The Seaweeds in Two Oceans Data

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1 The South African seaweed data

The data were collected for the regions defined in the table, below:

Table 1: The 58 × 50 km sections of the South African coastline, with approximate GPS coordinates, delineation of sections, and some well-known sites in each section. Taken with permission from Bolton and Stegenga (2002).

Site	Lon	Lat	Limits	Including
1	16.72	-28.98	Orange River to just south of Holgats River	
2	16.94	-29.38	To just south of Wedge Point	Port Nolloth
3	17.08	-29.83	To just south of Melkbos Point	Kleinzee
4	17.26	-30.26	To Swartlintjies River	Skulpfontein Point, Swartlintjies
5	17.48	-30.68	To 10 km north of Groen River	River Hondeklip Bay, Spoeg River
6	17.72	-31.09	To just north of Brak River	Groen River, Island Point, Blougat
7	18.00	-31.46	To just north of Duiwegat	Voëlklip, Sout River, Blinkwater Bay
8	18.25	-31.85	To just south of Doring Bay	Olifants River, Strandfontein, Doring Bay
9	18.34	-32.30	To just north of Elands Bay	Lambert's Bay, Lang River
10	18.20	-32.72	To just north of Laaiplek	Elands Bay, Die Vlei, Dwarskersbos
11	17.85	-32.83	To just south of Cape Columbine	Laaiplek, St Helena Bay, Paternoster
12	18.03	-33.03	To just east of Saldahna	
13	18.01	-33.15	To Postberg	Langebaan Lagoon
14	18.32	-33.50	To just south of Modder River	Yzerfontein, Dassen Is., Grotto Bay
15	18.47	-33.91	To Sea Point	Melkbosstrand, Table Bay, Green Point
16	18.37	-34.21	To just north of Scarborough	Camps Bay, Hout Bay, Kommetjie
17	18.47	-34.11	To just east of Kalk Bay	Scarborough, Cape Point, Fishoek
18	18.82	-34.19	To just south of Gordons Bay	Muizenburg, Strandfontein, Strand
19	19.07	-34.35	To just east of Kleinmond	Rooi Els, Hangklip, Betty's Bay
20	19.34	-34.59	To just south of Danger Point	Bot River, Sand Bay, Hermanus, Die Kelders
21	19.66	-34.79	To just east of Quoin Point	Danger Point, Pearly Beach, Dyer Island
22	20.07	-34.75	To just east of Struis Bay	Die Mond, Cape Agulhas
23	20.48	-34.49	To just east of Skipskop	Struis Bay, Arniston
24	20.87	-34.39	To just east of Cape Infanta	Koppie Alleen, Cape Infanta, Bree River, Witsand
25	21.36	-34.42	To just east of Grootjongensfontein	Puntjie, Skurwe Bay
26	21.83	-34.38	To just west of Gouritzmond	Stil Bay, Bloukrans, Bull Point
27	22.12	-34.16	To just north of Mossel Bay	Gouritzmond, Vlees Bay, Pinnacle Rock
28	22.54	-34.01	To just west of Victoria Bay	Hartenbos, Klein and Groot Brak rivers, Herolds Bay, Skuinsbank
29	23.02	-34.08	To just west of The Heads, Knysna	Victoria Bay, Wilderness, Platbank, Oesterbank, Walker Bay
30	23.36	-34.10	To Jack's Point, south of Plettenberg Bay	The Heads, Neusgate
31	23.78	-34.01	To Elandbos River	Plettenberg Bay, Arch Rock, Die Punt, Blousloep
32	24.27	-34.08	To Skuinsklip	Storms River, Voëlkrans, Skietgate
33	24.74	-34.19	To Thys Point	Aasvoëlklip, Tsitsikamma River, Klipdrif River
34	25.04	-33.97	To just west of Gamtoos River	Cape St Francis, Krom River, Seekoei River, Jeffreys Bay
35	25.52	-34.04	To just east of Sardinia Bay	Van Stadens River, Claasen Point
36	25.70	-33.79	To just east of St George's Beach	Chelsea Point, Port Elizabeth, Bluewater Bay
37	26.18	-33.72	To just west of Woody Cape	St Croix Is., Sundays River
38	26.65	-33.70	To just west of Kenton-on-Sea	Seal Is., Bird Is., Cape Padrone, Cannon Rocks, Boknes
39	27.10	-33.52	To just east of Kleinemonde	Kasouga, Port Alfred
40	27.52	-33.27	To just east of Keiskamma River	Great Fish River, Madagascar Reef
41	27.93	-33.01	To just east of East London	Kayser's Beach, Kidd's Beach, Cove Rock
42	28.30	-32.73	To Haga-Haga	Gonubie, Cintsa River
43	28.68	-32.44	To Qora River	Morgans Bay, Kei Mouth, Nxaxo River, Mazeppa Bay
44	29.05	-32.11	To just east of Xora River	Dwesa, The Haven
45	29.37	-31.76	To Sharks Point	Mncwasa River, Coffee Bay, Hluleka
46	29.74	-31.46	To Mkozi River	Boulder Bay, Port St Johns, Montshe, Ntsubane
47	30.12	-31.18	To Mnyameni River	Cathedral Rock, Lambasi Bay, Wild Coast
48	30.41	-30.81	To just north of St Michaels-on-Sea	Mzamba, Port Edward, Southbroom, Margate
49	30.68	-30.41	To just south of Pennington	Port Shepstone, Mzumbe, Sezela
50	30.93	-30.01	To just south of Isipingo Beach	Scottburgh, Park Rynie, Umkomaas, Illovo, Amanzimtoti
51	31.15	-29.62	To Desainagar	Durban, Umhlanga Rocks, Umdloti Beach
52	31.46	-29.26	To just north of Zinkwazi Beach	Westbrook, Ballito, Blythdale Beach
53	31.82	-28.94	To just east of Mtunzini	Tugela River, Dunn's Reserve
54	32.21	-28.70	To Mbonambi Beach	Richards Bay
55	32.46	-28.32	To just north of First Rocks	Dawson's Rocks, Cape St Lucia, St Lucia
56	32.59	-27.87	To Bhukwini	Mission Rocks, Cape Vidal, Leven Point
57	32.72	-27.42	To just north of Gobey's Point	Liefeldts Rocks, Sodwana Bay
58	32.87	-26.97	To Kosimeer	Hulley Point, Black Rock

I use two data sets. The first, Y (in the file 'seaweeds.csv') comprises distribution records of 847 macroalgal species within each of 58 × 50 km-long sections of the South African coast (updated from Bolton and Stegenga, 2002). This represents *ca*. 90% of the known seaweed flora of South Africa, but excludes some very small and/or very rare species for which data are insufficient. The data are from verifiable literature sources and John Bolton and Rob Anderson's own collections, assembled from information collected by teams of phycologists over three decades (Bolton, 1986; Bolton and Stegenga, 2002; De Clerck et al., 2005; Stegenga et al., 1997). The second, E (in 'env.csv'), is a dataset of *in situ* coastal seawater temperatures (Smit et al., 2013) derived from daily measurements over up to 40 years.

2 Setting up the analysis environment

This is **R**, so first I need to find, install and load various packages. Some of the packages will be available on CRAN and can be accessed and installed in the usual way, but others will have to be downloaded from R Forge.

```
library(tidyverse)
library(betapart)
library(vegan)
library(gridExtra)
library(BiodiversityR)
library(grid)
library(gridBase)
library(tidyr)
```

3 Species diversity

Let's load the data and see how it is structured:

```
# Read in the species data:
spp <- read.csv('../exercises/diversity/seaweeds.csv')
spp <- dplyr::select(spp, -1)

# Lets look at the data:
dim(spp)
```

```
## [1]  58 847
```

We see that our dataset has 58 rows and 847 columns. What is in the columns and rows? Start with the first 5 rows and 5 columns:

```
spp[1:5, 1:5]
```

```
##   ACECAL ACEMOE ACRVIR AROSP1 ANAWRI
## 1      0      0      0      0      0
## 2      0      0      0      0      0
## 3      0      0      0      0      0
## 4      0      0      0      0      0
## 5      0      0      0      0      0
```

Now the last 5 rows and 5 columns:

```
spp[(nrow(spp) - 5):nrow(spp), (ncol(spp) - 5):ncol(spp)]
```

```
##    WOMKWA WOMPAC WRAARG WRAPUR WURMIN ZONSEM
## 53      0      0      1      0      0      0
## 54      0      0      1      0      0      0
## 55      0      0      1      0      0      0
## 56      0      1      1      0      1      0
## 57      1      0      1      0      1      0
## 58      0      0      1      0      1      0
```

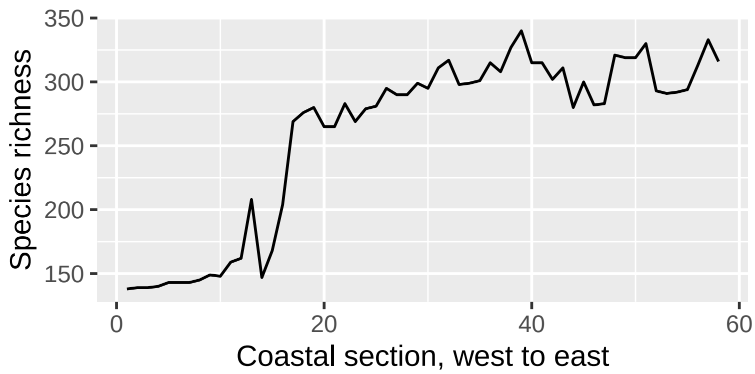
So, each of the rows correspond to a site (i.e. each of the coastal sections in Table 1), and the columns each contain a species. The species are arranged alphabetically, and they are indicated by a six-letter code.

3.1 Alpha diversity

We can represent α-diversity in three ways, i.e. 1) as species richness (S), 2) as a univariate diversity index, such as Shannon diversity (H') or Simpson's diversity (λ), or 3) as a dissimilarity index, e.g. Bray-Curtis or Jaccard dissimilarities. We will work through each in turn (but I will cover the dissimilarity indices under the 'Dissimilarity index' section later on).

First, species richness. In the seaweed biodiversity data—because we view each coastal section as the local scale (the smallest unit of sampling)—I simply count the number of species within each of the sections. The `diversityresult()` function in the **BiodiversityR** package does this easily:

```
spp_richness <- diversityresult(spp, index = 'richness', method = 'each site')
# spp_richness
ggplot(data = spp_richness, (aes(x = 1:58, y = richness))) +
  geom_line() + xlab("Coastal section, west to east") + ylab("Species richness")
```



If the **BiodiversityR** package does not work for you, there is also the `specnumber()` function in **vegan**:

```
# Use 'MARGIN = 1' to calculate the number of species within each row (site)
specnumber(spp, MARGIN = 1)
```

```
##  [1] 138 139 139 140 143 143 143 145 149 148 159 162 208 147 168 204 269 276 280
## [20] 265 265 283 269 279 281 295 290 290 299 295 311 317 298 299 301 315 308 327
## [39] 340 315 315 302 311 280 300 282 283 321 319 319 330 293 291 292 294 313 333
## [58] 316
```

In other instances, it makes more sense to calculate the mean species richness of all the sampling units (e.g. quadrats) taken inside the ecosystem of interest. You will have to decide based on your own data.

The second way in which we can express α-diversity is to use one of the univariate diversity indices such as Shannon's H' or Simpson's λ. Shannon's H' is sometimes called Shannon's diversity index, the Shannon–Wiener index, the Shannon–Weaver index, or the Shannon entropy. It is calculated as

$$H' = -\sum_{i=1}^{R} p_i \ln p_i$$

where p_i is the proportion of individuals belonging to the ith species, and R is the species richness.

Simpson's λ, or simply the Simpson index, is calculated as

$$\lambda = \sum_{i=1}^{R} p_i^2$$

where R is the species richness and p_i is the relative abundance of the ith species.

We cannot calculate either of these for the seaweed data because in order to do so we require abundance data – the seaweed data are presence-absence only. Let's load a fictitious dataset of the diversity of three different communities of plants, with each community corresponding to a different light environment (dim, mid and high light):

```
light <- read.csv("../exercises/diversity/light_levels.csv")
light
```

```
##         Site    A    B    C    D    E    F
## 1  low_light 0.75 0.62 0.24 0.33 0.21 0.14
## 2  mid_light 0.38 0.15 0.52 0.57 0.28 0.29
## 3 high_light 0.08 0.15 0.18 0.52 0.54 0.56
```

We can see above that in stead of having data with 1s and 0s for presence-absence, here we instead have some values that indicate the relative amounts of each of the species in the three light environments. We calculate species richness (as before), and also the Shannon and Simpson indices using **vegan**'s `diversity()` function:

```
light_div <- data.frame(
  site = c("low_light", "mid_light", "high_light"),
  richness = specnumber(light[, 2:7], MARGIN = 1),
  shannon = round(diversity(light[, 2:7], MARGIN = 1, index = "shannon"), 2),
  simpson = round(diversity(light[, 2:7], MARGIN = 1, index = "simpson"), 2)
)
light_div
```

```
##         site richness shannon simpson
## 1  low_light        6    1.62    0.78
## 2  mid_light        6    1.71    0.81
## 3 high_light        6    1.59    0.77
```

3.2 Gamma diversity

Returning again to the seaweed data, lets now look at γ-diversity – this would simply be the total number of species along the South African coastline in all 58 coastal sections:

```
ncol(spp)
```

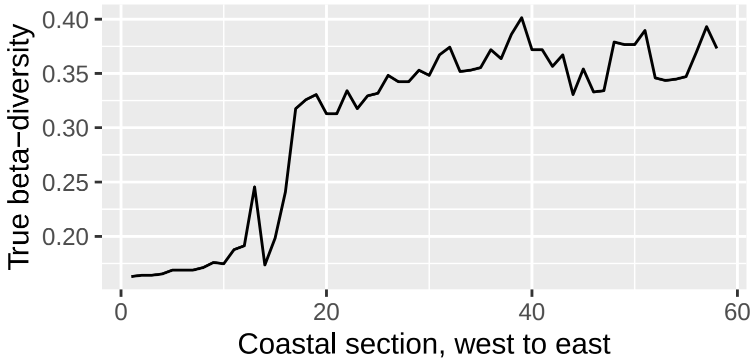
```
## [1] 847
```

Think before you calculate γ-diversity for your own data as it might not be as simple as here!

3.3 Beta diversity

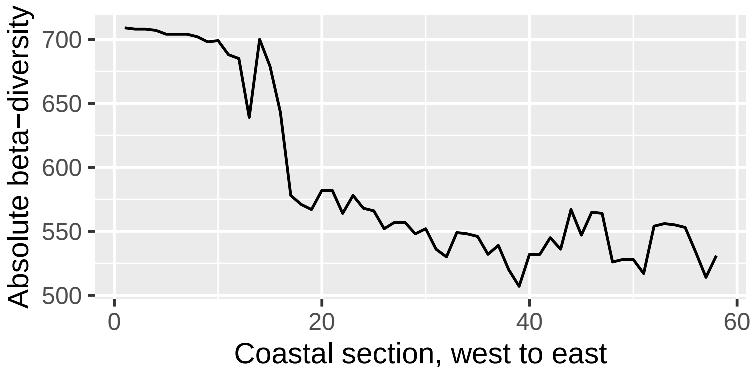
The first measure of β-diversity is *true β-diversity*. This is simply dividing the γ-diversity for the region by the α-diversity for a specific coastal section. We can calculate it all at once for the whole dataset and make a graph.

```
true_beta <- data.frame(
  beta = specnumber(spp, MARGIN = 1) / ncol(spp),
  section_no = c(1:58)
)
# true_beta
ggplot(data = true_beta, (aes(x = section_no, y = beta))) +
  geom_line() + xlab("Coastal section, west to east") + ylab("True beta-diversity")
```



The second measure of β-diversity is *absolute species turnover*, and to calculate this we simply simply substract α-diversity for each section from the region's γ-diversity.

```
abs_beta <- data.frame(
  beta = ncol(spp) - specnumber(spp, MARGIN = 1),
  section_no = c(1:58)
)
# abs_beta
ggplot(data = abs_beta, (aes(x = section_no, y = beta))) +
  geom_line() + xlab("Coastal section, west to east") + ylab("Absolute beta-diversity")
```



4 Dissimilarity indices

In this section we will cover the dissimilarity indices, which are special cases of diversity indices that use pairwise comparisons between sampling units, habitats, or ecosystems. Both α- and β-diversity can be expressed as dissimilarity indices, so let us look at each.

4.1 Alpha diversity

Recall from the lecture slides the Bray-Curtis and Jaccard dissimilarity indices for abundance data, and the Sørensen dissimilarity index for presence-absence data. The seaweed dataset is a presence-absence dataset, so we will use the Sørensen index here. The interpretation of the resulting square dissimilarity matrices is the same regardless of whether it is calculated from an abundance dataset or a presence-absence dataset. The values range from 0 to 1, with 0 meaning that the pair of sites being compared is identical (i.e. 0 dissimilarity) and 1 means the pair of sites is completely different (no species in common, hence 1 dissimilarity). In the square dissmilarity matrix the diagonal is 0, which essentially (and obviously) means that any site is identical to itself. Elsewhere the values will range from 0 to 1. Since this is a pairwise calculation (each site compared to every other site), our seaweed dataset will contain $(58 \times (58 - 1))/2 = 1653$ values, each one ranging from 0 to 1.

The first step involves the species table (Y). First I compute the Sørensen dissimilarity index ($\beta_{\text{sør}}$) to compare the dissimilarity of all pairs of coastal sections using on presence-absence data. The dissimilarity in species composition between two sections is calculated from three parameters, *viz.*, b and c, which represent the number of species unique to each of two sites, and a, the number of species in common between them. It is given by:

$$\beta_{\text{sør}} = \frac{b + c}{2a + b + c}$$

```
sor <- vegdist(spp, binary = TRUE)
```

[…to be completed…]

4.2 Beta diversity

β-diversity is a concept that describes how species assemblages (communities) measured within the ecosystem of interest vary from place to place, e.g. between the various transects or quadrats used to sample the ecosystem. β-diversity results from habitat heterogeneity (along gradients, or randomly). We have already seen two concepts of β-diversity, viz. true β-diversity and absolute species turnover – both of these rely on knowledge of species richness at local (a measure of α-diversity) and regional (γ-diversity) scales. Much more insight into species assembly processes can be extracted, however, when we view β-diversity as a dissmilarity index. In this view, we will see that there are two processes by which β-diversity might be affected (i.e. in which the patterning of communities over landscapes might arise):

Process 1 If a region is comprised of the species A, B, C, …, M (i.e. γ-diversity is 13), a subset of the regional flora as captured by one quadrat might be species **A**, **D**, E, whereas in another quadrat it might be species **A**, **D**, F. In this instance, the α-diversity is 3 in both instances, and heterogeneity (and hence β-diversity) results from the fact that the first quadrat has species E but the other has species F. In other words, here we have the same number of species in both quadrats, but only two of the species are the same. The process responsible for this form of β-diversity is species 'turnover' (β_{sim}). Turnover refers to processes that cause communities to differ due to species being lost and/or gained from section to section, i.e. the species composition changes between sections without corresponding changes in α-diversity.

Process 2 Consider again species A, B, C, …, M. Now we have the first quadrat with species **A**, **B**, C, D, **G**, H (α-diversity is 6) and the second quadrat has a subset of this, e.g. only species **A**, **B**, **G** (α-diversity 3). Here, β-diversity comes from the fact that even if the two places share the same species, the number of species can still differ amongst the quadrats (i.e. from place to place) due to one quadrat capturing only a subset of species present in the other. This form of β-diversity is called 'nestedness-resultant' β-diversity (β_{sne}), and it refers to processes that cause species to be gained or lost, and the community with the lowest α-diversity is a subset of the richer community.

The above two examples show that β-diversity is coupled not only with the identity of the species in the quadrats, but also α-diversity – with species richness in particular.

How do we calculate the turnover and nestedness-resultant components of β-diversity? The **betapart** package (Baselga et al., 2013) comes to the rescue. I decompose the dissimilarity into the β_{sim} and β_{sne} components (Baselga, 2010) using the `betapart.core()` and `betapart.pair()` functions. The outcomes of this partitioning calculation are placed into the matrices $Y1$ and $Y2$. These data can then be analysed further—e.g. I can apply a principal components analysis (PCA) or another multivariate analysis on Y to find the major patterns in the community data— but I will do this in a later section.

So what can we do with these two forms of β-diversity? What does it mean? Let's do a deeper analysis and create a figure to demonstrate these findings. I regress $\beta_{\text{sør}}$ on the spatial distance between section pairs (see below) and on the environmental distance (β_{E}) in each bioregion and used the magnitude of the slope (per 100 km) of this relationship as a metric of beta-diversity or 'distance decay' of dissimilarity. Since the connectivity between sections is constrained by their location along a shoreline, we calculated the distances between sections not as 'as the crow flies' distances (e.g. Section 1 is not connected in a straight line to Section 58 because of the intervening land in-between), but as the great circle geodesic distances between each pair of sections along a 'route'. Traveling from **1** to **58** therefore requires visiting **2**, then **3**, and eventually all the way up to **58**. The total distance between a pair of arbitrary sections is thus the cumulative sum of the great circle distances between each consecutive pair of intervening sections along the route.

```r
# Decompose total Sørensen dissimilarity into turnover and nestedness-resultant components:
Y.core <- betapart.core(spp)
Y.pair <- beta.pair(Y.core, index.family = "sor")

# Let Y1 be the turnover component (beta-sim):
Y1 <- as.matrix(Y.pair$beta.sim)
# save(Y1, file = "data/Y1.Rdata")
# load("data/Y1.Rdata")

# Let Y2 be the nestedness-resultant component (beta-sne):
Y2 <- as.matrix(Y.pair$beta.sne)
# save(Y2, file = "data/Y2.Rdata")
# load("data/Y2.Rdata")
```

4.3 Principal Components Analysis

In **vegan** a PCA is done using the `rda()` function and not supplying the constraints (*i.e.* the environment table, E, or the spatial table, S). The formal analysis will use the species data in distance-based redundancy analyses (db-RDA as per **vegan**'s `capscale()` function) by coupling them with E and S.

5 References

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Stegenga, H., Bolton, J. J., and Anderson, R. J. (1997). Seaweeds of the South African west coast. *Contributions of the Bolus Herbarium* 18, 3–637.