Computational Modeling of Gene Expression (Ramot)

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Prof. Tuller's lab is a leading computational lab that primarily focuses on and has extensive expertise studying and modeling diverse gene expression mechanisms and engineering gene expression based on computational and synthetic biology tools.

Computational Modeling of Gene Expression

- Development of computational predictive models to mathematically analyze and simulate the different stages of gene expression. The models are based on biophysical and stochastic aspects of this process.

Engineering of Gene Expression

- This research group devise supervised and unsupervised approaches for engineering gene expression for various biotechnological objectives.

Deciphering the Gene Expression Code

- Conducting large scale analyses of genomic data to discern the way various aspects of gene expression are encoded in the transcript.

Evolutionary Systems Biology

- Studying various questions related to the evolution of biological systems. Specifically, we endeavor to deduce the evolution of gene expression and the co-evolution of various intra-cellular components also during cancer.

Computational Study of Molecular Evolution

- Designing and analyzing algorithms for answering various questions in molecular evolution.

Gene Expression in Diseases

- Analyzing and modeling gene expression in autoimmune diseases and cancer to better understand their pathogenesis, for screening and diagnosis, and aiming at developing new therapeutic approaches.

Services

Gene expression optimization consultation

- Per hour consultation for any aspect related to gene expression optimization in various vectors/hosts/systems.

Bioinformatics consultation

- Per hour consultation for bioinformatics analysis strategy and support, in a wide range of expertise from different gene expression related topics to high throughput methodologies and statistical analysis.

Optimization of heterologous gene expression in various systems

- Computational design of various parts of the transcript and genome (e.g. promoter, UTRs, introns, coding regions, etc) for gene expression optimization for various objectives.

Computational modeling of gene expression

- Computational models of various aspects related to gene expression including transcription, splicing, translation, degradation, etc.

NGS and Microarray data analysis

Ribosome profiling analysis

- Analysis of ribosome profiling output data (Ribo-seq) across a multitude of parameters and queries, enabling a highly robust means of expression profiles and unique information such as ribosome/transcript ratios, codon effects, and identification of novel translation initiation sites, all based on ribosome footprints.

RNA-seq data analysis

- Raw data cleanup and preparation, alignment, read quantitation, geneset expression analysis, clustering, splicing events, identifying specific transcripts such as gene fusions/mutations.

Microarray expression profiling:

- Analysis of microarray data including alignment, clustering, functional annotations, and identification of pathway enrichment.

Hi-C data analysis

- Various types of Hi-C data analyses such as inferring 3D models and networks of gene proximity.

Systems biology

Gene pathway analysis

- Analysis and identification of enriched pathways in specified gene sets.

Spatial genomic organization in various conditions

- Comparative analysis of spatial eukaryotic genome organization in various conditions, tissues, and single cells, by analyzing Hi-C data output. This analysis can yield groups of genes and pathways that display similar spatial genome organization, suggesting possible evolutionary and functional relations.

Gene expression correlation

- Analysis of statistical correlation between expression of various gene expression profiles and features, including comparison across organisms.

Functional gene-set enrichment

- Analyses to derive functionality of enriched gene sets based on Gene Ontology annotations, pathways, and specific genes in expression data.

Plotting gene networks

- Elucidation plotting and analysis of gene/protein networks based on defined parameters (e.g. co-expression, interaction etc.).

Cancer mutation analysis

- Various mutational analyses such as gene translation efficiency, positional distribution, and determining dN/dS of mutations which can identify likelihood of protein structure and functional change, effect on gene expression.
- Analysis of various biological networks such as protein interaction networks, metabolic networks, gene expression networks, etc.:
- Various types of analysis such as clustering, differentially expressed pathways, motif analysis, networks comparisons, etc.

Analysis of co-functionality

- Co-functionality analysis is based on various parameters of genomic neighborhood, co-expression, gene fusion, and more

Protein interactions in disease

- Examination of gene network expression changes in diseases and their effect on protein-protein interaction networks.

Biophysical modeling of intracellular phenomena

mRNA folding predictions

- Prediction of mRNA folding patterns using various computational algorithms to determine folding energy of the secondary structure associated with the minimum free energy for an RNA sequence.

mRNA translation modeling

- models of translation that consider all central aspects of the process such as the number of ribosomes and mRNAs, decoding rates of each codon, initiation rates, size of the ribosomes, etc.

Biological sequence pattern analyses

Codon usage frequency calculation

- Calculation of DNA/mRNA codon usage frequency and various codon bias measures from given sequencing reads. Such comparisons could be performed to detect differences between gene groups, organisms, states etc.

Motif and feature detection in DNA sequences

- Identification and quantification of various motifs and features in DNA sequences, such as restriction enzyme sites, ORFs, TSS and more.

Molecular evolution

Phylogenetic analysis

- Assembly of hierarchical phylogenetic analysis and phylogenetic trees and networks.

Identification of horizontal gene transfer events

- Phylogenetic and heuristic based algorithms for identifying horizontal gene transfers across species.

Gene evolutionary analysis

- Methodologies to analyze gene evolution including co-evolution, mutation rate, and additional measures such as relative evolutionary rate, copy number pattern, and propensity for gene loss.

The research group has vast experience with:

- Engineering transcripts and genomes for optimizing gene expression.
- Analyses of various types of large scale gene expression measurements (e.g. RNA-seq, Ribo-seq, Hi-C, BS-seq, etc.).

Unique equipment found in the lab

- The lab has access to over 300 computing cores, a total of 720 GB RAM memory, and 56 TB storage memory.

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