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# Ordination analysis

## PCoA & NMDS (distance-based unconstrained ordination)

Theory R functions **Examples** Exercise 

### Example 1 - PCoA on the matrix of distances between European cities

We use data from the variable `eurodist`, which is available in R (you don't need to install any library, just type `euro dist`). This distance matrix contains real geographical distances among big European cities (driving distance, in km). We will use this matrix to calculate PCoA and draw the PCoA ordination diagram, and also a screeplot of eigenvalues for individual PCoA axes.

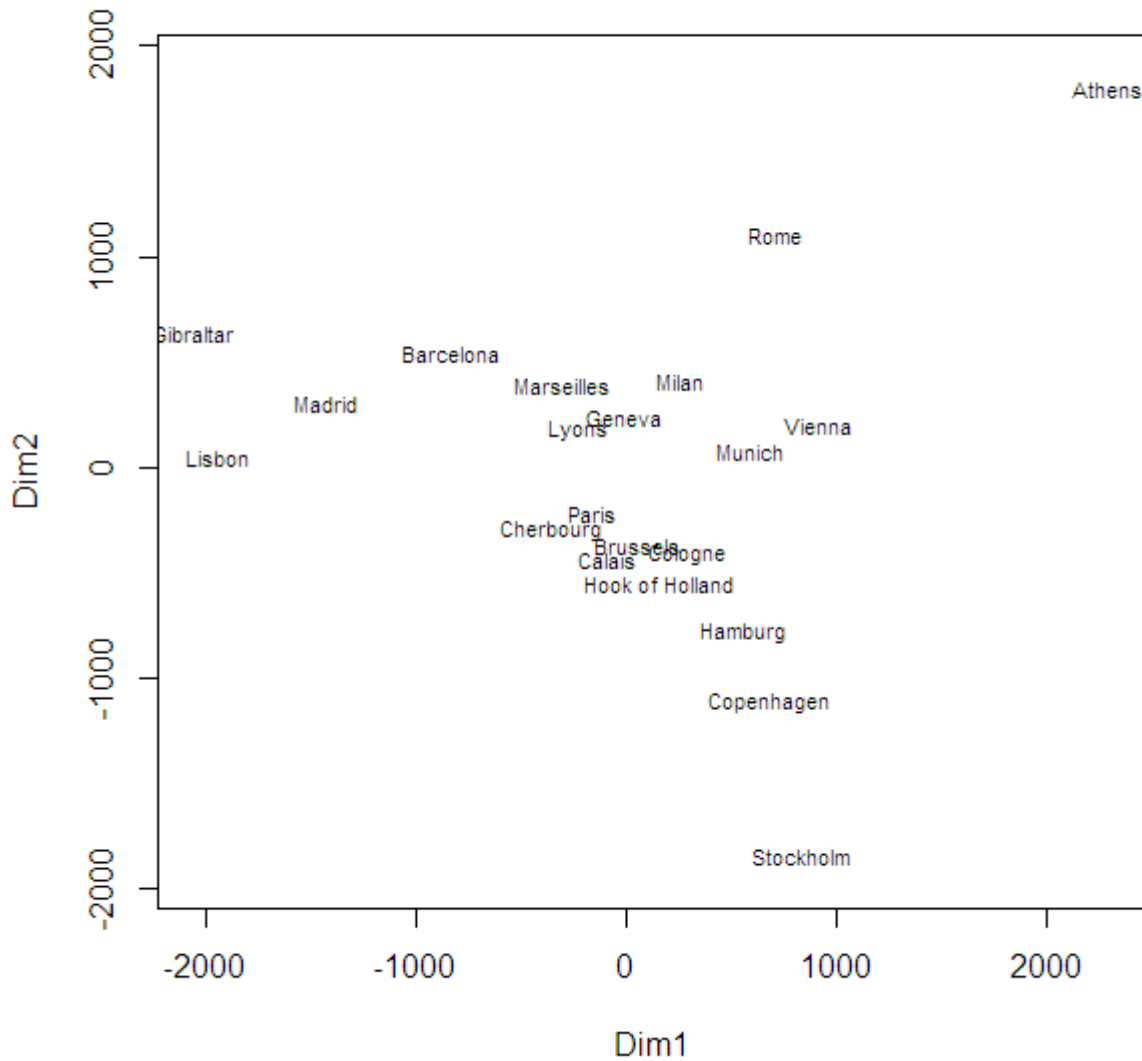
To calculate PCoA, use the base R function `cmdscale` (note that `vegan` contains the function `wcmdscale`, which in default setting is doing the same):

```
pcoa <- cmdscale (eurodist, eig = TRUE)
```

Note that I set up the argument `eig = TRUE` - in this way, the `cmdscale` function returns also the eigenvalues for individual axes (in the default setting this argument is set to `FALSE` and the function returns only the data frame of sample scores on individual PCoA axes).

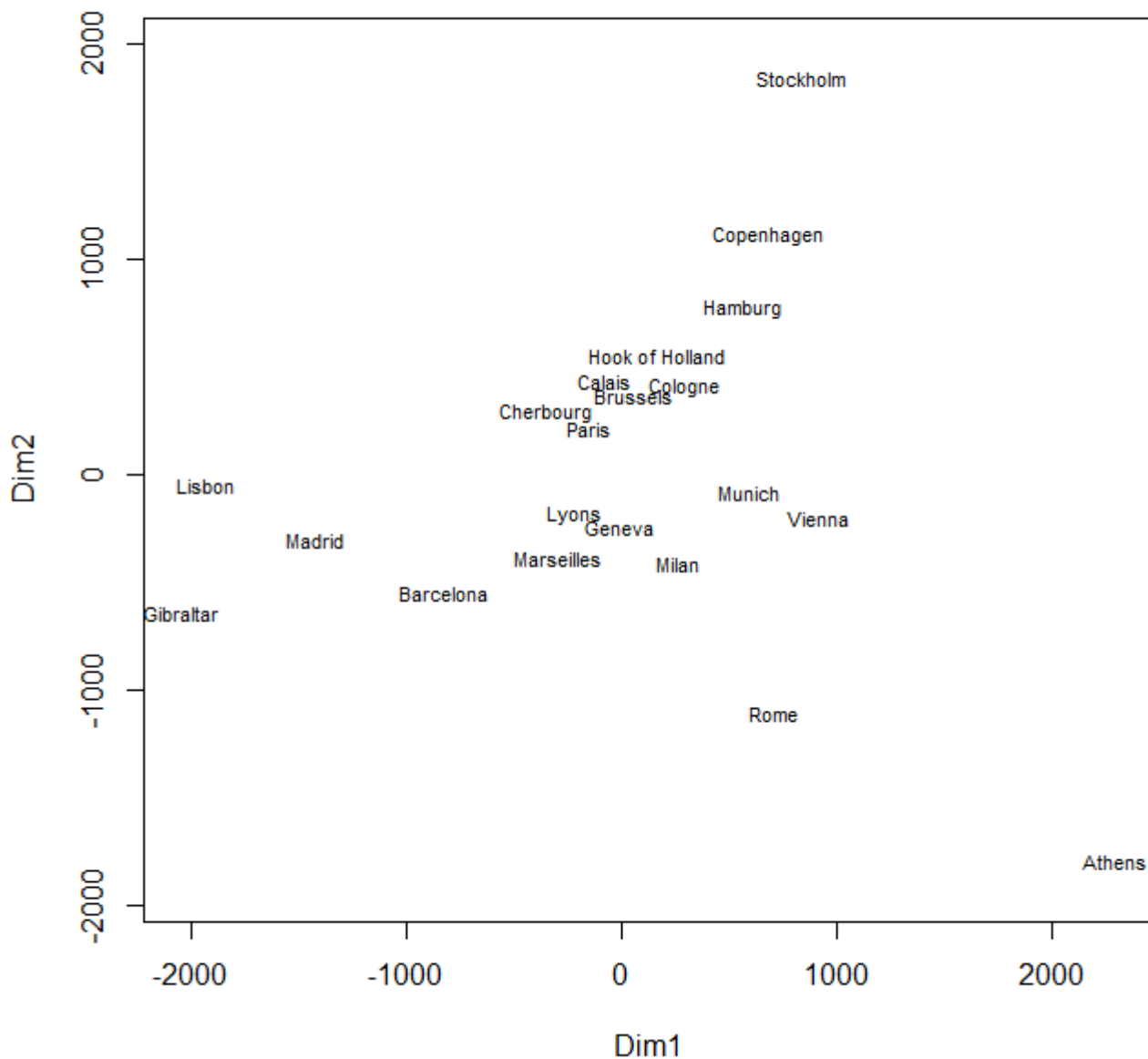
Now we can draw the ordination diagram of the cities:

```
library (vegan)  
ordiplot (pcoa, display = 'sites', type = 'text')
```



You can see that the distances between cities make intuitive sense (Athens are far from Stockholm, for example), and it almost looks like the map of Europe, except that Athens are at north and Stockholm at south. Let's flip the y-axis (the second axis of PCoA) and draw the ordination diagram again. The sample scores in PCoA ordination are in the object `pcoa`, in the component `points`<sup>1)</sup> (use `str(pcoa)` if you wish to see the structure of `pcoa` object).

```
pcoa[,2] <- -pcoa[,2]
ordiplot(pcoa, display = 'sites', type = 't')
```

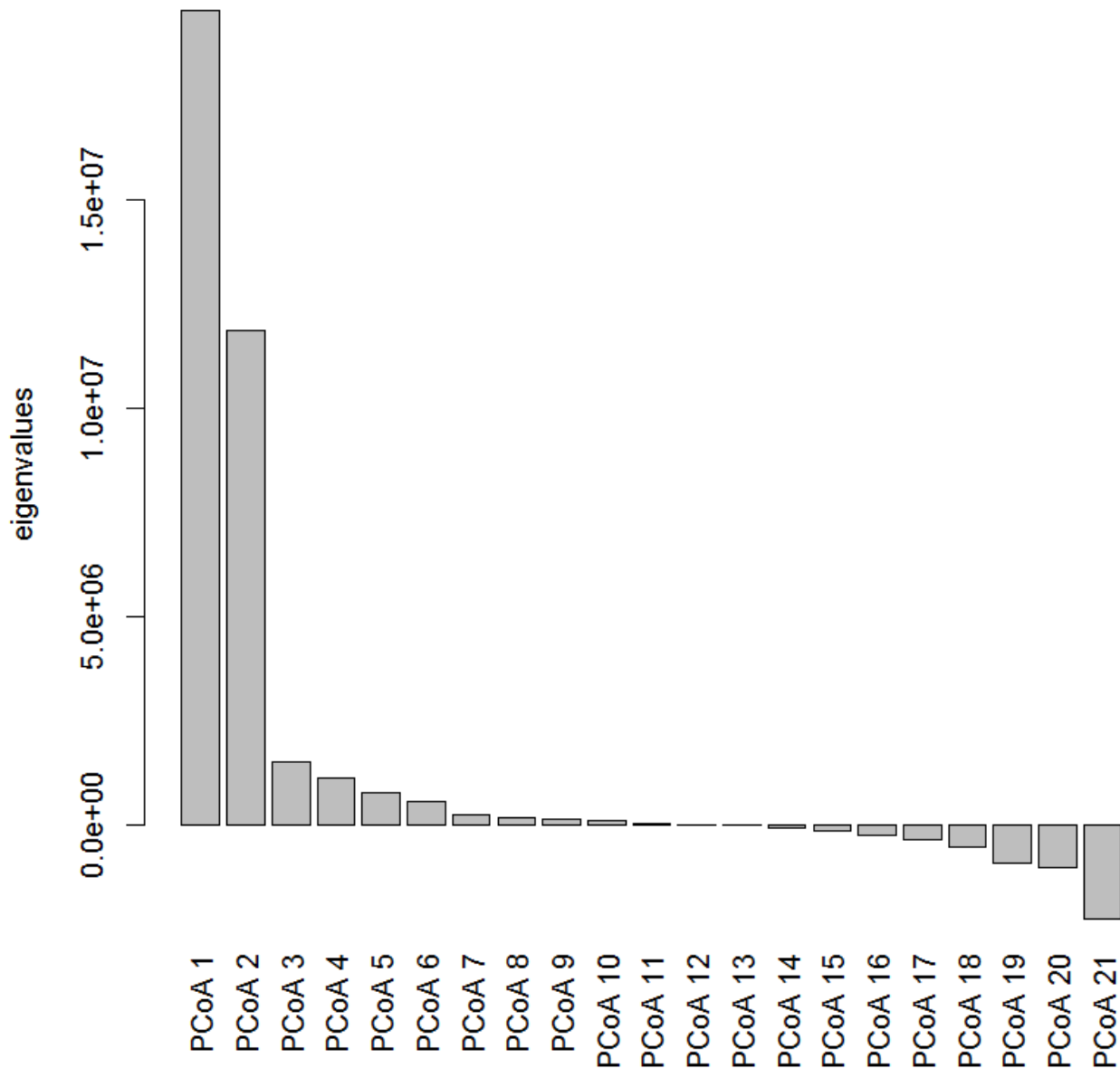


Now the distribution of cities make better geographical sense!

Finally, let's draw the screeplot with eigenvalues for individual axes; these eigenvalues are stored in the component `$eig` of the object `pcoa`:

```
barplot(pcoa$eig, names = paste('PCoA', 1:21), las = 3, ylab = 'eigenvalues')
```

Note that `names` argument adds the names to tickmarks on horizontal axis, `las` argument influences rotation of labels on both x and y axis (see `?par` for explanation) and `ylab` adds the label to the



## Example 2: NMDS on the Morse code confusion matrix

Use data about confusion of different Morse codes, originating from [Rothkopf's experiment with Morse codes](#). This is a classical data set, used by Shepard (1962)<sup>2)</sup> to demonstrate the use of NMDS analysis.

```
library (vegan)
morse.dist <- read.delim
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/data/morseco
des-dist.txt', row.names = 1, head = T)
names (morse.dist) <- rownames (morse.dist)
NMDS <- metaMDS (morse.dist)
NMDS
```

The stress values are in the following output:

```
Call:
metaMDS(comm = morse.dist)

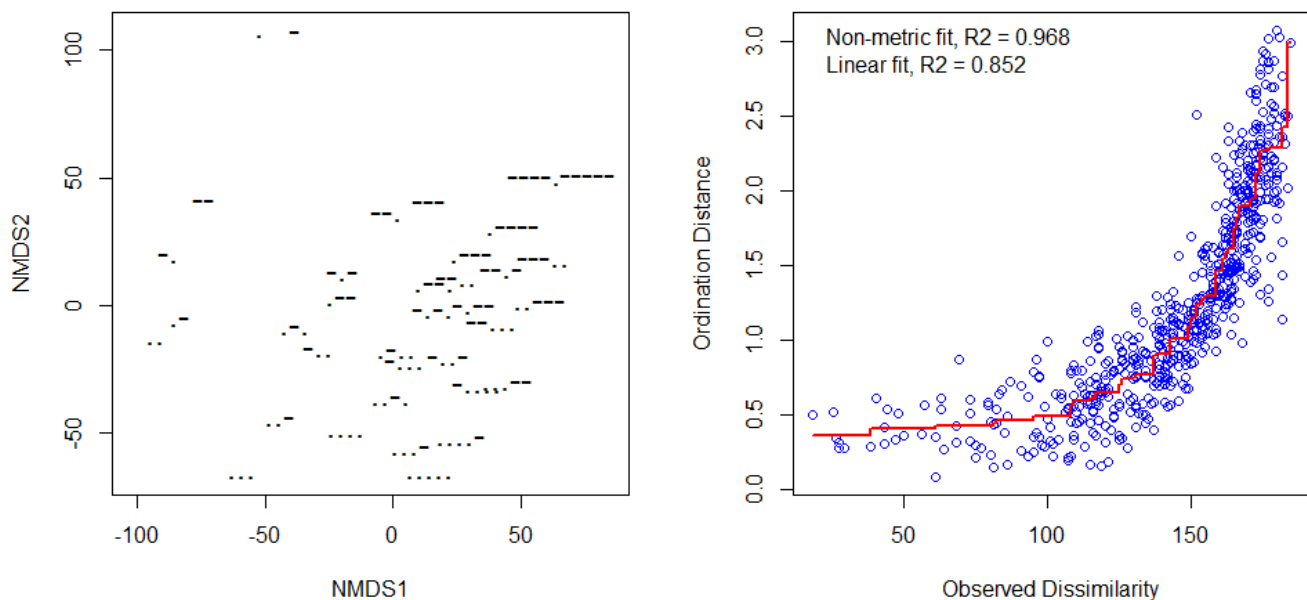
global Multidimensional Scaling using monoMDS

Data:      morse.dist
Distance:  user supplied

Dimensions: 2
Stress:    0.1800255
Stress type 1, weak ties
Two convergent solutions found after 1 tries
Scaling:   centring, PC rotation
Species:   scores missing
```

The ordination diagram and Shepard diagram could be drawn in the following way:

```
par (mfrow = c(1,2))
ordiplot (NMDS, cex = 1.5, type = 't')
stressplot (NMDS)
```



From left to right there is a gradient of increasing code length, from bottom up increases the proportion of long beeps within the code.

### Example 3: NMDS of river valley dataset

```
vltava.spe <- read.delim
('https://raw.githubusercontent.com/zdevalveindy/anadat-r/master/data/vltava-
spe.txt', row.names = 1)
```

```
NMDS <- metaMDS (vltava.spe)
```

```
Square root transformation  
Wisconsin double standardization  
Run 0 stress 0.2022791  
Run 1 stress 0.2193042  
Run 2 stress 0.2130607  
Run 3 stress 0.208742  
Run 4 stress 0.2022791  
... procrustes: rmse 9.278716e-06 max resid 3.31574e-05  
*** Solution reached
```

```
NMDS
```

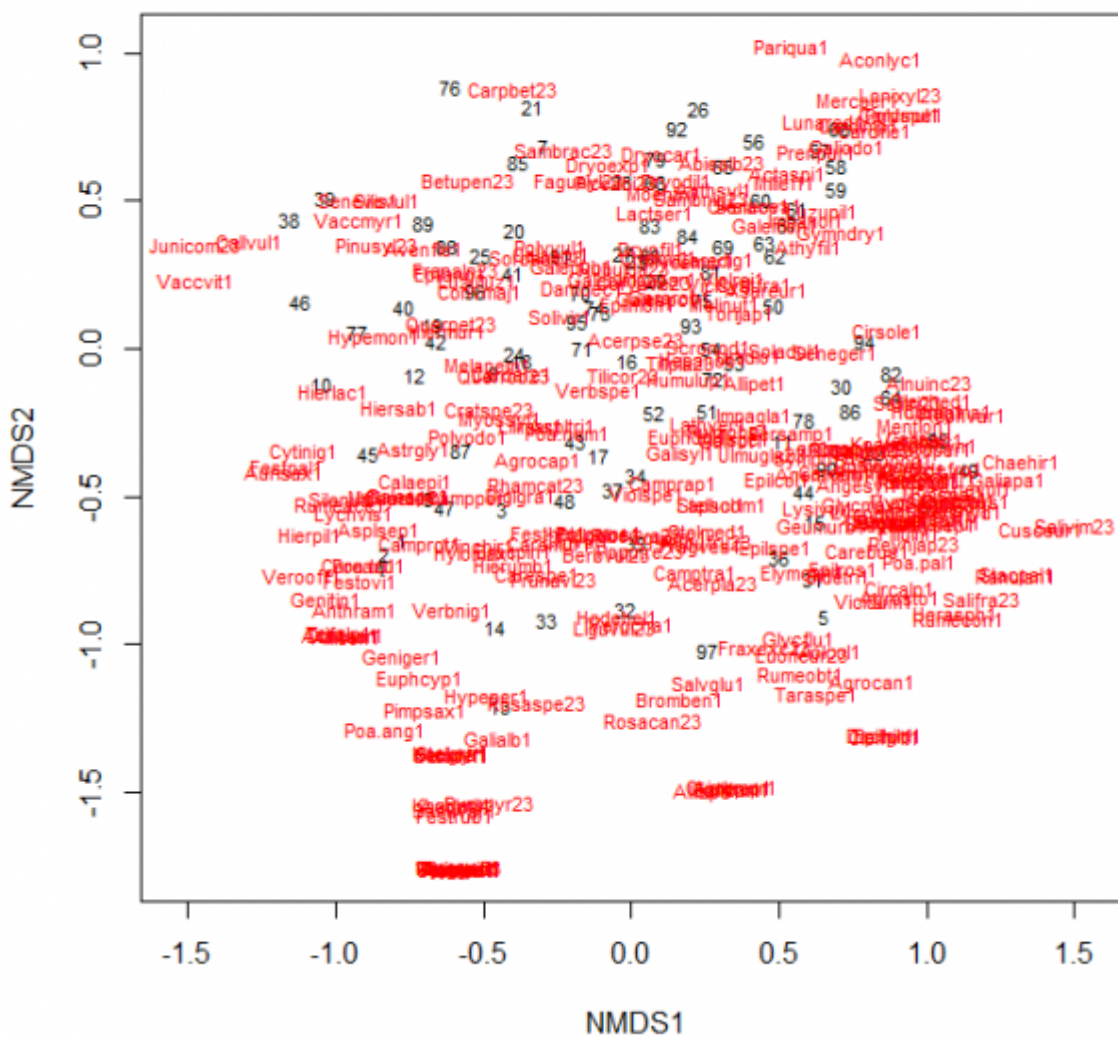
```
Call:  
metaMDS(comm = vltava.spe)  
  
global Multidimensional Scaling using monoMDS  
  
Data: wisconsin(sqrt(vltava.spe))  
Distance: bray  
  
Dimensions: 2  
Stress: 0.2022791  
Stress type 1, weak ties  
Two convergent solutions found after 4 tries  
Scaling: centring, PC rotation, halfchange scaling  
Species: expanded scores based on 'wisconsin(sqrt(vltava.spe))'
```

If the default setting of metaMDS function is used, the data are automatically (if necessary) transformed (in this case, combination of wisconsin and sqrt transformation was used). In this case, stress value is 20.2.

To draw the result, use the function ordiplot. In this case, using type = 't' will add text labels (default setting adds only points):

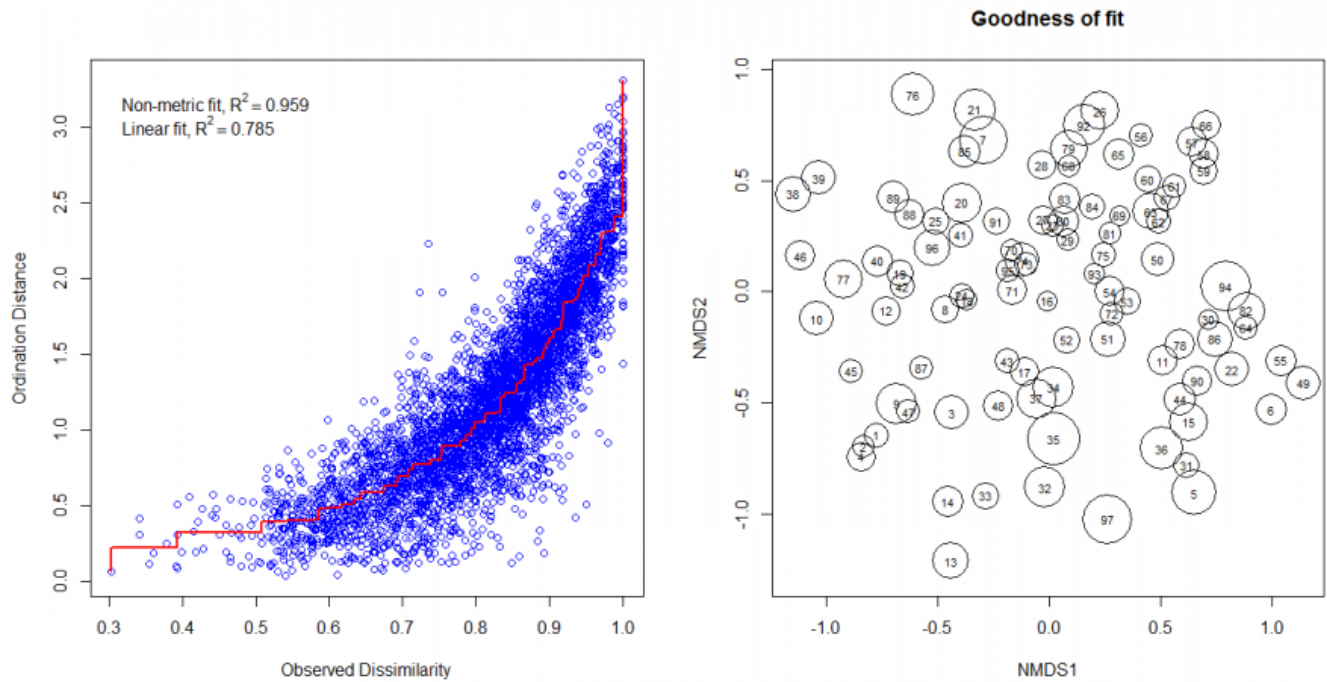
```
ordiplot (NMDS, type = 't')
```





```

par (mfrow = c(1,2)) # this function divides plotting window into two
columns
stressplot (NMDS)
plot (NMDS, display = 'sites', type = 't', main = 'Goodness of fit') # this
function draws NMDS ordination diagram with sites
points (NMDS, display = 'sites', cex = goodness (NMDS)*200) # and this adds
the points with size reflecting goodness of fit (bigger = worse fit)
    
```



1)

If we have calculated `cmdscale` with `eig = FALSE`, the structure of `pcoa` object would be simpler, it would be just a data frame with sample scores; with `eig = TRUE` the object became a list with the score data frame nested inside within the component `$points`.

2)

Shepard, R. N. (1962): The Analysis of Proximities: Multidimensional Scaling with an Unknown Distance Function, I and II. *Psychometrika*, 27: 125-139 and 219-246.

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