

Glossary of Terms / Abbreviations

A

Acc	Geometric Accuracy
AD	Average Distance
AdaBoost	Adaptive Boosting
ADM	Average Distance between Means
AL	Average Link
AP	Affinity Propagation
APN	Average Proportion of Non-overlap

B

Bagging	Bootstrap AGGREGatING
BGENS	Bipartite Graph Ensemble
BHI	Biological Homogeneity Index
BIRCH	Balanced Iterative Reducing and Clustering using Hierarchies
BLAST	Basic Local Alignment Search Tool
BN	Bayesian Network
BOK	Best-of-k
BOM	Best One-element Move
BP	Biological Process
BSI	Biological Stability Index

C

CART	Classification And Regression Tree
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CAST	Cluster Affinity Search Technique
CC	Cellular Component
cDNA	complementary Deoxy-Ribonucleic Acid
CFinder	Clique Finder
CGED	Cancer Gene Expression Database
CL	Complete Link
CLARA	Clustering LARge Applications
CLARANS	Clustering Algorithm based on Randomized Search
CLICK	CLuster Identification via Connectivity Kernels
ClusterONE	Cluster Overlapping Neighbourhood Expansion
CMC	Clustering based on Maximum Cliques
CNS	Central Nervous System
COACH	COre-AttaCHment
CPM	Clique Percolation Method
CSPA	Cluster-based Similarity Partitioning Algorithm
CURE	Clustering Using REpresentatives

D

DBSCAN	Density-Based Spatial Clustering of Applications with Noise
DECAFF	Dense-neighborhood Extraction using Connectivity And conFidence Features
DENCLUE	DENSity-based CLUstEring
DIANA	DIvisive ANALysis
DIP	Database of Interacting Proteins
DNA	Deoxy-Ribonucleic Acid
DPCLUS	Cluster Periphery-tracking

E

EC-BNMF Ensemble Clustering Bayesian Nonnegative Matrix Factorization

EM Expectation Maximization

F

FCM Fuzzy C-Means

FGENS Full Graph Ensemble

FOM Figure Of Merit

Frac Fraction of pairs

G

GA Genetic Algorithms

GENCLUST GENE CLUSTERing

GO Gene Ontology

GOSemSim Gene Ontology Semantic Similarity

H

HBGF Hybrid Bipartite Graph Formulation

HGPA HyperGraphs Partitioning Algorithm

I

IBk Instance-based classifier

IC Information Content

K

k NN k -Nearest Neighbour

L

LAC Locally Adaptive Clustering

M

MCDM Multiple Criteria Decision Making

MCL Markov Clustering

MCLA Meta-CLustering Algorithm

MCODE Molecular Complex Detection

MEI mutually exclusive interactions

MF Molecular Function

MICA Most Informative Common Ancestor

MIPS Munich Information Centre for Protein Sequences

MMR Maximum Matching Ratio

mRNA messenger Ribo-Nucleic Acid

N

NB Naïve Bayes

NMF Ensemble Non-negative Matrix Factorization

NMI Normalized Mutual Information

P

PAM Partitioning Around Medoids

PCDEN Protein Complex Detection Ensemble

PPI Protein-Protein Interaction

PPV Positive Predictive Value

ProCope Protein Complex Prediction and Evaluation

R

RNA	Ribo-Nucleic Acid
RNSC	Restricted Neighbourhood Search Clustering
ROCK	RObust Clustering using linKs
RRW	Repeated Random Walk

S

S3VM	Semi Supervised Support Vector Machine
SAOM	Simulated Annealing One-element Move
SGD	Saccharomyces Genome Database
SL	Single Link
Sn	Sensitivity
SOM	Self Organizing Map
SOTA	Self-Organizing Tree Algorithm
SPC	Super Paramagnetic Clustering
SVM	Support Vector Machine

T

tRNA	transfer Ribo-Nucleic Acid
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W

WBPA	Weighty Bipartite Partition Algorithm
WEKA	Waikato Environment for Knowledge Analysis
WPCK	Weighted Partition Consensus via Kernels
WSBPA	Weighted Subspace Bipartite Partitioning Algorithm

List of Notations

X	gene expression matrix, considered to be $m \times n$ matrix
x_{ij}	expression value for gene i in condition j
(g_i, g_j)	gene pair (object pair)
$d_{t,j}(x)$	support given by the t^{th} classifier to the j^{th} class for the instance x
w_j	weight of the t^{th} classifier
T	total number of classifiers
BC_i	the i^{th} base classifier
k	no. of clusters
$sim_{Resnick}$	<i>Resnick</i> semantic similarity
sim_{Lin}	<i>Lin</i> semantic similarity
sim_{Jiang}	<i>Jiang</i> and <i>Conrath</i> semantic similarity
$sim_{Schlicker}$	<i>Schlicker</i> semantic similarity
sim_{Wang}	<i>Wang</i> semantic similarity
$G = (V, E)$	graph G comprising of vertices V and edges E
$deg(v)$	degree of vertex v
$den(G)$	density of graph G
G_v	The neighbourhood graph of v
(n_i, n_j)	pair of nodes (proteins)
P_i	common set of nodes from corresponding complex sets
P_i^{GO}	protein complex set based on GO similarity
P_i^{Com}	protein complex set obtained from common set of nodes
P_i^{Fin}	final protein complex set