

## 2D varianta

```
simul.short.spe <- read.delim
('http://www.davidzeleny.net/anadat-r/data-download/simul.short.spe.txt',
row.names = 1)

simul.long.spe <- read.delim
('http://www.davidzeleny.net/anadat-r/data-download/simul.long.spe.txt',
row.names = 1)

simul.table <- simul.short.spe # choose which data to use, if
simul.short.spe or simul.long.spe
# simul.table <- simul.long.spe

library (vegan)

par (mfrow = c (2,2))

dca <- decorana (simul.table)
plot (dca$rproj, main = 'DCA')
for (i in seq (1, 70, by = 10)) lines (dca$rproj[i:(i+9), 1:2])
for (j in 0:9) lines (dca$rproj[seq (1, 70, by = 10)+j, 1:2])

nmds <- metaMDS (vegdist (simul.table))
plot (nmds$points, main = 'NMDS')
for (i in seq (1, 70, by = 10)) lines (nmds$points[i:(i+9),])
for (j in 0:9) lines (nmds$points[seq (1, 70, by = 10)+j,])

pca <- rda (simul.table)
plot (pca$CA$u[, 1:2], main = 'PCA')
for (i in seq (1, 70, by = 10)) lines (pca$CA$u[i:(i+9),1:2])
for (j in 0:9) lines (pca$CA$u[seq (1, 70, by = 10)+j,1:2])

ca <- cca (simul.table)
plot (ca$CA$u[, 1:2], main = 'CA')
for (i in seq (1, 70, by = 10)) lines (ca$CA$u[i:(i+9),1:2])
for (j in 0:9) lines (ca$CA$u[seq (1, 70, by = 10)+j,1:2])
```

## 3D varianta

```
simul.short.spe <- read.delim
('http://www.davidzeleny.net/anadat-r/data-download/simul.short.spe.txt',
row.names = 1)

simul.long.spe <- read.delim
('http://www.davidzeleny.net/anadat-r/data-download/simul.long.spe.txt',
row.names = 1)

simul.table <- simul.short.spe # choose which data to use, if
```

```
simul.short.spe or simul.long.spe
# simul.table <- simul.long.spe

library (vegan)

dca <- decorana (simul.table)
nmds <- metaMDS (vegdist (simul.table), trymax = 0, k = 3)
pca <- rda (simul.table)
ca <- cca (simul.table)

ordirgl (dca, col = 'black')
rgl.bg (color = 'white')
sites <- scores (dca, choices = c (1:3))
for (i in seq (1, 60)[seq (-10, -60, by = -10)]) rgl.quads (sites[c(i, i+1,
i+11, i+10),1], sites[c(i, i+1, i+11, i+10),2], sites[c(i, i+1, i+11,
i+10),3], col = 'blue', alpha = 0.5)

ordirgl (nmds)
rgl.bg (color = 'white')
sites <- scores (nmds, choices = c(1:3))
for (i in seq (1, 60)[seq (-10, -60, by = -10)]) rgl.quads (sites[c(i, i+1,
i+11, i+10),1], sites[c(i, i+1, i+11, i+10),2], sites[c(i, i+1, i+11,
i+10),3], col = 'blue', alpha = 0.5)

ordirgl (pca)
rgl.bg (color = 'white')
sites <- scores (pca, choices = c(1:3))$sites
for (i in seq (1, 60)[seq (-10, -60, by = -10)]) rgl.quads (sites[c(i, i+1,
i+11, i+10),1], sites[c(i, i+1, i+11, i+10),2], sites[c(i, i+1, i+11,
i+10),3], col = 'blue', alpha = 0.5)

ordirgl (ca)
rgl.bg (color = 'white')
sites <- scores (ca, choices = c (1:3))$sites
for (i in seq (1, 60)[seq (-10, -60, by = -10)]) rgl.quads (sites[c(i, i+1,
i+11, i+10),1], sites[c(i, i+1, i+11, i+10),2], sites[c(i, i+1, i+11,
i+10),3], col = 'blue', alpha = 0.5)
```

From:

<https://www.davidzeleny.net/anadat-r/> - **Analysis of community ecology data in R**

Permanent link:

[https://www.davidzeleny.net/anadat-r/doku.php/cs:mix:ordination\\_artefacts:solution](https://www.davidzeleny.net/anadat-r/doku.php/cs:mix:ordination_artefacts:solution)

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