

BIOINFORMATICS SERVICES

Quretec together with Department of Computer Science (University of Tartu) forms a joint Bioinformatics, Algorithmics, and Data Mining group BIIT. Our main research topics and capabilities include the gene regulation, gene expression data analysis, biological data mining, systems biology, combinatorial pattern matching, developing software for biomedical research databases, as well as partnering in stem cell and cancer related projects.

EXPERIENCE WITH

- mRNA expression analysis
 - RNA-seq
 - Affymetrix, Illumina microarray platforms
 - Q-RT-PCR
- Chromatin immunoprecipitation datasets
 - Epigenetic histone modifications
 - Transcription factor binding events
- Dual luciferase assays
- Compound dose response profiles
- Alternative splicing and tissue specific splice variant identification
- miRNA analysis and target prediction
- Motif discovery in nucleic acid and protein sequences
- Pattern matching
- Identification of point mutations and small indels associated with Mendelian diseases using NGS data
- Network reconstruction and modeling
- Data mining
- Machine learning

ACTIVITY IN EU FP6/7 PROJECTS

- AgedBrainSYSBIO – systems biology, network reconstruction, Alzheimer disease
- ATD – alternative splicing, tissue specific splice variants
- CIESCI – epigenetic signals in cancer initiation
- COBRED – expression, metabolomic, proteomic profiling of colon and breast cancer
- DETECTIVE – biomarker discovery using repeated dose toxicity
- ENFIN – systems biology, network reconstruction and modeling
- ESNATS – alternative compound testing using embryonic stem cells
- FUNGENES – expression profiling of embryonic stem cells
- IMI-EMIF-Platform - unifying medical data across Europe
- IMI-PREDECT – pathway analysis based on expression data to develop in vitro models of breast, lung and prostate cancer
- SIROCCO – identifying roles of short silencing RNAs in diseases

PUBLICLY AVAILABLE TOOLS

- DiffExp – differentially expressed genes finder
- ESCD – embryonic stem cell database, ChIP and expression perturbation datasets
- Expressview – gene expression dataset viewer
- g:Profiler – Gene Ontology enrichment, gene ID conversion, ortholog mapping
- GraphWeb – network reconstruction and mining
- KEGGAnim – gene expression mapping to known KEGG pathways
- MEM – gene expression similarity searches across thousands of experiments
- VISHIC – gene expression clustering based on Gene Ontology annotations

ONGOING COLLABORATIONS

- Estonian Genome Centre (Prof. Metspalu; Dr. Milani)
- University of Tartu, Medical Faculty (Prof. Salumets; Prof. Peterson)
- Protobios (Dr. Neuman)
- Tartu University Hospital, Anaesthesiology and Intensive Care Clinic (Prof. Starkopf)
- EGen Inc

METADATA MANAGEMENT

- Project specific databases and metadata collection and management solutions with Qure Data Management Platform
- Clinical Trial Management Systems
- Several national health registries
- Statistical surveys and e-census software (Statistics Estonia)