Paleoecology Laboratory #9 Upper Ordovician Brachiopod Assemblages – The Report

October 3, 2019

Goals:

- 1. Practice simple population statistics on Upper Ordovician brachiopod assemblages, including chi-squared and Shannon-Wiener measures.
- 2. Explore additional capabilities of the PAST3 statistics software package.
- 3. Start your second paleoecology lab report. (Due in Dropbox folder by 5:00 pm, Tuesday, October 22.)

Exercise:

Materials needed -- Three collections of Upper Ordovician brachiopods (Assemblages 1, 2 and 3) Your laptop computer or tablet with PAST3 ready to use Your data from the previous lab (three completed forms)

Procedure –

1. Open PAST3 and key in the taxa and data you collected from the three assemblages. List the taxa in column A and the abundance data from the three assemblages in columns B, C and D. Use "0" for any blanks. Your spreadsheet should resemble this made-up data–

		Α	В	С	D	E
1	•	Spirifer	21	10	30	
2	•	Syringothyris	15	7	0	
3	•	Orthis	13	6	12	
4	•	Rhynchonella	24	12	18	
5	•	Orbicularis	12	6	4	
6	•	Lingula	4	2	4	
7	•					

2. We have a hypothesis that Assemblages 1 and 2 (columns B and C) are from the same population of brachiopods, and that Assemblage 3 (Column D) is from a separate population. To test the first part of the hypothesis, we will examine the similarity of Assemblages 1 and 2 (B and C) by using a chi-squared test, with a p>0.05 indicating the assemblages likely came from the same population (or more accurately, that they cannot be excluded from being of the same population). Select the data in columns B and C, choose "Univariate" and then "Contingency table" to get a screen like this – (Ignore warning pop-up.)

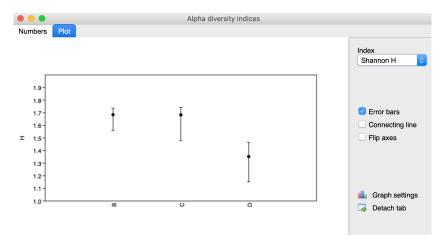
		A	В	С	D	E
1	• 5	Spirifer	21		30	
2	• 5	Syringothyris	15		0	
3	• (Drthis	13		12	
4	• F	Rhynchonella	24		18	
5	• (Drbicularis	12		4	
6	• [ingula	4		4	
7	•					
8	•		Contingency	table		
9	•	Tests Residuals				
10	•					
11	•		Chi square	ed		
12	•	Rows, columns: 6, 2	Deere	es freedom:		
13	•					
	•	Chi2: 0.03			,).99999	
13	•	Chi2: 0.03				
13 14	•	Chi2: 0.03				
13 14 15	•	Chi2: 0.03	1447 <i>p</i> (no	assoc.): (
13 14 15 16	•	Chi2: 0.03		assoc.): (
13 14 15 16 17	•	Chi2: 0.03	1447 <i>p</i> (no	assoc.): (-
13 14 15 16 17 18	•	Chi2: 0.03 Monte Carlo <i>p</i> : 1	1447 <i>p</i> (no	assoc.): (
13 14 15 16 17 18 19	•	Chi2: 0.03 Monte Carlo <i>p</i> : 1	1447 p(no Fisher´s ex	assoc.): (
13 14 15 16 17 18 19 20	• • • • • • • • • • • • • • • • • • • •	Chi2: 0.03 Monte Carlo <i>p</i> : 1	1447 <i>p</i> (no	assoc.): (
13 14 15 16 17 18 19 20 21	• • • • • • • • • • • • • • • • • • • •	Chi2: 0.03 Monte Carlo <i>p</i> : 1	1447 p (no Fisher´s ex Other statis	assoc.): (0.99999	
13 14 15 16 17 18 19 20 21 22	• • • • • • • • • • • • • • • • • • • •	Chi2: 0.03 Monte Carlo p : 1	1447 p (no Fisher's ex Other statis 5435 Conti	assoc.): (act tics ngency <i>C</i> : (0.99999	

Note the p value under chi-squared. Are the two assemblages from the same population?

- 3. Do the same chi-squared test with Assemblages 2 and 3 (columns C and D). Note the resulting p value. Are the assemblages from the same population or different populations?
- 4. Now we want to simply calculate a measure of the diversity of the three assemblages. We will calculate the Shannon-Wiener Diversity Index (H). Select all three data columns, choose "Diversity" and then "Diversity indices" --

A		В	С	D	E	F	G
• Sp	irifer	21					
Syringothyris		15					
Orthis		13	6				
Rhynchonella		24	12	18			
Orbicularis		12		4			
Lingula		4	2	4			
			Alpha di	versity indices			
Numbers	Plot						
	В	Lower	Upper	С	Lower	Upper	D
Taxa S	6	6	6	6	6	6	5
Individual	s 89	89	89	43	43	43	68
Dominanc	e_D 0.1983	0.1839	0.2395	0.1996	0.1823	0.272	0.302
Simpson_	1-D 0.8017	0.7605	0.8161	0.8004	0.728	0.8177	0.697
Shannon_	H 1.685	1.56	1.736	1.683	1.479	1.742	1.352
Evenness	_e^H/ 0.8986	0.7935	0.9453	0.8971	0.7356	0.9512	0.773
Brillouin	1.572	1.454	1.62	1.49	1.303	1.543	1.244
Menhinick	0.636	0.636	0.636	0.915	0.915	0.915	0.606
Margalef	1.114	1.114	1.114	1.329	1.329	1.329	0.948
Equitabilit	t y_J 0.9403	0.8709	0.9686	0.9394	0.8285	0.9721	0.840
Fisher_alp	oha 1.452	1.452	1.452	1.896	1.896	1.896	1.244
Berger-Pa	rker 0.2697	0.2247	0.3708	0.2791	0.2326	0.4186	0.441
Chao-1	6	6	6	6	6	6	5

There's lots there, but for now simply record the "Shannon-H" for columns B, C and D. Choose "Plot" and then "Shannon H" and "error bars" in that window and get something like this --



Screen-capture this plot, print to pdf or otherwise export it to your files. You're done with the statistics!

5. The lab report instructions. Again, you choose the format and style. The formal requirements are to address the following items and submit to the Dropbox folder a Word document by 5:00 pm on October 22. Note the time gives us a chance to discuss any questions in our October 15 lab session. The items to include in your report –

Locations and stratigraphy of the three brachiopod assemblages. Assemblages 1 and 2 are from the Whitewater Formation near Richmond, Indiana. Assemblage 3 is from the Liberty Formation near Liberty, Indiana. All are Upper Ordovician (Katian Stage).

List of identified taxa and abundances in each assemblage. (You can use your PAST3 spreadsheet or copy that data into your own table in Word. Don't forget to *italicize* genera and species names.)

Are assemblages 1 and 2 from the same brachiopod population? What is your evidence?

Are assemblages 2 and 3 from the same brachiopod population? What is your evidence?

What is the Shannon-Wiener Diversity Index for each assemblage, including error ranges? (Use your plot.)

Which brachiopod taxa are most prominent in each assemblage? How would you characterize the morphology of these dominant taxa? Can they tell us anything about the paleoenvironments? (Feel free to speculate on what you know about brachiopod ecology.)

As an appendix, please include one image of <u>each</u> brachiopod species in this study. The images need only a scale and a caption giving name and assemblage number.

That's it! Turn in your report to the Dropbox folder as a Word document by 5:00 pm on October 22.

