**References:**

# Materials and Methods

## List of data sets

### The analyzed data for morphological plasticity came from the saccharomyces cerevisiae morphology database (SCMD)

Yeast deletion mutation with known effects on morphology is available at the *Saccharomyces cerevisiae* Morphological Database (SCMD, http://scmd.gi.k.u-tokyo.ac.jp/). SCMD provides a list of 501 morphological parameters in four groups: cell shapes, bud sizes, nucleus locations, and actin localizations {Ohya, 2005 #534}.

### RLS

The RLS data used by the students contain RLS for 564 genes measured by the Kaeberlein group {Managbanag, 2008 #563}.

### Fitness

growth fitness measures in various conditions {Deutschbauer, 2005 #548;Steinmetz, 2002 #551}

### Network

Several network datasets will be used, including protein-protein interactions from DIP, BioGRID, and BIND {Xenarios, 2000 #1618;Bader, 2003 #2459;Stark, 2011 #2462}, protein complexes {Warringer, 2003 #261;Warringer, 2003 #1969;Warringer, 2003 #261;Warringer, 2003 #1969}, genetic interactions {Costanzo, 2010 #2074}.

### GFP CV, {Newman, 2006 #2467}

### GEO CV of 3821 (glucose pulse)

### The variances and coefficient of variation data was calculated

## Analysis Methods:

### R statistical software was used to perform linear and multiple regression analysis on the different variable factors that comprise robustness

### Firstly, regression analysis was performed between each fitness growth medium and RLS.

### Regression analysis was then conducted between replicative lifespan and each of the proxies of robustness.

### Multiple regression analysis was performed

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