Short description of the project

de.NBI-epi is a partner project in the HD-HuB node providing methods for epigenetics research. We provide expertise and high-end tools with an emphasis on DNA methylation analysis and integration. Services cover the full range from processing of raw data to validation, integration and exploration. MethylCtools extracts methylation calls from raw reads, which then can be further analyzed with RnBeads, while MeDeCom provides insights mimicking single-cell assays. Genomic regions of interest can then be further explored and integrated with external epigenetic data through EpiAnnotator, EpiExplorer or DeepBlue.

de.NBI services

- **Enrichment analysis in an easily accessible and responsive Shiny-interface.** Build with methylation data in mind but widely applicable to any type of genomic regions. (3 citations)

- **GUI-based application facilitating primary analysis of standard targeted sequenced bisulfite based assays.** (549 downloads, 582 citations)

**MethylCtools** A set of tools for the analysis of whole-genome bisulfite sequencing data and the study of DNA methylation. MethylCtools extends the popular short-read aligner BWA and generates high-quality methylation calls controlled for SNVs.

**RnBeads** An R package available through Bioconductor simplifying the analysis of DNA methylation in large datasets. The practical HTML report presents several analyses; giving a comprehensive view into the data. (2,571 downloads, 370 citations (original) + 10 (update))

**MeDeCom** A computational method for decomposition of heterogeneous DNA methylomes, recovering latent components of multi-cellular samples. (32 citations)

**EpiExplorer** A web-server allowing the user to explore sets of genomic regions in relation to multiple epigenetic and genetic annotations. (73 citations)

**DeepBlue** A Data Server and access point for processed epigenomic data, using controlled vocabularies and ontologies. DeepBlue can be be interfaced programmatically or through a web interface. (38 citations)

Progress report

In early 2019, an extensive update of RnBeads has been published including support of the Illumina EPIC array, extended methods to infer sample properties such as epigenetic age, and improved computational runtime. A workshop in the context of SCOG (single cell omics germany) was organized for single cell data analysis. DeepBlue can now be used to generate region databases based on various epigenomic data, which in turn can be used as an interpretation base for differentially methylated regions (RnBeads), or for various components that have been produced by MeDeCom. In addition these regions can be used for enrichment analysis of epigenomic data (LOLA). A three-stage protocol for reference-free deconvolution of complex DNA methylation data has been established and published, with MeDeCom as the core deconvolution tool.

**de.NBI Training and education**

- Internal course for Bioinformatics students at Saarland university "Epigenetic data processing", 23-25th, March 2020
- DNA Methylation: Design to Discovery, 18-1 9th, May, 2020

**Publications**


General information on the project

- No. of staff paid from de.NBI grant (FTE): 2.0
- Other staff involved : 0.2