Iron deficiency triggered transcriptome changes in bread wheat

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Abstract A short summary (max. 150 words) describing the original article, their results, your research, your results and end with a short discussion.

Introduction

In the introduction you will focus on two things; *(i)* the research subject from the original experiment. Take the article's abstract as inspiration but keep in mind that the target audience are your fellow students, the biology must be made understandable. In the next *(ii)* part you can explain your planned analysis; what is your research question, what steps are needed and if so, how will your analysis be different from the one in the original article?

Introductory section which may include references in parentheses (R Core Team, 2012), or cite a reference such as R Core Team (2012) in the text, see the last section in this document for a how-to on references.

Materials and Methods

Most likely this will be the largest section in your report (depending on the number of images you show in the `Results` section). Take a look at your experiments article to see how they organised its content to see if this is also suitable for your report.

This section must at the very least contain information about the **data**; how many samples from what organism + strain (if applicable), what kind of data is there available (not only saying **FPKM** but also the sequencer type that generated this data). Also, information about all the **software** that you used during your analysis (i.e. R and its libraries, `bioConductor`, `DESeq2`, etc.) and all **methods** that you applied (both filtering steps and statistical analysis steps). Try to use the proper terms and symbols if needed, i.e. "*We filtered for DEGs with an $\alpha < 0.05$*". Symbols need to be surrounded with $ signs, otherwise you will get an error when knitting.

Do not show any results in this section, for instance when stating that you filtered t-test p-values on a certain value, you do not list how many genes were left, that is for the next section.

Results

Here you will only focus on your own results, start at the beginning but only show the interesting results. This section works best if you alternate between text introducing some result, a figure or table showing the result, and a short text segment analyzing the presented result *and* introducing the next figure, etc.

Although we have worked in R a lot, the results are almost never pieces of R code. If you have written your own algorithm or analysis method try to present it in a formula *followed* by the R implementation, otherwise this section should mainly contain figures and tables.

There are multiple methods of including a figure in this section. Figure 1 shows the LATEXmethod (see the source code) giving very fine control over size and placement of a figure. The size of a figure is determined by the width of the text column, Figure 1 is scaled as 85% of the text width. The Wikibooks.org website shows some examples for placement (for instance, what the [htbp] means), scaling and captions.
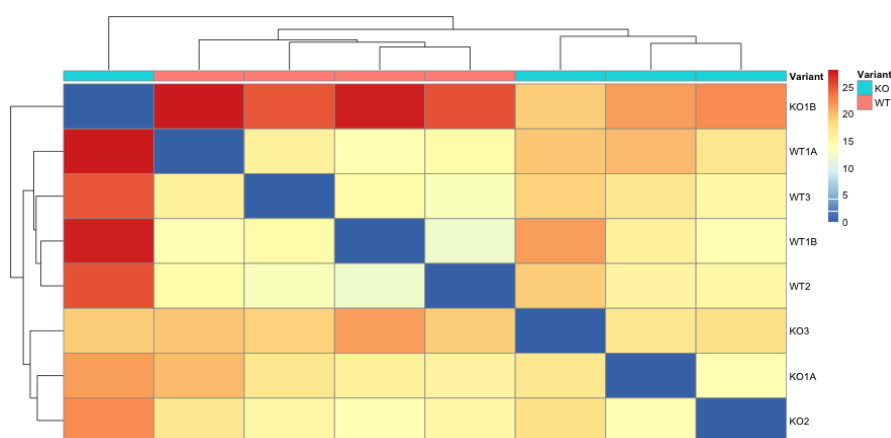
Figure 1: Heatmap showing sample distances and clustering.

Alternatively the previously shown `R` method using the `PNG` library can be used which allows changing the *heigth* and *width* of an image but lacks the possibility of referencing the figure in the text, aligning the figure (the heatmap is centered), providing a figure caption and automatic numbering of figures.

```
library(png)
library(grid)
img <- readPNG("images/mds.png")
grid.raster(img)
```
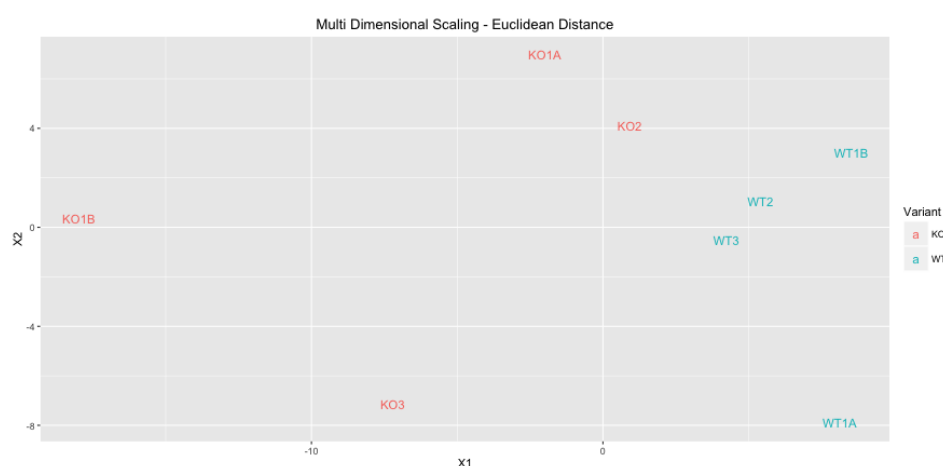

Conclusion

Limit to your *own* conclusions, based on what is shown in the **Results** section. Do not include any comparison to the original article as that is the content of the next section, the **Discussion**. Usually you refer back to all steps outlined in the results section since you included it there for a reason.

Discussion

An important section in your report; here you can compare your findings with the findings presented in the original article. If you found exactly the same results - and that was your goal from the start - this will be a bit shorter section and you should focus on other parts of your research that hasn't been discussed or shown in the article, i.e. any findings from the exploratory data analysis or differences in DEGs using the manual- and library-method.

Besides comparing the two 'experiments', this is also the place to discuss how reliable your results are. Did anything go wrong or did you get unexpected outcomes using some method and if so, what did you do to solve it or are there still open discussion points on this subject.

Notes on the `bibliography` section

The last section in the report contains all the used references that are used throughout the text in a section called the `Bibliography`. In the text you can link to references using the LATEXcommands (see the source of this file for instructions). These references must be present in a file named `RJreferences.bib` which is automatically generated once you click the `Knit` button for the first time in a folder with the same name as the current markdown file (`./report-template/RJreferences.bib` for this example file).

This file containing the references can be edited in RStudio too, browse to the folder (after Knitting) and click on the `.bib` file to edit. If, for example, I want to add the article that is available for the experiment used in the week 4 - 7 assignment document, I would first lookup the paper in PubMed to get the details and add these details to the `.bib` file as follows:

```
@article{garcia,
    author = {Duart-Garcia, Braunschweig},
    title = {Functional expression study of igf2 antisense transcript in mouse},
    journal = {International Journal of Genomics},
    doi = {10.1155/2014/390296},
    url = {http://dx.doi.org/10.1155/2014/390296},
    year = 2014
}
```

References added to this file do not automatically show up in your document, unless you actually refer to it. To add a reference, like so: (Duart-Garcia, 2014), you need to use the `\citep{}` or `\citer{}` LATEXcommand combined with the given ID which is `garcia` in our case.

Bibliography

B. Duart-Garcia. Functional expression study of igf2 antisense transcript in mouse. *International Journal of Genomics*, 2014. doi: 10.1155/2014/390296. URL http://dx.doi.org/10.1155/2014/390296. [p3]

R Core Team. *R: A Language and Environment for Statistical Computing*. R Foundation for Statistical Computing, Vienna, Austria, 2012. URL http://www.R-project.org/. ISBN 3-900051-07-0. [p1]

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