SACCHPOMB MULTIPLEX GPI NETWORK

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Reference and Acknowledgments

This README file accompanies the dataset representing the multiplex genetic and protein interactions network of the Saccharomyces Pombe. If you use this dataset in your work either for analysis or for visualization, you should acknowledge/cite the following papers:

```
"Biogrid: a general repository for interaction datasets"
C. Stark, B.-J. Breitkreutz, T. Reguly, L. Boucher, A. Breitkreutz, and M.
Tyers.
Nucleic Acids Research 2006 34 (1) D535–D539

"Structural reducibility of multilayer networks"
M. De Domenico, V. Nicosia, A. Arenas, and V. Latora
Nature Communications 2015 6, 6864
```

that can be found at the following URLs:

http://nar.oxfordjournals.org/content/34/suppl_1/D535.abstract

http://www.nature.com/ncomms/2015/150423/ncomms7864/abs/ncomms7864.html

Visit

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

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

for further details.

Description of the dataset

We consider different types of genetic interactions for organisms in the Biological General Repository for Interaction Datasets (BioGRID, thebiogrid.org), a public database that archives and disseminates genetic and protein interaction data from humans and model organisms. BioGRID currently includes more than 720,000 interactions that have been curated from both high-throughput data sets and individual focused studies using over 41,000 publications in the primary literature. We use BioGRID 3.2.108 (updated 1 Jan 2014).

The multiplex network used in the paper makes use of the following layers:

1. Direct interaction
2. Colocalization
3. Physical association
4. Suppressive genetic interaction defined by inequality
5. Synthetic genetic interaction defined by inequality
6. Additive genetic interaction defined by inequality
7. Association

There are 4092 nodes, labelled with integer ID between 1 and 4092, and 63676 connections. The multiplex is directed and unweighted, stored as edges list in the file

```
sacchpomb_genetic_multiplex.edges
```

with format

```
layerID nodeID nodeID weight
```

(Note: weight is 1 for all edges)

The IDs of all layers are stored in

```
sacchpomb_genetic_layers.txt
```

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

```
sacchpomb_genetic_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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