# edgeR: differential expression analysis of digital gene expression data

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edgeR (Robinson et al., 2010) is a package of the Bioconductor software development project. edgeR implements statistical methods for assessing differential expression from digital gene expression data developed by Robinson and Smyth (2007, 2008). The methodology can be applied to RNA-Seq, SAGE-Seq or ChIP-Seq data arising from sequencing technologies such as Illumina™, 454 or ABI SOLiD.

For a detailed introduction to the package, including a number of fully worked case studies, see the edgeR User's Guide.

# References

MD Robinson and GK Smyth. Moderated statistical tests for assessing differences in tag abundance. *Bioinformatics*, 23(21):2881–2887, 2007.

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