TeRAbytes

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A lack of tools is not the problem in maize hybrid RNA-seq

Cross-pollinated F1-hybrids are more vigorous than their parents, produce more biomass, have a faster development and greater fertility. This phenotypic variation between the parental mean and the hybrid is often accompanied by transcriptomic variance. The transcriptome is an important link between the genome and the phenotype of organisms. Sequencing the messenger RNA (mRNA) captures the coding transcriptome. In our study, RNA-seq is used to analyse hybrid vigour. The raw data are made publicly available. But different research questions often require a new experimental setup. If and how this data could be reused remains an open question. Further, there are a variety of tools for processing RNA-seq data. Most are computationally intensive, run on a server, and require scripting knowledge. Technical implementation details, complete parameters and analysis scripts are stored locally or on Sciebo. Improving the sharing of this technical knowledge remains one of the challenges.

Primary author: PITZ, Marion (uni-bonn)

Co-author: Prof. HOCHHOLDINGER, Frank (uni-bonn)

Presenter: PITZ, Marion (uni-bonn)

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