

# Co-expression analysis of RNA-seq data with the HTSCluster package

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*HTSCluster* version 2.0.2

## Abstract

This vignette explains the use of the *HTSCluster* package. For a presentation of the statistical method, please see our paper.

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## 1 Input data

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In this vignette, we will work with the gene level read counts from the ... data package.

## 2 Inference: Identifying co-expressed genes

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To be completed.

## 3 Further reading

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For more information on the statistical method, see [1].

## 4 Session Info

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```
> sessionInfo()

R version 3.1.1 (2014-07-10)
Platform: x86_64-w64-mingw32/x64 (64-bit)

locale:
[1] LC_COLLATE=French_France.1252 LC_CTYPE=French_France.1252 LC_MONETARY=French_France.1252
[4] LC_NUMERIC=C LC_TIME=French_France.1252

attached base packages:
[1] stats graphics grDevices utils datasets methods base

other attached packages:
```

```
[1] SweaveListingUtils_0.6.1 startupmsg_0.9          HTScluster_2.0.2
[4] RColorBrewer_1.0-5      ggplot2_1.0.0          plotrix_3.5-7
```

loaded via a namespace (and not attached):

```
[1] colorspace_1.2-4    digest_0.6.4      edgeR_3.4.2      grid_3.1.1
[5] gtable_0.1.2       limma_3.18.13    MASS_7.3-33     munsell_0.4.2
[9] plyr_1.8.1         poisson.glm.mix_1.2 proto_0.3-10    Rcpp_0.11.2
[13] reshape2_1.4       scales_0.2.4     stringr_0.6.2   tools_3.1.1
```

## References

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- [1] Andrea Rau, Cathy Maugis-Rabusseau, Marie-Laure Martin-Magniette, and Gilles Celeux. Co-expression analysis of high-throughput transcriptome sequencing data with Poisson mixture models. (*submitted*), 2014.