

Analysis of DNA methylation data using Galaxy

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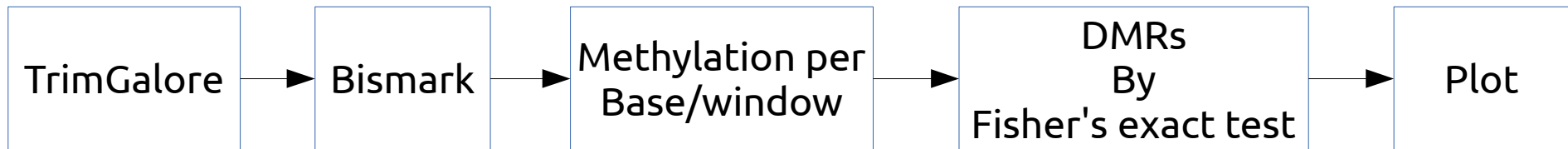
GCC2013, Oslo

- Addition of a methyl group to cytosine
- Epigenetic mechanism, involves in
 - gene expression regulation
 - gene silencing
 - X-chromosome inactivation
 - embryonic development
- Method for measuring DNA methylation: Bisulfite sequencing
- In mammals, 60-80% methylation at C-G dinucleotide contexts (CpG sites)
- Tools for genome-wide methylome analysis rather than reduced representation BS-seq (RRBS) ?

Methylation pipeline



- Thanks to Björn Grüning for writing the pipeline and galaxy wrappers
- One of the genome-wide DNA methylation analysis toolkits
- The first that is integrated into the galaxy



- Preprocessing: TrimGalore – wrapper around Cutadapt and FastQC
- Mapping: Bismark
 - Converts all Cs in to Ts in both reference and query
 - Uses bowtie for mapping
- Analysis - home made python scripts
 - Parallelized!

- TrimGalore and Bismark wrapper available in toolshed
 - http://toolshed.g2.bx.psu.edu/view/bgruening/trim_galore
 - <http://toolshed.g2.bx.psu.edu/view/bgruening/bismark>
- Methtools available at github
 - <https://github.com/bgruening/methtools>

By the way...



- ... our galaxy instance available at
- <http://galaxy.bi.uni-freiburg.de/>
 - RNA-seq, ChIP-seq, Methylation
 - Regular workshops on galaxy usage and analysis

Thank you!