Widespread genetic epistasis among cancer genes

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Joint work with Xiaoyue Wang[†], Megan E. McNerney,
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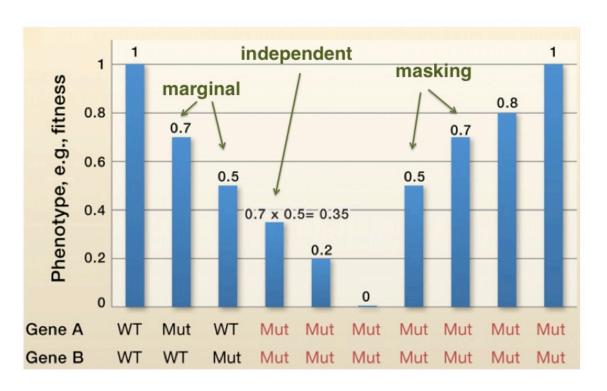
3rd TCGA Symposium, NIH

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Genetic epistasis/interaction

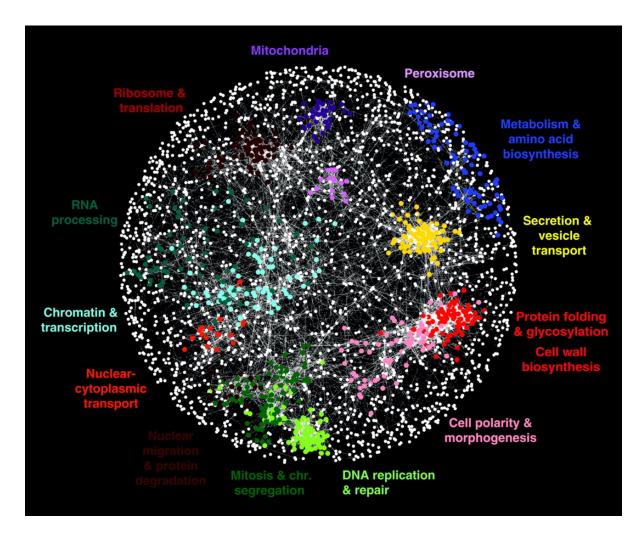


adapted from Ashworth et al. (2011), Cell

Epistasis:

- Bateson (1907): masking.
- Fisher (1918): departure from additive model.
- Departure from additive or multiplicative model.

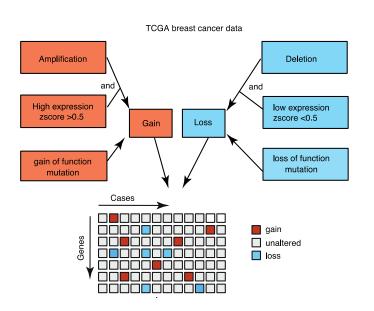
Genetic epistasis map in yeast



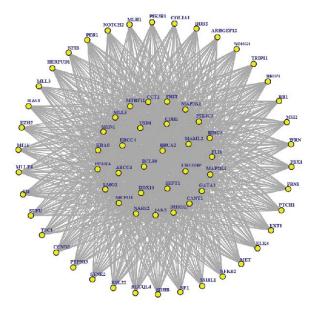
Costanzo et al. (2010), Science

- Selecting frequently co-altered cancer genes with statistical significance from TCGA;
- RNAi single and double knockdown experiment;
- Transformation and regression for inference of epistasis.

• Selection of candidate gene pairs (breast cancer data from cbioportal; 847 samples):

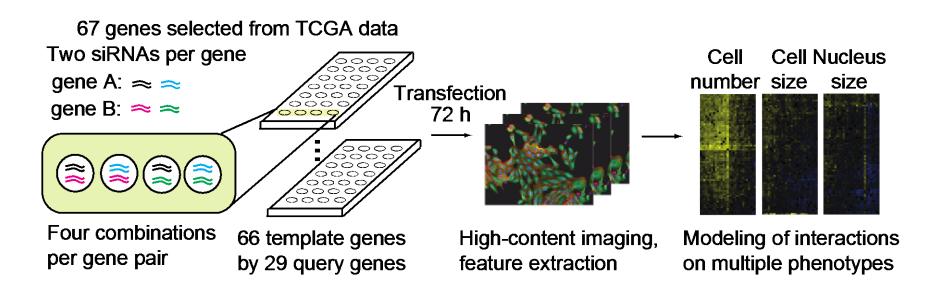


Experimental Design Map

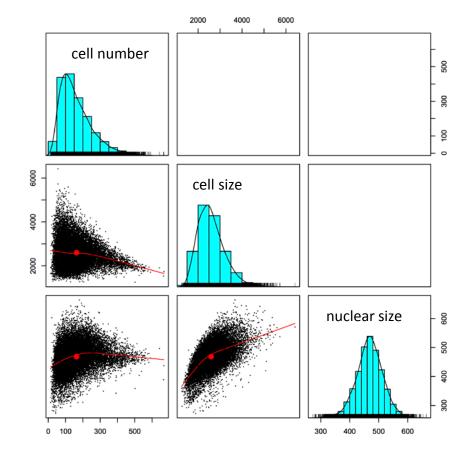


- Rank gene pairs using Fisher's exact test for co-alteration;
- Select pairs:
 - Containing cancer genes, drug targets or breast cancer GWAS hits;
 - Expressed in MCF10A breast epithelial cell line.
- 1508 gene pairs of 67 genes.

RNAi knockdown experiment (MCF10A breast epithelial cell line):



- Analysis of RNAi data:
- Interaction models:
 - Additive: nuclear size;
 - Multiplicative
 - cell number and cell size;
 - additive after log.
- Seemingly Unrelated Regression (SUR):
 - Account for dependence among phenotypes;
 - Account for batch effect.



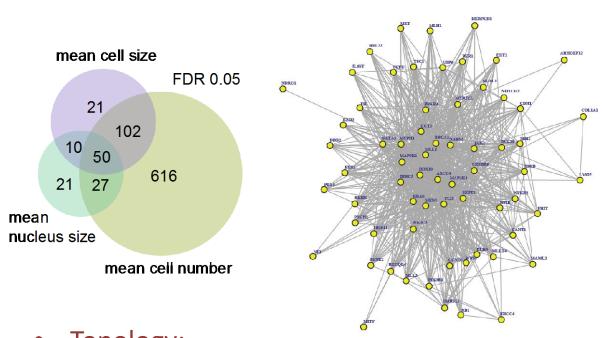
$$y_{pbijr} = \beta_0 + \beta_{1b} + \beta_2 G_i + \beta_3 G_j + \beta_4 (G_i \times G_j) + \varepsilon_{pbijr}$$

$$\varepsilon \sim Normal(0, \Omega)$$

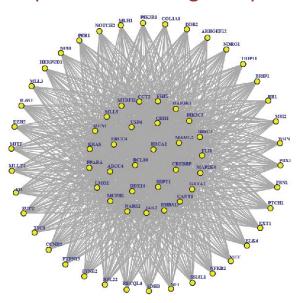
$$\Omega = \Sigma_{3\times 3} \otimes I_N$$

An epistasis map

• Inferred epistasis map (847 significant interactions):

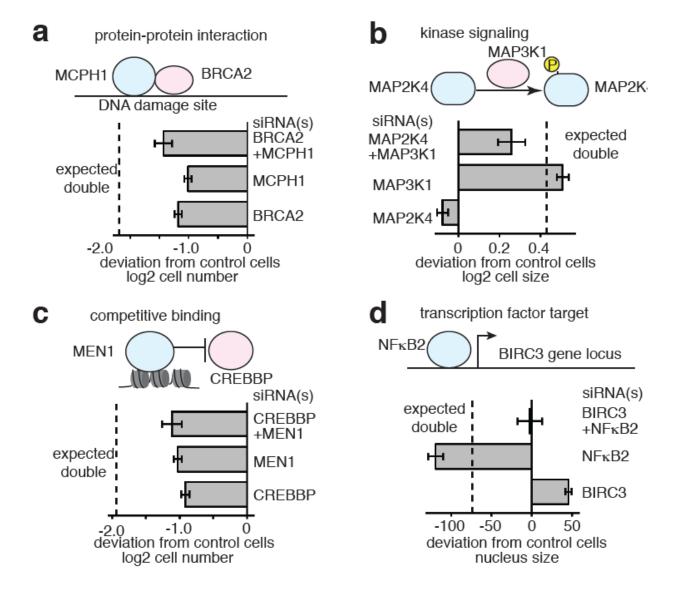


Experimental Design Map

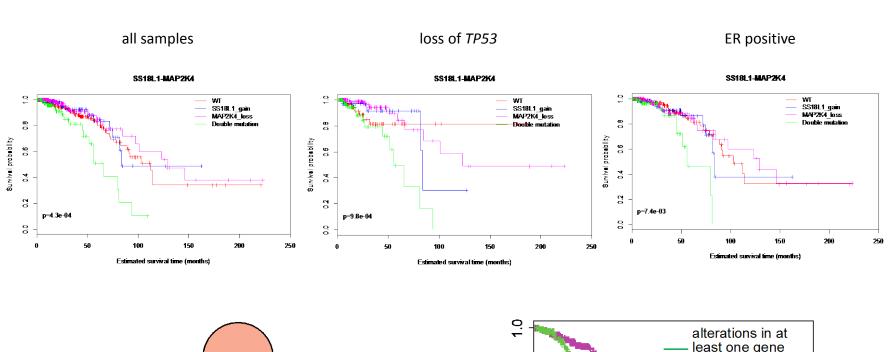


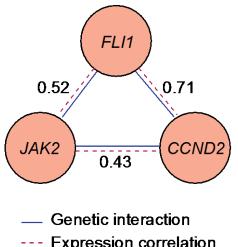
- Topology:
 - (Adjusted) connectivity: median 62%;
 - Small-worldness: 1.5 (1.1 for design map).
- Genetic interactions:
 - Majority (82%) are novel;
 - Over half exhibit masking effects.

Genetic interactions and molecular interactions

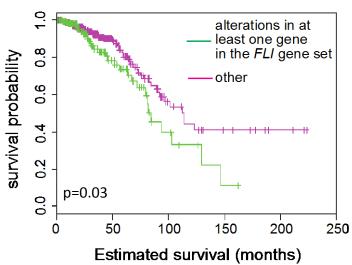


Genetic interactions and survival



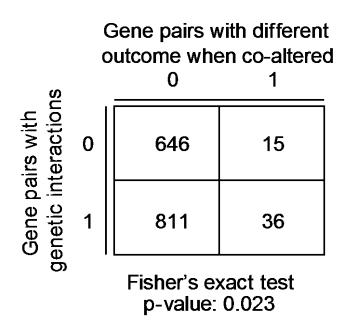


Expression correlation



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Genetic interactions and survival



Result: interacting gene pairs are enriched in gene pairs associated with reduced survival time (p=0.02; Fisher's exact test).

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- Other members in the White lab.

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