

Issue 124

2024-08-26

```
library(NetCoMi)

# Load data sets from American Gut Project (from SpiecEasi package)
data("amgut1.filt")

amgut_g1 <- amgut1.filt[1:140, ]
amgut_g2 <- amgut1.filt[141:280, ]

# Network construction:
amgut_net <- netConstruct(amgut_g1, data2 = amgut_g2,
                           measure = "pearson",
                           filtTax = "highestVar",
                           filtTaxPar = list(highestVar = 30),
                           zeroMethod = "pseudoZ0",
                           normMethod = "clr")

## Checking input arguments ... Done.
## Data filtering ...
## 102 taxa removed in each data set.
## 25 taxa and 140 samples remaining in group 1.
## 25 taxa and 140 samples remaining in group 2.
##
## Zero treatment in group 1:
## Zero counts replaced by 1
##
## Zero treatment in group 2:
## Zero counts replaced by 1
##
## Normalization in group 1:
## Execute clr(){SpiecEasi} ... Done.
##
## Normalization in group 2:
## Execute clr(){SpiecEasi} ... Done.
##
## Calculate 'pearson' associations ... Done.
##
## Calculate associations in group 2 ... Done.
##
## Sparsify associations via 't-test' ...
## Adjust for multiple testing via 'adaptBH' ... Done.
## Done.
##
## Sparsify associations in group 2 ...
## Adjust for multiple testing via 'adaptBH' ... Done.
## Done.
```

```

cor1 <- amgut_net$assoMat1
cor2 <- amgut_net$assoMat2

# construct networks
net.construct = netConstruct(data = as.matrix(cor1),
                             data2 = as.matrix(cor2),
                             dataType = "correlation",
                             sparsMethod = "none",
                             seed = 1234)

## Checking input arguments ... Done.
# identify differentially associated taxa
diff.res = diffnet(x=net.construct, diffMethod="fisherTest",
                    adjust = "none", n1 = 140, n2 = 140)

## Checking input arguments ...
## Done.

plot(diff.res, mar = c(2, 2, 4, 10))

```

