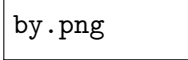


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1 Main Findings

What did I do so far?

programming and data

- Custom Analysis pipelines
- Evaluation of *de novo* Assembly Software with 454 data
- Evaluation of Assembly Software with Illumina data
- Chimeric contig detection
- Comparison of public datasets from different sources by complexity reduction

metabolism

- *Megathyrsus maximus* PEP-CK type C₄
- *Megathyrsus* blueprint for engineering C₄-cycle

transport

- *Megathyrsus* intercellular transport requirement
- *Megathyrsus* modular intracellular transport machinery

1.0.1 Custom analysis pipelines

this one is very generic so I will fit it in somewhere in between

1.0.2 Evaluation of assembly softwares

For de novo assembly of 454 pyrosequencing reads we tested six different assembly algorithms with simulated reads. These reads were extracted from the *Arabidopsis* genome and were therefore considered as perfect reads. To get a more realistic picture of assembly we additionally modified the reads with 1%/3%/5% *in silico* base changes.

2 Introduction

3 Conclusion

4 Appendix

The citations here will be replaced by hard-copies of the publications in the final, non-public version of this thesis, for I do not have the rights to publish them under CC-BY 4.0

Brautigam et al. (2011)

Schulze et al. (2012)

Hamisch et al. (2012)

Schliesky et al. (2012)

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