

HuPo 2016

# A genetic algorithm to locate responsive subpathways for time-course proteomic data

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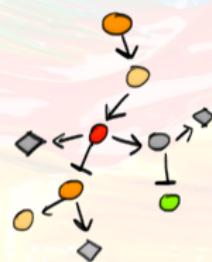
# Aim: The Active Module Identification Problem

Time-course  
Quantitative  
Data

time

Uniprot	Ratio
Q12345	2.5
P12357	1.8
P22341	-1.2

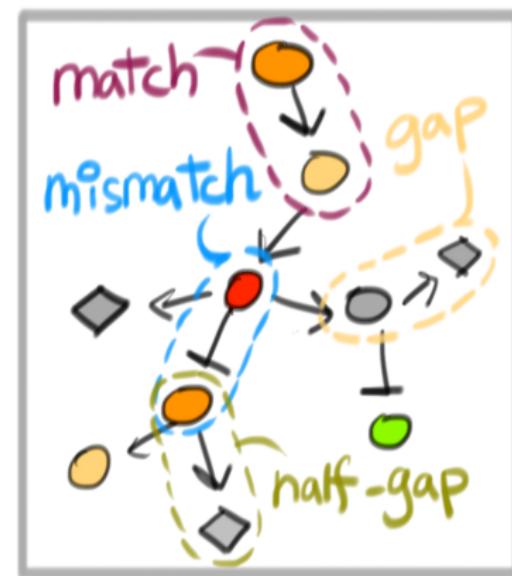
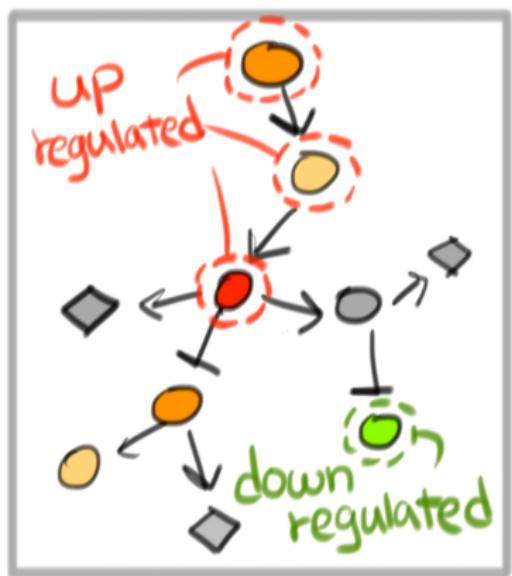
Pathway  
Database



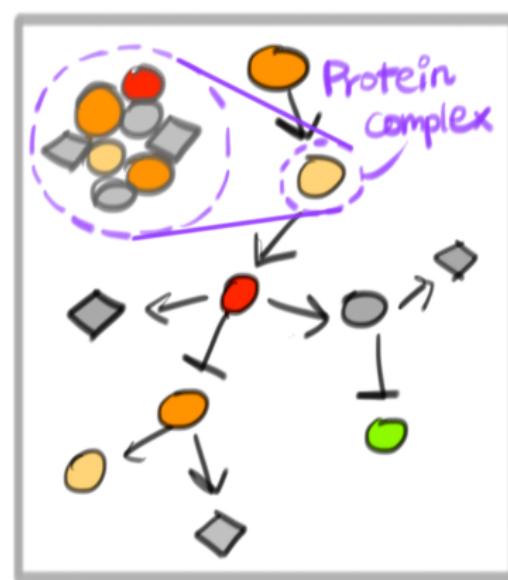
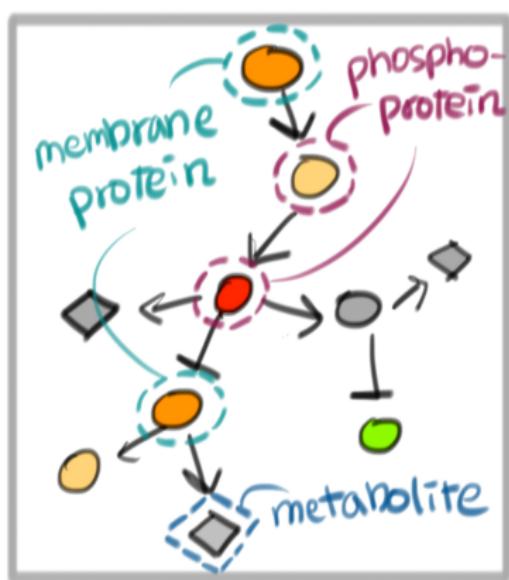
Corresponding  
Mechanism



## The Scoring Function considers:

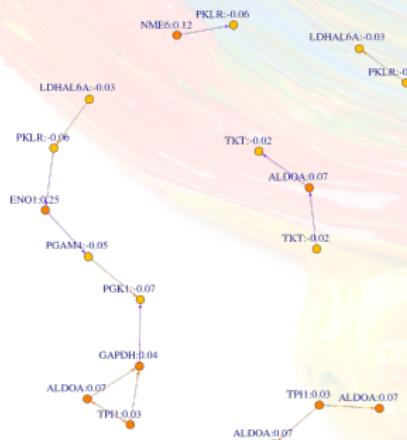


# Specific Concerns for Proteomic Data:

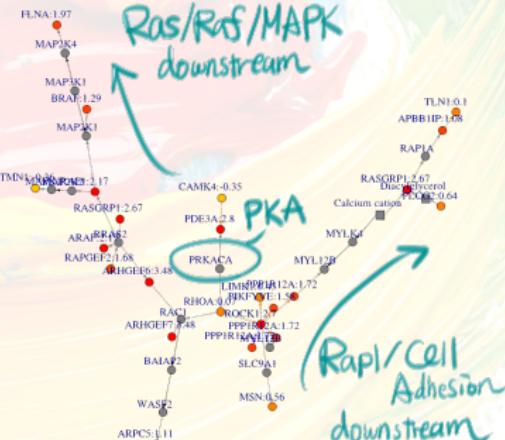


# Case Study: PKA downstream phosphoproteome

BioNet/Heinz algorithm



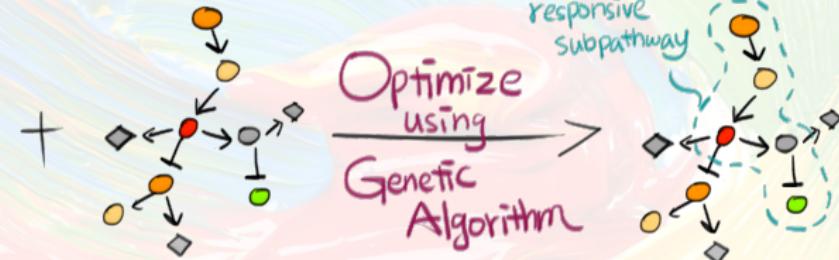
Genetic algorithm



# Overview

time

Uniprot	Ratio
Q12345	2.5
P12357	1.8
P22341	-1.2



- ▶ Expression ratio
- ▶ Regulation consistency
- ▶ Accessibility
- ▶ Complex



posters  
MO07-005

Thank you ❤