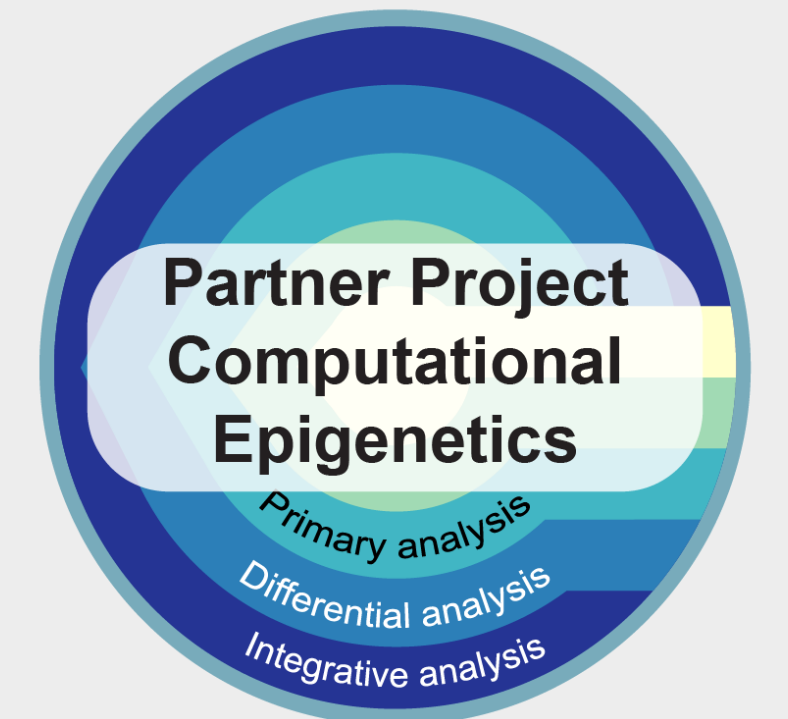


HD-HuB

Heidelberg Center for Human Bioinformatics Computational Epigenetics (de.NBI-epi)



Salhab A.¹, Scherer M.¹, Lutsik P.², Walter J.¹, Brors B.³

¹Saarland University, Epigenetics Department, Germany; ²Division Epigenomics and Cancer Risk Factors, German Cancer Research Center (DKFZ), Germany; ³Division of Applied Bioinformatics, DKFZ, Germany

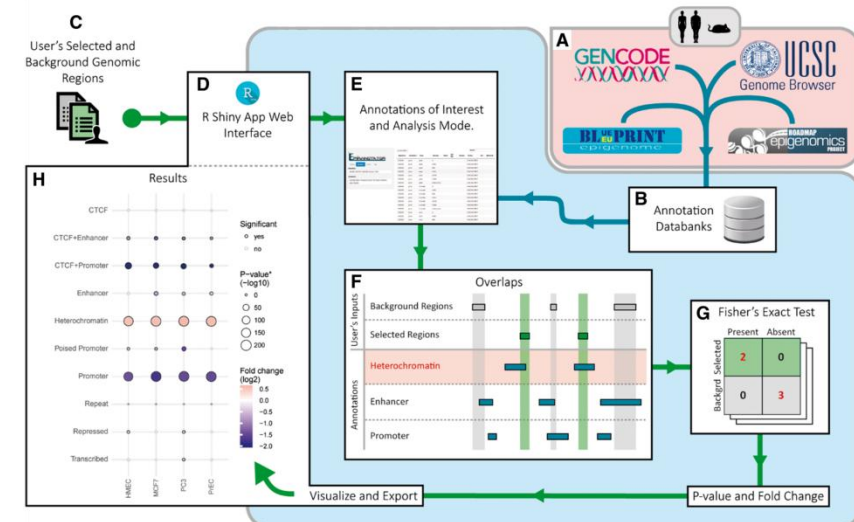
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Short description of the project

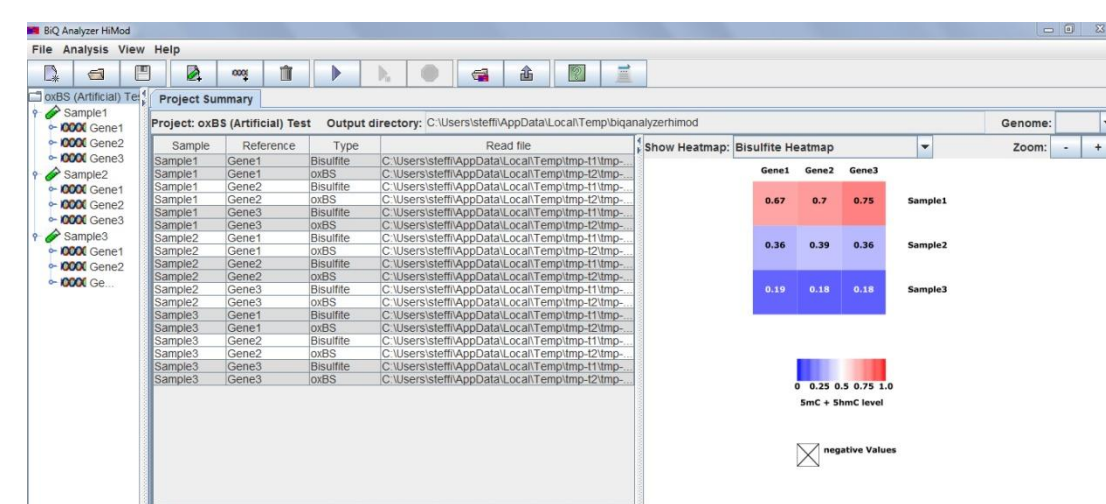
de.NBI-epi is a partner project in the HD-HuB node providing methods for epigenetics research. We provide expertise and high-end tools with an emphasis on DNA methylation analysis and integration. Services cover the full range from processing of raw data to validation, integration and exploration. *MethylCtools* 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

EPIANNOTATOR 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)

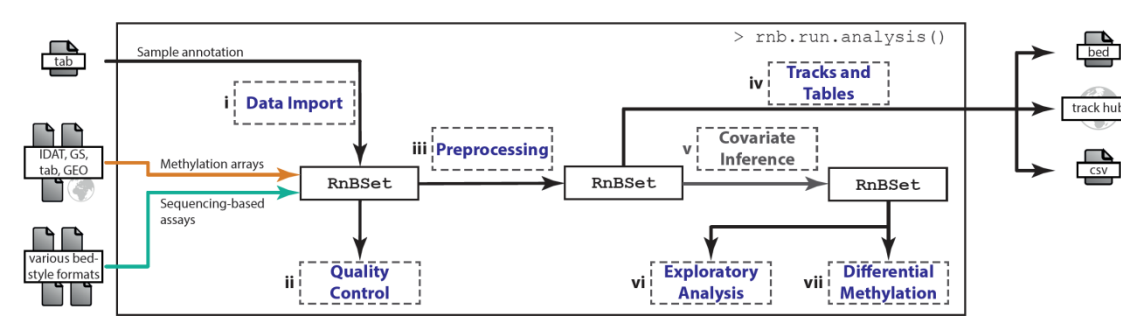


BiQ Analyzer GUI-based application facilitating primary analysis of standard targeted sequenced bisulfite based assays. (549 downloads, 582 citations)



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))

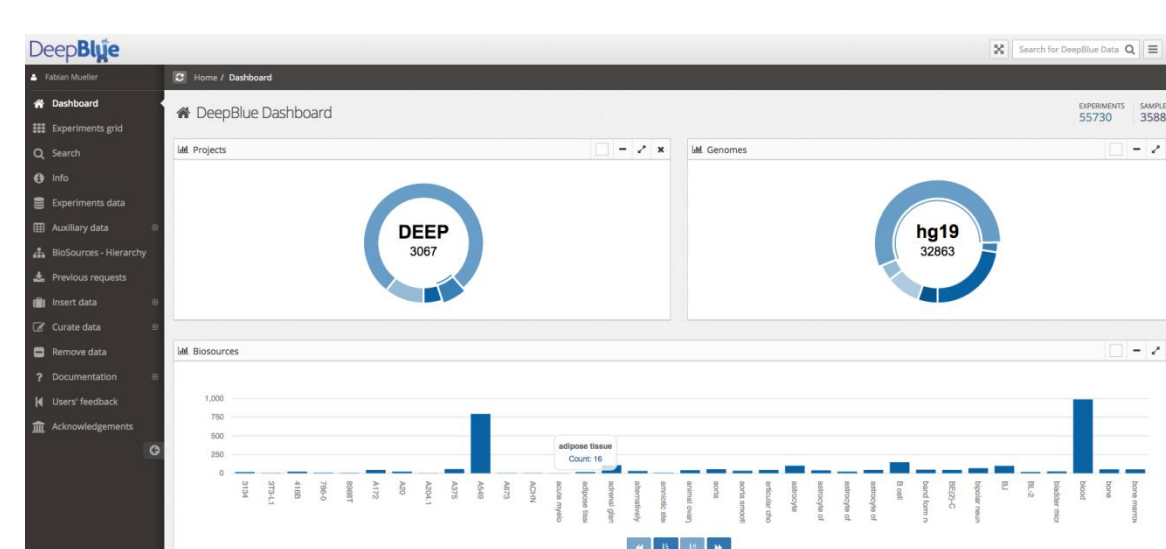


MeDeCom A computational method for decomposition of heterogeneous DNA methylomes, recovering latent components of multi-cellular samples. (32 citations)

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 interfaced programmatically or through a web interface. (38 citations)



General information on the project

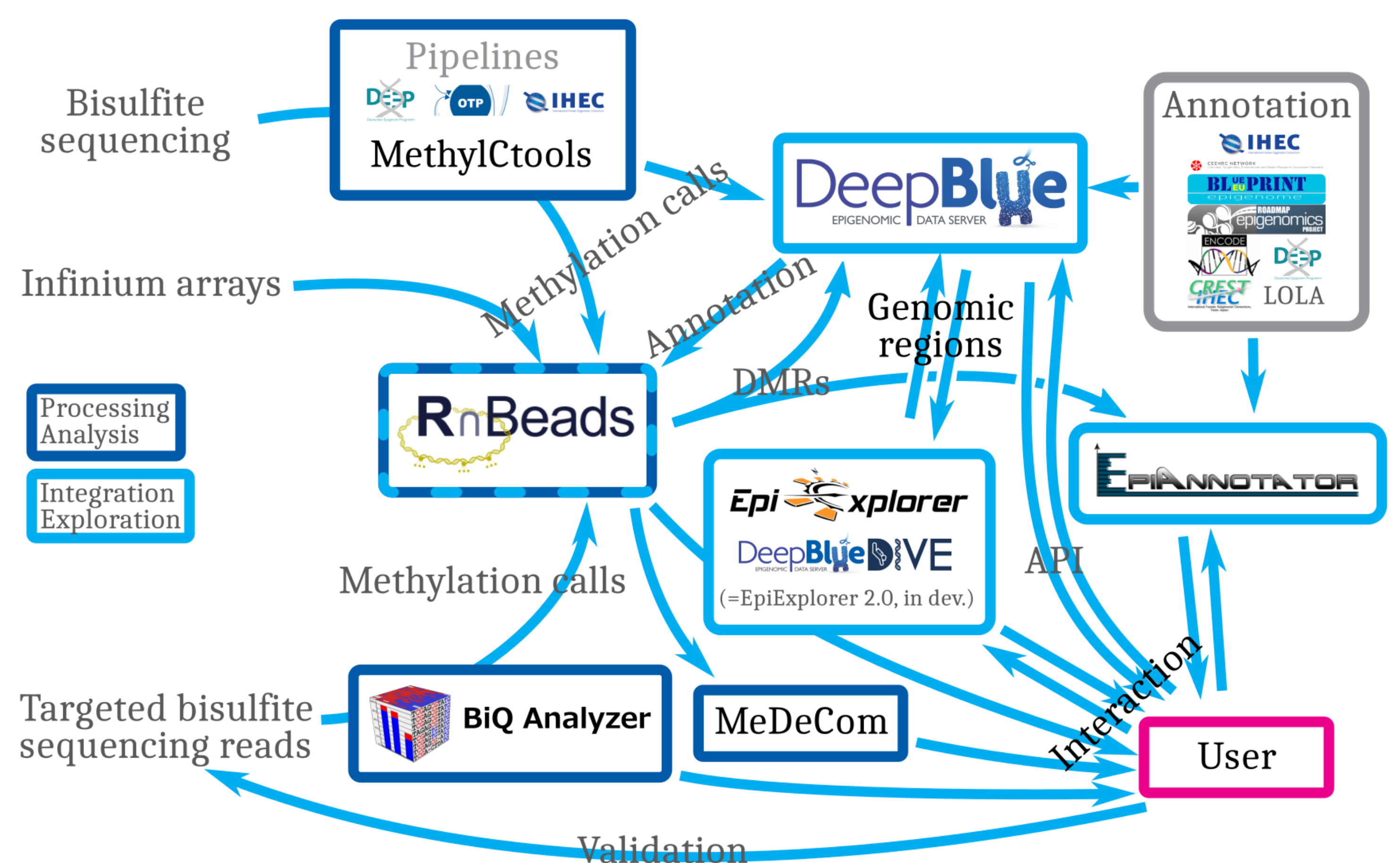
- No. of staff paid from de.NBI grant (FTE): 2.0
- Other staff involved : 0.2

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, 18-19th, May, 2020

Publications

- Scherer M, Nazarov P V, Toth R, Sahay S, Kaoma T, Plass C, Lengauer T, Walter J, Lutsik P. Reference-free deconvolution of complex DNA methylation data – a detailed protocol. bioRxiv (2019), <http://dx.doi.org/10.1101/853150>
- Nordström KJV, Schmidt F, Gasparoni N, Salhab A, Gasparoni G, Kattler K, et al. Unique and assay specific features of NOME-, ATAC- and DNase I-seq data. Nucleic Acids Res. 2019;47(20):10580–96.
- Müller F, Scherer M, Assenov Y, Lutsik P, Walter J, Lengauer T, Bock C. RnBeads 2.0: comprehensive analysis of DNA methylation data. Genome Biology. 2019;20(55)