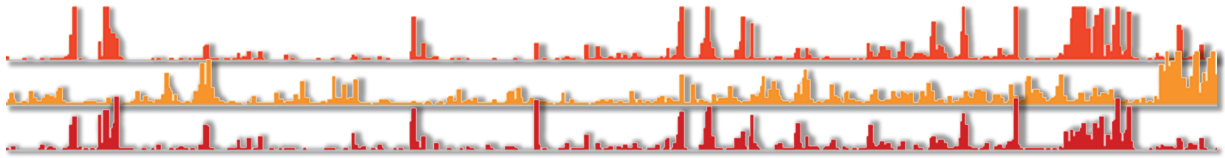


Finding regulatory motifs and extracting downstream targets



Mapping, peak calling and classification

The first steps in our ChIP-Seq workflow are mapping the reads and subsequently applying peak detection on the mapped data. Peak calling can be performed with either NGS Analyzer or MACS (Zhang et al. Genome Biology 2008). Both methods support the use of a control file and return statistically significant peaks. Performing a read/peak classification to verify enrichment e.g. in promoter regions provides a first level of quality control for the experiment.

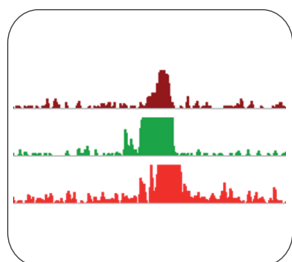
Promoter and TF analysis

For many transcription factors (TFs) DNA-binding motifs have been published in the scientific literature. MatBase - our transcription factor knowledge base - contains information on more than 17,000 TFs and almost 1,300 binding motifs. These motifs can be searched in the called peaks, and - using the information from EIDorado (our comprehensive annotation and promoter database) - overrepresented TF binding sites can be detected. Matching peaks can automatically be extracted for further analyses. In addition we identify pairs of TFs that bind with a specific distance profile and may have synergistic functions in gene regulation. To uncover novel TF binding sites motifs, CoreSearch can be applied to the peak sequences. Overall, the workflow allows to generate TF binding site motifs directly from your data with only a few mouse clicks.

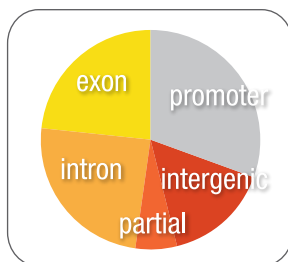
Downstream analysis

To understand the functional relevance of detected peaks, you can extract possible target genes by correlating peaks with promoter regions or primary transcripts. This enables you to uncover biological processes and canonical pathways regulated through the targeted factor by using the Genomatix Pathway System (GePS).

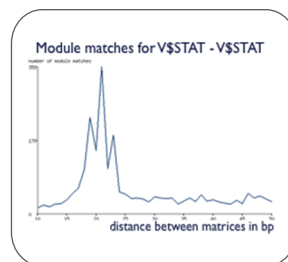
workflow



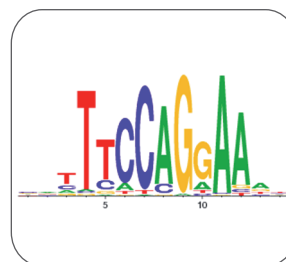
mapping



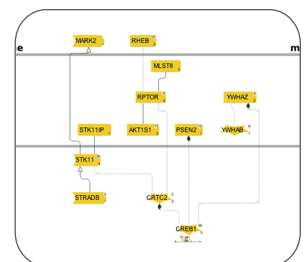
classification



TF modules

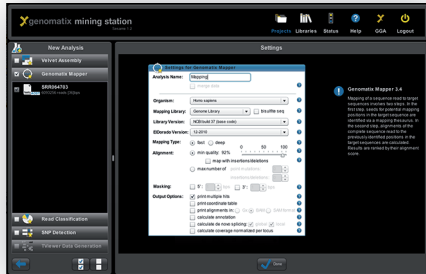


motifs



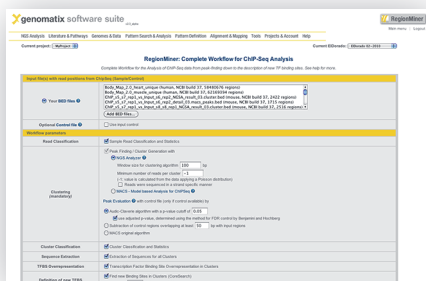
networks

Mapping, ChIP-Seq workflow and networks



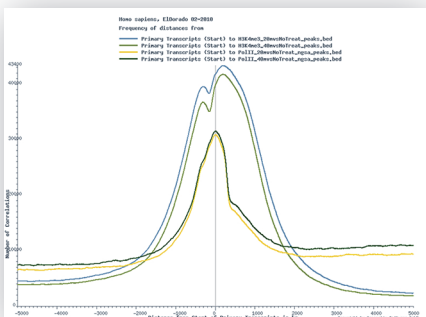
Mapping and read classification

ChIP-Seq reads are mapped to the genome with the Genomatix mapping algorithm. The mapping can be started via an intuitive user interface (see left). Alignment qualities for all unique and multiple hits are reported. After the mapping, read classification provides a first level of quality control.



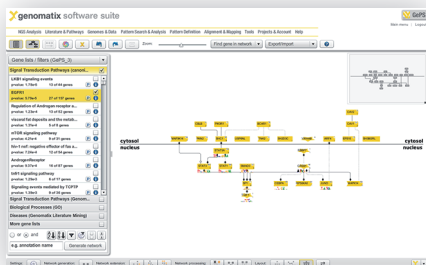
ChIP-Seq workflow

We have compiled a complete ChIP-Seq workflow including peak calling, peak classification, transcription factor binding site (TFBS) overrepresentation and definition of new TFBS motifs. Extending on this workflow, downstream analyses can be started (e.g. investigation of gene regulation using FrameWorker or finding potential target genes using GenomInspector).



Data integration

GenomInspector is a tool to correlate peaks with genomic regions, such as promoters, primary transcripts or microRNAs. In addition, different analyses can be compared to each other. For instance, replicates can be compared for their overlap or ChIP-Seq peaks can be compared to expressed genes from an RNA-Seq experiment. Correlated data can be exported for further analyses.



Networks and canonical pathways

To generate networks of regulated genes, GenomInspector can be used to extract target genes. These target genes can be loaded into the Genomatix Pathway System (GePS) to obtain gene enrichments and generate signaling networks or visualize relevant canonical pathways together with all available gene annotation.