**Supplementary Table S1.**Feature comparison between GEMMER and existing visualization tools for budding yeast.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Feature | GEMMER | STRING | BioGRID | APID | IntACT |
| HTML address | <http://gemmer.barberislab.com> | <http://string-db.org/> | <https://thebiogrid.org/> | <http://apid.dep.usal.es/> | <http://www.ebi.ac.uk/intact/> |
| Generating interaction networks seeded by two or more nodes | X |  | X\* |  | X |
| Browsing different organisms |  | X | X | X | X |
| Node size proportional to interactions in the visualized network | X |  | X |  |  |
| Edge size proportional to interactions in the visualized network | X |  | X | X |  |
| Coloring nodes based on their GO-term annotated function | X | X |  |  |  |
| Clustering nodes based on their GO-term annotated function | X |  | X | X |  |
| Clustering based on cellular compartments | X |  |  |  |  |
| Different possible visual layouts |  | X | X\*\* | X\*\* | X\*\* |
| Filtering and visualizing physical, regulatory and/or genetic interactions | X | X | X |  |  |
| Filtering interactions on number of experiments that show an interaction | X | X\*\*\* |  | X |  |
| Filtering interactions on number of unique experimental methods that show an interaction | X |  |  |  |  |
| Filtering nodes on network properties: degree, eigenvector and Katz centrality | X |  |  |  |  |
| Displaying peak of transcription levels | X |  |  |  |  |
| Link to original publication through PubMed | X | X | X |  |  |
| Additional information on node (PDB, Pfam, post-translational modifications) |  | X | X |  |  |
| Bitmap or vector image formats available for export | SVG | PNG, SVG | PNG | JPG, PNG |  |
| Table formats available for export | XLSX | TSV, TXT, XML |  | TXT |  |

\* network visualization of only user-supplied nodes

\*\* visualizations via Cytoscape

\*\*\* confidence factor exists but not explicit