

# Overcoming challenges in semantic alignment of therapeutics knowledge with TheraPy

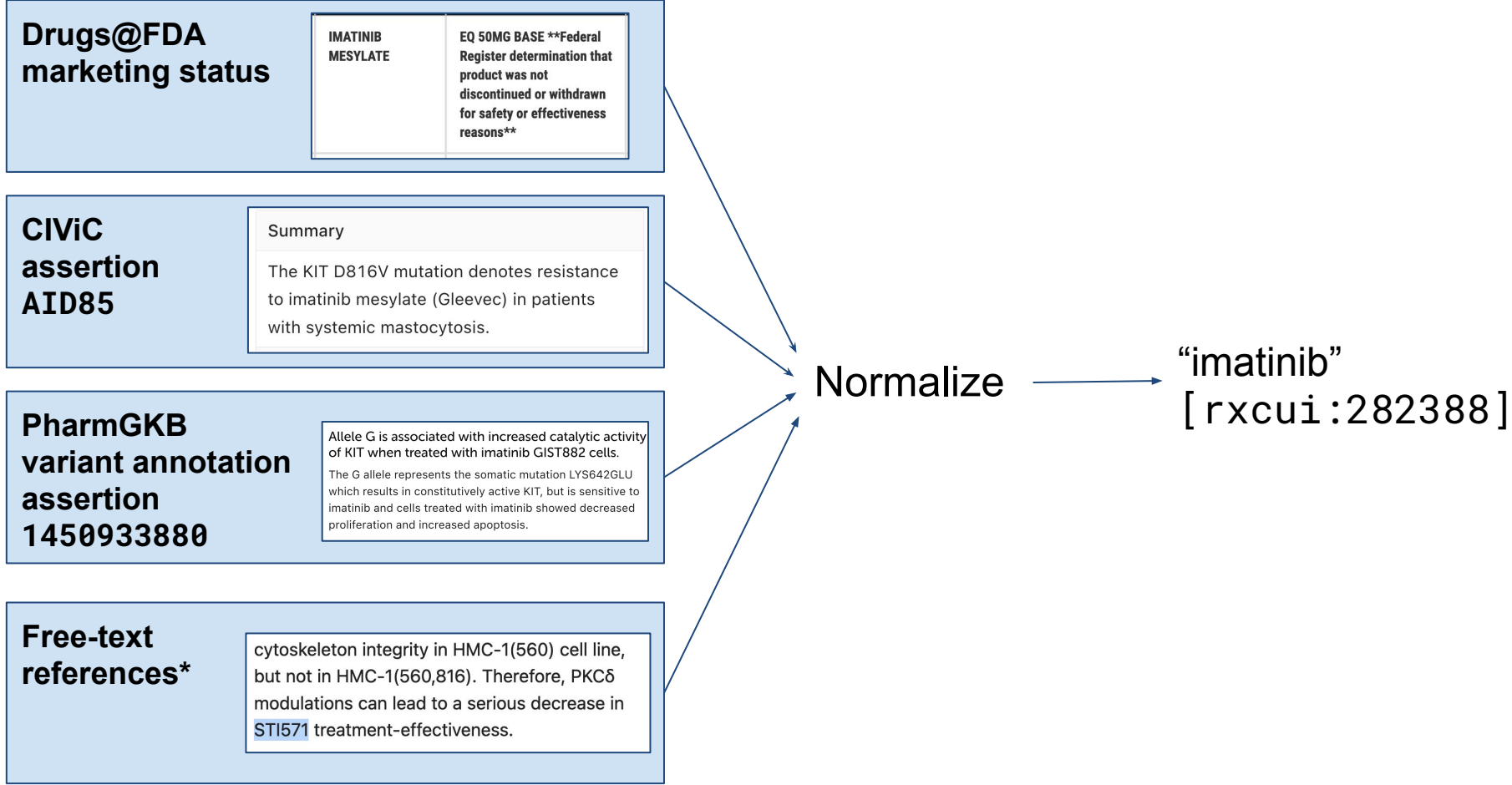
James Stevenson

# The mission

Align therapeutics data resources using **normalized drug and therapy concepts** to enable clinical data harmonization from open-access knowledgebases.

**VICC**

Variant Interpretation  
for Cancer Consortium



# Our problem

Data is

**fragmented,**

**imperfectly structured, and**

**inconsistently referenced.**

ChEMBL: **Imatinib**

MOA: *KIT exon 11 and 13 variants are sensitive to treatment with **Imatinib***

```
graph LR; A[ChEMBL: Imatinib] --> B[MOA: KIT exon 11 and 13 variants are sensitive to treatment with Imatinib]; C[Drugs@FDA: Gleevec] --> D[CIViC: KIT D816V is associated with resistance to Gleevec in patients with systemic mastocytosis]; E[ChemIDplus: Imatinib Mesylate];
```

Drugs@FDA: **Gleevec**

CIViC: *KIT D816V is associated with resistance to **Gleevec** in patients with systemic mastocytosis*

ChemIDplus:  
**Imatinib Mesylate**

**ChEMBL: Imatinib**

**Drugs@FDA: Gleevec**

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[Aggregate Imatinib concept]

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[Aggregate Imatinib concept]

# Referential ambiguity

<b>Generic name</b>	Sunitinib
<b>Brand name</b>	Sutent, Lucisun, Sunitix
<b>Active ingredient</b>	Sunitinib Malate
<b>Development ID</b>	SU-11248
<b>IUPAC chemical structure</b>	5-(5-Fluoro-2-oxo-1,2-dihydro...
<b>Database ID</b>	CHEMBL535, D0R0MW



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# Referential overlap

Aliases may be:

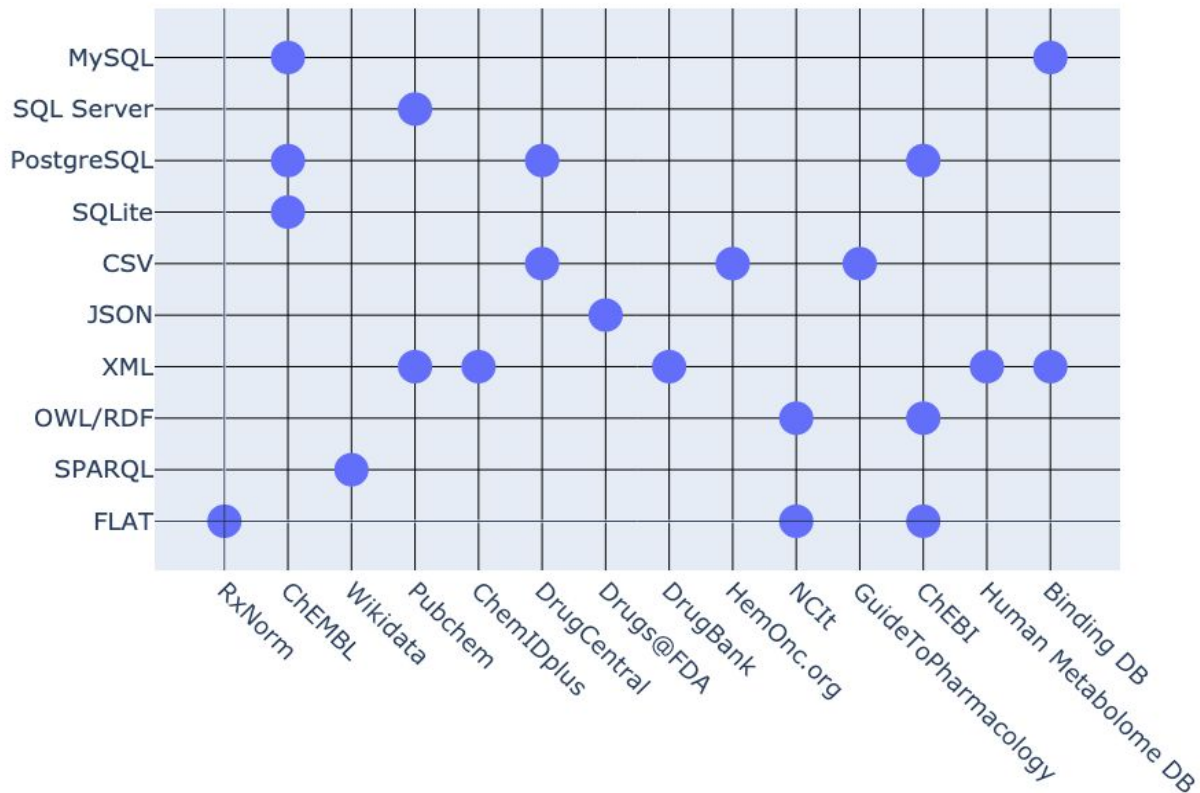
- Overly broad
  - “Ig gamma-1 chain C region”
  - “Anti-HER2”
- Indeterminate
  - “A6”

# Varying data structures

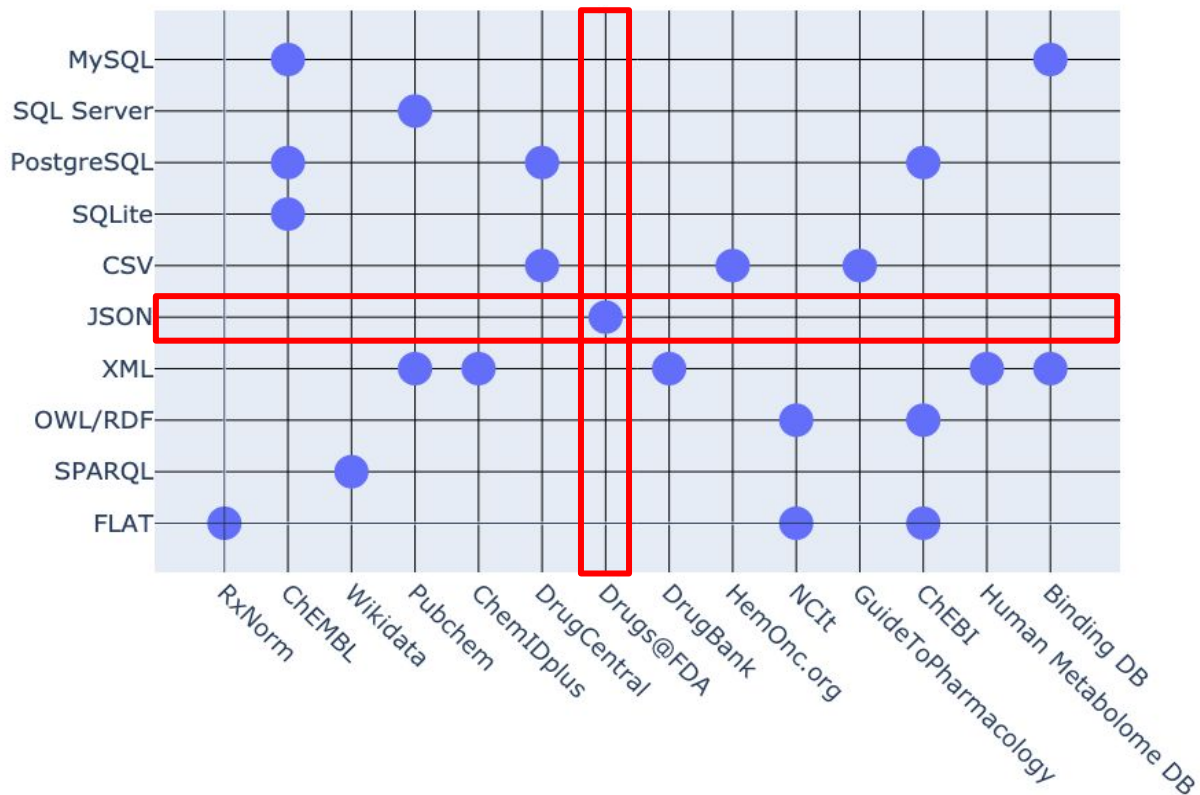
Data exports may be:

- **Relational** (SQL)
- **Key-value** (JSON)
- **Markup trees** (XML)
- **Semantic triples** (RDF, OWL)

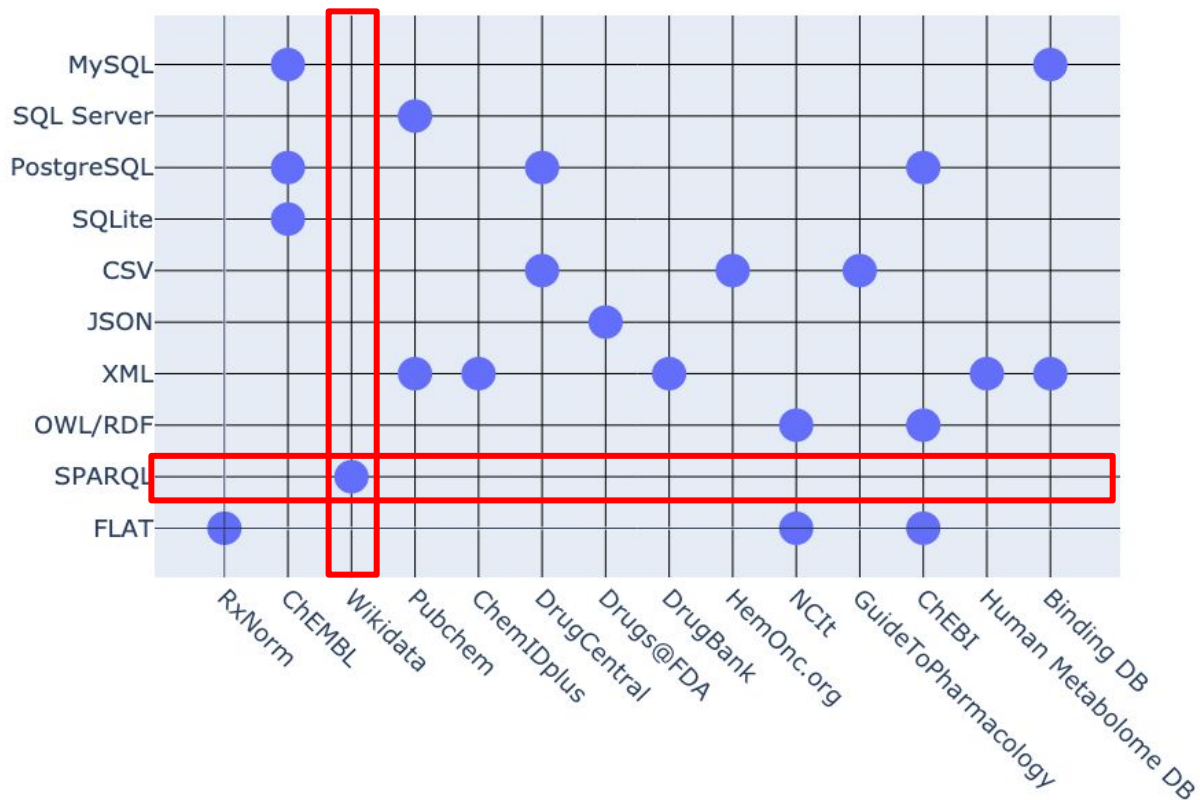
# Varying data structures



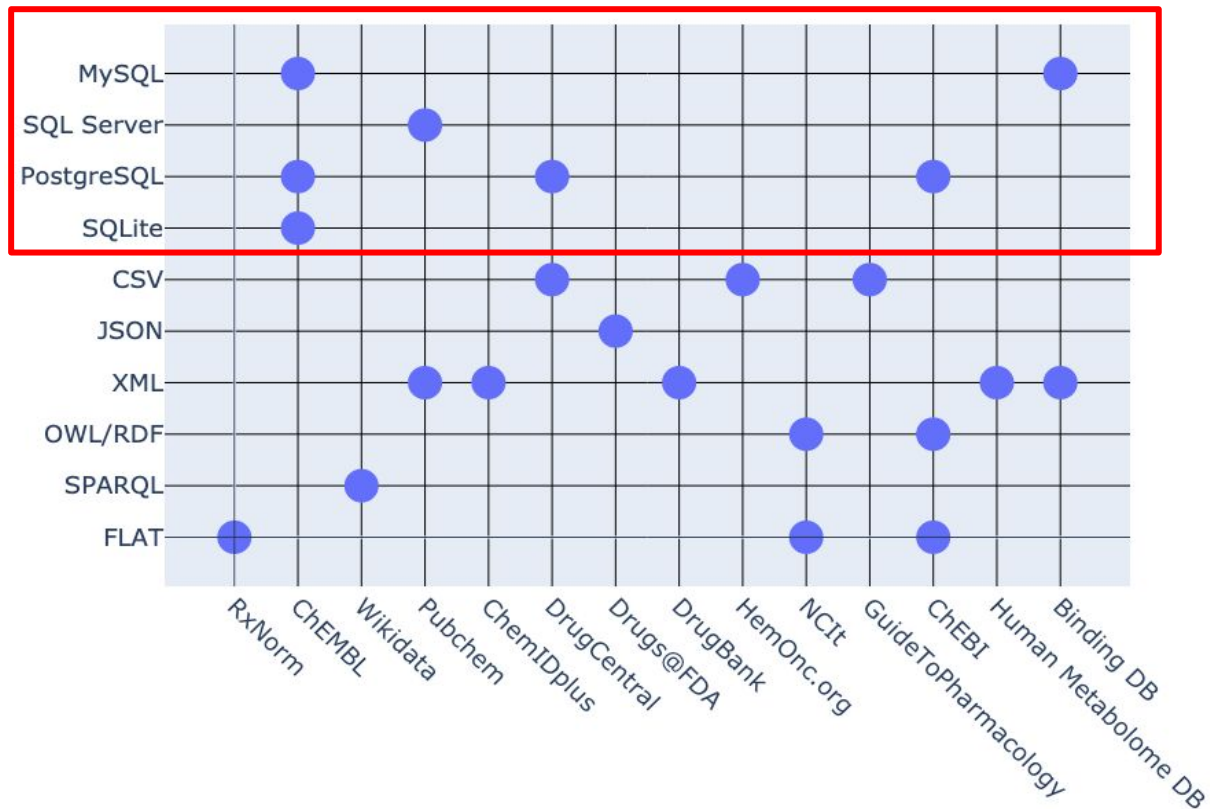
# Varying data structures



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# Varying data structures





# Incongruous conceptual structures

- “Chemicals”, “compounds”, “small molecules”
- “Ligands”
- “Drugs”
- “Drug products”
- Combination products, combination therapies

# Cross-referential ambiguity

- Is an xref to another source intended to convey...
  - A is equivalent to B?
  - A is contained by B?
  - A contains B?
  - A is related to B?

# Alignment framework and implementation: TheraPy



# TheraPy

Produces ~16,000  
multi-source, merged  
therapy concepts

## The VICC Therapy Normalizer

0.3.10 OAS3

</therapy/openapi.json>

Normalize drugs and other therapy terms.

[Alex H. Wagner - Website](#)

[Send email to Alex H. Wagner](#)

### default

GET

[/therapy  
/search](/therapy/search)

Given query, provide highest matches from each source.

GET

[/therapy  
/normalize](/therapy/normalize)

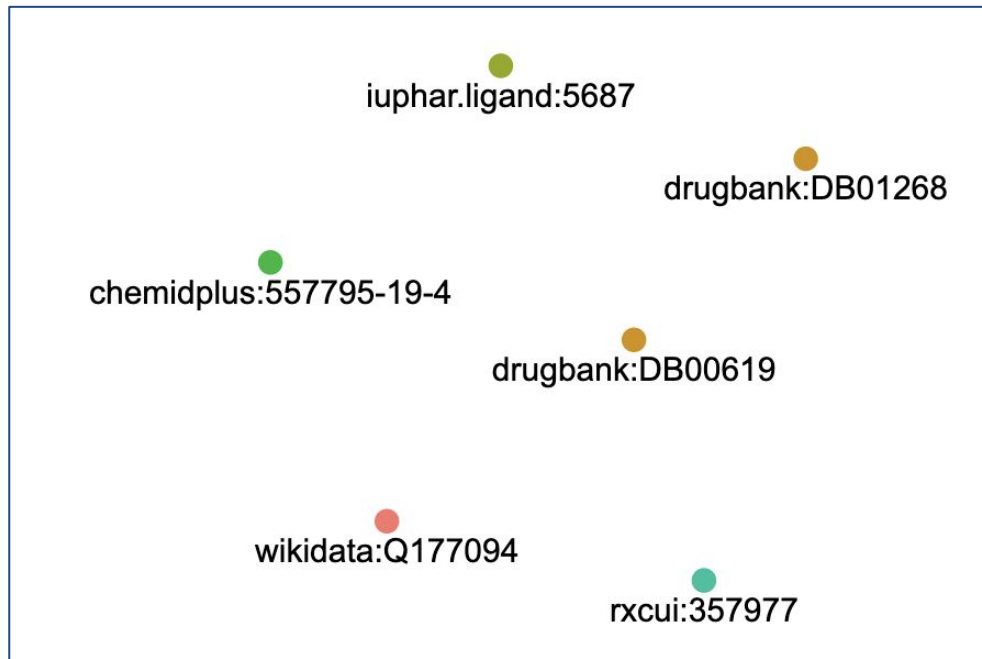
Given query, provide merged normalized record as a TherapyDescriptor.

GET

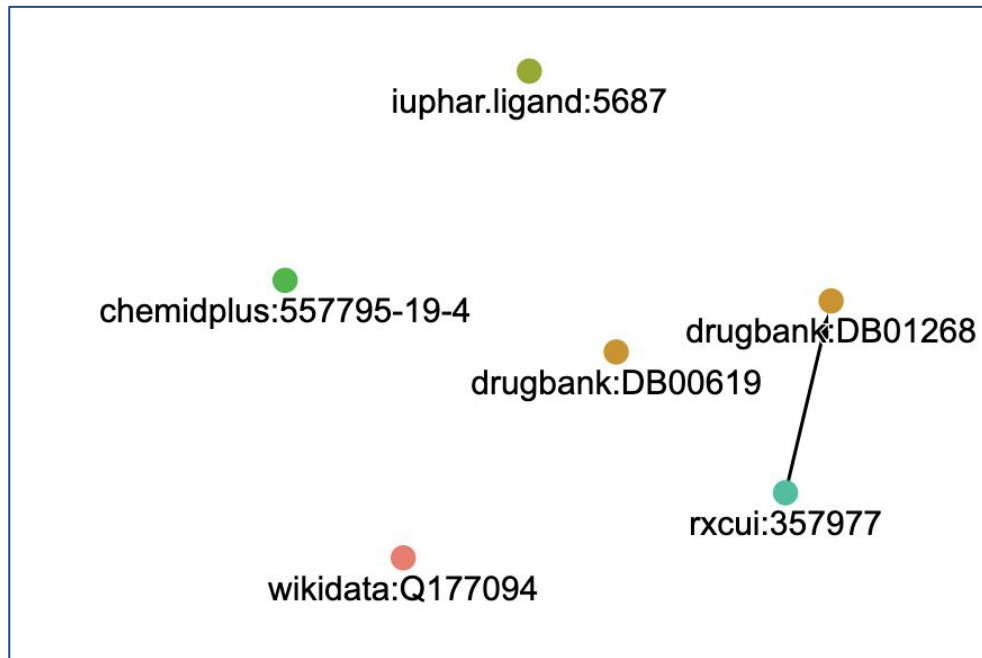
[/therapy  
/normalize\\_unmerged](/therapy/normalize_unmerged)

Given query, provide source records corresponding to normalized concept.

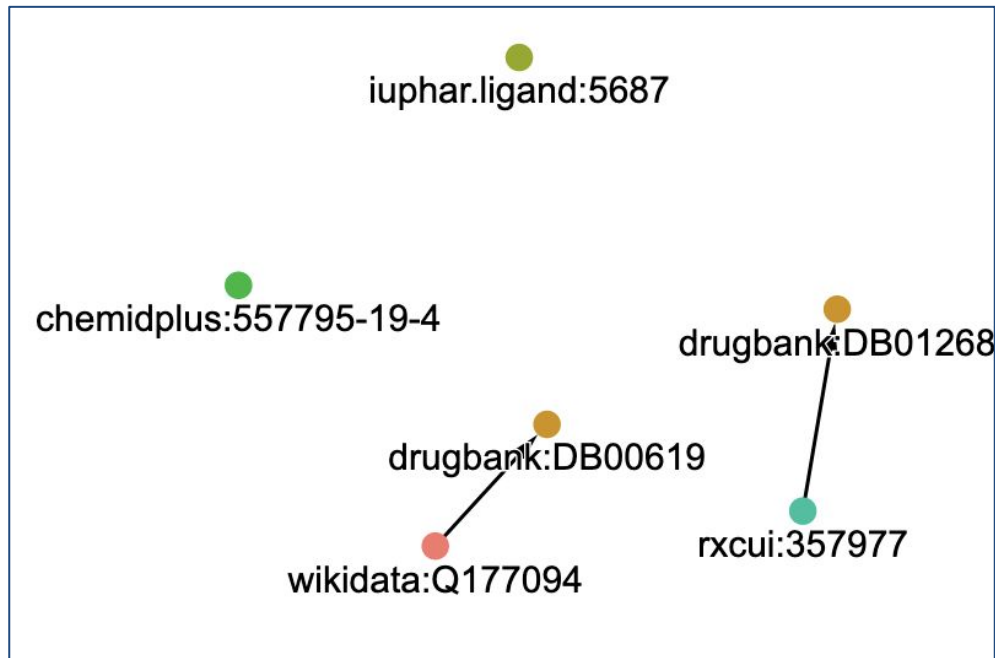
# Concept generation



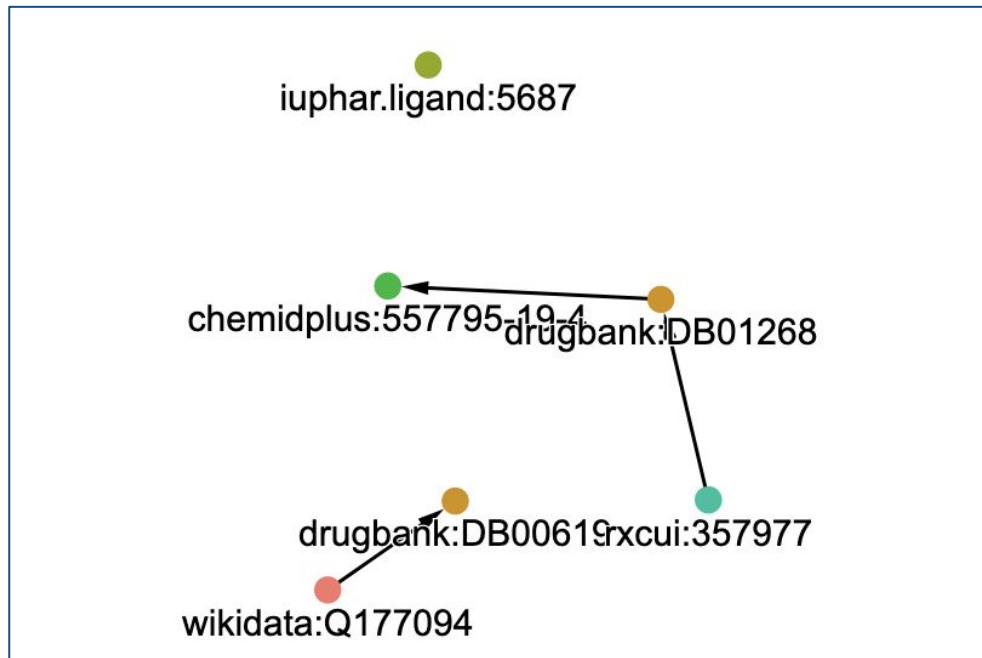
# Concept generation



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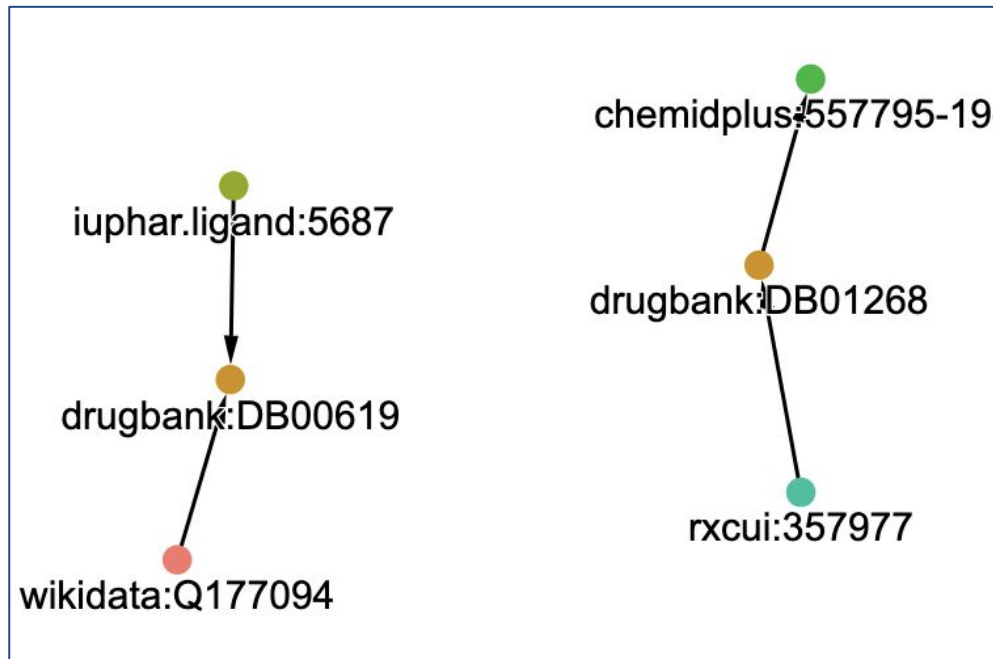


# Concept generation

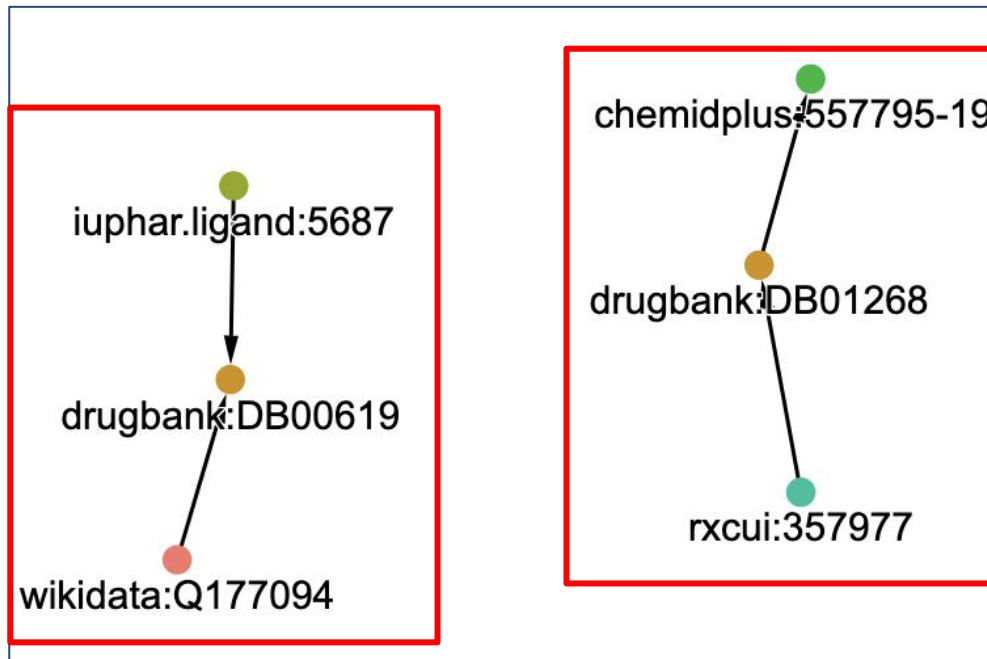




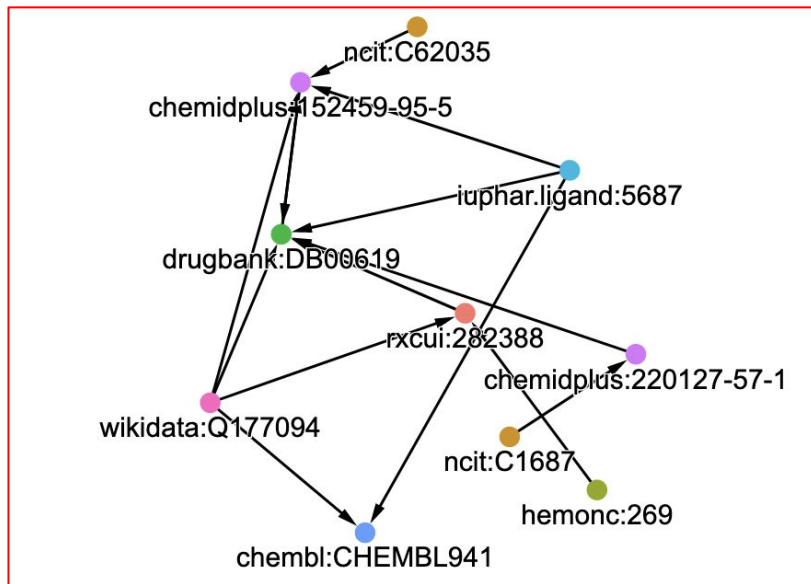
# Concept generation



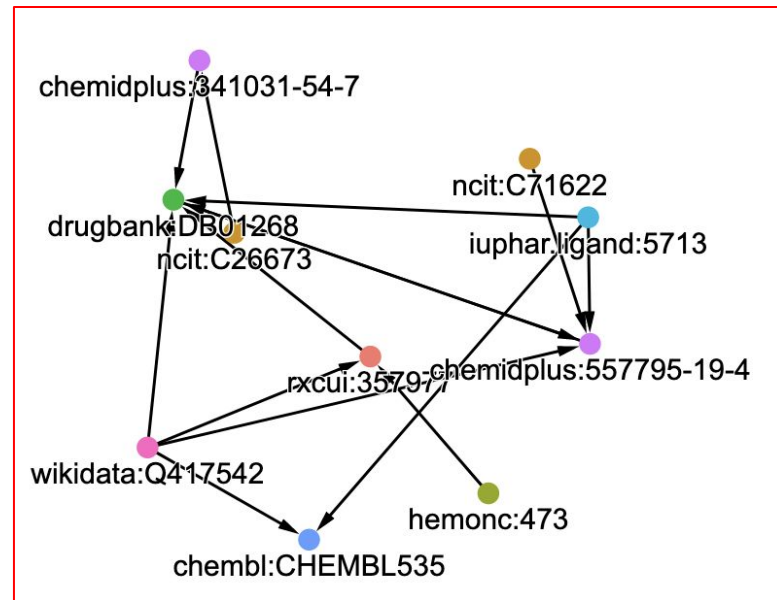
# Concept generation



# Concept generation



Imatinib [rxcul:282388]






Sunitinib [rxcul:357977]

**Monday, August 14, 2023 @ 11:45 AM**

**Improving interoperability of therapeutics and their targets for clinical and precision medicine applications**

Matthew Cannon, *Nationwide Children's Hospital*

## **Normalization of Drug and Therapeutic Concepts with TheraPy**

 Matthew Cannon, James Stevenson, Kori Kuzma, Susanna Kiwala, Jeremy L Warner,  Obi L Griffith, Malachi Griffith,  Alex H Wagner

**doi:** <https://doi.org/10.1101/2023.07.27.23293245>

# Future: Refining grouping

- Probabilistic mapping (Bayesian methods)
- Increased manual curation
- Additional data sources
- Applications in NLP

# Conclusion

- Open-source drug data is plentiful, but **structural inconsistencies** hamper inter-source alignment.
- TheraPy **pools drug descriptions** to define a normalized concept and mappings in support of data harmonization.

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- Adam Coffman

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# Get in touch

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- <https://go.osu.edu/tpy>
- <https://cancervariants.org/projects/integration/>

