Note: this document is a summary and skimps on some details. See runtime help for exact function syntax.

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```
One-liners are here! Analysis products are returned in a list as usual, addition-
ally containing the implied metagenome collection. For instance:
> p <- pco("4441679.3 4441680.3 4441696.3 4440463.3 4440464.3", main="my</pre>
title", color="blue")
> pco(p$collection, main="and now, in red", color="red")
Similarly implemented for: heatmap, sigtest.
These routines apply to any matrix:
dist(x, method="bray-curtis")
normalize(x)
remove.singletons(x, lim.entry=1 , lim.row=1)
randomize(x, n=1, method = c("sample", "dataset", "complete"), FUN=identity)
For collections, the default view in most circumstances (e.g. analysis functions
like pco) is the most recently constructed.
For API debugging use: messions$urls()
Read metagenome IDs from file with: collection(file="my-id-file.txt")
One ID per line, or name<tab>ID per line.
Read auth key from file with: msession$setAuth("my-key-file.txt")
Annotation hierarchies available with: rownames(collection, view, sep)
With sep=FALSE, the result is a matrix: one column per hierarchy level, one
row per annotation.
```

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For auth keys and other session configuration, use: msession (formerly mconfig)

For bug reporting, use: msession\$debug()

Collections now have four default views: raw counts (raw) normed counts (nrm) no singletons, raw counts (nsc) no singletons, normed counts (nsn) Command reference now available with: vignette("matR-quick-reference")
The same document is available via:

https://github.com/MG-RAST/matR/raw/master/inst/doc/matR-quick-reference.pdf

Runtime R-style help now available, such as: ?collection For the moment, docs are by and large limited to series of examples.

Significance testing of annotations available with: sigtest().

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This file available with: vignette("matR-change-log")

And at:

 $\verb|https://github.com/MG-RAST/matR/raw/master/inst/doc/matR-change-log.pdf| \\$