

Andreas Kloetgen

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Education

from / to	Degree, Place
2008 / June 2011	Bachelor of Science in Bioinformatics and Genome Research University Bielefeld, Germany
2011 / June 2013	Master of Science in Bioinformatics and Genome Research University Bielefeld, Germany
September 2013 / -	Ph.D. fellow in Computer Science Heinrich-Heine University Duesseldorf, Germany

Professional Experience

from / to	Institution	Tasks
2010 / 2012	Department for Genome Research, University Bielefeld	Design and implementation of bioinformatics software for GABI-Kat
November 2012 / January 2013	Department for Biomathematics, University Bielefeld	Preparing manuscript for a lecture series in Biomathematics
October 2012 / June 2013	Bayer Health Care, Wuppertal	Practical training; Design and implementation of bioinformatics software for GWAS analysis

Additional Skills

Languages

German and English, fluently spoken and written

Computational Skills

Programming languages: Java, C, Perl, R, PHP, MySQL / OracleSQL, LaTeX

Machine learning skills: HMMs, Bayesian networks, Cluster analysis

Statistics: sampling, statistical testing, statistical correlation analysis

Bioinformatics tools: Sequence analysis (Cutadapt, Trimmomatic, Bowtie, BWA, STAR, TopHat, fastqc, HTSeq, Bioconductor packages (including edgeR, spliceSites), cufflinks, samtools, ngsutils), GSEA, Ingenuity pathway analysis, Primer3 (PCR primer design), meme-suite (binding motif detection), RNAhybrid & Miranda (miRNA-target prediction)

Lab Skills

Standard molecular biology techniques (DNA/RNA purification and isolation, standard PCR, qRT-PCR, electrophoresis)
PAR-CLIP

Publications

Kleinboelting N et al., *GABI-Kat SimpleSearch: new features of the Arabidopsis thaliana T-DNA mutant database*, Nucleic Acids Res. 2012 Jan;40(Database issue):D1211-5.

Kloetgen A et al., *Biochemical and bioinformatic methods for elucidating the role of RNA–protein interactions in posttranscriptional regulation*, Brief Funct Genomics. 2015 Mar;14(2):102-14.

Hezaveh K et al., *Alterations of miRNAs and miRNA-regulated mRNA expression in GC B cell lymphomas determined by integrative sequencing analysis*. Haematologica. 2016 Jul 6. pii: haematol.2016.143891.

Doerrenberg M et al., *T-Cell Acute Lymphoblastic Leukemia in Infants Has Distinct Genetic and Epigenetic Features Compared to Childhood Cases*. Genes Chromosomes Cancer. 2016 Sep 26.

Kloetgen A et al., *The PARA-suite: PAR-CLIP specific sequence read simulation and processing*. PeerJ, accepted.

Manuscripts currently under review

Shinde P et al., *TNF mediated survival of CD169+ cells mediate innate and adaptive immune activation during viral infection*. (submitted to Nature Communications, currently under review)

Hoell JI et al., *Exome sequencing allows the identification of druggable targets in the majority of children with ALL relapse after allogeneic SCT*. (submitted to Blood, currently under review)

Awards

PhD scholarship granted by the Duesseldorf School of Oncology (DSO)

Poster presentations

Kloetgen A, Borkhardt A, Hoell JI, McHardy AC, *The PARA-suite: an easy to use toolkit for the analysis of error prone CLIP sequencing data*. ISMB/ECCB 2015, July 9-14 2015, Dublin, Ireland.