

Pypath & Omnipath: integrate, analyze and extract signaling networks from literature curated resources



Tissue patterns

2000

Intervention

Compound

Function

target binding

GSEA

Gene Ontology

Process description

GIANT

Prot.DB

GDSC

ChEMBL

UniChem

MSigDB

LINCS

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Unified network of pathways

Activity flow (12) Enzyme-substrate (8) Undirected PPI (8)

BioGRID

InnateDB

MatrixDB

Vidal HI-III

PANTHER

Reactome

WikiPathways

IntAct

MPPI

dbPTM*

DOMINO

HPRD-phos*

phospho.ELM*

PhosphoSite*

NCI-PID

NetPath

Process description (6)

ELM

with annotations

OmniPath &

pypath

Protein-protein interactio

resources (34)

ARN+

CancerCellMap³

DeathDomain

Macrophage+

NRF2ome+

PDZbase*

| Signor⁺

SPIKE+

TRIP+

| SignaLink3+

Guide2Pharma

Motivation

Literature curated information on signaling pathways is an extremely valuable resource for researchers studying different biological questions. These resources can help in the generation of hypothesis to explain experimental data and they provide support for the building of computational models.

The existing curated information is currently distributed throughout a large number of online resources. Gathering and retrieving this information in a consistent manner is a non-trivial endeavour.

Omnipath and Pypath greatly facilitate the integration and extraction of biological prior knowledge for analysis and model building, and they can be incorporated into wider data processing pipelines.

Available at http://omnipathdb.org

Quick start

import pypath pa = pypath.main.PyPath() pa.init network()

Features

Pypath is the Python package that gives full access to the Omnipath database:

- Easy protein ID conversion to gene IDs
- Ready integration of dozens of bioinformatics resources directly from the original source
- Incorporate new databases or your own networks and compare information between different databases
- Efficient handling of annotations: sources, literature references, directions, effect signs (stimulation/inhibition) and enzymesubstrate interactions
- Extract information on pathways, protein complexes, transcription factors and more
- Plot networks

The network is represented as an *igraph* object, giving access to plenty of graph analysis methods with excellent computational performance:

- complex node/edge queries
- shortest path searches
- statistical graph analysis (centrality, betweenness, community detection, and more)

Usage in PrECISE

PrECISE (Personalized Engine for Cancer Integrative Study and Evaluation) is a European H2020 project focused on prostate cancer, an international collaboration that aims to translate into clinical advances many of the technical and methodological developments achieved during the last years.

MOPRECISE

We will build interaction networks for increasing our understanding of prostate cancer tumours. The wealth of data generated will be encoded into mathematical models, both qualitative and quantitative.

The incorporation of prior biological knowledge into these models is eased by the usage of Omnipath and Pypath. Among other things, Omnipath helps in the definition of logic models that can later be simulated and used to make predictions about cell signalling pathways relevant to the biology of prostate cancer.

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Curated integration of multiple

Structure & Mechanism

Subcellular

localization (2)

3D structures (4)

Post-translational

modifications (9)

complexes (3)

ComPPI

Instruct

dbPTM

ELM

HPRD

LMPID

MIMP

Signor

CORUM

Phospho.ELM

PhosphoNetw.

PhosphoSite

3DComplexes

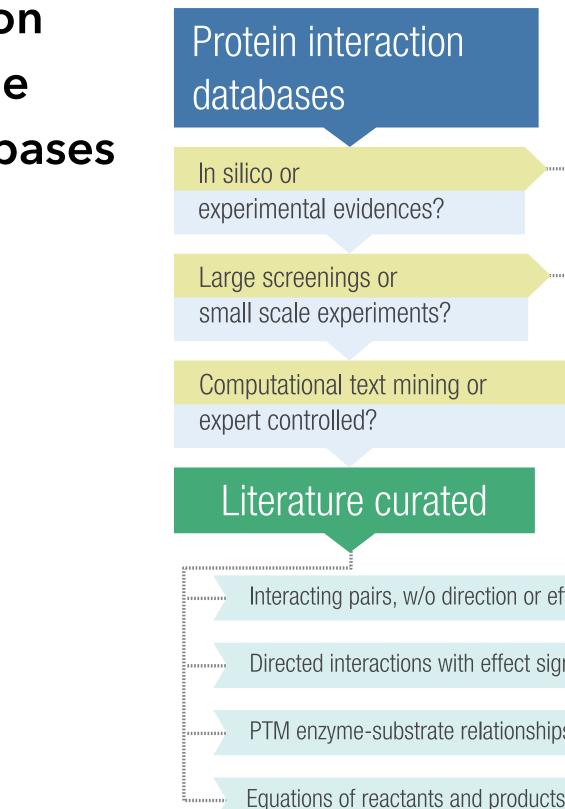
Havugimana

Gene Ontology

3DCompexes

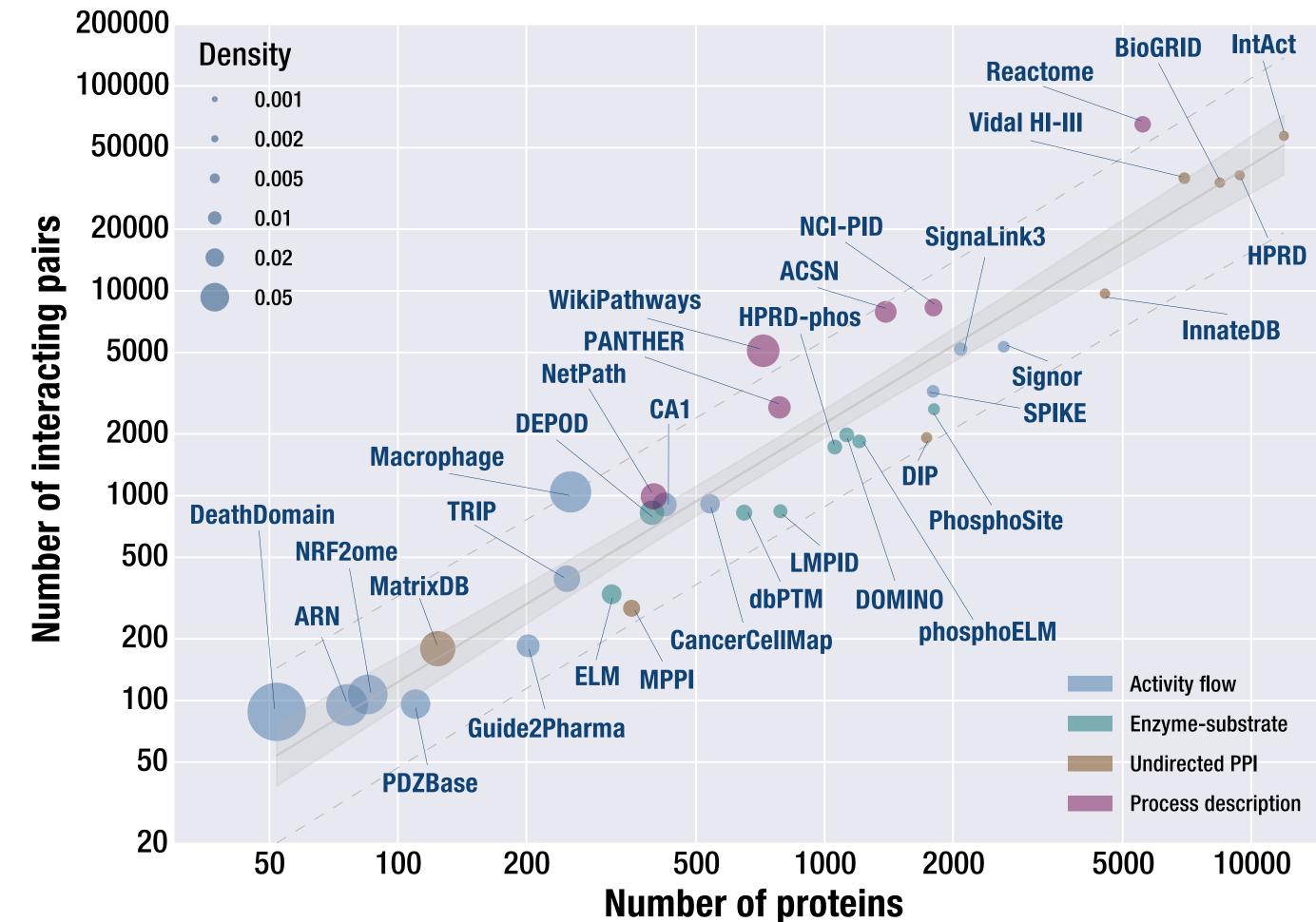
Interactome3D

databases



Protein interaction databases Predicted In silico or experimental evidences? High-throughput Large screenings or small scale experiments? Literature mined Computational text mining or expert controlled? Literature curated Undirected PPI Interacting pairs, w/o direction or effect Activity flow Directed interactions with effect sign PTM enzyme-substrate relationships Enzyme-substrate

Number of proteins, interactions and graph density



References

D Turei, T Korcsmaros and J Saez-Rodriguez: Guidelines for literature curated signaling pathway resources (under revision)

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