

QUICK REFERENCE

matR: metagenomics analysis tools for R (v0.9.9)

install & load

```
install.packages("matR", type="source", repo=
  "http://dunkirk.mcs.anl.gov/~braithwaite/matR")
library(matR)
dependencies(prompt=TRUE)
hazPackages()
msession$setAuth()
```

obtain the matR package for your system

load matR into your current session

obtain packages used by matR

show what dependencies are already installed

enter authentication key for private data

use `prompt=FALSE` for batch scripting

getting help

```
demo(package="matR")
demo2("demo")
```

see a list of available demos

step through *demo*

metagenome collections

```
cc <- collection(x, file=NULL)
collection(x, n1=v1, n2=v2, ...)
collection(x, L)
samples(cc)
names(cc) <- xx
groups(cc) <- xx
asFile(cc, view="count", file, ...)
```

create collection

create collection with custom views

create collection with views from a list

samples of a collection

name (or rename) samples

group samples

write view to text file

specify IDs with `x` or `file` but not both

`v1`, `v2`, ... are character vectors (see below)

`L` is a named list

`xx` is a character vector

`xx` is a factor

views of a collection

```
c(annot="function", ...)
view.params
cc$v <- xx
views(cc)
viewnames(cc) <- xx
cc$v
cc[["v", full=FALSE, plain=FALSE]]
```

view described by character vector

valid values for all view elements

add new view to existing collection

views of a collection

name (or rename) views

view, as ordinary matrix

view, with options

valid elements: `annot`, `entry`, `source`, `level`

`xx` describes the new view

`xx` is a character vector

`v` is the name of an existing view

`v` is the name of an existing view

metadata

```
mm <- metadata(x, file=NULL, ...)
metadata(cc)
mm[x, y, ..., bygroup=FALSE]
asFile(mm, file, ...)
```

metadata of metagenomes

metadata of collection

metadata elements

write metadata to text file

specify IDs with `x` or `file` but not both

`x`, `y`, ... are character vectors

analysis and visualization

```
render(cc, view="normed", ...)
pco(cc, view="normed", comp=c(1,2,3),
  method="bray-curtis", ...)
heatmap(cc, view="normed", rows=TRUE, ...)
sigtest(cc, view="normed", test, fdr.level, qvalue)
asFile(x, file, ...)
```

summarize view diversity

compute and plot principal components

compute and view heatmap dendrogram

apply significance test

write analysis to text file

graphical parameters as in *boxplot*

graphical parameters as in *plot* and *points*

graphical parameters as in *gplots::heatmap.2*

may also be applied to an ordinary matrix

EXAMPLES

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collections and views

```
view.params
default.views
collection(c("4441679.3","4441680.3","4441682.3"))
collection(x, L1 = c(lev="level1"), L2 = c(lev="level2"))
L <- list (spec = c(annot="organism"),
  phy = c(annot="organism", lev="phylum"),
  str = c(annot="organism", lev="strain"))
cc <- collection (c("4441679.3","4441680.3","4441682.3"), L)
names(cc) <- c("samp1", "samp2", "samp3")
groups(cc) <- c(1,1,2)
sub <- cc [c(1,2)]
```

show valid values of view parameters
show default collection views
create collection of specified samples (with default views)
create collection with custom views
create a list of views ...

... then create a collection with those views
name samples of the collection
assign a grouping to the samples
extract a subcollection of specified metagenomes

metadata

```
mm <- metadata(guts)
mm["0464"]
mm["body_product"]
mm["latitude", "longitude"]
mm["latitude", "longitude", bygroup=TRUE]
mm[c("0464", "env_package.data")]
mm[c("0464", "PI"), c("0464","seq_"), c("0464","biome")]
mm["host_common_name", "disease", ".age", bygroup=TRUE]
```

create metadata object (using predefined set of IDs)
single index of length one selects all fields from specified metagenome
single index of length one selects same field from all metagenomes
two indices, both length one, select same fields from all metagenomes
same, as data.frame
one index of length two selects multiple fields from one metagenome
three indices, all length two, select various fields
selected fields not common to all metagenomes

analysis and visualization

```
cc <- collection(guts)
render(cc)
render(cc, view="count", las=3, cex.axis=.7, ylab="my axis title")
P <- pco(cc, comp=c(1,2,3))
pco (cc, main = "My Title", pch = 19:25, color=c(rep("blue",5),rep("red",2)))
asFile(P, file="PC0.txt")
heatmap (cc, main="My Title", col=c("blue", "green"),cexCol=0.8)
heatmap (cc, rows=c(rep(TRUE, 100), rep(FALSE, 915)))
res <- sigtest(cc)
```

create collection (using predefined set of IDs)
boxplot for diversity overview
slightly customized boxplots
plot initial three principal components
and with customization
write principal components in text format
heatmap of all annotations with some customization
heatmap of selected annotations
apply default significance test