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Interests in Bioinformatics

- Analysis of genomes and transcriptomes
- Evaluation of genome wide gene expression data
- statistical analysis of Sequence data (candidate genes, whole exome, next generation sequencing)
- Evaluation of genome wide SNP data based on linkage disequilibrium and haplotype analysis
- Evaluation of funktional analysis within cellular models (polymorphisms, gene expression profiles, signaling pathways)

Software

- bowtie, bwa, gatk, picard, sam-tools, vcf-tools, annovar, clc, etc.

Current Research and Development Projects

DFG: Research Unit "Germ Cell Potential"

Projekt (TU 298/1-1, Research Unit FOR 1041)

“Role of structural genomic variation (copy number variants) in spermatogenetic failure”