BRES-MONVOISIN Chloé
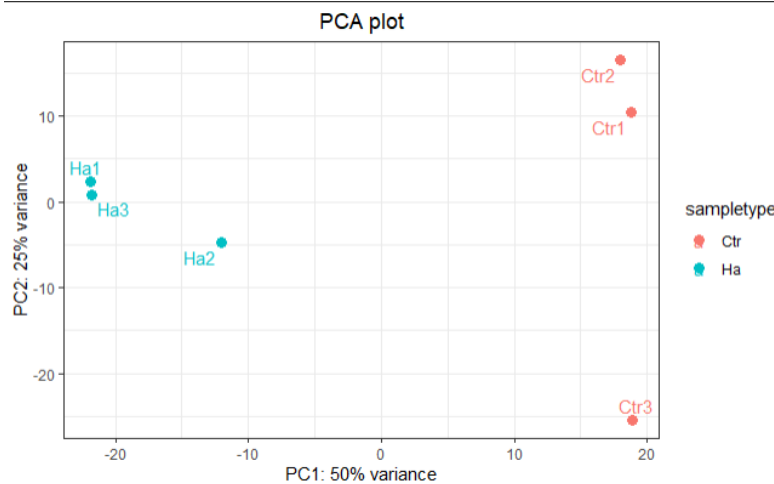**FOR 271 – Practical course in bioinformatic**

RNA-seq Summary of the Results

The data chosen represent scot pines growth inoculated by *Heterobasidion annousm* (Ha) and a control group (Ctr), which didn't receive any inoculation.

1. PCA Results

It is possible to discern 2 groups on the PCA plot: the control group and the one with Ha inoculation, which have grown less than Control group. The results coincide with bibliography, as *Heterobasidion annousm* is a pathogen of Scots pine.

The first and second axis explain 75% of the variance information, and indicate a high level of data quality.
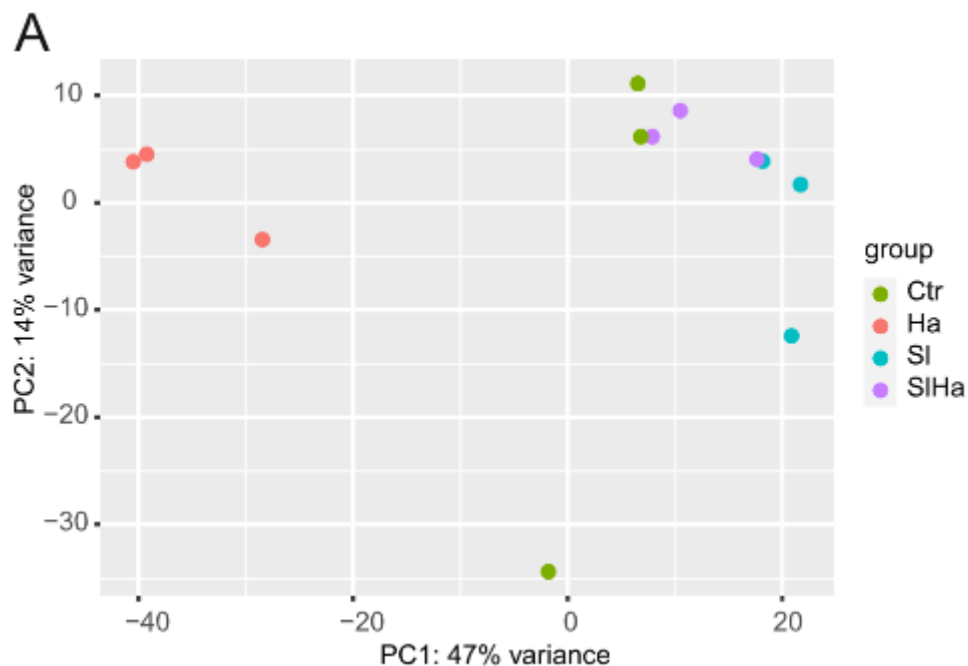
In application with all different groups, we can discern that Ha inoculation has a growth way less important than the control group or group with Sa inoculation. Those results coincide with *H. annousm* being a pathogen fungus, thus the scot pine has its growth reduce, and *Suillus luteus* is a symbiotic fungus, and helps the growth of the tree. The group inoculated by both fungi has a growth higher than the control, but lower than the Sl inoculation alone, and can be explain by the effect of the pathogen fungus lessen the effect of Sl without decreasing the global growth.

2. Heatmap
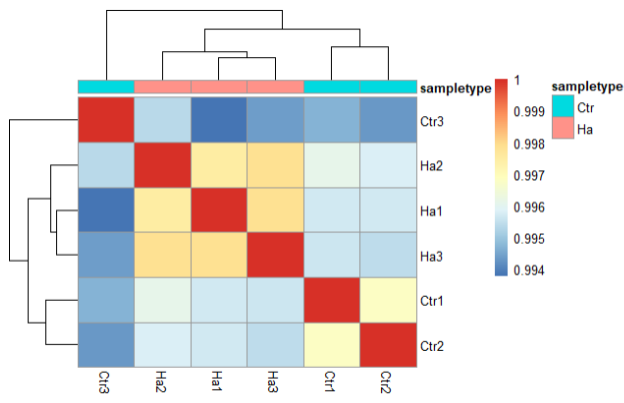
Same as the PCA, we can distinctively see the two groups of the experiment, even though there is one control individual that seems to behave differently than the rest, and may be an error.

3. Raw count distribution
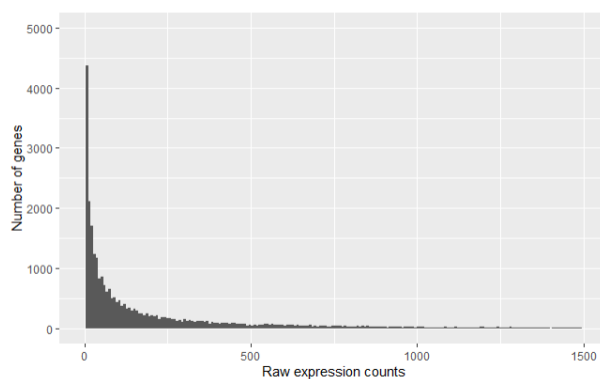
There are 51 000 genes, most of them (40 000) have zero values, which means they are not found. 5000 genes are near zero, and only a few have higher expression count, around a hundred.

4. MDS

MDS plot of RNA-Seq
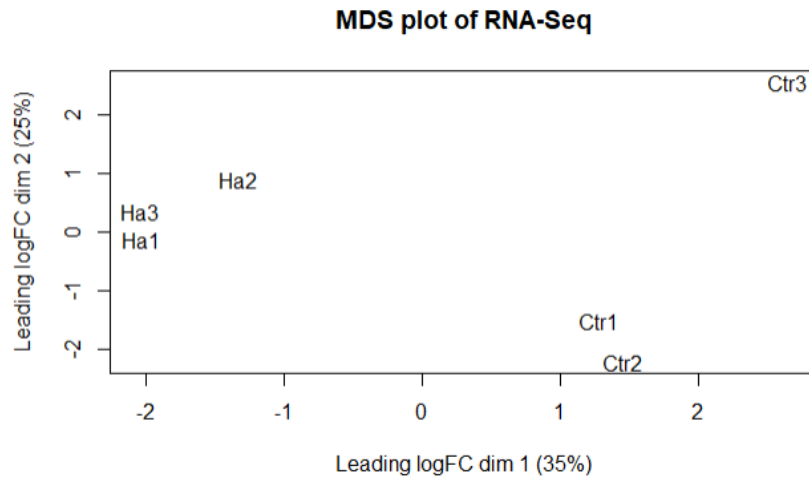
There is a clear separation between the Ha samples and the Ctr samples along the first dimension (dim 1). This separation suggests differential gene expression between the two groups, as seen earlier. The relatively high percentage of variance captured (35% + 25% = 60%) indicates that these two dimensions provide a good summary of the major differences.

For Sl plot, there is a separation between Sl and Ctr along the second dimension.

MDS plot of Mutualistic RNA-Seq