

# Magnetic: A Novel Algorithm for Identification of Cancer Therapeutics

Tech ID: 27348 / UC Case 2017-059-0

## INVENTION NOVELTY

Modular Analysis of Genomic NETWORKS In Cancer (MAGNETIC) is a novel algorithm that performs functional network analysis of molecular profiling data to identify tumor biomarkers and link them to therapies.

## VALUE PROPOSITION

Large-scale tumor sequencing efforts and machine learning methods have focused on identification of molecular aberrations in human cancers and exploiting these to better tailor therapies for patients. However, such efforts are yet to prove successful in predicting tumor response to a majority of drugs. This new algorithm provides a powerful way of integrating data across various molecular profiling platforms to identify tumor biomarkers, suggest treatment options, and potentially predict therapeutic outcomes.

## TECHNOLOGY DESCRIPTION

Researchers at the University of California, San Francisco have developed a robust algorithm that integrates various omics data (or patient and cell line data) across cancers to identify a set of functional networks or gene modules that have coordinated activities across patients and can inform new therapeutic targets and biomarkers. This method is robust to differences between the tumor microenvironments in patients versus cell lines and reveals a new approach to connect tumor genotype to therapy in a clinically relevant manner. The algorithm has been tested using relevant breast cancer data, but should have wide application across cancer subtypes.

## ADVANTAGES

- ▶ Decomposition of complex datasets into data driven modules
- ▶ Predict new targets in cancers based on pathway activity
- ▶ Tight integration of patient and cell line response data to predict new biomarkers
- ▶ Gain novel insight into the tumor microenvironment

## APPLICATION

- ▶ Identification of new gene networks and pathways
- ▶ Identification of clinically translatable biomarkers for cancers
- ▶ Identification of novel drug targets

## CONTACT

Ellen Kats  
[ellen.kats@ucsf.edu](mailto:ellen.kats@ucsf.edu)  
 tel: 415-758-1598.



## INVENTORS

- ▶ Bandyopadhyay, Sourav
- ▶ Webber, James

## OTHER INFORMATION

### KEYWORDS

Cancer biology, Pathways, Networks, Systems biology, Bioinformatics, Gene Regulatory Networks, Protein Interaction Mapping

### CATEGORIZED AS

- ▶ **Medical**
- ▶ **Software**

### RELATED CASES

2017-059-0

► Predict therapeutic response to cancer drugs

## LOOKING FOR PARTNERS

For commercial development

## STAGE OF DEVELOPMENT

Proof of Concept

## DATA AVAILABILITY

Under CDA/NDA

### ADDRESS

**UCSF**

**Innovation Ventures**

600 16th St, Genentech Hall, S-272,

San Francisco, CA 94158

### CONTACT

Tel:

[innovation@ucsf.edu](mailto:innovation@ucsf.edu)

<https://innovation.ucsf.edu>

Fax:

### CONNECT

 Follow  Connect

© 2017, The Regents of the University of  
California

[Terms of use](#) [Privacy Notice](#)