Insights into Analogy Completion from the Biomedical Domain

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BioNLP 2017
August 4, 2017

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TL;DR

Increasing work on training embedding-based models for biomedical applications, but not many resources to evaluate on.

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Findings:

- Current embeddings are good at direct chemical/biological relationships, not so good at clinical semantics.
- Changes need to be made to the standard analogy methods to reflect the complexity of real data.

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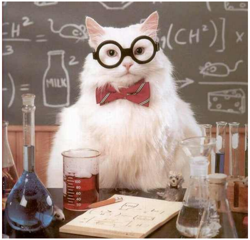
Outline

The analogy completion task

BMASS

How can we make analogies more realistic?

Findings and challenges on our dataset



The analogy completion task

London : England :: Paris : France

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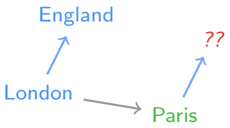
$$d^* = \text{argmax}_{d \in V}\left(\cos(d, \mathit{Eng} - \mathit{Lndn} + \mathit{Paris})\right)$$



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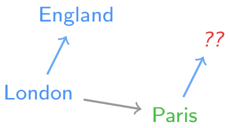

France
Switzerland
Italy
urology
swimming
purple
Latvia

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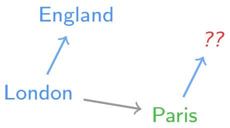

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Unified Medical Language System (UMLS)

BMASS - BioMedical Analogic Similarity Set

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Normalized concepts

C0009443 $\longrightarrow \left\{ \begin{array}{c} \text{common cold} \\ \text{cold} \\ \text{acute rhinitis} \end{array} \right\}$

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Relation triples

$$\begin{array}{c} \textit{subject} \\ \textit{relation} \\ \textit{object} \end{array} \left\langle \begin{array}{c} \text{C0450297} \\ \text{RO:has-finding-site} \\ \text{C0341532} \end{array} \right\rangle$$

BMASS - BioMedical Analogic Similarity Set

ID	Name	Amb
Lab/Rx		
L1	form-of	1.0
L2	has-lab-number	1.1
L3	has-tradename	1.5
L4	tradename-of	1.3
L5	associated-substance	1.6
L6	has-free-acid-or-base-form	1.0
L7	has-salt-form	1.1
L8	measured-component-of	1.3
Hierarchical		
H1	refers-to	1.0
H2	same-type	10.4
Morphological		
M1	adjectival-form-of	1.1
M2	noun-form-of	1.0

ID	Name	Amb
Clinical		
C1	associated-with-malfunction-of-gene-product	2.6
C2	gene-product-malfunction-associated-with-disease	1.5
C3	causative-agent-of	4.6
C4	has-causative-agent	2.0
C5	has-finding-site	1.9
C6	associated-with	1.2
Anatomy		
A1	anatomic-structure-is-part-of	1.6
A2	anatomic-structure-has-part	5.4
A3	is-located-in	1.4
Biology		
B1	regulated-by	1.0
B2	regulates	1.0
B3	gene-encodes-product	1.1
B4	gene-product-encoded-by	2.4

Cross-product of 50 samples for each relation:

2,450 analogies for each relation $\Rightarrow$ **61,250 total analogies**

This dataset represents real biomedical relationships. . .

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But it doesn't fit the standard paradigm!

"Unassuming" the standard assumptions

3 key assumptions in evaluation methodology:

- Single Answer
- Same Relationship(s)
- Informativity

Each is violated in recent analogy datasets

- Google[2], BATS[3], Sem-Para[4]

All are problematic in real-world data!

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[2] Mikolov et al. 2013
[3] Gladkova et al. 2016
[4] Köper et al. 2015

"Unassuming" the standard assumptions

Single Answer | Same Relationship | Informativity

The given analogy has only one correct target.

- Enforced by argmax over candidates for completing the analogy.
- If multiple analogies, must get at least one wrong.

Problem cases

$$\text{flu} : \text{nausea} :: \text{fever} : \left\{ \begin{array}{c} \text{sweating} \\ \text{weakness} \end{array} \right\}$$

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Easy fix!

Allow for multiple correct answers; also report on all of them, for fuller picture.

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Single Answer | **Same Relationship** | Informativity

All information relating exemplars a and b also relates query c to d.

- Enforced by treating full vector difference as relation of interest.
- Many relations have partial overlap with one another.

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$$\underbrace{\text{brother} : \text{sister}}_{\substack{\textbf{MaleCounterpart} \\ \text{SiblingOf}}} :: \underbrace{\text{husband} : \text{wife}}_{\substack{\textbf{MaleCounterpart} \\ \text{MarriedTo}}}$$

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$\underbrace{\text{wrist pain} : \text{shoulder pain}}_{\textbf{CoOccursWith}} :: \underbrace{\text{bipolar disorder} : \text{trazodone}}_{\substack{\textbf{CoOccursWith} \\ \text{TreatmentFor}}}$

"Unassuming" the standard assumptions

Single Answer | Same Relationship | **Informativity**

The relationship between exemplars a and b is specific enough to suggest the correct target d for query c.

- Issue with very broad semantic or hierarchical relationships.

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Generally related *(UMLS)*

socks : stockings :: Finns : Finnish language

"Unassuming" the standard assumptions

Single Answer | Same Relationship | **Informativity**

The relationship between exemplars *a* and *b* is specific enough to suggest the correct target *d* for query *c*.

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Fix during dataset generation

Review samples from each relation to ensure they're properly determined.

Modifying the evaluation methodology

$$a : b :: c : \underline{\quad\quad} \quad \longrightarrow \quad d^* = \text{argmax}_{d \in V}\left(\cos(d, b - a + c)\right)$$

Evaluating analogies under 3 settings:

Modifying the evaluation methodology

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Evaluating analogies under 3 settings:

Single-Answer (SA) Single candidate target for each analogy selected as the only "correct" answer.

flu : nausea :: fever : $\left\{ \begin{array}{c} \textbf{sweating} \\ \cancel{\text{weakness}} \end{array} \right\}$ $\longrightarrow$

~~weakness~~
temperature
sweating
nodule

✗

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Multi-Answer (MA) All candidate targets for each analogy are considered to be correct.

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Evaluating analogies under 3 settings:

Single-Answer (SA) Single candidate target for each analogy selected as the only “correct” answer.

Multi-Answer (MA) All candidate targets for each analogy are considered to be correct.

All-Info (AI) Use all possible exemplar objects and all candidate targets.

$$\text{flu} : \left\{ \begin{matrix} \text{nausea} \\ \text{cough} \end{matrix} \right\} :: \text{fever} : \left\{ \begin{matrix} \text{sweating} \\ \text{weakness} \end{matrix} \right\} \longrightarrow \begin{matrix} b - a \quad = \\ \frac{1}{2}\left(\begin{matrix} \text{nausea - flu} \\ + \text{ cough - flu} \end{matrix} \right) \end{matrix}$$

Evaluation methodology

Reporting 3 metrics over ranked candidates:

Acc_R Relaxed accuracy; correct if any valid answer is the top choice

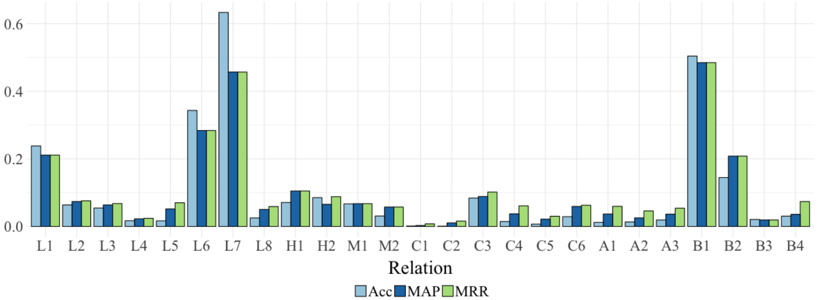
MAP Mean average precision

MRR Mean reciprocal rank

weakness
temperature
sweating
nodule

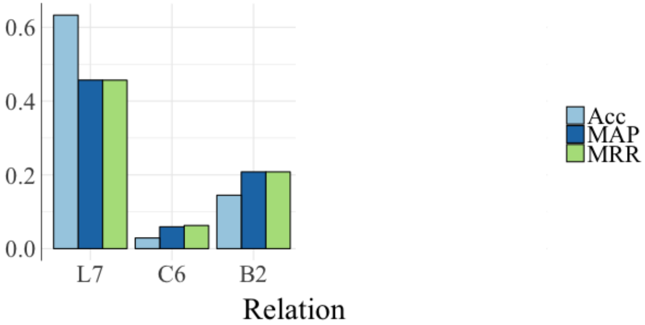
Acc_R	1.0
MAP	$\frac{5}{6}$
MRR	1.0

Overall results



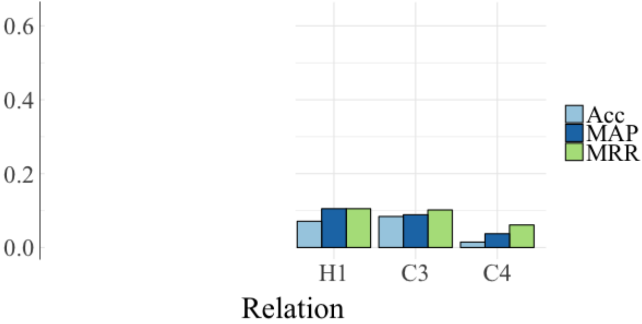
- Results shown for Multi-Answer setting.
- Average performance is around 11% on all metrics, with all embeddings. High variability between relationships!
- Used 5 different sets of embeddings trained on PubMed.

MAP/MRR give a better picture



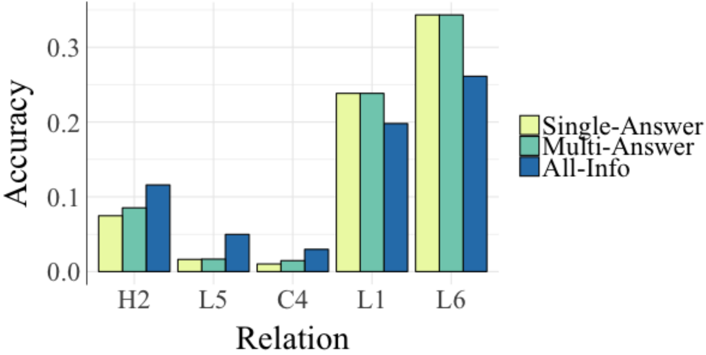
- MAP $<$ Acc_R indicates wider distribution of correct answers on *L7* (has-salt-form)
- MAP $>$ Acc_R shows that even if top answer is wrong, correct answers aren't far down on *C6* (associated-with), *B2* (regulates)

MAP/MRR give a better picture



- MRR $>$ Acc_R shows that the best correct answer stays near the top on *C4* (has-causative-agent)
- MRR $\approx$ Acc_R reflects more consistent positioning of nearest correct answer on *H1* (refers-to), *C3* (causative-agent-of)

All-Info benefits vary



- Extra examples help on *H2* (same-type), *L5* (associated-substance), and *C4* (has-causative-agent).
- But harm *L1* (form-of) (4% absolute) and *L6* (has-free-acid-or-base-form) (8% absolute)

Moving analogies forward

Single-Answer and Informativity assumptions addressed, but not Same Relationship(s).

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- Drozd et al (2016) use a parametric logistic regression that can be used to learn affine subspaces.

Standard linear offset method does not work for real-world data!

- Our changes help, but overall performance is still low (as with other recent datasets). Use MAP and MRR!
- **Analogies are useful!** We need to find better ways to tackle this task.

Thank you!

Dataset and source code at:
https://www.github.com/OSU-slatelab/BMASS

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