

QUICK REFERENCE

matR (0.9.9): metagenomics analysis tools for R

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installation and help

```
dependencies(prompt=)
msession$setAuth(file=)
demo(package="matR"); demo2("demo")
data(package="matR")
?command; library(help="matR"); msession$debug()
```

obtain supporting packages (with or without interactive prompting)
enter key for private data (use **file** to read from disk)
list demos; or step through demo named "**demo**"
list metagenome collections prepackaged
get help and examples for **command**; see index of help topics; create debug report

metagenome collections

```
cc <- collection(x, ..., file=)
samples(cc); projects(cc)
views(cc)
names(cc); names(cc) <- x
groups(cc); groups(cc) <- x
cc[sub]; as(x, "collection")
```

create collection with sample IDs as in **x** or **file**, and data views specified by ...
see samples in a collection, or projects appearing (fully or partially) in a collection
see data views included in a collection
see sample names; or name or rename samples
see sample grouping; or group samples of a collection
subset collection, retaining samples **sub**; formally convert matrix **x** to collection

data views in a collection

```
view.params; default.views
cc$raw
cc[["raw", full=, plain=]]
views(cc); viewnames(cc) <- x
x <- c(annot=, entry=, level=, source=, hit=)
cc$new <- x
```

see parameters that define data views and valid values; or see default data views
extract data view named **raw** as an ordinary matrix
extract data view named **raw** with options
see or rename data views of a collection
describe a data view by selecting values for view parameters
add data view named **new**, as described by **x**, to an existing collection

metadata

```
metadata(cc)
metadata(cc)["str"]
metadata(cc)["str1", "str2", ..., bygroup=]
mm <- metadata(x, file=)
```

all metadata of a collection
metadata fields matching specifier "**str**"
fields matching any of given specifiers; NA inserted as needed when **bygroup**=TRUE
retrieve (only) metadata of samples specified by ID by **x** or **file**

analysis utilities (x is matrix)

```
remove.singletons(x, lim.entry=, lim.row=)
normalize(x, method=)
dist(x, y=, groups=, method=)
sigtest(x, groups, test=, fdr.level=, qvalue=)
randomize(x, n=, method=, seed=, FUN=)
```

replace entries with zero and/or remove rows below a threshold
apply logarithmic transformation, scale, and center to [0,1]
compute distance between columns of **x**; from **y** to each; or m.p.d. of **groups**
apply significance **test** across rows to **groups** of columns of **x**
apply **FUN** to each of **n** permutations of **x** according to **method**

analysis routines (cc is collection)

```
boxplot(cc, ..., view=)
pco(cc, comp=, method=, ..., view=, rows=)
heatmap(cc, ..., view=, rows=)
parcoord(cc, groups=, test=, p.lim=, n.lim=, ..., view=)
```

summarize distribution of annotations per sample; graphical parameters as in *boxplot*
compute and plot principal coordinates; graphical parameters as in *plot* and *points*
compute and view heatmap dendrogram; graphical parameters as in *gplots::heatmap.2*
compute and plot parallel coordinates restricted by **p.lim** or **n.lim**