



## Differential gene expression analysis tools

### DESeq2

- Love MI, Huber W, Anders S. Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. *Genome Biology*. 2014;15(12). doi:<https://doi.org/10.1186/s13059-014-0550-8>

### Mitch

- Kaspi A, Ziemann M. mitch: multi-contrast pathway enrichment for multi-omics and single-cell profiling data. *BMC Genomics*. 2020;21(1). doi:<https://doi.org/10.1186/s12864-020-06856-9>
- <https://github.com/markziemann/mitch>
- <https://bioconductor.org/packages/mitch>

### R programming

- <https://www.r-project.org/>

### Kallisto

- Bray NL, Pimentel H, Melsted P, Pachter L. Near-optimal probabilistic RNA-seq quantification. *Nature Biotechnology*. 2016;34(5):525-527. doi:<https://doi.org/10.1038/nbt.3519>
- <https://github.com/pachterlab/kallisto>
- <https://pachterlab.github.io/kallisto/about>

## Data visualization tools

### Complexheatmap

- Gu Z, Eils R, Schlesner M. Complex heatmaps reveal patterns and correlations in multidimensional genomic data. *Bioinformatics*. 2016;32(18):2847-2849. doi:<https://doi.org/10.1093/bioinformatics/btw313>
- <https://github.com/jokergoo/ComplexHeatmap>

## ggplot2

- Wilkinson L. ggplot2: Elegant Graphics for Data Analysis by WICKHAM, H. *Biometrics*. 2011;67(2):678-679. doi:<https://doi.org/10.1111/j.1541-0420.2011.01616.x>

## Bioconductor visualization packages

- <https://bioconductor.org/>
- <https://www.bioconductor.org/packages/release/BiocViews.html#Visualization>

## Matplotlib

- <https://matplotlib.org/>

## Seaborn

- Waskom M. seaborn: statistical data visualization. *Journal of Open Source Software*. 2021;6(60):3021. doi:<https://doi.org/10.21105/joss.03021>
- <https://seaborn.pydata.org/>
- <https://pypi.org/project/seaborn/>

## Plotly

- <https://github.com/plotly/plotly.py>
- <https://plotly.com/python/>

## Integrative Genomics Viewer (IGV)

- Robinson JT, Thorvaldsdóttir H, Winckler W, et al. Integrative genomics viewer. *Nature Biotechnology*. 2011;29(1):24-26. doi:<https://doi.org/10.1038/nbt.1754>
- Thorvaldsdóttir H, Robinson JT, Mesirov JP. Integrative Genomics Viewer (IGV): high-performance genomics data visualization and exploration. *Briefings in Bioinformatics*. 2012;14(2):178-192. doi:<https://doi.org/10.1093/bib/bbs017>
- Robinson JT, Thorvaldsdóttir H, Wenger AM, Zehir A, Mesirov JP. Variant Review with the Integrative Genomics Viewer. *Cancer Research*. 2017;77(21):e31-e34. doi:<https://doi.org/10.1158/0008-5472.can-17-0337>
- Robinson JA, Thorvaldsdóttir H, Turner D, Mesirov JP. igv.js: an embeddable JavaScript implementation of the Integrative Genomics Viewer (IGV). *Bioinformatics*. 2020;39(1). doi:<https://doi.org/10.1101/2020.05.03.075499>
- <https://igv.org/>

## Samplot

- Belyeu JR, Chowdhury M, Brown JA, et al. Samplot: a platform for structural variant visual validation and automated filtering. *Genome Biology*. 2021;22(1). doi:<https://doi.org/10.1186/s13059-021-02380-5>
- <https://github.com/ryanlayer/samplot>

#### Circos

- Krzywinski M, Schein J, Birol I, et al. Circos: an information aesthetic for comparative genomics. *Genome Research*. 2009;19(9):1639-1645. doi:<https://doi.org/10.1101/gr.092759.109>
- <http://circos.ca/>

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