

SBC long term experiment trait analysis

2024-04-09

Preview of trait data:

```
head(trait_matrix)
```

	size_cm	thickness	position_to_benthos
Amphiroa beauvoisii	6	NA	upright or prostrate
Anisocladella pacifica	5	1	upright
Acrosorium ciliolatum	8	1	upright
Cryptopleura ruprechtiana	35	NA	upright
Bossiella orbigniana	8	4	upright
Calliarthron cheilosporioides	30	4	upright or prostrate

	articulated	stipe	midrib	branching	branch_shape
Amphiroa beauvoisii	y	<NA>	<NA>	<NA>	<NA>
Anisocladella pacifica	y	y	y	irregular	flattened
Acrosorium ciliolatum	y	n	n	irregular	flattened
Cryptopleura ruprechtiana	y	n	n	irregular	flattened
Bossiella orbigniana	y	n	y	irregular	flattened
Calliarthron cheilosporioides	y	n	n	pinnate	flattened

	blades	blade_category	coenocyte	attachment
Amphiroa beauvoisii	<NA>	<NA>	<NA>	<NA>
Anisocladella pacifica	leaflike	many	small	n discoid
Acrosorium ciliolatum	not leaflike	many	small	n discoid
Cryptopleura ruprechtiana	leaflike	many	small	n discoid
Bossiella orbigniana	not leaflike		none	n crustose
Calliarthron cheilosporioides	not leaflike		none	n crustose

	tissue_complexity	growth	calcification
Amphiroa beauvoisii		<NA>	<NA>
Anisocladella pacifica	pseudoparenchymatous	apical	n
Acrosorium ciliolatum	pseudoparenchymatous	apical	n
Cryptopleura ruprechtiana	pseudoparenchymatous	apical	n

Bossiella orbigniana	pseudoparenchymatous apical	y
Calliarthron cheilosporioides	pseudoparenchymatous apical	y

1. Gower dissimilarity on categorical and continuous traits

```
# creating gower dissimilarity matrix
trait_gower <- gowdis(trait_matrix)

# doing PCoA to get dimensions
trait_pcoa <- wcmdscale(d = trait_gower)

# just as a preview of the data
head(trait_pcoa)
```

	[,1]	[,2]	[,3]	[,4]
Amphiroa beauvoisii	-0.28275216	-0.26690479	0.003760472	0.21332256
Anisocladella pacifica	0.11639226	-0.28068909	0.028948850	-0.09941155
Acrosorium ciliolatum	-0.11379917	-0.12045930	-0.027511020	-0.08535320
Cryptopleura ruprechtiana	0.01081923	-0.16448543	-0.004747373	-0.07068760
Bossiella orbigniana	-0.28964673	-0.12713032	-0.080920019	-0.09163720
Calliarthron cheilosporioides	-0.30949915	-0.06472134	-0.197665699	0.07504598
	[,5]	[,6]	[,7]	
Amphiroa beauvoisii	-0.14572713	-0.1167242645	0.002048693	
Anisocladella pacifica	0.04379244	-0.0502039348	0.144508281	
Acrosorium ciliolatum	0.11299644	-0.0510114822	0.099897992	
Cryptopleura ruprechtiana	0.07381900	-0.0210256041	0.016038521	
Bossiella orbigniana	0.04943017	0.0008018006	0.025230975	
Calliarthron cheilosporioides	-0.04028799	0.0890891232	-0.077979394	
	[,8]	[,9]	[,10]	[,11]
Amphiroa beauvoisii	-0.07409646	-0.02878216	0.11611864	-0.10959305
Anisocladella pacifica	0.07728741	0.01615466	0.05315742	-0.06970876
Acrosorium ciliolatum	-0.04577692	0.03063915	0.01970792	0.08441170
Cryptopleura ruprechtiana	-0.03241060	0.01302801	0.02265702	0.03782363
Bossiella orbigniana	0.25790795	-0.01788080	-0.05599255	-0.06816622
Calliarthron cheilosporioides	0.04550333	-0.07484873	0.02867340	-0.02538714
	[,12]	[,13]	[,14]	
Amphiroa beauvoisii	0.001738049	-0.008814125	-0.021958745	
Anisocladella pacifica	-0.044992859	-0.060025324	-0.004235294	
Acrosorium ciliolatum	0.019480966	-0.082904277	0.001295995	
Cryptopleura ruprechtiana	0.031398471	0.006920731	-0.016650440	

Bossiella orbigniana	0.008551530	0.009040242	0.012004969
Calliarthron cheilosporioides	0.063702121	-0.012153117	0.040984948
	[,15]	[,16]	[,17]
Amphiroa beauvoisii	0.004382337	-0.0049661626	0.0005356715
Anisocladella pacifica	0.041565795	-0.0039633146	-0.0008563053
Acrosorium ciliolatum	0.038939857	-0.0055743480	0.0013679796
Cryptopleura ruprechtiana	-0.019944458	0.0172623391	-0.0033892310
Bossiella orbigniana	-0.015808450	-0.0118080908	-0.0004343998
Calliarthron cheilosporioides	0.009205501	-0.0003732535	-0.0113850588

```
# extracting scores
trait_pcoa_scores <- scores(trait_pcoa, choices = c(1, 2)) %>%
  as_tibble(rownames = NA) %>%
  rownames_to_column("scientific_name") %>%
  left_join(., algae_taxa, by = "scientific_name")

head(trait_pcoa_scores)
```

```
# A tibble: 6 x 8
  scientific_name      Dim1    Dim2 taxon_phylum taxon_class taxon_order
  <chr>              <dbl>   <dbl> <chr>          <chr>        <chr>
1 Amphiroa beauvoisii -0.283 -0.267 Rhodophyta     Florideoph~ Corallinal~
2 Anisocladella pacifica 0.116 -0.281 Rhodophyta     Florideoph~ Ceramiales
3 Acrosorium ciliolatum -0.114 -0.120 Rhodophyta     Florideoph~ Ceramiales
4 Cryptopleura ruprechtiana 0.0108 -0.164 Rhodophyta     Florideoph~ Ceramiales
5 Bossiella orbigniana -0.290 -0.127 Rhodophyta     Florideoph~ Corallinal~
6 Calliarthron cheilospori~ -0.309 -0.0647 Rhodophyta     Florideoph~ Corallinal~
# i 2 more variables: taxon_family <chr>, taxon_genus <chr>
```

2. Creating site by trait data

```
# creating species x trait data
spp_trait_data <- scores(trait_pcoa, choices = c(1, 2)) %>%
  as_tibble(rownames = NA) %>%
  # mutate(Dim1_new = Dim1 + 1,
  #        Dim2_new = Dim2 + 2) %>%
  # select(scientific_name, Dim1_new, Dim2_new) %>%
  # column_to_rownames("scientific_name") %>%
  as.matrix()
```

```
# monitoring data
comm_mat_algae_matrix <- comm_mat_algae %>%
  # putting the columns in the right order
  select(rownames(spp_trait_data)) %>%
  as.matrix()

# double checking that species are in the right order
# rownames(spp_trait_data) == colnames(comm_mat_algae_matrix)

# site x trait data
site_by_trait <- comm_mat_algae_matrix %*% spp_trait_data

head(site_by_trait)
```

	Dim1	Dim2
aque_continual_2010-07-22	22.917541	4.3318943
aque_continual_2010-10-13	7.519388	-3.0453523
aque_control_2010-07-22	23.446835	-0.5134383
aque_control_2010-10-13	22.823826	0.9096553
aque_continual_2011-01-11	2.811067	-2.7082835
aque_continual_2011-04-13	11.695224	-4.3894985

3. Doing NMDS

```
site_trait_nmnds <- metaMDS(comm = site_by_trait, distance = "gower")
```

'comm' has negative data: 'autotransform', 'noshare' and 'wascores' set to FALSE

```
Run 0 stress 0.01494331
Run 1 stress 0.0003993074
... New best solution
... Procrustes: rmse 0.02352697 max resid 0.2428537
Run 2 stress 0.00942237
Run 3 stress 0.001548849
Run 4 stress 0.007132751
Run 5 stress 0.006270073
Run 6 stress 0.003005712
Run 7 stress 0.005257521
```

```

Run 8 stress 0.01071588
Run 9 stress 0.005093949
Run 10 stress 0.001195935
Run 11 stress 0.00464888
Run 12 stress 0.001581629
Run 13 stress 0.004171129
Run 14 stress 0.009964542
Run 15 stress 0.001165374
Run 16 stress 0.009016671
Run 17 stress 0.005345855
Run 18 stress 0.005144234
Run 19 stress 0.008871419
Run 20 stress 0.004456321
*** Best solution was not repeated -- monoMDS stopping criteria:
    19: no. of iterations >= maxit
    1: scale factor of the gradient < sfgrmin

```

Warning in metaMDS(comm = site_by_trait, distance = "gower"): stress is (nearly) zero: you may have insufficient data

```
site_trait_nmds
```

```

Call:
metaMDS(comm = site_by_trait, distance = "gower")

```

global Multidimensional Scaling using monoMDS

```

Data:      site_by_trait
Distance:  gower

```

```

Dimensions: 2
Stress:      0.0003993074
Stress type 1, weak ties
Best solution was not repeated after 20 tries
The best solution was from try 1 (random start)
Scaling: centring, PC rotation
Species: scores missing

```

```

site_trait_scores <- scores(site_trait_nmds, choices = c(1, 2), display = "sites") %>%
  as_tibble(rownames = NA) %>%

```

```

rownames_to_column("sample_ID") %>%
left_join(., comm_meta_algae, by = "sample_ID") %>%
# taking out weird points for now
filter(!(sample_ID %in% c("napl_control_2023-05-18", "mohk_continual_2012-11-15")))

ggplot(site_trait_scores,
       aes(x = NMDS1, y = NMDS2)) +
  geom_point(aes(color = treatment))

```

