

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), mem-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.

Manuscripts currently under review

Kloetgen A et al., *The PARA-suite: processing and aligning error-prone CLIP sequencing reads with empirical error model inference*. (submitted to Bioinformatics, currently under review)

Hezaveh K et al., *Alterations of miRNAs and miRNA-regulated mRNA expression in GC B cell lymphomas determined by integrative sequencing analysis*. (submitted to Haematologica, 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)

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.