(protein) functional connectivity network

**Description**

Protein physical interactions (PPIs), typically taking place in protein complexes, have proved to be useful to functionally associate proteins or genes in a broad range of studies. Additional physical interactions, such as enzyme-substrate, also inform on functional relationships. Furthermore, therapeutic agents such as small molecules or antibodies can be regarded as inducers of perturbations in cellular networks, thus linking information related to drug targets and protein interaction networks naturally.

Here, we provide a compilation of an important corpus of physical interaction data extracted from large public data collections. The collected interactions fall in three different categories:

* Protein-protein interactions (PPI), mainly from measurements of physical association -e.g. affinity purification-mass spectrometry (AP-MS) and yeast two-hybrid (Y2H) experiments-;
* Kinase-substrate interactions (KSI), corresponding to phosphorylation reactions, obtained originally by both experimental and computational methods;
* Drug-protein interactions (DPI), which consist in known kinase inhibitors.

All together, the integration of PPI, KSI and DPI in large numbers provides the opportunity to study proteins or their coding genes in a broad functional context, and to further connect them with potential FDA-approved or tool compounds.

The integrated PPI network has been maintained and updated at CeMM over several years and the recent addition of KSIs and DPIs was undertaken during a study we published recently about kinase networks (<link>). In the future, we plan to complement this database with additional enzyme-substrate interactions, bioinformatics tools, and the generation of an equivalent mouse network. Release frequency is every six months.

**Data compilation algorithm**

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**Current release**

The current release, as of *20.August 2014*, includes:

* 14,146 proteins
* 487 protein kinases
* 104,979 *PPIs*
  + - sources: [*IntAct*](http://www.ebi.ac.uk/intact/)*,* [*MINT*](http://mint.bio.uniroma2.it/mint/Welcome.do)*,* [*InnateDB*](http://www.innatedb.com/)*,* [*DIP*](http://dip.doe-mbi.ucla.edu/dip/Main.cgi)*,* [*HPRD*](http://www.hprd.org/)*,* [*MatrixDB*](http://matrixdb.ibcp.fr/)*,* [*Reactome*](http://www.reactome.org/)*,* [*PID*](http://pid.nci.nih.gov/)*,* [*CORUM*](http://mips.helmholtz-muenchen.de/genre/proj/corum).
* 23,444 *KSIs* (8,539 experimental + 14,905 computational)
  + - sources: [*PhosphoSitePlus*](http://www.phosphosite.org/)*,* [*PhosphoNetworks*](http://phosphonetworks.org/)*,* [*Phospho.ELM*](http://phospho.elm.eu.org/)*,* [*Networkin*](http://networkin.info/), and some of the above such as[*IntAct*](http://www.ebi.ac.uk/intact/).
* 8,046 *DPIs*
  + - sources: *[DrugBank](http://www.drugbank.ca/" \t "_blank)*, and publications by[*Davis et al. 2011*](http://www.nature.com/nbt/journal/v29/n11/full/nbt.1990.html)*,* [*Anastassiadis et al. 2011*](http://www.nature.com/nbt/journal/v29/n11/full/nbt.2017.html)*,* [*Bantscheff et al. 2007*](http://www.nature.com/nbt/journal/v25/n9/full/nbt1328.html)*,* [*Rix et al. 2013*](http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0077155)*,* [*Rix et al. 2010*](http://www.nature.com/leu/journal/v24/n1/full/leu2009228a.html)*,* [*Rix et al. 2007*](http://www.bloodjournal.org/content/110/12/4055.long?sso-checked=true)*,* and[*Remsing Rix et al. 2009*](http://www.nature.com/leu/journal/v23/n3/full/leu2008334a.html).

The following heatmaps show the overlaps between different databases:

**Acknowledgements**

We are very grateful to the several public repositories from which we collected data for their effort in making these data available to the largest community and for the permission (general or given to us explicitly) to parse and redistribute their data.