Data Versus Abundance Data

Previous tests of the escalation hypothesis during the Jurassic have used occurrence data exclusively to track changes in proportions of ecological groups through time (Madin et al. 2006, Aberhan et al. 2006, Monarrez et al. 2017). This study, however, uses abundance data together with occurrence data to document how the ecological composition of faunal assemblages change from the Bajocian to Bathonian. Overall, occurrence data and abundance data (where available) appear to correspond fairly well with each other both in Utah and Europe. Despite changing in the same direction, the magnitude of change is greater in occurrence data than abundance data in Europe, where the strongest evidence consistent with escalation is observed. It is expected that if escalation occurred, occurrence and abundance data would shift in the same direction, but abundance data might lag behind as species would require some time after establishing to achieve their peak abundance (Foote et al. 2007, Liow and Stenseth 2007). Using abundance data to track ecological patterns is a more useful metric than taxonomic occurrences alone, as testing for escalation predicts a change in relative abundance.

This study represents the first quantitative ecosystem paleoecological test of the escalation hypothesis using field-based taxonomic and ecological data during the Mesozoic marine revolution. This study takes larger marine benthic ecosystems into account using field data and abundance data. Previous studies have used the escalation hypothesis to explain observed ecological patterns during the latter half of the Mesozoic without testing for escalation as the primary goal (e.g. Vorös 2010, Sessa et al. 2012). Other studies have focused on testing for escalation pressure on single groups of organisms, but not on larger ecosystems (e.g. Aronson 1989, Roy 1994, Kerr and Kelley

2015). Previous tests of the escalation hypothesis used regional and global database data using only diversity or occurrence data but not abundance data (e.g. Aberhan et al. 2006, Monarrez et al. 2017). Based on the analysis of the Utah data in this study, there is weak evidence that escalation played a significant role on macroevolutionary patterns from the Bajocian to the Bathonian stages of the Middle Jurassic from Utah occurrence and abundance data as expected, but there is evidence consistent with escalation in Europe.

Conclusions

1. Escalation-sensitive traits across the Bajocian and Bathonian show overall weak evidence of escalation throughout all three spatial scales, but the strongest evidence of escalation is observed in global abundance data. The Utah data weakly show evidence of escalation and supports Vermeij's (2004, 2008) hypothesis that optimal environmental conditions are required for escalatory interactions.
2. Proportional data suggests that while most comparisons of ecological trait groups among spatial scales are consistent with escalation, there are exceptions that were not expected. In Utah, cementers have larger proportions than the global data, whereas global epifaunal and sessile proportions are larger than the Utah data. These results highlight the importance of analyzing patterns at different scales to capture local and regional patterns that may be omitted in global patterns.
3. Global occurrence and abundance data do not agree across the Bajocian to Bathonian, but occurrence and abundance data agree in Utah. Lack of abundance data for North America does not allow for comparison. Whereas discordance in occurrence and abundance data at the global scale might reflect the importance of tracking abundance data over time to better understand ecological patterns, this

discordance can also be explained by the lack of abundance data and lack of standardization of abundance data uploaded to the Paleobiology Database.

Tables

Table 3.1. Expected escalatory pressure and predicted effects of escalation during the Jurassic, based on Vermeij (1987).

	Escalation Source	Escalation Prediction
Tiering		
Shallow Infaunal	Predation/Bioturbation	Increase
Epifaunal	Predation/Bioturbation	Decrease
Epifaunal Modes of Life		
Cementing	Predation	Increase
Motility		
Mobile	Predation/Bioturbation	Increase
Facultative Mobile	Predation/Bioturbation	Increase
Sessile	Predation	Decrease

Table 3.2. Proportions of life habit occurrences for the Bajocian and Bathonian from Utah field data and European data from the Paleobiology Database.

Life Habit	Utah		Europe	
	Bajocian	Bathonian	Bajocian	Bathonian
Shallow infaunal	0.07	0.08	0.02	0.25
Epifaunal	0.51	0.68	0.89	0.34
Cementing	0.37	0.18	0.01	0.17
Mobile	0.05	0.19	0.58	0.01
Facultatively mobile	0.07	0.08	0.07	0.34
Sessile	0.45	0.49	0.35	0.65

Table 3.3. Proportions of life habit abundance for the Bajocian and Bathonian from Utah field data and European data from the Paleobiology Database. Lack of abundance data reflects what was reported to the Paleobiology Database.

Life Habit	Utah		Europe	
	Bajocian	Bathonian	Bajocian	Bathonian
Shallow infaunal	0.01	0.03	NA	0.26
Epifaunal	0.56	0.82	0.98	0.70
Cementing	0.36	0.11	NA	NA
Mobile	0.01	0.06	0.92	NA
Facultatively mobile	0.01	0.03	0.04	0.46
Sessile	0.55	0.76	0.04	0.54

Figures

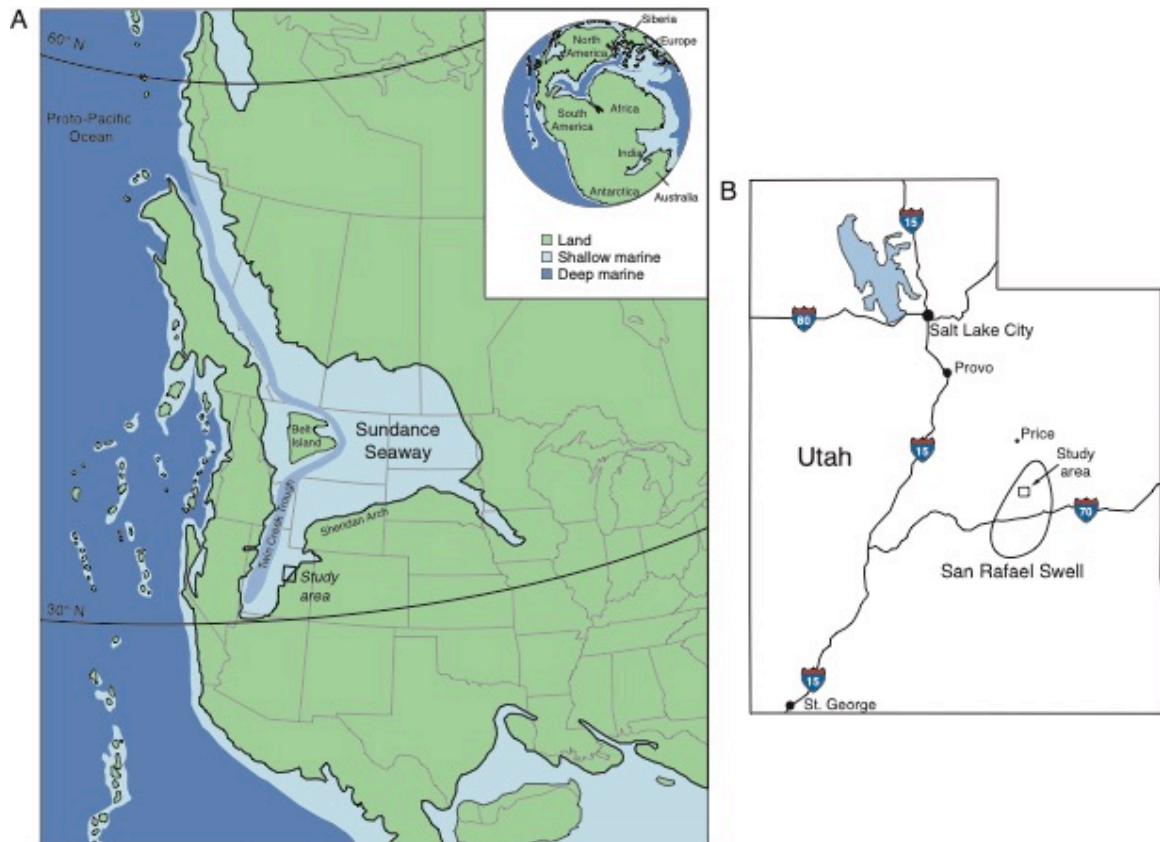


Figure 3.1. Paleogeographic and locality map of the Carmel Formation sampled for this study. A) Paleogeographic reconstruction of the western interior U.S. during the Bajocian Stage (~170 Ma). B) Locality map of the Carmel Formation in the San Rafael Swell in east-central Utah. Paleogeographic map modified from Clement and Holland (2016), adapted from Blakey (2015).

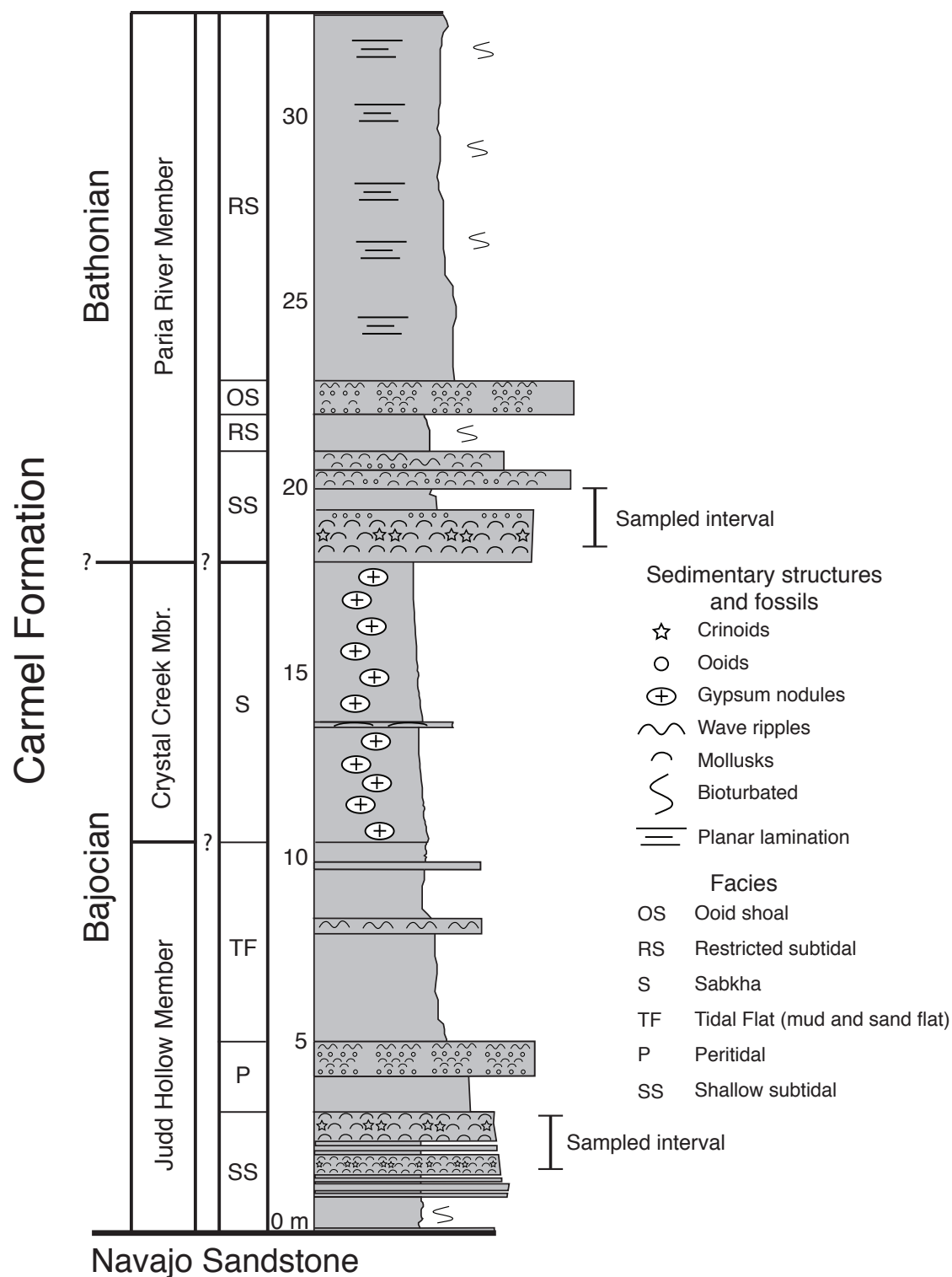


Figure 3.2. Composite stratigraphic section of the fossiliferous interval of the Carmel Formation exposed at Buckhorn Draw in the northwestern portion of the San Rafael Swell in east-central Utah, U.S.A. Stage assignments based on Doelling et al. (2013).

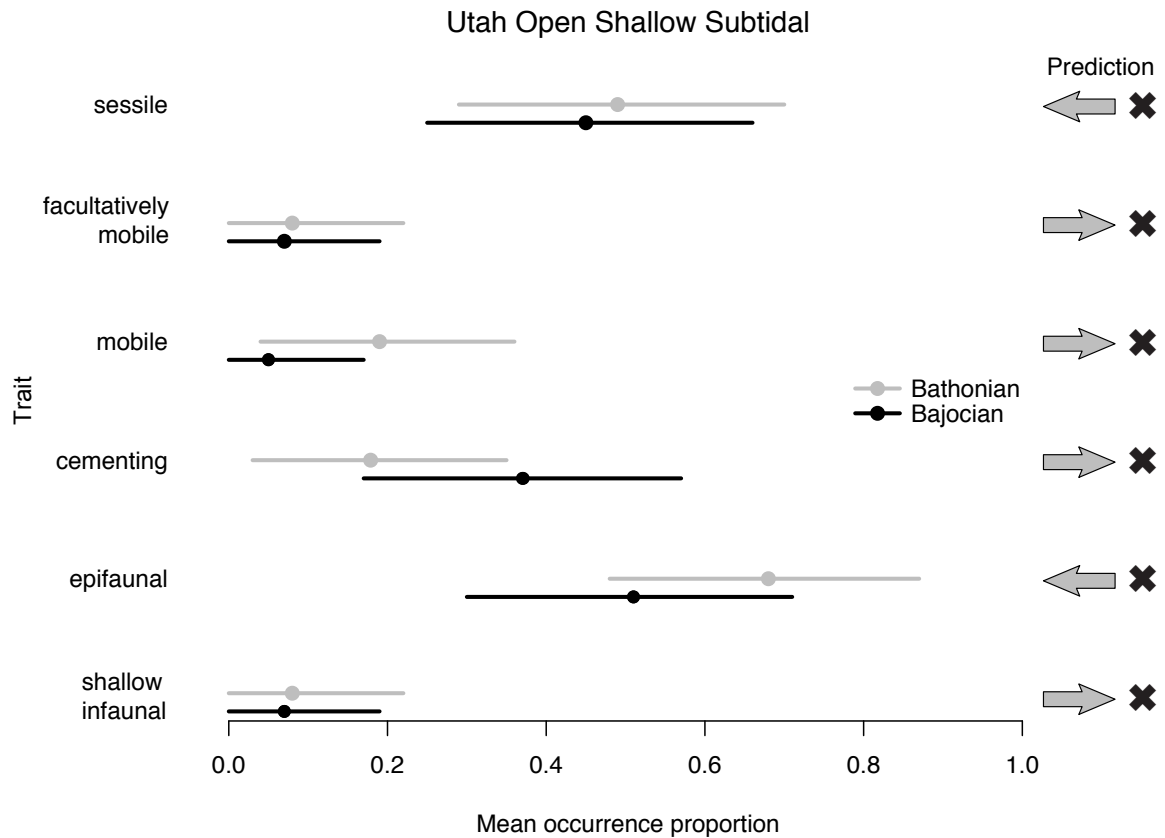


Figure 3.3. Temporal proportional changes of ecological-trait-group occurrences from the Carmel Formation in Utah. Changes in the proportion estimates of ecological trait groups with 95% confidence intervals are compared from the Bajocian (black) and Bathonian (gray), with predicted directions shown by the gray arrows. Overlap of Bajocian and Bathonian confidence intervals for each life habit group suggests no substantial temporal change, as indicated by the black X's.

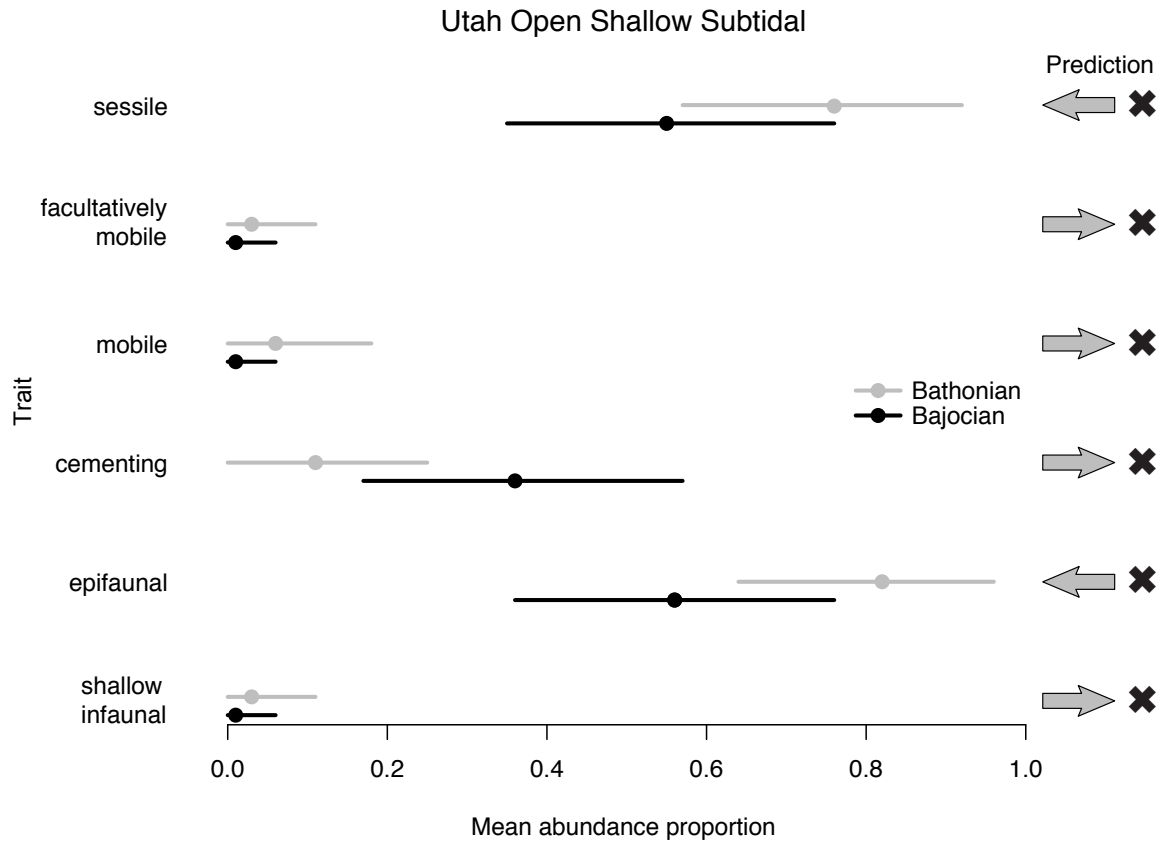


Figure 3.4. Temporal change in the proportional abundance of ecological trait groups from the Carmel Formation in Utah. Changes in the proportion estimates of ecological trait groups with 95% confidence intervals are compared from the Bajocian (black) and Bathonian (gray), with predicted directions shown by the gray arrows. Overlap of Bajocian and Bathonian confidence intervals for each life habit group suggests no substantial temporal change, as indicated by the black X's.

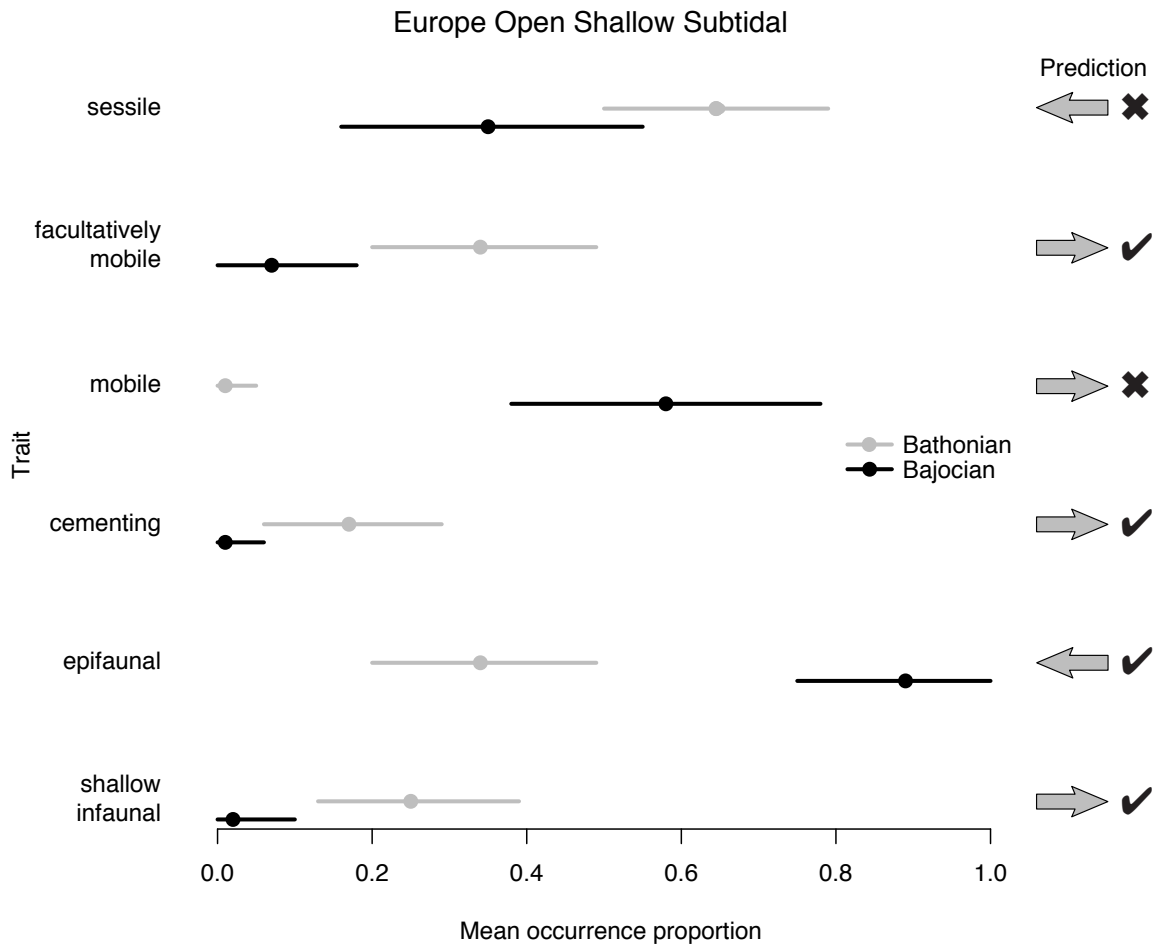


Figure 3.5. Temporal changes in the proportion of occurrences of ecological trait groups from European data from the Paleobiology Database. Changes in the estimates of proportional abundance of ecological trait groups with 95% confidence intervals are compared from the Bajocian (black) and Bathonian (gray), with predicted directions shown by the gray arrows. Overlap of Bajocian and Bathonian confidence intervals for each life habit group suggests no substantial temporal change as indicated by the black X's. Gaps between mean proportions indicate substantial temporal changes, as indicated by the black check marks.

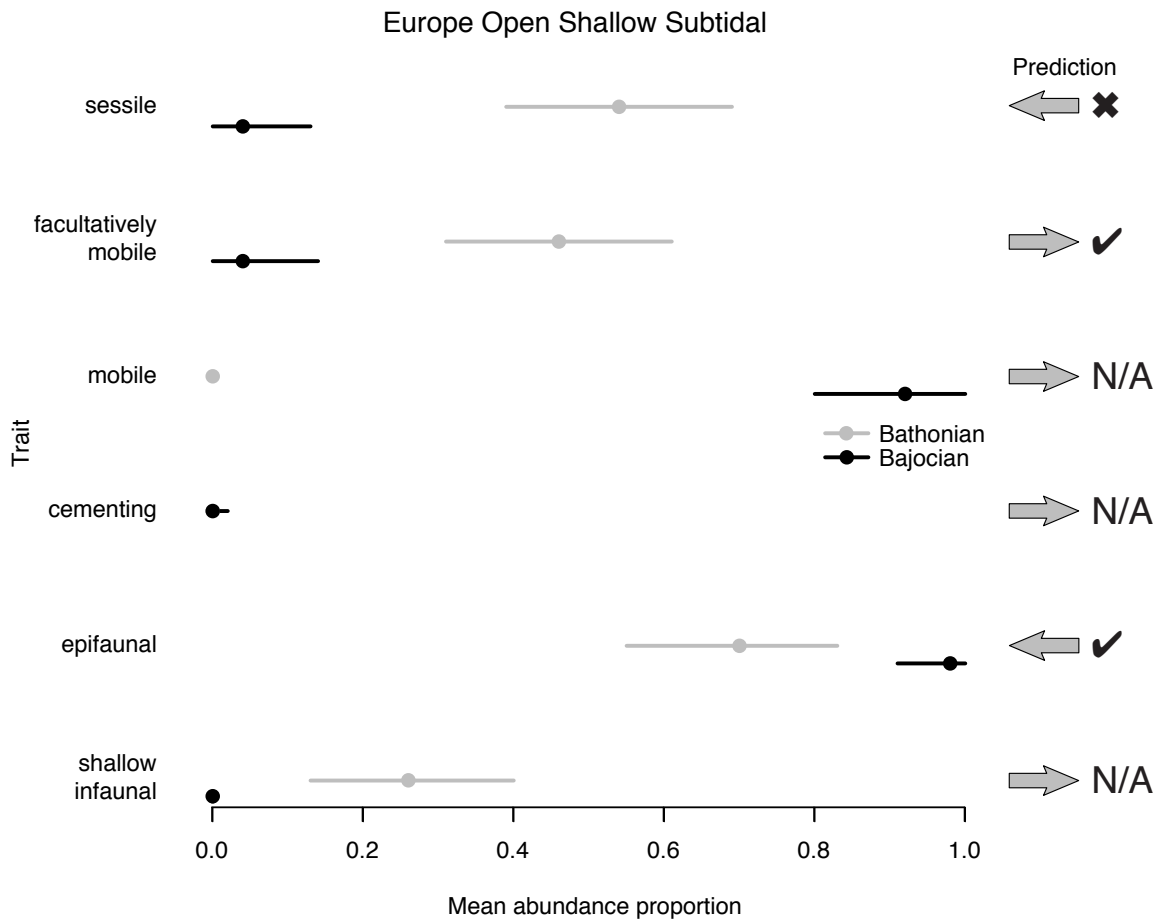


Figure 3.6. Temporal changes in the proportional abundance of ecological trait groups from European data from the Paleobiology Database. Changes in the proportion estimates of ecological trait groups with 95% confidence intervals are compared from the Bajocian (black) and Bathonian (gray), with predicted directions shown by the gray arrows. Overlap of Bajocian and Bathonian confidence intervals for each life habit group suggest no substantial temporal change as indicated by the black X's. Gaps between mean proportions indicate substantial temporal changes as indicated by the black check marks.

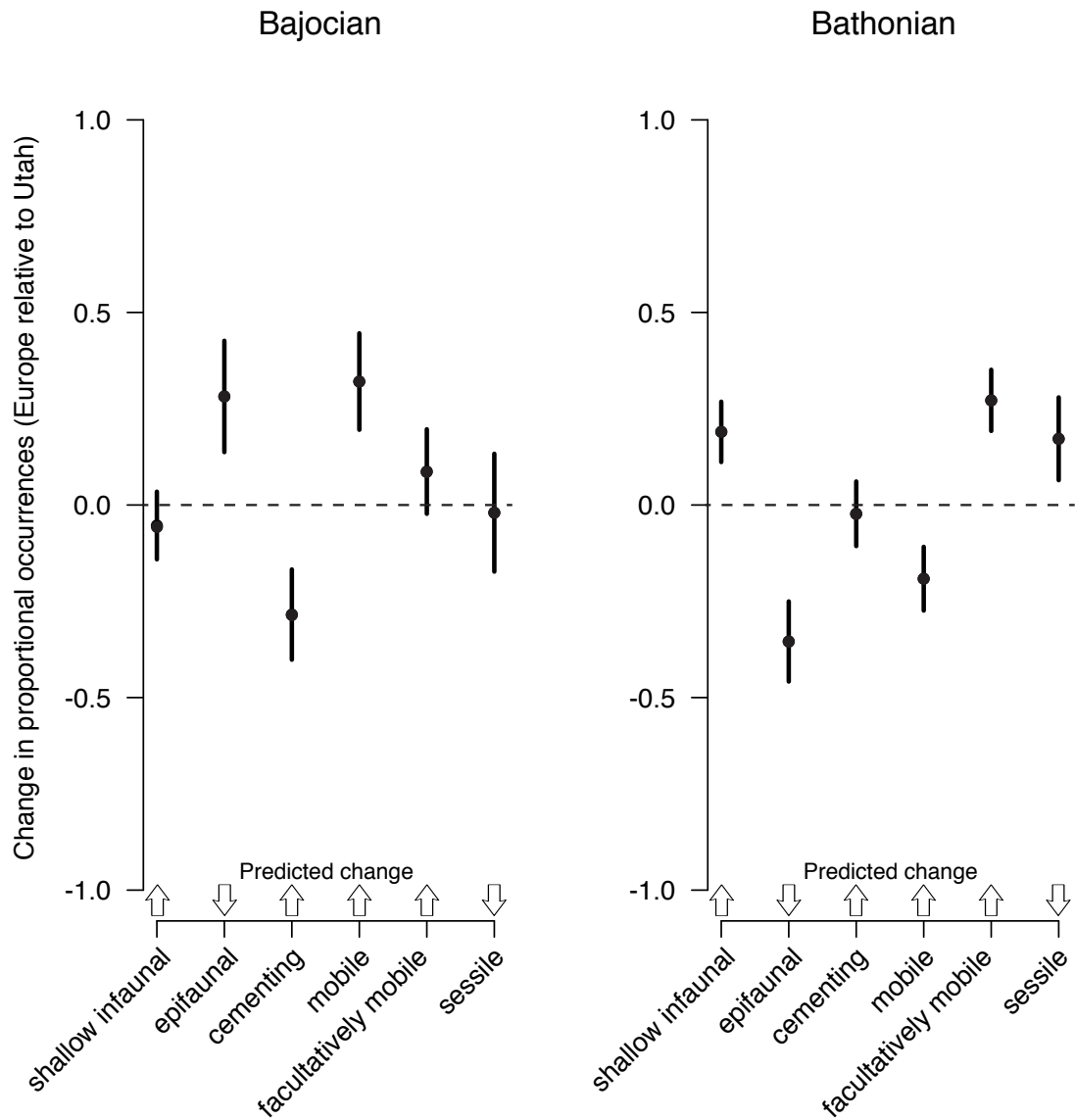


Figure 3.7. Proportional difference test of ecological group occurrences between European Paleobiology Database data and Utah field data. Estimates include 95% confidence intervals; arrows indicate predicted escalation changes. Dashed lines indicate zero change in proportional differences. Confidence intervals not shown where they are smaller than the data point.

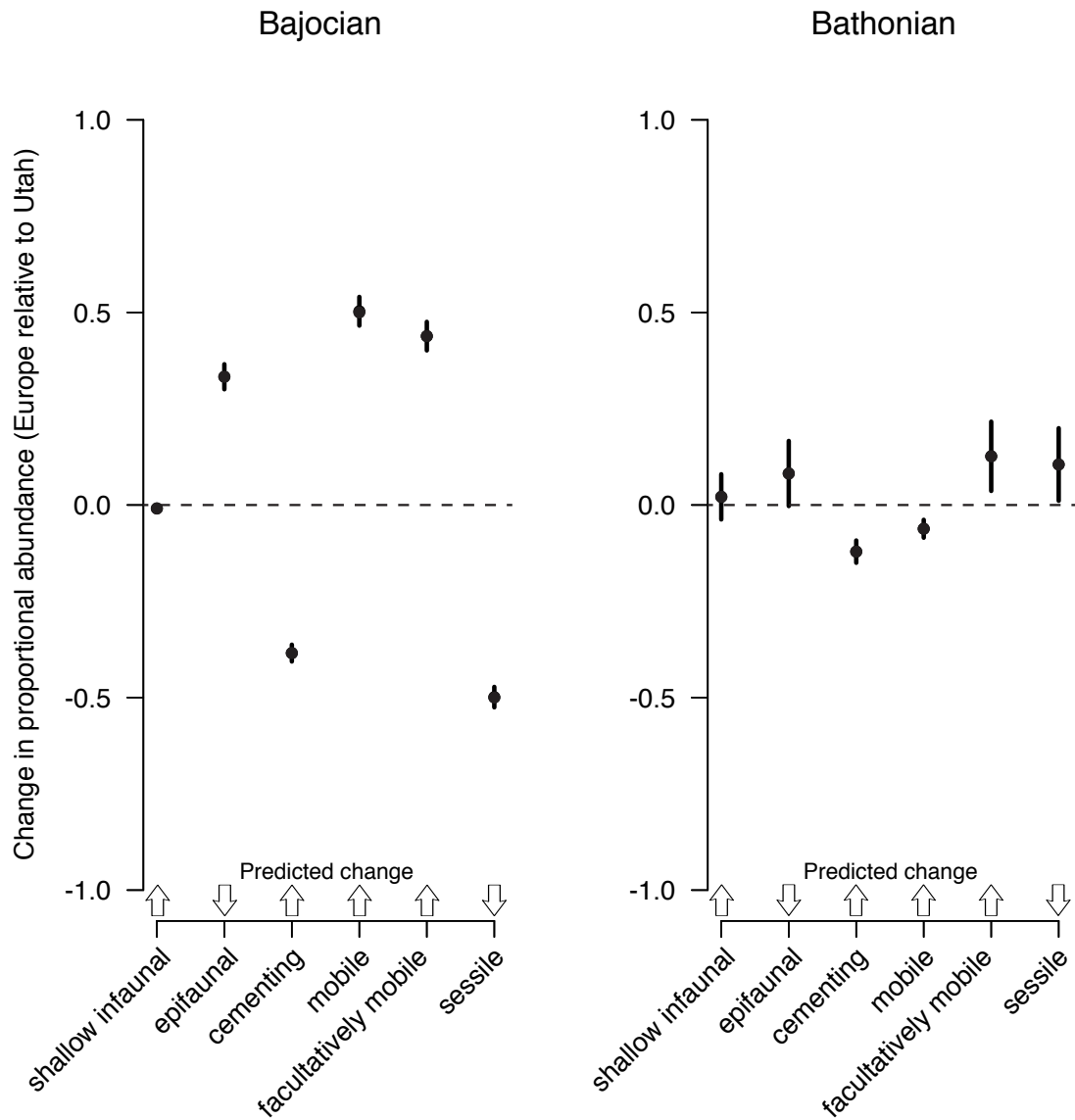


Figure 3.8. Proportional difference test of ecological group abundance between European Paleobiology Database data and Utah field data. Estimates include 95% confidence intervals; arrows indicate predicted escalation changes. Dashed lines indicate zero change in proportional differences. Confidence intervals not shown where they are smaller than the data point.

CHAPTER 4

INTRAREGIONAL TEST OF THE ESCALATION HYPOTHESIS, MIDDLE
JURASSIC SUNDANCE SEAWAY, U.S.A³

³ Monarrez, P.M. and S. Danise. Submitted to Paleobiology.

Abstract

Recent tests of the escalation hypothesis have demonstrated that geographic scale and environmental conditions are important determinants of escalation. Although escalation has been tested among continents, it has not been tested within a single sedimentary basin where environmental conditions can vary and might produce heterogeneous expressions of escalation. The Jurassic Sundance Seaway exhibits an environmental gradient, with environmental conditions improving to the north. This study tests if there is an escalation gradient that parallels the environmental gradient by comparing temporal changes from the Bajocian to Bathonian in 6 escalation-sensitive life habit groups (shallow infaunal, epifaunal, cementing, mobile, facultatively mobile, and sessile taxa) from two field-collected datasets in the Sundance Seaway. Unexpectedly, results show that temporal evidence of escalation does not parallel the observed environmental gradients and evidence for escalation decreases as environmental conditions improve spatially. In particular, we find that in the south there is an increase in infaunal and mobile taxa and a decrease in cementing epifaunal taxa through time, whereas in the north, infaunal and mobile taxa decrease but cementing epifaunal taxa increase. Other factors, other than escalation, might explain the detected changes in life habit groups, like changes in the availability of shelly substrates from the Bajocian to Bathonian. Despite evidence of escalation present in western Tethys during the Jurassic, this study demonstrates the regional variability of escalation and underscores the importance of testing for escalation among and within regions. It also emphasizes the importance of dissecting global data to understand perceived global patterns.

Introduction

Environmental conditions have been argued and shown to be an important limiting factor in promoting escalation, an asymmetrical, enemy-species driven selection (Vermeij 1987, 2004, 2008; Monarrez et al. 2017). This is the basis for Vermeij's (2008) argument that escalation should be tested at regional and local geographic scales to account for environmental heterogeneity. Escalatory interactions at local and regional scales during the Jurassic are argued to have collectively driven global macroevolutionary patterns of marine benthic invertebrates, particularly the observed increase in diversity (Vermeij, 2004, 2008). Although Jurassic biotic interactions occurred before the height of the Mesozoic marine revolution in the Late Cretaceous, they helped set up the events that would define the history of biotic change during the Mesozoic (Vermeij 1977, 1987, 2008). Recent tests of the escalation hypothesis during the Jurassic, however, demonstrate that although there is some evidence of escalation at the global scale, it is strong only in the Tethyan realm (Aberhan et al., 2006; Monarrez et al., 2017). Such global-scale variation raises the possibility that the intensity of escalation trends might vary even within sedimentary basins. Here, we test that hypothesis in the Sundance Seaway, a Jurassic epicontinental sea in western North America.

The Sundance Seaway was prone to poor ocean circulation, hypersalinity, and low oxygen conditions (di Gibert and Ekdale 1999), which were the result of a single, northern entry that created increasingly restricted conditions southward (Fig. 3.1). As such, the seaway is characterized by a latitudinal environmental gradient (Stanley 2010; Danise and Holland 2017, 2018). Here we evaluate the escalation hypothesis during the Middle Jurassic (Bajocian and Bathonian) using field data to: 1) test if the strength of

escalation reflects the environmental gradient in the Sundance Seaway (Stanley 2010; Danise and Holland 2017, 2018) and 2) test whether the northern region had greater proportions of ecological groups with escalation-sensitive life habits than areas farther south. As such, it is expected that strength of escalation should reflect the environmental and taxonomic gradient, with greater evidence of escalation in the northern part of the study relative to the southern portion and that the overall proportions of taxa with escalation-sensitive traits reflect the more favorable conditions in the north than in the south.

Geological Setting

The Sundance Seaway filled an elongate retroarc foreland basin in the western interior of North America from the Middle to Late Jurassic (Bjerrum and Dorsey 1995; Doelling et al. 2013). The seaway was over 2,000 km long, and extended from Utah, USA to British Columbia, Canada, with a single opening to the Panthalassa Ocean at its northern end (Fig. 4.1). Most of the fossiliferous strata in the southern half of the Sundance Seaway are assigned to four formations: the Carmel Formation, Twin Creek Limestone, Gypsum Springs Formation, and Sundance Formation. The Carmel Formation was deposited in the southern lobe of the Sundance Seaway in central and southern Utah (Nielson 1990; Brenner and Peterson 1994; de Gibert and Ekdale 1999). The Twin Creek Limestone was deposited along the foredeep along westernmost Wyoming, eastern Idaho, and north-central Utah (Imlay 1967). The Gypsum Springs and Sundance formations were deposited across most of Wyoming, in eastern South Dakota, and southern Montana (McMullen et al. 2014; Clement and Holland 2016; Danise and Holland, 2017, 2018).

The Bajocian and Bathonian intervals of the Carmel and Gypsum Springs Formations, and the Twin Creek Limestone are mainly carbonate, whereas the Sundance Formation consists of carbonates and siliciclastics. These lithostratigraphic units represent a wide range of environments, with the open shallow subtidal facies being the most fossiliferous and therefore the focus of this study.

The open shallow subtidal facies in the Carmel Formation is characterized by medium-bedded, bioturbated skeletal packstone and grainstone bounded by thin intervals of argillaceous mud at the base, and decreasing mud content and increasing ooid abundance towards the top. The limestone beds become amalgamated and thicker towards the top of each parasequence. Sedimentary structures are rare in this facies in the Carmel, but the high concentrations of shells and amalgamated beds suggest these are storm beds that formed above fairweather wave base.

The open shallow subtidal facies of the Gypsum Springs Formation and the Canyon Springs Member of the Sundance Formation are similar to that of the Carmel in lithology (lime mudstone to skeletal packstone), shell composition, bedding, and bioturbation (McMullen et al. 2014; Clement and Holland 2016). As with the Carmel Formation, the Gypsum Springs Formation and the Canyon Springs Member of the Sundance Formation contain rare sedimentary structures, but lithology and bedding also point to a storm-dominated, open shallow subtidal environment (McMullen et al. 2014; Clement and Holland 2016; Danise and Holland 2018). The open shallow subtidal facies of the Twin Creek Limestone is not as fossiliferous, but it is also characterized by bioturbated medium bedding, with rare sedimentary structures preserved. Based on

gradational contacts with deeper subtidal facies, the context suggests open shallow subtidal environment.

Overall, the environments of the Sundance Seaway were prone to restricted water circulation, hypersaline conditions, and low oxygen levels (Tang and Bottjer 1996; de Gibert and Ekdale 1999; McMullen et al. 2014; Clement and Holland 2016). Temperature and salinity conditions however, possibly improved towards the north. Such a gradient may have been produced because the seaway had a single open-ocean connection far to the north, which promoted warmer waters and increased salinity to the south (Stanley 2010). The shallow depth of the seaway could have impeded circulation, resulting in areas of low-oxygen conditions as a result of stagnation (di Gibert and Ekdale 1999; Stanley 2010). These environmental conditions are evidenced by the abundance of evaporite deposits throughout the seaway (Clement and Holland 2016), the low diversity of body and trace fossils (di Gibert and Ekdale 1999; Danise and Holland 2017), and the presence of microbialites throughout the seaway (Doelling 2013).

The fauna of the southern half of the Sundance Seaway contains mostly bivalves, as well as gastropods, belemnites, and echinoderms, but also rarer cheilostome bryozoans, corals, brachiopods, ammonites, serpulid worm tubes, decapods, and various ichnofossils (Imlay 1964; Sohl 1965; Cuffey and Ehleiter 1984; Blake 1986; Wilson and Palmer 1994; Wilson et al. 1998; Baker and Wilson 1999; Taylor and Wilson 1999; de Gibert and Ekdale 1999; Tang et al. 2000; Danise and Holland 2017). Predators are rare but diverse, and they include asteroides (Blake 1981, 1986), hybodont sharks (Wahl 2005), ichthyosaurs, pliosaurs, and plesiosaurs (Massare et al. 2013). Despite the diversity of higher taxonomic groups, the faunas of the Sundance Seaway are depauperate at the

species level relative to the Middle Jurassic faunas elsewhere, especially compared with Europe where bivalve species richness is twice that of the Sundance Seaway (Imlay 1964, 1967; Hallam 1976; Tang and Bottjer 1997; Danise & Holland 2017).

Testing for Escalation

Escalation can be tested by tracking physical traits, such as shell thickness, ornamentation, and size, and physiological traits, such as increased metabolic rates (Vermeij 1987). Although physiological traits cannot be observed in the fossil record, morphological features particularly shell characteristics, are readily observed. Interpreting changes in shell morphology as a response to escalation pressure, however, can be complicated and difficult to distinguish from other factors. For example, a recent study showed that spines in molluscs may not be a defensive adaptation (Chirat et al. 2013). Using a model for spine morphogenesis, Chirat et al. (2013) discovered that spine development can be accounted for by small changes in the mechanical process that controls shell accretion between the mantle edge and shell edge. As such, their study concludes that spines are not necessarily a result of functional adaptation from increased predation pressure.

Escalation can also be tested through its expected evolutionary consequences (Vermeij 1987). Trends in life habits are used in this study, because they are an important component to community structure and previously used to indicate escalation pressure (Vermeij 1987). Since escalation is thought to have restructured marine communities during the Mesozoic (Vermeij 1987, 2008), life habits of marine invertebrates within communities could indicate whether escalation played a role in shaping community

structure. Tracking life habits through time can provide a useful metric for escalation, if other factors that influence life habit patterns can be ruled out (Monarrez et al. 2017).

This study tests for escalation from the Bajocian to Bathonian because this is a period of rapid global diversification (Alroy et al. 2008; Alroy, 2010). This increase in diversity is also reflected in increased diversity of life habits (Bush and Bambach 2011). If escalation transformed marine communities during the Mesozoic and drove macroevolutionary patterns (Vermeij 1987, 2004, 2008), evidence of escalation should be observed during intervals of rapid diversification, especially in those life habits thought to be sensitive to escalation pressure.

Methods

This study tests for escalation using two approaches. First, we test for directional temporal change in ecological groups with life habits that are hypothesized to reflect changes caused by escalation from the Bajocian to Bathonian (Table 4.1). Second, we test for an escalation gradient in the seaway, assuming that environmental conditions improve and become more favorable northward, towards the open-marine entrance of the Sundance Seaway. We do this by assessing life habit groups in samples from two datasets collected from the Sundance Seaway. The northern dataset was collected from the Gypsum Springs Formation, the Canyon Springs Member of the Sundance Formation, and the Twin Creek Limestone in Wyoming by Danise and Holland (2017). The southern dataset was collected from the Carmel Formation from east-central Utah.

The open shallow subtidal collections from the Bajocian and Bathonian of the northern dataset analyzed in this study consist of 39 collections (23 Bajocian and 16 Bathonian), each with a minimum number of 25 individuals consisting of a total of 2,664

individuals among all collections, 55 genera, and 73 species, with a Bajocian species richness of 61 and Bathonian species richness of 31 (Danise and Holland 2017). The collections from Utah consist of 46 bulk samples from the Carmel Formation, 23 each from the open shallow subtidal facies for the Bajocian and Bathonian. Each bulk sample contains a minimum of 25 individuals for a total of 2,971 individuals among all collections, 18 genera and 24 species, with a Bajocian species richness of 23 and the same for the Bathonian. All fossils from both datasets were identified to the lowest taxonomic level possible and counted using the minimum number of individuals method (Gilinsky and Bennington 1994). Life habits including tiering, epifaunal mode of life, and motility of identified bivalves were determined from an unpublished ecological dataset of Jurassic bivalves assembled by Martin Aberhan (see Aberhan et al. 2006; Monarrez et al. 2017). Gastropod ecology was determined from unpublished data uploaded to the Paleobiology Database and from Kollman (2014). Crinoid ecology was determined from Donovan (1994).

Before testing for escalation, we calculated species diversity separately in the southern and northern study areas in the Sundance Seaway regions to determine if there is a latitudinal diversity gradient that parallels the environmental gradient in the seaway. Diversity was assessed by calculating the species richness and evenness (Simpson's D) for each stage in each region. Gamma, beta, and mean alpha diversity in richness and evenness were calculated using additive diversity partitioning (Whittaker 1956, 1960; Lande 1996; Holland 2010). Gamma diversity (γ) is the total diversity within a region; mean alpha diversity ($\bar{\alpha}$) is the mean diversity in all collections, and beta diversity (β) is the difference between gamma and mean alpha diversity (Lande 1996). Richness was

calculated using a function adapted from the functions of Holland (2010). Simpson's D was calculated using a modified *diversity* function from the Vegan package in R (Oksanen et al. 2009; R Core Team, 2018).

To test for escalation, we calculated the proportions of occurrences and abundances of ecological life habit groups from the northern and southern regions and compared the distributions and means across the Bajocian to Bathonian (Tables 4.2 and 4.3). We also compared the proportions of life habit groups from the northern region to those in the southern region to determine if the life habit proportions from the north differ as predicted by the escalation hypothesis. Abundance data are analyzed here in addition to occurrences because abundance reflects community structure. Additionally, the use of abundance data in conjunction with occurrence data allows the detection of ecological signals that may be decoupled from occurrence data, hence missed if occurrence data alone are analyzed (Foote et al. 2007; Liow and Stenseth 2007; Christie et al. 2013).

The proportions of life habit groups calculated in each dataset include shallow and deep infaunal, epifaunal (free-lying, sessile, cementing, and pedunculate), and motility (mobile, facultatively mobile, and sessile). The epifaunal category consists of non-cementing, sessile taxa, and the sessile category consists of non-cementing taxa. Because not every life habit observed in the northern region occurs in the southern region, only the 6 life habits present in both regions were compared (shallow infaunal, epifaunal, cementing, mobile, facultatively mobile, and sessile). These proportions were calculated and compared temporally within dataset and latitudinally between datasets using the *prop.test* function in R. All calculations were performed in R (R Core Team 2018).

Results

Sundance Seaway Diversity

Overall diversity is higher in the north relative to the south (Figs. 4.2 and 4.3), which is consistent with there being an environmental gradient that improved to the north. Richness and evenness are much higher in the north during the Bajocian, with gamma richness almost three times higher than the south (Fig. 4.2). Whereas richness decreases in the north from the Bajocian to Bathonian, gamma richness remains higher than the south, but not gamma evenness, which is higher in the south. The decrease in diversity in the north is driven by a decline in beta diversity, as mean alpha does not decrease as sharply. Whereas gamma diversity remains the same from the Bajocian to Bathonian in the south, mean alpha increases slightly in the Bathonian.

Temporal Comparison of Life Habits

Traits by occurrences.— Overall, the proportions of life habit occurrences do not change in the direction predicted by escalation, except for minor exceptions (Figs. 4.4 and 4.5). Specifically, only the mobile life habit in the south exhibits a pronounced increase consistent with escalation. In both the south and north, epifaunal and sessile occurrences increase, contrary to the escalation hypothesis. In the south, cementing occurrences decrease, also inconsistent with escalation. Conversely, shallow infaunal occurrences in the south and mobile occurrences in the north increase consistent with escalation, but both increases are negligible.

Traits by abundance— Abundance data show changes similar to occurrence data with most life habits changing in the direction opposite that predicted by escalation (Figs. 4.6 and 4.7). In both the south and north, the proportional abundance of epifaunal and

sessile taxa increases, which is not consistent with escalation. Proportional abundance of cementing taxa decreases in the south, and facultatively mobile taxa also decrease in the north, both not consistent with escalation. Conversely, the proportional abundance of shallow infaunal and facultatively mobile taxa increase in the south, which is consistent with escalation, but these increases are negligible. As with occurrences, the only change that is pronounced and consistent with escalation is the increase in mobile taxa in the south.

Spatial Comparison of Life Habits

Traits by occurrences .— Overall, the difference in proportions of life habits between the northern and the southern datasets are consistent with escalation for the Bajocian, but not for the Bathonian (Fig. 4.8a). Specifically, only the increase to the north in facultatively mobile taxa in the Bajocian is pronounced and consistent with a latitudinal gradient in escalation. During the Bajocian, the occurrences of shallow infaunal, epifaunal, mobile, facultatively mobile, and sessile taxa are all consistent with the prediction that the north had more favorable conditions to support escalation, but the differences are not statistically significant. Conversely, during the Bathonian, shallow infaunal, epifaunal, mobile, facultatively mobile, and sessile taxa do not support the prediction. The exception for these observations are cementing taxa, for which the spatial difference is not consistent with escalation during the Bajocian, but it is for the Bathonian.

Traits by abundance .— The regional differences in life habits based on abundance are very similar to the Bajocian occurrence data, and less so for the Bathonian. Spatial differences are more pronounced than in the occurrence data (Fig. 4.8b). As with

occurrence data, Bajocian proportional abundance for shallow infaunal, epifaunal, mobile, facultatively mobile, and sessile occurrences are all consistent with conditions in the north being more favorable for escalation, and all of these proportional differences are substantial. As with occurrence data, shallow infaunal, mobile and facultatively mobile proportional abundance in the Bathonian are not consistent with the north having favorable conditions for escalation. Unlike occurrence data, however, proportional abundance of Bathonian epifaunal, sessile, and cementing taxa are consistent with conditions favorable for escalation in the north and all of these differences are substantial.

Discussion

Is There Evidence of Escalation in the Sundance Seaway?

A comparison of life habit proportions across the Bajocian and Bathonian fails to show substantial evidence of escalation in the study area of the Sundance Seaway. In the southern dataset, only mobile taxa significantly change from the Bajocian to Bathonian in the direction consistent with escalation. Of the 12 total tests conducted, 6 life habits change in the opposite direction predicted by the escalation hypothesis. The other two life habits that do change in the directions consistent with escalation are shallow infaunal and facultatively mobile, but these increases are negligible. In the northern dataset, no ecological group shows changes from the Bajocian to Bathonian consistent with escalation. Whereas cementing and mobile species increase from the Bajocian to Bathonian, these increases are negligible and not significant. Additionally, of the possible 12 ecological changes from the Bajocian to Bathonian (including both occurrence and abundance data), 4 changes are strongly in the opposite direction predicted by the escalation hypothesis. Despite minor differences during the Bathonian, abundance data

corresponds fairly well with occurrence data. Based on these data alone, it is concluded that escalation did not play a major role in the benthic community life habit structure in the Sundance Seaway.

Is There Evidence of an Escalation Gradient in the Sundance Seaway?

Despite the lack of temporal changes consistent with escalation in this study, evidence indicates increasing escalation along a spatial gradient. Because environmental factors have been argued and shown to be important in promoting and sustaining escalation (Vermeij 2008; Monarrez et al. 2017), it was expected that evidence of escalation would be stronger in the northern dataset of this study. During the Bajocian, evidence suggests that conditions were more favorable for escalation to the north, which is supported by abundance data (Fig. 4.7). During the Bathonian, however, occurrence data do not support evidence of conditions favorable for escalation, but abundance data do for three traits (epifaunal, cementing, and sessile). Occurrence data overall do not support evidence of an escalation gradient, but abundance data support such a gradient during the Bajocian.

Alternative Explanation for Temporal Changes in Life Habit Groups

Subtle changes in lithology from the Bajocian to Bathonian could explain the observed differences in life habit proportions from south to north. At first glance, the lithology from open shallow subtidal facies of the Gypsum Spring Formation, Twin Creek Limestone and Canyon Springs Member of the Sundance Formation present to the north is similar to the Carmel Formation in Utah, as both consist of skeletal packstone and grainstone (Danise and Holland 2017). The biggest ecological difference between these two regions is in the proportions of shallow infaunal, cementers, and facultatively

mobile taxa, as the latitudinal changes in these groups are slightly inverted from the Bajocian to Bathonian (Fig. 4.8). One explanation of this pattern is that the southward decrease in cementers and increase in shallow infaunal, reflect a change to softer substrates in the south. Conversely, the northward increase in cementers and decrease in shallow infauna reflect greater availability of shells, and thus firm substrates, to the north. As most facultatively mobile taxa are shallow infauna, changes in shallow infaunal taxa would be mirrored by changes in facultatively mobile taxa. The importance of shelly substrate is also supported by other life habit groups that occur only in the northern dataset, specifically the Bathonian increase in free-lying taxa and decrease in shallow infaunal taxa. Increasingly shelly substrates in the north could have decreased the available habitat for burrowing and free-lying taxa and could have been an important underlying driver of community life habit structure.

Differences in proportional changes between the southern and northern datasets also parallel temporal changes in diversity. In the southern dataset, alpha richness slightly increases from the Bajocian to Bathonian, as does evenness (Figs. 4.2 and 4.3). The opposite occurs in the north, with alpha, beta, and gamma richness and evenness falling from the Bajocian to Bathonian (Figs. 4.2 and 4.3). Even so, gamma richness remains larger in the north than in the south. The temporal decrease in diversity in the north may also explain why evidence of escalation decreases as well. One of the conditions required to promote escalation is higher taxonomic diversity, as the high diversity is thought to promote more intense competition and predation among species (Vermeij 2004). The decrease in diversity may also be explained by changes in lithology, as shellier substrates could have sustained communities with lower diversity.

Testing for escalation across only two relatively short stages may fail to detect escalation if escalation is occurring across a longer time span. Evidence of escalation would not be expected to increase linearly through the Mesozoic, as the environmental conditions that support it may not be sustained for long periods of time in any given area (Vermeij 2004). As a result, it is expected that evidence of escalation should wax and wane. It is possible that a long-term temporal trend in escalation in the Sundance Seaway is masked by short term variation in escalation. However, based on the analysis of Jurassic North American occurrences from the Paleobiology Database, evidence of escalation is scant in North America during this period (Monarrez et al. 2017). Therefore, lack of escalation from the Bajocian to Bathonian in the Sundance Seaway is consistent with an overall lack of escalation in North America.

Reconciling Regional and Global Patterns

Escalation is tested across the Bajocian and Bathonian specifically because global diversity patterns indicate a sharp increase in taxonomic diversity that occurs during this time interval (Alroy et al. 2008; Alroy 2010). If escalation drove global macroevolutionary patterns during the Bajocian and Bathonian, then evidence of escalation should be detected. Despite this expectation, there is no evidence that escalation played a role in the temporal changes in ecological life habit group proportions in the Sundance Seaway. Even though there is no evidence from this study that escalatory interactions in the Sundance Seaway drove global diversity patterns based on life habit, it is possible that this is because global diversity patterns were not experienced everywhere but were driven by diversity in particular regions (Alroy et al. 2008; Alroy 2010).

Dissecting global data by regions for the Jurassic using data from the Paleobiology Database revealed scant evidence of escalation in North America during the Jurassic, with most evidence of escalation being concentrated in the western Tethyan realm during the latter half of the Jurassic (Monarrez et al. 2017). That study also found that ecological patterns from the European region were the major source of global patterns, as removing Europe from the global data yielded weak evidence of escalation (Monarrez et al. 2017). Moreover, approximately 55% of the Jurassic global occurrence data used from the Paleobiology Database comes from Europe (Monarrez et al. 2017). Since the Phanerozoic diversity curves of Alroy et al. (2008) and Alroy (2010) are based on occurrence data from the Paleobiology Database, the sharp increase in diversity across the Bajocian and Bathonian is driven by the dominance of European data, and Tethyan patterns were not representative of most patterns elsewhere in the Jurassic. Therefore, although escalation likely did not drive global diversity patterns during the Jurassic, they did so in the Tethyan realm where those patterns heavily influence observed global patterns.

Escalation took place in the Tethyan realm during the Jurassic, and the proliferation of groups with life habits that help fend off or escape enemy species may have spread out to other regions over time, particularly during the height of the Mesozoic marine revolution in the Cretaceous (Vermeij 1987). This possibility combined with how European data drives Jurassic global macroevolutionary patterns, may explain why evidence of escalation is not observed elsewhere, as in the Sundance Seaway.

The results of this study once more underscore the importance of dissecting global data to understand perceived global patterns (e.g. Miller 1997a, b, 2000, 2003; Vermeij

and Leighton 2003). As demonstrated by Monarrez et al. (2017), regional ecological patterns reveal that escalation plays a significant role in benthic ecosystems in the western Tethys realm, which heavily influences global patterns. This study goes further by assessing intraregional ecological data to determine if ecological gradients might correspond to a gradient in environmental conditions. Despite an environmental and an observed taxonomic richness gradient along the Sundance Seaway, evidence of escalation was not observed from the Bajocian to Bathonian, supporting previous results demonstrating a lack of escalation in the Jurassic of western North America (Monarrez et al. 2017).

Conclusions

1. An analysis of changes in escalation-sensitive life habits from the Bajocian to Bathonian show no evidence of increasing escalation in either the southern or northern areas of the Sundance Seaway. Spatial patterns of escalation are absent for occurrence data and moderately supported for abundance data.
2. Besides escalation, other factors, like changes in lithology, might explain the observed differences in proportions of life habits between the south and the north from the Bajocian to Bathonian. A temporal change to softer substrate in the south corresponds to an increase in infaunal taxa and a decrease in cementing taxa. In the north, the opposite trend occurs, with infaunal taxa decreasing and cementing species increasing through time, suggesting an increase in shelly substrates.
3. The lack of escalation in the northern studied part of the Seaway, despite higher taxonomic richness and improved environmental conditions, was unexpected. It is possible that escalation in the Middle Jurassic was limited to the western Tethyan realm,

and ecological traits sensitive to escalation that occurred in the western Tethys may not have proliferated elsewhere until much later. This is supported by the evidence that global increase in taxonomic diversity from the Bajocian to Bathonian is driven by diversification in the western Tethys.

Tables

Table 4.1. Expected escalatory pressure and predicted effects of escalation during the Jurassic, based on Vermeij (1987).

	Escalation Source	Escalation Prediction
Tiering		
Shallow Infaunal	Predation/Bioturbation	Increase
Epifaunal	Predation/Bioturbation	Decrease
Epifaunal Modes of Life		
Cementing	Predation	Increase
Motility		
Mobile	Predation/Bioturbation	Increase
Facultative Mobile	Predation/Bioturbation	Increase
Sessile	Predation	Decrease

Table 4.2. Proportions of life habit occurrences for the Bajocian and Bathonian in the south and north regions of the Sundance Seaway.

Life Habit	South		North	
	Bajocian	Bathonian	Bajocian	Bathonian
Shallow infaunal	0.07	0.09	0.19	0.06
Epifaunal	0.51	0.68	0.45	0.66
Cementing	0.37	0.18	0.17	0.26
Mobile	0.05	0.19	0.13	0.15
Facultatively mobile	0.07	0.09	0.27	0.07
Sessile	0.45	0.49	0.39	0.48

Table 4.3. Proportions of life habit abundance for the Bajocian and Bathonian in the south and north regions of the Sundance Seaway.

Life Habit	South		North	
	Bajocian	Bathonian	Bajocian	Bathonian
Shallow infaunal	0.01	0.03	0.13	0.04
Epifaunal	0.56	0.82	0.41	0.62
Cementing	0.37	0.11	0.27	0.33
Mobile	0.01	0.06	0.10	0.11
Facultatively mobile	0.01	0.03	0.22	0.04
Sessile	0.55	0.76	0.36	0.50

Figures

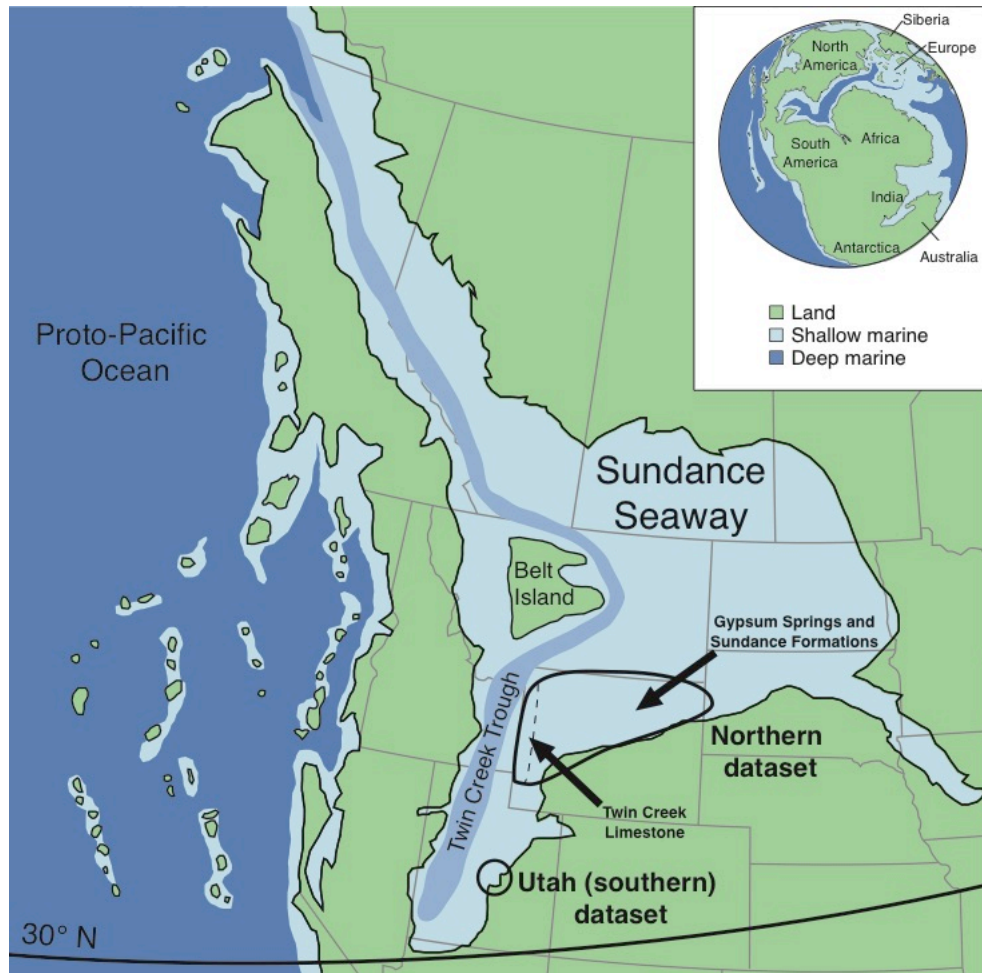


Figure 4.1. Paleogeographic map of western North America during the Middle Jurassic. The black circles indicate areas where data has been collected, with northern dataset collected by Danise and Holland (2017). Modified from Clement and Holland (2016), which was adapted from Blakey (2015).

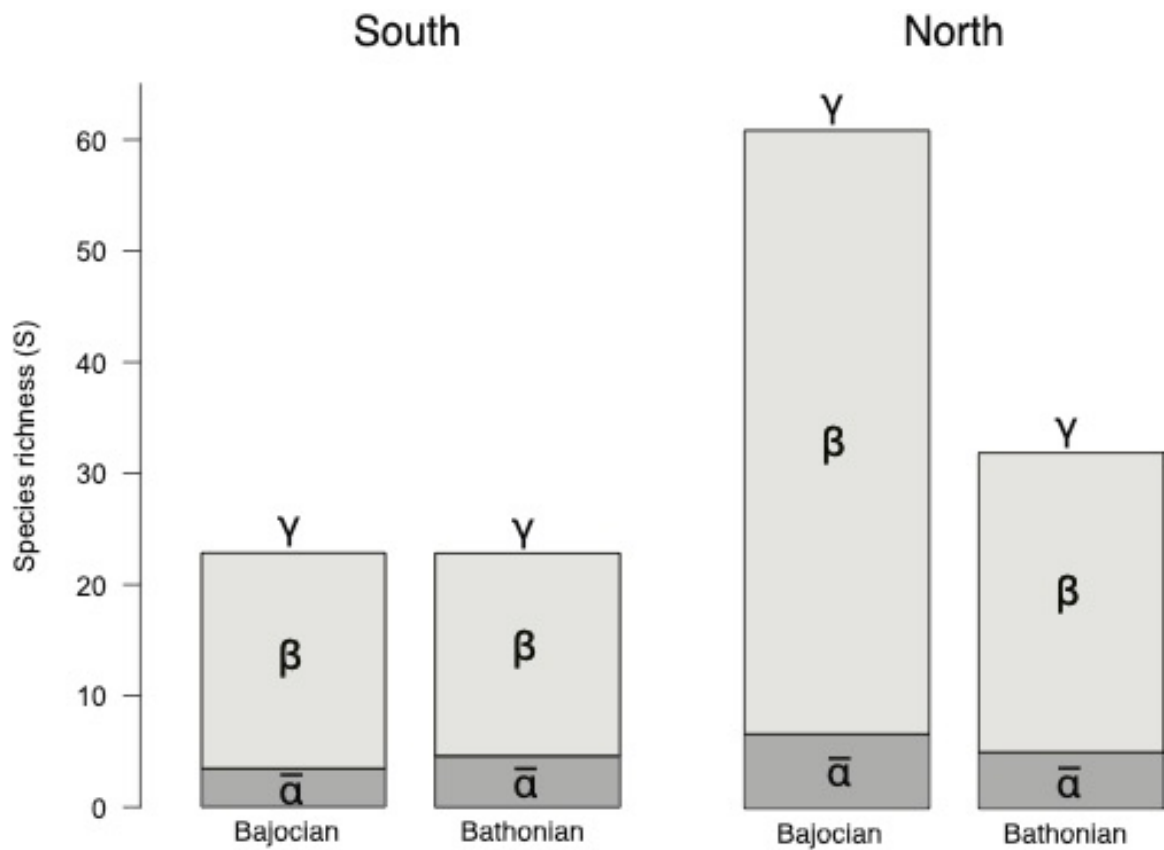


Figure 4.2. Additive diversity partitioning of species richness for the southern dataset and northern dataset from the Sundance Seaway for the Bajocian and Bathonian. Species richness is higher overall in the northern dataset but does exhibit a notable decrease from the Bajocian to Bathonian.

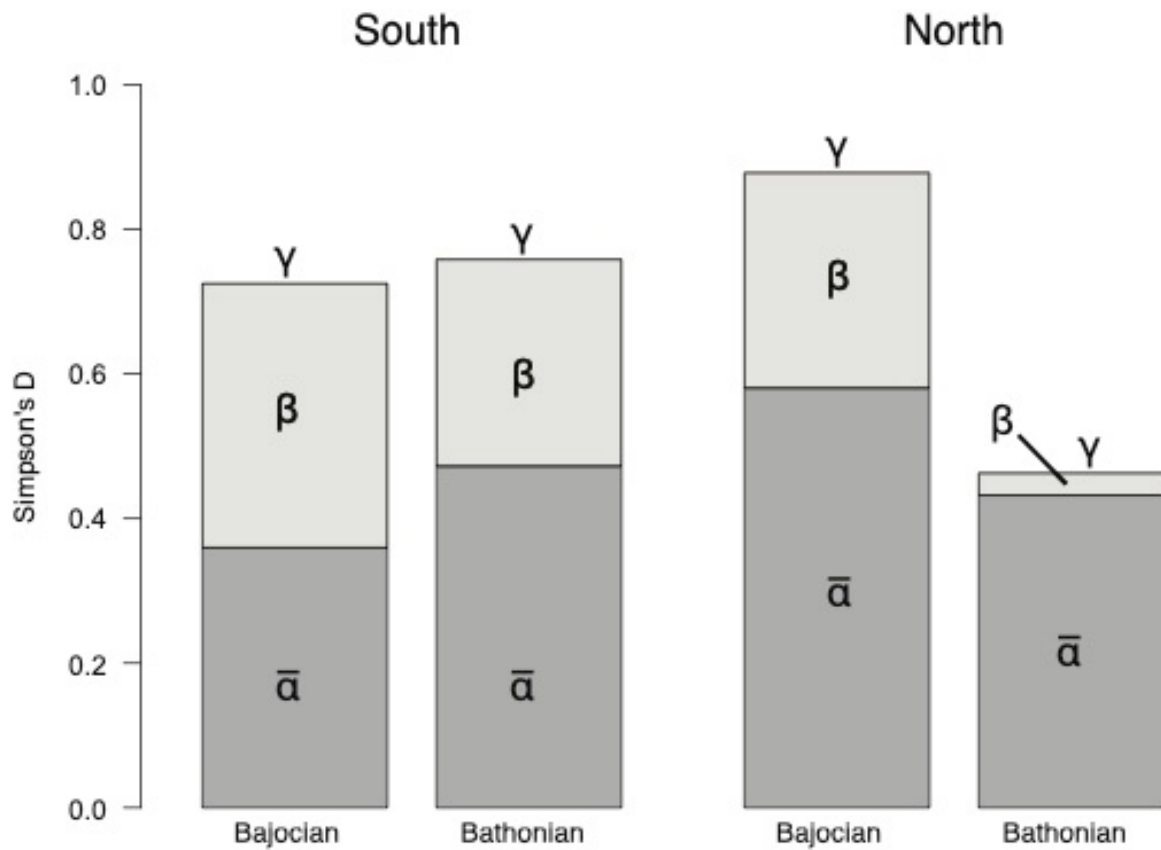


Figure 4.3. Additive diversity partitioning of evenness (Simpson's D) for the southern dataset and northern dataset from the Sundance Seaway for the Bajocian and Bathonian. Species evenness is higher overall in the northern dataset but does exhibit a notable decrease from the Bajocian to Bathonian.

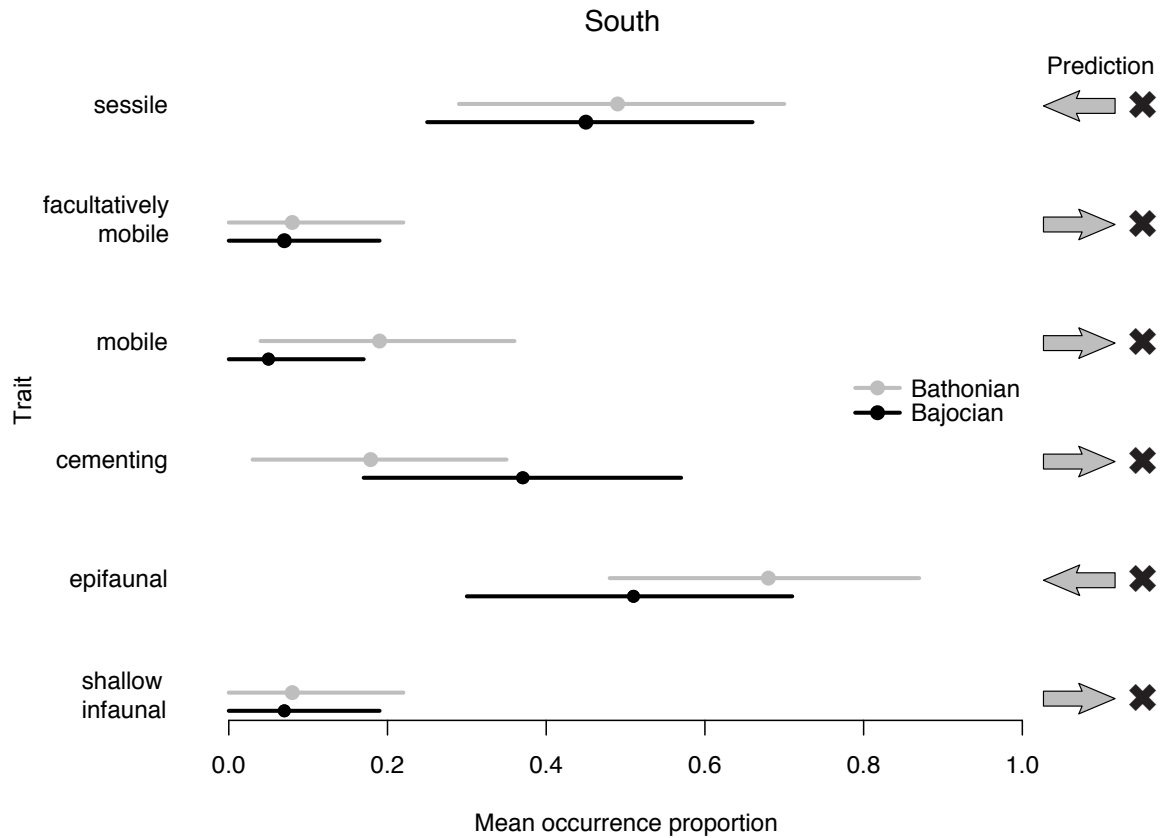


Figure 4.4. Temporal proportional changes of life habit occurrences of the southern Sundance Seaway. Changes in occurrence proportion estimates of life habits with 95% confidence intervals are compared from the Bajocian (black) and Bathonian (gray), with predicted directions shown by the gray arrows. Overlap of Bajocian and Bathonian confidence intervals for each life habit group suggest no substantial temporal change as indicated by the black X's.

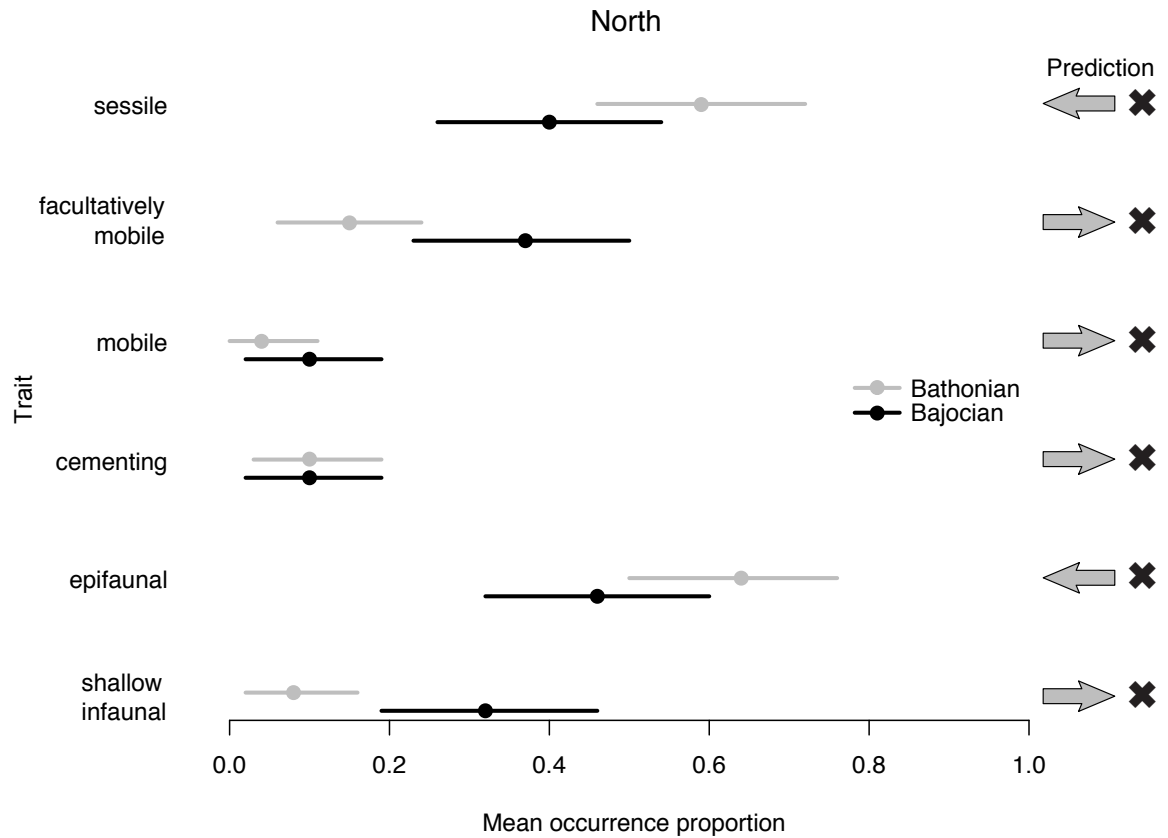


Figure 4.5. Temporal proportional changes of life habit occurrences of the northern Sundance Seaway dataset. Changes in occurrence proportion estimates of life habits with 95% confidence intervals are compared from the Bajocian (black) and Bathonian (gray), with predicted directions shown by the gray arrows. Overlap of Bajocian and Bathonian confidence intervals for each life habit group suggest no substantial temporal change as indicated by the black X's.

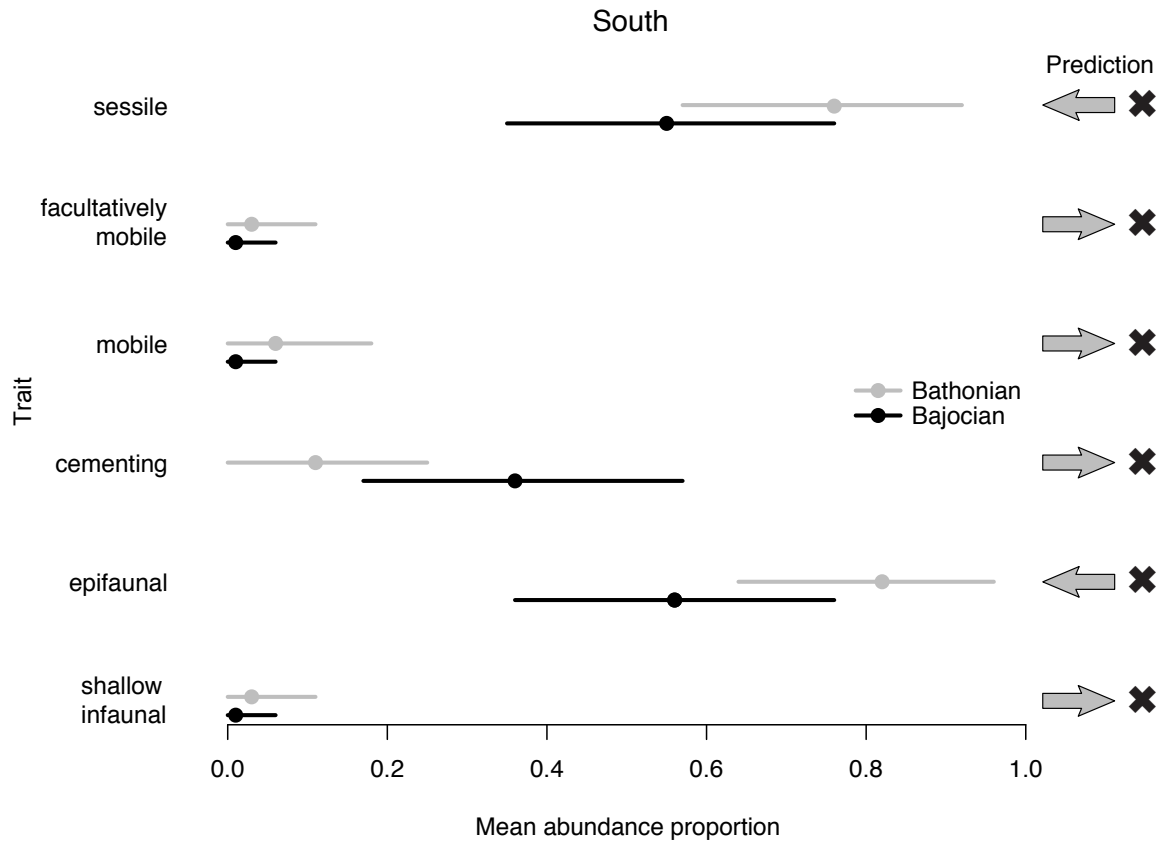


Figure 4.6. Temporal proportional changes of life habit abundance of the southern Sundance Seaway dataset. Changes in occurrence proportion estimates of life habits with 95% confidence intervals are compared from the Bajocian (black) and Bathonian (gray), with predicted directions shown by the gray arrows. Overlap of Bajocian and Bathonian confidence intervals for each life habit group suggest no substantial temporal change as indicated by the black X's.

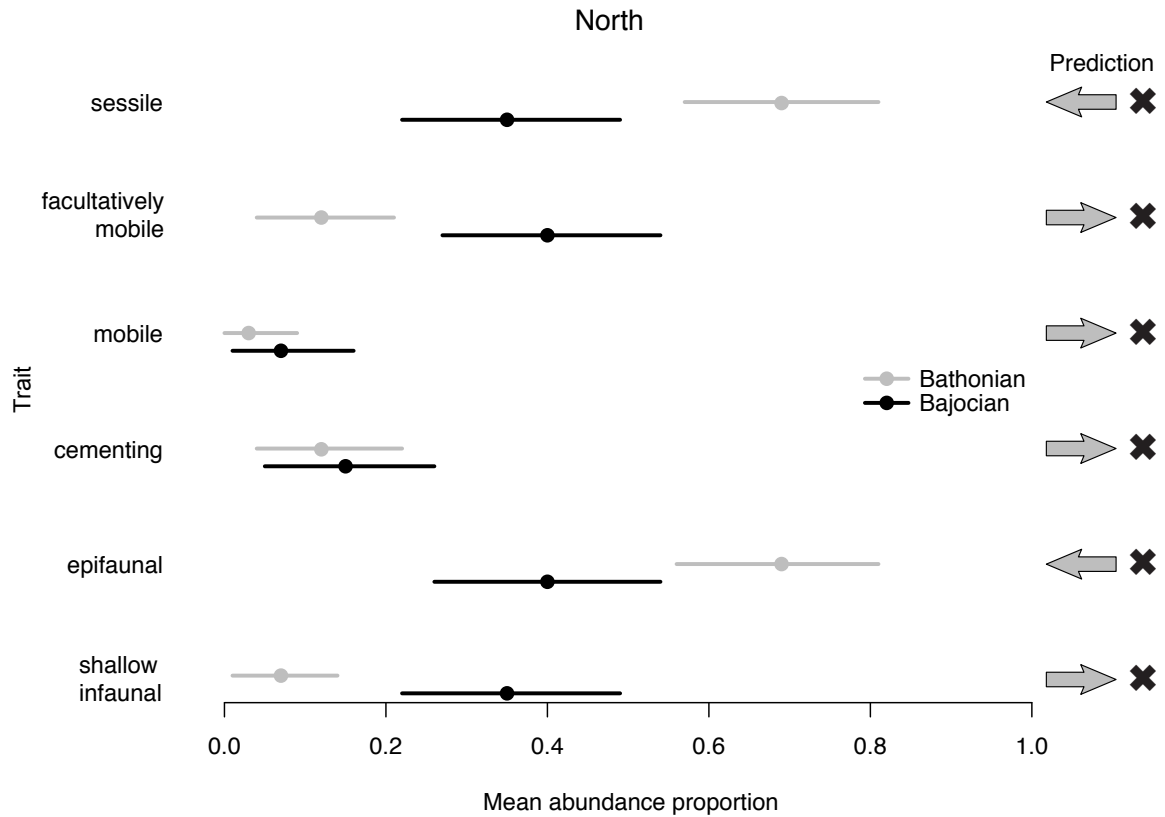


Figure 4.7. Temporal proportional changes of life habit abundance of the northern Sundance Seaway dataset. Changes in occurrence proportion estimates of life habits with 95% confidence intervals are compared from the Bajocian (black) and Bathonian (gray), with predicted directions shown by the gray arrows. Offset of Bajocian and Bathonian confidence intervals for each life habit group suggest substantial temporal change in proportions as indicated by the black X's, however, in the direction opposite that predicted by escalation.

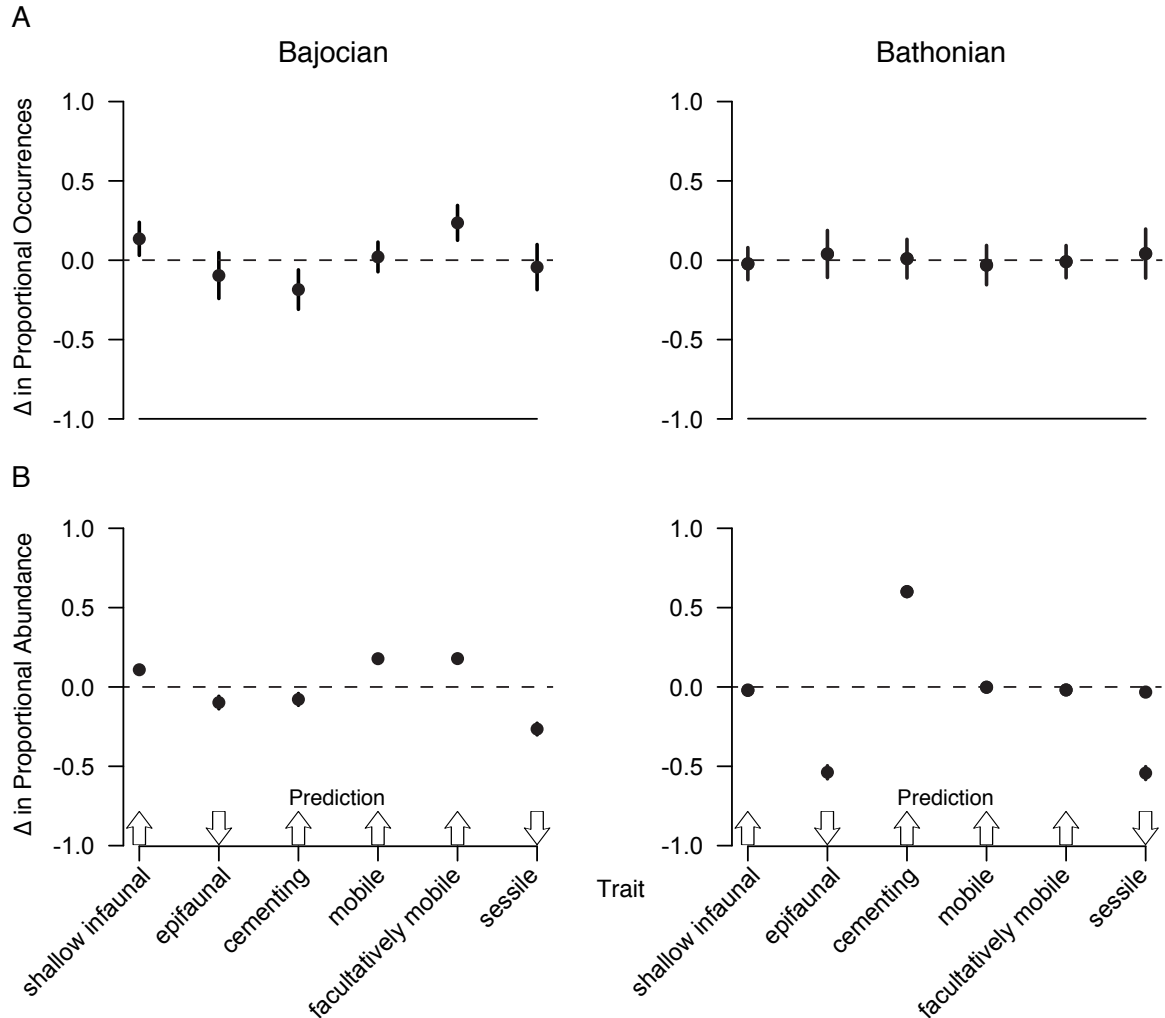


Figure 4.8. Latitudinal proportional changes of life habit occurrences (A) and abundance (B) of Sundance Seaway life habit groups. Estimates with 95% confidence intervals depict differences in proportions of life habit groups in the northern dataset relative to the southern dataset with arrows indicating escalation predictions. Dashed lines indicate zero change in latitudinal proportions. Missing confidence intervals occur where they are smaller than the data point.

CHAPTER 5

CONCLUSIONS

The Jurassic represents a crucial interval of the Mesozoic marine revolution when regional adaptive radiations resulting from escalation are hypothesized to have driven the diversification of many marine benthic invertebrate groups (Vermeij 2008). The Jurassic was also characterized by regions with the environmental conditions necessary to promote and sustain escalation (Vermeij 2004). The ecological adaptations that occurred during the Jurassic have been a critical component in support of biotic interactions having driven macroevolutionary patterns. The results of this dissertation support these two main pillars of the escalation hypothesis, that escalation was limited to particular regions (Europe in this case), and more importantly, that environmental conditions play a crucial role in promoting and sustaining escalation locally (Vermeij 2004, 2008).

Using Jurassic occurrence data from the Paleobiology Database in Chapter 2, the proportions of ecological life habit groups were calculated by region to determine if their trends are consistent with escalation. Five regions were selected based on the concentration of occurrences entered into the Paleobiology Database (Europe, North and South America, Middle East including parts of south Asia and Africa, and New Zealand). Overall, ecological life habit trends are heterogeneous across regions, with the strongest evidence of escalation concentrated in the western Tethys realm (Europe). This region was characterized by subtropical to tropical, primarily carbonate environments, with high biological productivity as well as potentially high nutrient availability. Other alternative

explanations behind the observed life habit trends in Europe can be ruled out, including both intrinsic and extrinsic factors, such as competitive displacement, availability of hard substrates, taphonomic effects of global seawater states, and statistical artifacts.

Furthermore, when all regions are combined, six of nine life habits trends are consistent with escalation and statistically significant. When the European data are excluded, only free-lying occurrences are consistent with escalation and statistically significant. This suggests that patterns in Europe drive the perceived global signal of escalation, and this resonates with previous calls that global data be dissected to lower geographic scales. Based on these results, it is plausible that escalation drove macroevolutionary patterns during Jurassic only in the western Tethyan realm.

Whereas Chapter 2 focused on testing for escalation among regions, Chapter 3 focused on the environmental aspect of the escalation hypothesis. Using field data collected from the Middle Jurassic Carmel Formation of east-central Utah, proportions of occurrences and abundance of ecological life habit groups were compared from the Bajocian to Bathonian. Because the Carmel Formation was deposited in the Sundance Seaway, which was prone to poor environmental conditions thought to preclude escalation, it was expected that evidence of escalation would be weak or lacking. These local proportions were then compared with European regional data from the Paleobiology Database to determine if the Utah proportions suggested weaker escalation relative to a region with escalation. In Utah, there is no evidence of escalation from the Bajocian to Bathonian with the exception of mobile taxa. European data show strong evidence of escalation. The results of this study suggest that environmental conditions play a crucial role in promoting escalation, and support Vermeij's (2004, 2008) argument that

environmental conditions that include warm, well-oxygenated, productive conditions are required to promote and sustain escalation.

Environmental conditions played a crucial role in determining whether evidence of escalation would be observed at the regional scale and in the Carmel Formation of Utah. Understanding the role of environmental conditions on escalation, Chapter 4 tests if the strength of escalation reflects an inferred environmental gradient in the Sundance Seaway. Using the dataset collected for Chapter 3, this study compared temporal change in life habit group proportions from the Bajocian to Bathonian in the Carmel Formation with a dataset collected in Wyoming and southern Montana (Danise and Holland 2017). Taxonomic richness increases south to north and it has been inferred that temperatures and salinity decrease to the north (Stanley 2010; Danise and Holland 2017). Changes in proportions of occurrences and abundances from the Bajocian to Bathonian in the northern dataset of Wyoming failed to show evidence of escalation. Additionally, overall evidence of escalation is weaker in the northern dataset than in the southern Utah dataset. The results were unexpected, as escalation did not parallel the inferred taxonomic and environmental gradients. The results, however, could also be explained by changes in substrate type. Nonetheless, the results of this chapter are consistent with the results of the first chapter that the Jurassic of North America does not show evidence of escalation.

Overall, the results of this dissertation demonstrate that there is some evidence of escalation during the Jurassic, and it is plausible that it played a role on macroevolutionary patterns, in at least the western Tethyan realm. Additionally, these results support the argument that evidence of escalation is limited to particular regions that experienced the right environmental conditions. These results contribute to the long-

standing debate behind the driver of Phanerozoic macroevolutionary patterns by demonstrating that at least in the western Tethys realm during the Jurassic, both biotic and abiotic factors synergistically drive macroevolutionary patterns. It is also possible that both biotic and abiotic factors drove macroevolutionary patterns at other times and regions as well. Furthermore, these findings suggest that abiotic factors played a bigger role on the structure of benthic invertebrate communities in the Sundance Seaway.

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APPENDIX A

R CODE, DATA, AND SUPPLEMENTARY MATERIAL FOR CHAPTER 2

Part 1: R Code

R code for all statistical analysis conducted, including functions, and scripts that run the commands. All code and data can be downloaded from the Dryad Digital Repository:

<http://dx.doi.org/10.5061/dryad.ds4gd>

R Function for calculating confidence intervals based on the method by Raup (1991). Transliterated for this project by Dr. Steven Holland.

```
percent.confint <- function(percentObserved, sampleSize,
  confidenceLevel=95) {
  # percentObserved should be between 0 and 100, not 0.0 and 1.0
  # sampleSize should be a positive integer
  # confidenceLevel should be positive and greater than 1,
  #   like 95, 99, or 99.9, not 0.95 or 0.99
  # Returns the upper and lower confidence limits as a two-element
  # vector

  # Return NaNs for input errors
  if (is.nan(percentObserved) || is.infinite(percentObserved) ||
    percentObserved < 0 || percentObserved > 100) {
    return(c(0/0, 0/0))
  } else if (sampleSize < 1) {
    return(c(0/0, 0/0))
  } else if (confidenceLevel <= 0 || confidenceLevel >= 100) {
    return(c(0/0, 0/0))
  }

  # Check for edge cases on percent observed
  # These are needed to avoid attempting log(0) when taking log(p)
  # or log(q) below
  if (percentObserved == 100) {
    return(c(100, 100))
  } else if (percentObserved == 0) {
    return(c(0,0))
  }

  AFlag <- 0
  BFlag <- 0
```

```

lowerLevel <- 0
upperLevel <- 0
probability <- 0
totalProbability <- 0
lowerProbability <- 0
higherProbability <- 0
lastLow <- 0
lastHigh <- 0
lastProbability <- 0
kLow <- 0
kHigh <- 0
probabilitySum <- 0

logFactorial <- vector(mode="numeric", length=sampleSize+1)
logFactorial[1] <- 0
for (i in 2:sampleSize+1) {
  logFactorial[i] <- logFactorial[i-1] + log(i-1)
}

p <- percentObserved/100
q <- 1-p

lowerLevel <- (100-confidenceLevel)/100/2
upperLevel <- 1-lowerLevel

for (k in 0:sampleSize) {
  probability <- logFactorial[sampleSize+1]-logFactorial[k+1]-
logFactorial[sampleSize-k+1]+k*log(p)+(sampleSize-k)*log(q)

  if (probability < -50 || probability > 50) {# checking for
overload
    probability <- 0
  } else {
    probability <- exp(probability)
  }

  totalProbability <- totalProbability + probability

  if (totalProbability >= lowerLevel) {
    AFlag <- AFlag + 1
  }

  if (totalProbability >= lowerLevel && AFlag == 1) {
    lowerProbability <- totalProbability
    kLow <- k
    lastLow <- lastProbability
  }

  if (totalProbability >= upperLevel) {
    BFlag <- BFlag + 1
  }

  if (totalProbability >= upperLevel && BFlag == 1) {

```

```

        higherProbability <- totalProbability
        kHigh <- k
        lastHigh <- lastProbability
    }

    lastProbability <- totalProbability
    probabilitySum = probabilitySum + probability
}

lowerLimit <- 0.5 + kLow + (lowerLevel-
lowerProbability)/(lowerProbability-lastLow)
upperLimit <- 0.5 + kHigh + (upperLevel-
higherProbability)/(higherProbability-lastHigh)

# lower confidence limit
if (lowerLimit/sampleSize > 0) {
    lowerLimit <- round(100*lowerLimit/sampleSize, 1)
} else {
    lowerLimit <- 0
}

# upper confidence limit
if (upperLimit/sampleSize < 1) {
    upperLimit <- round(100*upperLimit/sampleSize, 1)
} else {
    upperLimit <- 100
}

limits <- c(lowerLimit, upperLimit)
return(limits)
}

```

Script to assign geographic regions to the occurrence datafile downloaded from the Paleobiology Database.

```

##Point-in-polygons to designate regional clusters in global
Jurassic PBDB occurrence data

#Library with point-in-polygon function
library(SDMTools)

#Object with all occurrences
occurrences <- read.csv('occurrences.csv', header=TRUE,
stringsAsFactors=FALSE)

#Add new column to hold geographic cluster designation
occurrences[, "geo_cluster"] <- rep(0, nrow(occurrences))

#Plot of global occurrences

```

```

plot(occurrences[,1:2], main='Global Occurrences',
xlab='Paleolongitude', ylab='Paleolatitude', las=1, type='n',
axes=FALSE)
axis(1, at=seq(-180, 180, by=10), labels=seq(-180, 180, by=10))
axis(2, at=seq(-180, 180, by=10), labels=seq(-180, 180, by=10),
las=1)
points(occurrences[,1:2])

#Read polygon coordinates that were created manually from the
plot of global occurrences by using a screen shot of the plot in
illustrator and then extracted using GraphClick.
poly.coords <- read.csv("PolygonCoordinates.csv", header=TRUE)

#Extract coordinates vector for each polygon
NorthAmericapolypts <- poly.coords[poly.coords$Polygon=="Polygon
1", 1:2]
Europepolypts <- poly.coords[poly.coords$Polygon=="Polygon 2",
1:2]
SouthAmericapolypts <- poly.coords[poly.coords$Polygon=="Polygon
4", 1:2]
MiddleEastpolypts <- poly.coords[poly.coords$Polygon=="Polygon
5", 1:2]
NewZealandpolypts <- poly.coords[poly.coords$Polygon=="Polygon
6", 1:2]

#Plot polygons
polygon(NorthAmericapolypts, lwd = 2, border = "red")
text(-40, 80, labels = "North America", col = "red")
polygon(Europepolypts, lwd = 2, border = "blue")
text(-5, 5, labels = "Europe", col = "blue")
polygon(SouthAmericapolypts, lwd = 2, border = "green")
text(-70, -50, labels = "South America", col = "green")
polygon(MiddleEastpolypts, lwd = 2, border = "orange")
text(80, -20, labels = "Middle East", col = "orange")
polygon(NewZealandpolypts, lwd = 2, border = "light blue")
text(20, -80, labels = "New Zealand", col = "light blue")

#Create objects with the occurrences that occur in each polygon
NorthAmericapolyoccs <- pnt.in.poly(occurrences[,1:2],
NorthAmericapolypts)
Europepolyoccs <- pnt.in.poly(occurrences[,1:2], Europepolypts)
SouthAmericapolyoccs <- pnt.in.poly(occurrences[,1:2],
SouthAmericapolypts)
MiddleEastpolyoccs <- pnt.in.poly(occurrences[,1:2],
MiddleEastpolypts)
NewZealandpolyoccs <- pnt.in.poly(occurrences[,1:2],
NewZealandpolypts)

#Add list of points for each polygon to the geo_cluster vector in
the occurrences dataframe by modern continent/country: North
America, Europe, South America, Middle East, New Zealand,
Unassigned

```

```

#First, get rid of magic number by naming the column number with
the geoclust vector
geoClustercolumn <- 41

occurrences[NorthAmericapolyoccs$pip==1, geoClustercolumn] <-
"North America"
occurrences[Europepolyoccs$pip==1, geoClustercolumn] <- "Europe"
occurrences[SouthAmericapolyoccs$pip==1, geoClustercolumn] <-
"South America"
occurrences[MiddleEastpolyoccs$pip==1, geoClustercolumn] <-
"Middle East"
occurrences[NewZealandpolyoccs$pip==1, geoClustercolumn] <- "New
Zealand"
occurrences[occurrences$geo_cluster==0, geoClustercolumn] <-
"Unassigned"

#Make tables showing number of occurrences in each cluster for
each time interval
#By stage
with(occurrences, table(stage, geo_cluster))

#By PBDB 10my bin
with(occurrences, table(pbdb_bin, geo_cluster))

#Write new csv file that includes column with cluster
designations
write.table(occurrences, "clusteredOccurrences.csv",
row.names=FALSE, sep=",")

```

R function that calculates the proportion of ecological trait groups by geographic region with 95% confidence intervals.

```
percentEcolTrait <- function(x, traitCategory, desiredTraits,
  desiredStages = "allStages", desiredEnvts = "allEnvts",
  desiredGeoclusters = "allGeoclusters") {
  #Trait categories include life habit, diet, substrate stability,
  and motility
  #Environments are based on the categories used by Bottjer and
  Jablonski, 1988 (Palaios):
  # nearshore, inner shelf, middle shelf, outer shelf, slope and
  deep basin

  #If all stages, environments, and geoclusters are desired
  respectively:
  if (desiredStages[1] == "allStages") {
    desiredStages = unique(x$stage)
  }
  if (desiredEnvts[1] == "allEnvts") {
    desiredEnvts = unique(x$environment)
  }
  if (desiredGeoclusters[1] == "allGeoclusters") {
    desiredGeoclusters = unique(x$geo_cluster)
  }

  xS <- x[x$stage %in% desiredStages, ] #Assign desired stage
  to vector
  xSE <- xS[xS$environment %in% desiredEnvts, ] #Assign desired
  environments to stages vector
  xSEG <- xSE[xSE$geo_cluster %in% desiredGeoclusters, ] #Assign
  desired regional clusters to vector with stages and environments

  traitColumn <- which(colnames(x) %in% traitCategory)
  if (length(traitColumn) == 0) {
    errorMessage <- paste("Possible spelling error: column name
  '", traitCategory, "' was not found", sep="")
    warning(errorMessage)
  }
  xSEGL <- xSEG[xSEG[, traitColumn] %in% desiredTraits, ] #Assign
  ecological stage to vector

  matchingOccurrences <- nrow(xSEGL)
  totalOccurrences <- nrow(xSEG)

  percent <- rep(0, 3)
  percent[2] <- round(matchingOccurrences / totalOccurrences *
  100, 1)
  conf.int <- percent.confint(percent[2], totalOccurrences)
  percent[1] <- conf.int[1]
  percent[3] <- conf.int[2]
  percent
}
```

R command script that calculates the proportions of ecological group occurrences by region by Jurassic stage using data from the Paleobiology Database. This script also plots all the regional figures (Figs. 2.2–2.4) and performs all statistical tests for those regions (Table 2.3).

```
##Loop, plots, and Spearman's tests of ecological percentages of
PBDB Jurassic regional occurrences

#Read percent confidence interval function
source("percentConfidenceInterval.R")

#Read percent ecology function to calculate percentages with
confidence intervals
source("percentEcolTrait.R")

#Read dataset
occurrences2 <- read.csv('ClusteredOccurrences.csv', header=TRUE,
stringsAsFactors=FALSE)

#Create objects to define dimensions of matrices below
stagecolumn <- 4
JurassicStages <-
sort(unique(occurrences2[occurrences2$stage!="0", stagecolumn]))
geoClusters <- sort(unique(occurrences2$geo_cluster))

#Create empty matrices that will be used to fill estimated
percentages calculated by running loop
sinfaunalTableE <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))
dinfraunalTableE <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))
epifaunalTableE <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))
cementedTableE <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))
freelivingTableE <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))
pedunculateTableE <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))
mobileTableE <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))
limitedmobileTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
```

```

sessileTableE <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))

#Create empty matrices that will be used to fill lower confidence
limit percentages calculated by running loop
sinfaunalTableLCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))
dinfraunalTableLCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))
epifaunalTableLCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))
cementedTableLCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))
freelivingTableLCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))
pedunculateTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
mobileTableLCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))
limitedmobileTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
sessileTableLCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))

#Create empty matrices that will be used to fill upper
confidence limit percentages calculated by running loop
sinfaunalTableUCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))
dinfraunalTableUCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))
epifaunalTableUCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))
cementedTableUCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))
freelivingTableUCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))

```



```

pedunculateTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
mobileTableUCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))
limitedmobileTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
sessileTableUCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))

#Loop to calculate percentage of each ecological trait by cluster
for each stage
for (time in 1:length(JurassicStages)) {
  for (geo in 1:length(geoClusters)) {
    sinfaunal <- percentEcolTrait(occurrences2,
"life_habit", "shallow infaunal",
desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
    sinfaunalTableE[time, geo] <- sinfaunal[2]
    sinfaunalTableLCL[time, geo] <- sinfaunal[1]
    sinfaunalTableUCL[time, geo] <- sinfaunal[3]

    dinfaunal <- percentEcolTrait(occurrences2,
"life_habit", "deep infaunal",
desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
    dinfaunalTableE[time, geo] <- dinfaunal[2]
    dinfaunalTableLCL[time, geo] <- dinfaunal[1]
    dinfaunalTableUCL[time, geo] <- dinfaunal[3]

    epifaunal <- percentEcolTrait(occurrences2, "life_habit",
"epifaunal", desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
    epifaunalTableE[time, geo] <- epifaunal[2]
    epifaunalTableLCL[time, geo] <- epifaunal[1]
    epifaunalTableUCL[time, geo] <- epifaunal[3]

    cemented <- percentEcolTrait(occurrences2, "stability",
"cemented", desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
    cementedTableE[time, geo] <- cemented[2]
    cementedTableLCL[time, geo] <- cemented[1]
    cementedTableUCL[time, geo] <- cemented[3]

    freelifving <- percentEcolTrait(occurrences2, "stability",
"free-living", desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
    freelifvingTableE[time, geo] <- freelifving[2]
    freelifvingTableLCL[time, geo] <- freelifving[1]

```

```

freelivingTableUCL[time, geo] <- freeliving[3]

pedunculate <- percentEcolTrait(occurrences2, "stability",
"pedunculate", desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
pedunculateTableE[time, geo] <- pedunculate[2]
pedunculateTableLCL[time, geo] <- pedunculate[1]
pedunculateTableUCL[time, geo] <- pedunculate[3]

mobile <- percentEcolTrait(occurrences2, "motility",
"mobile", desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
mobileTableE[time, geo] <- mobile[2]
mobileTableLCL[time, geo] <- mobile[1]
mobileTableUCL[time, geo] <- mobile[3]

limitedmobile <- percentEcolTrait(occurrences2, "motility",
"limited mobile", desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
limitedmobileTableE[time, geo] <- limitedmobile[2]
limitedmobileTableLCL[time, geo] <- limitedmobile[1]
limitedmobileTableUCL[time, geo] <- limitedmobile[3]

sessile <- percentEcolTrait(occurrences2, "motility",
"sessile", desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
sessileTableE[time, geo] <- sessile[2]
sessileTableLCL[time, geo] <- sessile[1]
sessileTableUCL[time, geo] <- sessile[3]

}
}
-----
-----
-----
-----
##Plots

#Create vector of Jurassic stage boundary ages (Myr) based on the
2015 ICS Chronostratigraphy Chart
stageBoundaryAges <- c(201.3, 199.3, 190.8, 182.7, 174.1, 170.3,
168.3, 166.1, 163.5, 157.3, 152.1, 145.0)

#Duration of each stage (Myr) — Hettangian: 2.0, Sinemurian:
8.5, Pliensbachian: 8.1, Toarcian: 8.6, Aalenian: 3.8, Bajocian:
2.0, Bathonian: 2.2, Callovian: 2.6, Oxfordian: 6.2, Kimmeridian:
5.2, Tithonian: 7.1

#Calculate midpoint of each stage to include in plots
midpointAges <- stageBoundaryAges[-length(stageBoundaryAges)] +
diff(stageBoundaryAges)/2
midpointAges <- sort(midpointAges)

```

```

##Plots of percentages
#Plots of life habit
dev.new(width=4, length=7)
par(mfrow=(c(5,1)), mai=c(0.25, 0.35, 0.075, 0.25))

plot(midpointAges, sinfaunalTableE[,1], main='Europe', xlab='',
ylab='', ylim=range(0:100), las=1, type='n', axes=FALSE)
axis(1, labels=FALSE, lwd.ticks=0)
axis(2, at=seq(0, 100, by=20), las=1)
points(midpointAges, sinfaunalTableE[,1], type="o", pch=16,
lty=1, col="blue")
segments(midpointAges, sinfaunalTableLCL[, 1], midpointAges,
sinfaunalTableUCL[, 1], col="blue")
points(midpointAges, dinfaunalTableE[,1], type="o", pch=16,
lty=2, col="blue")
segments(midpointAges, dinfaunalTableLCL[, 1], midpointAges,
dinfaunalTableUCL[, 1], col="blue")
points(midpointAges, epifaunalTableE[,1], type="o", pch=16,
lty=3, col="red")
segments(midpointAges, epifaunalTableLCL[, 1], midpointAges,
epifaunalTableUCL[, 1], col="red")
legend("top", c("epifaunal", "shallow infaunal", "deep
infaunal"), bty="n", lty=c(3, 1, 2), col=c("red", "blue",
"blue"), horiz=TRUE, x.intersp=0.5)

plot(midpointAges, sinfaunalTableE[,2], main='Middle East',
xlab='', ylab='', ylim=range(0:100), las=1, type='n', axes=FALSE)
axis(1, labels=FALSE, lwd.ticks=0)
axis(2, at=seq(0, 100, by=20), las=1)
points(midpointAges, sinfaunalTableE[,2], type="o", pch=16,
lty=1, col="blue")
segments(midpointAges, sinfaunalTableLCL[, 2], midpointAges,
sinfaunalTableUCL[, 2], col="blue")
points(midpointAges, dinfaunalTableE[,2], type="o", pch=16,
lty=2, col="blue")
segments(midpointAges, dinfaunalTableLCL[, 2], midpointAges,
dinfaunalTableUCL[, 2], col="blue")
points(midpointAges, epifaunalTableE[,2], type="o", pch=16,
lty=3, col="red")
segments(midpointAges, epifaunalTableLCL[, 2], midpointAges,
epifaunalTableUCL[, 2], col="red")

plot(midpointAges, sinfaunalTableE[,3], main='New Zealand',
xlab='', ylab='', ylim=range(0:100), las=1, type='n', axes=FALSE)
axis(1, labels=FALSE, lwd.ticks=0)
axis(2, at=seq(0, 100, by=20), las=1)
points(midpointAges, sinfaunalTableE[,3], type="o", pch=16,
lty=1, col="blue")
segments(midpointAges, sinfaunalTableLCL[, 3], midpointAges,
sinfaunalTableUCL[, 3], col="blue")
points(midpointAges, dinfaunalTableE[,3], type="o", pch=16,
lty=2, col="blue")

```

```

segments(midpointAges, dinfaunalTableLCL[, 3], midpointAges,
dinfaunalTableUCL[, 3], col="blue")
points(midpointAges, epifaunalTableE[,3], type="o", pch=16,
lty=3, col="red")
segments(midpointAges, epifaunalTableLCL[, 3], midpointAges,
epifaunalTableUCL[, 3], col="red")

plot(midpointAges, sinfaunalTableE[,4], main='North America',
xlab='', ylab='', ylim=range(0:100), las=1, type='n', axes=FALSE)
axis(1, labels=FALSE, lwd.ticks=0)
axis(2, at=seq(0, 100, by=20), las=1)
points(midpointAges, sinfaunalTableE[,4], type="o", pch=16,
lty=1, col="blue")
segments(midpointAges, sinfaunalTableLCL[, 4], midpointAges,
sinfaunalTableUCL[, 4], col="blue")
points(midpointAges, dinfaunalTableE[,4], type="o", pch=16,
lty=2, col="blue")
segments(midpointAges, dinfaunalTableLCL[, 4], midpointAges,
dinfaunalTableUCL[, 4], col="blue")
points(midpointAges, epifaunalTableE[,4], type="o", pch=16,
lty=3, col="red")
segments(midpointAges, epifaunalTableLCL[, 4], midpointAges,
epifaunalTableUCL[, 4], col="red")

plot(midpointAges, sinfaunalTableE[,5], main='South America',
xlab='', ylab='', ylim=range(0:100), las=1, type='n', axes=FALSE)
axis(1, at=midpointAges, labels=c("He", "Si", "Pl", "To", "Aa",
"Baj", "Bat", "Ca", "Ox", "Ki", "Ti"), xlab='Jurassic Stages')
axis(2, at=seq(0, 100, by=20), las=1)
points(midpointAges, sinfaunalTableE[,5], type="o", pch=16,
lty=1, col="blue")
segments(midpointAges, sinfaunalTableLCL[, 5], midpointAges,
sinfaunalTableUCL[, 5], col="blue")
points(midpointAges, dinfaunalTableE[,5], type="o", pch=16,
lty=2, col="blue")
segments(midpointAges, dinfaunalTableLCL[, 5], midpointAges,
dinfaunalTableUCL[, 5], col="blue")
points(midpointAges, epifaunalTableE[,5], type="o", pch=16,
lty=3, col="red")
segments(midpointAges, epifaunalTableLCL[, 5], midpointAges,
epifaunalTableUCL[, 5], col="red")

##Substrate Stability (Epifaunal life modes) plots
dev.new(width=4, length=7)
par(mfrow=(c(5,1)), mai=c(0.25, 0.35, 0.075, 0.25))

plot(midpointAges, pedunculateTableE[,1], main='Europe', xlab='',
ylab='', ylim=range(0:100), las=1, type='n', axes=FALSE)
axis(1, labels=FALSE, lwd.ticks=0)
axis(2, at=seq(0, 100, by=20), las=1)
points(midpointAges, pedunculateTableE[,1], type="o", pch=16,
lty=1, col="red")

```

```

segments(midpointAges, pedunculateTableLCL[, 1], midpointAges,
pedunculateTableUCL[, 1], col="red")
points(midpointAges, cementedTableE[, 1], type="o", pch=16, lty=2,
col="blue")
segments(midpointAges, cementedTableLCL[, 1], midpointAges,
cementedTableUCL[, 1], col="blue")
points(midpointAges, freelivingTableE[, 1], type="o", pch=16,
lty=3, col="red")
segments(midpointAges, freelivingTableLCL[, 1], midpointAges,
freelivingTableUCL[, 1], col="red")
legend("top", c("pedunculate", "cemented", "free-living"),
bty="n", lty=c(1, 2, 3), col=c("red", "blue", "red"),
horiz=TRUE, x.intersp=0.5)

plot(midpointAges, pedunculateTableE[, 2], main='Middle East',
xlab='', ylab='', ylim=range(0:100), las=1, type='n', axes=FALSE)
axis(1, labels=FALSE, lwd.ticks=0)
axis(2, at=seq(0, 100, by=20), las=1)
points(midpointAges, pedunculateTableE[, 2], type="o", pch=16,
lty=1, col="red")
segments(midpointAges, pedunculateTableLCL[, 2], midpointAges,
pedunculateTableUCL[, 2], col="red")
points(midpointAges, cementedTableE[, 2], type="o", pch=16, lty=2,
col="blue")
segments(midpointAges, cementedTableLCL[, 2], midpointAges,
cementedTableUCL[, 2], col="blue")
points(midpointAges, freelivingTableE[, 2], type="o", pch=16,
lty=3, col="red")
segments(midpointAges, freelivingTableLCL[, 2], midpointAges,
freelivingTableUCL[, 2], col="red")

plot(midpointAges, pedunculateTableE[, 3], main='New Zealand',
xlab='', ylab='', ylim=range(0:100), las=1, type='n', axes=FALSE)
axis(1, labels=FALSE, lwd.ticks=0)
axis(2, at=seq(0, 100, by=20), las=1)
points(midpointAges, pedunculateTableE[, 3], type="o", pch=16,
lty=1, col="red")
segments(midpointAges, pedunculateTableLCL[, 3], midpointAges,
pedunculateTableUCL[, 3], col="red")
points(midpointAges, cementedTableE[, 3], type="o", pch=16, lty=2,
col="blue")
segments(midpointAges, cementedTableLCL[, 3], midpointAges,
cementedTableUCL[, 3], col="blue")
points(midpointAges, freelivingTableE[, 3], type="o", pch=16,
lty=3, col="red")
segments(midpointAges, freelivingTableLCL[, 3], midpointAges,
freelivingTableUCL[, 3], col="red")

plot(midpointAges, pedunculateTableE[, 4], main='North America',
xlab='', ylab='', ylim=range(0:100), las=1, type='n', axes=FALSE)
axis(1, labels=FALSE, lwd.ticks=0)
axis(2, at=seq(0, 100, by=20), las=1)

```

```

points(midpointAges, pedunculateTableE[,4], type="o", pch=16,
lty=1, col="red")
segments(midpointAges, pedunculateTableLCL[ , 4], midpointAges,
pedunculateTableUCL[ , 4], col="red")
points(midpointAges, cementedTableE[,4], type="o", pch=16, lty=2,
col="blue")
segments(midpointAges, cementedTableLCL[ , 4], midpointAges,
cementedTableUCL[ , 4], col="blue")
points(midpointAges, freelivingTableE[,4], type="o", pch=16,
lty=3, col="red")
segments(midpointAges, freelivingTableLCL[ , 4], midpointAges,
freelivingTableUCL[ , 4], col="red")

plot(midpointAges, pedunculateTableE[,5], main='South America',
xlab='', ylab='', ylim=range(0:100), las=1, type='n', axes=FALSE)
axis(1, at=midpointAges, labels=c("He", "Si", "Pl", "To", "Aa",
"Baj", "Bat", "Ca", "Ox", "Ki", "Ti"), xlab='Jurassic Stage')
axis(2, at=seq(0, 100, by=20), las=1)
points(midpointAges, pedunculateTableE[,5], type="o", pch=16,
lty=1, col="red")
segments(midpointAges, pedunculateTableLCL[ , 5], midpointAges,
pedunculateTableUCL[ , 5], col="red")
points(midpointAges, cementedTableE[,5], type="o", pch=16, lty=2,
col="blue")
segments(midpointAges, cementedTableLCL[ , 5], midpointAges,
cementedTableUCL[ , 5], col="blue")
points(midpointAges, freelivingTableE[,5], type="o", pch=16,
lty=3, col="red")
segments(midpointAges, freelivingTableLCL[ , 5], midpointAges,
freelivingTableUCL[ , 5], col="red")

##Plots of Motility
dev.new(width=4, length=7)
par(mfrow=(c(5,1)), mai=c(0.25, 0.35, 0.075, 0.25))

plot(midpointAges, mobileTableE[,1], main='Europe', xlab='',
ylab='', ylim=range(0:100), las=1, type='n', axes=FALSE)
axis(1, labels=FALSE, lwd.ticks=0)
axis(2, at=seq(0, 100, by=20), las=1)
points(midpointAges, mobileTableE[,1], type="o", pch=16, lty=1,
col="blue")
segments(midpointAges, mobileTableLCL[ , 1], midpointAges,
mobileTableUCL[ , 1], col="blue")
points(midpointAges, limitedmobileTableE[,1], type="o", pch=16,
lty=2, col="blue")
segments(midpointAges, limitedmobileTableLCL[ , 1], midpointAges,
limitedmobileTableUCL[ , 1], col="blue")
points(midpointAges, sessileTableE[,1], type="o", pch=16, lty=3,
col="red")
segments(midpointAges, sessileTableLCL[ , 1], midpointAges,
sessileTableUCL[ , 1], col="red")

```

```

legend("top", c("sessile", "limited mobile", "mobile"), bty="n",
lty=c(3, 2, 1), col=c("red", "blue", "blue"), horiz=TRUE,
x.intersp=0.5)

plot(midpointAges, mobileTableE[,2], main='Middle East', xlab='',
ylab='', ylim=range(0:100), las=1, type='n', axes=FALSE)
axis(1, labels=FALSE, lwd.ticks=0)
axis(2, at=seq(0, 100, by=20), las=1)
points(midpointAges, mobileTableE[,2], type="o", pch=16, lty=1,
col="blue")
segments(midpointAges, mobileTableLCL[, 2], midpointAges,
mobileTableUCL[, 2], col="blue")
points(midpointAges, limitedmobileTableE[,2], type="o", pch=16,
lty=2, col="blue")
segments(midpointAges, limitedmobileTableLCL[, 2], midpointAges,
limitedmobileTableUCL[, 2], col="blue")
points(midpointAges, sessileTableE[,2], type="o", pch=16, lty=3,
col="red")
segments(midpointAges, sessileTableLCL[, 2], midpointAges,
sessileTableUCL[, 2], col="red")

plot(midpointAges, mobileTableE[,3], main='New Zealand', xlab='',
ylab='', ylim=range(0:100), las=1, type='n', axes=FALSE)
axis(1, labels=FALSE, lwd.ticks=0)
axis(2, at=seq(0, 100, by=20), las=1)
points(midpointAges, mobileTableE[,3], type="o", pch=16, lty=1,
col="blue")
segments(midpointAges, mobileTableLCL[, 3], midpointAges,
mobileTableUCL[, 3], col="blue")
points(midpointAges, limitedmobileTableE[,3], type="o", pch=16,
lty=2, col="blue")
segments(midpointAges, limitedmobileTableLCL[, 3], midpointAges,
limitedmobileTableUCL[, 3], col="blue")
points(midpointAges, sessileTableE[,3], type="o", pch=16, lty=3,
col="red")
segments(midpointAges, sessileTableLCL[, 3], midpointAges,
sessileTableUCL[, 3], col="red")

plot(midpointAges, mobileTableE[,4], main='North America',
xlab='', ylab='', ylim=range(0:100), las=1, type='n', axes=FALSE)
axis(1, labels=FALSE, lwd.ticks=0)
axis(2, at=seq(0, 100, by=20), las=1)
points(midpointAges, mobileTableE[,4], type="o", pch=16, lty=1,
col="blue")
segments(midpointAges, mobileTableLCL[, 4], midpointAges,
mobileTableUCL[, 4], col="blue")
points(midpointAges, limitedmobileTableE[,4], type="o", pch=16,
lty=2, col="blue")
segments(midpointAges, limitedmobileTableLCL[, 4], midpointAges,
limitedmobileTableUCL[, 4], col="blue")
points(midpointAges, sessileTableE[,4], type="o", pch=16, lty=3,
col="red")

```

```

segments(midpointAges, sessileTableLCL[ , 4], midpointAges,
sessileTableUCL[ , 4], col="red")

plot(midpointAges, mobileTableE[,5], main='South America',
xlab='', ylab='', ylim=range(0:100), las=1, type='n', axes=FALSE)
axis(1, at=midpointAges, labels=c("He", "Si", "Pl", "To", "Aa",
"Baj", "Bat", "Ca", "Ox", "Ki", "Ti"), xlab='Jurassic Stage')
axis(2, at=seq(0, 100, by=20), las=1)
points(midpointAges, mobileTableE[,5], type="o", pch=16, lty=1,
col="blue")
segments(midpointAges, mobileTableLCL[ , 5], midpointAges,
mobileTableUCL[ , 5], col="blue")
points(midpointAges, limitedmobileTableE[,5], type="o", pch=16,
lty=2, col="blue")
segments(midpointAges, limitedmobileTableLCL[ , 5], midpointAges,
limitedmobileTableUCL[ , 5], col="blue")
points(midpointAges, sessileTableE[,5], type="o", pch=16, lty=3,
col="red")
segments(midpointAges, sessileTableLCL[ , 5], midpointAges,
sessileTableUCL[ , 5], col="red")

```

```

-----
-----
-----
-----
##Spearman's rank correlation tests of ecological metrics for
each region by Jurassic stages

```

```

#Spearman's rank correlation tests for Europe Cluster
cor.test(midpointAges, sinfaunalTableE[,1], method='spearman')
cor.test(midpointAges, dinfaunalTableE[,1], method='spearman')
cor.test(midpointAges, epifaunalTableE[,1], method='spearman')
cor.test(midpointAges, freelivingTableE[,1], method='spearman')
cor.test(midpointAges, cementedTableE[,1], method='spearman')
cor.test(midpointAges, pedunculateTableE[,1], method='spearman')
cor.test(midpointAges, sessileTableE[,1], method='spearman')
cor.test(midpointAges, limitedmobileTableE[,1],
method='spearman')
cor.test(midpointAges, mobileTableE[,1], method='spearman')

```

```

#Spearman's rank correlation tests for Middle East Cluster
cor.test(midpointAges, sinfaunalTableE[,2], method='spearman')
cor.test(midpointAges, dinfaunalTableE[,2], method='spearman')
cor.test(midpointAges, epifaunalTableE[,2], method='spearman')
cor.test(midpointAges, freelivingTableE[,2], method='spearman')
cor.test(midpointAges, cementedTableE[,2], method='spearman')
cor.test(midpointAges, pedunculateTableE[,2], method='spearman')
cor.test(midpointAges, sessileTableE[,2], method='spearman')
cor.test(midpointAges, limitedmobileTableE[,2],
method='spearman')
cor.test(midpointAges, mobileTableE[,2], method='spearman')

```

```

#Spearman's rank correlation tests for New Zealand Cluster

```



```

cor.test(midpointAges, sinfaunalTableE[,3], method='spearman')
cor.test(midpointAges, dinfaunalTableE[,3], method='spearman')
cor.test(midpointAges, epifaunalTableE[,3], method='spearman')
cor.test(midpointAges, freelivingTableE[,3], method='spearman')
cor.test(midpointAges, cementedTableE[,3], method='spearman')
cor.test(midpointAges, pedunculateTableE[,3], method='spearman')
cor.test(midpointAges, sessileTableE[,3], method='spearman')
cor.test(midpointAges, limitedmobileTableE[,3],
method='spearman')
cor.test(midpointAges, mobileTableE[,3], method='spearman')

#Spearman's rank correlation tests for North America Cluster
cor.test(midpointAges, sinfaunalTableE[,4], method='spearman')
cor.test(midpointAges, dinfaunalTableE[,4], method='spearman')
cor.test(midpointAges, epifaunalTableE[,4], method='spearman')
cor.test(midpointAges, freelivingTableE[,4], method='spearman')
cor.test(midpointAges, cementedTableE[,4], method='spearman')
cor.test(midpointAges, pedunculateTableE[,4], method='spearman')
cor.test(midpointAges, sessileTableE[,4], method='spearman')
cor.test(midpointAges, limitedmobileTableE[,4],
method='spearman')
cor.test(midpointAges, mobileTableE[,4], method='spearman')

#Spearman's rank correlation tests for South America Cluster
cor.test(midpointAges, sinfaunalTableE[,5], method='spearman')
cor.test(midpointAges, dinfaunalTableE[,5], method='spearman')
cor.test(midpointAges, epifaunalTableE[,5], method='spearman')
cor.test(midpointAges, freelivingTableE[,5], method='spearman')
cor.test(midpointAges, cementedTableE[,5], method='spearman')
cor.test(midpointAges, pedunculateTableE[,5], method='spearman')
cor.test(midpointAges, sessileTableE[,5], method='spearman')
cor.test(midpointAges, limitedmobileTableE[,5],
method='spearman')
cor.test(midpointAges, mobileTableE[,5], method='spearman')

```

R command script that calculates the proportions of ecological group occurrences by European environments by Jurassic stage using data from the Paleobiology Database. This script also plots all the environmental figures (Figs. 2.5–2.7) and performs all statistical tests for those environments (Table 2.4).

Environments from the Paleobiology Database occurrences used were consolidated into 5 environmental categories after Bottjer and Jablonski (1988): 1) nearshore, 2) inner shelf, 3) middle shelf, 4) outer shelf, and 5) slope and deep basin.

- 1) Nearshore: coastal indeterminate, delta plain, estuary/bay, foreshore, lagoonal, lagoonal/restricted shallow subtidal, marginal marine indeterminate, paralic indeterminate, peritidal, and sand shoal.
- 2) Inner shelf: open shallow subtidal, shallow subtidal indeterminate, and shoreface
- 3) Middle shelf: deep subtidal indeterminate, deep subtidal ramp, deep subtidal shelf, delta front, transition zone/lower shoreface.
- 4) Outer shelf: deep-water indeterminate, offshore, offshore ramp, offshore shelf, and prodelta.
- 5) Slope and deep basin: basinal (carbonate), basinal (siliceous), basinal (siliciclastic), slope, and submarine fan.

```
##Loop, plots, and Spearman's tests of ecological percentages of  
occurrences by depositional environment in Europe cluster
```

```
#Read percent confidence interval function  
source("percentConfidenceInterval.R")
```

```
#Read percent ecology function to calculate percentages with  
confidence intervals  
source("percentEcolTrait.R")
```

```
#Read dataset  
occurrences2 <- read.csv('ClusteredOccurrences.csv', header=TRUE,  
stringsAsFactors=FALSE)
```

```
#Create objects to define dimensions of matrices below  
stagecolumn <- 4  
JurassicStages <-  
sort(unique(occurrences2[occurrences2$stage!="0", stagecolumn]))  
Environments <- c("nearshore", "inner shelf", "middle shelf",  
"outer shelf", "slope and deep basin" )
```

```
#Create empty matrices that will be used to fill estimated  
percentages calculated by running loop  
EursinfaunalTableE <- matrix(data=0, nrow=length(JurassicStages),  
ncol=length(Environments), dimnames=list(JurassicStages,  
Environments))  
EuridinfaunalTableE <- matrix(data=0, nrow=length(JurassicStages),  
ncol=length(Environments), dimnames=list(JurassicStages,  
Environments))
```

```

EurepifaunalTableE <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(Environments), dimnames=list(JurassicStages,
Environments))
EurcementedTableE <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(Environments), dimnames=list(JurassicStages,
Environments))
EurfreelivingTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(Environments),
dimnames=list(JurassicStages, Environments))
EurpedunculateTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(Environments),
dimnames=list(JurassicStages, Environments))
EurmobileTableE <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(Environments), dimnames=list(JurassicStages,
Environments))
EurlimitedmobileTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(Environments),
dimnames=list(JurassicStages, Environments))
EursessileTableE <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(Environments), dimnames=list(JurassicStages,
Environments))

#Create empty matrices that will be used to fill lower confidence
limit percentages calculated by running loop
EursinfaunalTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(Environments),
dimnames=list(JurassicStages, Environments))
EurinfaunalTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(Environments),
dimnames=list(JurassicStages, Environments))
EurepifaunalTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(Environments),
dimnames=list(JurassicStages, Environments))
EurcementedTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(Environments),
dimnames=list(JurassicStages, Environments))
EurfreelivingTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(Environments),
dimnames=list(JurassicStages, Environments))
EurpedunculateTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(Environments),
dimnames=list(JurassicStages, Environments))
EurmobileTableLCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(Environments), dimnames=list(JurassicStages,
Environments))
EurlimitedmobileTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(Environments),
dimnames=list(JurassicStages, Environments))
EursessileTableLCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(Environments), dimnames=list(JurassicStages,
Environments))

```

```

#Create empty matrices that will be used to fill upper
condfidence limit percentages calculated by running loop
EursinfaunalTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(Environments),
dimnames=list(JurassicStages, Environments))
EurcinafaunalTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(Environments),
dimnames=list(JurassicStages, Environments))
EurepifaunalTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(Environments),
dimnames=list(JurassicStages, Environments))
EurcementedTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(Environments),
dimnames=list(JurassicStages, Environments))
EurfreelivingTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(Environments),
dimnames=list(JurassicStages, Environments))
EurpedunculateTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(Environments),
dimnames=list(JurassicStages, Environments))
EurmobileTableUCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(Environments), dimnames=list(JurassicStages,
Environments))
EurlimitedmobileTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(Environments),
dimnames=list(JurassicStages, Environments))
EursessileTableUCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(Environments), dimnames=list(JurassicStages,
Environments))

```

```

#Loop to calculate percentage of each ecological trait for each
environment group in the Europe cluster
for (time in 1:length(JurassicStages)) {
  for (env in 1:length(Environments)) {
    Eursinfaunal <- percentEcolTrait(occurrences2,
"life_habit", "shallow infaunal",
desiredStages=JurassicStages[time],
desiredEnvts=Environments[env], "Europe")
    EursinfaunalTableE[time, env] <- Eursinfaunal[2]
    EursinfaunalTableLCL[time, env] <- Eursinfaunal[1]
    EursinfaunalTableUCL[time, env] <- Eursinfaunal[3]

    Eurcinafaunal <- percentEcolTrait(occurrences2,
"life_habit", "deep infaunal",
desiredStages=JurassicStages[time],
desiredEnvts=Environments[env], "Europe")
    EurcinafaunalTableE[time, env] <- Eurcinafaunal[2]
    EurcinafaunalTableLCL[time, env] <- Eurcinafaunal[1]
    EurcinafaunalTableUCL[time, env] <- Eurcinafaunal[3]

```

```

    Eurepifaunal <- percentEcolTrait(occurrences2,
"life_habit", "epifaunal", desiredStages=JurassicStages[time],
desiredEnvts=Environments[env], "Europe")
    EurepifaunalTableE[time, env] <- Eurepifaunal[2]
    EurepifaunalTableLCL[time, env] <- Eurepifaunal[1]
    EurepifaunalTableUCL[time, env] <- Eurepifaunal[3]

    Eurcemented <- percentEcolTrait(occurrences2, "stability",
"cemented", desiredStages=JurassicStages[time],
desiredEnvts=Environments[env], "Europe")
    EurcementedTableE[time, env] <- Eurcemented[2]
    EurcementedTableLCL[time, env] <- Eurcemented[1]
    EurcementedTableUCL[time, env] <- Eurcemented[3]

    Eurfreeliving <- percentEcolTrait(occurrences2,
"stability", "free-living", desiredStages=JurassicStages[time],
desiredEnvts=Environments[env], "Europe")
    EurfreelivingTableE[time, env] <- Eurfreeliving[2]
    EurfreelivingTableLCL[time, env] <- Eurfreeliving[1]
    EurfreelivingTableUCL[time, env] <- Eurfreeliving[3]

    Eurpedunculate <- percentEcolTrait(occurrences2,
"stability", "pedunculate", desiredStages=JurassicStages[time],
desiredEnvts=Environments[env], "Europe")
    EurpedunculateTableE[time, env] <- Eurpedunculate[2]
    EurpedunculateTableLCL[time, env] <- Eurpedunculate[1]
    EurpedunculateTableUCL[time, env] <- Eurpedunculate[3]

    Eurmobile <- percentEcolTrait(occurrences2, "motility",
"mobile", desiredStages=JurassicStages[time],
desiredEnvts=Environments[env], "Europe")
    EurmobileTableE[time, env] <- Eurmobile[2]
    EurmobileTableLCL[time, env] <- Eurmobile[1]
    EurmobileTableUCL[time, env] <- Eurmobile[3]

    Eurlimitedmobile <- percentEcolTrait(occurrences2,
"motility", "limited mobile", desiredStages=JurassicStages[time],
desiredEnvts=Environments[env], "Europe")
    EurlimitedmobileTableE[time, env] <- Eurlimitedmobile[2]
    EurlimitedmobileTableLCL[time, env] <- Eurlimitedmobile[1]
    EurlimitedmobileTableUCL[time, env] <- Eurlimitedmobile[3]

    Eursessile <- percentEcolTrait(occurrences2, "motility",
"sessile", desiredStages=JurassicStages[time],
desiredEnvts=Environments[env], "Europe")
    EursessileTableE[time, env] <- Eursessile[2]
    EursessileTableLCL[time, env] <- Eursessile[1]
    EursessileTableUCL[time, env] <- Eursessile[3]
  }
}

```

```

-----
-----
-
##Plots

#Create vector of Jurassic stage boundary ages (Myr) based on the
2015 ICS Chronostratigraphy Chart
stageBoundaryAges <- c(201.3, 199.3, 190.8, 182.7, 174.1, 170.3,
168.3, 166.1, 163.5, 157.3, 152.1, 145.0)

#Duration of each stage — Hettangian: 2.0, Sinemurian: 8.5,
Pliensbachian: 8.1, Toarcian: 8.6, Aalenian: 3.8, Bajocian: 2.0,
Bathonian: 2.2, Callovian: 2.6, Oxfordian: 6.2, Kimmeridian: 5.2,
Tithonian: 7.1

#Calculate midpoint of each stage to include in plots
midpointAges <- stageBoundaryAges[-length(stageBoundaryAges)] +
diff(stageBoundaryAges)/2
midpointAges <- sort(midpointAges)

#Assign column number to environment type to avoid magic numbers
in plot code
nearshore <- 1
innershelf <- 2
middleshelf <- 3
outershelf <- 4
slopeandbasin <- 5

##Life habits
#Plots of percentages
dev.new(width=4, length=7)
par(mfrow=c(5,1)), mai=c(0.25, 0.35, 0.075, 0.25))

plot(midpointAges, EursinfaunalTableE[, nearshore],
main='Nearshore', xlab='', ylab='', ylim=range(0:100), las=1,
type='n', axes=FALSE)
axis(1, labels=FALSE, lwd.ticks=0)
axis(2, at=seq(0, 100, by=20), las=1)
points(midpointAges, EursinfaunalTableE[, nearshore], type="o",
pch=16, lty=1, col="blue")
segments(midpointAges, EursinfaunalTableLCL[,nearshore],
midpointAges, EursinfaunalTableUCL[, nearshore], col="blue")
points(midpointAges, EurdinfaunalTableE[,1], type="o", pch=16,
lty=2, col="blue")
segments(midpointAges, EurdinfaunalTableLCL[, nearshore],
midpointAges, EurdinfaunalTableUCL[, nearshore], col="blue")
points(midpointAges, EurepifaunalTableE[,1], type="o", pch=16,
lty=3, col="red")
segments(midpointAges, EurepifaunalTableLCL[, nearshore],
midpointAges, EurepifaunalTableUCL[, nearshore], col="red")
legend("top", c("epifaunal", "shallow infaunal", "deep
infaunal"), bty="n", lty=c(3, 1, 2), col=c("red", "blue",
"blue"), horiz=TRUE, x.intersp=0.5)

```

```

plot(midpointAges, EursinfaunalTableE[,innershelf], main='Inner
Shelf', xlab='', ylab='', ylim=range(0:100), las=1, type='n',
axes=FALSE)
axis(1, labels=FALSE, lwd.ticks=0)
axis(2, at=seq(0, 100, by=20), las=1)
points(midpointAges, EursinfaunalTableE[,innershelf], type="o",
pch=16, lty=1, col="blue")
segments(midpointAges, EursinfaunalTableLCL[, innershelf],
midpointAges, EursinfaunalTableUCL[, innershelf], col="blue")
points(midpointAges, EurdinfaunalTableE[,innershelf], type="o",
pch=16, lty=2, col="blue")
segments(midpointAges, EurdinfaunalTableLCL[, innershelf],
midpointAges, EurdinfaunalTableUCL[, innershelf], col="blue")
points(midpointAges, EurepifaunalTableE[,innershelf], type="o",
pch=16, lty=3, col="red")
segments(midpointAges, EurepifaunalTableLCL[, innershelf],
midpointAges, EurepifaunalTableUCL[, innershelf], col="red")

plot(midpointAges, EursinfaunalTableE[, middleshelf],
main='Middle Shelf', xlab='', ylab='', ylim=range(0:100), las=1,
type='n', axes=FALSE)
axis(1, labels=FALSE, lwd.ticks=0)
axis(2, at=seq(0, 100, by=20), las=1)
points(midpointAges, EursinfaunalTableE[, middleshelf], type="o",
pch=16, lty=1, col="blue")
segments(midpointAges, EursinfaunalTableLCL[, middleshelf],
midpointAges, EursinfaunalTableUCL[, middleshelf], col="blue")
points(midpointAges, EurdinfaunalTableE[,middleshelf], type="o",
pch=16, lty=2, col="blue")
segments(midpointAges, EurdinfaunalTableLCL[, middleshelf],
midpointAges, EurdinfaunalTableUCL[, middleshelf], col="blue")
points(midpointAges, EurepifaunalTableE[,middleshelf], type="o",
pch=16, lty=3, col="red")
segments(midpointAges, EurepifaunalTableLCL[, middleshelf],
midpointAges, EurepifaunalTableUCL[, middleshelf], col="red")

plot(midpointAges, EursinfaunalTableE[, outershelf], main='Outer
Shelf', xlab='', ylab='', ylim=range(0:100), las=1, type='n',
axes=FALSE)
axis(1, labels=FALSE, lwd.ticks=0)
axis(2, at=seq(0, 100, by=20), las=1)
points(midpointAges, EursinfaunalTableE[, outershelf], type="o",
pch=16, lty=1, col="blue")
segments(midpointAges, EursinfaunalTableLCL[, outershelf],
midpointAges, EursinfaunalTableUCL[, outershelf], col="blue")
points(midpointAges, EurdinfaunalTableE[,outershelf], type="o",
pch=16, lty=2, col="blue")
segments(midpointAges, EurdinfaunalTableLCL[, outershelf],
midpointAges, EurdinfaunalTableUCL[, outershelf], col="blue")
points(midpointAges, EurepifaunalTableE[, outershelf], type="o",
pch=16, lty=3, col="red")

```

```

segments(midpointAges, EurepifaunalTableLCL[, outershelf],
midpointAges, EurepifaunalTableUCL[, outershelf], col="red")

plot(midpointAges, EursinfaunalTableE[, slopeandbasin],
main='Slope and Deep Basin', xlab='', ylab='', ylim=range(0:100),
las=1, type='n', axes=FALSE)
axis(1, at=midpointAges, labels=c("He", "Si", "Pl", "To", "Aa",
"Baj", "Bat", "Ca", "Ox", "Ki", "Ti"), xlab='Jurassic Stage')
axis(2, at=seq(0, 100, by=20), las=1)
points(midpointAges, EursinfaunalTableE[, slopeandbasin],
type="o", pch=16, lty=1, col="blue")
segments(midpointAges, EursinfaunalTableLCL[, slopeandbasin],
midpointAges, EursinfaunalTableUCL[, slopeandbasin], col="blue")
points(midpointAges, EurdinfaunalTableE[, slopeandbasin],
type="o", pch=16, lty=2, col="blue")
segments(midpointAges, EurdinfaunalTableLCL[, slopeandbasin],
midpointAges, EurdinfaunalTableUCL[, slopeandbasin], col="blue")
points(midpointAges, EurepifaunalTableE[, slopeandbasin],
type="o", pch=16, lty=3, col="red")
segments(midpointAges, EurepifaunalTableLCL[, slopeandbasin],
midpointAges, EurepifaunalTableUCL[, slopeandbasin], col="red")

##Substrate Stability (Epifaunal life modes)

#Plots of percentages
dev.new(width=4, length=7)
par(mfrow=(c(5,1)), mai=c(0.25, 0.35, 0.075, 0.25))

plot(midpointAges, EurpedunculateTableE[, nearshore],
main='Nearshore', xlab='', ylab='', ylim=range(0:100), las=1,
type='n', axes=FALSE)
axis(1, labels=FALSE, lwd.ticks=0)
axis(2, at=seq(0, 100, by=20), las=1)
points(midpointAges, EurpedunculateTableE[, nearshore], type="o",
pch=16, lty=1, col="red")
segments(midpointAges, EurpedunculateTableLCL[, nearshore],
midpointAges, EurpedunculateTableUCL[, nearshore], col="red")
points(midpointAges, EurcementedTableE[, nearshore], type="o",
pch=16, lty=2, col="blue")
segments(midpointAges, EurcementedTableLCL[, nearshore],
midpointAges, EurcementedTableUCL[, nearshore], col="blue")
points(midpointAges, EurfreelivingTableE[, nearshore], type="o",
pch=16, lty=3, col="red")
segments(midpointAges, EurfreelivingTableLCL[, nearshore],
midpointAges, EurfreelivingTableUCL[, nearshore], col="red")
legend("top", c("pedunculate", "cemented", "free-living"),
bty="n", lty=c(1, 2, 3), col=c("red", "blue", "red"), horiz=TRUE,
x.intersp=0.5)

plot(midpointAges, EurpedunculateTableE[, innershelf],
main='Inner Shelf', xlab='', ylab='', ylim=range(0:100), las=1,
type='n', axes=FALSE)

```



```

axis(1, labels=FALSE, lwd.ticks=0)
axis(2, at=seq(0, 100, by=20), las=1)
points(midpointAges, EurpedunculateTableE[, innershelf],
type="o", pch=16, lty=1, col="red")
segments(midpointAges, EurpedunculateTableLCL[, innershelf],
midpointAges, EurpedunculateTableUCL[, innershelf], col="red")
points(midpointAges, EurcementedTableE[, innershelf], type="o",
pch=16, lty=2, col="blue")
segments(midpointAges, EurcementedTableLCL[, innershelf],
midpointAges, EurcementedTableUCL[, innershelf], col="blue")
points(midpointAges, EurfreelivingTableE[, innershelf], type="o",
pch=16, lty=3, col="red")
segments(midpointAges, EurfreelivingTableLCL[, innershelf],
midpointAges, EurfreelivingTableUCL[, innershelf], col="red")

plot(midpointAges, EurpedunculateTableE[, middleshelf],
main='Middle Shelf', xlab='', ylab='', ylim=range(0:100), las=1,
type='n', axes=FALSE)
axis(1, labels=FALSE, lwd.ticks=0)
axis(2, at=seq(0, 100, by=20), las=1)
points(midpointAges, EurpedunculateTableE[, middleshelf],
type="o", pch=16, lty=1, col="red")
segments(midpointAges, EurpedunculateTableLCL[, middleshelf],
midpointAges, EurpedunculateTableUCL[, middleshelf], col="red")
points(midpointAges, EurcementedTableE[, middleshelf], type="o",
pch=16, lty=2, col="blue")
segments(midpointAges, EurcementedTableLCL[, middleshelf],
midpointAges, EurcementedTableUCL[, middleshelf], col="blue")
points(midpointAges, EurfreelivingTableE[, middleshelf],
type="o", pch=16, lty=3, col="red")
segments(midpointAges, EurfreelivingTableLCL[, middleshelf],
midpointAges, EurfreelivingTableUCL[, middleshelf], col="red")

plot(midpointAges, EurpedunculateTableE[, outershelf],
main='Outer Shelf', xlab='', ylab='', ylim=range(0:100), las=1,
type='n', axes=FALSE)
axis(1, labels=FALSE, lwd.ticks=0)
axis(2, at=seq(0, 100, by=20), las=1)
points(midpointAges, EurpedunculateTableE[, outershelf],
type="o", pch=16, lty=1, col="red")
segments(midpointAges, EurpedunculateTableLCL[, outershelf],
midpointAges, EurpedunculateTableUCL[, outershelf], col="red")
points(midpointAges, EurcementedTableE[, outershelf], type="o",
pch=16, lty=2, col="blue")
segments(midpointAges, EurcementedTableLCL[, outershelf],
midpointAges, EurcementedTableUCL[, outershelf], col="blue")
points(midpointAges, EurfreelivingTableE[, outershelf], type="o",
pch=16, lty=3, col="red")
segments(midpointAges, EurfreelivingTableLCL[, outershelf],
midpointAges, EurfreelivingTableUCL[, outershelf], col="red")

```

```

plot(midpointAges, EurpedunculateTableE[, slopeandbasin],
main='Slope and Deep Basin', xlab='', ylab='', ylim=range(0:100),
las=1, type='n', axes=FALSE)
axis(1, at=midpointAges, labels=c("He", "Si", "Pl", "To", "Aa",
"Baj", "Bat", "Ca", "Ox", "Ki", "Ti"), xlab='Jurassic Stage')
axis(2, at=seq(0, 100, by=20), las=1)
points(midpointAges, EurpedunculateTableE[, slopeandbasin],
type="o", pch=16, lty=1, col="red")
segments(midpointAges, EurpedunculateTableLCL[, slopeandbasin],
midpointAges, EurpedunculateTableUCL[, slopeandbasin], col="red")
points(midpointAges, EurcementedTableE[, slopeandbasin],
type="o", pch=16, lty=2, col="blue")
segments(midpointAges, EurcementedTableLCL[, slopeandbasin],
midpointAges, EurcementedTableUCL[, slopeandbasin], col="blue")
points(midpointAges, EurfreelivingTableE[, slopeandbasin],
type="o", pch=16, lty=3, col="red")
segments(midpointAges, EurfreelivingTableLCL[, slopeandbasin],
midpointAges, EurfreelivingTableUCL[, slopeandbasin], col="red")

```

##Motility

#Plots of percentages

```

dev.new(width=4, length=7)
par(mfrow=(c(5,1)), mai=c(0.25, 0.35, 0.075, 0.25))

```

```

plot(midpointAges, EurmobileTableE[, nearshore],
main='Nearshore', xlab='', ylab='', ylim=range(0:100), las=1,
type='n', axes=FALSE)
axis(1, labels=FALSE, lwd.ticks=0)
axis(2, at=seq(0, 100, by=20), las=1)
points(midpointAges, EurmobileTableE[, nearshore], type="o",
pch=16, lty=1, col="blue")
segments(midpointAges, EurmobileTableLCL[, nearshore],
midpointAges, EurmobileTableUCL[, nearshore], col="blue")
points(midpointAges, EurlimitedmobileTableE[, nearshore],
type="o", pch=16, lty=2, col="blue")
segments(midpointAges, EurlimitedmobileTableLCL[, nearshore],
midpointAges, EurlimitedmobileTableUCL[, nearshore], col="blue")
points(midpointAges, EursessileTableE[, nearshore], type="o",
pch=16, lty=3, col="red")
segments(midpointAges, EursessileTableLCL[, nearshore],
midpointAges, EursessileTableUCL[, nearshore], col="red")
legend("top", c("sessile", "facultative mobile", "mobile"),
bty="n", lty=c(3, 2, 1), col=c("red", "blue", "blue"),
horiz=TRUE, x.intersp=0.5)

```

```

plot(midpointAges, EurmobileTableE[, innershelf], main='Inner
Shelf', xlab='', ylab='', ylim=range(0:100), las=1, type='n',
axes=FALSE)
axis(1, labels=FALSE, lwd.ticks=0)
axis(2, at=seq(0, 100, by=20), las=1)

```

```

points(midpointAges, EurmobileTableE[, innershelf], type="o",
pch=16, lty=1, col="blue")
segments(midpointAges, EurmobileTableLCL[, innershelf],
midpointAges, EurmobileTableUCL[, innershelf], col="blue")
points(midpointAges, EurlimitedmobileTableE[, innershelf],
type="o", pch=16, lty=2, col="blue")
segments(midpointAges, EurlimitedmobileTableLCL[, innershelf],
midpointAges, EurlimitedmobileTableUCL[, innershelf], col="blue")
points(midpointAges, EursessileTableE[, innershelf], type="o",
pch=16, lty=3, col="red")
segments(midpointAges, EursessileTableLCL[, innershelf],
midpointAges, EursessileTableUCL[, innershelf], col="red")

plot(midpointAges, EurmobileTableE[, middleshelf], main='Middle
Shelf', xlab='', ylab='', ylim=range(0:100), las=1, type='n',
axes=FALSE)
axis(1, labels=FALSE, lwd.ticks=0)
axis(2, at=seq(0, 100, by=20), las=1)
points(midpointAges, EurmobileTableE[, middleshelf], type="o",
pch=16, lty=1, col="blue")
segments(midpointAges, EurmobileTableLCL[, middleshelf],
midpointAges, EurmobileTableUCL[, middleshelf], col="blue")
points(midpointAges, EurlimitedmobileTableE[, middleshelf],
type="o", pch=16, lty=2, col="blue")
segments(midpointAges, EurlimitedmobileTableLCL[, middleshelf],
midpointAges, EurlimitedmobileTableUCL[, middleshelf],
col="blue")
points(midpointAges, EursessileTableE[, middleshelf], type="o",
pch=16, lty=3, col="red")
segments(midpointAges, EursessileTableLCL[, middleshelf],
midpointAges, EursessileTableUCL[, middleshelf], col="red")

plot(midpointAges, EurmobileTableE[, outershelf], main='Outer
Shelf', xlab='', ylab='', ylim=range(0:100), las=1, type='n',
axes=FALSE)
axis(1, labels=FALSE, lwd.ticks=0)
axis(2, at=seq(0, 100, by=20), las=1)
points(midpointAges, EurmobileTableE[, outershelf], type="o",
pch=16, lty=1, col="blue")
segments(midpointAges, EurmobileTableLCL[, outershelf],
midpointAges, EurmobileTableUCL[, outershelf], col="blue")
points(midpointAges, EurlimitedmobileTableE[, outershelf],
type="o", pch=16, lty=2, col="blue")
segments(midpointAges, EurlimitedmobileTableLCL[, outershelf],
midpointAges, EurlimitedmobileTableUCL[, outershelf], col="blue")
points(midpointAges, EursessileTableE[, outershelf], type="o",
pch=16, lty=3, col="red")
segments(midpointAges, EursessileTableLCL[, outershelf],
midpointAges, EursessileTableUCL[, outershelf], col="red")

```

```

-----
-----
-
##Spearman's rank correlation tests

#Spearman's rank correlation tests for Nearshore Environments
cor.test(midpointAges, EursinfaunalTableE[,1], method='spearman')
cor.test(midpointAges, EurdinfaunalTableE[,1], method='spearman')
cor.test(midpointAges, EurepifaunalTableE[,1], method='spearman')
cor.test(midpointAges, EurfreelivingTableE[,1],
method='spearman')
cor.test(midpointAges, EurcementedTableE[,1], method='spearman')
cor.test(midpointAges, EurpedunculateTableE[,1],
method='spearman')
cor.test(midpointAges, EursessileTableE[,1], method='spearman')
cor.test(midpointAges, EurlimitedmobileTableE[,1],
method='spearman')
cor.test(midpointAges, EurmobileTableE[,1], method='spearman')

#Spearman's rank correlation tests for Inner Shelf Environments
cor.test(midpointAges, EursinfaunalTableE[,2], method='spearman')
cor.test(midpointAges, EurdinfaunalTableE[,2], method='spearman')
cor.test(midpointAges, EurepifaunalTableE[,2], method='spearman')
cor.test(midpointAges, EurfreelivingTableE[,2],
method='spearman')
cor.test(midpointAges, EurcementedTableE[,2], method='spearman')
cor.test(midpointAges, EurpedunculateTableE[,2],
method='spearman')
cor.test(midpointAges, EursessileTableE[,2], method='spearman')
cor.test(midpointAges, EurlimitedmobileTableE[,2],
method='spearman')
cor.test(midpointAges, EurmobileTableE[,2], method='spearman')

#Spearman's rank correlation tests for Middle Shelf Environments
cor.test(midpointAges, EursinfaunalTableE[,3], method='spearman')
cor.test(midpointAges, EurdinfaunalTableE[,3], method='spearman')
cor.test(midpointAges, EurepifaunalTableE[,3], method='spearman')
cor.test(midpointAges, EurfreelivingTableE[,3],
method='spearman')
cor.test(midpointAges, EurcementedTableE[,3], method='spearman')
cor.test(midpointAges, EurpedunculateTableE[,3],
method='spearman')
cor.test(midpointAges, EursessileTableE[,3], method='spearman')
cor.test(midpointAges, EurlimitedmobileTableE[,3],
method='spearman')
cor.test(midpointAges, EurmobileTableE[,3], method='spearman')

#Spearman's rank correlation tests for Outer Shelf Environments
cor.test(midpointAges, EursinfaunalTableE[,4], method='spearman')
cor.test(midpointAges, EurdinfaunalTableE[,4], method='spearman')
cor.test(midpointAges, EurepifaunalTableE[,4], method='spearman')
cor.test(midpointAges, EurfreelivingTableE[,4],
method='spearman')

```

```

cor.test(midpointAges, EurcementedTableE[,4], method='spearman')
cor.test(midpointAges, EurpedunculateTableE[,4],
method='spearman')
cor.test(midpointAges, EursessileTableE[,4], method='spearman')
cor.test(midpointAges, EurlimitedmobileTableE[,4],
method='spearman')
cor.test(midpointAges, EurmobileTableE[,4], method='spearman')

#Spearman's rank correlation tests for Slope and Deep Basin
Environments
cor.test(midpointAges, EursinfaunalTableE[,5], method='spearman')
cor.test(midpointAges, EurdinfaunalTableE[,5], method='spearman')
cor.test(midpointAges, EurepifaunalTableE[,5], method='spearman')
cor.test(midpointAges, EurfreelivingTableE[,5],
method='spearman')
cor.test(midpointAges, EurcementedTableE[,5], method='spearman')
cor.test(midpointAges, EurpedunculateTableE[,5],
method='spearman')
cor.test(midpointAges, EursessileTableE[,5], method='spearman')
cor.test(midpointAges, EurlimitedmobileTableE[,5],
method='spearman')
cor.test(midpointAges, EurmobileTableE[,5], method='spearman')

```

R command script that calculates the proportions of ecological group occurrences for global data by Jurassic stage using data from the Paleobiology Database. This script also plots all the global ecological patterns figures (Fig. 2.8) and performs all statistical tests (Table 2.5).

```
###Loop, plots, and Spearman's tests of ecological percentages of  
PBDB Jurassic global occurrences
```

```
##This section sets up the loop to that will be used to calculate  
percentages of occurrences
```

```
#Read percent confidence interval function  
source("percentConfidenceInterval.R")
```

```
#Read percent ecology function to calculate percentages with  
confidence intervals  
source("percentEcolTrait.R")
```

```
#Read dataset  
globalOccurrences <- read.csv('ClusteredOccurrences.csv',  
header=TRUE, stringsAsFactors=FALSE)
```

```
#Create objects to define dimensions of matrices below  
stagecolumn <- 4  
JurassicStages <-  
sort(unique(globalOccurrences[globalOccurrences$stage!="0",  
stagecolumn]))
```

```
#Create empty matrices to be filled with percentage estimates  
calculated using the for loop for global  
sinfaunalTableE <- matrix(data=0, nrow=length(JurassicStages),  
ncol=1, dimnames=list(JurassicStages, "Global"))  
dinhaunalTableE <- matrix(data=0, nrow=length(JurassicStages),  
ncol=1, dimnames=list(JurassicStages, "Global"))  
epifaunalTableE <- matrix(data=0, nrow=length(JurassicStages),  
ncol=1, dimnames=list(JurassicStages, "Global"))  
pedunculateTableE <- matrix(data=0, nrow=length(JurassicStages),  
ncol=1, dimnames=list(JurassicStages, "Global"))  
cementedTableE <- matrix(data=0, nrow=length(JurassicStages),  
ncol=1, dimnames=list(JurassicStages, "Global"))  
freelivingTableE <- matrix(data=0, nrow=length(JurassicStages),  
ncol=1, dimnames=list(JurassicStages, "Global"))  
mobileTableE <- matrix(data=0, nrow=length(JurassicStages),  
ncol=1, dimnames=list(JurassicStages, "Global"))  
limitedmobileTableE <- matrix(data=0,  
nrow=length(JurassicStages), ncol=1,  
dimnames=list(JurassicStages, "Global"))  
sessileTableE <- matrix(data=0, nrow=length(JurassicStages),  
ncol=1, dimnames=list(JurassicStages, "Global"))
```

```
#Create empty matrices to be filled with lower confidence limit  
percentage calculated using the for loop
```

```

sinfaunalTableLCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=1, dimnames=list(JurassicStages, "Global"))
dinfraunalTableLCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=1, dimnames=list(JurassicStages, "Global"))
epifaunalTableLCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=1, dimnames=list(JurassicStages, "Global"))
pedunculateTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=1,
dimnames=list(JurassicStages, "Global"))
cementedTableLCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=1, dimnames=list(JurassicStages, "Global"))
freelivingTableLCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=1, dimnames=list(JurassicStages, "Global"))
mobileTableLCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=1, dimnames=list(JurassicStages, "Global"))
limitedmobileTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=1,
dimnames=list(JurassicStages, "Global"))
sessileTableLCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=1, dimnames=list(JurassicStages, "Global"))

```

#Create empty matrices to be filled with upper confidence limit percentage calculated using the for loop

```

sinfaunalTableUCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=1, dimnames=list(JurassicStages, "Global"))
dinfraunalTableUCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=1, dimnames=list(JurassicStages, "Global"))
epifaunalTableUCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=1, dimnames=list(JurassicStages, "Global"))
pedunculateTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=1,
dimnames=list(JurassicStages, "Global"))
cementedTableUCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=1, dimnames=list(JurassicStages, "Global"))
freelivingTableUCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=1, dimnames=list(JurassicStages, "Global"))
mobileTableUCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=1, dimnames=list(JurassicStages, "Global"))
limitedmobileTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=1,
dimnames=list(JurassicStages, "Global"))
sessileTableUCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=1, dimnames=list(JurassicStages, "Global"))

```

#Loop to calculate percentage of global occurrences for each ecological trait

```

for (time in 1:length(JurassicStages)) {
  sinfaunal <- percentEcolTrait(globalOccurrences,
"life_habit", "shallow infaunal",
desiredStages=JurassicStages[time])
  sinfaunalTableE[time] <- sinfaunal[2]
  sinfaunalTableLCL[time] <- sinfaunal[1]
}

```

```

        sinfaunalTableUCL[time] <- sinfaunal[3]

        dinfaunal <- percentEcolTrait(globalOccurrences,
"life_habit", "deep infaunal",
desiredStages=JurassicStages[time])
        dinfaunalTableE[time] <- dinfaunal[2]
        dinfaunalTableLCL[time] <- dinfaunal[1]
        dinfaunalTableUCL[time] <- dinfaunal[3]

        epifaunal <- percentEcolTrait(globalOccurrences,
"life_habit", "epifaunal", desiredStages=JurassicStages[time])
        epifaunalTableE[time] <- epifaunal[2]
        epifaunalTableLCL[time] <- epifaunal[1]
        epifaunalTableUCL[time] <- epifaunal[3]

        cemented <- percentEcolTrait(globalOccurrences,
"stability", "cemented", desiredStages=JurassicStages[time])
        cementedTableE[time] <- cemented[2]
        cementedTableLCL[time] <- cemented[1]
        cementedTableUCL[time] <- cemented[3]

        freeliving <- percentEcolTrait(globalOccurrences,
"stability", "free-living", desiredStages=JurassicStages[time])
        freelivingTableE[time] <- freeliving[2]
        freelivingTableLCL[time] <- freeliving[1]
        freelivingTableUCL[time] <- freeliving[3]

        pedunculate <- percentEcolTrait(globalOccurrences,
"stability", "pedunculate", desiredStages=JurassicStages[time])
        pedunculateTableE[time] <- pedunculate[2]
        pedunculateTableLCL[time] <- pedunculate[1]
        pedunculateTableUCL[time] <- pedunculate[3]

        mobile <- percentEcolTrait(globalOccurrences, "motility",
"mobile", desiredStages=JurassicStages[time])
        mobileTableE[time] <- mobile[2]
        mobileTableLCL[time] <- mobile[1]
        mobileTableUCL[time] <- mobile[3]

        limitedmobile <- percentEcolTrait(globalOccurrences,
"motility", "limited mobile", desiredStages=JurassicStages[time])
        limitedmobileTableE[time] <- limitedmobile[2]
        limitedmobileTableLCL[time] <- limitedmobile[1]
        limitedmobileTableUCL[time] <- limitedmobile[3]

        sessile <- percentEcolTrait(globalOccurrences, "motility",
"sessile", desiredStages=JurassicStages[time])
        sessileTableE[time] <- sessile[2]
        sessileTableLCL[time] <- sessile[1]
        sessileTableUCL[time] <- sessile[3]
}

```


##Plots and Spearman's Rank Correlation Tests

#Create vector of Jurassic stage boundary ages (Myr) based on the 2015 ICS Chronostratigraphy Chart

```
stageBoundaryAges <- c(201.3, 199.3, 190.8, 182.7, 174.1, 170.3, 168.3, 166.1, 163.5, 157.3, 152.1, 145.0)
```

#Duration of each stage – Hettangian: 2.0, Sinemurian: 8.5, Pliensbachian: 8.1, Toarcian: 8.6, Aalenian: 3.8, Bajocian: 2.0, Bathonian: 2.2, Callovian: 2.6, Oxfordian: 6.2, Kimmeridian: 5.2, Tithonian: 7.1

#Calculate midpoint of each stage to include in plots

```
midAges <- stageBoundaryAges[-length(stageBoundaryAges)] +  
diff(stageBoundaryAges)/2  
midAges <- sort(midAges)
```

#Plots of ecological percentages of global occurrences

```
dev.new(width=4, length=7)
```

```
par(mfrow=(c(3,1)), mai=c(0.25, 0.35, 0.075, 0.25))
```

```
plot(midAges, sinfaunalTableE[,1], main='Life Habit', xlab='',  
ylab='', ylim=range(0:100), las=1, type='n', axes=FALSE)  
axis(1, labels=FALSE, lwd.ticks=0)  
axis(2, at=seq(0, 100, by=20), las=1)  
points(midAges, sinfaunalTableE[,1], type="o", pch=16, lty=1,  
col="blue")  
segments(midAges, sinfaunalTableLCL[, 1], midAges,  
sinfaunalTableUCL[, 1], col="blue")  
points(midAges, dinfaunalTableE[,1], type="o", pch=16, lty=2,  
col="blue")  
segments(midAges, dinfaunalTableLCL[, 1], midAges,  
dinfaunalTableUCL[, 1], col="blue")  
points(midAges, epifaunalTableE[,1], type="o", pch=16, lty=3,  
col="red")  
segments(midAges, epifaunalTableLCL[, 1], midAges,  
epifaunalTableUCL[, 1], col="red")  
legend("top", c("epifaunal", "shallow infaunal", "deep  
infaunal"), bty="n", lty=c(3, 1, 2), col=c("red", "blue",  
"blue"), horiz=TRUE, x.intersp=0.5)
```

```
plot(midAges, pedunculateTableE[,1], main='Stability', xlab='',  
ylab='', ylim=range(0:100), las=1, type='n', axes=FALSE)  
axis(1, labels=FALSE, lwd.ticks=0)  
axis(2, at=seq(0, 100, by=20), las=1)  
points(midAges, pedunculateTableE[,1], type="o", pch=16, lty=1,  
col="red")  
segments(midAges, pedunculateTableLCL[, 1], midAges,  
pedunculateTableUCL[, 1], col="red")  
points(midAges, cementedTableE[,1], type="o", pch=16, lty=2,  
col="blue")  
segments(midAges, cementedTableLCL[, 1], midAges,  
cementedTableUCL[, 1], col="blue")
```

```

points(midAges, freelivingTableE[,1], type="o", pch=16, lty=3,
col="red")
segments(midAges, freelivingTableLCL[ , 1], midAges,
freelivingTableUCL[ , 1], col="red")
legend("top", c("pedunculate", "free-living", "cemented"),
bty="n", lty=c(1, 3, 2), col=c("red", "red", "blue"), horiz=TRUE,
x.intersp=0.5)

plot(midAges, mobileTableE[,1], main='Motility', xlab='',
ylab='', ylim=range(0:100), las=1, type='n', axes=FALSE)
axis(1, at=midAges, labels=c("He", "Si", "Pl", "To", "Aa", "Baj",
"Bat", "Ca", "Ox", "Ki", "Ti"), xlab='Jurassic Stage')
axis(2, at=seq(0, 100, by=20), las=1)
points(midAges, mobileTableE[,1], type="o", pch=16, lty=1,
col="blue")
segments(midAges, mobileTableLCL[ , 1], midAges, mobileTableUCL[
, 1], col="blue")
points(midAges, limitedmobileTableE[,1], type="o", pch=16, lty=2,
col="blue")
segments(midAges, limitedmobileTableLCL[ , 1], midAges,
limitedmobileTableUCL[ , 1], col="blue")
points(midAges, sessileTableE[,1], type="o", pch=16, lty=3,
col="red")
segments(midAges, sessileTableLCL[ , 1], midAges,
sessileTableUCL[ , 1], col="red")
legend("top", c("sessile", "limited mobile", "mobile"), bty="n",
lty=c(3, 2, 1), col=c("red", "blue", "blue"), horiz=TRUE,
x.intersp=0.5)

#Spearman's rank correlation tests
cor.test(midAges, sinfaunalTableE[,1], method='spearman')
cor.test(midAges, dinfaunalTableE[,1], method='spearman')
cor.test(midAges, epifaunalTableE[,1], method='spearman')
cor.test(midAges, freelivingTableE[,1], method='spearman')
cor.test(midAges, pedunculateTableE[,1], method='spearman')
cor.test(midAges, cementedTableE[,1], method='spearman')
cor.test(midAges, sessileTableE[,1], method='spearman')
cor.test(midAges, limitedmobileTableE[,1], method='spearman')
cor.test(midAges, mobileTableE[,1], method='spearman')

-----
##Percentages of global occurrences omitting Europe

#Create empty matrices to be filled with percentage estimates
calculated using the for loop for non-Europe global occurrences
noEUsinfaunalTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=1,
dimnames=list(JurassicStages, "Global"))
noEUDinfaunalTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=1,
dimnames=list(JurassicStages, "Global"))

```

```

noEUepifaunalTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=1,
dimnames=list(JurassicStages, "Global"))
noEUpedunculateTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=1,
dimnames=list(JurassicStages, "Global"))
noEUCementedTableE <- matrix(data=0, nrow=length(JurassicStages),
ncol=1, dimnames=list(JurassicStages, "Global"))
noEUfreelivingTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=1,
dimnames=list(JurassicStages, "Global"))
noEUmobileTableE <- matrix(data=0, nrow=length(JurassicStages),
ncol=1, dimnames=list(JurassicStages, "Global"))
noEUnlimitedmobileTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=1,
dimnames=list(JurassicStages, "Global"))
noEUsessileTableE <- matrix(data=0, nrow=length(JurassicStages),
ncol=1, dimnames=list(JurassicStages, "Global"))

```

#Create empty matrices to be filled with lower confidence limit percentage calculated using the for loop for non-Europe global occurrences

```

noEUsinfaunalTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=1,
dimnames=list(JurassicStages, "Global"))
noEUdinafaunalTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=1,
dimnames=list(JurassicStages, "Global"))
noEUepifaunalTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=1,
dimnames=list(JurassicStages, "Global"))
noEUpedunculateTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=1,
dimnames=list(JurassicStages, "Global"))
noEUCementedTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=1,
dimnames=list(JurassicStages, "Global"))
noEUfreelivingTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=1,
dimnames=list(JurassicStages, "Global"))
noEUmobileTableLCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=1, dimnames=list(JurassicStages, "Global"))
noEUnlimitedmobileTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=1,
dimnames=list(JurassicStages, "Global"))
noEUsessileTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=1,
dimnames=list(JurassicStages, "Global"))

```

#Create empty matrices to be filled with upper confidence limit percentage calculated using the for loop for non-Europe global occurrences

```

noEUsinfaunalTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=1,
dimnames=list(JurassicStages, "Global"))
noEUdinafaunalTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=1,
dimnames=list(JurassicStages, "Global"))
noEUepifaunalTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=1,
dimnames=list(JurassicStages, "Global"))
noEUpedunculateTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=1,
dimnames=list(JurassicStages, "Global"))
noEUCementedTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=1,
dimnames=list(JurassicStages, "Global"))
noEUfreelivingTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=1,
dimnames=list(JurassicStages, "Global"))
noEUmobileTableUCL <- matrix(data=0, nrow=length(JurassicStages),
ncol=1, dimnames=list(JurassicStages, "Global"))
noEULimitedmobileTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=1,
dimnames=list(JurassicStages, "Global"))
noEUsessileTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=1,
dimnames=list(JurassicStages, "Global"))

#Create vector holding different regional clusters and then
exclude the Europe cluster
geoClusters <- sort(unique(globalOccurrences$geo_cluster))
sansEurope <- geoClusters[-1]

#Loop to calculate percentage of each ecological trait for global
occurrences without Europe
for (time in 1:length(JurassicStages)) {
  noEUsinfaunal <- percentEcolTrait(globalOccurrences,
"life_habit", "shallow infaunal",
desiredStages=JurassicStages[time],
desiredGeoclusters=sansEurope)
  noEUsinfaunalTableE[time] <- noEUsinfaunal[2]
  noEUsinfaunalTableLCL[time] <- noEUsinfaunal[1]
  noEUsinfaunalTableUCL[time] <- noEUsinfaunal[3]

  noEUdinafaunal <- percentEcolTrait(globalOccurrences,
"life_habit", "deep infaunal",
desiredStages=JurassicStages[time],
desiredGeoclusters=sansEurope)
  noEUdinafaunalTableE[time] <- noEUdinafaunal[2]
  noEUdinafaunalTableLCL[time] <- noEUdinafaunal[1]
  noEUdinafaunalTableUCL[time] <- noEUdinafaunal[3]
}

```

```

    noEUepifaunal <- percentEcolTrait(globalOccurrences,
    "life_habit", "epifaunal", desiredStages=JurassicStages[time],
    desiredGeoclusters=sansEurope)
    noEUepifaunalTableE[time] <- noEUepifaunal[2]
    noEUepifaunalTableLCL[time] <- noEUepifaunal[1]
    noEUepifaunalTableUCL[time] <- noEUepifaunal[3]

    noEUcemented <- percentEcolTrait(globalOccurrences,
    "stability", "cemented", desiredStages=JurassicStages[time],
    desiredGeoclusters=sansEurope)
    noEUcementedTableE[time] <- noEUcemented[2]
    noEUcementedTableLCL[time] <- noEUcemented[1]
    noEUcementedTableUCL[time] <- noEUcemented[3]

    noEUfreeliving <- percentEcolTrait(globalOccurrences,
    "stability", "free-living", desiredStages=JurassicStages[time],
    desiredGeoclusters=sansEurope)
    noEUfreelivingTableE[time] <- noEUfreeliving[2]
    noEUfreelivingTableLCL[time] <- noEUfreeliving[1]
    noEUfreelivingTableUCL[time] <- noEUfreeliving[3]

    noEUpedunculate <- percentEcolTrait(globalOccurrences,
    "stability", "pedunculate", desiredStages=JurassicStages[time],
    desiredGeoclusters=sansEurope)
    noEUpedunculateTableE[time] <- noEUpedunculate[2]
    noEUpedunculateTableLCL[time] <- noEUpedunculate[1]
    noEUpedunculateTableUCL[time] <- noEUpedunculate[3]

    noEUmobilite <- percentEcolTrait(globalOccurrences,
    "motility", "mobile", desiredStages=JurassicStages[time],
    desiredGeoclusters=sansEurope)
    noEUmobiliteTableE[time] <- noEUmobilite[2]
    noEUmobiliteTableLCL[time] <- noEUmobilite[1]
    noEUmobiliteTableUCL[time] <- noEUmobilite[3]

    noEUnlimitedmobile <- percentEcolTrait(globalOccurrences,
    "motility", "limited mobile", desiredStages=JurassicStages[time],
    desiredGeoclusters=sansEurope)
    noEUnlimitedmobileTableE[time] <- noEUnlimitedmobile[2]
    noEUnlimitedmobileTableLCL[time] <- noEUnlimitedmobile[1]
    noEUnlimitedmobileTableUCL[time] <- noEUnlimitedmobile[3]

    noEUsessile <- percentEcolTrait(globalOccurrences,
    "motility", "sessile", desiredStages=JurassicStages[time],
    desiredGeoclusters=sansEurope)
    noEUsessileTableE[time] <- noEUsessile[2]
    noEUsessileTableLCL[time] <- noEUsessile[1]
    noEUsessileTableUCL[time] <- noEUsessile[3]
  }

  #Call tables with estimate percentages
  noEUsinfaunalTableE

```

```

noEUdinfraunalTableE
noEUepifaunalTableE
noEUpedunculateTableE
noEUCementedTableE
noEUfreelivingTableE
noEUMobileTableE
noEULimitedmobileTableE
noEUsessileTableE

#Call tables with lower condfidence limit percentages
noEUsinfraunalTableLCL
noEUdinfraunalTableLCL
noEUepifaunalTableLCL
noEUpedunculateTableLCL
noEUCementedTableLCL
noEUfreelivingTableLCL
noEUMobileTableLCL
noEULimitedmobileTableLCL
noEUsessileTableLCL

#Call tables with upper condfidence limit percentages
noEUsinfraunalTableUCL
noEUdinfraunalTableUCL
noEUepifaunalTableUCL
noEUpedunculateTableUCL
noEUCementedTableUCL
noEUfreelivingTableUCL
noEUMobileTableUCL
noEULimitedmobileTableUCL
noEUsessileTableUCL

#Plots of percentages
dev.new(width=4, length=7)
par(mfrow=(c(3,1)), mai=c(0.25, 0.35, 0.075, 0.25))

plot(midAges, noEUsinfraunalTableE[,1], main='Life Habit',
xlab='', ylab='', ylim=range(0:100), las=1, type='n', axes=FALSE)
axis(1, labels=FALSE, lwd.ticks=0)
axis(2, at=seq(0, 100, by=20), las=1)
points(midAges, noEUsinfraunalTableE[,1], type="o", pch=16, lty=1,
col="blue")
segments(midAges, noEUsinfraunalTableLCL[ , 1], midAges,
noEUsinfraunalTableUCL[ , 1], col="blue")
points(midAges, noEUdinfraunalTableE[,1], type="o", pch=16, lty=2,
col="blue")
segments(midAges, noEUdinfraunalTableLCL[ , 1], midAges,
noEUdinfraunalTableUCL[ , 1], col="blue")
points(midAges, noEUepifaunalTableE[,1], type="o", pch=16, lty=3,
col="red")
segments(midAges, noEUepifaunalTableLCL[ , 1], midAges,
noEUepifaunalTableUCL[ , 1], col="red")

```

```

legend("top", c("epifaunal", "shallow infaunal", "deep
infaunal"), bty="n", lty=c(3, 1, 2), col=c("red", "blue",
"blue"), horiz=TRUE, x.intersp=0.5)

plot(midAges, noEUpedunculateTableE[,1], main='Stability',
xlab='', ylab='', ylim=range(0:100), las=1, type='n', axes=FALSE)
axis(1, labels=FALSE, lwd.ticks=0)
axis(2, at=seq(0, 100, by=20), las=1)
points(midAges, noEUpedunculateTableE[,1], type="o", pch=16,
lty=1, col="red")
segments(midAges, noEUpedunculateTableLCL[, 1], midAges,
noEUpedunculateTableUCL[, 1], col="red")
points(midAges, noEUCementedTableE[,1], type="o", pch=16, lty=2,
col="blue")
segments(midAges, noEUCementedTableLCL[, 1], midAges,
noEUCementedTableUCL[, 1], col="blue")
points(midAges, noEUfreelivingTableE[,1], type="o", pch=16,
lty=3, col="red")
segments(midAges, noEUfreelivingTableLCL[, 1], midAges,
noEUfreelivingTableUCL[, 1], col="red")
legend("top", c("pedunculate", "free-living", "cemented"),
bty="n", lty=c(1, 3, 2), col=c("red", "red", "blue"), horiz=TRUE,
x.intersp=0.5)

plot(midAges, noEUMobileTableE[,1], main='Motility',
xlab='Jurassic stages', ylab='', ylim=range(0:100), las=1,
type='n', axes=FALSE)
axis(1, at=midAges, labels=c("He", "Si", "Pl", "To", "Aa", "Baj",
"Bat", "Ca", "Ox", "Ki", "Ti"), xlab='Jurassic Stage')
axis(2, at=seq(0, 100, by=20), las=1)
points(midAges, noEUMobileTableE[,1], type="o", pch=16, lty=1,
col="blue")
segments(midAges, noEUMobileTableLCL[, 1], midAges,
noEUMobileTableUCL[, 1], col="blue")
points(midAges, noEULimitedmobileTableE[,1], type="o", pch=16,
lty=2, col="blue")
segments(midAges, noEULimitedmobileTableLCL[, 1], midAges,
noEULimitedmobileTableUCL[, 1], col="blue")
points(midAges, noEUsessileTableE[,1], type="o", pch=16, lty=3,
col="red")
segments(midAges, noEUsessileTableLCL[, 1], midAges,
noEUsessileTableUCL[, 1], col="red")
legend("top", c("sessile", "limited mobile", "mobile"), bty="n",
lty=c(3, 2, 1), col=c("red", "blue", "blue"), horiz=TRUE,
x.intersp=0.5)

#Spearman's rank correlation tests for Global Data except Europe
cor.test(midAges, noEUsinfaunalTableE[,1], method='spearman')
cor.test(midAges, noEUdinafaunalTableE[,1], method='spearman')
cor.test(midAges, noEUepifaunalTableE[,1], method='spearman')
cor.test(midAges, noEUfreelivingTableE[,1], method='spearman')
cor.test(midAges, noEUpedunculateTableE[,1], method='spearman')

```

```
cor.test(midAges, noEUcementedTableE[,1], method='spearman')
cor.test(midAges, noEUsessileTableE[,1], method='spearman')
cor.test(midAges, noEUnlimitedmobileTableE[,1], method='spearman')
cor.test(midAges, noEUmobileTableE[,1], method='spearman')
```


R command script to perform a random permutation of time stages followed by Spearman's rank correlation tests using 10,000 iterations for all 45 tests conducted in all regions. (Fig. 2.9)

```
####10,000 iterations of a null model by conducting a random
permutation of time stages of global trends followed by
Spearman's rank correlation tests

##Loop, plots, and Spearman's tests of ecological percentages of
PBDB Jurassic regional occurrences

#Read percent confidence interval function
source("percentConfidenceInterval.R")

#Read percent ecology function to calculate percentages with
confidence intervals
source("percentEcolTrait.R")

#Read dataset
occurrences2 <- read.csv('ClusteredOccurrences.csv', header=TRUE,
stringsAsFactors=FALSE)

#Create object to hold results of 10,000 iteration null model
hold <- vector(mode = "numeric", length = 10000)

#Loop to calculate ecological trends by stage per region
for (i in 1:10000) {

    #Create objects to define dimensions of matrices below
    stagecolumn <- 4
    JurassicStages <-
sort(unique(occurrences2[occurrences2$stage!="0", stagecolumn]))
    geoClusters <- sort(unique(occurrences2$geo_cluster))

    #Create empty matrices that will be used to fill estimated
percentages calculated by running loop
    sinfaunalTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    dinfaunalTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    epifaunalTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    cementedTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    freelivingTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
```

```

    pedunculateTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    mobileTableE <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))
    limitedmobileTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    sessileTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))

    #Create empty matrices that will be used to fill lower
confidence limit percentages calculated by running loop
    sinfaunalTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    dinfaunalTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    epifaunalTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    cementedTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    freelivingTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    pedunculateTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    mobileTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    limitedmobileTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    sessileTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))

    #Create empty matrices that will be used to fill upper
condfidence limit percentages calculated by running loop
    sinfaunalTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    dinfaunalTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))

```

```

    epifaunalTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    cementedTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    freelivingTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    pedunculateTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    mobileTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    limitedmobileTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    sessileTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))

    #Loop to calculate percentage of each ecological trait by
    cluster for each stage
    for (time in 1:length(JurassicStages)) {
      for (geo in 1:length(geoClusters)) {
        sinfaunal <- percentEcolTrait(occurrences2,
"life_habit", "shallow infaunal",
desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
        sinfaunalTableE[time, geo] <- sinfaunal[2]
        sinfaunalTableLCL[time, geo] <- sinfaunal[1]
        sinfaunalTableUCL[time, geo] <- sinfaunal[3]

        dinfaunal <- percentEcolTrait(occurrences2,
"life_habit", "deep infaunal",
desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
        dinfaunalTableE[time, geo] <- dinfaunal[2]
        dinfaunalTableLCL[time, geo] <- dinfaunal[1]
        dinfaunalTableUCL[time, geo] <- dinfaunal[3]

        epifaunal <- percentEcolTrait(occurrences2,
"life_habit", "epifaunal", desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
        epifaunalTableE[time, geo] <- epifaunal[2]
        epifaunalTableLCL[time, geo] <- epifaunal[1]
        epifaunalTableUCL[time, geo] <- epifaunal[3]

        cemented <- percentEcolTrait(occurrences2,
"stability", "cemented", desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])

```

```

        cementedTableE[time, geo] <- cemented[2]
        cementedTableLCL[time, geo] <- cemented[1]
        cementedTableUCL[time, geo] <- cemented[3]

        freeliving <- percentEcolTrait(occurrences2,
"stability", "free-living", desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
        freelivingTableE[time, geo] <- freeliving[2]
        freelivingTableLCL[time, geo] <- freeliving[1]
        freelivingTableUCL[time, geo] <- freeliving[3]

        pedunculate <- percentEcolTrait(occurrences2,
"stability", "pedunculate", desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
        pedunculateTableE[time, geo] <- pedunculate[2]
        pedunculateTableLCL[time, geo] <- pedunculate[1]
        pedunculateTableUCL[time, geo] <- pedunculate[3]

        mobile <- percentEcolTrait(occurrences2,
"motility", "mobile", desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
        mobileTableE[time, geo] <- mobile[2]
        mobileTableLCL[time, geo] <- mobile[1]
        mobileTableUCL[time, geo] <- mobile[3]

        limitedmobile <- percentEcolTrait(occurrences2,
"motility", "limited mobile", desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
        limitedmobileTableE[time, geo] <-
limitedmobile[2]
        limitedmobileTableLCL[time, geo] <-
limitedmobile[1]
        limitedmobileTableUCL[time, geo] <-
limitedmobile[3]

        sessile <- percentEcolTrait(occurrences2,
"motility", "sessile", desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
        sessileTableE[time, geo] <- sessile[2]
        sessileTableLCL[time, geo] <- sessile[1]
        sessileTableUCL[time, geo] <- sessile[3]
    }
}

#Create vector of Jurassic stage boundary ages (Myr) based
on the 2015 ICS Chronostratigraphy Chart
stageBoundaryAges <- c(201.3, 199.3, 190.8, 182.7, 174.1,
170.3, 168.3, 166.1, 163.5, 157.3, 152.1, 145.0)

#Duration of each stage (Myr) – Hettangian: 2.0,
Sinemurian: 8.5, Pliensbachian: 8.1, Toarcian: 8.6, Aalenian:

```

3.8, Bajocian: 2.0, Bathonian: 2.2, Callovian: 2.6, Oxfordian:
6.2, Kimmeridian: 5.2, Tithonian: 7.1

```
#Calculate midpoint of each stage to include in plots
midpointAges <- stageBoundaryAges[-
length(stageBoundaryAges)] + diff(stageBoundaryAges)/2
midpointAges <- sort(midpointAges)

#Randomize stages
midpointAges <- sample(midpointAges, length(midpointAges))

#Create vector to hold number each p-value
pvalues <- vector(mode="numeric", length=45)

#Spearman's rank correlation tests for Europe Cluster
test1 <- cor.test(midpointAges, sinfaunalTableE[,1],
method='spearman')
test2 <- cor.test(midpointAges, dinfaunalTableE[,1],
method='spearman')
test3 <- cor.test(midpointAges, epifaunalTableE[,1],
method='spearman')
test4 <- cor.test(midpointAges, freelivingTableE[,1],
method='spearman')
test5 <- cor.test(midpointAges, cementedTableE[,1],
method='spearman')
test6 <- cor.test(midpointAges, pedunculateTableE[,1],
method='spearman')
test7 <- cor.test(midpointAges, sessileTableE[,1],
method='spearman')
test8 <- cor.test(midpointAges, limitedmobileTableE[,1],
method='spearman')
test9 <- cor.test(midpointAges, mobileTableE[,1],
method='spearman')

#Spearman's rank correlation tests for Middle East Cluster
test10 <- cor.test(midpointAges, sinfaunalTableE[,2],
method='spearman')
test11 <- cor.test(midpointAges, dinfaunalTableE[,2],
method='spearman')
test12 <- cor.test(midpointAges, epifaunalTableE[,2],
method='spearman')
test13 <- cor.test(midpointAges, freelivingTableE[,2],
method='spearman')
test14 <- cor.test(midpointAges, cementedTableE[,2],
method='spearman')
test15 <- cor.test(midpointAges, pedunculateTableE[,2],
method='spearman')
test16 <- cor.test(midpointAges, sessileTableE[,2],
method='spearman')
test17 <- cor.test(midpointAges, limitedmobileTableE[,2],
method='spearman')
test18 <- cor.test(midpointAges, mobileTableE[,2],
method='spearman')
```

```

#Spearman's rank correlation tests for New Zealand Cluster
test19 <- cor.test(midpointAges, sinfaunalTableE[,3],
method='spearman')
test20 <- cor.test(midpointAges, dinfaunalTableE[,3],
method='spearman')
test21 <- cor.test(midpointAges, epifaunalTableE[,3],
method='spearman')
test22 <- cor.test(midpointAges, freelivingTableE[,3],
method='spearman')
test23 <- cor.test(midpointAges, cementedTableE[,3],
method='spearman')
test24 <- cor.test(midpointAges, pedunculateTableE[,3],
method='spearman')
test25 <- cor.test(midpointAges, sessileTableE[,3],
method='spearman')
test26 <- cor.test(midpointAges, limitedmobileTableE[,3],
method='spearman')
test27 <- cor.test(midpointAges, mobileTableE[,3],
method='spearman')

#Spearman's rank correlation tests for North America
Cluster
test28 <- cor.test(midpointAges, sinfaunalTableE[,4],
method='spearman')
test29 <- cor.test(midpointAges, dinfaunalTableE[,4],
method='spearman')
test30 <- cor.test(midpointAges, epifaunalTableE[,4],
method='spearman')
test31 <- cor.test(midpointAges, freelivingTableE[,4],
method='spearman')
test32 <- cor.test(midpointAges, cementedTableE[,4],
method='spearman')
test33 <- cor.test(midpointAges, pedunculateTableE[,4],
method='spearman')
test34 <- cor.test(midpointAges, sessileTableE[,4],
method='spearman')
test35 <- cor.test(midpointAges, limitedmobileTableE[,4],
method='spearman')
test36 <- cor.test(midpointAges, mobileTableE[,4],
method='spearman')

#Spearman's rank correlation tests for South America
Cluster
test37 <- cor.test(midpointAges, sinfaunalTableE[,5],
method='spearman')
test38 <- cor.test(midpointAges, dinfaunalTableE[,5],
method='spearman')
test39 <- cor.test(midpointAges, epifaunalTableE[,5],
method='spearman')
test40 <- cor.test(midpointAges, freelivingTableE[,5],
method='spearman')

```

```

test41 <- cor.test(midpointAges, cementedTableE[,5],
method='spearman')
test42 <- cor.test(midpointAges, pedunculateTableE[,5],
method='spearman')
test43 <- cor.test(midpointAges, sessileTableE[,5],
method='spearman')
test44 <- cor.test(midpointAges, limitedmobileTableE[,5],
method='spearman')
test45 <- cor.test(midpointAges, mobileTableE[,5],
method='spearman')

```

```

#Fill pvalues vector with p-values of each Speaman's
correlation test

```

```

pvalues[1] <- test1$p.value
pvalues[2] <- test2$p.value
pvalues[3] <- test3$p.value
pvalues[4] <- test4$p.value
pvalues[5] <- test5$p.value
pvalues[6] <- test6$p.value
pvalues[7] <- test7$p.value
pvalues[8] <- test8$p.value
pvalues[9] <- test9$p.value
pvalues[10] <- test10$p.value
pvalues[11] <- test11$p.value
pvalues[12] <- test12$p.value
pvalues[13] <- test13$p.value
pvalues[14] <- test14$p.value
pvalues[15] <- test15$p.value
pvalues[16] <- test16$p.value
pvalues[17] <- test17$p.value
pvalues[18] <- test18$p.value
pvalues[19] <- test19$p.value
pvalues[20] <- test20$p.value
pvalues[21] <- test21$p.value
pvalues[22] <- test22$p.value
pvalues[23] <- test23$p.value
pvalues[24] <- test24$p.value
pvalues[25] <- test25$p.value
pvalues[26] <- test26$p.value
pvalues[27] <- test27$p.value
pvalues[28] <- test28$p.value
pvalues[29] <- test29$p.value
pvalues[30] <- test30$p.value
pvalues[31] <- test31$p.value
pvalues[32] <- test32$p.value
pvalues[33] <- test33$p.value
pvalues[34] <- test34$p.value
pvalues[35] <- test35$p.value
pvalues[36] <- test36$p.value
pvalues[37] <- test37$p.value
pvalues[38] <- test38$p.value
pvalues[39] <- test39$p.value
pvalues[40] <- test40$p.value

```

```

    pvalues[41] <- test41$p.value
    pvalues[42] <- test42$p.value
    pvalues[43] <- test43$p.value
    pvalues[44] <- test44$p.value
    pvalues[45] <- test45$p.value

    #Fill vector with number of pvalues at or lesser than 0.05
    for each iteration
        hold[i] <- length(pvalues[pvalues <= 0.05])
    }

    #Create file with histogram of randomized iterations
    pdf("histogramGlobal.pdf", width=7, height=7)
        hist(hold, xlab="# of sig. trends", main="10000 Trials
(Global)", las=1, col="gray")
        abline(v=8, col="red")
    dev.off()

```


R command script to perform a random permutation of time stages followed by Spearman's rank correlation tests using 10,000 iterations for all 9 tests conducted in Europe. (Fig. 2.10)

```
####10,000 iterations of a null model by conducting a random
permutation of time stages of global trends followed by
Spearman's rank correlation tests

##Loop, plots, and Spearman's tests of ecological percentages of
PBDB Jurassic regional occurrences

#Read percent confidence interval function
source("percentConfidenceInterval.R")

#Read percent ecology function to calculate percentages with
confidence intervals
source("percentEcolTrait.R")

#Read dataset
occurrences2 <- read.csv('ClusteredOccurrences.csv', header=TRUE,
stringsAsFactors=FALSE)

#Create object to hold results of 10,000 iteration null model
hold <- vector(mode = "numeric", length = 10000)

#Loop to calculate ecological trends by stage per region
for (i in 1:10000) {

    #Create objects to define dimensions of matrices below
    stagecolumn <- 4
    JurassicStages <-
sort(unique(occurrences2[occurrences2$stage!="0", stagecolumn]))
    geoClusters <- sort(unique(occurrences2$geo_cluster))

    #Create empty matrices that will be used to fill estimated
percentages calculated by running loop
    sinfaunalTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    dinfaunalTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    epifaunalTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    cementedTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    freelivingTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
```

```

pedunculateTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
mobileTableE <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))
limitedmobileTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
sessileTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))

```

#Create empty matrices that will be used to fill lower confidence limit percentages calculated by running loop

```

sinfaunalTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
dinfraunalTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
epifaunalTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
cementedTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
freelivingTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
pedunculateTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
mobileTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
limitedmobileTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
sessileTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))

```

#Create empty matrices that will be used to fill upper confidence limit percentages calculated by running loop

```

sinfaunalTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
dinfraunalTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))

```

```

    epifaunalTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    cementedTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    freelivingTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    pedunculateTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    mobileTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    limitedmobileTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    sessileTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))

    #Loop to calculate percentage of each ecological trait by
cluster for each stage
    for (time in 1:length(JurassicStages)) {
      for (geo in 1:length(geoClusters)) {
        sinfaunal <- percentEcolTrait(occurrences2,
"life_habit", "shallow infaunal",
desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
        sinfaunalTableE[time, geo] <- sinfaunal[2]
        sinfaunalTableLCL[time, geo] <- sinfaunal[1]
        sinfaunalTableUCL[time, geo] <- sinfaunal[3]

        dinfaunal <- percentEcolTrait(occurrences2,
"life_habit", "deep infaunal",
desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
        dinfaunalTableE[time, geo] <- dinfaunal[2]
        dinfaunalTableLCL[time, geo] <- dinfaunal[1]
        dinfaunalTableUCL[time, geo] <- dinfaunal[3]

        epifaunal <- percentEcolTrait(occurrences2,
"life_habit", "epifaunal", desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
        epifaunalTableE[time, geo] <- epifaunal[2]
        epifaunalTableLCL[time, geo] <- epifaunal[1]
        epifaunalTableUCL[time, geo] <- epifaunal[3]

        cemented <- percentEcolTrait(occurrences2,
"stability", "cemented", desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])

```

```

        cementedTableE[time, geo] <- cemented[2]
        cementedTableLCL[time, geo] <- cemented[1]
        cementedTableUCL[time, geo] <- cemented[3]

        freeliving <- percentEcolTrait(occurrences2,
"stability", "free-living", desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
        freelivingTableE[time, geo] <- freeliving[2]
        freelivingTableLCL[time, geo] <- freeliving[1]
        freelivingTableUCL[time, geo] <- freeliving[3]

        pedunculate <- percentEcolTrait(occurrences2,
"stability", "pedunculate", desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
        pedunculateTableE[time, geo] <- pedunculate[2]
        pedunculateTableLCL[time, geo] <- pedunculate[1]
        pedunculateTableUCL[time, geo] <- pedunculate[3]

        mobile <- percentEcolTrait(occurrences2,
"motility", "mobile", desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
        mobileTableE[time, geo] <- mobile[2]
        mobileTableLCL[time, geo] <- mobile[1]
        mobileTableUCL[time, geo] <- mobile[3]

        limitedmobile <- percentEcolTrait(occurrences2,
"motility", "limited mobile", desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
        limitedmobileTableE[time, geo] <-
limitedmobile[2]
        limitedmobileTableLCL[time, geo] <-
limitedmobile[1]
        limitedmobileTableUCL[time, geo] <-
limitedmobile[3]

        sessile <- percentEcolTrait(occurrences2,
"motility", "sessile", desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
        sessileTableE[time, geo] <- sessile[2]
        sessileTableLCL[time, geo] <- sessile[1]
        sessileTableUCL[time, geo] <- sessile[3]
    }
}

#Create vector of Jurassic stage boundary ages (Myr) based
on the 2015 ICS Chronostratigraphy Chart
stageBoundaryAges <- c(201.3, 199.3, 190.8, 182.7, 174.1,
170.3, 168.3, 166.1, 163.5, 157.3, 152.1, 145.0)

#Duration of each stage (Myr) – Hettangian: 2.0,
Sinemurian: 8.5, Pliensbachian: 8.1, Toarcian: 8.6, Aalenian:

```

3.8, Bajocian: 2.0, Bathonian: 2.2, Callovian: 2.6, Oxfordian:
6.2, Kimmeridian: 5.2, Tithonian: 7.1

```
#Calculate midpoint of each stage to include in plots
midpointAges <- stageBoundaryAges[-
length(stageBoundaryAges)] + diff(stageBoundaryAges)/2
midpointAges <- sort(midpointAges)

#Randomize stages
midpointAges <- sample(midpointAges, length(midpointAges))

#Create vector to hold number each p-value
pvalues <- vector(mode="numeric", length=9)

#Spearman's rank correlation tests for Europe Cluster
test1 <- cor.test(midpointAges, sinfaunalTableE[,1],
method='spearman')
test2 <- cor.test(midpointAges, dinfaunalTableE[,1],
method='spearman')
test3 <- cor.test(midpointAges, epifaunalTableE[,1],
method='spearman')
test4 <- cor.test(midpointAges, freelivingTableE[,1],
method='spearman')
test5 <- cor.test(midpointAges, cementedTableE[,1],
method='spearman')
test6 <- cor.test(midpointAges, pedunculateTableE[,1],
method='spearman')
test7 <- cor.test(midpointAges, sessileTableE[,1],
method='spearman')
test8 <- cor.test(midpointAges, limitedmobileTableE[,1],
method='spearman')
test9 <- cor.test(midpointAges, mobileTableE[,1],
method='spearman')

#Fill pvalues vector with p-values of each Spearman's
correlation test
pvalues[1] <- test1$p.value
pvalues[2] <- test2$p.value
pvalues[3] <- test3$p.value
pvalues[4] <- test4$p.value
pvalues[5] <- test5$p.value
pvalues[6] <- test6$p.value
pvalues[7] <- test7$p.value
pvalues[8] <- test8$p.value
pvalues[9] <- test9$p.value

#Fill vector with number of pvalues at or lesser than 0.05
for each iteration
  hold[i] <- length(pvalues[pvalues <= 0.05])
}

#Create file with histogram of randomized iterations
pdf("histogramEurope.pdf", width=7, height=7)
```

```
hist(hold, xlab="# of sig. trends", main="10000 Trials  
(Europe)", las=1, col="gray")  
abline(v=4, col="red")  
dev.off()
```

R command script to calculate percent occurrences of European taxonomic groups by tiering. (Fig. 2.11)

```
##Loop, plots, and Spearman's tests of ecological percentages of
PBDB Jurassic regional occurrences

#Read percent confidence interval function
source("percentConfidenceInterval.R")

#Read percent ecology function to calculate percentages with
confidence intervals
source("percentEcolTrait.R")

#Read dataset
occurrences2 <- read.csv('ClusteredOccurrences.csv', header=TRUE,
stringsAsFactors=FALSE)
bivalves <- occurrences2
brachiopods <- occurrences2
everythingElse <- occurrences2
bivalves[bivalves$class_name!="Bivalvia", 18] <- 0
brachiopods[brachiopods$class_name!="Rhynchonellata" &
brachiopods$class_name!="Lingulata", 18] <- 0
everythingElse[everythingElse$class_name=="Rhynchonellata" |
everythingElse$class_name=="Lingulata" |
everythingElse$class_name=="Bivalvia", 18] <- 0

#Create objects to define dimensions of matrices below
stagecolumn <- 4
JurassicStages <-
sort(unique(occurrences2[occurrences2$stage!="0", stagecolumn]))
geoClusters <- sort(unique(occurrences2$geo_cluster))

#Create empty matrices that will be used to fill estimated
percentages calculated by running loop
bi_sinfaunalTableE <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))
bi_dinfaunalTableE <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))
bi_epifaunalTableE <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))
br_sinfaunalTableE <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))
br_dinfaunalTableE <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))
br_epifaunalTableE <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))
```

```

ee_sinfraunalTableE <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))
ee_dinfraunalTableE <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))
ee_epifaunalTableE <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))

```

#Create empty matrices that will be used to fill lower confidence limit percentages calculated by running loop

```

bi_sinfraunalTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
bi_dinfraunalTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
bi_epifaunalTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
br_sinfraunalTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
br_dinfraunalTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
br_epifaunalTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
ee_sinfraunalTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
ee_dinfraunalTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
ee_epifaunalTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))

```

#Create empty matrices that will be used to fill upper confidence limit percentages calculated by running loop

```

bi_sinfraunalTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
bi_dinfraunalTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
bi_epifaunalTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))

```



```

br_sinfraunalTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
br_dinfraunalTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
br_epifaunalTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
ee_sinfraunalTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
ee_dinfraunalTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
ee_epifaunalTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))

#Loop to calculate percentage of each ecological trait by cluster
for each stage
for (time in 1:length(JurassicStages)) {
  for (geo in 1:length(geoClusters)) {
    bi_sinfraunal <- percentEcolTrait(bivalves,
"life_habit", "shallow infaunal",
desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
    bi_sinfraunalTableE[time, geo] <- bi_sinfraunal[2]
    bi_sinfraunalTableLCL[time, geo] <- bi_sinfraunal[1]
    bi_sinfraunalTableUCL[time, geo] <- bi_sinfraunal[3]

    bi_dinfraunal <- percentEcolTrait(bivalves,
"life_habit", "deep infaunal",
desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
    bi_dinfraunalTableE[time, geo] <- bi_dinfraunal[2]
    bi_dinfraunalTableLCL[time, geo] <- bi_dinfraunal[1]
    bi_dinfraunalTableUCL[time, geo] <- bi_dinfraunal[3]

    bi_epifaunal <- percentEcolTrait(bivalves, "life_habit",
"epifaunal", desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
    bi_epifaunalTableE[time, geo] <- bi_epifaunal[2]
    bi_epifaunalTableLCL[time, geo] <- bi_epifaunal[1]
    bi_epifaunalTableUCL[time, geo] <- bi_epifaunal[3]

    br_sinfraunal <- percentEcolTrait(brachiopods, "life_habit",
"shallow infaunal", desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
    br_sinfraunalTableE[time, geo] <- br_sinfraunal[2]
    br_sinfraunalTableLCL[time, geo] <- br_sinfraunal[1]
    br_sinfraunalTableUCL[time, geo] <- br_sinfraunal[3]
  }
}

```

```

        br_dinfaunal <- percentEcolTrait(brachiopods,
"life_habit", "deep infaunal",
desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
        br_dinfaunalTableE[time, geo] <- br_dinfaunal[2]
        br_dinfaunalTableLCL[time, geo] <- br_dinfaunal[1]
        br_dinfaunalTableUCL[time, geo] <- br_dinfaunal[3]

        br_epifaunal <- percentEcolTrait(brachiopods, "life_habit",
"epifaunal",, desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
        br_epifaunalTableE[time, geo] <- br_epifaunal[2]
        br_epifaunalTableLCL[time, geo] <- br_epifaunal[1]
        br_epifaunalTableUCL[time, geo] <- br_epifaunal[3]

        ee_sinfaunal <- percentEcolTrait(everythingElse,
"life_habit", "shallow infaunal",
desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
        ee_sinfaunalTableE[time, geo] <- ee_sinfaunal[2]
        ee_sinfaunalTableLCL[time, geo] <- ee_sinfaunal[1]
        ee_sinfaunalTableUCL[time, geo] <- ee_sinfaunal[3]

        ee_dinfaunal <- percentEcolTrait(everythingElse,
"life_habit", "deep infaunal",
desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
        ee_dinfaunalTableE[time, geo] <- ee_dinfaunal[2]
        ee_dinfaunalTableLCL[time, geo] <- ee_dinfaunal[1]
        ee_dinfaunalTableUCL[time, geo] <- ee_dinfaunal[3]

        ee_epifaunal <- percentEcolTrait(everythingElse,
"life_habit", "epifaunal", desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
        ee_epifaunalTableE[time, geo] <- ee_epifaunal[2]
        ee_epifaunalTableLCL[time, geo] <- ee_epifaunal[1]
        ee_epifaunalTableUCL[time, geo] <- ee_epifaunal[3]

    }
}

#Call tables with estimate percentages
bi_sinfaunalTableE
bi_dinfaunalTableE
bi_epifaunalTableE
br_sinfaunalTableE
br_dinfaunalTableE
br_epifaunalTableE
ee_sinfaunalTableE
ee_dinfaunalTableE
ee_epifaunalTableE

```

```

#Call tables with lower condfidence limit percentages
bi_sinfaunalTableLCL
bi_dinfaunalTableLCL
bi_epifaunalTableLCL
br_sinfaunalTableLCL
br_dinfaunalTableLCL
br_epifaunalTableLCL
ee_sinfaunalTableLCL
ee_dinfaunalTableLCL
ee_epifaunalTableLCL

#Call tables with upper condfidence limit percentages
bi_sinfaunalTableUCL
bi_dinfaunalTableUCL
bi_epifaunalTableUCL
br_sinfaunalTableUCL
br_dinfaunalTableUCL
br_epifaunalTableUCL
ee_sinfaunalTableUCL
ee_dinfaunalTableUCL
ee_epifaunalTableUCL
-----
-----
-----
-----
-----

##Plots

#Create vector of Jurassic stage boundary ages (Myr) based on the
2015 ICS ChronostratigraphyChart
stageBoundaryAges <- c(201.3, 199.3, 190.8, 182.7, 174.1, 170.3,
168.3, 166.1, 163.5, 157.3, 152.1, 145.0)

#Duration of each stage (Myr) – Hettangian: 2.0, Sinemurian:
8.5, Pliensbachian: 8.1, Toarcian: 8.6, Aalenian: 3.8, Bajocian:
2.0, Bathonian: 2.2, Callovian: 2.6, Oxfordian: 6.2, Kimmeridian:
5.2, Tithonian: 7.1

#Calculate midpoint of each stage to include in plots
midpointAges <- stageBoundaryAges[-length(stageBoundaryAges)] +
diff(stageBoundaryAges)/2
midpointAges <- sort(midpointAges)

##Plots of percentages
#Plots of life habit
dev.new(width=4, length=7)
par(mfrow=(c(3,1)), mai=c(0.25, 0.35, 0.075, 0.25))

plot(midpointAges, bi_sinfaunalTableE[,1], main='European
Bivalves', xlab='', ylab='', ylim=range(0:100), las=1, type='n',
axes=FALSE)
axis(1, labels=FALSE, lwd.ticks=0)
axis(2, at=seq(0, 100, by=20), las=1)

```

```

points(midpointAges, bi_sinfraunalTableE[,1], type="o", pch=16,
lty=1, col="blue")
segments(midpointAges, bi_sinfraunalTableLCL[, 1], midpointAges,
bi_sinfraunalTableUCL[, 1], col="blue")
points(midpointAges, bi_dinfraunalTableE[,1], type="o", pch=16,
lty=2, col="blue")
segments(midpointAges, bi_dinfraunalTableLCL[, 1], midpointAges,
bi_dinfraunalTableUCL[, 1], col="blue")
points(midpointAges, bi_epifaunalTableE[,1], type="o", pch=16,
lty=3, col="red")
segments(midpointAges, bi_epifaunalTableLCL[, 1], midpointAges,
bi_epifaunalTableUCL[, 1], col="red")
legend("top", c("epifaunal", "shallow infaunal", "deep
infaunal"), bty="n", lty=c(3, 1, 2), col=c("red", "blue",
"blue"), horiz=TRUE, x.intersp=0.5)

```

```

plot(midpointAges, br_sinfraunalTableE[,1], main='European
Brachiopods', xlab='', ylab='', ylim=range(0:100), las=1,
type='n', axes=FALSE)
axis(1, labels=FALSE, lwd.ticks=0)
axis(2, at=seq(0, 100, by=20), las=1)
points(midpointAges, br_sinfraunalTableE[,1], type="o", pch=16,
lty=1, col="blue")
segments(midpointAges, br_sinfraunalTableLCL[, 1], midpointAges,
br_sinfraunalTableUCL[, 1], col="blue")
points(midpointAges, br_dinfraunalTableE[,1], type="o", pch=16,
lty=2, col="blue")
segments(midpointAges, br_dinfraunalTableLCL[, 1], midpointAges,
br_dinfraunalTableUCL[, 1], col="blue")
points(midpointAges, br_epifaunalTableE[,1], type="o", pch=16,
lty=3, col="red")
segments(midpointAges, br_epifaunalTableLCL[, 1], midpointAges,
br_epifaunalTableUCL[, 1], col="red")

```

```

plot(midpointAges, ee_sinfraunalTableE[,1], main='European
Everything Else', xlab='', ylab='', ylim=range(0:100), las=1,
type='n', axes=FALSE)
axis(1, at=midpointAges, labels=c("He", "Si", "Pl", "To", "Aa",
"Baj", "Bat", "Ca", "Ox", "Ki", "Ti"), xlab='Jurassic Stages')
axis(2, at=seq(0, 100, by=20), las=1)
points(midpointAges, ee_sinfraunalTableE[,1], type="o", pch=16,
lty=1, col="blue")
segments(midpointAges, ee_sinfraunalTableLCL[, 1], midpointAges,
ee_sinfraunalTableUCL[, 1], col="blue")
points(midpointAges, ee_dinfraunalTableE[,1], type="o", pch=16,
lty=2, col="blue")
segments(midpointAges, ee_dinfraunalTableLCL[, 1], midpointAges,
ee_dinfraunalTableUCL[, 1], col="blue")
points(midpointAges, ee_epifaunalTableE[,1], type="o", pch=16,
lty=3, col="red")
segments(midpointAges, ee_epifaunalTableLCL[, 1], midpointAges,
ee_epifaunalTableUCL[, 1], col="red")

```

```

-----
-----
-----
-----
##Spearman's rank correlation tests of ecological metrics for
each region by Jurassic stages

#Spearman's rank correlation tests for Europe Bivalves
cor.test(midpointAges, bi_sinfaunalTableE[,1], method='spearman')
cor.test(midpointAges, bi_dinfaunalTableE[,1], method='spearman')
cor.test(midpointAges, bi_epifaunalTableE[,1], method='spearman')

#Spearman's rank correlation tests for Europe Brachiopods
cor.test(midpointAges, br_sinfaunalTableE[,1], method='spearman')
cor.test(midpointAges, br_dinfaunalTableE[,1], method='spearman')
cor.test(midpointAges, br_epifaunalTableE[,1], method='spearman')

#Spearman's rank correlation tests for Europe Everything Else
cor.test(midpointAges, ee_sinfaunalTableE[,1], method='spearman')
cor.test(midpointAges, ee_dinfaunalTableE[,1], method='spearman')
cor.test(midpointAges, ee_epifaunalTableE[,1], method='spearman')

```

R command script to perform frequency distribution of statistically significant trends in Europe. This method uses a random permutation of occurrences by region followed by Spearman's rank correlation tests using 10,000 iterations for all nine tests conducted. (Fig. 2.12)

```
#####10,000 iterations of a null model by conducting a random
permutation of ecological trends by shuffling regions then
followed by Spearman's rank correlation tests
#(note that this script takes at least 26 hours to run)

##Loop, plots, and Spearman's tests of ecological percentages of
PBDB Jurassic regional occurrences

#Read percent confidence interval function
source("percentConfidenceInterval.R")

#Read percent ecology function to calculate percentages with
confidence intervals
source("percentEcolTrait.R")

#Read dataset
occurrences2 <- read.csv('ClusteredOccurrences.csv', header=TRUE,
stringsAsFactors=FALSE)

#Create object to hold results of 10,000 iteration null model
hold <- vector(mode = "numeric", length = 10000)
EU_hold <- vector(mode = "numeric", length = 10000)

#Create objects to define dimensions of matrices below
stagecolumn <- 4
JurassicStages <-
sort(unique(occurrences2[occurrences2$stage!="0", stagecolumn]))
geoClusters <- sort(unique(occurrences2$geo_cluster))

#Loop to calculate ecological trends by stage per region
for (i in 1:10000) {
  geoClusters <- sample(geoClusters, length(geoClusters))
#regional shuffle

  #Create empty matrices that will be used to fill estimated
percentages calculated by running loop
  sinfaunalTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
  dinfaunalTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
  epifaunalTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
```

```

    cementedTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    freelifvingTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    pedunculateTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    mobileTableE <- matrix(data=0, nrow=length(JurassicStages),
ncol=length(geoClusters), dimnames=list(JurassicStages,
geoClusters))
    limitedmobileTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    sessileTableE <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))

    #Create empty matrices that will be used to fill lower
confidence limit percentages calculated by running loop
    sinfaunalTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    dinfaunalTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    epifaunalTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    cementedTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    freelifvingTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    pedunculateTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    mobileTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    limitedmobileTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    sessileTableLCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))

    #Create empty matrices that will be used to fill upper
condfidence limit percentages calculated by running loop

```

```

    sinfaunalTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    dinfaunalTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    epifaunalTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    cementedTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    freelivingTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    pedunculateTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    mobileTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    limitedmobileTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))
    sessileTableUCL <- matrix(data=0,
nrow=length(JurassicStages), ncol=length(geoClusters),
dimnames=list(JurassicStages, geoClusters))

    #Loop to calculate percentage of each ecological trait by
cluster for each stage
    for (time in 1:length(JurassicStages)) {
        for (geo in 1:length(geoClusters)) {

            sinfaunal <- percentEcolTrait(occurrences2,
"life_habit", "shallow infaunal",
desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
            sinfaunalTableE[time, geo] <- sinfaunal[2]
            sinfaunalTableLCL[time, geo] <- sinfaunal[1]
            sinfaunalTableUCL[time, geo] <- sinfaunal[3]

            dinfaunal <- percentEcolTrait(occurrences2,
"life_habit", "deep infaunal",
desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
            dinfaunalTableE[time, geo] <- dinfaunal[2]
            dinfaunalTableLCL[time, geo] <- dinfaunal[1]
            dinfaunalTableUCL[time, geo] <- dinfaunal[3]

            epifaunal <- percentEcolTrait(occurrences2,
"life_habit", "epifaunal", desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
            epifaunalTableE[time, geo] <- epifaunal[2]

```



```

        epifaunalTableLCL[time, geo] <- epifaunal[1]
        epifaunalTableUCL[time, geo] <- epifaunal[3]

        cemented <- percentEcolTrait(occurrences2,
"stability", "cemented", desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
        cementedTableE[time, geo] <- cemented[2]
        cementedTableLCL[time, geo] <- cemented[1]
        cementedTableUCL[time, geo] <- cemented[3]

        freeliving <- percentEcolTrait(occurrences2,
"stability", "free-living", desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
        freelivingTableE[time, geo] <- freeliving[2]
        freelivingTableLCL[time, geo] <- freeliving[1]
        freelivingTableUCL[time, geo] <- freeliving[3]

        pedunculate <- percentEcolTrait(occurrences2,
"stability", "pedunculate", desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
        pedunculateTableE[time, geo] <- pedunculate[2]
        pedunculateTableLCL[time, geo] <- pedunculate[1]
        pedunculateTableUCL[time, geo] <- pedunculate[3]

        mobile <- percentEcolTrait(occurrences2,
"motility", "mobile", desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
        mobileTableE[time, geo] <- mobile[2]
        mobileTableLCL[time, geo] <- mobile[1]
        mobileTableUCL[time, geo] <- mobile[3]

        limitedmobile <- percentEcolTrait(occurrences2,
"motility", "limited mobile", desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
        limitedmobileTableE[time, geo] <-
limitedmobile[2]
        limitedmobileTableLCL[time, geo] <-
limitedmobile[1]
        limitedmobileTableUCL[time, geo] <-
limitedmobile[3]

        sessile <- percentEcolTrait(occurrences2,
"motility", "sessile", desiredStages=JurassicStages[time],
desiredGeoclusters=geoClusters[geo])
        sessileTableE[time, geo] <- sessile[2]
        sessileTableLCL[time, geo] <- sessile[1]
        sessileTableUCL[time, geo] <- sessile[3]
    }
}

```

```

#Create vector of Jurassic stage boundary ages (Myr) based
on the 2015 ICS Chronostratigraphy Chart

```

```
stageBoundaryAges <- c(201.3, 199.3, 190.8, 182.7, 174.1,
170.3, 168.3, 166.1, 163.5, 157.3, 152.1, 145.0)
```

```
#Duration of each stage (Myr) – Hettangian: 2.0,
Sinemurian: 8.5, Pliensbachian: 8.1, Toarcian: 8.6, Aalenian:
3.8, Bajocian: 2.0, Bathonian: 2.2, Callovian: 2.6, Oxfordian:
6.2, Kimmeridian: 5.2, Tithonian: 7.1
```

```
#Calculate midpoint of each stage to include in plots
midpointAges <- stageBoundaryAges[-
length(stageBoundaryAges)] + diff(stageBoundaryAges)/2
midpointAges <- sort(midpointAges)
```

```
#Create vector to hold number each p-value
pvalues <- vector(mode="numeric", length=45)
EU_pvalues <- vector(mode="numeric", length=9)
```

```
#Spearman's rank correlation tests for Europe Cluster
test1 <- cor.test(midpointAges, sinfaunalTableE[,1],
method='spearman')
test2 <- cor.test(midpointAges, dinfaunalTableE[,1],
method='spearman')
test3 <- cor.test(midpointAges, epifaunalTableE[,1],
method='spearman')
test4 <- cor.test(midpointAges, freelivingTableE[,1],
method='spearman')
test5 <- cor.test(midpointAges, cementedTableE[,1],
method='spearman')
test6 <- cor.test(midpointAges, pedunculateTableE[,1],
method='spearman')
test7 <- cor.test(midpointAges, sessileTableE[,1],
method='spearman')
test8 <- cor.test(midpointAges, limitedmobileTableE[,1],
method='spearman')
test9 <- cor.test(midpointAges, mobileTableE[,1],
method='spearman')
```

```
#Spearman's rank correlation tests for Middle East Cluster
test10 <- cor.test(midpointAges, sinfaunalTableE[,2],
method='spearman')
test11 <- cor.test(midpointAges, dinfaunalTableE[,2],
method='spearman')
test12 <- cor.test(midpointAges, epifaunalTableE[,2],
method='spearman')
test13 <- cor.test(midpointAges, freelivingTableE[,2],
method='spearman')
test14 <- cor.test(midpointAges, cementedTableE[,2],
method='spearman')
test15 <- cor.test(midpointAges, pedunculateTableE[,2],
method='spearman')
test16 <- cor.test(midpointAges, sessileTableE[,2],
method='spearman')
```

```

    test17 <- cor.test(midpointAges, limitedmobileTableE[,2],
method='spearman')
    test18 <- cor.test(midpointAges, mobileTableE[,2],
method='spearman')

    #Spearman's rank correlation tests for New Zealand Cluster
    test19 <- cor.test(midpointAges, sinfaunalTableE[,3],
method='spearman')
    test20 <- cor.test(midpointAges, dinfaunalTableE[,3],
method='spearman')
    test21 <- cor.test(midpointAges, epifaunalTableE[,3],
method='spearman')
    test22 <- cor.test(midpointAges, freelivingTableE[,3],
method='spearman')
    test23 <- cor.test(midpointAges, cementedTableE[,3],
method='spearman')
    test24 <- cor.test(midpointAges, pedunculateTableE[,3],
method='spearman')
    test25 <- cor.test(midpointAges, sessileTableE[,3],
method='spearman')
    test26 <- cor.test(midpointAges, limitedmobileTableE[,3],
method='spearman')
    test27 <- cor.test(midpointAges, mobileTableE[,3],
method='spearman')

    #Spearman's rank correlation tests for North America
    Cluster
    test28 <- cor.test(midpointAges, sinfaunalTableE[,4],
method='spearman')
    test29 <- cor.test(midpointAges, dinfaunalTableE[,4],
method='spearman')
    test30 <- cor.test(midpointAges, epifaunalTableE[,4],
method='spearman')
    test31 <- cor.test(midpointAges, freelivingTableE[,4],
method='spearman')
    test32 <- cor.test(midpointAges, cementedTableE[,4],
method='spearman')
    test33 <- cor.test(midpointAges, pedunculateTableE[,4],
method='spearman')
    test34 <- cor.test(midpointAges, sessileTableE[,4],
method='spearman')
    test35 <- cor.test(midpointAges, limitedmobileTableE[,4],
method='spearman')
    test36 <- cor.test(midpointAges, mobileTableE[,4],
method='spearman')

    #Spearman's rank correlation tests for South America
    Cluster
    test37 <- cor.test(midpointAges, sinfaunalTableE[,5],
method='spearman')
    test38 <- cor.test(midpointAges, dinfaunalTableE[,5],
method='spearman')

```

```

test39 <- cor.test(midpointAges, epifaunalTableE[,5],
method='spearman')
test40 <- cor.test(midpointAges, freelivingTableE[,5],
method='spearman')
test41 <- cor.test(midpointAges, cementedTableE[,5],
method='spearman')
test42 <- cor.test(midpointAges, pedunculateTableE[,5],
method='spearman')
test43 <- cor.test(midpointAges, sessileTableE[,5],
method='spearman')
test44 <- cor.test(midpointAges, limitedmobileTableE[,5],
method='spearman')
test45 <- cor.test(midpointAges, mobileTableE[,5],
method='spearman')

```

```

#Fill pvalues vector with p-values of each Spearman's
correlation test

```

```

pvalues[1] <- test1$p.value
pvalues[2] <- test2$p.value
pvalues[3] <- test3$p.value
pvalues[4] <- test4$p.value
pvalues[5] <- test5$p.value
pvalues[6] <- test6$p.value
pvalues[7] <- test7$p.value
pvalues[8] <- test8$p.value
pvalues[9] <- test9$p.value
pvalues[10] <- test10$p.value
pvalues[11] <- test11$p.value
pvalues[12] <- test12$p.value
pvalues[13] <- test13$p.value
pvalues[14] <- test14$p.value
pvalues[15] <- test15$p.value
pvalues[16] <- test16$p.value
pvalues[17] <- test17$p.value
pvalues[18] <- test18$p.value
pvalues[19] <- test19$p.value
pvalues[20] <- test20$p.value
pvalues[21] <- test21$p.value
pvalues[22] <- test22$p.value
pvalues[23] <- test23$p.value
pvalues[24] <- test24$p.value
pvalues[25] <- test25$p.value
pvalues[26] <- test26$p.value
pvalues[27] <- test27$p.value
pvalues[28] <- test28$p.value
pvalues[29] <- test29$p.value
pvalues[30] <- test30$p.value
pvalues[31] <- test31$p.value
pvalues[32] <- test32$p.value
pvalues[33] <- test33$p.value
pvalues[34] <- test34$p.value
pvalues[35] <- test35$p.value
pvalues[36] <- test36$p.value

```

```

pvalues[37] <- test37$p.value
pvalues[38] <- test38$p.value
pvalues[39] <- test39$p.value
pvalues[40] <- test40$p.value
pvalues[41] <- test41$p.value
pvalues[42] <- test42$p.value
pvalues[43] <- test43$p.value
pvalues[44] <- test44$p.value
pvalues[45] <- test45$p.value

#Fill vector with number of pvalues at or lesser than 0.05
for each iteration
  hold[i] <- length(pvalues[pvalues <= 0.05])

  EU_pvalues[1] <- test1$p.value
  EU_pvalues[2] <- test2$p.value
  EU_pvalues[3] <- test3$p.value
  EU_pvalues[4] <- test4$p.value
  EU_pvalues[5] <- test5$p.value
  EU_pvalues[6] <- test6$p.value
  EU_pvalues[7] <- test7$p.value
  EU_pvalues[8] <- test8$p.value
  EU_pvalues[9] <- test9$p.value

  EU_hold[i] <- length(EU_pvalues[EU_pvalues <= 0.05])
}

#Create file with histogram of randomized iterations
pdf("histogramGlobal.pdf", width=7, height=7)
  hist(hold, xlab="# of sig. trends", main="10000 Trials
(Global)", las=1, col="gray")
  abline(v=8, col="red")
  dev.off()

pdf("histogramEurope.pdf", width=7, height=7)
  hist(EU_hold, xlab="# of sig. trends", main="10000 Trials
(Europe)", las=1, col="gray")
  abline(v=4, col="red")
  dev.off()

#Calculate p-values
length(hold[hold >= 8])/10000
length(EU_hold[EU_hold >= 4])/10000s

```

Part 2: Data

Coordinates used to parse global Paleobiology Database data into different regions.

Longitude	Latitude	Polygon	Longitude	Latitude	Polygon
-41.114	75.639	Polygon 1	176.892	55.292	Polygon 3
-52.04	65.859	Polygon 1	180.09	63.404	Polygon 3
-64.763	41.244	Polygon 1	179.54	89.616	Polygon 3
-68.668	28.542	Polygon 1	172.819	92.757	Polygon 3
-67.45	22.521	Polygon 1	146.396	88.916	Polygon 3
-66.708	16.804	Polygon 1	138.019	87.345	Polygon 3
-58.732	12.173	Polygon 1	129.24	86.298	Polygon 3
-47.102	7.221	Polygon 1	125.47	85.795	Polygon 3
-35.092	11.167	Polygon 1	122.365	85.02	Polygon 3
-28.501	32.851	Polygon 1	-28.291	-18.393	Polygon 4
-28.634	40.862	Polygon 1	-29.223	-27.549	Polygon 4
-33.431	47.583	Polygon 1	-30.425	-37.292	Polygon 4
-31.279	60.668	Polygon 1	-31.302	-47.052	Polygon 4
-26.577	73.37	Polygon 1	-31.303	-52.61	Polygon 4
-41.114	75.639	Polygon 1	-26.619	-52.61	Polygon 4
17.143	54.215	Polygon 2	-19.196	-52.611	Polygon 4
-1.838	42.601	Polygon 2	-6.347	-49.751	Polygon 4
-2.296	35.395	Polygon 2	-6.346	-42.566	Polygon 4
-2.297	27.062	Polygon 2	-6.346	-38.741	Polygon 4
0.424	17.462	Polygon 2	-10.133	-29.038	Polygon 4
5.734	11.081	Polygon 2	-12.664	-21.81	Polygon 4
24.162	2.606	Polygon 2	-13.997	-18.828	Polygon 4
44.629	9.489	Polygon 2	-22.831	-18.324	Polygon 4
46.439	20.6	Polygon 2	-28.291	-18.393	Polygon 4
39.701	35.68	Polygon 2	46.485	5.774	Polygon 5
40.766	38.699	Polygon 2	38.622	-0.183	Polygon 5
39.397	40.412	Polygon 2	34.949	-6.52	Polygon 5
35.037	45.124	Polygon 2	28.725	-19.017	Polygon 5
27.043	53.379	Polygon 2	22.211	-40.573	Polygon 5
17.143	54.215	Polygon 2	28.605	-47.478	Polygon 5
122.365	85.02	Polygon 3	50.187	-47.318	Polygon 5
121.925	73.751	Polygon 3	50.511	-43.171	Polygon 5
128.754	50.06	Polygon 3	52.912	-29.258	Polygon 5
146.778	41.142	Polygon 3	48.345	-21.287	Polygon 5
155.686	39.23	Polygon 3	49.716	-11.423	Polygon 5
176.434	45.892	Polygon 3	51.125	-0.091	Polygon 5

Longitude	Latitude	Polygon
46.485	5.774	Polygon 5
77.683	-60.361	Polygon 6
55.715	-72.754	Polygon 6
55.713	-91.132	Polygon 6
80.723	-90.953	Polygon 6
96.982	-90.773	Polygon 6
113.752	-90.774	Polygon 6
184.265	-90.617	Polygon 6
184.266	-80.588	Polygon 6
150.404	-75.776	Polygon 6
132.112	-73.683	Polygon 6
120.158	-71.768	Polygon 6
108.948	-68.406	Polygon 6
98.61	-65.547	Polygon 6
82.754	-61.381	Polygon 6
77.683	-60.361	Polygon 6

Paleobiology Database Collections Used

1198	1199	1200	1201	1202	1203
1204	1205	1206	1207	1210	1212
1214	1215	1216	1218	1219	1220
1221	1222	1225	1226	1227	1228
1229	1230	1231	1232	1233	1234
1235	1236	1237	1238	1239	1240
1241	1242	1243	1244	1245	1246
1247	1248	1249	1250	1251	1252
1253	1254	1255	1256	1257	1258
1259	1260	1261	1262	1263	1264
1265	1266	1267	1268	1269	1270
1271	1272	1273	1274	1275	1276
1277	1278	1279	1280	1281	1405
1406	1407	1408	1409	1410	1412
1456	1458	1459	1460	1461	1462
1463	1464	1465	1466	1467	1468
1469	1470	1471	1472	1473	1474
1475	1476	1477	1478	1479	1480
1481	1482	1483	1494	1495	1496
1497	1498	1499	1500	1501	1502
1504	1505	1506	1507	1508	1555
1556	1557	1558	1559	1560	1561
1562	1563	1565	1566	1567	1568
1569	1570	1571	1572	1573	1574
1598	1599	1602	1603	1604	1605
1606	1607	1608	1609	1610	1611
1612	1613	1899	1900	1901	1903
1904	1906	1907	1909	1911	1912
1914	1915	1917	1920	2092	2093
2095	2096	2098	2101	2103	2104
2105	2106	2107	2108	2109	2110
2111	2136	2137	2138	2139	2140
2141	2142	2143	2144	2550	2551
2552	2553	2554	2555	2556	2557
2558	2560	2562	2563	2564	2565
2566	2567	2582	2583	2584	2586
2587	2588	2589	2590	2591	2592
2593	2594	2595	2596	2597	2598
2599	2600	2601	2603	2604	2605

2606	2607	2608	2609	2610	2611
2615	2618	2649	2651	2652	2653
2654	2656	2657	2658	2659	2660
2662	2663	2664	2665	2666	2667
2668	2669	2670	4077	4078	4079
4080	4081	4082	4084	4085	4086
4087	4088	4089	4090	4091	4092
4093	4094	4095	4096	4097	4098
4777	4778	4779	4780	4781	4782
4783	4784	4785	4786	4787	4788
4789	4848	4849	4850	4853	4854
4855	4856	4857	4858	4859	4860
4861	4881	4882	4883	4903	4904
4905	4906	4907	4908	4909	4910
4911	4912	4913	4914	4915	4916
4917	4918	4919	4920	4921	4923
4924	4925	4926	5199	5200	5203
5206	5207	5208	5209	5210	5211
5214	5221	5223	5227	5228	5229
5231	5232	5236	5237	5238	5239
5240	5242	5243	5244	5245	5246
5247	5248	5249	5443	5446	5450
5455	5467	5470	5472	5475	5487
5489	5490	5936	5937	5938	5939
5940	5957	5958	5988	6010	6011
6013	6872	7054	7055	7056	7057
7058	7059	7075	7076	7077	7078
7079	7080	7081	7082	7083	7393
7394	7395	7406	7407	7408	7409
7410	7411	7412	7413	7414	7415
7416	7417	7418	7419	7420	7421
7422	7423	7424	7425	7426	7427
7428	7429	7430	7431	7432	7433
7434	7435	7436	7868	7869	7870
7877	7888	7889	7891	7892	7893
7894	7895	7896	7913	7914	7915
7916	8040	8041	8042	8043	8044
8045	8046	8098	8099	8100	8101
8151	8152	8153	8154	8155	8156
8157	8158	8159	8160	8161	8162

8163	8164	8165	8166	8168	8169
8170	8184	8185	8201	8202	8203
8204	8205	8206	8282	8283	8285
8287	8317	8318	8319	8335	8336
8337	8363	8364	8365	8400	8401
8402	8425	8426	8427	8511	8512
8513	8514	8516	8517	8518	8519
8520	8521	8522	8525	8526	8574
8600	8601	8602	8603	8604	8608
8652	8653	8654	8655	8656	8657
8658	8659	8660	8661	8666	8667
8668	8670	8671	8672	8673	8674
8805	8806	8807	8834	8835	8836
9138	9140	9141	10701	10702	11818
11820	12005	12006	12007	12008	12009
12010	12011	12012	12013	12014	12015
12016	12017	12018	12019	12020	12084
12085	12086	12087	12088	12089	12090
12091	12092	12093	12094	12095	12096
12097	12098	12099	12100	12110	12123
12124	12125	12126	12127	12128	12129
12130	12131	12132	12133	12134	12135
12136	12137	12138	12139	12140	12141
12142	12150	12151	12152	12153	12340
12363	12924	12925	12926	12927	12978
12979	12980	12981	12982	13029	13030
13031	13032	13033	13034	13035	13036
13037	13055	13056	13057	13058	13059
13111	13112	13113	13114	13115	13116
13117	13118	13119	13120	13121	13122
13123	13124	13125	13126	13147	13148
13149	13150	13151	13367	13368	13369
13370	13371	13372	13373	13374	13375
13376	13377	13378	13379	13380	13381
13382	13383	13384	13385	13386	13387
13388	13389	13390	13391	13392	13393
13394	13395	13396	13397	13398	13399
13400	13401	13504	13505	13506	13507
13508	13509	13510	13514	13515	13516
13517	13518	13519	13520	13583	13584

13585	13586	13587	13588	13589	13590
13607	13608	13609	13610	13611	13612
13613	13614	13659	13660	13661	13662
13663	13664	13665	13666	13667	13668
13676	13677	13688	13689	13783	13784
13785	13786	13788	13789	13790	13791
13792	13793	13794	13795	13796	13797
13809	13810	13811	13813	13856	13857
13858	13860	13863	13864	13865	13866
13867	13868	13869	13870	13871	13898
13899	13900	13901	13902	13903	13904
13905	13950	13951	13952	13953	21186
21252	21268	22785	23624	23625	23626
23627	23628	23812	23814	23815	23816
23817	23818	23833	23839	23840	23841
23842	23843	23844	23845	23846	23847
23848	23849	23850	23851	23852	23853
23854	23855	23856	23857	23858	23859
23860	23862	23863	23864	23865	23866
23868	23871	23872	24862	25211	25212
25213	25214	25215	25216	25217	25218
25416	25417	25418	25419	25502	25608
25609	25610	25611	25612	25613	25614
25615	25616	25617	25618	25619	25620
25621	25661	25662	25663	25664	25665
25666	25667	25668	25669	25670	25671
25672	25673	25674	25675	25771	25772
25773	25774	25775	25776	25777	25778
25779	25780	25781	25782	25783	25784
25879	25880	25881	25882	25883	25885
25886	25887	25888	25936	25937	25938
25939	25940	25941	25942	25943	25944
25945	25946	25947	25948	25949	25950
25951	25952	25953	25954	25955	25956
25957	25958	25959	25960	25961	25962
25963	25964	25965	25966	25967	25968
26137	26138	26139	26140	26141	26142
26143	26144	26145	26146	26147	26148
26149	26150	26151	26152	26153	26154
26155	26156	26321	26322	26323	26324

26325	26326	26327	26328	26329	26330
26332	26334	26335	26336	26382	26383
26384	26385	26386	26387	26388	26389
26390	26391	26393	26395	26397	26398
26400	26401	26403	26639	26790	26795
27224	27225	27226	27227	27228	27354
27355	27356	27890	28444	28506	28839
28842	28844	28845	28847	28867	28868
28869	28870	28871	28872	28873	28874
28875	28876	28877	28878	28879	28880
28881	28882	28883	28884	28885	28886
28887	28888	28889	28890	28891	28892
28893	28894	28895	28896	28897	28929
28930	28931	28932	28933	28934	28935
28936	28939	28940	28941	28942	28944
28945	28948	28949	28952	28958	28960
28962	28965	29024	29025	29027	29028
29030	29031	29032	29033	29034	29035
29036	29037	29038	29039	29040	29042
29043	29044	29045	29046	29047	29048
29049	29050	29051	29052	29053	29054
29055	29056	29057	29058	29060	29061
29062	29063	29064	29081	29082	29083
29084	29085	29086	29087	29088	29089
29090	29091	29092	29093	29113	29114
29115	29163	29164	29165	29166	29167
29168	29169	29170	29171	29172	29173
29174	29175	29176	29177	29178	29179
29180	29181	29182	29183	29184	29185
29186	29187	29225	29226	29227	29228
29230	29231	29232	29233	29234	29235
29236	29237	29238	29239	29240	29241
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170483	170484	170485	170486	170489	170490
170492	170493	170494	170495	170496	170497
170498	170499	170500	170501	170511	170518
170528	170532	170533	170534	170536	170537
170538	170539	170540	170541	170542	170543
170544	170545	170549	170551	170553	170554
170555	170556	170558	170559	170560	170565
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170585	170586	170591	170593	170608	170609
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170623	170625	170626	170627	170628	170629
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171017	171043	171044	171045	171046	171047
171048	171053	171057	171059	171060	171061
171062	171063	171126	171127	171128	171129
171130	171131	171132	171133	171134	171135
171136	171137	171138	171139	171140	171141
171142	171143	171144	171145	171313	171314
171315	171316	171317	171318	171319	171320
171321	171322	171323	171324	171325	171326
171327	171328	171329	171330	171333	171334
171335	171336	171338	171339	171340	171341
171342	171347	171348	171349	171363	171364
171386	171387	171389	171412	171413	171414
171415	171416	171417	171418	171419	171420
171421	171422	171432	171436	171440	171441
171442	171443	171444	171448	171450	171552
171616	171669	171670	171671	171726	171727
171853	171854	171855	171856	171857	171858
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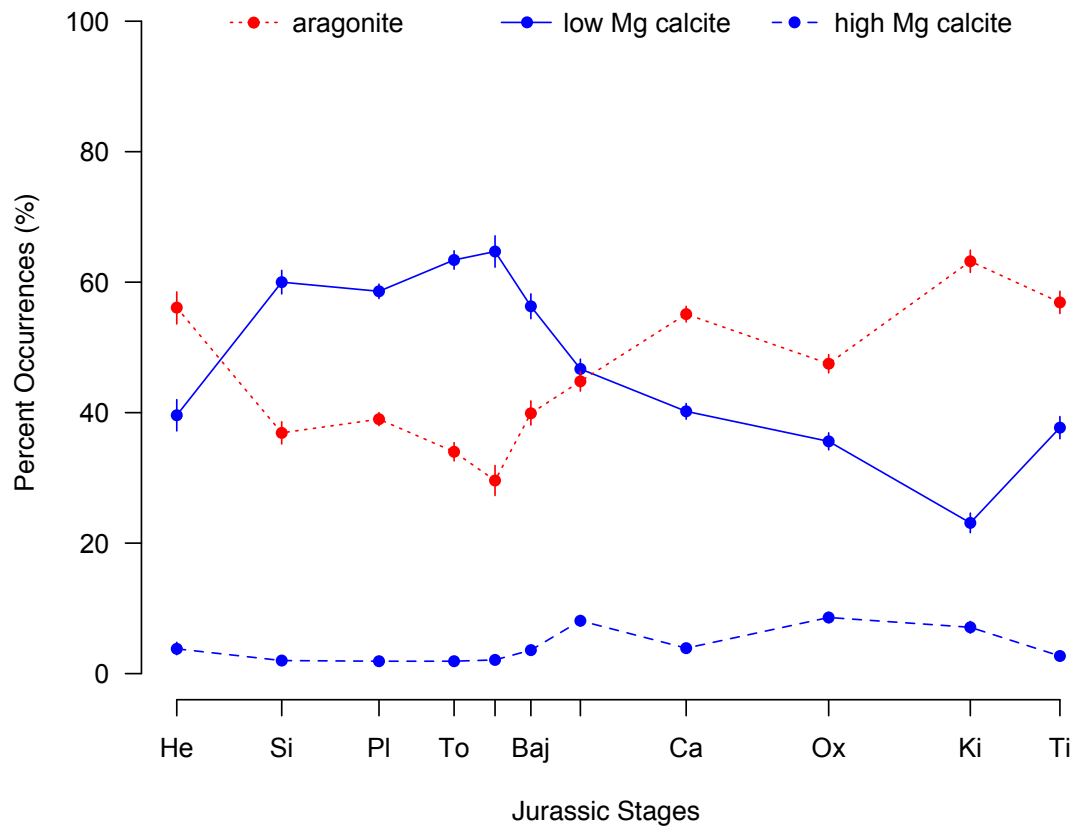
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171892	171893	171905	171906	171907	171909
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171917	171918	171919	171920	171924	171925
171926	171927	171928	171929	171930	171941
171946	171947	171948	171949	171950	171951
171952	171953	171954	171955	171956	171957
171958	171959	171960	171961	171962	171963
171965	171966	171967	171968	171970	171971
171972	171973	171974	171975	171976	171977
171978	171979	171980	171981	171982	171983
171984	171985	171986	171987	171988	171989
171990	171992	171993	172004	172005	172006
172007	172008	172009	172010	172011	172012
172013	172014	172015	172016	172017	172018
172019	172020	172021	172022	172023	172024
172025	172026	172027	172028	172029	172031
172032	172033	172034	172035	172036	172037
172038	172039	172040	172041	172042	172043
172044	172045	172046	172047	172590	172591
172592	172981	172982	172983	172984	172985
172986	173593	173631	173632	173635	173641
173642	174250	174255	174256	174261	174265
174266	174267	174295	174296	174297	174298
174299	174302	174304	174305	174306	174308
174309	174310	174311	174312	174313	174318
174319	174358	174359	174423	174424	174425
174426	174427	174428	174429	174430	174431
174432	174433	174434	174435	174436	174437
174438	174439	174440	174441	174442	174443
174444	174445	174446	174447	174448	174449
174450	174451	174610	174611	174612	174613
174614	174615	174630	174631	174632	174633
174634	174635	174636	174637	174638	174639
174640	174641	174642	174690	174691	174692
174693	174694	174695	174696	174697	174698
174699	174700	175360	175363	175828	175832
176060	176124				

Part 3: Supplementary Material

Spearman's rank correlation test of changes in tiering by taxonomic groups over time during the Jurassic in Europe. Bold font indicates trends that are in the expected direction, with the sign of the correlation coefficient indicating direction of predicted escalatory pattern. Values of Spearman's ρ shown with significance codes for p -values: ***: $p < 0.001$; **: $p < 0.01$; *: $p < 0.05$; •: $p < 0.1$. This table summarizes the trends in Figure 2.11.

Ecologic Metric/Region	Europe
Bivalves	
shallow infaunal	0.56•
deep infaunal	0.59•
epifaunal	0.23
Brachiopods	
shallow infaunal	0.16
deep infaunal	NA
epifaunal	-0.59•
Other Fauna	
shallow infaunal	-0.04
deep infaunal	NA
epifaunal	0.25

Global Shell Mineralogy



Percent occurrences of all taxa by shell mineralogy. This plot was created to test whether the escalatory trends observed during the Late Jurassic are attributed to the taphonomic effects of global ocean seawater chemistry. See Discussion section of Chapter 2.

APPENDIX B

MONOGRAPH, DATA, AND R CODE FOR CHAPTER 3

Part 1: Taxonomic Monograph

Plate 1

Bivalvia

- A. *Astarte?* sp. (sample BD-2A-8)
- B. *Corbula?* sp. (sample BD-2A-18)
- C. *Liostrea* sp. (sample BD-1A-2)
- D. *Liostrea strigecula* (sample BD-2A-16)
- E. *Plagiostoma* sp. (sample BD-1A15)

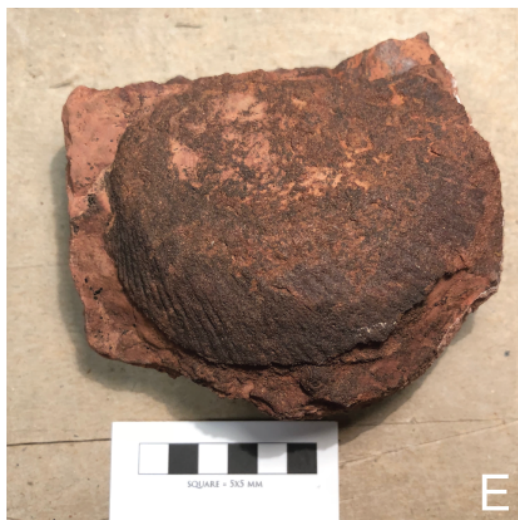
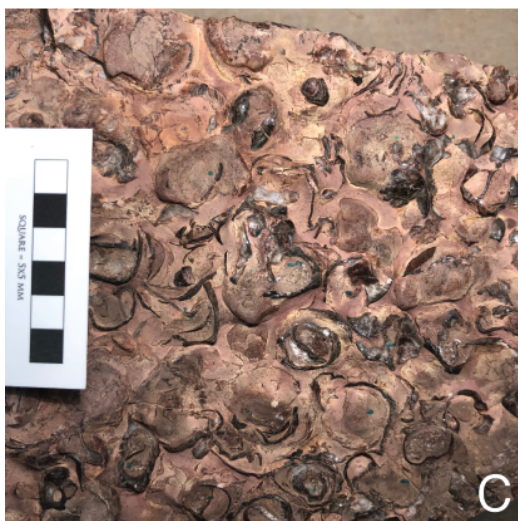


Plate 1

Plate 2

Bivalvia

- A. *Isognomon?* sp. (sample BD-2A-21)
- B. *Isognomon perplana* (sample BD-2A-23)
- C. *Myophorella* sp. (sample BD-1A-10)
- D. *Myophorella montanaensis?* (sample BD-1A-13)
- E. *Vaugonia* sp. (BD-2A-8)
- F. *Vaugonia conradi* (BD-1A-10)

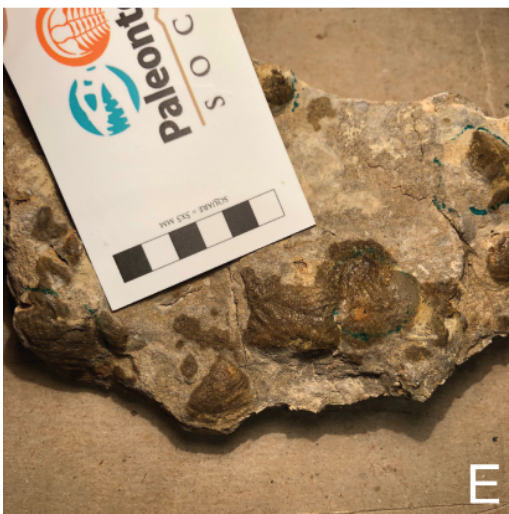


Plate 2

Plate 3

Bivalvia

- A. *Actinostreon* sp. (sample BD-1A-2)
- B. *Camptonectes* sp. (sample BD-1A-7)
- C. *Camptonectes platessioformis* (sample BD-1A-13)
- D. *Camptonectes stygius* (sample BD-2A-12)
- E. *Plicatula* sp. (sample BD-1A-1)
- F. *Trigonia?* sp. (sample BD-2A-1)

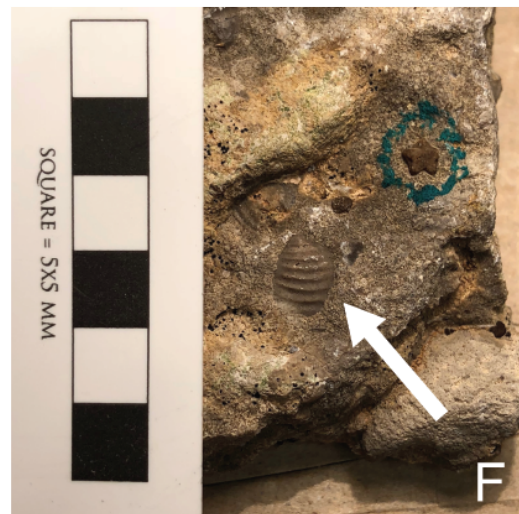
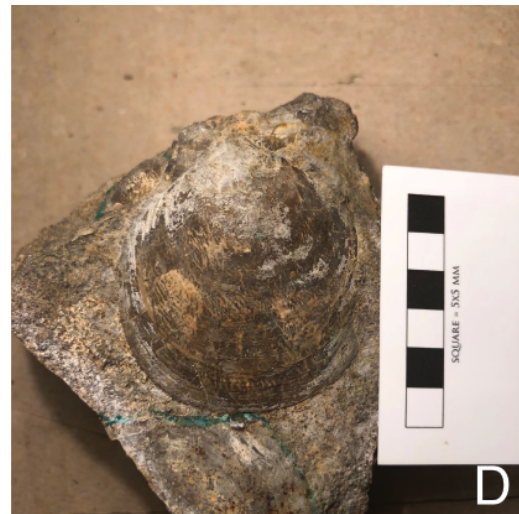
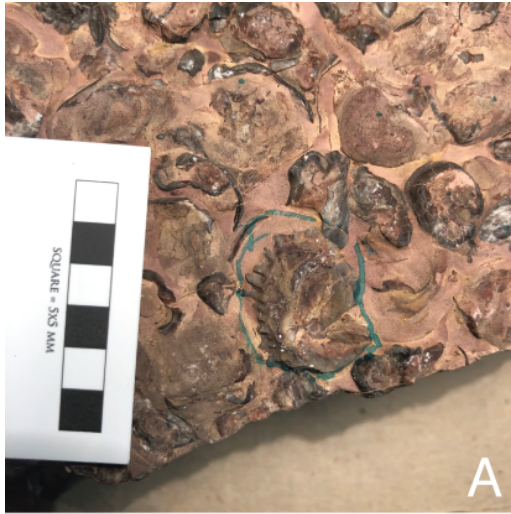


Plate 3

Plate 4

Bivalvia

- A. Bivalve indet. (sample BD-1A-10)
- B. Bivalve indet. A (sample BD-1A-13)
- C. Bivalve indet. B (sample BD-1A-13)



Plate 4

Plate 5

Gastropoda

- A. *Cylindrobullina* sp. (sample BD-2A-4)
- B. *Cossmonnea* sp. (sample BD-2A-15)
- C. *Neritina phaseolaris* (sample BD-1A-15)
- D. *Procerithium?* sp. (sample BD-1A-14)
- E. *Rhabdocolpus* sp. (sample BD-1A-14)

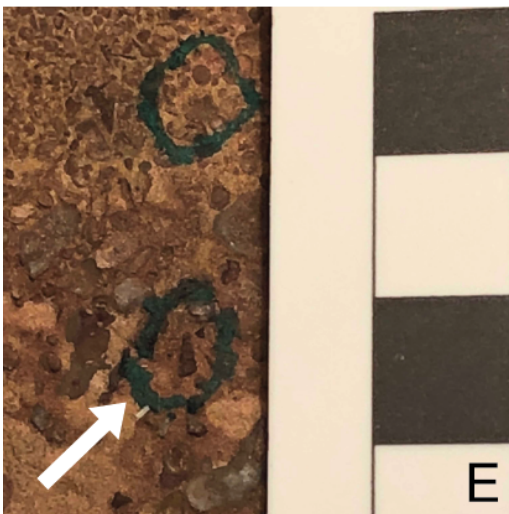


Plate 5

Plate 6

Gastropoda

- A. Gastropod indet. (sample BD-2A-4)
- B. Gastropod indet. A (sample BD-2A-7)



Plate 6

Plate 7

Echinodermata

- A. Isocrinus sp. (sample BD-1A-14)
- B. Crionid indet. (sample BD-2A-4)
- C. Echinoid spine indet. (sample BD-1A-15)



Plate

Part 2: Data

Field Sampling

Prior to field sampling, I spent several days scouting the outcrops in the area and describing the lithology to interpret facies and create a facies model. The facies model consists of a wave-dominated carbonate ramp setting with open shallow subtidal facies, oolitic shoals, restricted shallow subtidal/lagoon facies, tidal flat, and sabkha. This facies model is consistent with the facies model created for the Carmel Formation in this region of Utah by di Gibert and Ekdale (1999), and it is similar to the carbonate facies models of similar age farther north along the Sundance Seaway in Wyoming and Montana (McMullen et al. 2014, Clement and Holland 2016, Danise and Holland 2017, 2018). After creating a facies model, I measured five partial stratigraphic sections that I used to create a single composite section (Fig. 3.2).

A total of 46 samples were collected from the Bajocian and Bathonian portion of the Carmel Formation in the northern portion of San Rafael Swell in central-east Utah. Each sample consists of 2 gallons (7.57 liters) of rock material containing at least 25 individuals. The 23 Bajocian samples were collected near the base of the exposed Carmel Formation above the sharp contact with the underlying Temple Cap/Navajo Formation. This part of the Carmel consists of open shallow subtidal facies. The 23 Bathonian samples were collected from the open shallow subtidal facies that sharply overlies a gypsum-rich sabkha facies. This contact is interpreted as a sequence boundary, and it is correlated with other outcrops in the San Rafael Swell region interpreted as Bathonian based on dinoflagellate biostratigraphy (Doelling et al 2013).

All counted species are outlined in the table below. This table is formatted to follow the Paleobiology Database occurrence format, which allows a single function to be used to calculate the proportions of species by ecological trait for both datasets.

Collection	Species	Stage	Life Habit	Stability	Motility	Abundance	Environment	Lithology
BD-1A-1	Trigonia sp.	Bajocian	shallow infaunal	0	facultatively mobile	1	Open Shallow Subtidal	skeletal grainstone
BD-1A-1	Bivalve indet.	Bajocian	0	0	0	1	Open Shallow Subtidal	skeletal grainstone
BD-1A-1	Liostrea sp.	Bajocian	epifaunal (cementing)	cementing	sessile (cementing)	84	Open Shallow Subtidal	skeletal grainstone
BD-1A-1	Plicatula sp.	Bajocian	epifaunal (cementing)	cementing	sessile (cementing)	1	Open Shallow Subtidal	skeletal grainstone
BD-1A-1	Camptonectes sp.	Bajocian	epifaunal	epibyssate	sessile	8	Open Shallow Subtidal	skeletal grainstone
BD-1A-2	Trigonia sp.	Bajocian	shallow infaunal	0	facultatively mobile	1	Open Shallow Subtidal	skeletal grainstone
BD-1A-2	Actinostreon? sp.	Bajocian	epifaunal (cementing)	cementing	sessile (cementing)	2	Open Shallow Subtidal	skeletal grainstone
BD-1A-2	Liostrea sp.	Bajocian	epifaunal (cementing)	cementing	sessile (cementing)	182	Open Shallow Subtidal	skeletal grainstone
BD-1A-2	Camptonectes sp.	Bajocian	epifaunal	epibyssate	sessile	5	Open Shallow Subtidal	skeletal grainstone

BD-1A-3	Liostrea sp.	Bajocian	epifaunal (cementing)	cementing	sessile (cementing)	9	Open Shallow Subtidal	skeletal grainstone
BD-1A-3	Camptonectes sp.	Bajocian	epifaunal	epibyssate	sessile	67	Open Shallow Subtidal	skeletal grainstone
BD-1A-4	Liostrea sp.	Bajocian	epifaunal (cementing)	cementing	sessile (cementing)	27	Open Shallow Subtidal	skeletal grainstone
BD-1A-4	Camptonectes sp.	Bajocian	epifaunal	epibyssate	sessile	27	Open Shallow Subtidal	skeletal grainstone
BD-1A-5	Astarte? sp.	Bajocian	shallow infaunal	0	facultatively mobile	1	Open Shallow Subtidal	skeletal grainstone
BD-1A-5	Bivalve indet.	Bajocian	0	0	0	1	Open Shallow Subtidal	skeletal grainstone
BD-1A-5	Liostrea sp.	Bajocian	epifaunal (cementing)	cementing	sessile (cementing)	69	Open Shallow Subtidal	skeletal grainstone
BD-1A-5	Camptonectes sp.	Bajocian	epifaunal	epibyssate	sessile	5	Open Shallow Subtidal	skeletal grainstone
BD-1A-6	Liostrea sp.	Bajocian	epifaunal (cementing)	cementing	sessile (cementing)	59	Open Shallow Subtidal	skeletal grainstone
BD-1A-6	Camptonectes sp.	Bajocian	epifaunal	epibyssate	sessile	40	Open Shallow Subtidal	skeletal grainstone

BD-1A-7	Liostrea sp.	Bajocian	epifaunal (cementing)	cementing	sessile (cementing)	55	Open Shallow Subtidal	skeletal grainstone
BD-1A-7	Camptonectes sp.	Bajocian	epifaunal	epibyssate	sessile	58	Open Shallow Subtidal	skeletal grainstone
BD-1A-8	Procerithium? sp.	Bajocian	epifaunal	0	mobile	1	Open Shallow Subtidal	skeletal grainstone
BD-1A-8	Isocrinus sp.	Bajocian	epifaunal	attached	sessile	6	Open Shallow Subtidal	skeletal grainstone
BD-1A-8	Liostrea sp.	Bajocian	epifaunal (cementing)	cementing	sessile (cementing)	35	Open Shallow Subtidal	skeletal grainstone
BD-1A-8	Camptonectes sp.	Bajocian	epifaunal	epibyssate	sessile	43	Open Shallow Subtidal	skeletal grainstone
BD-1A-9	Liostrea sp.	Bajocian	epifaunal (cementing)	cementing	sessile (cementing)	17	Open Shallow Subtidal	skeletal grainstone
BD-1A-9	Camptonectes sp.	Bajocian	epifaunal	epibyssate	sessile	27	Open Shallow Subtidal	skeletal grainstone
BD-1A-10	Myophorella sp.	Bajocian	shallow infaunal	0	facultatively mobile	1	Open Shallow Subtidal	skeletal grainstone
BD-1A-10	Trigonia sp.	Bajocian	shallow infaunal	0	facultatively mobile	1	Open Shallow Subtidal	skeletal grainstone

BD-1A-10	Vaugonia conradi	Bajocian	shallow infaunal	0	facultatively mobile	8	Open Shallow Subtidal	skeletal grainstone
BD-1A-10	Bivalve indet.	Bajocian	0	0	0	50	Open Shallow Subtidal	skeletal grainstone
BD-1A-10	Gastropod indet.	Bajocian	epifaunal	0	mobile	1	Open Shallow Subtidal	skeletal grainstone
BD-1A-10	Liostrea sp.	Bajocian	epifaunal (cementing)	cementing	sessile (cementing)	14	Open Shallow Subtidal	skeletal grainstone
BD-1A-10	Camptonectes sp.	Bajocian	epifaunal	epibyssate	sessile	22	Open Shallow Subtidal	skeletal grainstone
BD-1A-11	Bivalve indet.	Bajocian	0	0	0	32	Open Shallow Subtidal	skeletal grainstone
BD-1A-11	Camptonectes sp.	Bajocian	epifaunal	epibyssate	sessile	30	Open Shallow Subtidal	skeletal grainstone
BD-1A-12	Isocrinus sp.	Bajocian	epifaunal	attached	sessile	2	Open Shallow Subtidal	skeletal grainstone
BD-1A-12	Liostrea sp.	Bajocian	epifaunal (cementing)	cementing	sessile (cementing)	5	Open Shallow Subtidal	skeletal grainstone
BD-1A-12	Camptonectes sp.	Bajocian	epifaunal	epibyssate	sessile	35	Open Shallow Subtidal	skeletal grainstone

BD-1A-13	Bivalve indet. A	Bajocian	0	0	0	35	Open Shallow Subtidal	skeletal grainstone
BD-1A-13	Bivalve indet. B	Bajocian	0	0	0	1	Open Shallow Subtidal	skeletal grainstone
BD-1A-13	<i>Myophorella montanaensis?</i>	Bajocian	shallow infaunal	0	facultatively mobile	5	Open Shallow Subtidal	skeletal grainstone
BD-1A-13	<i>Isocrinus</i> sp.	Bajocian	epifaunal	attached	sessile	2	Open Shallow Subtidal	skeletal grainstone
BD-1A-13	<i>Actinostreon?</i> sp.	Bajocian	epifaunal (cementing)	cementing	sessile (cementing)	1	Open Shallow Subtidal	skeletal grainstone
BD-1A-13	<i>Liostrea</i> sp.	Bajocian	epifaunal (cementing)	cementing	sessile (cementing)	39	Open Shallow Subtidal	skeletal grainstone
BD-1A-13	<i>Camptonectes platessiformis</i>	Bajocian	epifaunal	epibyssate	sessile	2	Open Shallow Subtidal	skeletal grainstone
BD-1A-13	<i>Camptonectes</i> sp.	Bajocian	epifaunal	epibyssate	sessile	5	Open Shallow Subtidal	skeletal grainstone
BD-1A-14	Gastropod indet.	Bajocian	epifaunal	0	mobile	7	Open Shallow Subtidal	skeletal grainstone
BD-1A-14	<i>Procerithium?</i> sp.	Bajocian	epifaunal	0	mobile	5	Open Shallow Subtidal	skeletal grainstone

BD-1A-14	Rhabdocolpus sp.	Bajocian	epifaunal	0	mobile	1	Open Shallow Subtidal	skeletal grainstone
BD-1A-14	Isocrinus sp.	Bajocian	epifaunal	attached	sessile	3	Open Shallow Subtidal	skeletal grainstone
BD-1A-14	Liostrea sp.	Bajocian	epifaunal (cementing)	cementing	sessile (cementing)	60	Open Shallow Subtidal	skeletal grainstone
BD-1A-14	Camptonectes sp.	Bajocian	epifaunal	epibyssate	sessile	9	Open Shallow Subtidal	skeletal grainstone
BD-1A-14	Camptonectes stygius	Bajocian	epifaunal	epibyssate	sessile	6	Open Shallow Subtidal	skeletal grainstone
BD-1A-15	Echinoid indet.	Bajocian	epifaunal	0	mobile	1	Open Shallow Subtidal	skeletal grainstone
BD-1A-15	Gastropod indet.	Bajocian	epifaunal	0	mobile	1	Open Shallow Subtidal	skeletal grainstone
BD-1A-15	Neritina phaseolaris?	Bajocian	epifaunal	0	mobile	1	Open Shallow Subtidal	skeletal grainstone
BD-1A-15	Isocrinus sp.	Bajocian	epifaunal	attached	sessile	2	Open Shallow Subtidal	skeletal grainstone
BD-1A-15	Liostrea sp.	Bajocian	epifaunal (cementing)	cementing	sessile (cementing)	42	Open Shallow Subtidal	skeletal grainstone

BD-1A-15	<i>Camptonectes</i> sp.	Bajocian	epifaunal	epibyssate	sessile	19	Open Shallow Subtidal	skeletal grainstone
BD-1A-15	<i>Plagiostoma</i> <i>occidentalis</i> ?	Bajocian	epifaunal	epibyssate	sessile	1	Open Shallow Subtidal	skeletal grainstone
BD-1A-16	<i>Liostrea</i> <i>strigilecula</i>	Bajocian	epifaunal (cementing)	cementing	sessile (cementing)	11	Open Shallow Subtidal	skeletal grainstone
BD-1A-16	<i>Camptonectes</i> <i>stygius</i>	Bajocian	epifaunal	epibyssate	sessile	93	Open Shallow Subtidal	skeletal grainstone
BD-1A-17	<i>Liostrea</i> <i>strigilecula</i>	Bajocian	epifaunal (cementing)	cementing	sessile (cementing)	23	Open Shallow Subtidal	skeletal grainstone
BD-1A-17	<i>Camptonectes</i> <i>stygius</i>	Bajocian	epifaunal	epibyssate	sessile	89	Open Shallow Subtidal	skeletal grainstone
BD-1A-18	<i>Isocrinus</i> sp.	Bajocian	epifaunal	attached	sessile	1	Open Shallow Subtidal	skeletal grainstone
BD-1A-18	<i>Liostrea</i> sp.	Bajocian	epifaunal (cementing)	cementing	sessile (cementing)	7	Open Shallow Subtidal	skeletal grainstone
BD-1A-18	<i>Camptonectes</i> <i>stygius</i>	Bajocian	epifaunal	epibyssate	sessile	91	Open Shallow Subtidal	skeletal grainstone
BD-1A-19	<i>Liostrea</i> <i>strigilecula</i>	Bajocian	epifaunal (cementing)	cementing	sessile (cementing)	6	Open Shallow Subtidal	skeletal grainstone

BD-1A-19	<i>Camptonectes stygius</i>	Bajocian	epifaunal	epibyssate	sessile	81	Open Shallow Subtidal	skeletal grainstone
BD-1A-20	<i>Isocrinus</i> sp.	Bajocian	epifaunal	attached	sessile	1	Open Shallow Subtidal	skeletal grainstone
BD-1A-20	<i>Liostrea</i> sp.	Bajocian	epifaunal (cementing)	cementing	sessile (cementing)	21	Open Shallow Subtidal	skeletal grainstone
BD-1A-20	<i>Camptonectes</i> sp.	Bajocian	epifaunal	epibyssate	sessile	51	Open Shallow Subtidal	skeletal grainstone
BD-1A-21	<i>Liostrea</i> sp.	Bajocian	epifaunal (cementing)	cementing	sessile (cementing)	8	Open Shallow Subtidal	skeletal grainstone
BD-1A-21	<i>Camptonectes stygius</i>	Bajocian	epifaunal	epibyssate	sessile	95	Open Shallow Subtidal	skeletal grainstone
BD-1A-22	<i>Liostrea</i> sp.	Bajocian	epifaunal (cementing)	cementing	sessile (cementing)	17	Open Shallow Subtidal	skeletal grainstone
BD-1A-22	<i>Camptonectes stygius</i>	Bajocian	epifaunal	epibyssate	sessile	135	Open Shallow Subtidal	skeletal grainstone
BD-1A-23	<i>Vaugonia</i> sp.	Bajocian	shallow infaunal	0	facultatively mobile	1	Open Shallow Subtidal	skeletal grainstone
BD-1A-23	<i>Liostrea strigilecula</i>	Bajocian	epifaunal (cementing)	cementing	sessile (cementing)	21	Open Shallow Subtidal	skeletal grainstone

BD-1A-23	<i>Camptonectes stygius</i>	Bajocian	epifaunal	epibyssate	sessile	79	Open Shallow Subtidal	skeletal grainstone
BD-2A-1	Bivalve indet.	Bathonian	0	0	0	16	Open Shallow Subtidal	skeletal packstone
BD-2A-1	Gastropod indet.	Bathonian	epifaunal	0	mobile	1	Open Shallow Subtidal	skeletal packstone
BD-2A-1	<i>Trigonia</i> sp.	Bathonian	shallow infaunal	0	facultatively mobile	2	Open Shallow Subtidal	skeletal packstone
BD-2A-1	<i>Vaugonia conradi</i>	Bathonian	shallow infaunal	0	facultatively mobile	1	Open Shallow Subtidal	skeletal packstone
BD-2A-1	<i>Isocrinus</i> sp.	Bathonian	epifaunal	attached	sessile	1	Open Shallow Subtidal	skeletal packstone
BD-2A-1	<i>Liostrea</i> sp.	Bathonian	epifaunal (cementing)	cementing	sessile (cementing)	8	Open Shallow Subtidal	skeletal packstone
BD-2A-1	<i>Camptonectes</i> sp.	Bathonian	epifaunal	epibyssate	sessile	15	Open Shallow Subtidal	skeletal packstone
BD-2A-2	<i>Cossmannea</i> sp.	Bathonian	epifaunal	0	mobile	2	Open Shallow Subtidal	skeletal packstone
BD-2A-2	<i>Isocrinus</i> sp.	Bathonian	epifaunal	attached	sessile	1	Open Shallow Subtidal	skeletal packstone

BD-2A-2	Camptonectes sp.	Bathonian	epifaunal	epibyssate	sessile	27	Open Shallow Subtidal	skeletal packstone
BD-2A-3	Bivalve indet.	Bathonian	0	0	0	12	Open Shallow Subtidal	skeletal packstone
BD-2A-3	Gastropod indet.	Bathonian	epifaunal	0	mobile	2	Open Shallow Subtidal	skeletal packstone
BD-2A-3	Liostrea sp.	Bathonian	epifaunal (cementing)	cementing	sessile (cementing)	2	Open Shallow Subtidal	skeletal packstone
BD-2A-3	Camptonectes sp.	Bathonian	epifaunal	epibyssate	sessile	31	Open Shallow Subtidal	skeletal packstone
BD-2A-4	Bivalve indet.	Bathonian	0	0	0	7	Open Shallow Subtidal	skeletal packstone
BD-2A-4	Crinoid indet.	Bathonian	epifaunal	0	0	1	Open Shallow Subtidal	skeletal packstone
BD-2A-4	Cylindrobullina sp.	Bathonian	epifaunal	0	mobile	2	Open Shallow Subtidal	skeletal packstone
BD-2A-4	Gastropod indet.	Bathonian	epifaunal	0	mobile	3	Open Shallow Subtidal	skeletal packstone
BD-2A-4	Liostrea sp.	Bathonian	epifaunal (cementing)	cementing	sessile (cementing)	4	Open Shallow Subtidal	skeletal packstone

BD-2A-4	Camptonectes sp.	Bathonian	epifaunal	epibyssate	sessile	10	Open Shallow Subtidal	skeletal packstone
BD-2A-4	Astarte? sp.	Bathonian	shallow infaunal	0	facultatively mobile	1	Open Shallow Subtidal	skeletal packstone
BD-2A-5	Gastropod indet.	Bathonian	epifaunal	0	mobile	4	Open Shallow Subtidal	skeletal packstone
BD-2A-5	Liostrea sp.	Bathonian	epifaunal (cementing)	cementing	sessile (cementing)	6	Open Shallow Subtidal	skeletal packstone
BD-2A-5	Camptonectes sp.	Bathonian	epifaunal	epibyssate	sessile	32	Open Shallow Subtidal	skeletal packstone
BD-2A-6	Liostrea sp.	Bathonian	epifaunal (cementing)	cementing	sessile (cementing)	2	Open Shallow Subtidal	skeletal packstone
BD-2A-6	Camptonectes sp.	Bathonian	epifaunal	epibyssate	sessile	32	Open Shallow Subtidal	skeletal packstone
BD-2A-7	Astarte? sp.	Bathonian	shallow infaunal	0	facultatively mobile	1	Open Shallow Subtidal	skeletal packstone
BD-2A-7	Cossmannia sp.	Bathonian	epifaunal	0	mobile	3	Open Shallow Subtidal	skeletal packstone
BD-2A-7	Gastropod indet.	Bathonian	epifaunal	0	mobile	1	Open Shallow Subtidal	skeletal packstone

BD-2A-7	Gastropod indet. B	Bathonian	epifaunal	0	mobile	1	Open Shallow Subtidal	skeletal packstone
BD-2A-7	Vaugonia sp.	Bathonian	shallow infaunal	0	facultatively mobile	1	Open Shallow Subtidal	skeletal packstone
BD-2A-7	Liostrea sp.	Bathonian	epifaunal (cementing)	cementing	sessile (cementing)	4	Open Shallow Subtidal	skeletal packstone
BD-2A-7	Camptonectes sp.	Bathonian	epifaunal	epibyssate	sessile	35	Open Shallow Subtidal	skeletal packstone
BD-2A-8	Astarte? sp.	Bathonian	shallow infaunal	0	facultatively mobile	2	Open Shallow Subtidal	skeletal packstone
BD-2A-8	Gastropod indet.	Bathonian	epifaunal	0	mobile	1	Open Shallow Subtidal	skeletal packstone
BD-2A-8	Myophorella sp.	Bathonian	shallow infaunal	0	facultatively mobile	1	Open Shallow Subtidal	skeletal packstone
BD-2A-8	Vaugonia conradi	Bathonian	shallow infaunal	0	facultatively mobile	1	Open Shallow Subtidal	skeletal packstone
BD-2A-8	Vaugonia sp.	Bathonian	shallow infaunal	0	facultatively mobile	12	Open Shallow Subtidal	skeletal packstone
BD-2A-8	Liostrea sp.	Bathonian	epifaunal (cementing)	cementing	sessile (cementing)	9	Open Shallow Subtidal	skeletal packstone

BD-2A-8	Camptonectes sp.	Bathonian	epifaunal	epibyssate	sessile	18	Open Shallow Subtidal	skeletal packstone
BD-2A-9	Cossmannea sp.	Bathonian	epifaunal	0	mobile	2	Open Shallow Subtidal	skeletal packstone
BD-2A-9	Gastropod indet.	Bathonian	epifaunal	0	mobile	2	Open Shallow Subtidal	skeletal packstone
BD-2A-9	Isocrinus sp.	Bathonian	epifaunal	attached	sessile	1	Open Shallow Subtidal	skeletal packstone
BD-2A-9	Liostrea sp.	Bathonian	epifaunal (cementing)	cementing	sessile (cementing)	7	Open Shallow Subtidal	skeletal packstone
BD-2A-9	Camptonectes sp.	Bathonian	epifaunal	epibyssate	sessile	19	Open Shallow Subtidal	skeletal packstone
BD-2A-10	Liostrea sp.	Bathonian	epifaunal (cementing)	cementing	sessile (cementing)	2	Open Shallow Subtidal	skeletal packstone
BD-2A-10	Camptonectes sp.	Bathonian	epifaunal	epibyssate	sessile	27	Open Shallow Subtidal	skeletal packstone
BD-2A-10	Isognomon perplana	Bathonian	epifaunal	epibyssate	sessile	5	Open Shallow Subtidal	skeletal packstone
BD-2A-11	Cossmannea sp.	Bathonian	epifaunal	0	mobile	1	Open Shallow Subtidal	skeletal packstone

BD-2A-11	<i>Liostrea</i> sp.	Bathonian	epifaunal (cementing)	cementing	sessile (cementing)	2	Open Shallow Subtidal	skeletal packstone
BD-2A-11	<i>Camptonectes</i> <i>stygius</i>	Bathonian	epifaunal	epibyssate	sessile	29	Open Shallow Subtidal	skeletal packstone
BD-2A-11	<i>Isognomon</i> sp.	Bathonian	epifaunal	epibyssate	sessile	2	Open Shallow Subtidal	skeletal packstone
BD-2A-12	<i>Camptonectes</i> <i>stygius</i>	Bathonian	epifaunal	epibyssate	sessile	26	Open Shallow Subtidal	skeletal packstone
BD-2A-12	<i>Isognomon</i> <i>perplana</i>	Bathonian	epifaunal	epibyssate	sessile	3	Open Shallow Subtidal	skeletal packstone
BD-2A-13	<i>Cossmanea</i> sp.	Bathonian	epifaunal	0	mobile	2	Open Shallow Subtidal	skeletal packstone
BD-2A-13	Gastropod indet.	Bathonian	epifaunal	0	mobile	8	Open Shallow Subtidal	skeletal packstone
BD-2A-13	<i>Trigonia</i> sp.	Bathonian	shallow infaunal	0	facultatively mobile	1	Open Shallow Subtidal	skeletal packstone
BD-2A-13	<i>Vaugonia</i> sp.	Bathonian	shallow infaunal	0	facultatively mobile	1	Open Shallow Subtidal	skeletal packstone
BD-2A-13	<i>Actinostreon</i> ? sp.	Bathonian	epifaunal (cementing)	cementing	sessile (cementing)	1	Open Shallow Subtidal	skeletal packstone

BD-2A-13	<i>Liostrea</i> sp.	Bathonian	epifaunal (cementing)	cementing	sessile (cementing)	24	Open Shallow Subtidal	skeletal packstone
BD-2A-13	<i>Camptonectes</i> sp.	Bathonian	epifaunal	epibyssate	sessile	13	Open Shallow Subtidal	skeletal packstone
BD-2A-13	<i>Camptonectes</i> <i>stygius</i>	Bathonian	epifaunal	epibyssate	sessile	7	Open Shallow Subtidal	skeletal packstone
BD-2A-13	<i>Isognomon</i> <i>perplana</i>	Bathonian	epifaunal	epibyssate	sessile	1	Open Shallow Subtidal	skeletal packstone
BD-2A-14	<i>Camptonectes</i> <i>stygius</i>	Bathonian	epifaunal	epibyssate	sessile	21	Open Shallow Subtidal	skeletal packstone
BD-2A-14	<i>Isognomon</i> <i>perplana</i>	Bathonian	epifaunal	epibyssate	sessile	4	Open Shallow Subtidal	skeletal packstone
BD-2A-15	<i>Cossmannea</i> sp.	Bathonian	epifaunal	0	mobile	5	Open Shallow Subtidal	skeletal packstone
BD-2A-15	Gastropod indet.	Bathonian	epifaunal	0	mobile	6	Open Shallow Subtidal	skeletal packstone
BD-2A-15	<i>Liostrea</i> sp.	Bathonian	epifaunal (cementing)	cementing	sessile (cementing)	12	Open Shallow Subtidal	skeletal packstone
BD-2A-15	<i>Camptonectes</i> sp.	Bathonian	epifaunal	epibyssate	sessile	15	Open Shallow Subtidal	skeletal packstone

BD-2A-16	Bivalve indet.	Bathonian	0	0	0	3	Open Shallow Subtidal	skeletal packstone
BD-2A-16	Cossmannea sp.	Bathonian	epifaunal	0	mobile	3	Open Shallow Subtidal	skeletal packstone
BD-2A-16	Vaugonia conradi	Bathonian	shallow infaunal	0	facultatively mobile	1	Open Shallow Subtidal	skeletal packstone
BD-2A-16	Liostrea strigilecula	Bathonian	epifaunal (cementing)	cementing	sessile (cementing)	5	Open Shallow Subtidal	skeletal packstone
BD-2A-16	Camptonectes sp.	Bathonian	epifaunal	epibyssate	sessile	20	Open Shallow Subtidal	skeletal packstone
BD-2A-17	Bivalve indet.	Bathonian	0	0	0	1	Open Shallow Subtidal	skeletal packstone
BD-2A-17	Liostrea sp.	Bathonian	epifaunal (cementing)	cementing	sessile (cementing)	1	Open Shallow Subtidal	skeletal packstone
BD-2A-17	Camptonectes sp.	Bathonian	epifaunal	epibyssate	sessile	5	Open Shallow Subtidal	skeletal packstone
BD-2A-17	Camptonectes stygius	Bathonian	epifaunal	epibyssate	sessile	17	Open Shallow Subtidal	skeletal packstone
BD-2A-17	Isognomon perplana	Bathonian	epifaunal	epibyssate	sessile	1	Open Shallow Subtidal	skeletal packstone

BD-2A-17	Isognomon sp.	Bathonian	epifaunal	epibyssate	sessile	1	Open Shallow Subtidal	skeletal packstone
BD-2A-18	Corbula sp.	Bathonian	shallow infaunal	0	facultatively mobile	2	Open Shallow Subtidal	skeletal packstone
BD-2A-18	Liostrea strigilecula	Bathonian	epifaunal (cementing)	cementing	sessile (cementing)	2	Open Shallow Subtidal	skeletal packstone
BD-2A-18	Camptonectes stygius	Bathonian	epifaunal	epibyssate	sessile	15	Open Shallow Subtidal	skeletal packstone
BD-2A-18	Isognomon perplana	Bathonian	epifaunal	epibyssate	sessile	10	Open Shallow Subtidal	skeletal packstone
BD-2A-19	Bivalve indet. A	Bathonian	0	0	0	1	Open Shallow Subtidal	skeletal packstone
BD-2A-19	Bivalve indet. B	Bathonian	0	0	0	1	Open Shallow Subtidal	skeletal packstone
BD-2A-19	Cylindrobullina sp.	Bathonian	epifaunal	0	mobile	1	Open Shallow Subtidal	skeletal packstone
BD-2A-19	Liostrea sp.	Bathonian	epifaunal (cementing)	cementing	sessile (cementing)	5	Open Shallow Subtidal	skeletal packstone
BD-2A-19	Camptonectes sp.	Bathonian	epifaunal	epibyssate	sessile	16	Open Shallow Subtidal	skeletal packstone

BD-2A-19	<i>Camptonectes stygius</i>	Bathonian	epifaunal	epibyssate	sessile	8	Open Shallow Subtidal	skeletal packstone
BD-2A-19	<i>Isognomon perplana</i>	Bathonian	epifaunal	epibyssate	sessile	6	Open Shallow Subtidal	skeletal packstone
BD-2A-20	<i>Cossmannea</i> sp.	Bathonian	epifaunal	0	mobile	1	Open Shallow Subtidal	skeletal packstone
BD-2A-20	<i>Liostrea</i> sp.	Bathonian	epifaunal (cementing)	cementing	sessile (cementing)	2	Open Shallow Subtidal	skeletal packstone
BD-2A-20	<i>Camptonectes stygius</i>	Bathonian	epifaunal	epibyssate	sessile	39	Open Shallow Subtidal	skeletal packstone
BD-2A-20	<i>Isognomon perplana</i>	Bathonian	epifaunal	epibyssate	sessile	3	Open Shallow Subtidal	skeletal packstone
BD-2A-21	Gastropod indet.	Bathonian	epifaunal	0	mobile	1	Open Shallow Subtidal	skeletal packstone
BD-2A-21	<i>Camptonectes</i> sp.	Bathonian	epifaunal	epibyssate	sessile	2	Open Shallow Subtidal	skeletal packstone
BD-2A-21	<i>Camptonectes stygius</i>	Bathonian	epifaunal	epibyssate	sessile	19	Open Shallow Subtidal	skeletal packstone
BD-2A-21	<i>Isognomon perplana</i>	Bathonian	epifaunal	epibyssate	sessile	2	Open Shallow Subtidal	skeletal packstone

BD-2A-21	Isognomon sp.	Bathonian	epifaunal	epibyssate	sessile	3	Open Shallow Subtidal	skeletal packstone
BD-2A-21	Lima sp.	Bathonian	epifaunal	epibyssate	sessile	1	Open Shallow Subtidal	skeletal packstone
BD-2A-22	Camptonectes stygius	Bathonian	epifaunal	epibyssate	sessile	30	Open Shallow Subtidal	skeletal packstone
BD-2A-22	Isognomon perplana	Bathonian	epifaunal	epibyssate	sessile	9	Open Shallow Subtidal	skeletal packstone
BD-2A-23	Liostrea strigilecula	Bathonian	epifaunal (cementing)	cementing	sessile (cementing)	6	Open Shallow Subtidal	skeletal packstone
BD-2A-23	Camptonectes stygius	Bathonian	epifaunal	epibyssate	sessile	41	Open Shallow Subtidal	skeletal packstone
BD-2A-23	Cossmannea sp.	Bathonian	epifaunal	epibyssate	mobile	1	Open Shallow Subtidal	skeletal packstone
BD-2A-23	Isognomon perplana	Bathonian	epifaunal	epibyssate	sessile	10	Open Shallow Subtidal	skeletal packstone

Paleobiology Collection Numbers Used

97941	97940	97939	97937	97936	97934
97933	97903	97899	97894	97891	97888
96194	96193	96191	96190	96187	96186
96183	96182	96180	96179	96177	96176
96173	96172	96171	96170	96169	96165
96164	96163	96161	96160	96159	96158
96156	96155	96153	96152	96150	96148
96147	96146	96145	90024	87402	87400
87399	59772	59032	51555	37510	32036
169200	169190	169189	169188	169180	132951
132950	125457	125456	125455	125454	125432

Part 3: R Code

R code for all statistical analysis conducted, including functions, and scripts that run the commands.

Functions used to extract collection data

```
#Set of functions to extract desired subdata sets from main
occurrence data file.

extractPBDBCollections <- function(x, stage, desiredRegions =
  "allRegions", desiredEnvironments = "allEnvironments",
  desiredFacies = "allFacies"){

  if (desiredRegions[1] == "allRegions") {
    desiredRegions = unique(x$geo_cluster)
  }

  if (desiredEnvironments[1] == "allEnvironments") {
    desiredEnvironments = unique(x$environment)
  }

  if (desiredFacies[1] == "allFacies") {
    desiredFacies = unique(x$facies)
  }

  xS <- x[x$stage %in% stage, ] #Assign desired stage to vector
  xSR <- xS[xS$geo_cluster %in% desiredRegions, ] #Assign
  desired regional clusters to vector
  xSRE <- xSR[xSR$environment %in% desiredEnvironments,]
  xSREF <- xSRE[xSRE$facies %in% desiredFacies,]
  xSREFC<- sort(unique(xSREF$collection_no))
```

```
}  
  
extractFieldCollections <- function(x, stage){  
  
  xS <- x[x$stage %in% stage, ] #Assign desired stage to vector  
  xSC <- sort(unique(xS$collection_no))  
}  
  
metricsForCollections <- function(x){  
  xV <- vector(mode = "numeric", length = length(x))  
}
```

Functions used to calculate percentage of occurrences by ecological trait.

```
percentEcolTrait <- function(x, traitCategory, desiredTraits,
  desiredCollections= "allCollections", desiredEnvts = "allEnvts")
{
  #Trait categories include life habit, diet, substrate stability,
  and motility
  #Environments are based on the categories used by Bottjer and
  Jablonski, 1988 (Palaos):
  # nearshore, inner shelf, middle shelf, outer shelf, slope and
  deep basin

  if (desiredCollections[1] == "allCollections") {
    desiredCollections = unique(x$collection_no)
  }
  if (desiredEnvts[1] == "allEnvts") {
    desiredEnvts = unique(x$environment)
  }

  xC <- x[x$collection_no %in% desiredCollections, ] #Assign
  desired environments to stages vector
  xCE <- xC[xC$environment %in% desiredEnvts, ] #Assign desired
  environments to stages vector

  traitColumn <- which(colnames(x) %in% traitCategory)
  if (length(traitColumn) == 0) {
    errorMessage <- paste("Possible spelling error: column name
  '", traitCategory, "' was not found", sep="")
    warning(errorMessage)
  }
  xCET <- xCE[xCE[, traitColumn] %in% desiredTraits, ] #Assign
  ecological stage to vector

  matchingOccurrences <- nrow(xCET)
  totalOccurrences <- nrow(xCE)

  prop <- rep(0, 3)
  prop[2] <- round((matchingOccurrences / totalOccurrences) *100,
  2)
  conf.int <- percent.confint(prop[2], totalOccurrences)
  prop[1] <- conf.int[1]
  prop[3] <- conf.int[2]
  prop
}
```

Functions used to calculate abundance percentage by ecological trait.

```
abundance_percentEcolTrait <- function(x, traitCategory,
desiredTraits, desiredCollections= "allCollections") {
  #Trait categories include life habit, diet, substrate stability,
  and motility
  #Environments are based on the categories used by Bottjer and
  Jablonski, 1988 (Palaos):
  #  nearshore, inner shelf, middle shelf, outer shelf, slope and
  deep basin

  if (desiredCollections[1] == "allCollections") {
    desiredCollections = unique(x$collection_no)
  }

  xC <- x[x$collection_no %in% desiredCollections, ] #Assign
  desired environments to stages vector

  traitColumn <- which(colnames(x) %in% traitCategory)
  if (length(traitColumn) == 0) {
    errorMessage <- paste("Possible spelling error: column name
'", traitCategory, "' was not found", sep="")
    warning(errorMessage)
  }
  xCT <- xC[xC[, traitColumn] %in% desiredTraits, ] #Assign
  ecological stage to vector

  matchingOccurrences <- sum(xCT$abundance)
  totalOccurrences <- sum(xC$abundance)

  percent <- rep(0, 3)
  percent[2] <- round((matchingOccurrences /
  totalOccurrences)*100, 2)
  conf.int <- percent.confint(percent[2], totalOccurrences)
  percent[1] <- conf.int[1]
  percent[3] <- conf.int[2]
  percent
}
```

R command script to calculate the mean proportion of occurrences and abundance in each collection and compare them from the Bajocian to Bathonian in Utah and Europe. (Figs. 3.3–3.6)

```
##Loop and plots of temporal ecological proportions of
occurrences by depositional environment in Utah and Europe

#Read source files
source("percentConfidenceInterval.R")
source("mod_percentEcolTrait.R")
source("extractionFunctions.R")

#Read Datasets
global <- read.csv('clusteredGlobalNEW.csv', header=TRUE,
stringsAsFactors=FALSE)
carmel <- read.csv('carmel.csv', header=TRUE,
stringsAsFactors=FALSE)

#Extract collections by stage from Utah data
UT_BajocianCollections <- extractFieldCollections(carmel,
"Bajocian")
UT_BathonianCollections <- extractFieldCollections(carmel,
"Bathonian")

#Extract collections by stage and environment from European data
EU_BajocianCollectionsSS <- extractPBDBCollections(global,
"Bajocian", "Europe", "open shallow subtidal",
desiredFacies="allFacies")
EU_BathonianCollectionsSS <- extractPBDBCollections(global,
"Bathonian", "Europe", "open shallow subtidal",
desiredFacies="allFacies")

#Create empty vectors that will be used to fill estimated
percentages calculated by running loop for Bajocian occurrences
UT_BajosinfaunalVectorE <-
metricsForCollections(UT_BajocianCollections)
UT_BajodinfraunalVectorE <-
metricsForCollections(UT_BajocianCollections)
UT_BajoepifaunalVectorE <-
metricsForCollections(UT_BajocianCollections)
UT_BajocementingVectorE <-
metricsForCollections(UT_BajocianCollections)
UT_BajofreelyingVectorE <-
metricsForCollections(UT_BajocianCollections)
UT_BajopedunculateVectorE <-
metricsForCollections(UT_BajocianCollections)
UT_BajoepibyssateVectorE <-
metricsForCollections(UT_BajocianCollections)
UT_BajomobileVectorE <-
metricsForCollections(UT_BajocianCollections)
```

```

UT_BajofacultativelymobileVectorE <-
metricsForCollections(UT_BajocianCollections)
UT_BajosessileVectorE <-
metricsForCollections(UT_BajocianCollections)

EU_BajosinfaunalSSVectorE <-
metricsForCollections(EU_BajocianCollectionsSS)
EU_BajodinfraunalSSVectorE <-
metricsForCollections(EU_BajocianCollectionsSS)
EU_BajoepifaunalSSVectorE <-
metricsForCollections(EU_BajocianCollectionsSS)
EU_BajocementingSSVectorE <-
metricsForCollections(EU_BajocianCollectionsSS)
EU_BajofreelyingSSVectorE <-
metricsForCollections(EU_BajocianCollectionsSS)
EU_BajopedunculateSSVectorE <-
metricsForCollections(EU_BajocianCollectionsSS)
EU_BajoepibyssateSSVectorE <-
metricsForCollections(EU_BajocianCollectionsSS)
EU_BajomobileSSVectorE <-
metricsForCollections(EU_BajocianCollectionsSS)
EU_BajofacultativelymobileSSVectorE <-
metricsForCollections(EU_BajocianCollectionsSS)
EU_BajosessileSSVectorE <-
metricsForCollections(EU_BajocianCollectionsSS)

#Create empty vectors that will be used to fill estimates
calculated by running loop for Bathonian occurrences
UT_BatsinfaunalVectorE <-
metricsForCollections(UT_BathonianCollections)
UT_BatdinfraunalVectorE <-
metricsForCollections(UT_BathonianCollections)
UT_BatepifaunalVectorE <-
metricsForCollections(UT_BathonianCollections)
UT_BatcementingVectorE <-
metricsForCollections(UT_BathonianCollections)
UT_BatepibyssateVectorE <-
metricsForCollections(UT_BathonianCollections)
UT_BatfreelyingVectorE <-
metricsForCollections(UT_BathonianCollections)
UT_BatpedunculateVectorE <-
metricsForCollections(UT_BathonianCollections)
UT_BatmobileVectorE <-
metricsForCollections(UT_BathonianCollections)
UT_BatfacultativelymobileVectorE <-
metricsForCollections(UT_BathonianCollections)
UT_BatsessileVectorE <-
metricsForCollections(UT_BathonianCollections)

EU_BatsinfaunalSSVectorE <-
metricsForCollections(EU_BathonianCollectionsSS)
EU_BatdinfraunalSSVectorE <-
metricsForCollections(EU_BathonianCollectionsSS)

```

```

EU_BatepifaunalSSVectorE <-
metricsForCollections(EU_BathonianCollectionsSS)
EU_BatcementingSSVectorE <-
metricsForCollections(EU_BathonianCollectionsSS)
EU_BatepibyssateSSVectorE <-
metricsForCollections(EU_BathonianCollectionsSS)
EU_BatfreelyingSSVectorE <-
metricsForCollections(EU_BathonianCollectionsSS)
EU_BatpedunculateSSVectorE <-
metricsForCollections(EU_BathonianCollectionsSS)
EU_BatmobileSSVectorE <-
metricsForCollections(EU_BathonianCollectionsSS)
EU_BatfacultativelymobileSSVectorE <-
metricsForCollections(EU_BathonianCollectionsSS)
EU_BatsessileSSVectorE <-
metricsForCollections(EU_BathonianCollectionsSS)

#Loop to calculate percentage of each ecological trait by cluster
for European Bajocian occurrences
  for (coll in 1:length(UT_BajocianCollections)) {

      UT_Bajosinfaunal <- percentEcolTrait(carmel,
"life_habit", "shallow infaunal",
desiredCollections=UT_BajocianCollections[coll])
      UT_BajosinfaunalVectorE[coll] <-
UT_Bajosinfaunal[2]

      UT_Bajodinfaunal <- percentEcolTrait(carmel,
"life_habit", "deep infaunal",
desiredCollections=UT_BajocianCollections[coll])
      UT_BajodinfaunalVectorE[coll] <-
UT_Bajodinfaunal[2]

      UT_Bajoepifaunal <- percentEcolTrait(carmel,
"life_habit", "epifaunal",
desiredCollections=UT_BajocianCollections[coll])
      UT_BajoepifaunalVectorE[coll] <-
UT_Bajoepifaunal[2]

      UT_Bajocementing <- percentEcolTrait(carmel,
"stability", "cementing",
desiredCollections=UT_BajocianCollections[coll])
      UT_BajocementingVectorE[coll] <-
UT_Bajocementing[2]

      UT_Bajofreelying <- percentEcolTrait(carmel,
"stability", "free-lying",
desiredCollections=UT_BajocianCollections[coll])
      UT_BajofreelyingVectorE[coll] <-
UT_Bajofreelying[2]

```



```

        UT_Bajopedunculate <- percentEcolTrait(carmel,
"stability", "pedunculate",
desiredCollections=UT_BajocianCollections[coll])
        UT_BajopedunculateVectorE[coll] <-
UT_Bajopedunculate[2]

        UT_Bajoepibyssate <- percentEcolTrait(carmel,
"stability", "epibyssate",
desiredCollections=UT_BajocianCollections[coll])
        UT_BajoepibyssateVectorE[coll] <-
UT_Bajoepibyssate[2]

        UT_Bajomobile <- percentEcolTrait(carmel,
"motility", "mobile",
desiredCollections=UT_BajocianCollections[coll])
        UT_BajomobileVectorE[coll] <- UT_Bajomobile[2]

        UT_Bajofacultativelymobile <-
percentEcolTrait(carmel, "motility", "facultatively mobile",
desiredCollections=UT_BajocianCollections[coll])
        UT_BajofacultativelymobileVectorE[coll] <-
UT_Bajofacultativelymobile[2]

        UT_Bajosessile <- percentEcolTrait(carmel,
"motility", "sessile",
desiredCollections=UT_BajocianCollections[coll])
        UT_BajosessileVectorE[coll] <- UT_Bajosessile[2]

    }

#Loop to calculate percentage of each ecological trait by cluster
for European Bathonian occurrences
    for (coll in 1:length(UT_BathonianCollections)) {

        UT_Batsinfaunal <- percentEcolTrait(carmel,
"life_habit", "shallow infaunal",
desiredCollections=UT_BathonianCollections[coll])
        UT_BatsinfaunalVectorE[coll] <-
UT_Batsinfaunal[2]

        UT_Batdinafaunal <- percentEcolTrait(carmel,
"life_habit", "deep infaunal",
desiredCollections=UT_BathonianCollections[coll])
        UT_BatdinafaunalVectorE[coll] <-
UT_Batdinafaunal[2]

        UT_Batepifaunal <- percentEcolTrait(carmel,
"life_habit", "epifaunal",
desiredCollections=UT_BathonianCollections[coll])
        UT_BatepifaunalVectorE[coll] <-
UT_Batepifaunal[2]

```

```

        UT_Batcementing <- percentEcolTrait(carmel,
"stability", "cementing",
desiredCollections=UT_BathonianCollections[coll])
        UT_BatcementingVectorE[coll] <-
UT_Batcementing[2]

        UT_Batfreelying <- percentEcolTrait(carmel,
"stability", "free-lying",
desiredCollections=UT_BathonianCollections[coll])
        UT_BatfreelyingVectorE[coll] <-
UT_Batfreelying[2]

        UT_Batpedunculate <- percentEcolTrait(carmel,
"stability", "pedunculate",
desiredCollections=UT_BathonianCollections[coll])
        UT_BatpedunculateVectorE[coll] <-
UT_Batpedunculate[2]

        UT_Batepibyssate <- percentEcolTrait(carmel,
"stability", "epibyssate",
desiredCollections=UT_BathonianCollections[coll])
        UT_BatepibyssateVectorE[coll] <-
UT_Batepibyssate[2]

        UT_Batmobile <- percentEcolTrait(carmel,
"motility", "mobile",
desiredCollections=UT_BathonianCollections[coll]) #achievement
unlocked
        UT_BatmobileVectorE[coll] <- UT_Batmobile[2]

        UT_Batfacultativelymobile <-
percentEcolTrait(carmel, "motility", "facultatively mobile",
desiredCollections=UT_BathonianCollections[coll])
        UT_BatfacultativelymobileVectorE[coll] <-
UT_Batfacultativelymobile[2]

        UT_Batsessile <- percentEcolTrait(carmel,
"motility", "sessile",
desiredCollections=UT_BathonianCollections[coll])
        UT_BatsessileVectorE[coll] <- UT_Batsessile[2]
    }

#Loop to calculate percentage of each ecological trait for
European Bajocian occurrences
    for (coll in 1:length(EU_BajocianCollectionsSS)) {

        EU_Bajosinfaunal <- percentEcolTrait(global,
"life_habit", "shallow infaunal",
desiredCollections=EU_BajocianCollectionsSS[coll])
        EU_BajosinfaunalSSVectorE[coll] <-
EU_Bajosinfaunal[2]

```

```

EU_Bajodinfraunal <- percentEcolTrait(global,
"life_habit", "deep infraunal",
desiredCollections=EU_BajocianCollectionsSS[coll])
EU_BajodinfraunalSSVectorE[coll] <-
EU_Bajodinfraunal[2]

EU_Bajoepifaunal <- percentEcolTrait(global,
"life_habit", "epifaunal",
desiredCollections=EU_BajocianCollectionsSS[coll])
EU_BajoepifaunalSSVectorE[coll] <-
EU_Bajoepifaunal[2]

EU_Bajocementing <- percentEcolTrait(global,
"stability", "cementing",
desiredCollections=EU_BajocianCollectionsSS[coll])
EU_BajocementingSSVectorE[coll] <-
EU_Bajocementing[2]

EU_Bajofreelying <- percentEcolTrait(global,
"stability", "free-lying",
desiredCollections=EU_BajocianCollectionsSS[coll])
EU_BajofreelyingSSVectorE[coll] <-
EU_Bajofreelying[2]

EU_Bajopedunculate <- percentEcolTrait(global,
"stability", "pedunculate",
desiredCollections=EU_BajocianCollectionsSS[coll])
EU_BajopedunculateSSVectorE[coll] <-
EU_Bajopedunculate[2]

EU_Bajoepibyssate <- percentEcolTrait(global,
"stability", "epibyssate",
desiredCollections=EU_BajocianCollectionsSS[coll])
EU_BajoepibyssateSSVectorE[coll] <-
EU_Bajoepibyssate[2]

EU_Bajomobile <- percentEcolTrait(global,
"motility", "mobile",
desiredCollections=EU_BajocianCollectionsSS[coll])
EU_BajomobileSSVectorE[coll] <- EU_Bajomobile[2]

EU_Bajofacultativelymobile <-
percentEcolTrait(global, "motility", "facultatively mobile",
desiredCollections=EU_BajocianCollectionsSS[coll])
EU_BajofacultativelymobileSSVectorE[coll] <-
EU_Bajofacultativelymobile[2]

EU_Bajosessile <- percentEcolTrait(global,
"motility", "sessile",
desiredCollections=EU_BajocianCollectionsSS[coll])
EU_BajosessileSSVectorE[coll] <-
EU_Bajosessile[2]

```

```

    }

#Loop to calculate percentage of each ecological trait by cluster
for Global Bathonian occurrences
  for (coll in 1:length(EU_BathonianCollectionsSS)) {

    EU_Batsinfaunal <- percentEcolTrait(global,
"life_habit", "shallow infaunal",
desiredCollections=EU_BathonianCollectionsSS[coll])
    EU_BatsinfaunalSSVectorE[coll] <-
EU_Batsinfaunal[2]

    EU_Batdinafaunal <- percentEcolTrait(global,
"life_habit", "deep infaunal",
desiredCollections=EU_BathonianCollectionsSS[coll])
    EU_BatdinafaunalSSVectorE[coll] <-
EU_Batdinafaunal[2]

    EU_Batepifaunal <- percentEcolTrait(global,
"life_habit", "epifaunal",
desiredCollections=EU_BathonianCollectionsSS[coll])
    EU_BatepifaunalSSVectorE[coll] <-
EU_Batepifaunal[2]

    EU_Batcementing <- percentEcolTrait(global,
"stability", "cementing",
desiredCollections=EU_BathonianCollectionsSS[coll])
    EU_BatcementingSSVectorE[coll] <-
EU_Batcementing[2]

    EU_Batfreelying <- percentEcolTrait(global,
"stability", "free-lying",
desiredCollections=EU_BathonianCollectionsSS[coll])
    EU_BatfreelyingSSVectorE[coll] <-
EU_Batfreelying[2]

    EU_Batpedunculate <- percentEcolTrait(global,
"stability", "pedunculate",
desiredCollections=EU_BathonianCollectionsSS[coll])
    EU_BatpedunculateSSVectorE[coll] <-
EU_Batpedunculate[2]

    EU_Batepibyssate <- percentEcolTrait(global,
"stability", "epibyssate",
desiredCollections=EU_BathonianCollectionsSS[coll])
    EU_BatepibyssateSSVectorE[coll] <-
EU_Batepibyssate[2]

    EU_Batmobile <- percentEcolTrait(global,
"motility", "mobile",
desiredCollections=EU_BathonianCollectionsSS[coll]) #achievement
    unlocked
    EU_BatmobileSSVectorE[coll] <- EU_Batmobile[2]
  }
}

```

```

        EU_Batfacultativelymobile <-
percentEcolTrait(global, "motility", "facultatively mobile",
desiredCollections=EU_BathonianCollectionsSS[coll])
        EU_BatfacultativelymobileSSVectorE[coll] <-
EU_Batfacultativelymobile[2]

        EU_Batsessile <- percentEcolTrait(global,
"motility", "sessile",
desiredCollections=EU_BathonianCollectionsSS[coll])
        EU_BatsessileSSVectorE[coll] <- EU_Batsessile[2]

    }

#Calculate confidence intervals
UtahMeanBajoProp <- matrix(rep(0), nrow=6, ncol=3,
dimnames=list(c("shallow infaunal", "epifaunal", "cementing",
"mobile", "facultatively mobile", "sessile" ), c("LCL", "E",
"UCL")))
UtahMeanBajoProp[1,2] <- round(mean(UT_BajosinfaunalVectorE), 1)
CI1 <- percent.confint(mean(UT_BajosinfaunalVectorE),
length(UT_BajosinfaunalVectorE), 95)
UtahMeanBajoProp[1,1] <- CI1[1]
UtahMeanBajoProp[1,3] <- CI1[2]
UtahMeanBajoProp[2,2] <- round(mean(UT_BajoepifaunalVectorE), 1)
CI2 <- percent.confint(mean(UT_BajoepifaunalVectorE),
length(UT_BajoepifaunalVectorE), 95)
UtahMeanBajoProp[2,1] <- CI2[1]
UtahMeanBajoProp[2,3] <- CI2[2]
UtahMeanBajoProp[3,2] <- round(mean(UT_BajocementingVectorE), 1)
CI3 <- percent.confint(mean(UT_BajocementingVectorE),
length(UT_BajocementingVectorE), 95)
UtahMeanBajoProp[3,1] <- CI3[1]
UtahMeanBajoProp[3,3] <- CI3[2]
UtahMeanBajoProp[4,2] <- round(mean(UT_BajomobileVectorE), 1)
CI4 <- percent.confint(mean(UT_BajomobileVectorE),
length(UT_BajomobileVectorE), 95)
UtahMeanBajoProp[4,1] <- CI4[1]
UtahMeanBajoProp[4,3] <- CI4[2]
UtahMeanBajoProp[5,2] <-
round(mean(UT_BajofacultativelymobileVectorE), 1)
CI5 <- percent.confint(mean(UT_BajofacultativelymobileVectorE),
length(UT_BajofacultativelymobileVectorE), 95)
UtahMeanBajoProp[5,1] <- CI5[1]
UtahMeanBajoProp[5,3] <- CI5[2]
UtahMeanBajoProp[6,2] <- round(mean(UT_BajosessileVectorE), 1)
CI6 <- percent.confint(mean(UT_BajosessileVectorE),
length(UT_BajosessileVectorE), 95)
UtahMeanBajoProp[6,1] <- CI6[1]
UtahMeanBajoProp[6,3] <- CI6[2]

#Calculate confidence intervals

```

```

UtahMeanBatProp <- matrix(rep(0), nrow=6, ncol=3,
dimnames=list(c("shallow infaunal", "epifaunal", "cementing",
"mobile", "facultatively mobile", "sessile" ), c("LCL", "E",
"UCL")))
UtahMeanBatProp[1,2] <- round(mean(UT_BatsinfaunalVectorE), 1)
CI1 <- percent.confint(mean(UT_BatsinfaunalVectorE),
length(UT_BatsinfaunalVectorE), 95)
UtahMeanBatProp[1,1] <- CI1[1]
UtahMeanBatProp[1,3] <- CI1[2]
UtahMeanBatProp[2,2] <- round(mean(UT_BatepifaunalVectorE), 1)
CI2 <- percent.confint(mean(UT_BatepifaunalVectorE),
length(UT_BatepifaunalVectorE), 95)
UtahMeanBatProp[2,1] <- CI2[1]
UtahMeanBatProp[2,3] <- CI2[2]
UtahMeanBatProp[3,2] <- round(mean(UT_BatcementingVectorE), 1)
CI3 <- percent.confint(mean(UT_BatcementingVectorE),
length(UT_BatcementingVectorE), 95)
UtahMeanBatProp[3,1] <- CI3[1]
UtahMeanBatProp[3,3] <- CI3[2]
UtahMeanBatProp[4,2] <- round(mean(UT_BatmobileVectorE), 1)
CI4 <- percent.confint(mean(UT_BatmobileVectorE),
length(UT_BatmobileVectorE), 95)
UtahMeanBatProp[4,1] <- CI4[1]
UtahMeanBatProp[4,3] <- CI4[2]
UtahMeanBatProp[5,2] <-
round(mean(UT_BatfacultativelymobileVectorE), 1)
CI5 <- percent.confint(mean(UT_BatfacultativelymobileVectorE),
length(UT_BatfacultativelymobileVectorE), 95)
UtahMeanBatProp[5,1] <- CI5[1]
UtahMeanBatProp[5,3] <- CI5[2]
UtahMeanBatProp[6,2] <- round(mean(UT_BatsessileVectorE), 1)
CI6 <- percent.confint(mean(UT_BatsessileVectorE),
length(UT_BatsessileVectorE), 95)
UtahMeanBatProp[6,1] <- CI6[1]
UtahMeanBatProp[6,3] <- CI6[2]

#Calculate confidence intervals
EUMeanBajoPropSS <- matrix(rep(0), nrow=6, ncol=3,
dimnames=list(c("shallow infaunal", "epifaunal", "cementing",
"mobile", "facultatively mobile", "sessile" ), c("LCL", "E",
"UCL")))
EUMeanBajoPropSS[1,2] <- round(mean(EU_BajosinfaunalSSVectorE),
1)
CI1 <- percent.confint(mean(EU_BajosinfaunalSSVectorE),
length(EU_BajosinfaunalSSVectorE), 95)
EUMeanBajoPropSS[1,1] <- CI1[1]
EUMeanBajoPropSS[1,3] <- CI1[2]
EUMeanBajoPropSS[2,2] <- round(mean(EU_BajoepifaunalSSVectorE),
1)
CI2 <- percent.confint(mean(EU_BajoepifaunalSSVectorE),
length(EU_BajoepifaunalSSVectorE), 95)
EUMeanBajoPropSS[2,1] <- CI2[1]
EUMeanBajoPropSS[2,3] <- CI2[2]

```

```

EUMeanBajoPropSS[3,2] <- round(mean(EU_BajocementingSSVectorE),
1)
CI3 <- percent.confint(mean(EU_BajocementingSSVectorE),
length(EU_BajocementingSSVectorE), 95)
EUMeanBajoPropSS[3,1] <- CI3[1]
EUMeanBajoPropSS[3,3] <- CI3[2]
EUMeanBajoPropSS[4,2] <- round(mean(EU_BajomobileSSVectorE), 1)
CI4 <- percent.confint(mean(EU_BajomobileSSVectorE),
length(EU_BajomobileSSVectorE), 95)
EUMeanBajoPropSS[4,1] <- CI4[1]
EUMeanBajoPropSS[4,3] <- CI4[2]
EUMeanBajoPropSS[5,2] <-
round(mean(EU_BajofacultativelymobileSSVectorE), 1)
CI5 <- percent.confint(mean(EU_BajofacultativelymobileSSVectorE),
length(EU_BajofacultativelymobileSSVectorE), 95)
EUMeanBajoPropSS[5,1] <- CI5[1]
EUMeanBajoPropSS[5,3] <- CI5[2]
EUMeanBajoPropSS[6,2] <- round(mean(EU_BajosessileSSVectorE), 1)
CI6 <- percent.confint(mean(EU_BajosessileSSVectorE),
length(EU_BajosessileSSVectorE), 95)
EUMeanBajoPropSS[6,1] <- CI6[1]
EUMeanBajoPropSS[6,3] <- CI6[2]

#Calculate confidence intervals
EUMeanBatPropSS <- matrix(rep(0), nrow=6, ncol=3,
dimnames=list(c("shallow infaunal", "epifaunal", "cementing",
"mobile", "facultatively mobile", "sessile" ), c("LCL", "E",
"UCL")))
EUMeanBatPropSS[1,2] <- round(mean(EU_BatsinfaunalSSVectorE), 1)
CI1 <- percent.confint(mean(EU_BatsinfaunalSSVectorE),
length(EU_BatsinfaunalSSVectorE), 95)
EUMeanBatPropSS[1,1] <- CI1[1]
EUMeanBatPropSS[1,3] <- CI1[2]
EUMeanBatPropSS[2,2] <- round(mean(EU_BatepifaunalSSVectorE), 1)
CI2 <- percent.confint(mean(EU_BatepifaunalSSVectorE),
length(EU_BatepifaunalSSVectorE), 95)
EUMeanBatPropSS[2,1] <- CI2[1]
EUMeanBatPropSS[2,3] <- CI2[2]
EUMeanBatPropSS[3,2] <- round(mean(EU_BatcementingSSVectorE), 1)
CI3 <- percent.confint(mean(EU_BatcementingSSVectorE),
length(EU_BatcementingSSVectorE), 95)
EUMeanBatPropSS[3,1] <- CI3[1]
EUMeanBatPropSS[3,3] <- CI3[2]
EUMeanBatPropSS[4,2] <- round(mean(EU_BatmobileSSVectorE), 1)
CI4 <- percent.confint(mean(EU_BatmobileSSVectorE),
length(EU_BatmobileSSVectorE), 95)
EUMeanBatPropSS[4,1] <- CI4[1]
EUMeanBatPropSS[4,3] <- CI4[2]
EUMeanBatPropSS[5,2] <-
round(mean(EU_BatfacultativelymobileSSVectorE), 1)
CI5 <- percent.confint(mean(EU_BatfacultativelymobileSSVectorE),
length(EU_BatfacultativelymobileSSVectorE), 95)
EUMeanBatPropSS[5,1] <- CI5[1]

```

```

EUMeanBatPropSS[5,3] <- CI5[2]
EUMeanBatPropSS[6,2] <- round(mean(EU_BatsessileSSVectorE), 1)
CI6 <- percent.confint(mean(EU_BatsessileSSVectorE),
length(EU_BatsessileSSVectorE), 95)
EUMeanBatPropSS[6,1] <- CI6[1]
EUMeanBatPropSS[6,3] <- CI6[2]

#Convert percentages to proportions
UtahMeanBajoProp <- round(UtahMeanBajoProp/100, 2)
UtahMeanBatProp <- round(UtahMeanBatProp/100,2)
EUMeanBajoPropSS <- round(EUMeanBajoPropSS/100, 2)
EUMeanBatPropSS <- round(EUMeanBatPropSS/100, 2)

UtahMeanBajoProp
UtahMeanBatProp
EUMeanBajoPropSS
EUMeanBatPropSS

#Create axes for plots
traits <- factor(c("shallow infaunal", "epifaunal", "cementing",
"mobile", "facultatively mobile", "sessile"),
as.ordered(c("shallow infaunal", "epifaunal", "cementing",
"mobile", "facultatively mobile", "sessile")))
yaxis <- c(1, 2, 3, 4, 5, 6)

##Plots of temporal proportions for each geographic scale

#Utah
dev.new(width=7, length=7)
plot(UtahMeanBajoProp[,2], yaxis, main='Utah', xlab='Mean
proportion', ylab='Trait', xlim=range(0:1), las=1, type='n',
axes=FALSE)
axis(1,)
axis(2, at=yaxis, las=1, labels=traits)
points(UtahMeanBajoProp[,2], yaxis, type="p", pch=16,
col="black")
segments(UtahMeanBajoProp[,1], yaxis, UtahMeanBajoProp[,3],
yaxis, col="black")
points(UtahMeanBatProp[,2], yaxis, type="p", pch=16, col="gray")
segments(UtahMeanBatProp[,1], yaxis, UtahMeanBatProp[,3], yaxis,
col="gray")
legend("right", c("Bajocian", "Bathonian"), bty="n", lty=1,
col=c("black", "gray"), horiz=FALSE, x.intersp=0.5)

#Europe
dev.new(width=7, length=7)
plot(EUMeanBajoPropSS[,2], yaxis, main='Europe Open Shallow
Subtidal', xlab='Mean proportion', ylab='Trait', xlim=range(0:1),
las=1, type='n', axes=FALSE)
axis(1,)
axis(2, at=yaxis, las=1, labels=traits)
points(EUMeanBajoPropSS[,2], yaxis, type="p", pch=16,
col="black")

```



```

segments(EUMeanBajoPropSS[,1], yaxis, EUMeanBajoPropSS[,3],
yaxis, col="black")
points(EUMeanBatPropSS[,2], yaxis, type="p", pch=16, col="gray")
segments(EUMeanBatPropSS[,1], yaxis, EUMeanBatPropSS[,3], yaxis,
col="gray")
legend("right", c("Bajocian", "Bathonian"), bty="n", lty=1,
col=c("black", "gray"), horiz=FALSE, x.intersp=0.5)

-----
-----
-----
-----

##Loop and plots of temporal ecological proportions of abundances
by depositional environment in Utah and Europe

#Read source files
source("percentConfidenceInterval.R")
source("mod_abundance_percentEcolTrait.R")
source("extractionFunctions.R")

#Read Datasets
global <- read.csv('clusteredGlobalNEW.csv', header=TRUE,
stringsAsFactors=FALSE)
carmel <- read.csv('carmel.csv', header=TRUE,
stringsAsFactors=FALSE)

#Extract collections by stage
UT_BajocianCollections <- extractFieldCollections(carmel,
"Bajocian")
UT_BathonianCollections <- extractFieldCollections(carmel,
"Bathonian")

#Extract collections by stage and environment
EU_BajocianCollectionsSS <- extractPBDBCollections(global,
"Bajocian", "Europe", "open shallow subtidal",
desiredFacies="allFacies")
EU_BathonianCollectionsSS <- extractPBDBCollections(global,
"Bathonian", "Europe", "open shallow subtidal",
desiredFacies="allFacies")

#Create empty vectors that will be used to fill estimated
percentages calculated by running loop for Bajocian occurrences
UT_BajosinfaunalVectorE <-
metricsForCollections(UT_BajocianCollections)
UT_BajodinfaunalVectorE <-
metricsForCollections(UT_BajocianCollections)
UT_BajoepifaunalVectorE <-
metricsForCollections(UT_BajocianCollections)
UT_BajocementingVectorE <-
metricsForCollections(UT_BajocianCollections)
UT_BajofreelyingVectorE <-
metricsForCollections(UT_BajocianCollections)

```

```

UT_BajopedunculateVectorE <-
metricsForCollections(UT_BajocianCollections)
UT_BajoepibyssateVectorE <-
metricsForCollections(UT_BajocianCollections)
UT_BajomobileVectorE <-
metricsForCollections(UT_BajocianCollections)
UT_BajofacultativelymobileVectorE <-
metricsForCollections(UT_BajocianCollections)
UT_BajosessileVectorE <-
metricsForCollections(UT_BajocianCollections)

EU_BajosinfaunalSSVectorE <-
metricsForCollections(EU_BajocianCollectionsSS)
EU_BajodinfaunalSSVectorE <-
metricsForCollections(EU_BajocianCollectionsSS)
EU_BajoepifaunalSSVectorE <-
metricsForCollections(EU_BajocianCollectionsSS)
EU_BajocementingSSVectorE <-
metricsForCollections(EU_BajocianCollectionsSS)
EU_BajofreelyingSSVectorE <-
metricsForCollections(EU_BajocianCollectionsSS)
EU_BajopedunculateSSVectorE <-
metricsForCollections(EU_BajocianCollectionsSS)
EU_BajoepibyssateSSVectorE <-
metricsForCollections(EU_BajocianCollectionsSS)
EU_BajomobileSSVectorE <-
metricsForCollections(EU_BajocianCollectionsSS)
EU_BajofacultativelymobileSSVectorE <-
metricsForCollections(EU_BajocianCollectionsSS)
EU_BajosessileSSVectorE <-
metricsForCollections(EU_BajocianCollectionsSS)

#Create empty vectors that will be used to fill estimates
calculated by running loop for Bathonian occurrences
UT_BatsinfaunalVectorE <-
metricsForCollections(UT_BathonianCollections)
UT_BatdinfaunalVectorE <-
metricsForCollections(UT_BathonianCollections)
UT_BatepifaunalVectorE <-
metricsForCollections(UT_BathonianCollections)
UT_BatcementingVectorE <-
metricsForCollections(UT_BathonianCollections)
UT_BatepibyssateVectorE <-
metricsForCollections(UT_BathonianCollections)
UT_BatfreelyingVectorE <-
metricsForCollections(UT_BathonianCollections)
UT_BatpedunculateVectorE <-
metricsForCollections(UT_BathonianCollections)
UT_BatmobileVectorE <-
metricsForCollections(UT_BathonianCollections)
UT_BatfacultativelymobileVectorE <-
metricsForCollections(UT_BathonianCollections)

```

```

UT_BatsessileVectorE <-
metricsForCollections(UT_BathonianCollections)

EU_BatsinfaunalSSVectorE <-
metricsForCollections(EU_BathonianCollectionsSS)
EU_BatdinhaunalSSVectorE <-
metricsForCollections(EU_BathonianCollectionsSS)
EU_BatepifaunalSSVectorE <-
metricsForCollections(EU_BathonianCollectionsSS)
EU_BatcementingSSVectorE <-
metricsForCollections(EU_BathonianCollectionsSS)
EU_BatepibyssateSSVectorE <-
metricsForCollections(EU_BathonianCollectionsSS)
EU_BatfreelyingSSVectorE <-
metricsForCollections(EU_BathonianCollectionsSS)
EU_BatpedunculateSSVectorE <-
metricsForCollections(EU_BathonianCollectionsSS)
EU_BatmobileSSVectorE <-
metricsForCollections(EU_BathonianCollectionsSS)
EU_BatfacultativelymobileSSVectorE <-
metricsForCollections(EU_BathonianCollectionsSS)
EU_BatsessileSSVectorE <-
metricsForCollections(EU_BathonianCollectionsSS)

#Loop to calculate percentage of each ecological trait by cluster
for Global Bajocian occurrences
  for (coll in 1:length(UT_BajocianCollections)) {

      UT_Bajosinhaunal <-
abundance_percentEcolTrait(carmel, "life_habit", "shallow
inhaunal", desiredCollections=UT_BajocianCollections[coll])
      UT_BajosinhaunalVectorE[coll] <-
UT_Bajosinhaunal[2]

      UT_Bajodinhaunal <-
abundance_percentEcolTrait(carmel, "life_habit", "deep inhaunal",
desiredCollections=UT_BajocianCollections[coll])
      UT_BajodinhaunalVectorE[coll] <-
UT_Bajodinhaunal[2]

      UT_Bajoepifaunal <-
abundance_percentEcolTrait(carmel, "life_habit", "epifaunal",
desiredCollections=UT_BajocianCollections[coll])
      UT_BajoepifaunalVectorE[coll] <-
UT_Bajoepifaunal[2]

      UT_Bajocementing <-
abundance_percentEcolTrait(carmel, "stability", "cementing",
desiredCollections=UT_BajocianCollections[coll])
      UT_BajocementingVectorE[coll] <-
UT_Bajocementing[2]

```

```

        UT_Bajofreelying <-
abundance_percentEcolTrait(carmel, "stability", "free-lying",
desiredCollections=UT_BajocianCollections[coll])
        UT_BajofreelyingVectorE[coll] <-
UT_Bajofreelying[2]

        UT_Bajopedunculate <-
abundance_percentEcolTrait(carmel, "stability", "pedunculate",
desiredCollections=UT_BajocianCollections[coll])
        UT_BajopedunculateVectorE[coll] <-
UT_Bajopedunculate[2]

        UT_Bajoepibyssate <-
abundance_percentEcolTrait(carmel, "stability", "epibyssate",
desiredCollections=UT_BajocianCollections[coll])
        UT_BajoepibyssateVectorE[coll] <-
UT_Bajoepibyssate[2]

        UT_Bajomobile <-
abundance_percentEcolTrait(carmel, "motility", "mobile",
desiredCollections=UT_BajocianCollections[coll])
        UT_BajomobileVectorE[coll] <- UT_Bajomobile[2]

        UT_Bajofacultativelymobile <-
abundance_percentEcolTrait(carmel, "motility", "facultatively
mobile", desiredCollections=UT_BajocianCollections[coll])
        UT_BajofacultativelymobileVectorE[coll] <-
UT_Bajofacultativelymobile[2]

        UT_Bajosessile <-
abundance_percentEcolTrait(carmel, "motility", "sessile",
desiredCollections=UT_BajocianCollections[coll])
        UT_BajosessileVectorE[coll] <- UT_Bajosessile[2]

    }

#Loop to calculate percentage of each ecological trait by cluster
for Global Bathonian occurrences
    for (coll in 1:length(UT_BathonianCollections)) {

        UT_Batsinfaunal <-
abundance_percentEcolTrait(carmel, "life_habit", "shallow
infaunal", desiredCollections=UT_BathonianCollections[coll])
        UT_BatsinfaunalVectorE[coll] <-
UT_Batsinfaunal[2]

        UT_Batdinafaunal <-
abundance_percentEcolTrait(carmel, "life_habit", "deep infaunal",
desiredCollections=UT_BathonianCollections[coll])
        UT_BatdinafaunalVectorE[coll] <-
UT_Batdinafaunal[2]

```

```

        UT_Batepifaunal <-
abundance_percentEcolTrait(carmel, "life_habit", "epifaunal",
desiredCollections=UT_BathonianCollections[coll])
        UT_BatepifaunalVectorE[coll] <-
UT_Batepifaunal[2]

        UT_Batcementing <-
abundance_percentEcolTrait(carmel, "stability", "cementing",
desiredCollections=UT_BathonianCollections[coll])
        UT_BatcementingVectorE[coll] <-
UT_Batcementing[2]

        UT_Batfreelying <-
abundance_percentEcolTrait(carmel, "stability", "free-lying",
desiredCollections=UT_BathonianCollections[coll])
        UT_BatfreelyingVectorE[coll] <-
UT_Batfreelying[2]

        UT_Batpedunculate <-
abundance_percentEcolTrait(carmel, "stability", "pedunculate",
desiredCollections=UT_BathonianCollections[coll])
        UT_BatpedunculateVectorE[coll] <-
UT_Batpedunculate[2]

        UT_Batepibyssate <-
abundance_percentEcolTrait(carmel, "stability", "epibyssate",
desiredCollections=UT_BathonianCollections[coll])
        UT_BatepibyssateVectorE[coll] <-
UT_Batepibyssate[2]

        UT_Batmobile <-
abundance_percentEcolTrait(carmel, "motility", "mobile",
desiredCollections=UT_BathonianCollections[coll]) #achievement
unlocked
        UT_BatmobileVectorE[coll] <- UT_Batmobile[2]

        UT_Batfacultativelymobile <-
abundance_percentEcolTrait(carmel, "motility", "facultatively
mobile", desiredCollections=UT_BathonianCollections[coll])
        UT_BatfacultativelymobileVectorE[coll] <-
UT_Batfacultativelymobile[2]

        UT_Batsessile <-
abundance_percentEcolTrait(carmel, "motility", "sessile",
desiredCollections=UT_BathonianCollections[coll])
        UT_BatsessileVectorE[coll] <- UT_Batsessile[2]

    }

#Loop to calculate percentage of each ecological trait for
European Bajocian occurrences
    for (coll in 1:length(EU_BajocianCollectionsSS)) {

```

```

EU_Bajosinfaunal <-
abundance_percentEcolTrait(global, "life_habit", "shallow
infaunal", desiredCollections=EU_BajocianCollectionsSS[coll])
EU_BajosinfaunalSSVectorE[coll] <-
EU_Bajosinfaunal[2]

EU_Bajodinfaunal <-
abundance_percentEcolTrait(global, "life_habit", "deep infaunal",
desiredCollections=EU_BajocianCollectionsSS[coll])
EU_BajodinfaunalSSVectorE[coll] <-
EU_Bajodinfaunal[2]

EU_Bajoepifaunal <-
abundance_percentEcolTrait(global, "life_habit", "epifaunal",
desiredCollections=EU_BajocianCollectionsSS[coll])
EU_BajoepifaunalSSVectorE[coll] <-
EU_Bajoepifaunal[2]

EU_Bajocementing <-
abundance_percentEcolTrait(global, "stability", "cementing",
desiredCollections=EU_BajocianCollectionsSS[coll])
EU_BajocementingSSVectorE[coll] <-
EU_Bajocementing[2]

EU_Bajofreelying <-
abundance_percentEcolTrait(global, "stability", "free-lying",
desiredCollections=EU_BajocianCollectionsSS[coll])
EU_BajofreelyingSSVectorE[coll] <-
EU_Bajofreelying[2]

EU_Bajopedunculate <-
abundance_percentEcolTrait(global, "stability", "pedunculate",
desiredCollections=EU_BajocianCollectionsSS[coll])
EU_BajopedunculateSSVectorE[coll] <-
EU_Bajopedunculate[2]

EU_Bajoepibyssate <-
abundance_percentEcolTrait(global, "stability", "epibyssate",
desiredCollections=EU_BajocianCollectionsSS[coll])
EU_BajoepibyssateSSVectorE[coll] <-
EU_Bajoepibyssate[2]

EU_Bajomobile <-
abundance_percentEcolTrait(global, "motility", "mobile",
desiredCollections=EU_BajocianCollectionsSS[coll])
EU_BajomobileSSVectorE[coll] <- EU_Bajomobile[2]

EU_Bajofacultativelymobile <-
abundance_percentEcolTrait(global, "motility", "facultatively
mobile", desiredCollections=EU_BajocianCollectionsSS[coll])
EU_BajofacultativelymobileSSVectorE[coll] <-
EU_Bajofacultativelymobile[2]

```

```

        EU_Bajosessile <-
abundance_percentEcolTrait(global, "motility", "sessile",
desiredCollections=EU_BajocianCollectionsSS[coll])
        EU_BajosessileSSVectorE[coll] <-
EU_Bajosessile[2]

    }

#Loop to calculate percentage of each ecological trait by cluster
for Global Bathonian occurrences
    for (coll in 1:length(EU_BathonianCollectionsSS)) {

        EU_Batsinfaunal <-
abundance_percentEcolTrait(global, "life_habit", "shallow
infaunal", desiredCollections=EU_BathonianCollectionsSS[coll])
        EU_BatsinfaunalSSVectorE[coll] <-
EU_Batsinfaunal[2]

        EU_Batdinafaunal <-
abundance_percentEcolTrait(global, "life_habit", "deep infaunal",
desiredCollections=EU_BathonianCollectionsSS[coll])
        EU_BatdinafaunalSSVectorE[coll] <-
EU_Batdinafaunal[2]

        EU_Batepifaunal <-
abundance_percentEcolTrait(global, "life_habit", "epifaunal",
desiredCollections=EU_BathonianCollectionsSS[coll])
        EU_BatepifaunalSSVectorE[coll] <-
EU_Batepifaunal[2]

        EU_Batcementing <-
abundance_percentEcolTrait(global, "stability", "cementing",
desiredCollections=EU_BathonianCollectionsSS[coll])
        EU_BatcementingSSVectorE[coll] <-
EU_Batcementing[2]

        EU_Batfreelying <-
abundance_percentEcolTrait(global, "stability", "free-lying",
desiredCollections=EU_BathonianCollectionsSS[coll])
        EU_BatfreelyingSSVectorE[coll] <-
EU_Batfreelying[2]

        EU_Batpedunculate <-
abundance_percentEcolTrait(global, "stability", "pedunculate",
desiredCollections=EU_BathonianCollectionsSS[coll])
        EU_BatpedunculateSSVectorE[coll] <-
EU_Batpedunculate[2]

        EU_Batepibyssate <-
abundance_percentEcolTrait(global, "stability", "epibyssate",
desiredCollections=EU_BathonianCollectionsSS[coll])
        EU_BatepibyssateSSVectorE[coll] <-
EU_Batepibyssate[2]

```

```

        EU_Batmobile <-
abundance_percentEcolTrait(global, "motility", "mobile",
desiredCollections=EU_BathonianCollectionsSS[coll]) #achievement
unlocked

        EU_BatmobileSSVectorE[coll] <- EU_Batmobile[2]

        EU_Batfacultativelymobile <-
abundance_percentEcolTrait(global, "motility", "facultatively
mobile", desiredCollections=EU_BathonianCollectionsSS[coll])
        EU_BatfacultativelymobileSSVectorE[coll] <-
EU_Batfacultativelymobile[2]

        EU_Batsessile <-
abundance_percentEcolTrait(global, "motility", "sessile",
desiredCollections=EU_BathonianCollectionsSS[coll])
        EU_BatsessileSSVectorE[coll] <- EU_Batsessile[2]

    }

#Calculate confidence intervals for Bajocian abundances from Utah
UtahMeanBajoProp <- matrix(rep(0), nrow=6, ncol=3,
dimnames=list(c("shallow infaunal", "epifaunal", "cementing",
"mobile", "facultatively mobile", "sessile" ), c("LCL", "E",
"UCL")))
UtahMeanBajoProp[1,2] <- round(mean(UT_BajosinfaunalVectorE,
na.rm=TRUE), 1)
CI1 <- percent.confint(mean(UT_BajosinfaunalVectorE, na.rm=TRUE),
length(UT_BajosinfaunalVectorE), 95)
UtahMeanBajoProp[1,1] <- CI1[1]
UtahMeanBajoProp[1,3] <- CI1[2]
UtahMeanBajoProp[2,2] <- round(mean(UT_BajoepifaunalVectorE,
na.rm=TRUE), 1)
CI2 <- percent.confint(mean(UT_BajoepifaunalVectorE, na.rm=TRUE),
length(UT_BajoepifaunalVectorE), 95)
UtahMeanBajoProp[2,1] <- CI2[1]
UtahMeanBajoProp[2,3] <- CI2[2]
UtahMeanBajoProp[3,2] <- round(mean(UT_BajocementingVectorE,
na.rm=TRUE), 1)
CI3 <- percent.confint(mean(UT_BajocementingVectorE, na.rm=TRUE),
length(UT_BajocementingVectorE), 95)
UtahMeanBajoProp[3,1] <- CI3[1]
UtahMeanBajoProp[3,3] <- CI3[2]
UtahMeanBajoProp[4,2] <- round(mean(UT_BajomobileVectorE,
na.rm=TRUE), 1)
CI4 <- percent.confint(mean(UT_BajomobileVectorE, na.rm=TRUE),
length(UT_BajomobileVectorE), 95)
UtahMeanBajoProp[4,1] <- CI4[1]
UtahMeanBajoProp[4,3] <- CI4[2]
UtahMeanBajoProp[5,2] <-
round(mean(UT_BajofacultativelymobileVectorE, na.rm=TRUE), 1)
CI5 <- percent.confint(mean(UT_BajofacultativelymobileVectorE,
na.rm=TRUE), length(UT_BajofacultativelymobileVectorE), 95)

```



```

UtahMeanBajoProp[5,1] <- CI5[1]
UtahMeanBajoProp[5,3] <- CI5[2]
UtahMeanBajoProp[6,2] <- round(mean(UT_BajosessileVectorE,
na.rm=TRUE), 1)
CI6 <- percent.confint(mean(UT_BajosessileVectorE, na.rm=TRUE),
length(UT_BajosessileVectorE), 95)
UtahMeanBajoProp[6,1] <- CI6[1]
UtahMeanBajoProp[6,3] <- CI6[2]

#Calculate confidence intervals for Bathonian abundances from
Utah
UtahMeanBatProp <- matrix(rep(0), nrow=6, ncol=3,
dimnames=list(c("shallow infaunal", "epifaunal", "cementing",
"mobile", "facultatively mobile", "sessile" ), c("LCL", "E",
"UCL")))
UtahMeanBatProp[1,2] <- round(mean(UT_BatsinfaunalVectorE,
na.rm=TRUE), 1)
CI1 <- percent.confint(mean(UT_BatsinfaunalVectorE, na.rm=TRUE),
length(UT_BatsinfaunalVectorE), 95)
UtahMeanBatProp[1,1] <- CI1[1]
UtahMeanBatProp[1,3] <- CI1[2]
UtahMeanBatProp[2,2] <- round(mean(UT_BatepifaunalVectorE,
na.rm=TRUE), 1)
CI2 <- percent.confint(mean(UT_BatepifaunalVectorE, na.rm=TRUE),
length(UT_BatepifaunalVectorE), 95)
UtahMeanBatProp[2,1] <- CI2[1]
UtahMeanBatProp[2,3] <- CI2[2]
UtahMeanBatProp[3,2] <- round(mean(UT_BatcementingVectorE,
na.rm=TRUE), 1)
CI3 <- percent.confint(mean(UT_BatcementingVectorE, na.rm=TRUE),
length(UT_BatcementingVectorE), 95)
UtahMeanBatProp[3,1] <- CI3[1]
UtahMeanBatProp[3,3] <- CI3[2]
UtahMeanBatProp[4,2] <- round(mean(UT_BatmobileVectorE,
na.rm=TRUE), 1)
CI4 <- percent.confint(mean(UT_BatmobileVectorE, na.rm=TRUE),
length(UT_BatmobileVectorE), 95)
UtahMeanBatProp[4,1] <- CI4[1]
UtahMeanBatProp[4,3] <- CI4[2]
UtahMeanBatProp[5,2] <-
round(mean(UT_BatfacultativelymobileVectorE, na.rm=TRUE), 1)
CI5 <- percent.confint(mean(UT_BatfacultativelymobileVectorE,
na.rm=TRUE), length(UT_BatfacultativelymobileVectorE), 95)
UtahMeanBatProp[5,1] <- CI5[1]
UtahMeanBatProp[5,3] <- CI5[2]
UtahMeanBatProp[6,2] <- round(mean(UT_BatsessileVectorE,
na.rm=TRUE), 1)
CI6 <- percent.confint(mean(UT_BatsessileVectorE, na.rm=TRUE),
length(UT_BatsessileVectorE), 95)
UtahMeanBatProp[6,1] <- CI6[1]
UtahMeanBatProp[6,3] <- CI6[2]

```

```

#Calculate confidence intervals for Bajocian abundances from
Europe
EUMeanBajoPropSS <- matrix(rep(0), nrow=6, ncol=3,
dimnames=list(c("shallow infaunal", "epifaunal", "cementing",
"mobile", "facultatively mobile", "sessile" ), c("LCL", "E",
"UCL")))
EUMeanBajoPropSS[1,2] <- round(mean(EU_BajosinfaunalSSVectorE,
na.rm=TRUE), 1)
CI1 <- percent.confint(mean(EU_BajosinfaunalSSVectorE,
na.rm=TRUE), length(EU_BajosinfaunalSSVectorE), 95)
EUMeanBajoPropSS[1,1] <- CI1[1]
EUMeanBajoPropSS[1,3] <- CI1[2]
EUMeanBajoPropSS[2,2] <- round(mean(EU_BajoepifaunalSSVectorE,
na.rm=TRUE), 1)
CI2 <- percent.confint(mean(EU_BajoepifaunalSSVectorE,
na.rm=TRUE), length(EU_BajoepifaunalSSVectorE), 95)
EUMeanBajoPropSS[2,1] <- CI2[1]
EUMeanBajoPropSS[2,3] <- CI2[2]
EUMeanBajoPropSS[3,2] <- round(mean(EU_BajocementingSSVectorE,
na.rm=TRUE), 1)
CI3 <- percent.confint(mean(EU_BajocementingSSVectorE,
na.rm=TRUE), length(EU_BajocementingSSVectorE), 95)
EUMeanBajoPropSS[3,1] <- CI3[1]
EUMeanBajoPropSS[3,3] <- CI3[2]
EUMeanBajoPropSS[4,2] <- round(mean(EU_BajomobileSSVectorE,
na.rm=TRUE), 1)
CI4 <- percent.confint(mean(EU_BajomobileSSVectorE, na.rm=TRUE),
length(EU_BajomobileSSVectorE), 95)
EUMeanBajoPropSS[4,1] <- CI4[1]
EUMeanBajoPropSS[4,3] <- CI4[2]
EUMeanBajoPropSS[5,2] <-
round(mean(EU_BajofacultativelymobileSSVectorE, na.rm=TRUE), 1)
CI5 <- percent.confint(mean(EU_BajofacultativelymobileSSVectorE,
na.rm=TRUE), length(EU_BajofacultativelymobileSSVectorE), 95)
EUMeanBajoPropSS[5,1] <- CI5[1]
EUMeanBajoPropSS[5,3] <- CI5[2]
EUMeanBajoPropSS[6,2] <- round(mean(EU_BajosessileSSVectorE,
na.rm=TRUE), 1)
CI6 <- percent.confint(mean(EU_BajosessileSSVectorE, na.rm=TRUE),
length(EU_BajosessileSSVectorE), 95)
EUMeanBajoPropSS[6,1] <- CI6[1]
EUMeanBajoPropSS[6,3] <- CI6[2]

#Calculate confidence intervals for Bathonian abundances from
Europe
EUMeanBatPropSS <- matrix(rep(0), nrow=6, ncol=3,
dimnames=list(c("shallow infaunal", "epifaunal", "cementing",
"mobile", "facultatively mobile", "sessile" ), c("LCL", "E",
"UCL")))
EUMeanBatPropSS[1,2] <- round(mean(EU_BatsinfaunalSSVectorE,
na.rm=TRUE), 1)
CI1 <- percent.confint(mean(EU_BatsinfaunalSSVectorE,
na.rm=TRUE), length(EU_BatsinfaunalSSVectorE), 95)

```

```

EUMeanBatPropSS[1,1] <- CI1[1]
EUMeanBatPropSS[1,3] <- CI1[2]
EUMeanBatPropSS[2,2] <- round(mean(EU_BatepifaunalSSVectorE,
na.rm=TRUE), 1)
CI2 <- percent.confint(mean(EU_BatepifaunalSSVectorE,
na.rm=TRUE), length(EU_BatepifaunalSSVectorE), 95)
EUMeanBatPropSS[2,1] <- CI2[1]
EUMeanBatPropSS[2,3] <- CI2[2]
EUMeanBatPropSS[3,2] <- round(mean(EU_BatcementingSSVectorE,
na.rm=TRUE), 1)
CI3 <- percent.confint(mean(EU_BatcementingSSVectorE),
length(EU_BatcementingSSVectorE), 95)
EUMeanBatPropSS[3,1] <- CI3[1]
EUMeanBatPropSS[3,3] <- CI3[2]
EUMeanBatPropSS[4,2] <- round(mean(EU_BatmobileSSVectorE,
na.rm=TRUE), 1)
CI4 <- percent.confint(mean(EU_BatmobileSSVectorE, na.rm=TRUE),
length(EU_BatmobileSSVectorE), 95)
EUMeanBatPropSS[4,1] <- CI4[1]
EUMeanBatPropSS[4,3] <- CI4[2]
EUMeanBatPropSS[5,2] <-
round(mean(EU_BatfacultativelymobileSSVectorE, na.rm=TRUE), 1)
CI5 <- percent.confint(mean(EU_BatfacultativelymobileSSVectorE,
na.rm=TRUE), length(EU_BatfacultativelymobileSSVectorE), 95)
EUMeanBatPropSS[5,1] <- CI5[1]
EUMeanBatPropSS[5,3] <- CI5[2]
EUMeanBatPropSS[6,2] <- round(mean(EU_BatsessileSSVectorE,
na.rm=TRUE), 1)
CI6 <- percent.confint(mean(EU_BatsessileSSVectorE, na.rm=TRUE),
length(EU_BatsessileSSVectorE), 95)
EUMeanBatPropSS[6,1] <- CI6[1]
EUMeanBatPropSS[6,3] <- CI6[2]

#Convert percentages to proportions
UtahMeanBajoProp <- round(UtahMeanBajoProp/100, 2)
UtahMeanBatProp <- round(UtahMeanBatProp/100,2)
EUMeanBajoPropSS <- round(EUMeanBajoPropSS/100, 2)
EUMeanBatPropSS <- round(EUMeanBatPropSS/100, 2)

UtahMeanBajoProp
UtahMeanBatProp
EUMeanBajoPropSS
EUMeanBatPropSS

#Create axes for plots
traits <- factor(c("shallow infaunal", "epifaunal", "cementing",
"mobile", "facultatively mobile", "sessile"),
as.ordered(c("shallow infaunal", "epifaunal", "cementing",
"mobile", "facultatively mobile", "sessile")))
yaxis <- c(1, 2, 3, 4, 5, 6)

```

```

##Plots of temporal proportions for each geographic scale

#Utah
dev.new(width=7, length=7)
plot(UtahMeanBajoProp[,2], yaxis, main='Utah', xlab='Mean
proportion', ylab='Trait', xlim=range(0:1), las=1, type='n',
axes=FALSE)
axis(1,)
axis(2, at=yaxis, las=1, labels=traits)
points(UtahMeanBajoProp[,2], yaxis, type="p", pch=16,
col="black")
segments(UtahMeanBajoProp[,1], yaxis, UtahMeanBajoProp[,3],
yaxis, col="black")
points(UtahMeanBatProp[,2], yaxis, type="p", pch=16, col="gray")
segments(UtahMeanBatProp[,1], yaxis, UtahMeanBatProp[,3], yaxis,
col="gray")
legend("right", c("Bajocian", "Bathonian"), bty="n", lty=1,
col=c("black", "gray"), horiz=FALSE, x.intersp=0.5)

#Europe
dev.new(width=7, length=7)
plot(EUMeanBajoPropSS[,2], yaxis, main='Europe Open Shallow
Subtidal', xlab='Mean proportion', ylab='Trait', xlim=range(0:1),
las=1, type='n', axes=FALSE)
axis(1,)
axis(2, at=yaxis, las=1, labels=traits)
points(EUMeanBajoPropSS[,2], yaxis, type="p", pch=16,
col="black")
segments(EUMeanBajoPropSS[,1], yaxis, EUMeanBajoPropSS[,3],
yaxis, col="black")
points(EUMeanBatPropSS[,2], yaxis, type="p", pch=16, col="gray")
segments(EUMeanBatPropSS[,1], yaxis, EUMeanBatPropSS[,3], yaxis,
col="gray")
legend("right", c("Bajocian", "Bathonian"), bty="n", lty=1,
col=c("black", "gray"), horiz=FALSE, x.intersp=0.5)

```

R command script to calculate the mean proportion of occurrences and abundance in each collection and compare them between Utah and European collections for the Bajocian and Bathonian. (Figs. 3.7 and 3.8)

```
###Proportion test of life habit occurrence and abundance between  
Utah field data and European and Global PBDB data
```

```
##Occurrences
```

```
#Read source files  
source("PropEcolTrait.R")  
source("extractionFunctions.R")
```

```
#Read Datasets  
global <- read.csv('clusteredGlobalNEW.csv', header=TRUE,  
stringsAsFactors=FALSE)  
carmel <- read.csv('carmel.csv', header=TRUE,  
stringsAsFactors=FALSE)
```

```
UT_Bajocian <- carmel[carmel$stage=="Bajocian",]  
UT_Bathonian <- carmel[carmel$stage=="Bathonian",]
```

```
EU_Bajocian <- global[global$stage=="Bajocian" &  
global$geo_cluster=="Europe",]  
EU_Bathonian <- global[global$stage=="Bathonian" &  
global$geo_cluster=="Europe",]
```

```
EU_BajocianSS <- global[global$stage=="Bajocian" &  
global$geo_cluster=="Europe" & global$environment=="open shallow  
subtidal",]  
EU_BathonianSS <- global[global$stage=="Bathonian" &  
global$geo_cluster=="Europe" & global$environment=="open shallow  
subtidal",]
```

```
#Calculate Bajocian proportions of each life habit group in the  
Utah dataset  
UT_Bajosinfaunal <- propEcolTrait(UT_Bajocian, "life_habit",  
"shallow infaunal")  
UT_Bajodinfaunal <- propEcolTrait(UT_Bajocian, "life_habit",  
"deep infaunal")  
UT_Bajoepifaunal <- propEcolTrait(UT_Bajocian, "life_habit",  
"epifaunal")  
UT_Bajocementing <- propEcolTrait(UT_Bajocian, "stability",  
"cementing")  
UT_Bajofreelying <- propEcolTrait(UT_Bajocian, "stability",  
"free-lying")  
UT_Bajopedunculate <- propEcolTrait(UT_Bajocian, "stability",  
"pedunculate")  
UT_Bajoepibyssate <- propEcolTrait(UT_Bajocian, "stability",  
"epibyssate")  
UT_Bajomobile <- propEcolTrait(UT_Bajocian, "motility", "mobile")
```

```

UT_Bajofacultativelymobile <- propEcolTrait(UT_Bajocian,
"motility", "facultatively mobile")
UT_Bajosessile <- propEcolTrait(UT_Bajocian, "motility",
"sessile")

UT_Bajosinfaunal
UT_Bajodinafaunal
UT_Bajoepifaunal
UT_Bajocementing
UT_Bajofreelying
UT_Bajopedunculate
UT_Bajoepibyssate
UT_Bajomobile
UT_Bajofacultativelymobile
UT_Bajosessile

#Calculate Bathonian proportions of each life habit group in the
northern dataset
UT_Batsinafaunal <- propEcolTrait(UT_Bathonian, "life_habit",
"shallow infaunal")
UT_Batdinafaunal <- propEcolTrait(UT_Bathonian, "life_habit",
"deep infaunal")
UT_Batepifaunal <- propEcolTrait(UT_Bathonian, "life_habit",
"epifaunal")
UT_Batcementing <- propEcolTrait(UT_Bathonian, "stability",
"cementing")
UT_Batfreelying <- propEcolTrait(UT_Bathonian, "stability",
"free-lying")
UT_Batpedunculate <- propEcolTrait(UT_Bathonian, "stability",
"pedunculate")
UT_Batepibyssate <- propEcolTrait(UT_Bathonian, "stability",
"epibyssate")
UT_Batmobile <- propEcolTrait(UT_Bathonian, "motility", "mobile")

UT_Batfacultativelymobile <- propEcolTrait(UT_Bathonian,
"motility", "facultatively mobile")
UT_Batsessile <- propEcolTrait(UT_Bathonian, "motility",
"sessile")

UT_Batsinafaunal
UT_Batdinafaunal
UT_Batepifaunal
UT_Batcementing
UT_Batfreelying
UT_Batpedunculate
UT_Batepibyssate
UT_Batmobile
UT_Batfacultativelymobile
UT_Batsessile

#Calculate BajocianSS proportions of each life habit group in the
southern dataset

```

```

EU_BajosinfaunalSS <- propEcolTrait(EU_BajocianSS, "life_habit",
"shallow infaunal")
EU_BajodinafaunalSS <- propEcolTrait(EU_BajocianSS, "life_habit",
"deep infaunal")
EU_BajoepifaunalSS <- propEcolTrait(EU_BajocianSS, "life_habit",
"epifaunal")
EU_BajocementingSS <- propEcolTrait(EU_BajocianSS, "stability",
"cementing")
EU_BajofreelyingSS <- propEcolTrait(EU_BajocianSS, "stability",
"free-lying")
EU_BajopedunculateSS <- propEcolTrait(EU_BajocianSS, "stability",
"pedunculate")
EU_BajoepibyssateSS <- propEcolTrait(EU_BajocianSS, "stability",
"epibyssate")
EU_BajomobileSS <- propEcolTrait(EU_BajocianSS, "motility",
"mobile")
EU_BajofacultativelymobileSS <- propEcolTrait(EU_BajocianSS,
"motility", "facultatively mobile")
EU_BajosessileSS <- propEcolTrait(EU_BajocianSS, "motility",
"sessile")

EU_BajosinfaunalSS
EU_BajodinafaunalSS
EU_BajoepifaunalSS
EU_BajocementingSS
EU_BajofreelyingSS
EU_BajopedunculateSS
EU_BajoepibyssateSS
EU_BajomobileSS
EU_BajofacultativelymobileSS
EU_BajosessileSS

#Calculate Bathonian proportions of each life habit group in the
European dataset
EU_BatsinfaunalSS <- propEcolTrait(EU_BathonianSS, "life_habit",
"shallow infaunal")
EU_BatdinafaunalSS <- propEcolTrait(EU_BathonianSS, "life_habit",
"deep infaunal")
EU_BatepifaunalSS <- propEcolTrait(EU_BathonianSS, "life_habit",
"epifaunal")
EU_BatcementingSS <- propEcolTrait(EU_BathonianSS, "stability",
"cementing")
EU_BatfreelyingSS <- propEcolTrait(EU_BathonianSS, "stability",
"free-lying")
EU_BatpedunculateSS <- propEcolTrait(EU_BathonianSS, "stability",
"pedunculate")
EU_BatepibyssateSS <- propEcolTrait(EU_BathonianSS, "stability",
"epibyssate")
EU_BatmobileSS <- propEcolTrait(EU_BathonianSS, "motility",
"mobile")
EU_BatfacultativelymobileSS <- propEcolTrait(EU_BathonianSS,
"motility", "facultatively mobile")

```

```
EU_BatsessileSS <- propEcolTrait(EU_BathonianSS, "motility",
"sessile")
```

```
EU_BatsinfaunalSS
EU_BatdinhaunalSS
EU_BatepifaunalSS
EU_BatcementingSS
EU_BatfreelyingSS
EU_BatpedunculateSS
EU_BatepibyssateSS
EU_BatmobileSS
EU_BatfacultativelymobileSS
EU_BatsessileSS
```

```
#Combine Bajocian proportions of life habit groups from Utah and
Europe into a vector
```

```
ESSUT_BajoShallowinfaunalProp <- c(EU_BajosinhaunalSS,
UT_Bajosinhaunal)
ESSUT_BajoEpifaunalProp <- c(EU_BajoepifaunalSS,
UT_Bajoepifaunal)
ESSUT_BajoCementingProp <- c(EU_BajocementingSS,
UT_Bajocementing)
ESSUT_BajoMobileProp <- c(EU_BajomobileSS, UT_Bajomobile)
ESSUT_BajoFacmobileProp <- c(EU_BajofacultativelymobileSS,
UT_Bajofacultativelymobile)
ESSUT_BajoSessileProp <- c(EU_BajosessileSS, UT_Bajosessile)
```

```
#Combine Bathonian proportions of life habit groups from Utah and
Europe into a vector
```

```
ESSUT_BatShallowinfaunalProp <- c(EU_BatsinhaunalSS,
UT_Batsinhaunal)
ESSUT_BatEpifaunalProp <- c(EU_BatepifaunalSS, UT_Batepifaunal)
ESSUT_BatCementingProp <- c(EU_BatcementingSS, UT_Batcementing)
ESSUT_BatMobileProp <- c(EU_BatmobileSS, UT_Batmobile)
ESSUT_BatFacmobileProp <- c(EU_BatfacultativelymobileSS,
UT_Batfacultativelymobile)
ESSUT_BatSessileProp <- c(EU_BatsessileSS, UT_Batsessile)
```

```
ESSUT_BajoShallowinfaunalProp
ESSUT_BajoEpifaunalProp
ESSUT_BajoCementingProp
ESSUT_BajoMobileProp
ESSUT_BajoFacmobileProp
ESSUT_BajoSessileProp
```

```
ESSUT_BatShallowinfaunalProp
ESSUT_BatEpifaunalProp
ESSUT_BatCementingProp
ESSUT_BatMobileProp
ESSUT_BatFacmobileProp
ESSUT_BatSessileProp
```



```

#Combine total number of occurrences from Utah and Europe into
one vector
ESSUT_BajocianTotal <- c(nrow(EU_BajocianSS), nrow(UT_Bajocian))
ESSUT_BathonianTotal <- c(nrow(EU_BathonianSS),
nrow(UT_Bathonian))

#Proportional test of life habits during the Bajocian
ESSUTbajoinfprop.test <- prop.test(ESSUT_BajoShallowinfaunalProp,
ESSUT_BajocianTotal)
ESSUTbajoepiprop.test <- prop.test(ESSUT_BajoEpifaunalProp,
ESSUT_BajocianTotal)
ESSUTbajocemp.test <- prop.test(ESSUT_BajoCementingProp,
ESSUT_BajocianTotal)
ESSUTbajomobprop.test <- prop.test(ESSUT_BajoMobileProp,
ESSUT_BajocianTotal)
ESSUTbajofacmobprop.test <- prop.test(ESSUT_BajoFacmobileProp,
ESSUT_BajocianTotal)
ESSUTbajosesprop.test <- prop.test(ESSUT_BajoSessileProp,
ESSUT_BajocianTotal)

#Proportional test of life habits during the Bathonian
ESSUTbatinfprop.test <- prop.test(ESSUT_BatShallowinfaunalProp,
ESSUT_BathonianTotal)
ESSUTbatepiprop.test <- prop.test(ESSUT_BatEpifaunalProp,
ESSUT_BathonianTotal)
ESSUTbatcemp.test <- prop.test(ESSUT_BatCementingProp,
ESSUT_BathonianTotal)
ESSUTbatmobprop.test <- prop.test(ESSUT_BatMobileProp,
ESSUT_BathonianTotal)
ESSUTbatfacmobprop.test <- prop.test(ESSUT_BatFacmobileProp,
ESSUT_BathonianTotal)
ESSUTbatsesprop.test <- prop.test(ESSUT_BatSessileProp,
ESSUT_BathonianTotal)

#Create axes for plots
traits <- factor(c("shallow infaunal", "epifaunal", "cementing",
"mobile", "facultatively mobile", "sessile"),
as.ordered(c("shallow infaunal", "epifaunal", "cementing",
"mobile", "facultatively mobile", "sessile")))
xaxis <- c(1, 2, 3, 4, 5, 6)
estimates <- c(diff(ESSUTbajoinfprop.test$estimate),
diff(ESSUTbajoepiprop.test$estimate),
diff(ESSUTbajocemp.test$estimate),
diff(ESSUTbajomobprop.test$estimate),
diff(ESSUTbajofacmobprop.test$estimate),
diff(ESSUTbajosesprop.test$estimate))

##Plots of proportional differences between Utah and Europe
dev.new(width=7, height=7)
par(mfrow=(c(1,2)))

```

```

plot(xaxis, estimates, main='Bajocian', xlab='', ylab='Change in
Proportional Occurrences (Open Shallow Subtidal)', ylim=range(-
1:1), las=1, type='n', axes=FALSE)
axis(1, at=xaxis, labels=FALSE)
text(xaxis, par("usr")[3] - 0.2, labels = traits, srt = 45, pos =
1, xpd = TRUE)
axis(2, las=1)
points(xaxis[1], ESSUTbajoinfprop.test$estimate[1]-
ESSUTbajoinfprop.test$estimate[2], type="p", pch=16, col="black")
segments(xaxis[1], ESSUTbajoinfprop.test$conf.int[1], xaxis[1],
ESSUTbajoinfprop.test$conf.int[2], col="black")
points(xaxis[2], ESSUTbajoepiprop.test$estimate[1]-
ESSUTbajoepiprop.test$estimate[2], type="p", pch=16, col="black")
segments(xaxis[2], ESSUTbajoepiprop.test$conf.int[1], xaxis[2],
ESSUTbajoepiprop.test$conf.int[2], col="black")
points(xaxis[3], ESSUTbajocempnop.test$estimate[1]-
ESSUTbajocempnop.test$estimate[2], type="p", pch=16, col="black")
segments(xaxis[3], ESSUTbajocempnop.test$conf.int[1], xaxis[3],
ESSUTbajocempnop.test$conf.int[2], col="black")
points(xaxis[4], ESSUTbajomobprop.test$estimate[1]-
ESSUTbajomobprop.test$estimate[2], type="p", pch=16, col="black")
segments(xaxis[4], ESSUTbajomobprop.test$conf.int[1], xaxis[4],
ESSUTbajomobprop.test$conf.int[2], col="black")
points(xaxis[5], ESSUTbajofacmobprop.test$estimate[1]-
ESSUTbajofacmobprop.test$estimate[2], type="p", pch=16,
col="black")
segments(xaxis[5], ESSUTbajofacmobprop.test$conf.int[1],
xaxis[5], ESSUTbajofacmobprop.test$conf.int[2], col="black")
points(xaxis[6], ESSUTbajosesprop.test$estimate[1]-
ESSUTbajosesprop.test$estimate[2], type="p", pch=16, col="black")
segments(xaxis[6], ESSUTbajosesprop.test$conf.int[1], xaxis[6],
ESSUTbajosesprop.test$conf.int[2], col="black")

plot(xaxis, estimates, main='Bathonian', xlab='', ylab='',
ylim=range(-1:1), las=1, type='n', axes=FALSE)
axis(1, at=xaxis, labels=FALSE)
text(xaxis, par("usr")[3] - 0.2, labels = traits, srt = 45, pos =
1, xpd = TRUE)
axis(2, las=1)
points(xaxis[1], ESSUTbatinfprop.test$estimate[1]-
ESSUTbatinfprop.test$estimate[2], type="p", pch=16, col="black")
segments(xaxis[1], ESSUTbatinfprop.test$conf.int[1], xaxis[1],
ESSUTbatinfprop.test$conf.int[2], col="black")
points(xaxis[2], ESSUTbatepiprop.test$estimate[1]-
ESSUTbatepiprop.test$estimate[2], type="p", pch=16, col="black")
segments(xaxis[2], ESSUTbatepiprop.test$conf.int[1], xaxis[2],
ESSUTbatepiprop.test$conf.int[2], col="black")
points(xaxis[3], ESSUTbatcempnop.test$estimate[1]-
ESSUTbatcempnop.test$estimate[2], type="p", pch=16, col="black")
segments(xaxis[3], ESSUTbatcempnop.test$conf.int[1], xaxis[3],
ESSUTbatcempnop.test$conf.int[2], col="black")
points(xaxis[4], ESSUTbatmobprop.test$estimate[1]-
ESSUTbatmobprop.test$estimate[2], type="p", pch=16, col="black")

```

```

segments(xaxis[4], ESSUTbatmobprop.test$conf.int[1], xaxis[4],
ESSUTbatmobprop.test$conf.int[2], col="black")
points(xaxis[5], ESSUTbatfacmobprop.test$estimate[1]-
ESSUTbatfacmobprop.test$estimate[2], type="p", pch=16,
col="black")
segments(xaxis[5], ESSUTbatfacmobprop.test$conf.int[1], xaxis[5],
ESSUTbatfacmobprop.test$conf.int[2], col="black")
points(xaxis[6], ESSUTbatsesprop.test$estimate[1]-
ESSUTbatsesprop.test$estimate[2], type="p", pch=16, col="black")
segments(xaxis[6], ESSUTbatsesprop.test$conf.int[1], xaxis[6],
ESSUTbatsesprop.test$conf.int[2], col="black")

```

```
##Abundance
```

```
###Proportion test of life habit occurrence and abundance between
Utah, European, and Global datasets
```

```
#Read source files
```

```
source("abundance_PropEcolTrait.R")
```

```
source("extractionFunctions.R")
```

```
#Read datasets
```

```
global <- read.csv('clusteredGlobalNEW.csv', header=TRUE,
stringsAsFactors=FALSE)
```

```
carmel <- read.csv('carmel.csv', header=TRUE,
stringsAsFactors=FALSE)
```

```
UT_Bajocian <- carmel[carmel$stage=="Bajocian",]
```

```
UT_Bathonian <- carmel[carmel$stage=="Bathonian",]
```

```
EU_Bajocian <- global[global$stage=="Bajocian" &
```

```
global$geo_cluster=="Europe",]
```

```
EU_Bathonian <- global[global$stage=="Bathonian" &
```

```
global$geo_cluster=="Europe",]
```

```
EU_BajocianSS <- global[global$stage=="Bajocian" &
```

```
global$geo_cluster=="Europe" & global$environment=="open shallow
subtidal",]
```

```
EU_BathonianSS <- global[global$stage=="Bathonian" &
```

```
global$geo_cluster=="Europe" & global$environment=="open shallow
subtidal",]
```

```
#Calculate Bajocian proportions of each life habit group in the
Utah dataset
```

```
UT_Bajosinfaunal <- abundance_propEcolTrait(UT_Bajocian,
"life_habit", "shallow infaunal")
```

```
UT_Bajodinfaunal <- abundance_propEcolTrait(UT_Bajocian,
"life_habit", "deep infaunal")
```

```
UT_Bajoepifaunal <- abundance_propEcolTrait(UT_Bajocian,
"life_habit", "epifaunal")
```

```
UT_Bajocementing <- abundance_propEcolTrait(UT_Bajocian,
"stability", "cementing")
```

```

UT_Bajofreelying <- abundance_propEcolTrait(UT_Bajocian,
"stability", "free-lying")
UT_Bajopedunculate <- abundance_propEcolTrait(UT_Bajocian,
"stability", "pedunculate")
UT_Bajoepibyssate <- abundance_propEcolTrait(UT_Bajocian,
"stability", "epibyssate")
UT_Bajomobile <- abundance_propEcolTrait(UT_Bajocian, "motility",
"mobile")
UT_Bajofacultativelymobile <-
abundance_propEcolTrait(UT_Bajocian, "motility", "facultatively
mobile")
UT_Bajosessile <- abundance_propEcolTrait(UT_Bajocian,
"motility", "sessile")

```

```

UT_Bajosinfaunal
UT_Bajodinafaunal
UT_Bajoepifaunal
UT_Bajocementing
UT_Bajofreelying
UT_Bajopedunculate
UT_Bajoepibyssate
UT_Bajomobile
UT_Bajofacultativelymobile
UT_Bajosessile

```

```

#Calculate Bathonian proportions of each life habit group in the
Utah dataset

```

```

UT_Batsinfaunal <- abundance_propEcolTrait(UT_Bathonian,
"life_habit", "shallow infaunal")
UT_Batdinafaunal <- abundance_propEcolTrait(UT_Bathonian,
"life_habit", "deep infaunal")
UT_Batepifaunal <- abundance_propEcolTrait(UT_Bathonian,
"life_habit", "epifaunal")
UT_Batcementing <- abundance_propEcolTrait(UT_Bathonian,
"stability", "cementing")
UT_Batfreelying <- abundance_propEcolTrait(UT_Bathonian,
"stability", "free-lying")
UT_Batpedunculate <- abundance_propEcolTrait(UT_Bathonian,
"stability", "pedunculate")
UT_Batepibyssate <- abundance_propEcolTrait(UT_Bathonian,
"stability", "epibyssate")
UT_Batmobile <- abundance_propEcolTrait(UT_Bathonian, "motility",
"mobile")
UT_Batfacultativelymobile <-
abundance_propEcolTrait(UT_Bathonian, "motility", "facultatively
mobile")
UT_Batsessile <- abundance_propEcolTrait(UT_Bathonian,
"motility", "sessile")

```

```

UT_Batsinfaunal
UT_Batdinafaunal
UT_Batepifaunal
UT_Batcementing

```

```

UT_Batfreelying
UT_Batpedunculate
UT_Batepibyssate
UT_Batmobile
UT_Batfacultativelymobile
UT_Batsessile

```

```

#Calculate BajocianSS proportions of each life habit group in the
European dataset

```

```

EU_BajosinfaunalSS <- abundance_propEcolTrait(EU_BajocianSS,
"life_habit", "shallow infaunal")
EU_BajodinfaunalSS <- abundance_propEcolTrait(EU_BajocianSS,
"life_habit", "deep infaunal")
EU_BajoepifaunalSS <- abundance_propEcolTrait(EU_BajocianSS,
"life_habit", "epifaunal")
EU_BajocementingSS <- abundance_propEcolTrait(EU_BajocianSS,
"stability", "cementing")
EU_BajofreelyingSS <- abundance_propEcolTrait(EU_BajocianSS,
"stability", "free-lying")
EU_BajopedunculateSS <- abundance_propEcolTrait(EU_BajocianSS,
"stability", "pedunculate")
EU_BajoepibyssateSS <- abundance_propEcolTrait(EU_BajocianSS,
"stability", "epibyssate")
EU_BajomobileSS <- abundance_propEcolTrait(EU_BajocianSS,
"motility", "mobile")
EU_BajofacultativelymobileSS <-
abundance_propEcolTrait(EU_BajocianSS, "motility", "facultatively
mobile")
EU_BajosessileSS <- abundance_propEcolTrait(EU_BajocianSS,
"motility", "sessile")

```

```

EU_BajosinfaunalSS
EU_BajodinfaunalSS
EU_BajoepifaunalSS
EU_BajocementingSS
EU_BajofreelyingSS
EU_BajopedunculateSS
EU_BajoepibyssateSS
EU_BajomobileSS
EU_BajofacultativelymobileSS
EU_BajosessileSS

```

```

#Calculate Bathonian proportions of each life habit group in the
European dataset

```

```

EU_BatsinfaunalSS <- abundance_propEcolTrait(EU_BathonianSS,
"life_habit", "shallow infaunal")
EU_BatdinfaunalSS <- abundance_propEcolTrait(EU_BathonianSS,
"life_habit", "deep infaunal")
EU_BatepifaunalSS <- abundance_propEcolTrait(EU_BathonianSS,
"life_habit", "epifaunal")
EU_BatcementingSS <- abundance_propEcolTrait(EU_BathonianSS,
"stability", "cementing")

```

```

EU_BatfreelyingSS <- abundance_propEcolTrait(EU_BathonianSS,
"stability", "free-lying")
EU_BatpedunculateSS <- abundance_propEcolTrait(EU_BathonianSS,
"stability", "pedunculate")
EU_BatepibyssateSS <- abundance_propEcolTrait(EU_BathonianSS,
"stability", "epibyssate")
EU_BatmobileSS <- abundance_propEcolTrait(EU_BathonianSS,
"motility", "mobile")
EU_BatfacultativelymobileSS <-
abundance_propEcolTrait(EU_BathonianSS, "motility",
"facultatively mobile")
EU_BatsessileSS <- abundance_propEcolTrait(EU_BathonianSS,
"motility", "sessile")

```

```

EU_BatsinfaunalSS
EU_BatdinhaunalSS
EU_BatepifaunalSS
EU_BatcementingSS
EU_BatfreelyingSS
EU_BatpedunculateSS
EU_BatepibyssateSS
EU_BatmobileSS
EU_BatfacultativelymobileSS
EU_BatsessileSS

```

```

#Combine Bajocian proportions of life habit groups from Utah and
Europe into a vector

```

```

ESSUT_BajoShallowinfaunalProp <- c(EU_BajosinfaunalSS,
UT_Bajosinfaunal)
ESSUT_BajoEpifaunalProp <- c(EU_BajoepifaunalSS,
UT_Bajoepifaunal)
ESSUT_BajoCementingProp <- c(EU_BajocementingSS,
UT_Bajocementing)
ESSUT_BajoMobileProp <- c(EU_BajomobileSS, UT_Bajomobile)
ESSUT_BajoFacmobileProp <- c(EU_BajofacultativelymobileSS,
UT_Bajofacultativelymobile)
ESSUT_BajoSessileProp <- c(EU_BajosessileSS, UT_Bajosessile)

```

```

#Combine Bathonian proportions of life habit groups from Utah and
Europe into a vector

```

```

ESSUT_BatShallowinfaunalProp <- c(EU_BatsinfaunalSS,
UT_Batsinfaunal)
ESSUT_BatEpifaunalProp <- c(EU_BatepifaunalSS, UT_Batepifaunal)
ESSUT_BatCementingProp <- c(EU_BatcementingSS, UT_Batcementing)
ESSUT_BatMobileProp <- c(EU_BatmobileSS, UT_Batmobile)
ESSUT_BatFacmobileProp <- c(EU_BatfacultativelymobileSS,
UT_Batfacultativelymobile)
ESSUT_BatSessileProp <- c(EU_BatsessileSS, UT_Batsessile)

```

```

ESSUT_BajoShallowinfaunalProp
ESSUT_BajoEpifaunalProp
ESSUT_BajoCementingProp
ESSUT_BajoMobileProp

```

```

ESSUT_BajoFacmobileProp
ESSUT_BajoSessileProp

ESSUT_BatShallowinfaunalProp
ESSUT_BatEpifaunalProp
ESSUT_BatCementingProp
ESSUT_BatMobileProp
ESSUT_BatFacmobileProp
ESSUT_BatSessileProp

#Combine total abundance from Utah and Europe into one vector
ESSUT_BajocianTotal <- c(sum(EU_BajocianSS$abundance),
sum(UT_Bajocian$abundance))
ESSUT_BathonianTotal <- c(sum(EU_BathonianSS$abundance),
sum(UT_Bathonian$abundance))

#Proportional test of life habits during the Bajocian
ESSUTbajoinfprop.test <- prop.test(ESSUT_BajoShallowinfaunalProp,
ESSUT_BajocianTotal)
ESSUTbajoepiprop.test <- prop.test(ESSUT_BajoEpifaunalProp,
ESSUT_BajocianTotal)
ESSUTbajocemp.test <- prop.test(ESSUT_BajoCementingProp,
ESSUT_BajocianTotal)
ESSUTbajomobprop.test <- prop.test(ESSUT_BajoMobileProp,
ESSUT_BajocianTotal)
ESSUTbajofacmobprop.test <- prop.test(ESSUT_BajoFacmobileProp,
ESSUT_BajocianTotal)
ESSUTbajosessprop.test <- prop.test(ESSUT_BajoSessileProp,
ESSUT_BajocianTotal)

#Proportional test of life habits during the Bathonian
ESSUTbatinfprop.test <- prop.test(ESSUT_BatShallowinfaunalProp,
ESSUT_BathonianTotal)
ESSUTbatepiprop.test <- prop.test(ESSUT_BatEpifaunalProp,
ESSUT_BathonianTotal)
ESSUTbatcemp.test <- prop.test(ESSUT_BatCementingProp,
ESSUT_BathonianTotal)
ESSUTbatmobprop.test <- prop.test(ESSUT_BatMobileProp,
ESSUT_BathonianTotal)
ESSUTbatfacmobprop.test <- prop.test(ESSUT_BatFacmobileProp,
ESSUT_BathonianTotal)
ESSUTbatsessprop.test <- prop.test(ESSUT_BatSessileProp,
ESSUT_BathonianTotal)

#Create axes for plots
traits <- factor(c("shallow infaunal", "epifaunal", "cementing",
"mobile", "facultatively mobile", "sessile"),
as.ordered(c("shallow infaunal", "epifaunal", "cementing",
"mobile", "facultatively mobile", "sessile")))
xaxis <- c(1, 2, 3, 4, 5, 6)
estimates <- c(diff(ESSUTbajoinfprop.test$estimate),
diff(ESSUTbajoepiprop.test$estimate),
diff(ESSUTbajocemp.test$estimate),

```

```

diff(ESSUTbajomobprop.test$estimate),
diff(ESSUTbajofacmobprop.test$estimate),
diff(ESSUTbajosprop.test$estimate))

##Plots of temporal proportions for each geographic scale
dev.new()
par(mfrow=(c(1,2)))
plot(xaxis, estimates, main='Bajocian', xlab='', ylab='Change in
Proportional Occurrences (Open Shallow Subtidal)', ylim=range(-
1:1), las=1, type='n', axes=FALSE)
axis(1, at=xaxis, labels=FALSE)
text(xaxis, par("usr")[3] - 0.2, labels = traits, srt = 45, pos =
1, xpd = TRUE)
axis(2, las=1)
points(xaxis[1], ESSUTbajoinfprop.test$estimate[1]-
ESSUTbajoinfprop.test$estimate[2], type="p", pch=16, col="black")
segments(xaxis[1], ESSUTbajoinfprop.test$conf.int[1], xaxis[1],
ESSUTbajoinfprop.test$conf.int[2], col="black")
points(xaxis[2], ESSUTbajoepiprop.test$estimate[1]-
ESSUTbajoepiprop.test$estimate[2], type="p", pch=16, col="black")
segments(xaxis[2], ESSUTbajoepiprop.test$conf.int[1], xaxis[2],
ESSUTbajoepiprop.test$conf.int[2], col="black")
points(xaxis[3], ESSUTbajocempromprop.test$estimate[1]-
ESSUTbajocempromprop.test$estimate[2], type="p", pch=16, col="black")
segments(xaxis[3], ESSUTbajocempromprop.test$conf.int[1], xaxis[3],
ESSUTbajocempromprop.test$conf.int[2], col="black")
points(xaxis[4], ESSUTbajomobprop.test$estimate[1]-
ESSUTbajomobprop.test$estimate[2], type="p", pch=16, col="black")
segments(xaxis[4], ESSUTbajomobprop.test$conf.int[1], xaxis[4],
ESSUTbajomobprop.test$conf.int[2], col="black")
points(xaxis[5], ESSUTbajofacmobprop.test$estimate[1]-
ESSUTbajofacmobprop.test$estimate[2], type="p", pch=16,
col="black")
segments(xaxis[5], ESSUTbajofacmobprop.test$conf.int[1],
xaxis[5], ESSUTbajofacmobprop.test$conf.int[2], col="black")
points(xaxis[6], ESSUTbajosprop.test$estimate[1]-
ESSUTbajosprop.test$estimate[2], type="p", pch=16, col="black")
segments(xaxis[6], ESSUTbajosprop.test$conf.int[1], xaxis[6],
ESSUTbajosprop.test$conf.int[2], col="black")

plot(xaxis, estimates, main='Bathonian', xlab='', ylab='',
ylim=range(-1:1), las=1, type='n', axes=FALSE)
axis(1, at=xaxis, labels=FALSE)
text(xaxis, par("usr")[3] - 0.2, labels = traits, srt = 45, pos =
1, xpd = TRUE)
axis(2, las=1)
points(xaxis[1], ESSUTbatinfprop.test$estimate[1]-
ESSUTbatinfprop.test$estimate[2], type="p", pch=16, col="black")
segments(xaxis[1], ESSUTbatinfprop.test$conf.int[1], xaxis[1],
ESSUTbatinfprop.test$conf.int[2], col="black")
points(xaxis[2], ESSUTbatepiprop.test$estimate[1]-
ESSUTbatepiprop.test$estimate[2], type="p", pch=16, col="black")

```



```

segments(xaxis[2], ESSUTbatepiprop.test$conf.int[1], xaxis[2],
ESSUTbatepiprop.test$conf.int[2], col="black")
points(xaxis[3], ESSUTbatcempnop.test$estimate[1]-
ESSUTbatcempnop.test$estimate[2], type="p", pch=16, col="black")
segments(xaxis[3], ESSUTbatcempnop.test$conf.int[1], xaxis[3],
ESSUTbatcempnop.test$conf.int[2], col="black")
points(xaxis[4], ESSUTbatmobprop.test$estimate[1]-
ESSUTbatmobprop.test$estimate[2], type="p", pch=16, col="black")
segments(xaxis[4], ESSUTbatmobprop.test$conf.int[1], xaxis[4],
ESSUTbatmobprop.test$conf.int[2], col="black")
points(xaxis[5], ESSUTbatfacmobprop.test$estimate[1]-
ESSUTbatfacmobprop.test$estimate[2], type="p", pch=16,
col="black")
segments(xaxis[5], ESSUTbatfacmobprop.test$conf.int[1], xaxis[5],
ESSUTbatfacmobprop.test$conf.int[2], col="black")
points(xaxis[6], ESSUTbatsesprop.test$estimate[1]-
ESSUTbatsesprop.test$estimate[2], type="p", pch=16, col="black")
segments(xaxis[6], ESSUTbatsesprop.test$conf.int[1], xaxis[6],
ESSUTbatsesprop.test$conf.int[2], col="black")

```

APPENDIX C

R CODE AND DATA FOR CHAPTER 4

Part 1: R Code

The R code used to calculate proportions of taxa by ecological group is the same as that for Chapter 3.

R script commands that performs the Additive Diversity Partitioning analysis in this chapter and creates the figures (Figs. 4.2 and 4.3). This code is modified from Holland (2010).

```
# All functions assume that x is a presence-absence data frame,
with
# columns corresponding to taxa and rows corresponding to
sampling
# units. Data frame must be culled, such that all samples contain
at
# least one taxon, and all taxa occur in at least one sample.

#Read Datasets
carmelBajocian <- read.csv('carmelBajocianpa.csv', header=TRUE,
row.names=1, stringsAsFactors=FALSE)
carmelBathonian <- read.csv('carmelBathonianpa.csv', header=TRUE,
row.names=1, stringsAsFactors=FALSE)

sundanceBajocian <- read.csv('sundanceBajocianpa.csv',
header=TRUE, row.names=1, stringsAsFactors=FALSE)
sundanceBathonian <- read.csv('sundanceBathonianpa.csv',
header=TRUE, row.names=1, stringsAsFactors=FALSE)

carmelBajociancounts <- read.csv('carmelBajociancounts.csv',
header=TRUE, row.names=1, stringsAsFactors=FALSE)
carmelBathoniancounts <- read.csv('carmelBathoniancounts.csv',
header=TRUE, row.names=1, stringsAsFactors=FALSE)

sundanceBajociancounts <- read.csv('sundanceBajociancounts.csv',
header=TRUE, row.names=1, stringsAsFactors=FALSE)
sundanceBathoniancounts <-
read.csv('sundanceBathoniancounts.csv', header=TRUE, row.names=1,
stringsAsFactors=FALSE)
```

```

#Additive diversity partitioning function
ADP <- function(x, method){ #method can include richness or
Simpson's D

    colSums <- apply(x, 2, sum)
    gamma <- method(colSums)

    alpha <- method(x)
    meanalpha <- mean(alpha)

    beta <- gamma - meanalpha

    partitions <- c(gamma, beta, meanalpha)
    names(partitions) <- c("gamma", "beta", "meanalpha")
    partitions

}

simpsonD <- function (x, index = "simpson", MARGIN = 1, base =
exp(1)){
  x <- drop(as.matrix(x))
  if (any(x < 0, na.rm = TRUE))
    stop("input data must be non-negative")
  INDICES <- c("shannon", "simpson", "invsimpson")
  index <- match.arg(index, INDICES)
  if (length(dim(x)) > 1) {
    total <- apply(x, MARGIN, sum)
    x <- sweep(x, MARGIN, total, "/")
  }
  else {
    x <- x/(total <- sum(x))
  }
  if (index == "shannon")
    x <- -x * log(x, base)
  else x <- x * x
  if (length(dim(x)) > 1)
    H <- apply(x, MARGIN, sum, na.rm = TRUE)
  else H <- sum(x, na.rm = TRUE)
  if (index == "simpson")
    H <- 1 - H
  else if (index == "invsimpson")
    H <- 1/H
  if (any(is.na(total)))
    is.na(H) <- is.na(total)
  H
}

shannonH <- function (x, index = "shannon", MARGIN = 1, base =
exp(1)){
  x <- drop(as.matrix(x))
  if (any(x < 0, na.rm = TRUE))
    stop("input data must be non-negative")

```

```

INDICES <- c("shannon", "simpson", "invsimpson")
index <- match.arg(index, INDICES)
if (length(dim(x)) > 1) {
  total <- apply(x, MARGIN, sum)
  x <- sweep(x, MARGIN, total, "/")
}
else {
  x <- x/(total <- sum(x))
}
if (index == "shannon")
  x <- -x * log(x, base)
else x <- x * x
if (length(dim(x)) > 1)
  H <- apply(x, MARGIN, sum, na.rm = TRUE)
else H <- sum(x, na.rm = TRUE)
if (index == "simpson")
  H <- 1 - H
else if (index == "invsimpson")
  H <- 1/H
if (any(is.na(total)))
  is.na(H) <- is.na(total)
H
}

richness <- function(x){

gamma <- ncol(x)

meanalpha <- mean(apply(x, 1, sum))

beta <- gamma - meanalpha

partitions <- c(gamma, beta, meanalpha)
names(partitions) <- c("gamma", "beta", "meanalpha")
partitions

}

CarmelBajocianRichness <- richness(carmelBajocian)
CarmelBathonianRichness <- richness(carmelBathonian)

SundanceBajocianRichness <- richness(sundanceBajocian)
SundanceBathonianRichness <- richness(sundanceBathonian)

CarmelBajocianSimpson <- ADP(carmelBajociancounts, simpsonD)
CarmelBathonianSimpson <- ADP(carmelBathoniancounts, simpsonD)

SundanceBajocianSimpson <- ADP(sundanceBajociancounts, simpsonD)
SundanceBathonianSimpson <- ADP(sundanceBathoniancounts,
simpsonD)

```

```
CarmelBajocianRichness
CarmelBathonianRichness
```

```
SundanceBajocianRichness
SundanceBathonianRichness
```

```
CarmelBajocianSimpson
CarmelBathonianSimpson
```

```
SundanceBajocianSimpson
SundanceBathonianSimpson
```

```
#Plots
```

```
dev.new()
barplot(as.matrix(CarmelBajocianRichness[3:2]), ylim=range(0:65),
las=1, ylab="Species richness (S)", main="Carmel Bajocian
Richness", legend=names(CarmelBajocianRichness[3:2]))
```

```
dev.new()
barplot(as.matrix(CarmelBathonianRichness[3:2]),
ylim=range(0:65), las=1, ylab="Species richness (S)",
main="Carmel Bathonian Richness",
legend=names(CarmelBathonianRichness[3:2]))
```

```
dev.new()
barplot(as.matrix(SundanceBajocianRichness[3:2]),
ylim=range(0:65), las=1, ylab="Species richness (S)",
main="Sundance Bajocian Richness",
legend=names(SundanceBajocianRichness[3:2]))
```

```
dev.new()
barplot(as.matrix(SundanceBathonianRichness[3:2]),
ylim=range(0:65), las=1, ylab="Species richness (S)",
main="Sundance Bathonian Richness",
legend=names(SundanceBathonianRichness[3:2]))
```

```
dev.new()
barplot(as.matrix(CarmelBajocianSimpson[3:2]), ylim=range(0:1),
las=1, ylab="Simpson's D", main="Carmel Bajocian Evenness",
legend=names(CarmelBajocianSimpson[3:2]))
```

```
dev.new()
barplot(as.matrix(CarmelBathonianSimpson[3:2]), ylim=range(0:1),
las=1, ylab="Simpson's D", main="Carmel Bathonian Evenness",
legend=names(CarmelBathonianSimpson[3:2]))
```

```
dev.new()
barplot(as.matrix(SundanceBajocianSimpson[3:2]), ylim=range(0:1),
las=1, ylab="Simpson's D", main="Sundance Bajocian Evenness",
legend=names(SundanceBajocianSimpson[3:2]))
```

```
dev.new()
barplot(as.matrix(SundanceBathonianSimpson[3:2]),
ylim=range(0:1), las=1, ylab="Simpson's D", main="Sundance
Bathonian Evenness", legend=names(SundanceBathonianSimpson[3:2]))
```

Part 2: Data

The datafile for the northern Sundance Seaway data from Danise and Holland (2017) can be accessed from the Dryad Digital Data Repository: <https://doi.org/10.5061/dryad.fg220>

The specific collections used are outlined below:

ACC-15-23	ACC-15-7	ACC-15-9	ASB-15-A	ASB-15-B
BBL2	BBL3	BBL4	BBL5	BBL6
BLMA-15-1	BLMB-15-8	BTC-15-30	BTC-15-7	CCK-16-132
CCK-16-182	CCK-16-184	CHMNY-1	CHMNY-2	CHMNY-3
CODY-2	CODY-3	CODY-4	CODY-6	CR1138-1
CR1138-2	CR1138-6	CWK-16-A	CWK-16-B	DGS-15-42
DGS-15-A	DGS-15-B	DGS-15-C	DYT-15-5	EMR-15-B
GSR-1	GSR-16	GSR-18	GSR-19	GSR-2
GSR-3	GSR-4	GSR-6	HMR-15-15	HMR-15-9
HMR-15-9.5	HYATT-1	JBR1-16-45	LBC-16-A	LBC-16-B
LBC-16-C	LBC-16-D	LBC-16-E	LBC-16-F	LCK-16-A
LCK-16-B	LCK-16-D	LCK-16-E	LCK-16-F	LCK-16-G
LCK-16-H	LSL-15-21	LSL-15-23.8	LSL-15-45	LSL-15-45.5
LSL-15-87	LSL-15-97.5	LSM-N-1	LSM-N-3	LSM-N-4
NWL1	NWL2	NWL3	NWL4	RDG1
RDM1	RDM3	RDM4	RDM5	RED-2
RED-3	RED-7	SFH-15-A	SFH-15-B	SM-E-6
SM-E-8	SM-PANTO-1	SM-PANTO-2	SM-PANTO-6	SRC-16-A
SWCB-15-A	TCK-16-A	TFK-16-A	TFK-16-B	TFK-16-C
THERMO-1	TPCK-1	TPCK-2	TPCK-3	TPCK-4
TPCK-5	TSS-16-3a	TSS-16-3b	ACC-15-23	ACC-15-7