# HUMAN-HERPES4 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 Epstein–Barr virus, also known as human herpes-virus 4 (HHV-4). 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
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"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

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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 present folder concerns human herpes virus 4.

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

- 1. Direct interaction
- 2. Physical associatio
- 3. Association
- 4. Colocalization

There are 216 nodes, labelled with integer ID between 1 and 216, and 259 connections. The multiplex is directed and unweighted, stored as edges list in the file

humanHerpes4\_genetic\_multiplex.edges

with format

layerID nodeID nodeID weight

(Note: weight is 1 for all edges)

The IDs of all layers are stored in

humanHerpes4\_genetic\_layers.txt

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

humanHerpes4\_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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