Discovery of Feature Matrices: Gene vs. Cancer Dual

Relationships

謝復興

Department of Statistics University of California, Davis

Abstract

A brand new concept of feature matrix is computed and discovered via computational dual relationships of gene vs cancer or gene vs drug in high dimensional gene-expression and drug-activity data. Such a feature matrix is demonstrated to be an efficient platform for constructing supervised and semi-supervised learning algorithm. All technical developments are illustrated on several real datasets throughout.