

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 IlluminaTM, 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.
- MD Robinson and GK Smyth. Small-sample estimation of negative binomial dispersion, with applications to SAGE data. *Biostatistics*, 9(2):321–332, 2008.
- MD Robinson, DJ McCarthy, and GK Smyth. edgeR: a bioconductor package for differential expression analysis of digital gene expression data. *Bioinformatics*, 26(1):139–40, Jan 2010.