UNCONSTRAINED ORDINATION: NON-METRIC MULTIDIMENSIONAL SCALING

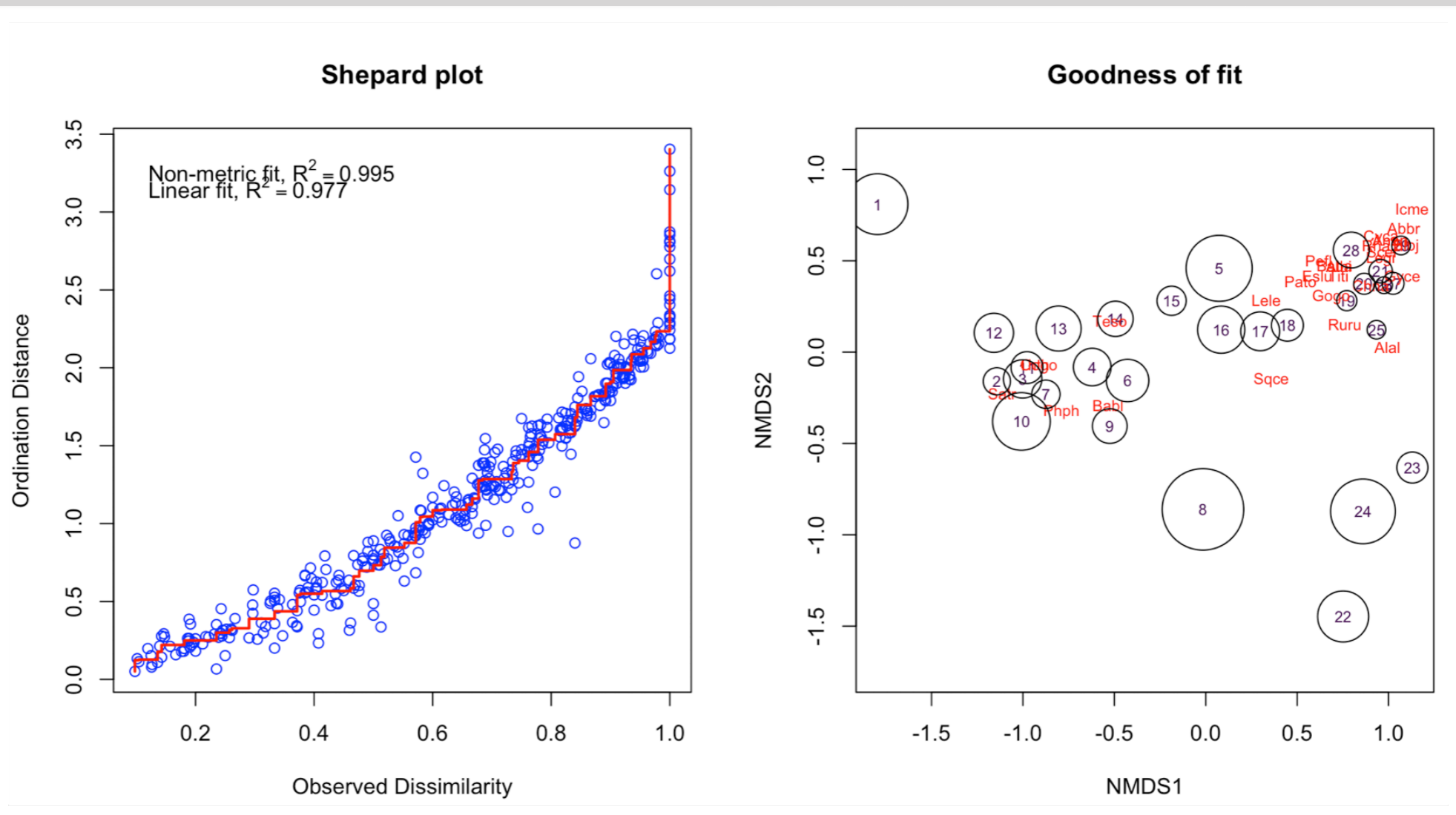# Non-Metric Multidimensional Scaling (nMDS)

- see https://sites.google.com/site/mb3gustame/dissimilarity-based-methods/nmds and https://www.davidzeleny.net/anadat-r/doku.php/en:pcoa_nmds
- like PCoA, nMDS can **produce ordinations of objects from any distance or dissimilarity matrix**
- does not preserve the exact distances among objects in an ordination plot
  - represent as well as possible **the ordering (rank) relationships among objects** in a small and specified number of axes
- non-linear mapping of dissimilarities onto a low-dimensional ordination
  - i.e. Euclidean distances of points in the ordination space are rank-order similar to community dissimilarities
    - the ordination space is metric, but the regression is non-metric
- rank orders of dissimilarities cannot be exactly preserved by rank-orders of ordination distances in low-dimensional space, and this causes stress
- stress: scatter of observed dissimilarities against expected monotone regression
- due to rank-ordering, it is a robust method if data are not well represented by a specific distribution and can use use quantitative, semi-quantitative, qualitative, or mixed variables

Non-Metric Multidimensional Scaling (NMDS)

```r
spe.nmds <- metaMDS(spe, distance = "bray")
spe.nmds
spe.nmds$stress
# dev.new(title="NMDS on fish species - Percentage difference")
plot(spe.nmds, type = "t", main = paste("NMDS/Percentage difference - Stress =", round(spe
.nmds$stress,3)))
```

```r
# Shepard plot and goodness of fit
# dev.new(title="NMDS - Shepard plot", width=12, height=6)
par(mfrow = c(1, 2))
stressplot(spe.nmds, main = "Shepard plot")
gof <- goodness(spe.nmds)
plot(spe.nmds, type = "t", main = "Goodness of fit")
points(spe.nmds, display = "sites", cex = gof * 300)
```

non-Metric Multidimensional Scaling (nMDS)

- nMDS can be subjected to environmental interpretation after analysis, using the **vegan** functions, `envfit()` and/or `ordisurf()`
- note that this is not a formal constrained ordination, which is something we shall see in the next section
- or use PERMANOVA to test differences that might be due to group effects

Questions (for yourself):

1. produce the code to run this analysis on the seaweed species data
2. how does the interpretation compare to that in the CA and PCoA?
3. produce a multivariate analysis of the seaweed environmental data, and use this to explain the patterns observed in the species data (re-use your earlier results if you have done this before)

Re-cap and assessment

Questions:

1. using two unconstrained ordination techniques of your choice, analyse the **mite data** in the {vegan} package; provide a brief description and discussion of what you have found, and produce the R code

2. using two unconstrained ordination techniques of your choice (not already used in 1), above, analyse the **dune data** in the {vegan} package; provide a brief description and discussion of what you have found, and produce the R code

Non-Metric Multidimensional Scaling (NMDS)

```
# Before doing the PERMANOVA, first check to see if the dispersion is the same
# Homogeneity of groups
# betadisper studies the differences in group homogeneities
# analogous to Levene's test of the equality of variances;
# the null hypothesis that the population variances are equal;
# can only use one factor as an independent variable
# par(mfrow = c(2, 2))
(mod.spp <- with(env, betadisper(spp.log.dis, host_spp)))
# plot(mod.spp, sub = NULL)
# boxplot(mod.spp)
anova(mod.spp)
permutest(mod.spp)

(mod.size <- with(env, betadisper(spp.log.dis, host_size)))
# plot(mod.size)
# boxplot(mod.size)
anova(mod.size)
permutest(mod.size)
```

```
spp.nmds <- metaMDS(spp.log, k = 2, trymax = 100,
                    distance = "bray", wascores = TRUE)
```