

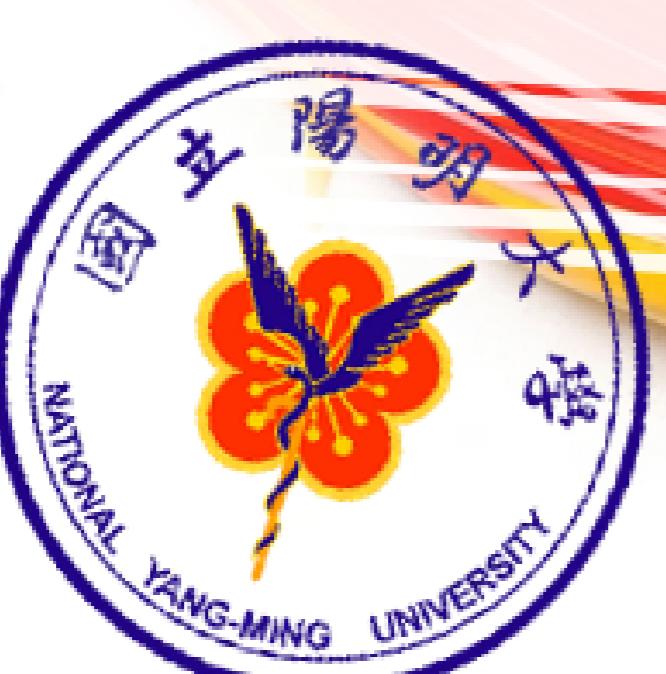
A genetic algorithm to locate responsive subpathways for time-course proteomic data

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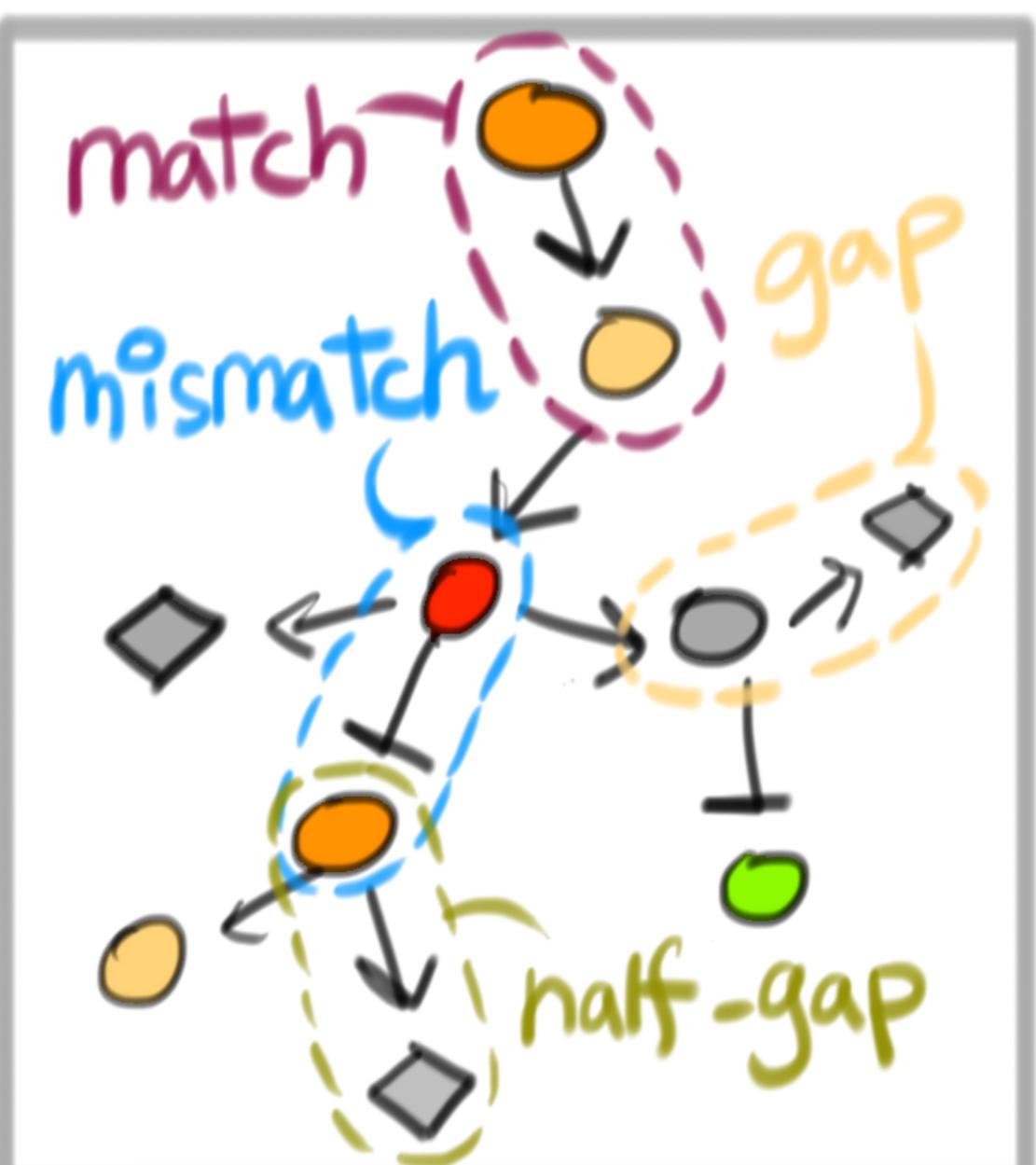
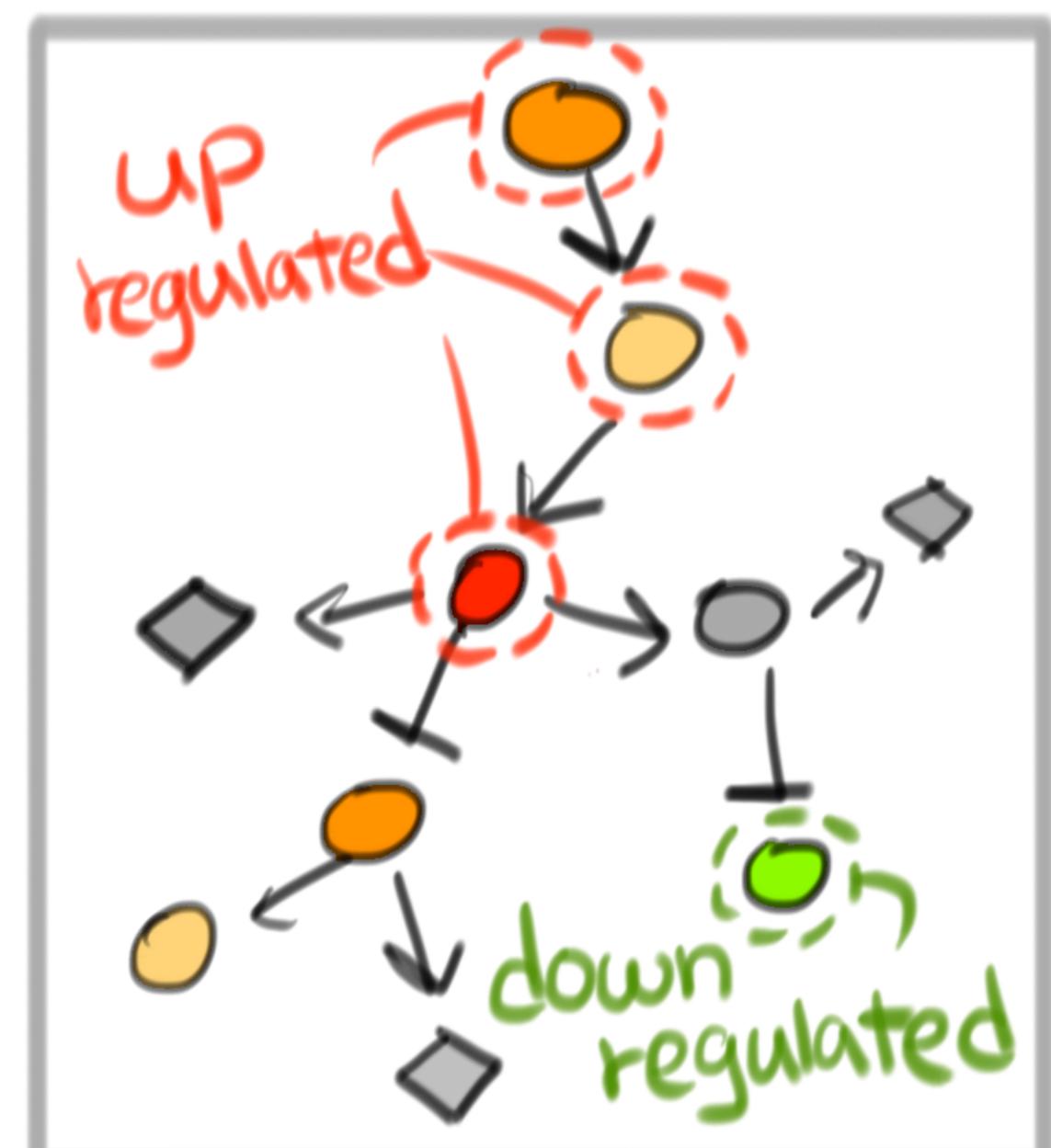
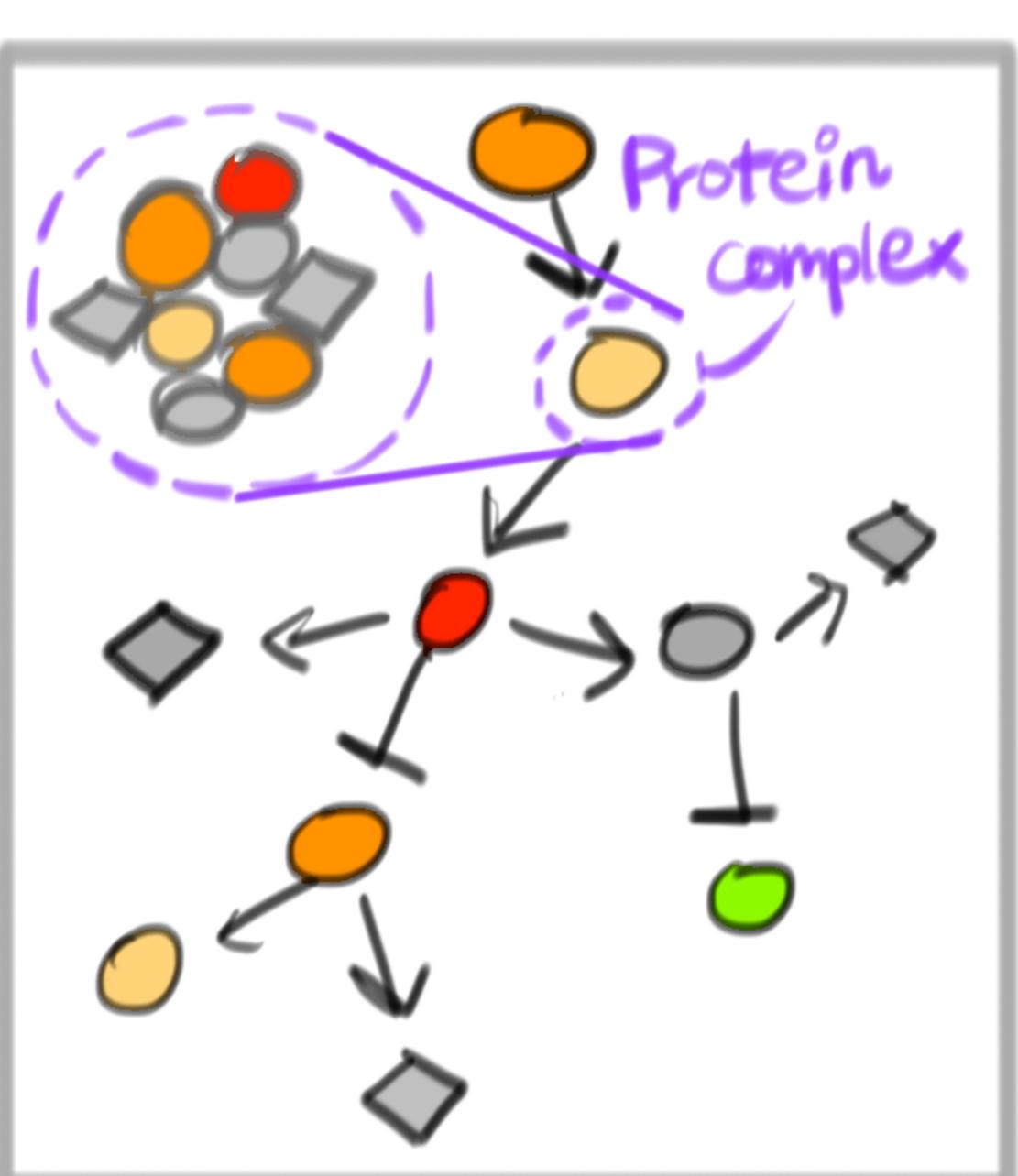
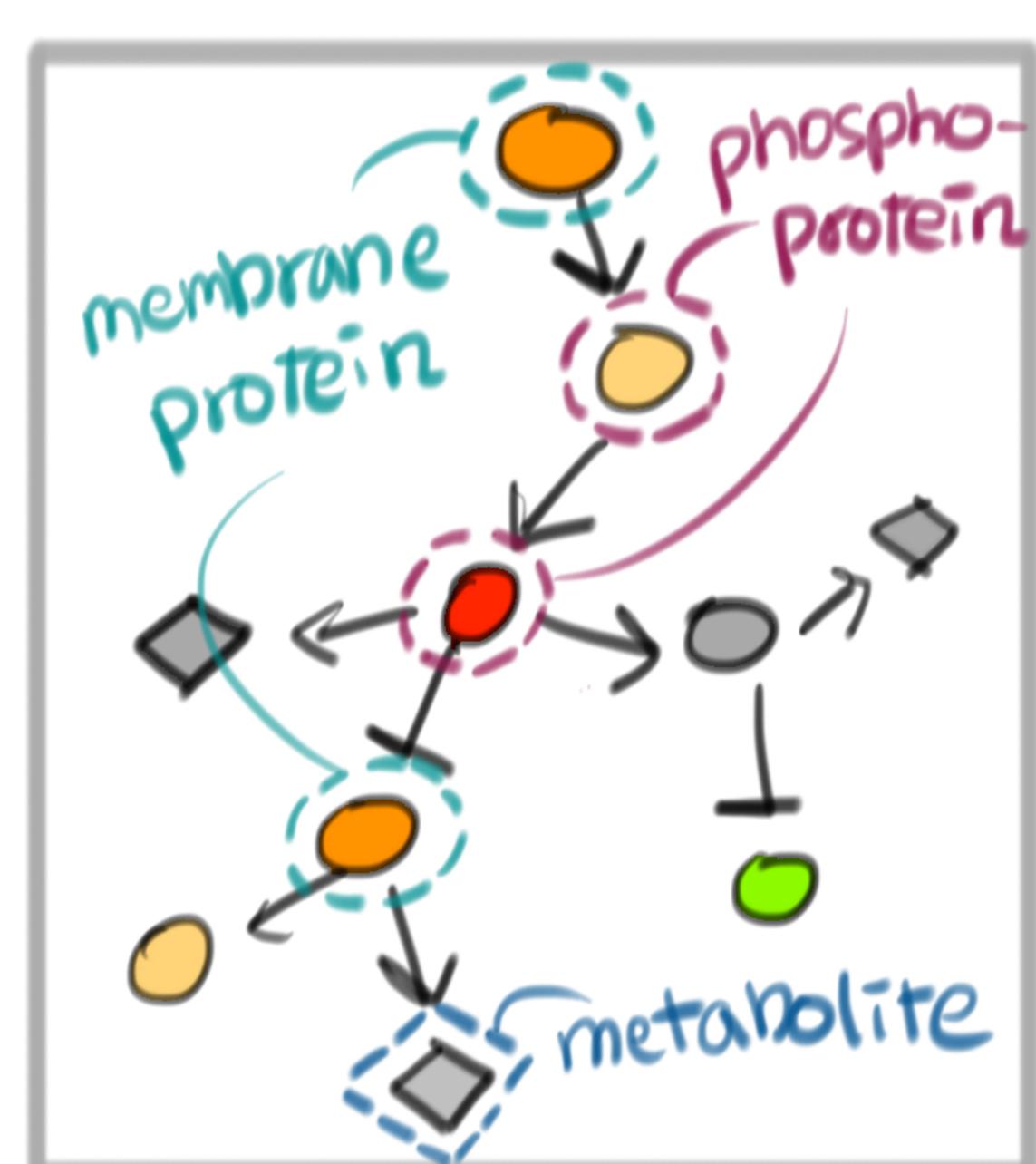
Motivation: Active module identification problem + Time-course proteomic data

UniProt	ratio
Q13245	2.5
P22322	0.3
P01356	-1.2
:	:



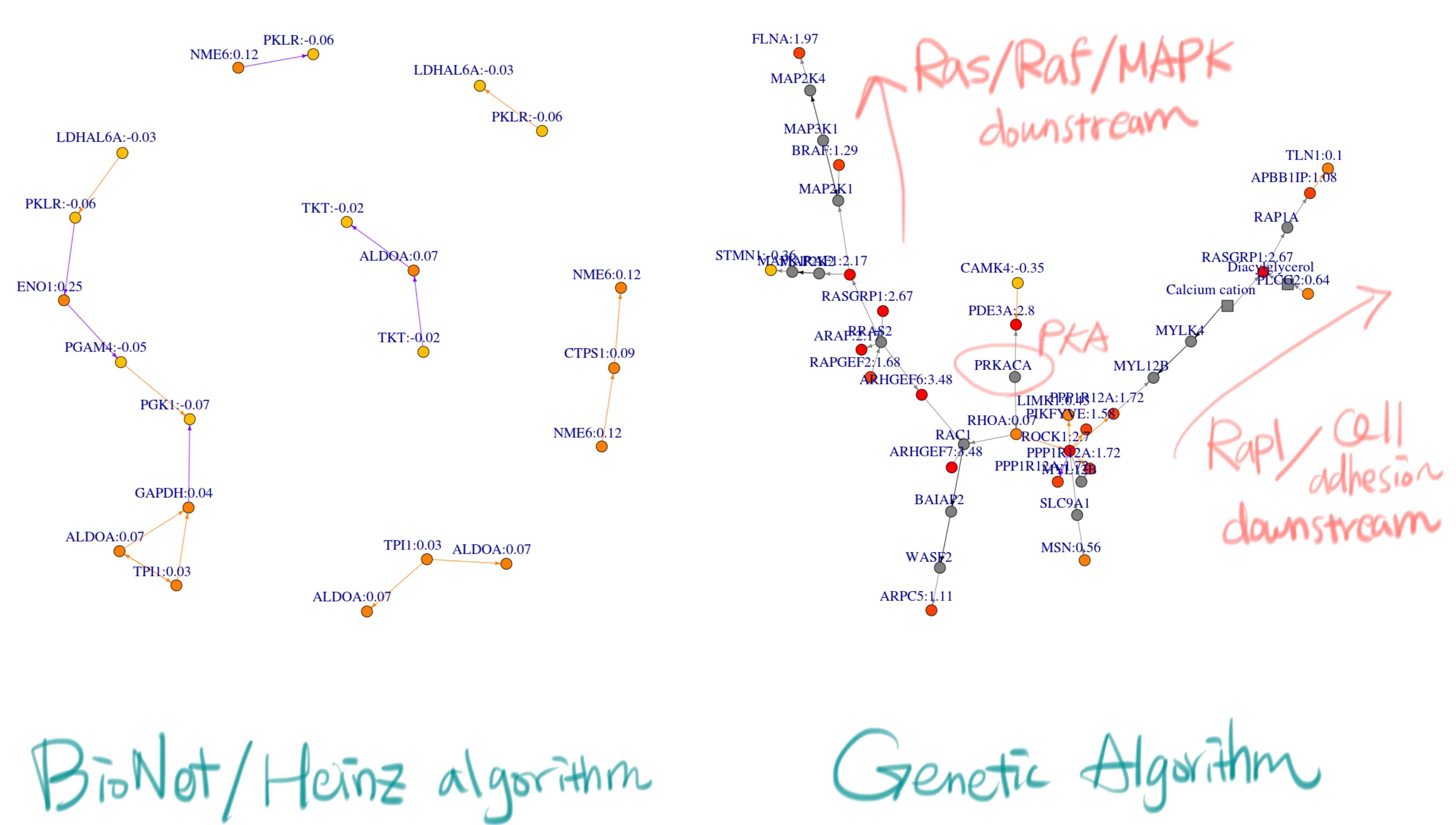
Scoring function considering:

Demo result: cAMP signaling phosphoproteome



Experimental setting:

PGE2 → cAMP → PKA → downstream pathways



BioNet/Heinz algorithm

Genetic Algorithm