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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/~numericecology/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/CA.newr.R')

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

# screestick
```

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

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

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

First edition (Borcard et al. 2011)

The source of the scripts can be downloaded from here:

http://adn.biol.umontreal.ca/~numeralecology/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/CA.R')

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

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

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

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

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

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

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

# panelutils
source
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/scripts/NumEcolR1/panelutils.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://davidzeleny.net/anadat-r/> - **Analysis of community ecology data in R**

Permanent link:

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

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