Representation and Extraction of Causality Statements

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In collaboration with

EBI – Reactome, PSI-MI
Institut Curie
ENS





The DrugLogics project

Towards the development of precision and personalised medicine

DrugLogics

Crossover Research

Structured Knowledge Commons resource DbTF curation Scicura **Drug Combinations**

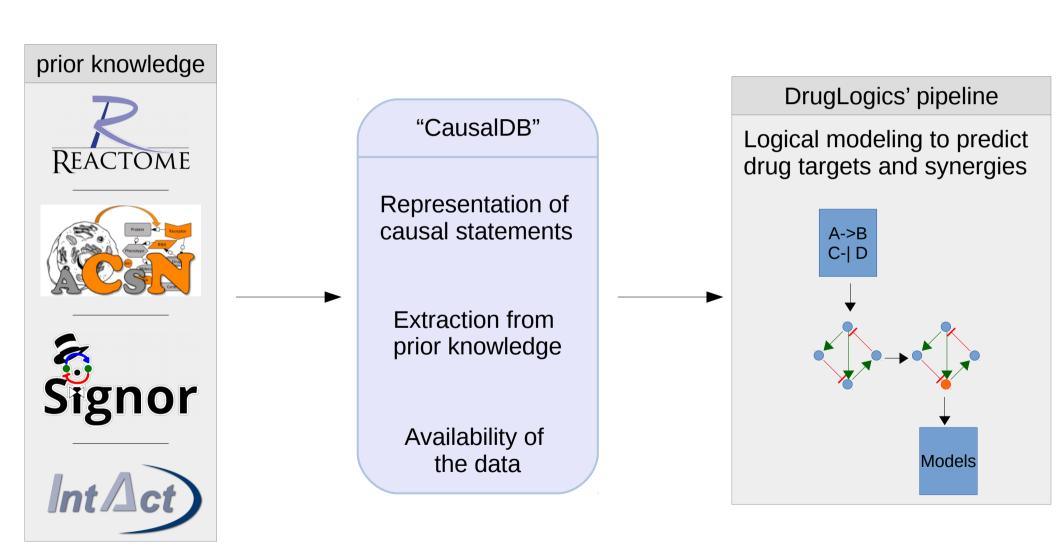
Development of anticancer combinations **COLOSYS**

Drug resistance prediction in colon cancer via computer models

My tasks within the DrugLogics/NTNU-Health project



Facilitate the process of building biological models with causal statements



Causal interaction between two biological entities (gene, RNA, protein, complexes, etc...)

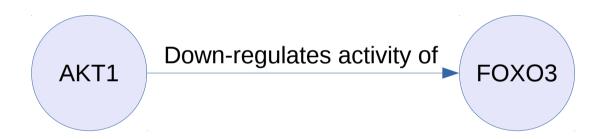


How to represent meaningful causal interactions?

What is FOXO3's state? (active/inactive)

When and where does this interaction occurs?

Which molecular function is down-regulated?



What is the regulation type? (phosphorylation, acetylation, dephosphorylation)

Is it a direct or indirect Interaction?

Research ideas on information that should be ideally encoded

Entity – Source (Regulator) / Target (Regulated)

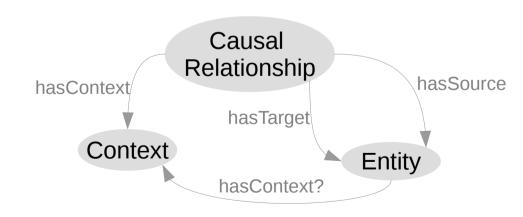
- ID ex:causalDB:FOXO3
- Reference ID HGNC; Uniprot; Entrez
 - For Complex: ComplexPortal ID?
 - For Families?
- Name ex:FOXO3
- Molecule type gene, RNA, protein, complex
- Acting entity Reference ID
- Molecular function GO:MF
- State active / inactive

Context

- Species TaxID
- Tissue type Brenda Tissue Ontology (BTO), Uberon?
- Cell type BTO, Cell Line Ontology (CLO)?
- Experimental conditions if evidence is experimental
- Tissue / Cell state

Causal Relationship

- Regulation type down-regulates
- Mechanism PSI MOD?
- Modified residue Tyr@P202
- Interaction depth 0 (direct); 1; 2; etc...
- Text Scicura (http://scicura.org/info.html)
- Provenance ex:Reactome
- Evidence ECO
- Confidence score?



Controlled Vocabulary and Ontologies – essential to make data sustainable, shareable and interoperable

Controlled vocabulary / ontologies for representing causal interaction type

Effect	Gene Ontology	PSI-MI causal interaction	Relation Ontology	BEL statement	IntAct	Signalink
Positive regulation	positively regulates	up-regulates	activity directly positively regulates activity of	increases	activates	stimulation
Negative regulation	negatively regulates	down-regulates	activity directly negatively regulates activity of	decreases	inhibits	inhibition

→ Need unification

Extraction from prior knowledge

Aggregation of causal data from several existing resources



Pathways, reactions



Pathways of cancer related signaling networks



DB of causal interactions



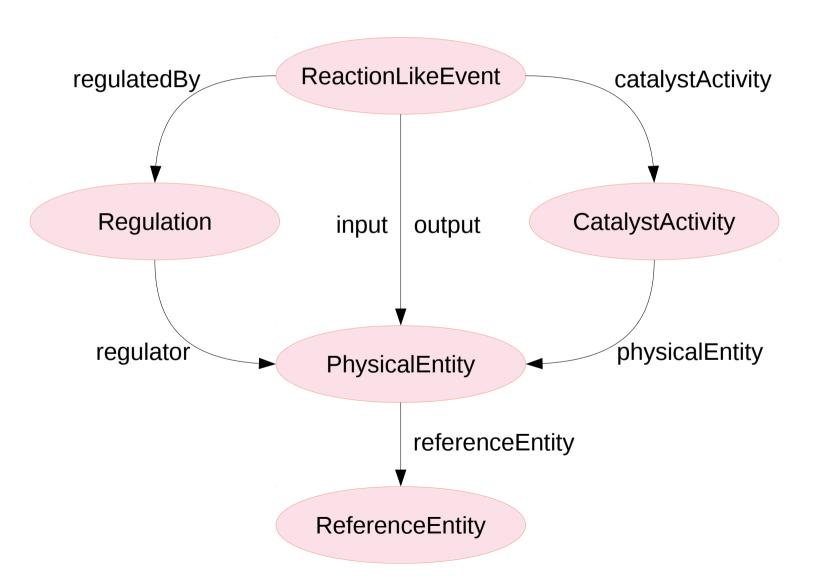
DB of molecular interactions

Example: extraction from Reactome



Reactome data model extraction using Neo4j and Cypher Query language





Example: extraction from Reactome



Reactome data model extraction using Neo4j and Cypher Query language



Example: Get all reactions regulated by a physical entity or catalysed by a catalyst activity

MATCH (rle:ReactionLikeEvent)-[:regulatedBy|catalystActivity]->(o)-[:regulator|physicalEntity]->(source:PhysicalEntity)

OPTIONAL MATCH (input:PhysicalEntity)<-[:input]-(rle)-[:output]->(output:PhysicalEntity)

RETURN rle.stld AS ReactionID,

rle.displayName AS Reaction,

COLLECT(input.displayName) AS Inputs,

COLLECT(output.displayName) AS Outputs,

o.simpleLabel AS Regulation,

source.displayName AS Regulator

Example: Resulting outputs



ReactionId	Reaction	Compartment	Inputs	Effect	Outputs	Regulator
R-HSA- 452338	Expression of TDGF1 (CRIPTO)	cytosol	["TDGF1 gene [nucleoplasm]"]	NegativeGeneExp ressionRegulation	["N-aspartyl- glycosylphosphatidyli nositolethanolamine- TDGF1(31-188) [plasma membrane]"]	NR6A1(GCNF):TDGF1 gene [nucleoplasm]
R-HSA- 8936628	GP1BA gene transcription is stimulated by the complex containing RUNX1, PRMT1 and GATA1 and inhibited by the complex of RUNX1, SIN3A and PRMT6	plasma membrane	["GP1BA gene [nucleoplasm]"]	NegativeGeneExp ressionRegulation	["GP1BA [plasma membrane]"]	RUNX1:CBFB:SIN3A, (SIN3B):PRMT6:HDA C1:GP1BA gene:H3K4me2,H3R2 me2a-Nucleosome [nucleoplasm]
R-HSA- 8944497	PTEN mRNA translation is negatively regulated by microRNAs	cytosol	["PTEN mRNA [cytosol]"]	NegativeGeneExp ressionRegulation	["PTEN [cytosol]"]	miR-20 RISC:PTEN mRNA [cytosol]

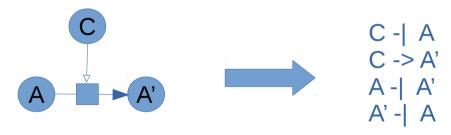


Example: questions / issues raised



Exclude trivial molecules

- Missing IDs for the modified mechanism type
- How to transform a reaction network to causal statements?



- Definition of necessary and sufficient contextual information
 - → MICAST: Minimum Information for representing Causality Statements?

Current work

- Collaboration with Curie and ENS Paris
 - Define the representation of causal statements
 - Extraction of causal statements from ACSN
 - Consensus representations with GO, PSI-MI,
 COLOMOTO
 - Standardisation of the pipeline → SBML-Qual?





Thank you for your attention!

The DrugLogics team

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