

a flexible platform for exploring deepsequencing data

Björn Grüning - Galaxy Community Conference 2014

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Before deepTools

NGS analyses often characterized by

- Specialized and custom-made scripts
- Hidden filtering strategies
- Lack of standardization and reproducibility

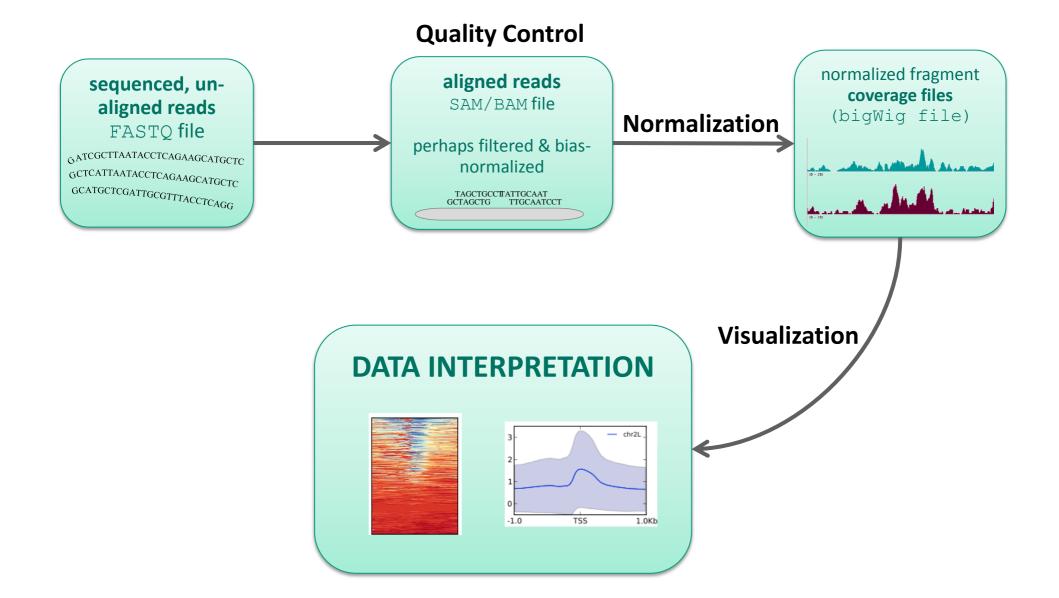
Existing tools:

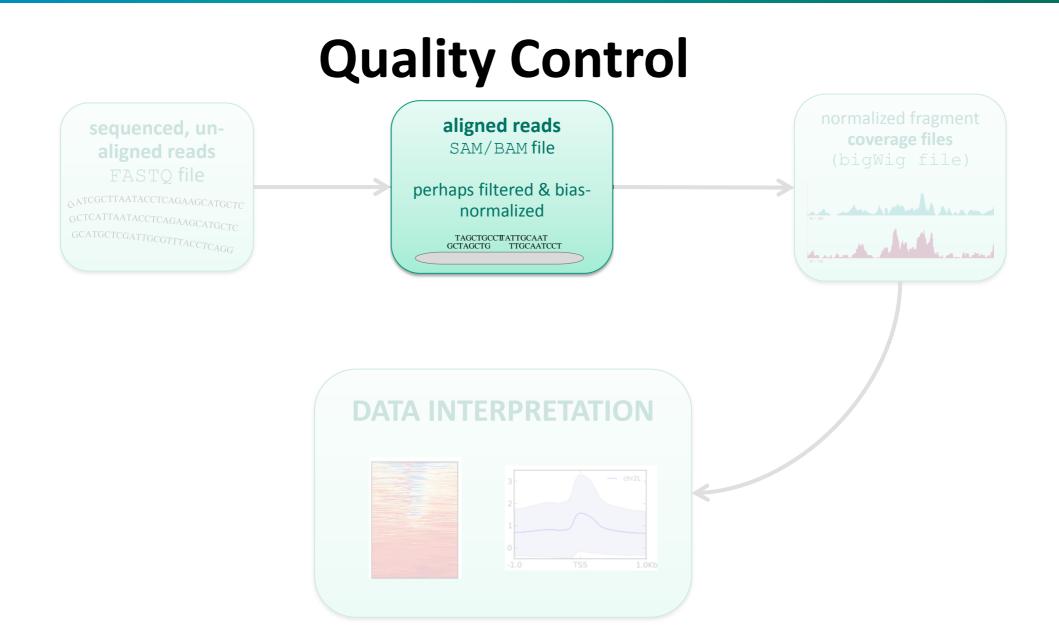
- Require experience with command-line
- No graphical output to guide interpretation of results

Several biases in NGS data

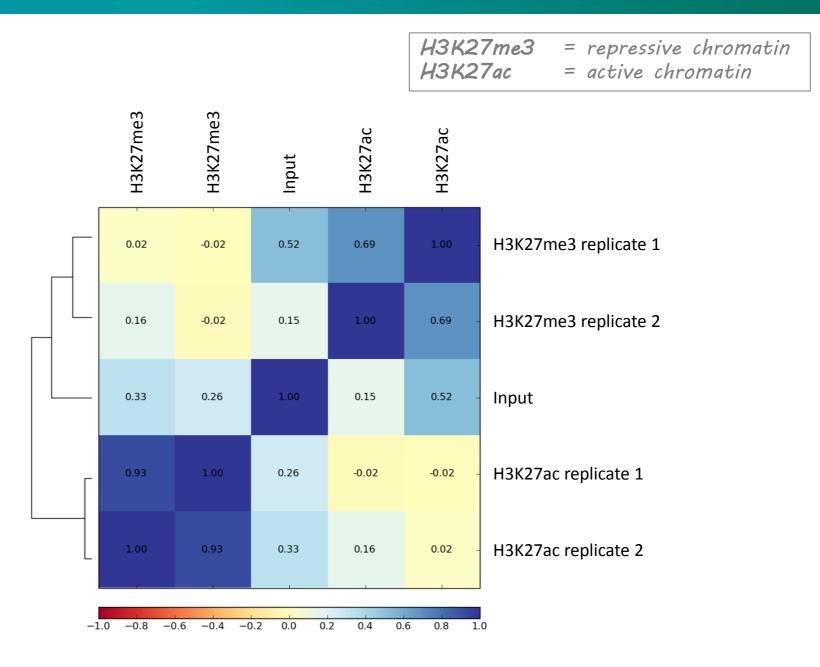
> Deters biologists from taking part in analysis of their data

deepTools data processing workflow



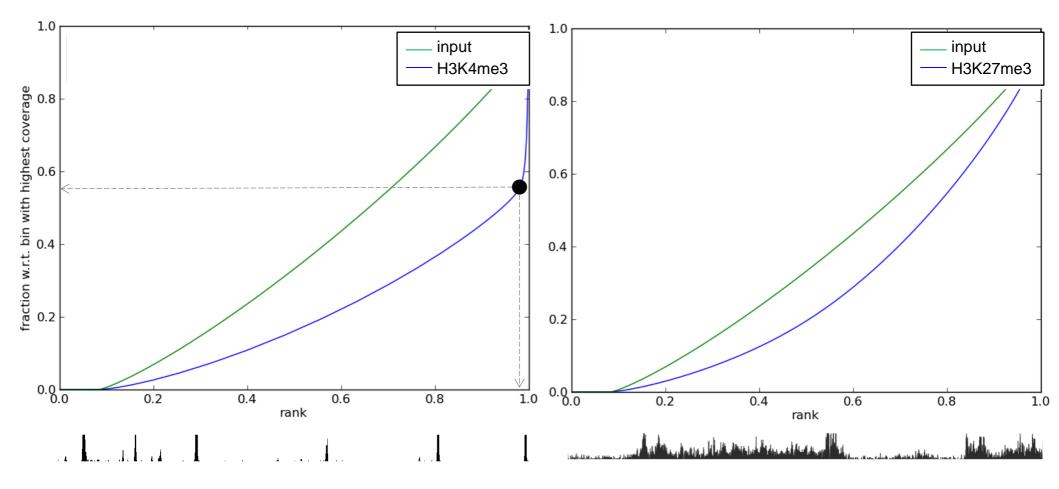


bamCorrelate



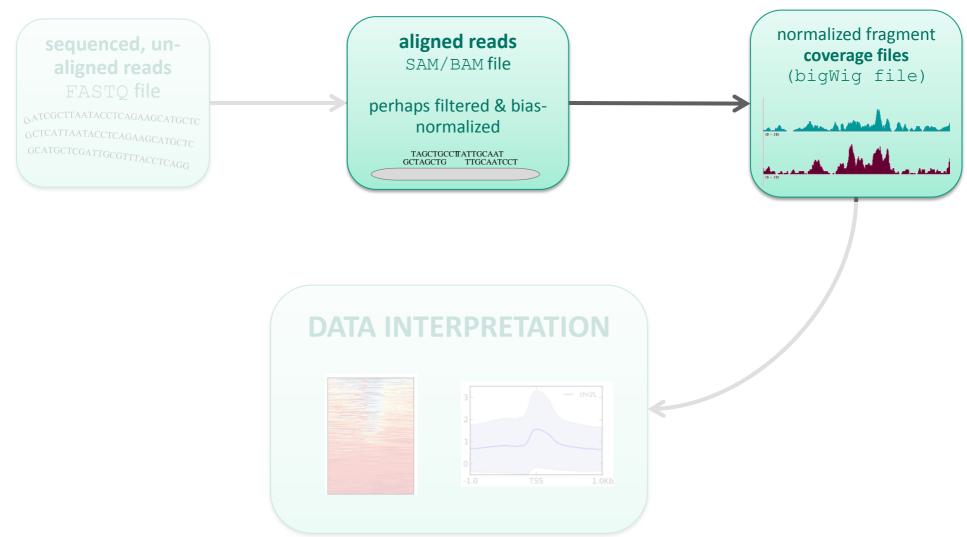
bamFingerprint

How well can the signal in the ChIP-seq sample be differentiated from the background?

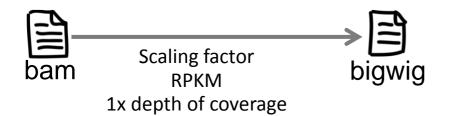


Diaz A., Park K., Lim D.A., Song J.S. Normalization, bias correction, and peak calling for ChIP-seq. Stat. Appl. Genet. Mol. Biol. 2012;11:9. University of Freiburg – Department of Computer Science | Björn Grüning 01.07.2014 | PAGE 6

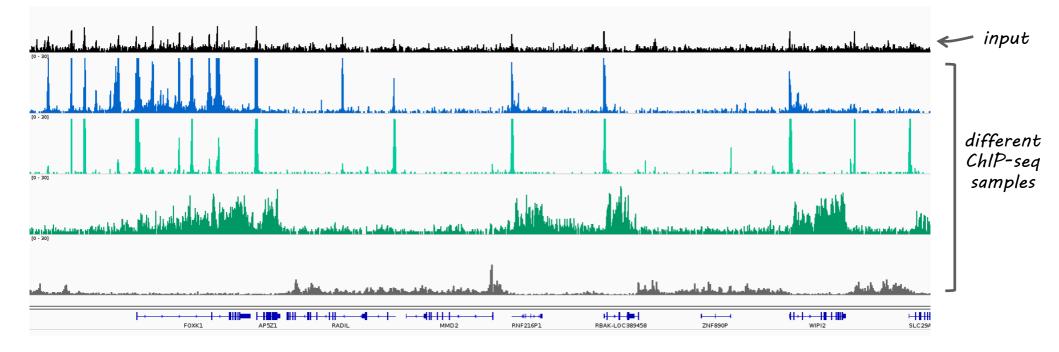
Normalization



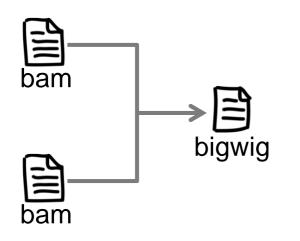
bamCoverage



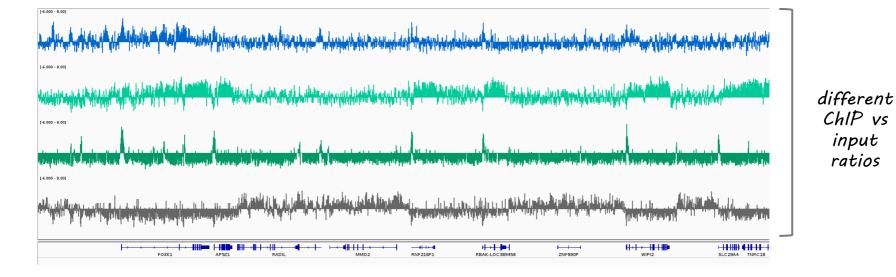
- Data sharing & storage
- Visualization in Genome Browsers (e.g. IGV)
- More efficient downstream analyses



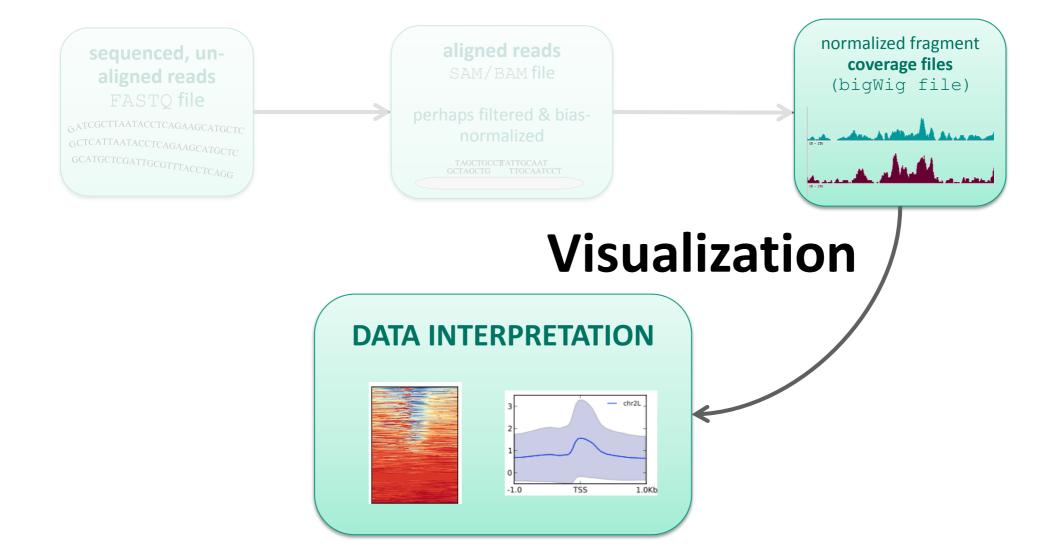
bamCompare



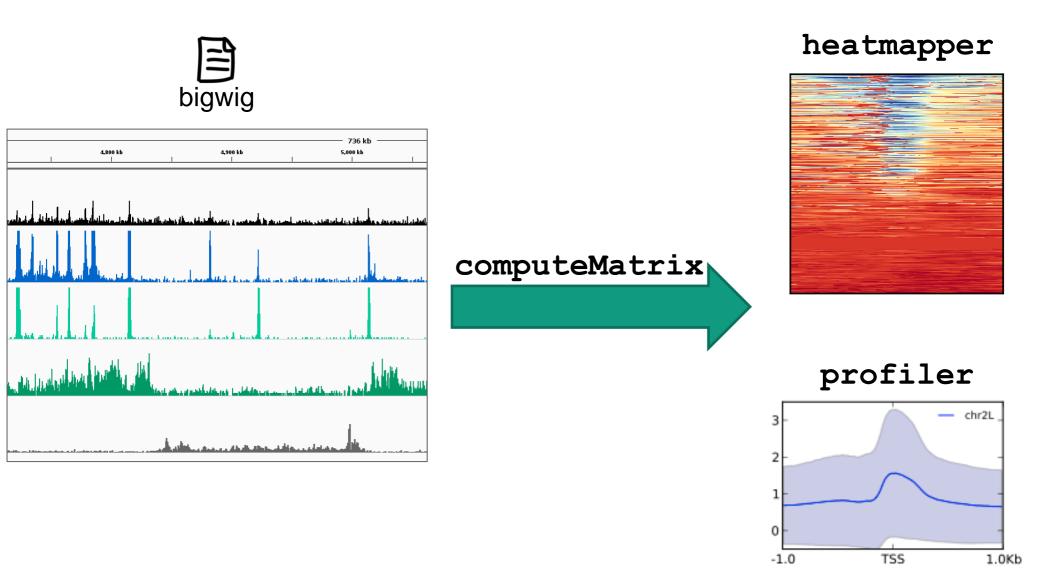
- Reported value:Ratio of number of reads per bin
 - Log2 ratio
 - Difference
- Scaling:
 - Read counts
 - SES method by Diaz et al.



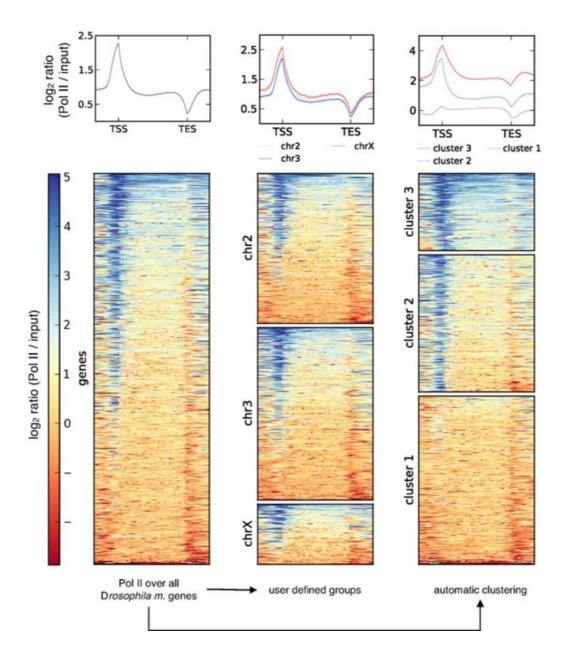
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Local to global



heatmapper



Implementation

- Efficiency and highly parallelized processing
- Customized down-stream analyses (store intermediate data)
- Standardized output files
- Modular approach compatibility, flexibility, scalability
- Automatic installation with dependencies
 - Command-line version: Python Package Index (easy_install, pip)
 - Galaxy: from main toolshed
 - Docker image
- Public Galaxy Server: deepTools.ie-freiburg.mpg.de

Analyze more, process less!

Acknowledgements



MPI-IE

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- Thomas Manke

More information & support: deepTools.github.io

All users of deepTools for their feedback

docker run -d -p 8080:80 bgruening/galaxy-deeptools

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