Using NGS to answer biological questions

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As generating next generation sequencing (NGS) data has become much cheaper, it is becoming more and more commonly used to address questions hitherto tackled by microarrays or by costly large scale EST sequencing. However, the computational challenge to analyse and interpret these data still remains.

Here we present some tools for the processing of NGS data. Focusing on RNA-seq data we show that using these tools, it is possible to get a first idea about major biological stories and to get a first overview which can then be used to develop biological hypotheses which can then be tested in more detail.

One example entails the often performed NGS analysis of non-model plant species and the exploration of metabolic pathways within these species (Lohse *et al.*, 2014). Having established these annotations, NGS data can then be analysed for statistical changes and explored for differences in expression which is demonstrated here (see Figure 1).

A main take home message however is that, even though these tools will help the experimenter in data analysis and interpretation, knowledge of the underlying biological system is of course required.

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References

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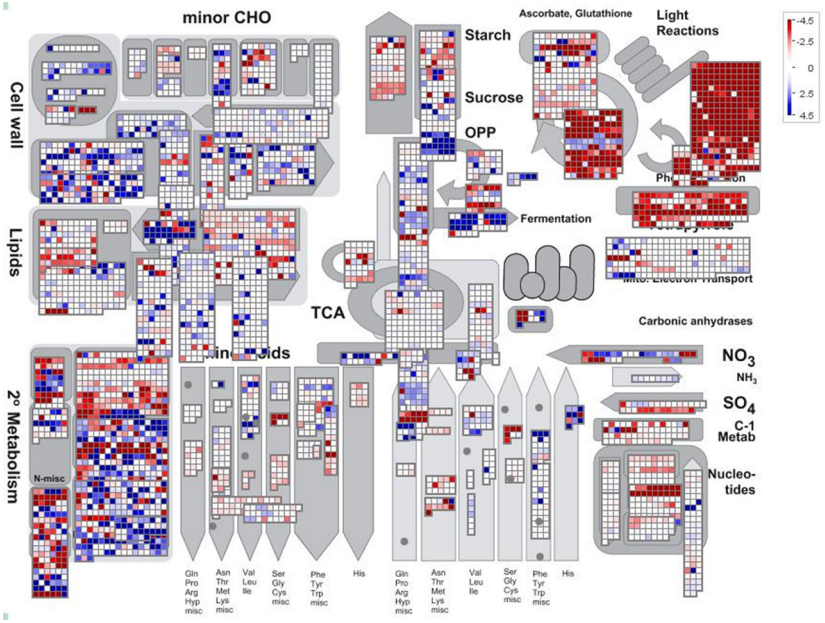

Figure 1.