**Seminari Gennaio**

**Update 25/9/2017 – Titoli già assegnati**  
Identification of a small set of plasma signalling proteins using neural network for prediction of Alzheimer’s disease  
Identifying representative drug resistant mutants of HIV  
Pattern recognition methods to relate time profiles of gene expression with phenotypic data: a comparative study  
TIPR: transcription initiation pattern recognition on a genome scale  
In-vitro diagnosis of single and poly microbial species targeted for diabetic foot infection using e-nose technology*  
viralmiR: a support vector machine based method for predicting viral microRNA precursors  
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  
Differential diagnosis of pleural mesothelioma using Logic Learning Machine  
A computational method for drug repositioning using publicly available gene expression data  
HMVarfunc: a new method for predicting the functional outcome of genetic variants  
Automated identification of copepods using digital image processing and artificial neural network  
An auditory feature detection circuit for sound pattern recognition  
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

**Seminari Singoli**

Identifying cancer-related microRNAs based on gene expression data  
Faster sequence homology searches by clustering subseparateclues.  
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 heterodimemric 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

---

**Pagina 1**