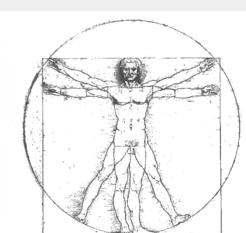
Open Phenotypic Drug Discovery Resource (OPDDR)

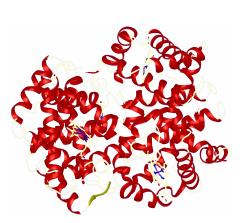




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Collaboration

- Lilly OIDD phenotypic assays
- NIH NCATS Pharmaceutical Collection (NPC) compounds
- Data2Discovery/IU informatics, semantics

Experiments

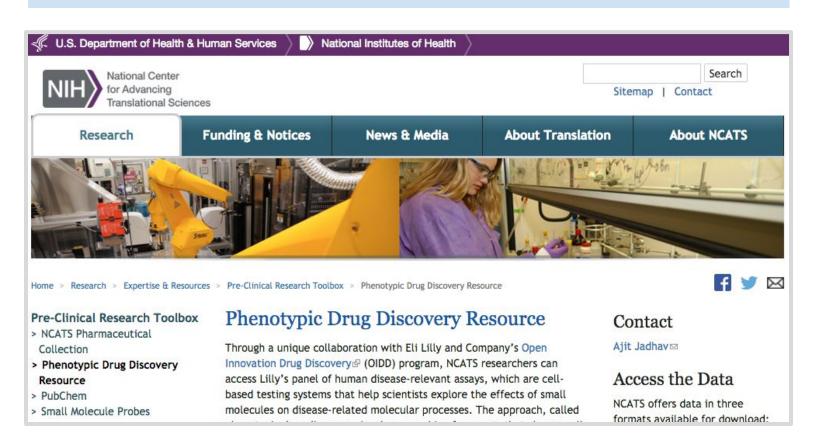
- NCATS (NPC) compounds (2509)
- OIDD phenotypic assays (35 assays across 5 modules)
- Relevance: cardiovascular, diabetes, cancer, endocrine

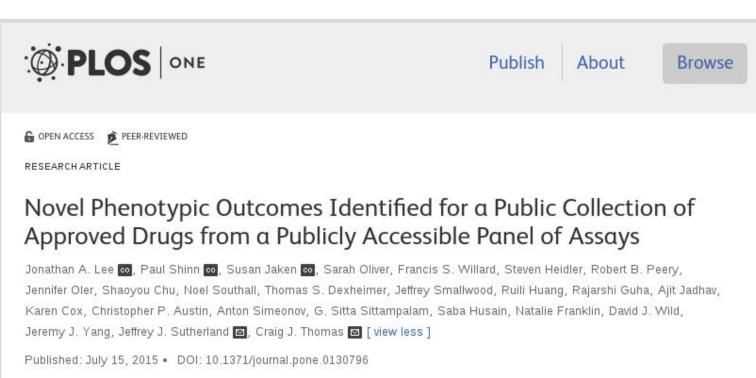
Why phenotypic?

- Phenotypic assays more biologically relevant.
- But, require analytics for molecular inferences.
- Phenomics reflects systems biology.
- Phenotypic assay phenotypes are rigorously defined, observable biological effects, often well associated with disease states.

Semantic engineering

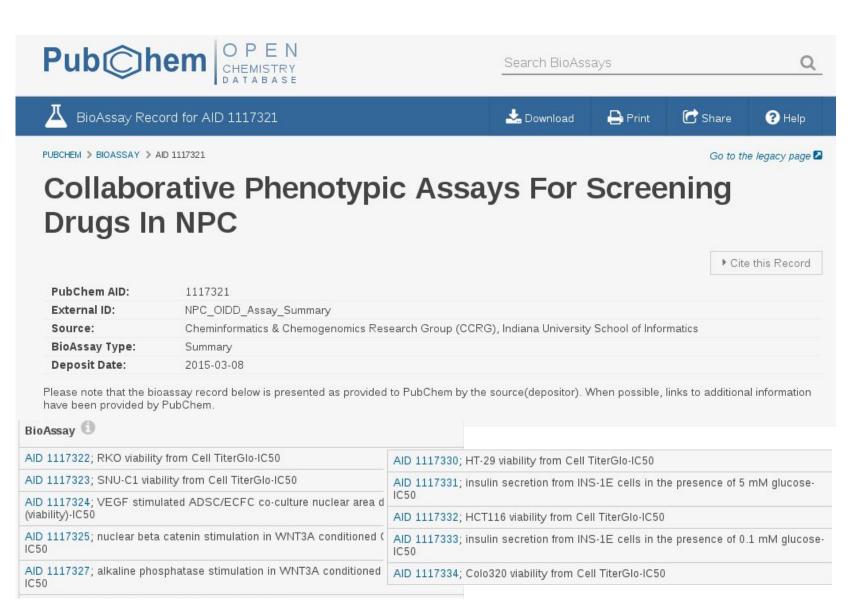
- OPDDR RDB to RDF transformation
- Manual annotation via BAO
- Integration: PubChem, Chembl, Open PHACTS

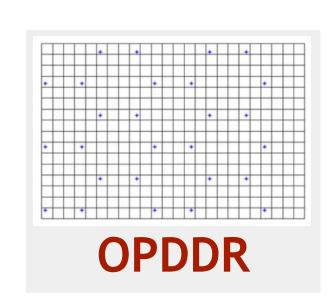


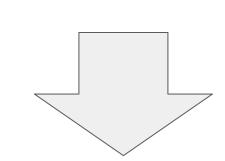


Publication

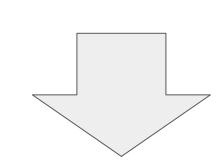
- PubChem Bioassay (March 2015)
- PLOS One (July 2015)
- NCATS site: https://ncats.nih.gov/expertise/preclinical/pd2



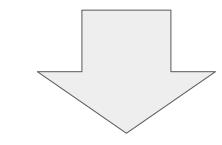


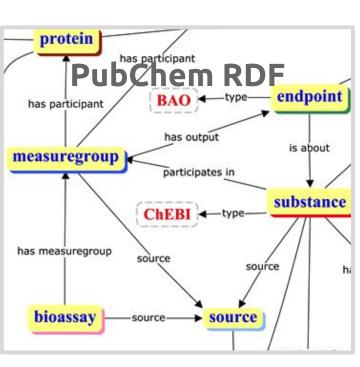


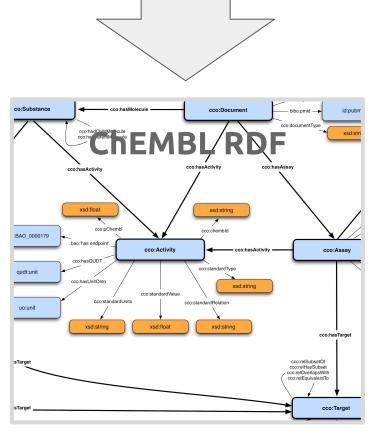


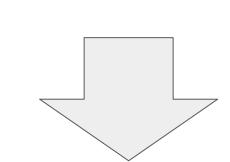














Community semantics

- Cooperation with PubChem, ChEMBL, Open PHACTS, BAO
- Shared goal: biomedical knowledge discovery ecosystem
- Phenotypic knowledge management as new opportunity

RDF community progress

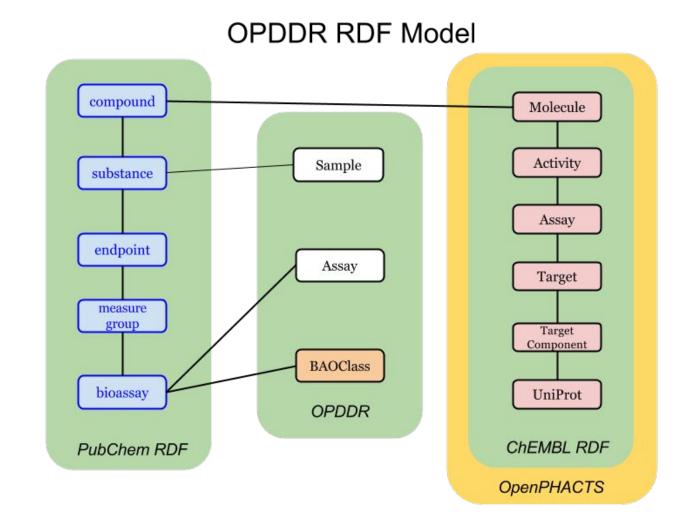
- PubChem RDF major revision June 2015, REST API
- ChEMBL RDF, ChEMBL Core Ontology, Sparql enpoint
- Aligned efforts leading to greater results.

Related projects

- BioAssay Ontology (BAO)
- BioAssay Research Database (BARD)
- Illuminating the Druggable Genome (IDG)
 - Heterogeneous knowledge integration
- D2D: NSF SBIR Predictive Phenotypic Profiler

Open PHACTS integration

- Open PHACTS v2.0 includes OPDDR beta version
- OPDDR revision plan:
 - ChEMBL RDF schema for tighter API integration
 - Phenotypic curation, e.g. cell line associations
 - Additional BAO annotations



Applications and use cases

Cross-domain query

- Semantic assay analytics; finding related data.
- Noise reduction; more data usually allows better sampling.
- Target, MOA deconvolution; interpreting phenotypes. Disease relevant lead discovery; diseases as phenotypes.

