

Real_data_comparison.r

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```
rm(list=ls(all=TRUE)) # remove all existing items from the workspace

source("Rfunctions/rXY_permutation.r")
source("rfunctions/Test_CCA_functions.r")
#mysvd <- svd if eig1 test is needed
mysvd<- dummysvd # if no eig1 tests are needed (avoids svd)

library(ade4)
library(vegan)

nrepet = 1999
with_vegan_ade4 <- TRUE
#with_vegan_ade4 <- FALSE
Pvals <- list()

# data from ade4 -----
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data("doubts", package = "ade4")

(Pvals[[length(Pvals)+1]] <-
test_vegan_ade4_randperm_CCA_transf(doubts$fish,doubts$env, nrepet = nrepet,
with_vegan_ade4 =with_vegan_ade4 ))

##          CCA_Y CCA_Ycan3  vegan  ade4 CCA_X
## pow_1    5e-04      5e-04 5e-04 5e-04 5e-04
## pow_0.5  5e-04      5e-04 5e-04 5e-04 5e-04
## pow_0    5e-04      5e-04 5e-04 5e-04 5e-04

data("dunedata", package = "ade4" )
(Pvals[[length(Pvals)+1]] <-
test_vegan_ade4_randperm_CCA_transf(dunedata$veg,dunedata$envir, nrepet =
nrepet, with_vegan_ade4 =with_vegan_ade4 ))

##          CCA_Y CCA_Ycan3  vegan  ade4 CCA_X
## pow_1    0.0020      0.0020 0.0020 0.001 0.001
## pow_0.5  0.0015      0.0015 0.0015 0.001 0.001
## pow_0    0.0015      0.0015 0.0015 0.001 0.001

# data from vegan -----
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data("mite", "mite.env", "mite.xy", package = "vegan")
# test on effect of env on the species data
(Pvals[[length(Pvals)+1]] <-
test_vegan_ade4_randperm_CCA_transf(mite, mite.env, nrepet = nrepet,
with_vegan_ade4 = with_vegan_ade4 ))

##          CCA_Y CCA_Ycan3 vegan  ade4 CCA_X
## pow_1    5e-04      5e-04 5e-04 5e-04 5e-04
## pow_0.5  5e-04      5e-04 5e-04 5e-04 5e-04
## pow_0    5e-04      5e-04 5e-04 5e-04 5e-04

names(mite.xy)[2] <- "yy" # y-> yy to avoid name conflict in
ade4::randtest(cca1,...)
# test on geographic trend in the species data
(Pvals[[length(Pvals)+1]] <-
test_vegan_ade4_randperm_CCA_transf(mite, mite.xy, nrepet = nrepet,
with_vegan_ade4 = with_vegan_ade4 ))

##          CCA_Y CCA_Ycan3 vegan  ade4 CCA_X
## pow_1    5e-04      5e-04 5e-04 5e-04 5e-04
## pow_0.5  5e-04      5e-04 5e-04 5e-04 5e-04
## pow_0    5e-04      5e-04 5e-04 5e-04 5e-04

# effect of env conditional on linear geography
(Pvals[[length(Pvals)+1]] <-
test_vegan_ade4_randperm_CCA_transf(mite, mite.env, Zdf = mite.xy, nrepet =
nrepet, with_vegan_ade4 = with_vegan_ade4 ))

##          CCA_Y CCA_Ycan3 vegan  ade4 CCA_X
## pow_1    5e-04      5e-04 5e-04   NA 5e-04
## pow_0.5  5e-04      5e-04 5e-04   NA 5e-04
## pow_0    5e-04      5e-04 5e-04   NA 5e-04

data("BCI", package = "vegan")
data("BCI.env", package = "vegan")
# set constant or near constant variables to null
BCI.env$Geology <- BCI.env$Age.cat <- BCI.env$Precipitation <-
BCI.env$Elevation <- NULL
# effect of env on the species data?
(Pvals[[length(Pvals)+1]] <-
test_vegan_ade4_randperm_CCA_transf(BCI, BCI.env[, -c(1,2)], nrepet = nrepet,
with_vegan_ade4 = with_vegan_ade4 ))

##          CCA_Y CCA_Ycan3 vegan  ade4 CCA_X
## pow_1    5e-04      5e-04 5e-04 5e-04 5e-04
## pow_0.5  5e-04      5e-04 5e-04 5e-04 5e-04
## pow_0    5e-04      5e-04 5e-04 5e-04 5e-04

# geography trend (linear) in species data?
(Pvals[[length(Pvals)+1]] <-

```

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test_vegan_ade4_randperm_CCA_transf(BCI,BCI.env[, c(1,2)], nrepet = nrepet,
with_vegan_ade4 =with_vegan_ade4 ))

##          CCA_Y CCA_Ycan3  vegan  ade4 CCA_X
## pow_1    5e-04      5e-04 5e-04 5e-04 5e-04
## pow_0.5  5e-04      5e-04 5e-04 5e-04 5e-04
## pow_0    5e-04      5e-04 5e-04 5e-04 5e-04

# effect of env conditional on linear geographic trend?
(Pvals[[length(Pvals)+1]] <-
test_vegan_ade4_randperm_CCA_transf(BCI,BCI.env[, -c(1,2)],BCI.env[, c(1,2)],
nrepet = nrepet, with_vegan_ade4 =with_vegan_ade4 ))

##          CCA_Y CCA_Ycan3  vegan  ade4 CCA_X
## pow_1    5e-04      5e-04 5e-04   NA 5e-04
## pow_0.5  5e-04      5e-04 5e-04   NA 5e-04
## pow_0    5e-04      5e-04 5e-04   NA 5e-04

data("sipoo", package = "vegan")
data("sipoo.map", package = "vegan")
names(sipoo.map)

## [1] "N"      "E"      "area"

# effect of area
(Pvals[[length(Pvals)+1]] <-
test_vegan_ade4_randperm_CCA_transf(sipoo,sipoo.map$area, nrepet = nrepet,
with_vegan_ade4 =with_vegan_ade4 ))

##          CCA_Y CCA_Ycan3  vegan  ade4 CCA_X
## pow_1    0.001      5e-04 5e-04 5e-04 5e-04
## pow_0.5  0.001      5e-04 5e-04 5e-04 5e-04
## pow_0    0.001      5e-04 5e-04 5e-04 5e-04

# geographic trend?
(Pvals[[length(Pvals)+1]] <-
test_vegan_ade4_randperm_CCA_transf(sipoo,sipoo.map[, c(1,2)], nrepet =
nrepet, with_vegan_ade4 =with_vegan_ade4 ))

##          CCA_Y CCA_Ycan3  vegan  ade4 CCA_X
## pow_1    0.148      0.121 0.121 0.5155 0.5155
## pow_0.5  0.148      0.121 0.121 0.5155 0.5155
## pow_0    0.148      0.121 0.121 0.5155 0.5155

# effect of area conditional on linear geography trend
(Pvals[[length(Pvals)+1]] <-
test_vegan_ade4_randperm_CCA_transf(sipoo,sipoo.map$area,sipoo.map[, c(1,2)],
nrepet = nrepet, with_vegan_ade4 =with_vegan_ade4 ))

##          CCA_Y CCA_Ycan3  vegan  ade4 CCA_X
## pow_1    0.002      0.002 0.002   NA 0.001

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## pow_0.5 0.002      0.002 0.002  NA 0.001
## pow_0   0.002      0.002 0.002  NA 0.001

data("varespec", package = "vegan")
data("varechem", package = "vegan")
# too many predictor variables for this small dataset?
(Pvals[[length(Pvals)+1]] <-
test_vegan_ade4_randperm_CCA_transf(varespec,varechem, nrepet = nrepet,
with_vegan_ade4 =with_vegan_ade4 ))

##          CCA_Y CCA_Ycan3  vegan  ade4  CCA_X
## pow_1    0.0320    0.0320 0.0320 0.0365 0.0365
## pow_0.5  0.0635    0.0630 0.0630 0.0785 0.0785
## pow_0    0.0720    0.0715 0.0715 0.1015 0.1015

# data from mvabund -----
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data("spider", package = "mvabund")
colnames(spider$x)

## [1] "soil.dry"      "bare.sand"      "fallen.leaves" "moss"
## [5] "herb.layer"     "reflection"

(Pvals[[length(Pvals)+1]] <-
test_vegan_ade4_randperm_CCA_transf(spider$abund,spider$x, nrepet = nrepet,
with_vegan_ade4 =with_vegan_ade4 ))

##          CCA_Y CCA_Ycan3  vegan  ade4  CCA_X
## pow_1    5e-04    5e-04 5e-04 5e-04 5e-04
## pow_0.5  5e-04    5e-04 5e-04 5e-04 5e-04
## pow_0    5e-04    5e-04 5e-04 5e-04 5e-04

data("tikus", package = "mvabund")
#View(tikus$abund)
str(tikus$x)

## 'data.frame':   60 obs. of  2 variables:
## $ time: Factor w/ 6 levels "81","83","84",...: 1 1 1 1 1 1 1 1 1 1 ...
## $ rep : Factor w/ 10 levels "1","2","3","4",...: 1 2 3 4 5 6 7 8 9 10 ...

(Pvals[[length(Pvals)+1]] <-
test_vegan_ade4_randperm_CCA_transf(tikus$abund,tikus$x, nrepet = nrepet,
with_vegan_ade4 =with_vegan_ade4 ))

##          CCA_Y CCA_Ycan3  vegan  ade4  CCA_X
## pow_1    5e-04    5e-04 5e-04 5e-04 5e-04
## pow_0.5  5e-04    5e-04 5e-04 5e-04 5e-04
## pow_0    5e-04    5e-04 5e-04 5e-04 5e-04

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(Pvals[[length(Pvals)+1]] <-
test_vegan_ade4_randperm_CCA_transf(tikus$abund,tikus$x$time, nrepet =
nrepet, with_vegan_ade4 =with_vegan_ade4 ))

##          CCA_Y CCA_Ycan3  vegan  ade4 CCA_X
## pow_1    5e-04      5e-04 5e-04 5e-04 5e-04
## pow_0.5  5e-04      5e-04 5e-04 5e-04 5e-04
## pow_0    5e-04      5e-04 5e-04 5e-04 5e-04

# location effect ignoring time
# interest?
(Pvals[[length(Pvals)+1]] <-
test_vegan_ade4_randperm_CCA_transf(tikus$abund,tikus$x$rep, nrepet = nrepet,
with_vegan_ade4 =with_vegan_ade4 ))

##          CCA_Y CCA_Ycan3  vegan  ade4 CCA_X
## pow_1    5e-04      5e-04 5e-04 0.0005 0.0005
## pow_0.5  5e-04      5e-04 5e-04 0.0010 0.0010
## pow_0    5e-04      5e-04 5e-04 0.0025 0.0025

# time given location (rep)
(Pvals[[length(Pvals)+1]] <-
test_vegan_ade4_randperm_CCA_transf(tikus$abund,tikus$x$time,Z = tikus$x$rep,
nrepet = nrepet, with_vegan_ade4 =with_vegan_ade4 ))

##          CCA_Y CCA_Ycan3  vegan  ade4 CCA_X
## pow_1    5e-04      5e-04 5e-04  NA 5e-04
## pow_0.5  5e-04      5e-04 5e-04  NA 5e-04
## pow_0    5e-04      5e-04 5e-04  NA 5e-04

# location given time (rep)
(Pvals[[length(Pvals)+1]] <-
test_vegan_ade4_randperm_CCA_transf(tikus$abund,tikus$x$rep, Z =
tikus$x$time, nrepet = nrepet, with_vegan_ade4 =with_vegan_ade4 ))

##          CCA_Y CCA_Ycan3  vegan  ade4 CCA_X
## pow_1    5e-04      5e-04 5e-04  NA 5e-04
## pow_0.5  5e-04      5e-04 5e-04  NA 5e-04
## pow_0    5e-04      5e-04 5e-04  NA 5e-04

data("antTraits", package = "mvabund")
names(antTraits)

## [1] "abund" "env" "traits"

#str(antTraits$env)
#str(antTraits$abund)
#str(antTraits$traits)
# effect of effect on the abundance
(Pvals[[length(Pvals)+1]] <-
test_vegan_ade4_randperm_CCA_transf(antTraits$abund,antTraits$env,nrepet =
nrepet, with_vegan_ade4 =with_vegan_ade4 ))

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##          CCA_Y CCA_Ycan3 vegan  ade4 CCA_X
## pow_1    5e-04      5e-04 5e-04 5e-04 5e-04
## pow_0.5  5e-04      5e-04 5e-04 5e-04 5e-04
## pow_0    5e-04      5e-04 5e-04 5e-04 5e-04

# no effect of traits on the abundance detected
(Pvals[[length(Pvals)+1]] <-
test_vegan_ade4_randperm_CCA_transf(t(antTraits$abund),antTraits$traits,nrepet
t = nrepet, with_vegan_ade4 =with_vegan_ade4 ))

##          CCA_Y CCA_Ycan3 vegan  ade4  CCA_X
## pow_1    0.4680      0.433 0.433 0.7675 0.7675
## pow_0.5  0.6940      0.662 0.662 0.2960 0.2960
## pow_0    0.6385      0.603 0.603 0.2130 0.2130

data("solberg", package = "mvabund")
names(solberg)

## [1] "abund" "x"

# almost constant site totals (98-102), very variable species totals (1-189)
# untransformed: no effect detectable; after sqrt or log: effect detectable
(Pvals[[length(Pvals)+1]] <-
test_vegan_ade4_randperm_CCA_transf(solberg$abund,solberg$x,nrepet = nrepet,
with_vegan_ade4 =with_vegan_ade4 ))

##          CCA_Y CCA_Ycan3 vegan  ade4  CCA_X
## pow_1    0.1840      0.1840 0.1840 0.1770 0.1770
## pow_0.5  0.0295      0.0285 0.0285 0.0300 0.0300
## pow_0    0.0180      0.0180 0.0180 0.0175 0.0175

data("Tasmania", package = "mvabund")
names(Tasmania)

## [1] "abund"      "copepods"  "nematodes" "treatment" "block"
## [6] "tr.block"

(Pvals[[length(Pvals)+1]] <-
test_vegan_ade4_randperm_CCA_transf(Tasmania$abund,Tasmania$treatment,Z=
Tasmania$block, nrepet = nrepet, with_vegan_ade4 =with_vegan_ade4 ))

##          CCA_Y CCA_Ycan3  vegan ade4 CCA_X
## pow_1    0.0015      0.0015 0.0015  NA 1e-03
## pow_0.5  0.0010      0.0005 0.0005  NA 5e-04
## pow_0    0.0005      0.0005 0.0005  NA 5e-04

# data from TraitEnvMLMWA -----

#install.packages("remotes")
#remotes::install_github("CajoterBraak/TraitEnvMLMWA")
data("Revisit", package = "TraitEnvMLMWA")
#str(Revisit)

```

```

#str(Revisit$y)
Y <- matrix(Revisit$y[,1], nrow = 52, ncol =75)
X <- Revisit$env[1:52]
T1 <-matrix(Revisit$trait, nrow = 52, ncol =75)[1,]
# a strong environment gradient topographic moisture gradient
(Pvals[[length(Pvals)+1]] <- test_vegan_ade4_randperm_CCA_transf(Y,X, nrepet
= nrepet, with_vegan_ade4 =with_vegan_ade4 ))

##          CCA_Y CCA_Ycan3 vegan  ade4 CCA_X
## pow_1    5e-04      5e-04 5e-04 5e-04 5e-04
## pow_0.5  5e-04      5e-04 5e-04 5e-04 5e-04
## pow_0    5e-04      5e-04 5e-04 5e-04 5e-04

# a weak trait response, stronger with sqrt and log-transformation in
predictor permutation,
# for the log perhaps helped by the trait main effect; see
https://doi.org/10.1111/2041-210X.13278
(Pvals[[length(Pvals)+1]] <- test_vegan_ade4_randperm_CCA_transf(t(Y),X= T1,
nrepet = nrepet, with_vegan_ade4 =with_vegan_ade4 ))

##          CCA_Y CCA_Ycan3 vegan  ade4 CCA_X
## pow_1    5e-04      5e-04 5e-04 0.0420 0.0420
## pow_0.5  5e-04      5e-04 5e-04 0.0085 0.0085
## pow_0    5e-04      5e-04 5e-04 0.0045 0.0045

length(Pvals)

## [1] 24

#save.image("real_data.rdata")

```