Numerical Ecology with R: Custom R functions

Second edition (Borcard et al. 2018)

The source of the scripts below can be found here: http://adn.biol.umontreal.ca/~numericalecology/numecolR/. The link to GitHub repository of all NumEcolR functions: https://github.com/zdealveindy/anadat-r/tree/master/scripts/NumEcolR2

In the list below, find the name of the function, and use the `source` command to download it into your R.

```
# CA.newr
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR2/C
A.newr.R')

# PCA.newr
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR2/P
CA.newr.R')

# Rao
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR2/R
ao.R')

# bartlett.perm
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR2/b
artlett.perm.R')

# boxplerk
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR2/b
oxplerk.R')

# boxplert
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR2/b
oxplert.R')

# cleanplot.pca
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR2/c
leanplot.pca.R')

# coldiss
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR2/c
oldiss.R')

# drawmap
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR2/d
```

```
rawmap.R')

# drawmap3
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR2/d
rawmap3.R')

# hcoplot
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR2/h
coplot.R')

# panelutils
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR2/p
anelutils.R')

# plot.lda
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR2/p
lot.lda.R')

# plot.links
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR2/p
lot.links.R')

# polyvars
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR2/p
olyvars.R')

# quickMEM
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR2/q
uickMEM.R')

# scalog
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR2/s
calog.R')

# screestick
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR2/s
creestick.R')

# sr.value
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR2/s
r.value.R')

# triplot.rda
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR2/t
riplot.rda.R')
```

First edition (Borcard et al. 2011)

The source of the scripts can be downloaded from here: http://adn.biol.umontreal.ca/~numericalecology/numecolR/NEwR_1st_edition_R332.zip. The link to GitHub repository of all NumEcolR functions: https://github.com/zdealveindy/anadat-r/tree/master/scripts/NumEcolR1.

In the list below, find the name of the function, and use the `source` command to download it into your R.

```
# CA
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR1/C
A.R')

# PCA
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR1/P
CA.R')

# cleanplot.pca
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR1/c
leanplot.pca.R')

# coldiss
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR1/c
oldiss.R')

# create.MEM.model
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR1/c
reate.MEM.model.R')

# evplot
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR1/e
vplot.R')

# grpdist
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR1/g
rpdist.R')

# hcoplot
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR1/h
coplot.R')

# panelutils
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR1/p
anelutils.R')

# pcacircle
source
```

```
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR1/pcacircle.R')

# plot.distmat.links
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR1/plot.distmat.links.R')

# plot.links
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR1/plot.links.R')

# sr.value
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR1/sr.value.R')

# test.a
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR1/test.a.R')
```

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

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https://anadat-r.davidzeleny.net/doku.php/en:numecolr

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