HEPATITUSC MULTIPLEX GPI NETWORK

Last update: 1 July 2014

Reference and Acknowledgments

This README file accompanies the dataset representing the multiplex genetic and protein interactions network of the Hepatitus C virus. 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

"MuxViz: A Tool for Multilayer Analysis and Visualization of Networks"
Manlio De Domenico, Mason A. Porter, and Alex Arenas
Journal of Complex Networks 2015 3 (2) 159-176
```

that can be found at the following URLs:

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

http://comnet.oxfordjournals.org/content/3/2/159

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. Physical association
2. Direct interaction
3. Colocalization

There are 105 nodes, labelled with integer ID between 1 and 105, and 137 connections. The multiplex is directed and unweighted, stored as edges list in the file

```
hepatitusC_genetic_multiplex.edges
```

with format

```
layerID nodeID nodeID weight
```

(Note: weight is 1 for all edges)

The IDs of all layers are stored in

```
hepatitusC_genetic_layers.txt
```

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

```
hepatitusC_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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Manlio De Domenico
Universitat Rovira i Virgili
Tarragona (Spain)
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email: manlio.dedomenico@urv.cat

web: http://deim.urv.cat/~manlio.dedomenico/