The de.NBI project de.STAIR 1 – Alternative splicing and differential expression

*The de.STAIR 1 project at the University Leipzig is a partner project dedicated to design flexible pipelines for RNA-Seq analysis, Leipzig implements workflows for the (split-alignment) of RNA-Seq reads, the detection of transcription changes and the integration of transcriptomic data with epigenetic marks.*

Located at the Interdisciplinary Center for Bioinformatics, the Leipzig site evaluates and implements various customizable GALAXY workflows for the alignment of RNA-Seq data and the subsequent analysis steps. The users shall be enabled to quickly and reproducibly analyze data of various RNA-Seq protocols using one-touch pipelines (e.g. for mRNA-Seq, miRNA-Seq or dRNA-Seq) and to integrate their results with epigenetic data and experiments.

**The topics of the Leipzig partner of de.STAIR:**

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* Integration and output harmonization of various NGS aligners to the GALAXY workflows of de.STAIR; design and implementation of comprehensive mapping quality reports
* Integration and harmonization of tools for the detection of differential expression; automated, comparative reports on differentially expressed transcripts.
* Development of improved methods for the detection of differential, alternative splicing. Integration and harmonization of existing methods.
* Development and integration of .methods to link transcriptomic and epigenetic changes

**Currently developed and maintained software:**

* segemehl, a versatile NGS aligner that supports various protocols such as mRNA-Seq (split-read mapping) or bisulfite conversions.
* metilene, a tool for ultra-fast detection of differentially methylated regions.

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* BAT: a comprehensive pipeline for the joint analysis of transcriptomic and epigenomic data.