

Distributed: Fri. March 11, 2016

Due: Weds. March 23, 2016

Instructions: Copy and paste your answers below and turn in a word file and two excel files by the end of due day via email to khyrenba@gmail.com. Please use email title "MARS 6300 hw#5" and label all files with you're a suffix including your name (e.g., MARS6300_hw5_hyrenbach). Unlabeled emails / files will be penalized 10% of points.

The objectives of this homework are:

- A) To critically evaluate the "biological indicator" literature.
- B) To perform and interpret Weighted Averaging Analysis.
- C) To perform and interpret Polar Ordination Analysis.

To complete this homework, you will need:

- Instruction file: "BIOL6300_hw5.doc" (open with word file) – **Turn this file in**
- "Biogeography_data.xls" data file: (open with excel) – **Turn this file in**
- Two pdfs: Dufrene & Legendre 1997, McGeoch & Chow 1998
- "Biogeography_environment.xls" & "Biogeography_samples.xls"
- "Biogeography_weights.xls" is a template, to show you how to organize file. Modify with your data and use in PC-ORD.

1) Reviewing Indicator Species:

Read Dufrene & Legendre 1997, McGeoch & Chow 1998 and answer the following questions:

- Define "specificity" in plain words

This refers to the average abundance (or density) of a particular species of interest within all sites of one particular habitat, and is often compared across habitats al. Basically, this shows how "specific" one particular species is to one particular habitat. It may or may not be found in all sites within a habitat – if it is found in all sites of one habitat (and no other habitats), it is considered a true symmetrical indicator. If it is found in only a few sites within one habitat (and no other habitats), it is considered an asymmetrical indicator – it cannot be predicted to be in all sites of one habitat, but does contribute to the habitat's specificity. A species will have a high specificity value if the species were truly unique to a particular habitat, independent of other species assemblages.

- Provide an equation for calculating "specificity"

$A_{ij} = \text{Nindividuals}_{ij} / \text{Nindividuals}_i$, where i = each species, j = each site group, A_{ij} = the mean abundance of species i in the sites of group j compared to all groups within the study, Nindividuals_{ij} = the average number of individuals of species i across sites of group j , and Nindividuals_i = the sum of the mean numbers of individuals of species i over all groups.

- Define "fidelity" in plain words

This refers to the relative frequency of a particular species of interest (species presence/absence rather than its average abundance) within one particular habitat. For instance, knowing a

species' ecological preferences, it can be determined how frequently a certain species should be present within a habitat. A species would have a high fidelity value if it is both abundant and widespread within one particular habitat (not just being unique to the habitat, like specificity).

- Provide an equation for calculating “fidelity”

$B_{ij} = N_{sites_{ij}} / N_{sites_j}$, where i = each species, j = each site group, B_{ij} = the relative frequency of occurrence of species i in the sites of group j , $N_{sites_{ij}}$ = the number of sites in cluster j where species i is present, and N_{sites_j} = total number of sites in cluster j .

The key idea is that to determine the indicator value of a species, it must fulfill the criteria of both specificity and fidelity – the species must be unique to a particular habitat, and it must be both abundant and widespread throughout the habitat (no rare species).

Discuss how these three ways of integrating the “fidelity” and the “specificity” metrics will affect the resulting indicator value: (i) sum (specificity + fidelity) , (ii) multiplication (fidelity * specificity), (iii) sqrt (fidelity * specificity), and (iv) ratio (specificity / fidelity). To inform your discussion, consider these two series of specificity and fidelity values, listed below:

fidelity	specificity	SUM	PRODUCT	SQRT (PRODUCT)	RATIO
0	0.25	0.25	0	0	#DIV/0!
0.25	0.25	0.50	0.0625	0.25	1
0.5	0.25	0.75	0.125	0.353553391	0.5
0.75	0.25	1.00	0.1875	0.433012702	0.3333
1	0.25	1.25	0.25	0.5	0.25
0	0.5	0.5	0	0	#DIV/0!
0.25	0.5	0.75	0.125	0.353553391	2
0.5	0.5	1.00	0.25	0.5	1
0.75	0.5	1.25	0.375	0.612372436	0.6667
1	0.5	1.50	0.5	0.707106781	0.5
0	0.75	0.75	0	0	#DIV/0!
0.25	0.75	1.00	0.1875	0.433012702	3
0.5	0.75	1.25	0.375	0.612372436	1.5
0.75	0.75	1.50	0.5625	0.75	1
1	0.75	1.75	0.75	0.866025404	0.75
0	1	1.00	0	0	#DIV/0!
0.25	1	1.25	0.25	0.5	4
0.5	1	1.50	0.5	0.707106781	2
0.75	1	1.75	0.75	0.866025404	1.3333
1	1	2.00	1	1	1

- What is the problem with the SUM algorithm?

The problem with the SUM algorithm is that it is not possible to tell the relative contribution from both the specificity and fidelity values. Also, it may be more difficult to interpret a scale of 0 to 2 (as opposed to scales of 0-1 or 0-100), but this shouldn't cause too much of a problem as it is still just a scale like any other.

- What is the problem with the PRODUCT algorithm?

The problem with the PRODUCT algorithm is that once again it is not possible to determine the relative contribution of either the fidelity or specificity value. Also, the overall product is either

equal to or smaller than the smaller of the specificity or fidelity values, potentially causing one to think the indicator value of the species may be lower than it actually is.

- What is the problem with the SQRT(PRODUCT) algorithm?

The problem with the SQRT(PRODUCT) algorithm is that once again it is not possible to determine the relative contribution of either the fidelity or specificity values. Additionally, there is not necessarily a square relationship between the two values, so taking the square root does not necessarily make sense, and results in a number which may confuse the reader.

- What is the problem with the RATIO algorithm?

The problem with the RATIO algorithm is twofold – 1) if the fidelity value is zero, it is impossible to divide a value by zero; 2) although this method DOES give an idea of the relative contribution of both specificity and fidelity, it does not tell the exact values of either. For instance, a ratio of 0.5/1 will be the same value as a ratio of 0.25/0.5.

- 2) Next, you will apply these concepts to three species lists from distinct biogeographic domains: “subtropical”, “convergence” and “sub-Antarctic.

For each biogeographic domain, identify those species that would be valuable indicators using both the “specificity” (density) and the “fidelity” (presence / absence) concepts. Hint: To do this, combine the information from all three domains, so you consider the abundance and the occurrence of each species across all three domains at once.

Explain below how you would do this:

To determine which species would be valuable indicators for each biogeographic domain, it will be necessary to use the equation stated in both of the readings: $IndVal_{ij} = A_{ij} \times B_{ij} \times 100$, where $IndVal$ is the indicator value of species i in site cluster j . To calculate A_{ij} and B_{ij} , the equations written above in question #1 will be used.

Use this approach to calculate the indicator values for each species in each Report the “indicator values” for each species

Use the column / row summary tool in PC_ORD and calculate column / row totals for the data in matrix 1. Paste the three sets of excel file cells below, showing the species list, specificity value, fidelity value, and overall indicator value for all three biogeographic domains:

- **Subtropical:**

Table 1. Species, specificity value, fidelity value, and overall indicator value for the Subtropical biogeographic domain.

subtropical species	subtropical specificity	subtropical fidelity	subtropical overall indicator value
ANTE	0	0.00	0.00
AUSH	1	1.00	100.00
BBAL	0	0.00	0.00
BBSP	0.10519412	1.00	10.52
BLPT	0	0.00	0.00
BRPT	1	1.00	100.00
BRSK	0	0.00	0.00
BUPT	1	1.00	100.00
CAPT	0	0.00	0.00
COSH	0.00655518	1.00	0.66
DKSH	0	0.00	0.00
dkte	1	1.00	100.00
dpsp	0	0.00	0.00
FFSH	0.13965275	1.00	13.97
GBSP	0	0.00	0.00
GHAL	0	0.00	0.00
GRSH	1	1.00	100.00
GWPT	0.84350044	1.00	84.35
JFPT	1	1.00	100.00
KEGU	0	0.00	0.00
KEPT	0	0.00	0.00
KESH	0	0.00	0.00
KIPN	0	0.00	0.00
LISH	0.32173584	1.00	32.17
LMSA	0.12685068	1.00	12.69
LTJA	0.25271053	1.00	25.27
MAPN	0	0.00	0.00
MSPT	1	1.00	100.00
NGPT	0	0.00	0.00
prion	0	0.00	0.00
ROPN	0	0.00	0.00
SAAL	0.35110074	1.00	35.11
SGPT	0.07982029	1.00	7.98
SOAL	0.03481885	1.00	3.48
SOSH	0	0.00	0.00
SPPT	0.1180704	1.00	11.81

WAAL	0.09271591	1.00	9.27
WBSP	0	0.00	0.00
WCAL	0	0.00	0.00
WCPT	0.06270173	1.00	6.27
WFSP	0.06334934	1.00	6.33
WHPT	0	0.00	0.00
WISP	0.02797651	1.00	2.80
wnpt	1	1.00	100.00
WTSB	1	1.00	100.00
WTTR	1	1.00	100.00
YNAL	0.08233805	1.00	8.23

- **Convergence Zone:**

Table 2. Species, specificity value, fidelity value, and overall indicator value for the Convergence Zone biogeographic domain.

convergence species	convergence specificity	convergence fidelity	convergence overall indicator value
ANTE	1	1	100.00
AUSH	0	0	0.00
BBAL	0.053842283	1	5.38
BBSP	0.691264875	1	69.13
BLPT	0.213166296	1	21.32
BRPT	0	0	0.00
BRSK	0	0	0.00
BUPT	0	0	0.00
CAPT	0.100124817	1	10.01
COSH	0.993444824	1	99.34
DKSH	1	1	100.00
dkte	0	0	0.00
dpsp	0	0	0.00
FFSH	0.86034725	1	86.03
GBSP	0	0	0.00
GHAL	0	0	0.00
GRSH	0	0	0.00
GWPT	0.156499559	1	15.65
JFPT	0	0	0.00
KEGU	0	0	0.00
KEPT	0	0	0.00
KESH	0	0	0.00
KIPN	0	0	0.00
LISH	0.660697198	1	66.07
LMSA	0.156295712	1	15.63
LTJA	0.747289468	1	74.73

MAPN	0	0	0.00
MSPT	0	0	0.00
NGPT	0.305478913	1	30.55
prion	0.09319831	1	9.32
ROPN	0.979780601	1	97.98
SAAL	0.648899262	1	64.89
SGPT	0.295045386	1	29.50
SOAL	0.93309958	1	93.31
SOSH	0.983653807	1	98.37
SPPT	0.753837045	1	75.38
WAAL	0.599746703	1	59.97
WBSP	0.879432369	1	87.94
WCAL	1	1	100.00
WCPT	0.338739092	1	33.87
WFSP	0.936650657	1	93.67
WHPT	0	0	0.00
WISP	0.351599286	1	35.16
wnpt	0	0	0.00
WTSH	0	0	0.00
WTTR	0	0	0.00
YNAL	0.913055862	1	91.31

- **Sub-Antarctic:**

Table 3. Species, specificity value, fidelity value, and overall indicator value for the Sub-Antarctic biogeographic domain.

sub-Antarctic species	sub-Antarctic specificity	sub-Antarctic fidelity	sub-Antarctic overall indicator value
ANTE	0	0	0.00
AUSH	0	0	0.00
BBAL	0.946157717	1	94.62
BBSP	0.203541	1	20.35
BLPT	0.786833704	1	78.68
BRPT	0	0	0.00
BRSK	1	1	100.00
BUPT	0	0	0.00
CAPT	0.899875183	1	89.99
COSH	0	0	0.00
DKSH	0	0	0.00
dkte	0	0	0.00
dpsp	1	1	100.00
FFSH	0	0	0.00
GBSP	1	1	100.00

GHAL	1	1	100.00
GRSH	0	0	0.00
GWPT	0	0	0.00
JFPT	0	0	0.00
KEGU	1	1	100.00
KEPT	1	1	100.00
KESH	1	1	100.00
KIPN	1	1	100.00
LISH	0.017566967	1	1.76
LMSA	0.716853613	1	71.69
LTJA	0	0	0.00
MAPN	1	1	100.00
MSPT	0	0	0.00
NGPT	0.694521087	1	69.45
prion	0.90680169	1	90.68
ROPN	0.020219399	1	2.02
SAAL	0	0	0.00
SGPT	0.625134325	1	62.51
SOAL	0.032081568	1	3.21
SOSH	0.016346193	1	1.63
SPPT	0.128092557	1	12.81
WAAL	0.307537383	1	30.75
WBSP	0.120567631	1	12.06
WCAL	0	0	0.00
WCPT	0.598559177	1	59.86
WFSP	0	0	0.00
WHPT	1	1	100.00
WISP	0.620424204	1	62.04
wnpt	0	0	0.00
WTSH	0	0	0.00
WTTR	0	0	0.00
YNAL	0.004606092	1	0.46

3) Perform weighted averaging analyses:

Using the overall indicator values you calculated, create three matrix2's: one for each biogeographic domain. These matrices will show the weights for each species as indicators of each biogeographic domain.

Load the sample data "biogeography_samples.xls" and perform three Weighted Averaging Analyses, using the three matrix 2 "weights" you just created.

For each analysis, paste a plot of the samples arranged along a 1-D axis (Note: ask for 2-D plot), showing the abundance of the best indicators for that biogeographic domains (based on your answers from section 1).

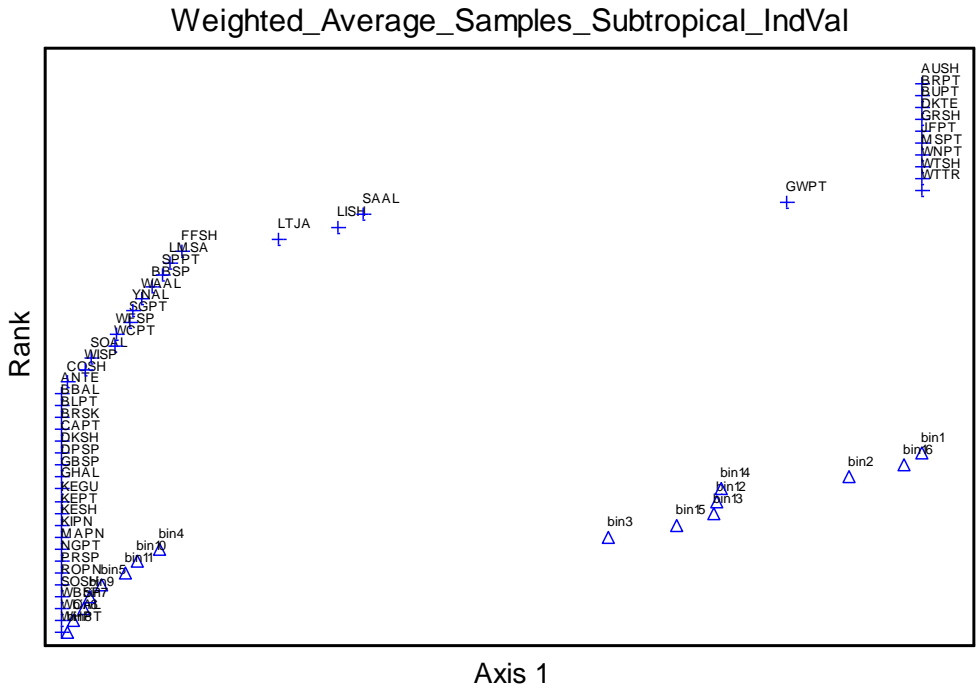


Figure 1. Plot of the 47 species and 16 bins in a weighted average analysis along a 1-D axis, using the Subtropical indicator values as the weight.

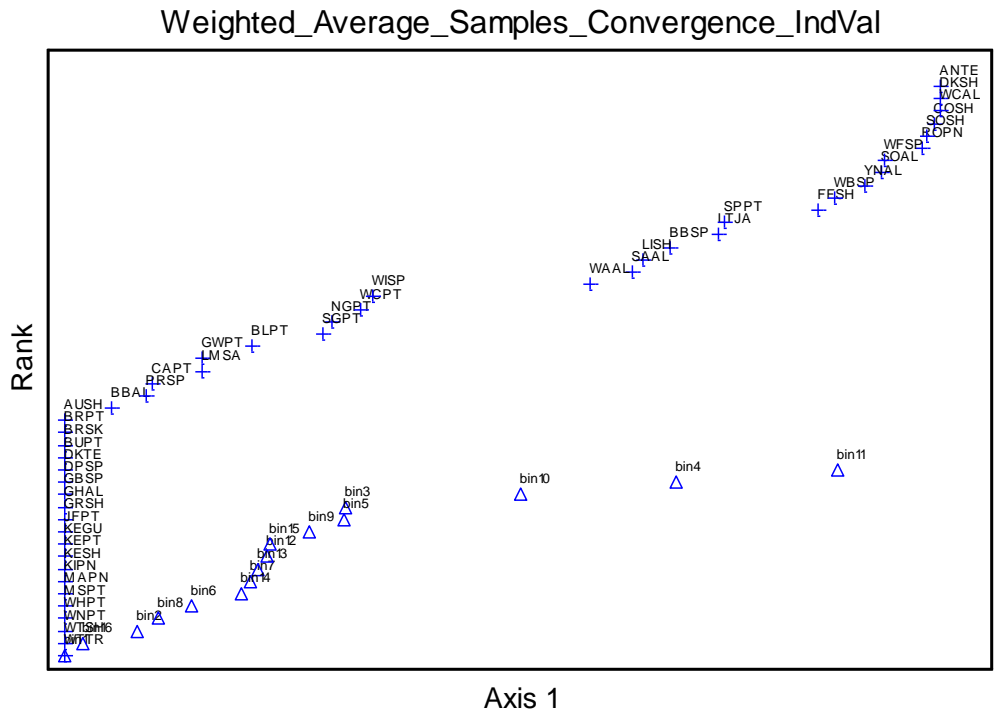


Figure 2. Plot of the 47 species and 16 bins in a weighted average analysis along a 1-D axis, using the Convergence Zone indicator values as the weight.

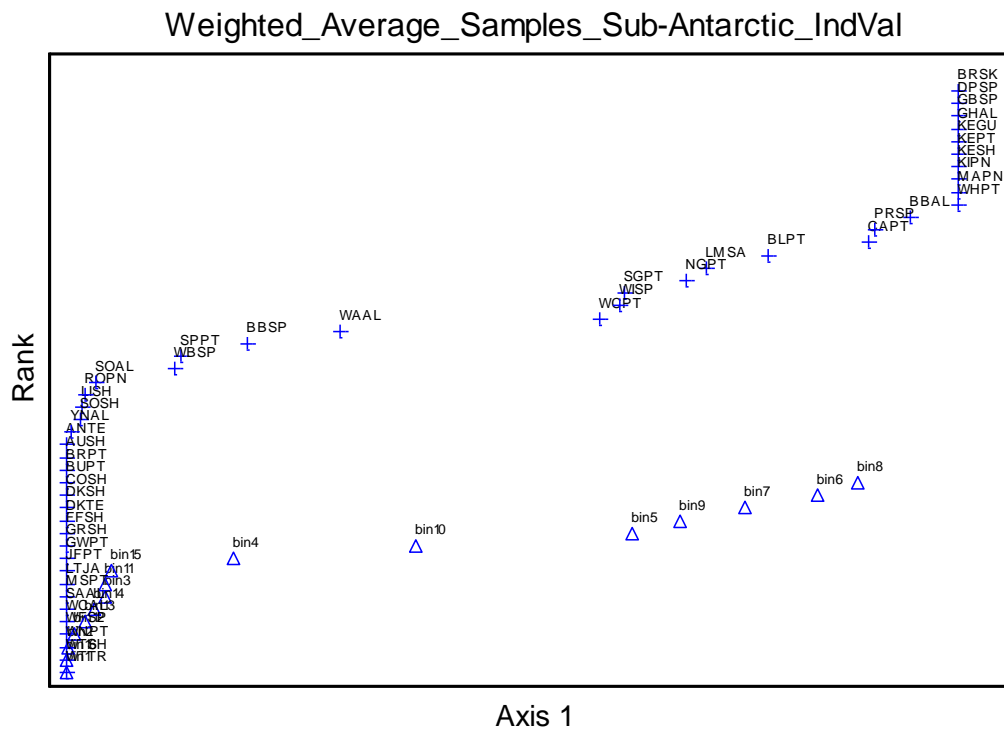
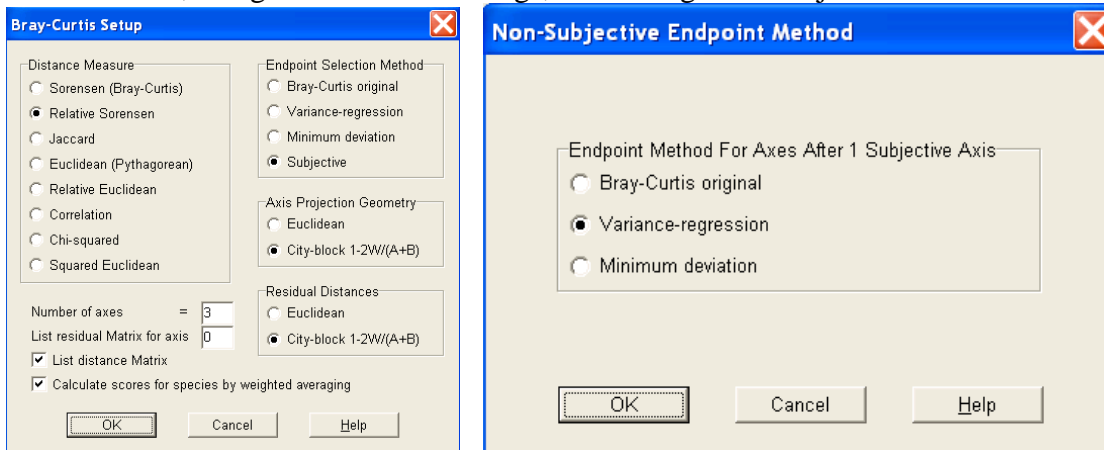


Figure 3. Plot of the 47 species and 16 bins in a weighted average analysis along a 1-D axis, using the Sub-Antarctic indicator values as the weight.

Final question: based on the results of the three weighted averaging analyses, classify each sample as belonging to one of the three biogeographic domains, below. For each “bin” sample, show its score in the three analyses you run and then use this information to classify the sample as one of the three biogeographic domains:

	Subtropical	Convergence	Sub-Antarctic	Classification
bin1	100.00	0.00	0.00	Subtropical
bin2	91.52	8.26	0.22	Subtropical
bin3	63.57	32.03	4.40	Subtropical
bin4	11.32	69.88	18.80	Convergence
bin5	4.73	31.87	63.39	Sub-Antarctic
bin6	1.31	14.47	84.22	Sub-Antarctic
bin7	2.58	21.28	76.14	Sub-Antarctic
bin8	0.67	10.65	88.68	Sub-Antarctic
bin9	3.28	27.90	68.83	Sub-Antarctic
bin10	8.78	52.01	39.21	Convergence
bin11	7.35	88.23	4.42	Convergence
bin12	76.14	23.08	0.79	Subtropical
bin13	75.90	22.02	2.09	Subtropical
bin14	76.75	20.18	3.07	Subtropical
bin15	71.47	23.53	5.00	Subtropical
bin16	97.87	2.09	0.03	Subtropical

4) **Perform Polar-Ordination analyses:** Open the “biogeography_environment.xls” file and use this information to test three hypotheses about the organization of the samples: (H1): water temperature (SST) is most important ecotone, (H2) productivity (CHL) is most important ecotone, and (3) latitude is most important ecotone. To make this test, perform three Polar Ordination (Bray Curtis) tests, in the Ordination menu, using these default settings, and asking for 1 subjective axis:



- (i) SST: Identify the two poles for this analysis:
 “warm bin”: Bin1 (highest SST) “cold bin”: Bin8 (lowest SST)

Perform analysis and paste the following results, below:

- Report amount of variance for axis 1 (objective): 49.26%

Endpoints for axis 1: bin1 bin8
Distances (ordination scores) are from bin1

Sum of squares of non-redundant distances
in original matrix = .894480E+02

Axis 1 extracted 49.26% of the original distance matrix
Cumulative: 49.26%
Sum of squares of residual distances remaining = .453847E+02

Ordination scores on axis 1

Seq.	Name	Score	Seq.	Name	Score	Seq.	Name	Score	Seq.	Name	Score
1	bin1	0.000	2	bin2	0.384	3	bin3	0.451	4	bin4	0.537
5	bin5	0.732	6	bin6	0.938	7	bin7	0.783	8	bin8	1.000
9	bin9	0.638	10	bin10	0.645	11	bin11	0.517	12	bin12	0.504
13	bin13	0.517	14	bin14	0.510	15	bin15	0.508	16	bin16	0.348

- Report amount of variance for axis 2 (subjective): 34.23%

Endpoints for axis 2: bin13 bin4
Distances (ordination scores) are from bin13

Regression coefficient for this axis = -6.40
Variance in distances from the first endpoint = 1.26

Axis 2 extracted 34.23% of the original distance matrix
Cumulative: 83.49%
Sum of squares of residual distances remaining = .147675E+02

Ordination scores on axis 2

Seq.	Name	Score	Seq.	Name	Score	Seq.	Name	Score	Seq.	Name	Score
1	bin1	0.472	2	bin2	0.488	3	bin3	0.320	4	bin4	0.925
5	bin5	0.656	6	bin6	0.514	7	bin7	0.547	8	bin8	0.472
9	bin9	0.547	10	bin10	0.662	11	bin11	0.456	12	bin12	0.033
13	bin13	0.000	14	bin14	0.040	15	bin15	0.149	16	bin16	0.462

- Report amount of variance for axis 3 (subjective): 9.67%

Endpoints for axis 3: bin3 bin11
Distances (ordination scores) are from bin3

Regression coefficient for this axis = -0.10
Variance in distances from the first endpoint = 0.89

Axis 3 extracted 9.67% of the original distance matrix
Cumulative: 93.16%
Sum of squares of residual distances remaining = .611857E+01

Ordination scores on axis 3

Seq.	Name	Score	Seq.	Name	Score	Seq.	Name	Score	Seq.	Name	Score
1	bin1	0.306	2	bin2	0.306	3	bin3	0.000	4	bin4	0.175
5	bin5	0.230	6	bin6	0.298	7	bin7	0.312	8	bin8	0.306
9	bin9	0.313	10	bin10	0.253	11	bin11	0.785	12	bin12	0.200
13	bin13	0.175	14	bin14	0.168	15	bin15	0.147	16	bin16	0.328

- (ii) CHL: Identify the two poles for this analysis:
 “highest bin”: **Bin 11** “lowest bin”: **Bin 1 or Bin 15**. I am choosing to use **Bin 1** as this bin is surrounded by other chlorophyll levels which are also on the lower end, whereas **Bin 15** is surrounded by chlorophyll levels which are higher.

Perform analysis and paste the following results, below:

- Report amount of variance for axis 1 (objective): **34.25%**

Endpoints for axis 1: bin1 bin11
 Distances (ordination scores) are from bin1

Sum of squares of non-redundant distances
 in original matrix = .894480E+02

Axis 1 extracted 34.25% of the original distance matrix
 Cumulative: 34.25%
 Sum of squares of residual distances remaining = .588133E+02

Ordination scores on axis 1

Seq.	Name	Score	Seq.	Name	Score	Seq.	Name	Score	Seq.	Name	Score
1	bin1	0.000	2	bin2	0.384	3	bin3	0.455	4	bin4	0.526
5	bin5	0.530	6	bin6	0.521	7	bin7	0.540	8	bin8	0.517
9	bin9	0.536	10	bin10	0.583	11	bin11	1.000	12	bin12	0.555
13	bin13	0.542	14	bin14	0.529	15	bin15	0.500	16	bin16	0.348

- Report amount of variance for axis 2 (subjective): **49.76%**

Endpoints for axis 2: bin12 bin7
 Distances (ordination scores) are from bin12

Regression coefficient for this axis = -8.79
 Variance in distances from the first endpoint = 1.81

Axis 2 extracted 49.76% of the original distance matrix
 Cumulative: 84.01%
 Sum of squares of residual distances remaining = .142996E+02

Ordination scores on axis 2

Seq.	Name	Score	Seq.	Name	Score	Seq.	Name	Score	Seq.	Name	Score
1	bin1	0.479	2	bin2	0.479	3	bin3	0.204	4	bin4	0.571
5	bin5	0.801	6	bin6	0.788	7	bin7	0.973	8	bin8	0.758
9	bin9	0.752	10	bin10	0.703	11	bin11	0.479	12	bin12	0.000
13	bin13	0.038	14	bin14	0.047	15	bin15	0.114	16	bin16	0.450

- Report amount of variance for axis 3 (subjective): **10.11%**

Endpoints for axis 3: bin8 bin4
 Distances (ordination scores) are from bin8

Regression coefficient for this axis = -3.11
 Variance in distances from the first endpoint = 0.60

Axis 3 extracted 10.11% of the original distance matrix
 Cumulative: 94.13%
 Sum of squares of residual distances remaining = .525399E+01

Ordination scores on axis 3

Seq.	Name	Score	Seq.	Name	Score	Seq.	Name	Score	Seq.	Name	Score
------	------	-------	------	------	-------	------	------	-------	------	------	-------

1 bin1	0.275	2 bin2	0.291	3 bin3	0.416	4 bin4	0.729
5 bin5	0.442	6 bin6	0.099	7 bin7	0.282	8 bin8	0.000
9 bin9	0.421	10 bin10	0.481	11 bin11	0.275	12 bin12	0.282
13 bin13	0.276	14 bin14	0.277	15 bin15	0.337	16 bin16	0.294

- (iii) Latitude: Identify the two poles for this analysis:
 “northern-most bin”: **Bin 1** “southern-most bin”: **Bin 8**

Perform analysis and paste the following results, below:

- Report amount of variance for axis 1 (objective): **49.26%**

Endpoints for axis 1: bin1 bin8
 Distances (ordination scores) are from bin1

Sum of squares of non-redundant distances
 in original matrix = .894480E+02

Axis 1 extracted 49.26% of the original distance matrix
 Cumulative: 49.26%
 Sum of squares of residual distances remaining = .453847E+02

Ordination scores on axis 1

Seq.	Name	Score	Seq.	Name	Score	Seq.	Name	Score	Seq.	Name	Score
1	bin1	0.000	2	bin2	0.384	3	bin3	0.451	4	bin4	0.537
5	bin5	0.732	6	bin6	0.938	7	bin7	0.783	8	bin8	1.000
9	bin9	0.638	10	bin10	0.645	11	bin11	0.517	12	bin12	0.504
13	bin13	0.517	14	bin14	0.510	15	bin15	0.508	16	bin16	0.348

- Report amount of variance for axis 2 (subjective): **34.23%**

Endpoints for axis 2: bin13 bin4
 Distances (ordination scores) are from bin13

Regression coefficient for this axis = -6.40
 Variance in distances from the first endpoint = 1.26

Axis 2 extracted 34.23% of the original distance matrix
 Cumulative: 83.49%
 Sum of squares of residual distances remaining = .147675E+02

Ordination scores on axis 2

Seq.	Name	Score	Seq.	Name	Score	Seq.	Name	Score	Seq.	Name	Score
1	bin1	0.472	2	bin2	0.488	3	bin3	0.320	4	bin4	0.925
5	bin5	0.656	6	bin6	0.514	7	bin7	0.547	8	bin8	0.472
9	bin9	0.547	10	bin10	0.662	11	bin11	0.456	12	bin12	0.033
13	bin13	0.000	14	bin14	0.040	15	bin15	0.149	16	bin16	0.462

- Report amount of variance for axis 3 (subjective): **9.67%**

Endpoints for axis 3: bin3 bin11
 Distances (ordination scores) are from bin3

Regression coefficient for this axis = -0.10
 Variance in distances from the first endpoint = 0.89

Axis 3 extracted 9.67% of the original distance matrix
 Cumulative: 93.16%
 Sum of squares of residual distances remaining = .611857E+01

Ordination scores on axis 3

Seq.	Name	Score	Seq.	Name	Score	Seq.	Name	Score	Seq.	Name	Score
1	bin1	0.306	2	bin2	0.306	3	bin3	0.000	4	bin4	0.175
5	bin5	0.230	6	bin6	0.298	7	bin7	0.312	8	bin8	0.306
9	bin9	0.313	10	bin10	0.253	11	bin11	0.785	12	bin12	0.200
13	bin13	0.175	14	bin14	0.168	15	bin15	0.147	16	bin16	0.328

Final question: Which analyses gave the best result?

- Which of the three “objective” axes performed better – higher variance explained?

Both the SST and Latitude “objective” axes tied for the better score, with a variance explained of 49.26% compared to 34.25% explained in the CHL “objective” axis.

- Which analyses explained the most variance overall?

Overall, both the SST and Latitude analyses explained a total of 93.16% of the variance while the CHL analysis explained 94.13%.

To determine which answer gives the best result, we must consider the answers to both of these mini-questions: Both SST and Latitude give the highest amount of explained variance with a single axis, but CHL explains slightly more overall variance, but only by just under 1% more. Therefore, I believe that the SST and Latitude analyses give the best results.

- 5) **Synthesis:** To finish, calculate the weighted average scores for the pole “samples” you used in the three Polar Ordinations. Using the proportional species composition of the samples and the indicator values you calculated in question 1, calculate the following:

- **SST hypothesis:**

	Subtropical	Convergence	Sub-Antarctic
“warm” pole bin	100.00	0.00	0.00
“cold” pole bin	0.67	10.65	88.68

- **CHL hypothesis:**

	Subtropical	Convergence	Sub-Antarctic
“highest CHL ” pole bin	7.35	88.23	4.42
“lowest CHL” pole bin	100.00	0.00	0.00

- **LAT hypothesis:**

	Subtropical	Convergence	Sub-Antarctic
“northern-most” pole bin	100.00	0.00	0.00
“southern-most” pole bin	0.67	10.65	88.68

Discuss (qualitatively) whether the poles you identified agree with the species indicator values you calculated? Hint: do subtropical species indicate warm / low CHL / low LAT poles? What environmental poles do the sub-Antarctic species indicate?

Yes, the poles we identified for the SST, CHL, and LAT hypotheses do agree with the species indicator values we calculated for each biogeographic region:

SUBTROPICAL: For SST, I chose poles of bin 1 (warmest) and bin 8 (coldest). Looking at the weighted averages for the Subtropical biogeographic region (Figure 1), bin 1 is all the way on the right, along with many species which have the highest indicator value for the Subtropical biogeographic region. Likewise, bin 8 is all the way on the left, along with the species which have the lowest indicator values for the region. This is the exact same as LAT – the same bins, and the same species with the highest indicator values aligned with bin 1, and the lowest indicator values aligned with bin 8. For CHL, the bins of 11 (highest) and 1 (lowest) were chosen. Again, looking at figure 1, the species with the highest indicator values are aligned with bin 1, and the species aligned with bin 11 (high CHL) are right in the middle, which makes sense as the Subtropical zone is in the middle of the 3 biogeographic zones of the weighted average score for highest CHL. The environmental poles that the Subtropical species indicate are warm / low CHL / low LAT on the right, and cold / high CHL / high LAT on the left.

CONVERGENCE: For SST and LAT, bin 1 (highest, most southern) and bin 8 (lowest, most northern) were chosen as the poles. Looking at Figure 2 (weighted averages of bins and species in the convergence zone), bins 1 and 8 are in the middle of the 1-D plot, and the species which align with them have indicator values which are not on the extreme end of being high or low. For CHL, bin 11 was chosen as the highest, and bin 1 was chosen as the lowest – bin 11 is indeed all the way on the right in Figure 2 and those species aligned with it have the highest indicator values for this biogeographic region. The environmental poles that the Convergence species indicate are cold / high CHL / mid-Lat on the right, and cold / low CHL / mid-Lat on the left.

SUB-ANTARCTIC: For SST and LAT, bin 1 (highest, most southern) and bin 8 (lowest, most northern) were chosen as the poles, just like the other 2 regions. Looking at Figure 3 (weighted averages of bins and species within the Sub-Antarctic Zone), bins 1 and 8 are again the endpoints, with bin 8 all the way on the right, and bin 1 all the way on the left (opposite of the subtropical region). With these 2 bins, the species with the highest indicator values are aligned with bin 8, and those with the lowest indicator values are aligned with bin 1. For CHL, bin 11 was chosen as the highest CHL value, and bin 1 was chosen as the lowest (same as for all biogeographic regions). In figure 3, bin 1 is all the way on the left, and bin 11 is also very near the left side which matches with the species in the same location – they also have low indicator values for this region. This makes sense as the least amount of CHL is found in this area. The environmental poles that the Sub-Antarctic species indicate are cold / high CHL / high LAT on the right, and warm / low CHL / low LAT on the left.