

LIST OF ABSTRACTS: BIOINFORMATICS AT ALL SCALES OF LIFE



Oral
Presentation



Software
Demo

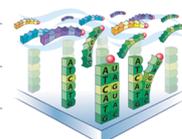
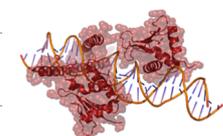
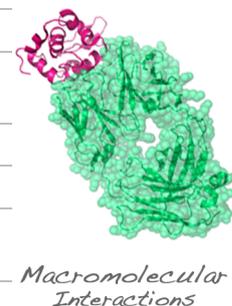
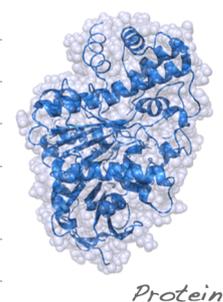
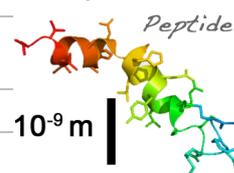
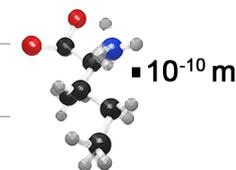


Poster
Commercial

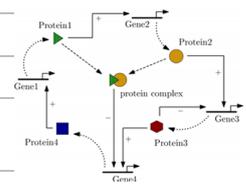


Poster
Presentation

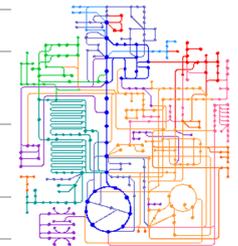
- 1 Artefacts in the refinement of isoleucine.
- 2 Identifying cholestasis-causing drug compounds: a validated ligand-based pharmacophore model.
- 3 Prediction of protein residues contacts with deep learning and direct information methods.
- 4 Logistic regression for the classification of PSMS: a simple method for a complex problem.
- 5 Focus on relatively hydrophilic peptides for targeted proteomics.
- 6 Coding regions subject to multiple constraints tend to encode intrinsically disordered protein segments.
- 7 Spatially cohesive amino acids and their role in protein molecular structures.
- 8 In silico stability analysis method applied to bovine seminal ribonuclease.
- 9 Mapping intra-protein communication – the FYN SH2 snap-lock mechanism.
- 10 DynaMine: from protein sequence to dynamics and disorder.
- 11 pE-DB: a database of structural ensembles of intrinsically disordered and of unfolded proteins.
- 12 The selectivity of the voltage-dependent anion channel towards inorganic ions.
- 13 Protein fold recognition through hybrid geometric kernel integration of different protein features with complementary information.
- 14 Protein thermal stability prediction by statistical potential.
- 15 Computational analysis of antigen-antibody compared to other protein-protein interactions.
- 16 Pairwise kernel methods for predicting molecular interactions.
- 17 CAPRI: the diverse challenges of computational protein-protein docking.
- 18 Identifying degrons: how are proteins targeted for degradation by the ubiquitin proteasome system ?
- 19 Superclusteroid 2: the easy-to-use tool to analyse your protein-protein interaction data.
- 20 Improving the detection of biologically meaningful clusters in protein interaction networks through integrated functional analysis.
- 21 Integrative analysis of regulatory tracks for the identification of direct TF-target interactions.
- 22 Prediction of transcriptional targets using advanced enhancer models.
- 23 Stable feature selection techniques for microarray data.
- 24 Experiment-specific probe set annotation for Affymetrix gene expression data.
- 25 Bi-clustering gene expression data under constraints.
- 26 Galahad - a web server for gene expression data analysis in support of drug development.
- 27 Comparison of methods for pattern recognition in toxicogenomics time series.
- 28 Unveiling the mechanisms of action and the side effects of drugs by comparative module analysis.
- 29 Protein identification based on ribosome targeted mRNA fragments.
- 30 PROBIC-II: simultaneously detecting coexpression modules and their regulatory patterns.



- 31 Mechanistic interpretation of gene lists using interaction networks.
- 32 Inferring the direction of gene interactions.
- 33 Network inference by integrating biclustering and feature selection.
- 34 Netter: re-ranking gene regulatory network predictions using structure properties.
- 35 The rank minrelation for transcriptional network inference.
- 36 The cell nucleus helps regulate not only the dynamics of gene expression, but also its noise.
- 37 Data-driven validation of gene regulatory networks using knock-down data.
- 38 CUTTER: GPU-based reconstruction of biological networks from perturbation experiments.
- 39 FASTCORE: an algorithm for fast reconstruction of context-specific metabolic network models.
- 40 Network deregulation analysis in complex diseases via the pairwise elastic net.
- 41 NODE and CATCH: two algorithms to get more accurate 16S rRNA sequencing data.
- 42 Applications of large-scale genome-wide DNA methylation profiling.
- 43 SNP-guided identification of monoallelic DNA-methylation events from enrichment-based sequencing data.
- 44 Mining the garbage fragments of methylation-specific enriched DNA sequencing.
- 45 Assessing the outcome of 16S rDNA-based community analysis by comprehensive simulations.
- 46 Rapid identification of potential antimicrobial drug targets.
- 47 The complex intron landscape and massive intron invasion in a picoeukaryote provides insights into intron evolution.
- 48 Toxin-antitoxin module dynamics can cause persister cell formation in *E. coli*.
- 49 Whole-genome sequence-based identification of epidemic plasmids spreading Extended-Spectrum Beta-Lactamase genes among *Escherichia coli* from different hosts.
- 50 Evolution following whole genome duplication in the yeast gene regulatory network.
- 51 Comparative transcriptomics of helper T cells.
- 52 Effect of UNBS1450 on histiocytic lymphoma cell line U937: a transcriptomics analysis.
- 53 RNA-sequencing identifies NOVA1 as a major splicing regulator in pancreatic beta cells.
- 54 CellMissy: a tool for management, storage, dissemination and analysis of cell migration data.
- 55 GWAS-M: genome-wide association studies for microbes.
- 56 AFKSNP: assembly-free K-mer based SNP comparison of bacterial WGS samples.
- 57 Comparative analysis of biome-specific microbial association networks.
- 58 Towards a software-independent taxonomic profiling method of microbial metagenomes.
- 59 Identifying interaction patterns in human microbiota.
- 60 Comparative metagenomics by cross-assembly.

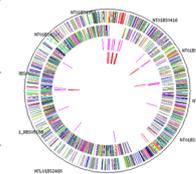


Gene regulation Networks

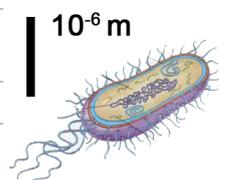


Metabolism

Genome

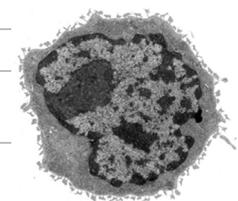


Sequencing



Cell

10^{-5} m

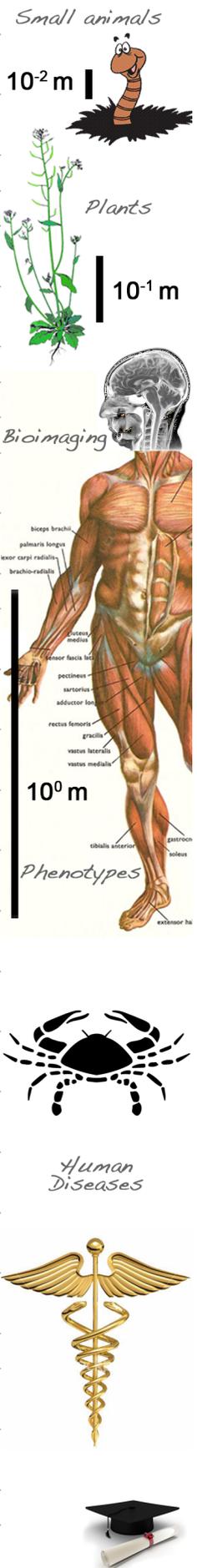


Cell population



Metagenome

-  **61** ORCAE: online resource for community annotation of eukaryotes.
-   **62** Comparing fragmentation spectra from two parasitic worm species to discover unique peptides.
-  **63** Identifying losses and expansions of selected genes families in incomplete genomic datasets.
-  **64** Unravelling the genetic basis of *Fusarium* sugarbeet wilt disease.
-  **65** Sequence based genotyping: applications for plant breeding.
-  **66** Convergent gene loss following gene and genome duplications creates single-copy families in flowering plants.
-   **67** Integrating gene regulatory network inference solutions for the abiotic stress response in *Arabidopsis thaliana*.
-  **68** Visual analysis of spermatozoa, oocytes and early embryonic transcripts.
-  **69** Tensor decomposition for data reduction in mass spectrometry imaging.
-  **70** Large-scale bioimage analysis using web services and machine learning.
-  **71** Accuracy of an automated vessel counting algorithm in four different tumor types.
-  **72** Guided exploration of mass spectrometry imaging data through integration with anatomical information.
-  **73** eXtasy : variant prioritization by genomic data fusion.
-   **74** Prediction accuracy for deleterious and disease causing mutations in healthy individuals.
-  **75** Convert your favourite protein modelling program into a mutation predictor: “MODICT”.
-  **76** Unravelling the regulatory mechanisms behind inter-genic cardiac quantitative trait loci through systems genetics approaches.
-  **77** Connecting phenotypes and traits to biological processes and molecular functions.
-  **78** A class representative model for pure parsimony haplotyping under uncertain data.
-  **79** Classifying the progression of ductal carcinoma from single-cell sampled data: a case study.
-   **80** Comprehensive analysis of transcriptome variation uncovers known and novel driver events in T-cell acute lymphoblastic leukemia.
-   **81** Detecting master regulators and cis-regulatory interactions in human cancer related gene networks.
-  **82** Long non-coding RNAs in lung cancer: comparison of microarray and RNA-seq techniques.
-  **83** Extracting signatures from high-dimensional unbalanced biological data: the cases of DNA methylation and LNCRNA in breast cancer.
-  **84** BELLEROPHON: a hybrid method for detecting interchromosomal rearrangements at base pair resolution using next-generation sequencing data.
-  **85** A human-specific endogenous retroviral insert serves as an enhancer for the schizophrenia-linked gene *PRODH*.
-   **86** In silico drug repurposing in Parkinson’s disease.
-  **87** Assessment of reference networks for pathway analysis and mechanistic interpretation of disease data.
-   **88** Integrated analysis of transcript level regulation of metabolism reveals disease relevant nodes of the human metabolic network.
-  **89** Biomedical text mining for disease gene discovery.
-  **90** Bioinformatics and systems biology masters: bridging the gap between heterogeneous student backgrounds.



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|---|--|---|
|   | 91 jqcML: A Java API for quality control for mass spectrometry experiments. | |
|  | 92 Identifying interesting frequent patterns in complex biological data with MIME. | <i>Human group</i> |
|   | 93 Facilitating computational biology and bioinformatics on HPC systems using EasyBuild. |  |
|  | 94 NGS logistics: data infrastructure for efficient analysis of NGS sequence variants. | <i>Logistics</i> |
|   | 95 DBXP: investigating the future of integrative bioinformatics research infrastructures in Europe. | <i>Infrastructure</i> |
|  | 96 Data integration & stewardship centre: tackling the big data challenge in life science research. | |
|  | 97 Bioinformatics @ DSM biotechnology centre | |
|  | 98 PacBio: single molecule sequencing to improve the Norway Spruce genome annotation. | |
|  | 99 A random forests based breast cancer diagnosis tool using circulating miRNA expression. |  |
|  | 100 Regression with enriched random forest. | 10¹ m |
|  | 101 Transposable element annotation using relational random forests. | |
|  | 102 Small decision models: capitalizing on feature selection. | <i>Forest</i> |
|  | 103 Predicting tryptic cleavage from proteomics data using decision tree ensembles. | |
|  | 104 Promoting a functional and comparative understanding of the conifer genome- implementing applied aspects for more productive and adapted forests. | <i>Cloud</i> |
|  | 105 NMR_REDO: Large-scale recalculation of NMR structures in the cloud. |  |
|   | 106 Comparative motif discovery in the cloud. | 10³ m |
|  | 107 Large-scale ancestral route reconstruction of the Luxembourgian HIV cohort in international context. | |
|  | 108 Species interactions in the world's oceans. |  10⁷ m |