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Geosci 541

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Lab 13

Problem Set 1  
  
1) What is the total biodiversity (generic richness) of OrdovicianMatrix and SilurianMatrix? In the alpha, beta, and gamma ADDITIVE diversity partitioning paradigm, does this number represent alpha, beta, or gamma biodiversity? Show your code.

#GAMMA DIVERSITY

>dimnames(OrdovicianMatrix)[[2]]

> ncol(OrdovicianMatrix)  
[1] 211

> ncol(SilurianMatrix)  
[1] 423

The genric richness is represented by the total number of columns in this matrix. This represents the gamma biodiversity, which is the total biodiversity over the entire region.

2) What is the average biodiversity of all sample (stratigraphic units) in OrdovicianMatrix and SilurianMatrix? In the alpha, beta, and gamma ADDITIVE diversity partitioning paradigm, does this number represent alpha, beta, or gamma biodiversity? Show your code.

> #AVERAGE BIODIVERSITY OF ALL SAMPLES  
> #ORDOVICIAN  
> mean(rowSums(OrdovicianMatrix))  
[1] 26.60526  
>   
> #SILURIAN  
> mean(rowSums(SilurianMatrix))  
[1] 42.79167

These numbers represent the alpha diversity.  
  
3) What is the difference between the average biodiversity of all samples (stratigraphic units) in OrdovicianMatrix and the total biodiversity of OrdovicianMatrix. What about for the Silurian? In the alpha, beta, and gamma ADDITIVE diveristy partitioning paradigm, does this number represent alpha, beta, or gamma biodiversity? Show your code.

The difference between the average biodiversity and the total biodiversity for the Ordovician/Silurian matrices would represent the beta biodiversity.

Beta biodiversity = total biodiversity - mean biodiversity

> #ORDOVICIAN BETA

> ncol(OrdovicianMatrix)-mean(rowSums(OrdovicianMatrix))

[1] 184.3947

>

> #SILURIAN BETA

> ncol(SilurianMatrix)-mean(rowSums(SilurianMatrix))

[1] 380.2083

4) Using the same ADDITIVE diversity partitioning schema, does alpha diveristy increase between the Ordovician and Silurian? Does beta diversity? Does gamma diversity? By how much?

#ALPHA DIVERSITY (INCREASE IN THE SILURIAN)

> mean(rowSums(SilurianMatrix))-mean(rowSums(OrdovicianMatrix))

[1] 16.1864

#BETA DIVERSITY (INCREASE IN THE SILURIAN)

>(ncol(SilurianMatrix)-mean(rowSums(SilurianMatrix)))-(ncol(OrdovicianMatrix)-mean(rowSums(OrdovicianMatrix)))  
[1] 195.8136

#GAMMA DIVERSITY (INCREASE IN THE SILURIAN

> ncol(SilurianMatrix)-ncol(OrdovicianMatrix)

[1] 212  
  
5) Sampling is different between the Ordovician and Silurian, which makes a direct comparison of the numbers questionable. Sometimes we try to get around this by representing alpha and beta as percentages of gamma.  
  
A. What is the alpha diveristy of OrdovicianMatrix and SilurianMatrix as a percentage of their respective gamma diversities?

#ALPHA AS A PERCENT OF GAMMA

> (mean(rowSums(OrdovicianMatrix))/ncol(OrdovicianMatrix))\*100  
[1] 12.60913

> (mean(rowSums(SilurianMatrix))/ncol(SilurianMatrix))\*100

[1] 10.11623

B. What is the beta diversity of OrdovicianMatrix and SilurianMatrix as a percentage of their respective gamma diversities?

> #BETA AS A PERCENT OF GAMMA

> (ncol(OrdovicianMatrix)-mean(rowSums(OrdovicianMatrix)))/(ncol(OrdovicianMatrix))\*100

[1] 87.39087

> (ncol(SilurianMatrix)-mean(rowSums(SilurianMatrix)))/(ncol(SilurianMatrix))\*100

[1] 89.88377

C. Does beta increase or decrease across the Ordovician Silurian boundary when measured as a percentage?

> 89.88377-87.39087  
[1] 2.4929

Beta increases slightly by 2.5% across the boundary.

D. Conceptually does this mean that Silurian faunas are more cosmopolitan (found in more places around North America) or are less cosmopolitan (found in fewer places around North America) following the Ordovician/Silurian mass extinction.

I looked this up on Google Scholar but I’m not super sure about my reasoning.

Beta measures the changes in species diversity. Conceptually an increase in beta means that organisms experienced an increase in diversity. If a fauna is more diverse and has been split into smaller groups, that means the geographic ranges in general for individual species have decreased (because of crowding/competition). This then means that faunas became less cosmopolitan across the boundary.

E. Does this match what we learned about Silurian cosmopolitanism in class?

6) What is one drawback of using percentages to compare changing alpha, beta, and gamma biodiversity between two time intervals?

It doesn’t give an idea of specific numbers because it uses percents. For example 10% of 10 is 1, but 10% of 100 is 10. Therefore this type of data reporting can be misleading sometimes.

Problem Set 2  
  
1) Using what we did above as a guide, download comparable datasets for the End-Permian extinction and End-Cretaceous extinction and process them as we did above (Steps 2-5). Show your code.

> # Download data from the PBDB  
>LatePermian<-downloadPBDB(Taxa="Animalia",StartInterval="Guadalupian",StopInterval="Lopingian")  
> EarlyTriassic<-downloadPBDB(Taxa="Animalia",StartInterval="Induan",StopInterval="Ladinian")  
>LateCretaceous<-downloadPBDB(Taxa="Animalia",StartInterval="Santonian",StopInterval="Maastrichtian")  
> EarlyPaleogene<-downloadPBDB(Taxa="Animalia",StartInterval="Danian",StopInterval="Lutetian")  
>   
> # Clean up bad genus names  
> LatePermian<-cleanRank(LatePermian,"genus")  
> EarlyTriassic<-cleanRank(EarlyTriassic,"genus")  
> LateCretaceous<-cleanRank(LateCretaceous,"genus")  
> EarlyPaleogene<-cleanRank(EarlyPaleogene,"genus")  
>   
> # Constrain data to only occurrences limited to a single epoch  
> LatePermian<-constrainAges(LatePermian,Epochs)  
> EarlyTriassic<-constrainAges(EarlyTriassic,Epochs)  
> LateCretaceous<-constrainAges(LateCretaceous,Epochs)  
> EarlyPaleogene<-constrainAges(EarlyPaleogene,Epochs)  
>   
> # Download stratigraphic unit information from the Macrostrat database and match it to the PBDB data  
> LatePermian<-macrostratMatch(LatePermian)  
> EarlyTriassic<-macrostratMatch(EarlyTriassic)  
> LateCretaceous<-macrostratMatch(LateCretaceous)  
> EarlyPaleogene<-macrostratMatch(EarlyPaleogene)  
>   
> # Community matrix in order  
> PermianMatrix<-presenceMatrix(LatePermian,SampleDefinition="unit\_name",TaxonRank="genus")  
> TriassicMatrix<-presenceMatrix(EarlyTriassic,SampleDefinition="unit\_name",TaxonRank="genus")  
>CretaceousMatrix<-presenceMatrix(LateCretaceous,SampleDefinition="unit\_name",TaxonRank="genuss")  
>PaleogeneMatrix<-presenceMatrix(EarlyPaleogene,SampleDefinition="unit\_name",TaxonRank="genus")  
>   
> # Cull  
> PermianMatrix<-cullMatrix(PermianMatrix,2,10)  
> TriassicMatrix<-cullMatrix(TriassicMatrix,2,10)  
> CretaceousMatrix<-cullMatrix(CretaceousMatrix,2,10)  
> PaleogeneMatrix<-cullMatrix(PaleogeneMatrix,2,10)

2) What are the Alpha, Beta, and Gamma biodiversitites for each downloaded time-interval (not measured as a percentage)? Show your code.

> #ALPHA

> mean(rowSums(PermianMatrix))

[1] 57.63636

> mean(rowSums(TriassicMatrix))

[1] 35.15385

> mean(rowSums(CretaceousMatrix))

[1] 57.96875

> mean(rowSums(PaleogeneMatrix))

[1] 52.85

>

> #BETA

> ncol(PermianMatrix)-mean(rowSums(PermianMatrix))

[1] 253.3636

> ncol(TriassicMatrix)-mean(rowSums(TriassicMatrix))

[1] 122.8462

> ncol(CretaceousMatrix)-mean(rowSums(CretaceousMatrix))

[1] 717.0312

> ncol(PaleogeneMatrix)-mean(rowSums(PaleogeneMatrix))

[1] 978.15

>

> #GAMMA

> ncol(PermianMatrix)

[1] 311

> ncol(TriassicMatrix)

[1] 158

> ncol(CretaceousMatrix)

[1] 775

> ncol(PaleogeneMatrix)

[1] 1031  
  
  
3) What are the Alpha and Beta biodiversities for each downloaded time-interval (when measured as a percentage of gamma)? Show your code.

> #ALPHA AS A PERCENT OF GAMMA

> (mean(rowSums(PermianMatrix))/ncol(PermianMatrix))\*100

[1] 18.53259

> (mean(rowSums(TriassicMatrix))/ncol(TriassicMatrix))\*100

[1] 22.24927

> (mean(rowSums(CretaceousMatrix))/ncol(CretaceousMatrix))\*100

[1] 7.479839

> (mean(rowSums(PaleogeneMatrix))/ncol(PaleogeneMatrix))\*100

[1] 5.126091

>

> #BETA AS A PERCENT OF GAMMA

> (ncol(PermianMatrix)-mean(rowSums(PermianMatrix)))/(ncol(PermianMatrix))\*100

[1] 81.46741

> (ncol(TriassicMatrix)-mean(rowSums(TriassicMatrix)))/(ncol(TriassicMatrix))\*100

[1] 77.75073

> (ncol(CretaceousMatrix)-mean(rowSums(CretaceousMatrix)))/(ncol(CretaceousMatrix))\*100

[1] 92.52016

> (ncol(PaleogeneMatrix)-mean(rowSums(PaleogeneMatrix)))/(ncol(PaleogeneMatrix))\*100

[1] 94.87391

4) Does Alpha biodiversity increase or decrease after each extinction event (not measured as a percentage)? Show your code.

> #Does ALPHA increase of decrease after each extinction event?   
>   
> #ALPHA P/T:   
> mean(rowSums(TriassicMatrix))-mean(rowSums(PermianMatrix))  
[1] -22.48252  
>   
> #ALPHA K-T:  
> mean(rowSums(PaleogeneMatrix))-mean(rowSums(CretaceousMatrix))  
[1] -5.11875

Alpha decreases across both events.

5) Does Alpha biodiversity increase or decrease after each extinction event (when measured as a percentage of gamma)? Show your code.

> #Does ALPHA AS A PERCENT OF GAMMA increase or decrease?  
> ((mean(rowSums(TriassicMatrix))/ncol(TriassicMatrix))\*100)-((mean(rowSums(PermianMatrix))/ncol(PermianMatrix))\*100)  
[1] 3.716677  
> ((mean(rowSums(PaleogeneMatrix))/ncol(PaleogeneMatrix))\*100)-((mean(rowSums(CretaceousMatrix))/ncol(CretaceousMatrix))\*100)  
[1] -2.353748

Alpha as a percent of gamma increases across the P/T extinction, but it decreases across the K/T.

Problem Set 3  
  
It is also possible to measure biodiversity using metrics other than generic richness, such as exponentiated Shannon's Entropy. Let's see what the biodiversity pattern looks like when analyzed in this way.  
  
Hint: You may use the vegan package of previous labs to calculate Shannon's H

1) Using what we did above as a guide, download comparable datasets for the End-Ordovician, End-Permian, and End-Cretaceous extinctions and process them as we did above (Steps 2-5). BUT, this time, use the abundanceMatrix( ) function instead of presenceMatrix( ).  
  
> # Download data from the PBDB  
>LateOrdovician<-downloadPBDB(Taxa="Animalia",StartInterval="Sandbian",StopInterval="Hirnantian")  
>EarlySilurian<-downloadPBDB(Taxa="Animalia",StartInterval="Llandovery",StopInterval="Wenlock")  
>LatePermian<-downloadPBDB(Taxa="Animalia",StartInterval="Guadalupian",StopInterval="Lopingian")  
> EarlyTriassic<-downloadPBDB(Taxa="Animalia",StartInterval="Induan",StopInterval="Ladinian")  
>LateCretaceous<-downloadPBDB(Taxa="Animalia",StartInterval="Santonian",StopInterval="Maastrichtian")  
> EarlyPaleogene<-downloadPBDB(Taxa="Animalia",StartInterval="Danian",StopInterval="Lutetian")  
>   
> # Clean up genus names  
> LateOrdovician<-cleanRank(LateOrdovician,"genus")  
> EarlySilurian<-cleanRank(EarlySilurian,"genus")  
> LatePermian<-cleanRank(LatePermian,"genus")  
> EarlyTriassic<-cleanRank(EarlyTriassic,"genus")  
> LateCretaceous<-cleanRank(LateCretaceous,"genus")  
> EarlyPaleogene<-cleanRank(EarlyPaleogene,"genus")  
>   
> # Constrain data to only occurrences limited to a single epoch  
> LateOrdovician<-constrainAges(LateOrdovician,Epochs)  
> EarlySilurian<-constrainAges(EarlySilurian,Epochs)  
> LatePermian<-constrainAges(LatePermian,Epochs)  
> EarlyTriassic<-constrainAges(EarlyTriassic,Epochs)  
> LateCretaceous<-constrainAges(LateCretaceous,Epochs)  
> EarlyPaleogene<-constrainAges(EarlyPaleogene,Epochs)  
>   
> # Download stratigraphic unit information from the Macrostrat database and match it to the PBDB data  
> LateOrdovician<-macrostratMatch(LateOrdovician)  
> EarlySilurian<-macrostratMatch(EarlySilurian)  
> LatePermian<-macrostratMatch(LatePermian)  
> EarlyTriassic<-macrostratMatch(EarlyTriassic)  
> LateCretaceous<-macrostratMatch(LateCretaceous)  
> EarlyPaleogene<-macrostratMatch(EarlyPaleogene)  
>   
> # Community matrix in order  
>OrdovicianMatrix<-abundanceMatrix(LateOrdovician,SampleDefinition="unit\_name",TaxonRank="genus")  
> SilurianMatrix<-abundanceMatrix(EarlySilurian,SampleDefinition="unit\_name",TaxonRank="genus")  
> PermianMatrix<-abundanceMatrix(LatePermian,SampleDefinition="unit\_name",TaxonRank="genus")  
> TriassicMatrix<-abundanceMatrix(EarlyTriassic,SampleDefinition="unit\_name",TaxonRank="genus")  
>CretaceousMatrix<-abundanceMatrix(LateCretaceous,SampleDefinition="unit\_name",TaxonRank="genus")  
>PaleogeneMatrix<-abundanceMatrix(EarlyPaleogene,SampleDefinition="unit\_name",TaxonRank="genus")  
>   
> # Cull  
> OrdovicianMatrix<-cullMatrix(OrdovicianMatrix,2,10)  
> SilurianMatrix<-cullMatrix(SilurianMatrix,2,10)  
> PermianMatrix<-cullMatrix(PermianMatrix,2,10)  
> TriassicMatrix<-cullMatrix(TriassicMatrix,2,10)  
> CretaceousMatrix<-cullMatrix(CretaceousMatrix,2,10)  
> PaleogeneMatrix<-cullMatrix(PaleogeneMatrix,2,10)

2) What are the Alpha, Beta, and Gamma biodiversity for each downloaded time-interval (not measured as a percentage) if biodiversity is measured as the exponentiated Shannon's Entropy? Show your code.

3) What are the Alpha, Beta, and Gamma biodiversity for each downloaded time-interval (when measured as a percentage of gamma) if biodiversity is measured as the exponentiated Shannon's Entropy? Show your code.  
  
4) Does Alpha biodiversity increase or decrease after each extinction event (not measured as a percentage)? Show your code.