A Quantitative Pipeline for the Identification of Combinations of Targets for Claudin-Low Triple Negative Breast Cancer Reversion

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Abstract

Intro/Background

* CL TNBC is bad
  + Molecular characteristics/phenotype
* No therapeutics
* Clinical trials studying combinations of therapies
* Tumor Reversion
  + What is it
  + Has been achieved before
* Dynamical Systems Theory
* Sructure Based Control
* SFA
* Boolean modeling
* Epigenetic Landscape
* Kauffman
  + Cancer attractor
  + Attractors == phenotypes
* Multi omics signaling networks?

Methods

* Data collection/sources
* Construction of multi-omics network
  + Binom / funDEGs
  + Transfac
  + Transpath
  + Ipa
  + Rekinect
  + Cosmic
  + Vep
  + Genexplain
* Landscape Simulation
  + Approximation with SFA
  + 100,000 random inits
  + Unsupervised k-means clustering to associate phenotypes
  + Refer to SFA exploration
* Target identification
  + Structure based control
  + In silico perturbations
  + DAC
  + Knn classification

Results

Conclusions

Discussion

* Proteomics networks
* Multi-layer networks
* Data-driven approach