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Identification of a small set of plasma signalling proteins using neural network for prediction of Alzheimer's disease
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Pattern recognition methods to relate time profiles of gene expression with phenotypic data: a comparative study
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Learning from healthy and stable eyes: a new approach for detection of glaucomatous progression
A Gaussian mixture model based cost function for parameter estimation of chaotic biological systems
Gene selection for the reconstruction of stem cell differentiation trees: a linear programming approach
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A computational method for drug repositioning using publicly available gene expression data
HMMvar-func: a new method for predicting the functional outcome of genetic variants
Automated identification of copepods using digital image processing and artificial neural network
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Inferring dynamic gene regulatory networks in cardiac differentiation through the integration of multi-dimensional data
Robust feature selection to predict tumor treatment outcome
Data-intensive analysis of HIV mutations
Hierarchical boosting: a machine-learning framework to detect and classify hard selective sweeps in human populations
DINGO: Differential Network Analysis in Genomics

Identifying cancer-related microRNAs based on gene expression data
Faster sequence homology searches by clustering subsequences.
An adaptive genetic algorithm for selection of blood-based biomarkers for prediction of Alzheimer's disease progression
Characterizing informative sequence descriptors and predicting binding affinities of heterodimeric protein complexes
A probabilistic approach for pediatric epilepsy diagnosis using brain functional connectivity networks
Analysis of miRNA expression profiles in breast cancer using biclustering
Cardiac magnetic resonance image-based classification of the risk of arrhythmias in post-myocardial infarction patients
Deep convolutional neural networks for annotating gene expression patterns in the mouse brain
Automated parameter estimation for biological models using Bayesian statistical model checking
Computational and analytical challenges in single-cell transcriptomics
Classification of bioinformatics workflows using weighted versions of partitioning and hierarchical clustering algorithms
MixChIP: a probabilistic method for cell type specific protein-DNA binding analysis