

# Differential expression analysis of RNA-seq data with the HTSDiff package

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*HTSDiff* version 1.0.1

## Abstract

This vignette explains the use of the *HTSDiff* 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 differentially 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] and [2] .

## 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] HTSDiff_1.0.1	HTSCluster_2.0.3	RColorBrewer_1.0-5
[4] ggplot2_1.0.0	plotrix_3.5-7	SweaveListingUtils_0.6.1
[7] startupmsg_0.9		

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.
- [2] S. Balzergue, G. Rigaiil, V. Brunaud, E. Blondet, A. Rau, O. Rogier, J. Caius, C. Maugis-Rabusseau, L. Soubigou-Taconnat, S. Aubourg, C. Lurin, E. Delannoy, and M.-L. Martin-Magniette. Htsdiff: a sensitive analysis of differential gene expression by rna-seq. (*submitted*), 2014.