

# YEAST LANDSCAPE MULTIPLEX NETWORK

Last update: 1 July 2014

## Reference and Acknowledgments

This README file accompanies the dataset representing the multiplex genetic interaction network of the *Saccharomyces Cerevisiae*, a species of yeast. If you use this dataset in your work either for analysis or for visualization, you should acknowledge/cite the following papers:

“The Genetic Landscape of a Cell”

M. Costanzo et al

Science 2010 327 (5964) 425-431

“MuxViz: A Tool for Multilayer Analysis and Visualization of Networks”

Manlio De Domenico, Mason A. Porter, and Alex Arenas

Journal of Complex Networks, 2014 (DOI: 10.1093/comnet/cnu038)

that can be found at the following URLs:

<http://www.sciencemag.org/content/327/5964/425>

<http://comnet.oxfordjournals.org/content/early/2014/10/12/comnet.cnu038.full>

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Visit

PLEXMATH: <http://www.plexmath.eu/>

ALEPHSYS: <http://deim.urv.cat/~alephsys/>

for further details.

## Description of the dataset

Multiplex in which the layers correspond to interaction networks of genes in *Saccharomyces cerevisiae* (which was obtained via a synthetic genetic-array methodology) and correlation-based networks in which genes with similar interaction profiles are connected to each other. Positive and negative interactions, as well as positive and negative correlations, are considered.

Thus, the provided layers are:

1. Positive interactions
2. Negative interactions
3. Positive correlations
4. Negative correlations

There are 4458 nodes, labelled with integer ID between 1 and 4458, and 8473997 connections. The multiplex is undirected and unweighted, although in the file

```
yeast_landscape_multiplex.edges
```

with format

```
layerID nodeID nodeID r
```

are provided all the edges present in the original dataset. Here,  $r$  is either the genetic interaction score (for layers concerning interactions) or the Pearson correlation coefficient (for layers concerning correlations).

**NOTE: filter the interactions you might want to keep applying your preferred threshold**

**to  $r$**

**Don't use the edges list as it is.**

The values for  $r$  are provided to allow flexible analyses. For further details see the original paper by Costanzo et al.

The IDs of all layers are stored in

```
yeast_landscape_layers.txt
```

The IDs of nodes, together with their name can be found in the file

```
yeast_landscape_nodes.txt
```

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## Contacts

If you find any error in the dataset or you have questions, please contact

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