Hypothesis Generation with AGATHA

Accelerate Scientific Discovery with Deep Learning

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Motivation: Drug Discovery

- Solution strategy:
 - Identify ~1000 target substances
 - Determine ~10 candidates
 - Conduct ~1 human trial
- Challenges:
 - Expensive early investment
 - Uncertain results

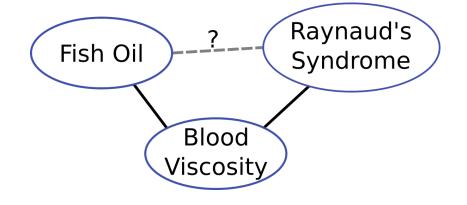
Available Data

- National Library of Medicine provides public databases
- MEDLINE contains nearly 30 million biomedical abstracts
- Data available through PubMed
- New papers per-year is increasing!
 - Nearly 1 million last year
 - New paper every 35 sec



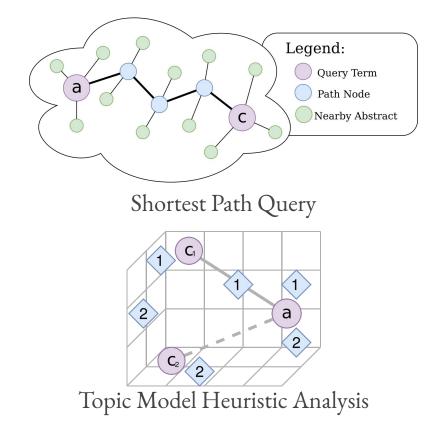
Background: ARROWSMITH (1986)

- Pattern:
 - Given two terms: A, C
 - Find words related to A
 - Find words related to C
 - Find overlap
- Key Limitations:
 - Only simple connections
 - Biased to incremental results



Background: MOLIERE (2017)

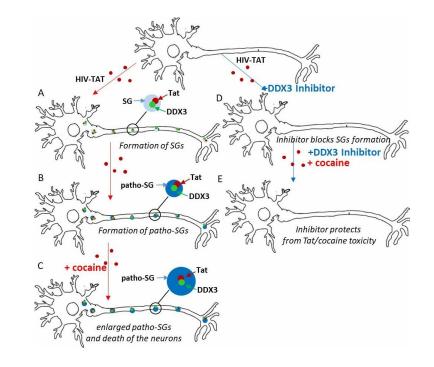
- Our first hypothesis generation system
- Process:
 - Construct semantic network
 - Shortest path queries
 - Topic modeling
 - Heuristic analysis
- Limitations:
 - Minutes per query
 - Heuristic analysis



Moliere: Automatic biomedical hypothesis generation system Sybrandt, Shtutman, Safro

Success with HIV-Associated Dementia

- Moliere ranked 40,000 genes
- DDX3 ranked highly
- Confirmed in laboratory



Inhibition of the DDX3 prevents HIV-1 Tat and cocaine-induced neurotoxicity by targeting microglia activation Aksenovam, Sybrandt, Chu, Sikirzhytski, Ji, Odhiambo, Lucius, Turner, Broude, Pena, Lizzaraga, Zhu, Safro, Wyatt, Shtutman JNP'19

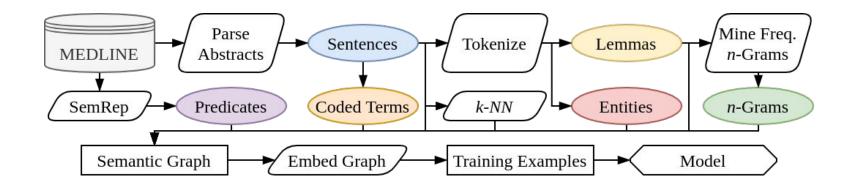


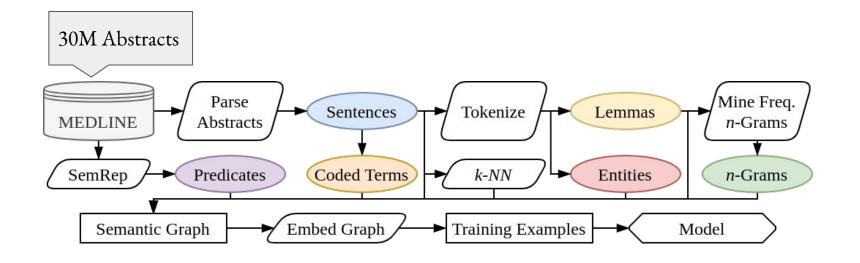
- Process:
 - Parse MEDLINE
 - Construct semantic network
 - Train embedding & model
 - Validate through ranking

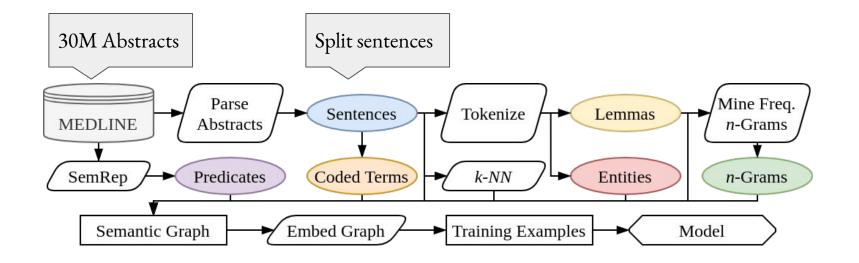
• Intuition:

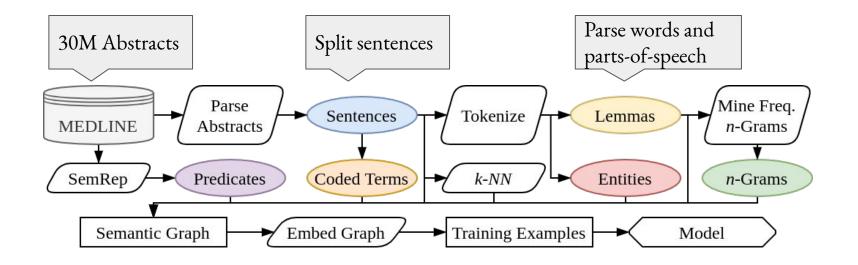
- Remove heuristics
- Add data-driven insights
- Speed up hypothesis queries

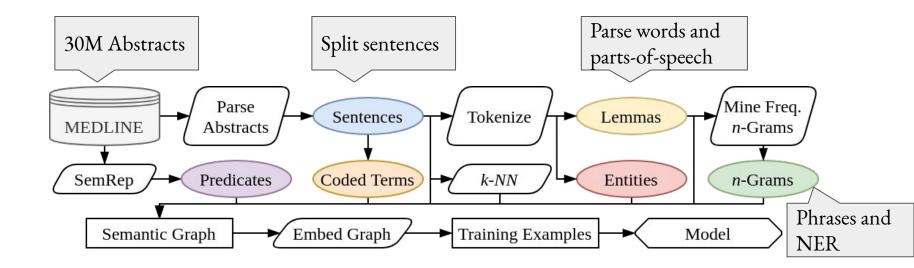
Agatha Pipeline Summary



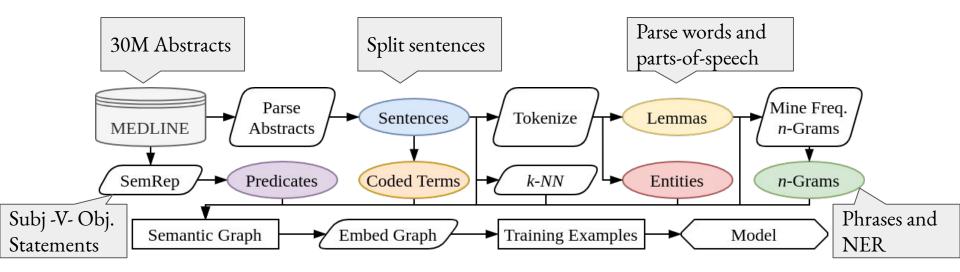






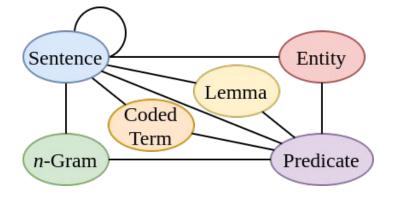


Agatha Pipeline Summary



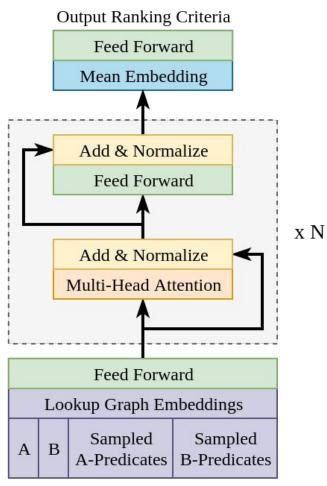
Semantic Graph

- Sentences:
 - Connected by nearest-neighbors
 - Edges to contained elements
- Predicates
 - Edges to info supplied by SemMedDB
- Size:
 - 2015 Release:
 - 188 M. Nodes
 - 2020 Release:
 - 270 M. Nodes



Agatha Deep Learning Model

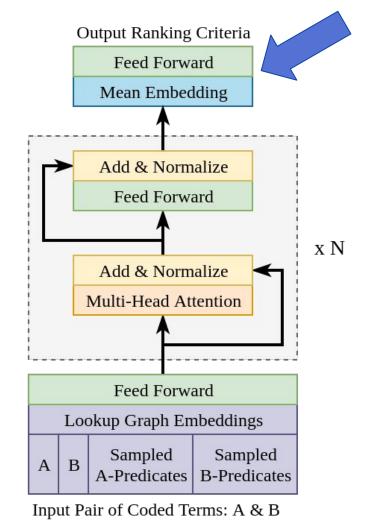
- Goal: train a transformer encoder to accept two query terms and produce ranking criteria
- Objective: Margin Ranking Loss
- Model: Transformer Encoder
- Graph Embedding



Input Pair of Coded Terms: A & B

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Predicate Modeling Objective

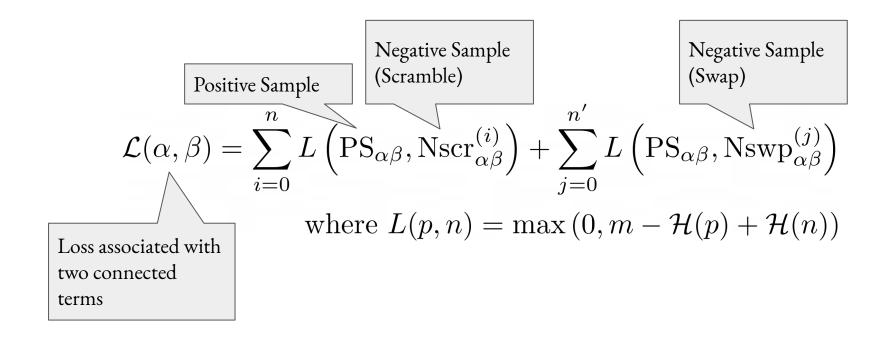
$$\mathcal{L}(\alpha,\beta) = \sum_{i=0}^{n} L\left(\mathrm{PS}_{\alpha\beta}, \mathrm{Nscr}_{\alpha\beta}^{(i)}\right) + \sum_{j=0}^{n'} L\left(\mathrm{PS}_{\alpha\beta}, \mathrm{Nswp}_{\alpha\beta}^{(j)}\right)$$

where $L(p,n) = \max\left(0, m - \mathcal{H}(p) + \mathcal{H}(n)\right)$

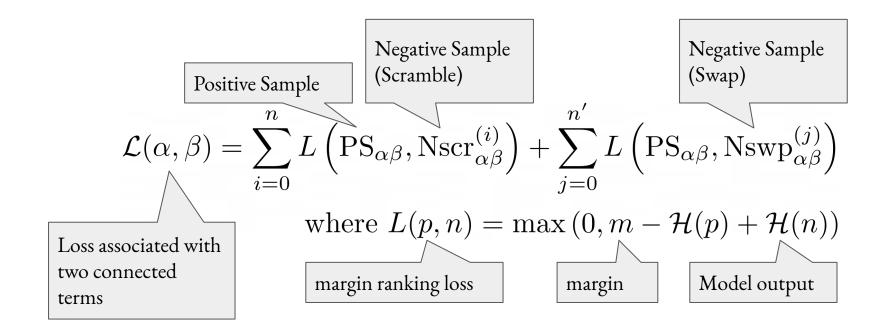
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Predicate Modeling Objective



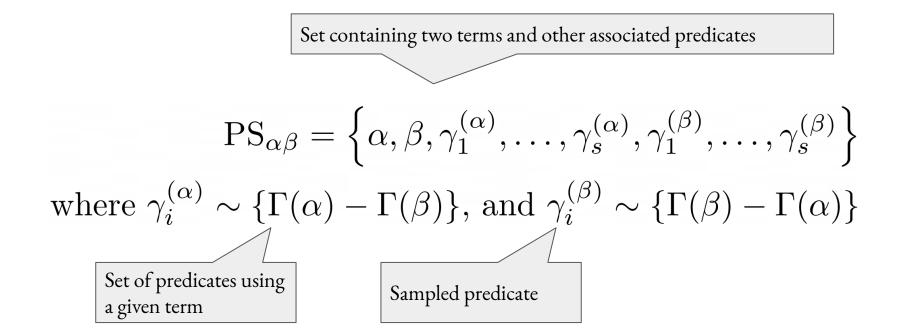
Predicate Modeling Objective



Predicate Formulation

$$\mathrm{PS}_{\alpha\beta} = \left\{ \alpha, \beta, \gamma_1^{(\alpha)}, \dots, \gamma_s^{(\alpha)}, \gamma_1^{(\beta)}, \dots, \gamma_s^{(\beta)} \right\}$$

where $\gamma_i^{(\alpha)} \sim \{\Gamma(\alpha) - \Gamma(\beta)\}$, and $\gamma_i^{(\beta)} \sim \{\Gamma(\beta) - \Gamma(\alpha)\}$



Negative Samples

• Scramble (easy):

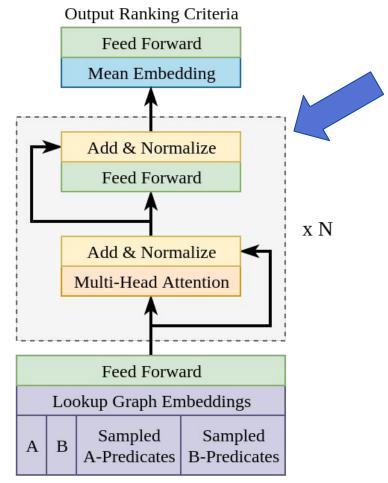
NScr_{$$\alpha\beta$$} = { $x, y, \gamma_1, \dots, \gamma_{2s}$ }
where $x, y \sim T$,
and $\gamma_i \sim P$,
s.t. $\Gamma(x) \cap \Gamma(y) = \emptyset$

• Swap (hard):

$$\begin{split} \mathrm{NSwp}_{\alpha\beta} &= \left\{ x, y, \gamma_1^{(x)}, \dots, \gamma_s^{(x)}, \gamma_1^{(y)}, \dots, \gamma_s^{(y)} \right\} \\ \mathrm{where} \ x, y \sim T, \\ \mathrm{and} \ \gamma_i^{(x)} &\sim \{ \Gamma(x) - \Gamma(y) \}, \\ \mathrm{and} \ \gamma_i^{(y)} &\sim \{ \Gamma(y) - \Gamma(x) \}, \\ \mathrm{s.t.} \ \Gamma(x) \cap \Gamma(y) &= \emptyset \end{split}$$

Agatha Deep Learning Model

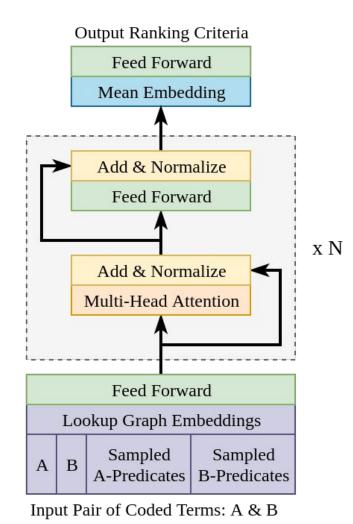
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Model Formalism

- Prediction Model: $\mathcal{H}(X) = \text{sigmoid}(\mathcal{M}W)$ $\mathcal{M} = \frac{1}{|X|} \sum_{x_i \in X} E_N(FF(e(x_i)))$ $E_{i+1}(x) = \mathcal{E}(E_i(x)), \text{ and } E_0(x) = x$
- Encoder Block: $\mathcal{E}(X) = \text{LayerNorm}(FF(\alpha) + \alpha)$ where $FF(Y) = \max(0, YW)W'$ and $\alpha = \text{LayerNorm}(\text{MultiHead}(X) + X)$



• Attention: learned weighted averages

Attention
$$(Q, K, V) = \operatorname{softmax}\left(\frac{QK^{\intercal}}{\sqrt{d_k}}\right)V$$

• Attention: learned weighted averages

Attention
$$(Q, K, V) =$$
softmax

$$\left(\frac{QK^{\mathsf{T}}}{\sqrt{d_k}}\right)V$$
... then add in value

Think: if key matches query

• Attention: learned weighted averages

Attention
$$(Q, K, V) = \operatorname{softmax}\left(\frac{QK^{\intercal}}{\sqrt{d_k}}\right)V$$

• Multi Head Self Attention:

MultiHead
$$(X) = [h_1; \dots; h_k] W^{(4)}$$

where $h_i = \text{Attention} \left(X W_i^{(1)}, X W_i^{(2)}, X W_i^{(3)} \right)$

• Attention: learned weighted averages

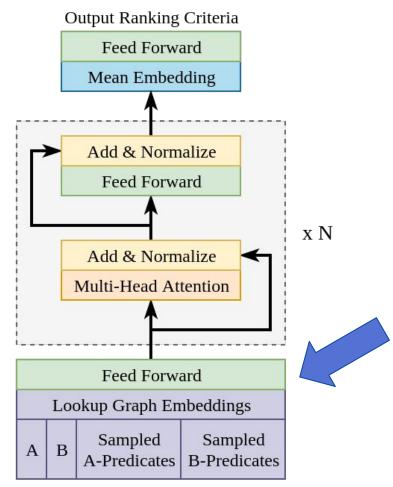
Attention
$$(Q, K, V) = \operatorname{softmax}\left(\frac{QK^{\intercal}}{\sqrt{d_k}}\right)V$$

• Multi Head Self Attention:

MultiHead(X) =
$$[h_1; ...; h_k]W^{(4)}$$
 Compute multiple
times and merge
where h_i = Attention $\left(XW_i^{(1)}, XW_i^{(2)}, XW_i^{(3)}\right)$
Derive Q, K, and V from X

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Graph Embedding Objective

- PyTorch-BigGraph (PTBG) distributed embedding
- Produce embedding per node in network
- Trained separate from Agatha ranking model
- Minimizes Softmax Loss:
 - Positive probability close to 1
 - All negative probabilities close to 0

$$\begin{aligned} \text{GraphLoss}_{ij} &= -s(ij) + \log \sum_{n=0}^{100} \exp\left(s\left(x_n^{(ij)}y_n^{(ij)}\right)\right) \\ & \\ \text{Similarity assoc.} \\ & \text{w/ existing edge} \end{aligned}$$

- Similarity measure:
 - biased transformed dot product of nodes
 - includes typed translation

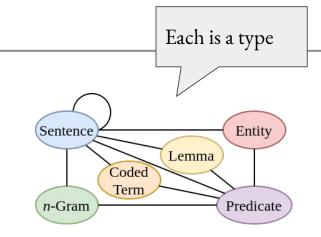
$$s(ij) = e(i)_1 + e(j)_1 + T_1^{(t_i t_j)} + \sum_{k=2}^N e(i)_k \left(e(j)_k + T_k^{(t_i t_j)} \right)$$

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Estimated sim. btwn. i and j

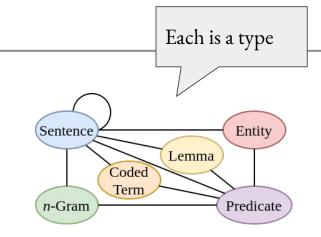
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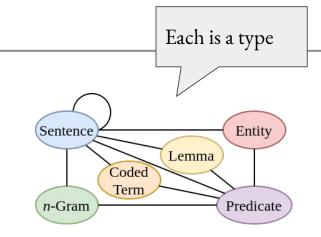
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Estimated sim.
btwn. i and j
Translated dot
product
T translates
between types

- Similarity measure:
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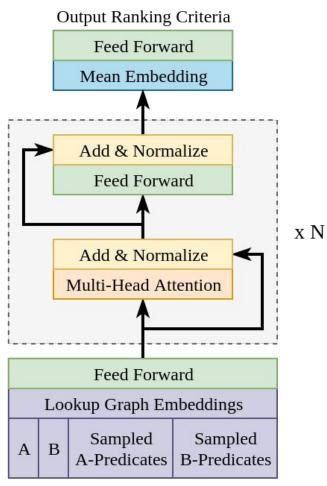


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Estimated sim.
btwn. i and j
First dim. is bias
First dim. is bias
Translated dot
product
T translates
between types

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How to Validate

- Challenge: looking for novel information
- Existing methods:
 - Recreate 7 experiments from early 90's
 - Domain-specific statistics
 - Expert interpretation
 - Publish in medicine
- Complications:
 - Too narrow: Only specific domains
 - Too slow: Human in the loop
 - Too small: Datasets of <10 hypotheses

How to Validate

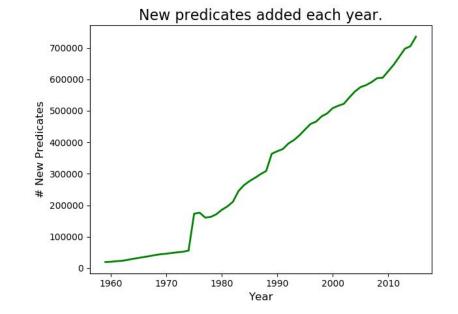
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Large-scale validation of hypothesis generation systems via candidate ranking *Sybrandt, Shtutman, Safro*

BigData'18

Validation via Ranking

- Drug discovery is ranking
- Positive test set
 - Recently introduced predicates
- Negative test set
 - Never introduced predicates
- Perform temporal holdout



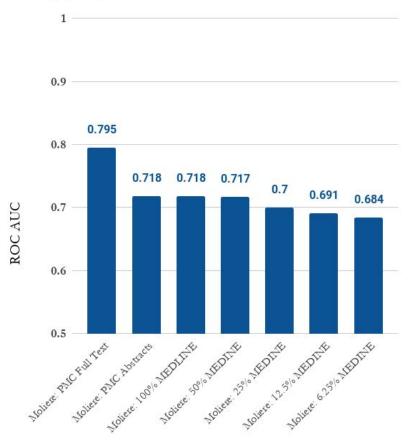
Moliere Baseline

- Train on data before 2015
- Explore different training datasets
- Rank recent predicates with heuristic criteria
- Found that full text papers outperform abstracts by 10%

Are abstracts enough for hypothesis generation? Sybrandt, Carrabba, Herzog, Safro

BigData'18

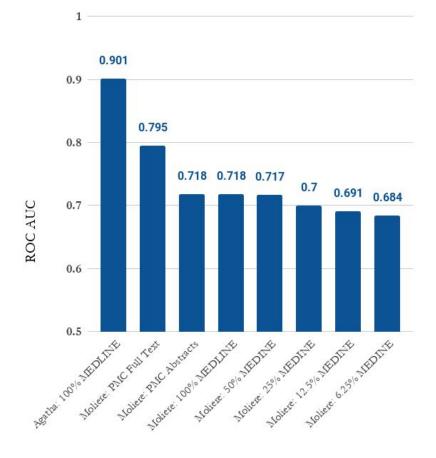
Ranking Quality on 2015 Baseline



Agatha performance on Moliere Benchmark

- Trained on same holdout as Moliere experiments (2015)
 - Used only abstracts
- Same set of predicates
- 100's queries per minute

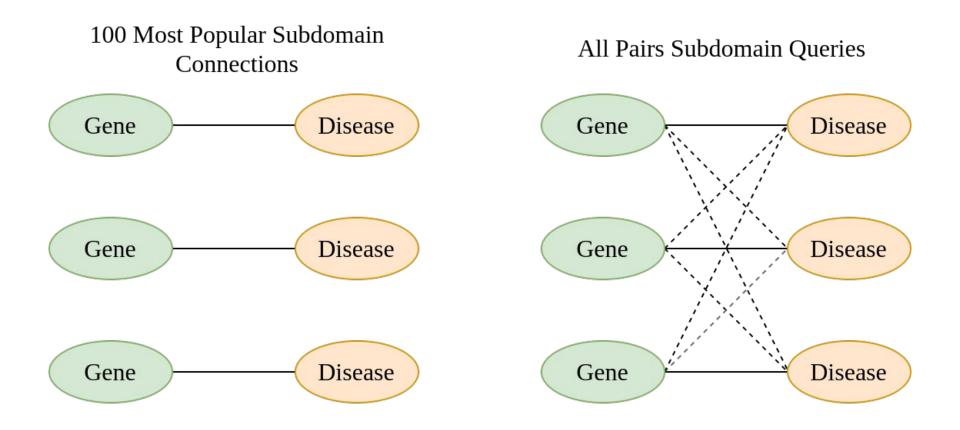
Ranking Quality on 2015 Baseline



Beyond the Moliere Benchmark

- Moliere benchmark had significant issues
 - Balanced classes
 - Non-representative negative samples
- New validation task
 - Subdomain all-pairs recommendation
- Procedure:
 - Identify popular types of predicates
 - Find 100 most popular new findings within each predicate type
 - Predict all pairs of queries within popular entities
 - 0 Rank
 - Compute recommendation system metrics

All Pairs Recommendation Example



Gene to Cell Function

Top 100 predicates of this type.

- Area under curves:
 - PR: 0.44
 - ROC: 0.62
- Top ranked predicate is positive
- Half of the top-10 are positive
- Each one-to-many query on average:
 - Positive result within first two

Gene to Neoplastic Process

Top 100 predicates of this type.

- Area under curves:
 - PR: 0.34
 - ROC: 0.65
- Second ranked predicate is positive
- Half of the top-10 are positive
- Each one-to-many query on average:
 - Positive result within first two

Try it yourself

```
# Its now incredibly easy to run your own
# Hypothesis Generation Queries!
import torch
agatha_data_dir = "..."
model = torch.load(f"{agatha_data_dir}/model.pt")
model.set_data_root(agatha_data_dir)
model.init()
# Now you can rank arbitrary UMLS term pairs!
# Keywords: Cancer(C0006826), Tobacco(C0040329)
model.predict_from_terms([("C0006826", "C0040329")])
>>> [0.78358984]
# Check us out at github.com/jsybrandt/agatha
```

In Summary

- Agatha:
 - Deep learning model built on graph embeddings and the transformer
 - Ranks user queries
 - High quality recommendation
- Learn more:
 - Email: jsybran@clemson.edu
 - Project: <u>sybrandt.com/2020/agatha</u>
 - Github: <u>github.com/jsybrandt/agatha</u>