

microbiome

R package and protocols

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The microbiome package includes standard R routines for preprocessing, analysis and visualization of microbiomics profiling data. The package is jointly developed by researchers from the Molecular Ecology group, Laboratory of Microbiology, Wageningen University, Netherlands, and Gut Group, Department of Veterinary Bioscience, University of Helsinki, Finland.

The current version is in beta. The features and documentation are unstable and under development. For further information, check the website: <http://microbiome.github.com> or contact the admins through microbiome-admin@googlegroups.com

For installation instructions and other documentation, see <https://github.com/microbiome/microbiome/wiki/>

To citation information, check in R: `citation("microbiome")`

1 Version information

```
> sessionInfo()
```

```
R version 2.15.1 (2012-06-22)
```

```
Platform: x86_64-pc-linux-gnu (64-bit)
```

```
locale:
```

```
[1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
[3] LC_TIME=en_US.UTF-8      LC_COLLATE=en_US.UTF-8
[5] LC_MONETARY=en_US.UTF-8  LC_MESSAGES=en_US.UTF-8
[7] LC_PAPER=C               LC_NAME=C
[9] LC_ADDRESS=C             LC_TELEPHONE=C
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
```

```
attached base packages:
```

```
[1] tcltk      parallel  grid      stats      graphics  grDevices  utils
[8] datasets  methods   base
```

```
other attached packages:
```

```
[1] vegan_2.0-4      permute_0.7-0      svDialogs_0.9-52
[4] svMisc_0.9-65    svGUI_0.9-53       RPA_1.13.04
[7] affydata_1.11.16 R2HTML_2.2         reshape_0.8.4
[10] qvalue_1.30.0    preprocessCore_1.18.0 plyr_1.7.1
```

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[13] outliers_0.14	NMF_0.5.06	nlme_3.1-104
[16] mixOmics_4.0-2	pheatmap_0.7.2	lattice_0.20-10
[19] rgl_0.92.892	igraph0_0.5.5-2	limma_3.12.1
[22] gplots_2.11.0	MASS_7.3-21	KernSmooth_2.23-8
[25] caTools_1.13	bitops_1.0-4.1	gdata_2.11.0
[28] gtools_2.7.0	ggplot2_0.9.2	fields_6.6.3
[31] spam_0.29-2	DBI_0.2-5	brew_1.0-6
[34] affy_1.34.0	Biobase_2.16.0	BiocGenerics_0.2.0
[37] staticdocs_0.1		

loaded via a namespace (and not attached):

[1] affyio_1.24.0	BiocInstaller_1.4.7	codetools_0.2-8
[4] colorspace_1.1-1	devtools_0.7.1	dichromat_1.2-4
[7] digest_0.5.2	evaluate_0.4.2	gtable_0.1.1
[10] highlight_0.3.2	httr_0.1.1	labeling_0.1
[13] markdown_0.5.2	memoise_0.1	munsell_0.3
[16] parser_0.0-16	proto_0.3-9.2	RColorBrewer_1.0-5
[19] Rcpp_0.9.13	RCurl_1.91-1	reshape2_1.2.1
[22] scales_0.2.2	stringr_0.6.1	testthat_0.7
[25] tools_2.15.1	whisker_0.1	zlibbioc_1.2.0