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Combining DNase hypersensitivity data and transcription factor expression to identify putative regulatory regions in leukemia

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Acute myeloid leukemia (AML) is the most common acute leukemia in adults with about 2-2.5 million new cases per year worldwide. Only 27% of patients survive 5 years or more after being diagnosed with the disease. Within the EU-funded BLUEPRINT project several epigenetic markers as well as expression data were generated from blood and bone marrow samples of several AML patients. We have used DNase hypersensitivity and expression data from the project to identify putative transcriptional regulators and regulatory regions by combining omics data with literature. The approach included identifying DNase-HS regions that were common among AML patients but absent in samples from healthy individuals. We then used RNA-Seq data from the project to identify transcription factor binding sites that were differentially regulated between the case and control group. Finally we used Genomati'x MatInspector software to pick regions that had both differences in DNase-HS as well as putative binding sites for the differentially expressed transcription factors. Potential target genes were selected by a next-neighbor approach and the findings were evaluated based on gene disease associations from Genomati'x literature database.

Biography

Korbinian Grote is a Senior Scientist at Genomatix AG, Germany. His expertise is in bioinformatics of gene regulation, neural networks and deep learning. For BLUEPRINT, he coordinated the project activities at Genomatix which included the development of a processing pipeline for various omics data and the creation of a visual interface to allow non-bioinformaticians easy access to the data in a biological context.

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