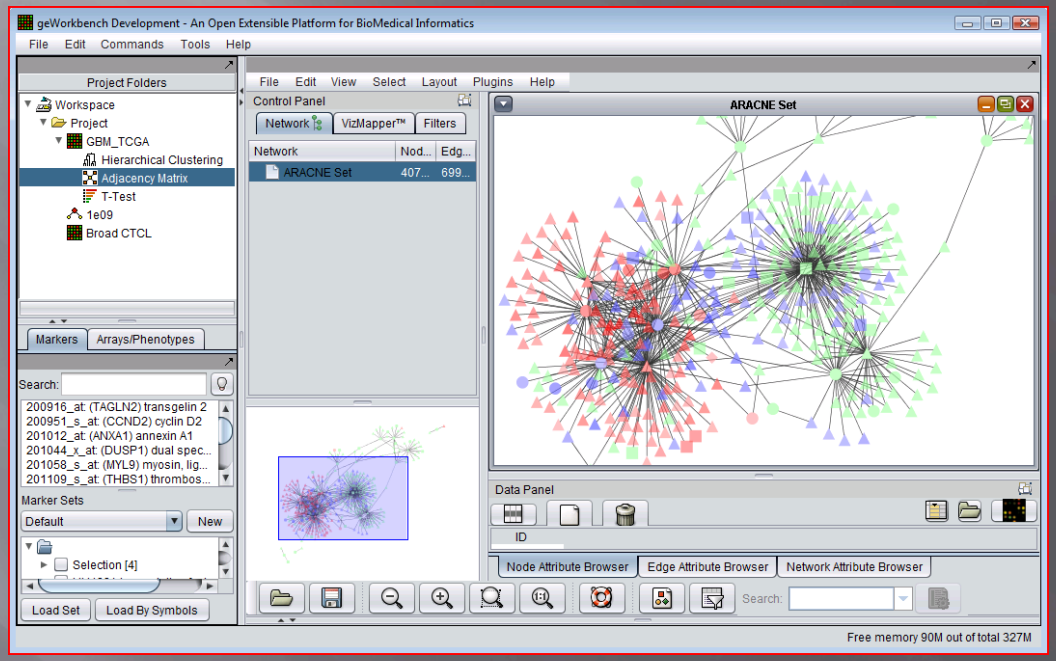
geWorkbench (Genomics Workbench)

Accessing LINCS drug synergy data and systems biology tools for mechanism of action prediction

Aris Floratos (Flash talk) & Kenneth Smith (Demo)
Columbia University

geWorkbench Overview

MAGNet: National Center for the Multiscale Analysis of Genomic and Cellular Networks: *http://magnet.c2b2.columbia.edu*



Integrated access to MAGNet Center and 3rd party tools. Java, open source, extensible platform. 70+ analytical and visualization modules. *http://www.geworkbench.org*

Demonstration

3 new geWorkbench modules (data and tools from Andrea Califano's lab @ Columbia):

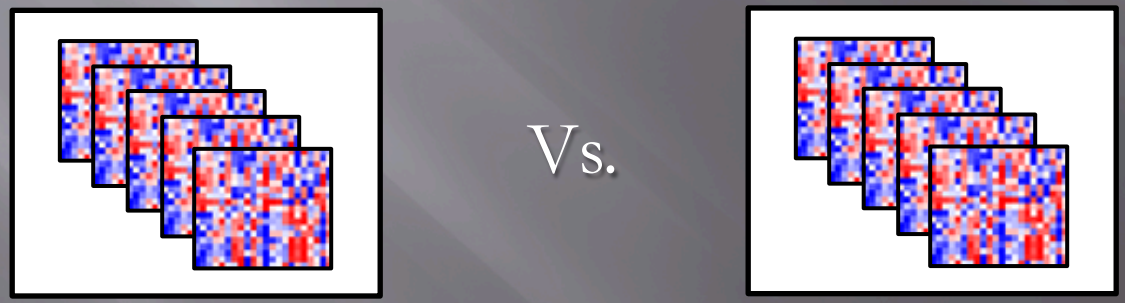
LINCS Drug Synergy Data	Querying interface for computational synergy predictions and experimental validation assays *(Mariano Alvarez)*
VIPER	Virtual Inference of Protein-activity by Regulon Readout *(Mariano Alvarez)*
DeMAND	Drug Mechanism of Action using Network Dysregulation *(Yishai Shimoni)*

LINCS Drug Synergy Data

Step 1: Interactome construction.

Public GE data

Step 2: Identification of differentially expressed genes.



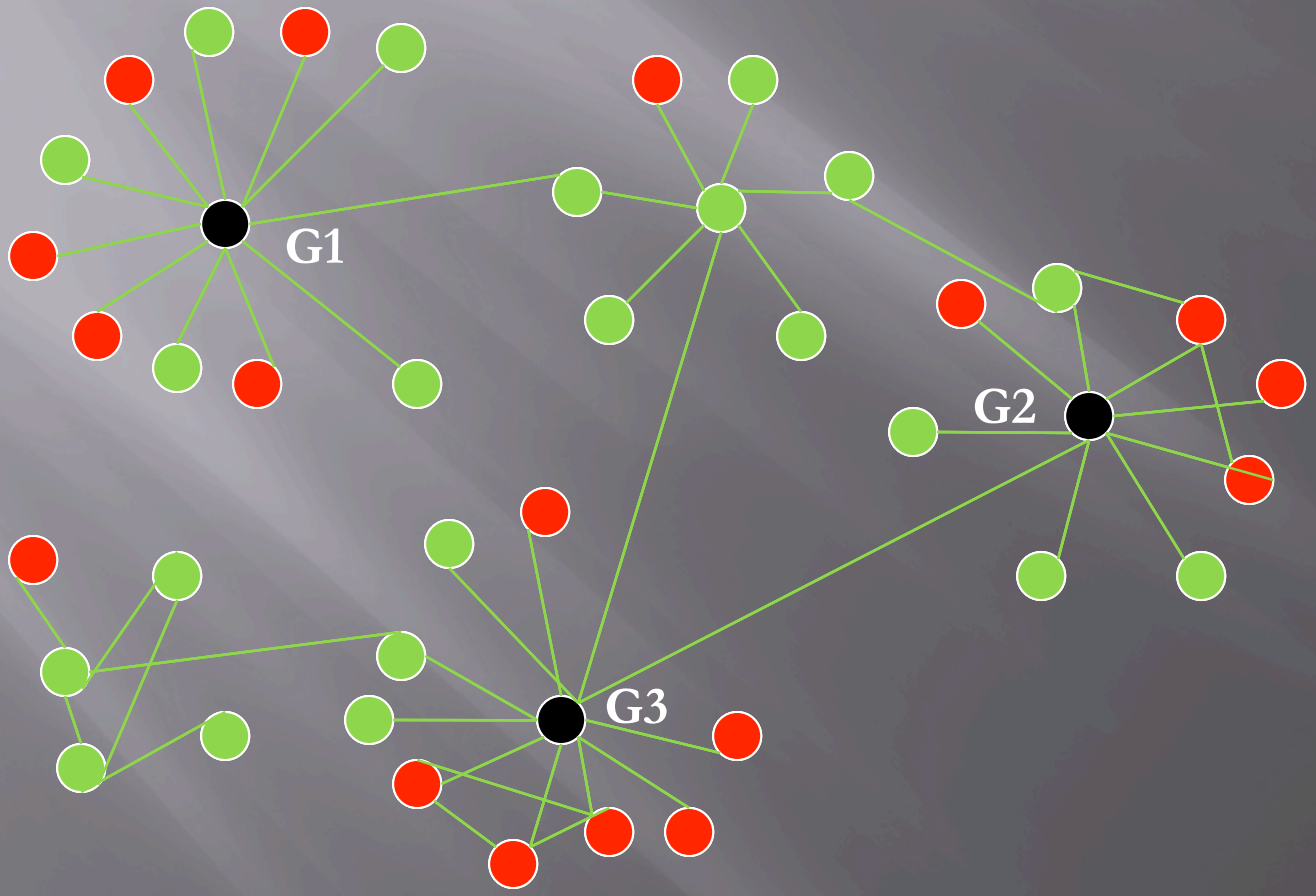
LINCS Cell Line (untreated)

LINCS Cell Line (Drug D treated)

Differentially expressed genes

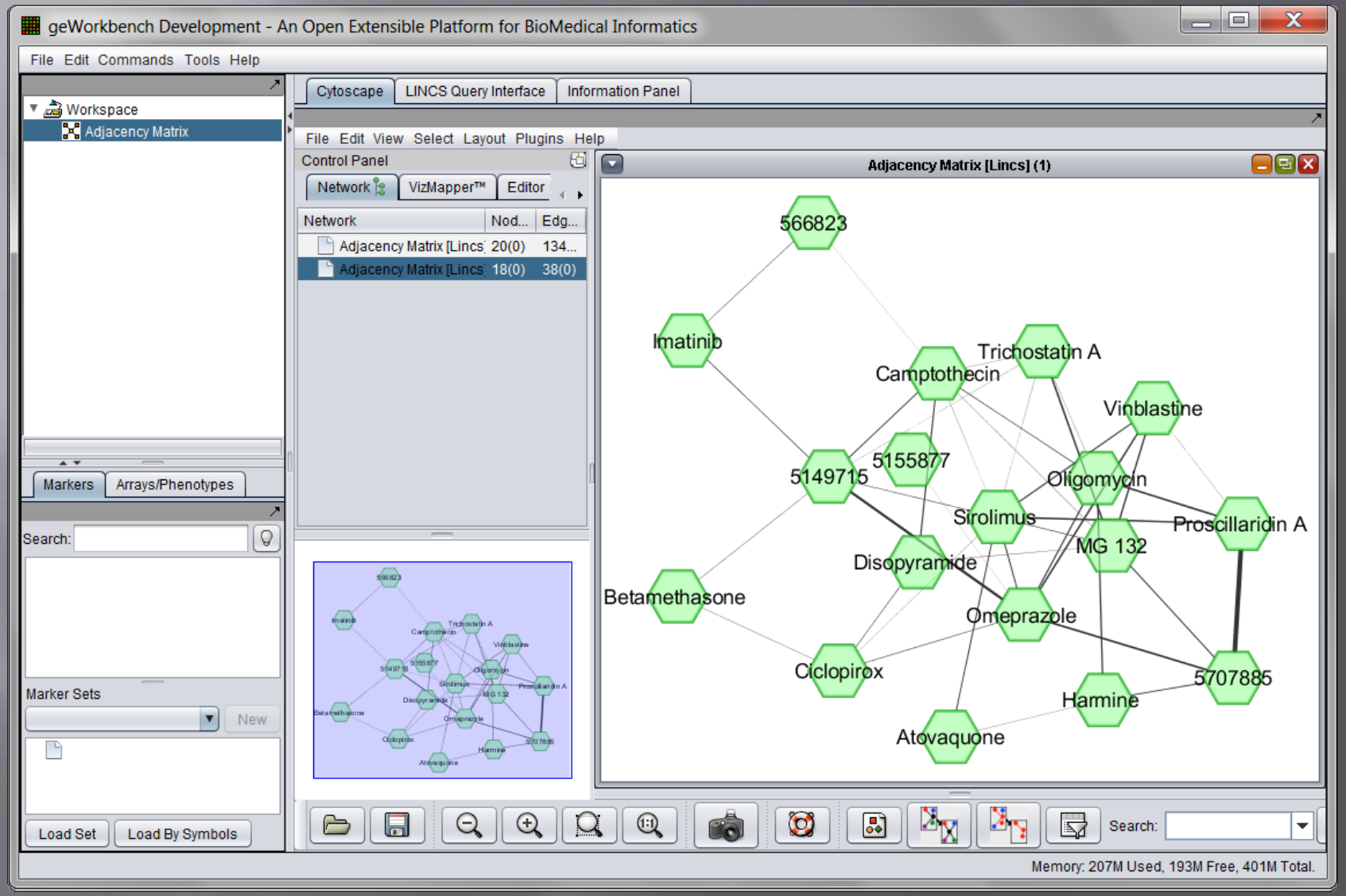
LINCS Drug Synergy Data

Step 3: Inference of drug functional mechanism of action.



fMoA (Drug D) = {G1, G2, G3}

Querying Interface



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geWorkbench dev team

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