# WIlsON: Fancy visualization of RNA-seq data

Download and extract Wilson from the following link: WIlsON: Webbased Interactive Omics visualizatioN

- In R-Studio run the following commands:

```
install.packages("devtools")
devtools::install_github(repo = "loosolab/wilson",
host="github.molgen.mpg.de/api/v3")
```

- Restart R-Studio and in *File - New project* select the *wilson-basic* folder where Wilson was extracted.
- Open app.R and click on *run App*.
- You can practice with the sample datasets, where they compare expression levels in wildtype and mutant. Go to feature selection and in the left panel you can pick the one of RNAseq.
- To use your own data, paste your file in *wilson-apps-master/wilson-basic/data /*.



## Example I: Scatterplot to view overexpressed genes when comparing RNA-seq data from two conditions.

- In the menu - feature selection you will have two tabs: Data contains all your sequences, and in Highlight you can set your filters to find the genes of interest (in our example, we want to highlight a fold change outside the -3 to 3 range).
- In the Scatterplot tab, left panel, you can indicate Wilson to label the genes that you selected for highlight in the previous step.

 





## Example II.- Heatmap of relevant genes

- Wilson can only generate heatmaps for 11000 genes; for this example, from *Feature selection - Data* we selected the first 10 genes with an adjusted P-value between 0 and 0.05, sorted by mean (note that you might not only need to type the ranges in the text boxes, but also move the scroll to capture the range).
- Heatmap

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