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Relation Discovery between Indirectly Connected Biomedical Concepts

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Raynaud's syndrome & fish oil

*"Beneficial effect of **fish oil** on **blood viscosity** in peripheral vascular disease"*
[Woodcock et al., 1984]

Blood viscosity

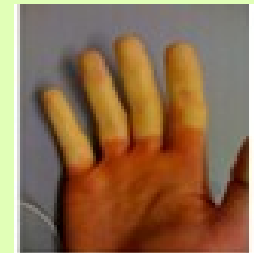
*"...blood was studied in 20 patients with **Raynaud's syndrome**... studies demonstrate increased **blood viscosity** ..."*
[Tietjen et al., 1975]

Fish oil



Blood viscosity

Raynaud's disease



Blood viscosity

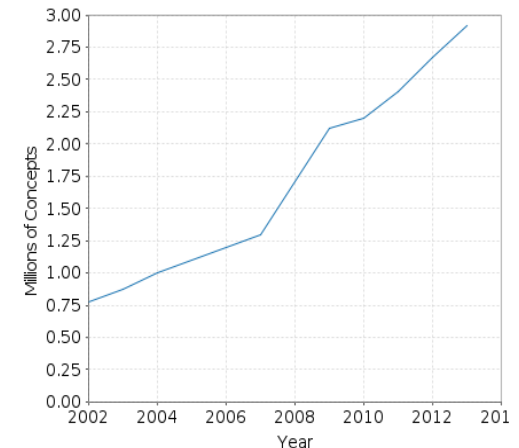
Hypothesis:
Fish oil **treats** Raynaud's syndrome
[Swanson, 1986]

Confirmation:
clinical study [DiGiacomo et al., 1989]

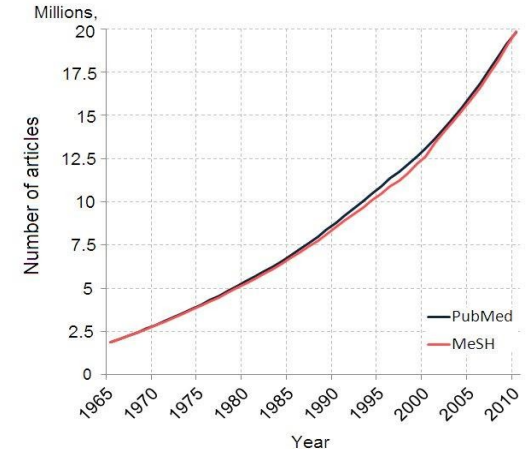
Motivation

- fast growth of knowledge sources → *data mining*
- combination of facts can lead to new knowledge (e.g., Swanson)
- focus of similar work mainly on word statistics neglecting linguistic information

Growth of UMLS



Growth of MEDLINE



Structured vs. Unstructured Knowledge

Structured knowledge:

- from databases like the *UMLS*, *DrugBank*
- **fixed** set of **concepts** and **relations**

DRUGBANK
Open Data Drug & Drug Target Database



Unstructured knowledge:

- *MEDLINE* abstracts, annotated by *MetaMap*
- natural language text, expression of **concepts** and their **relations** in **ambiguous** and **synonymous** ways



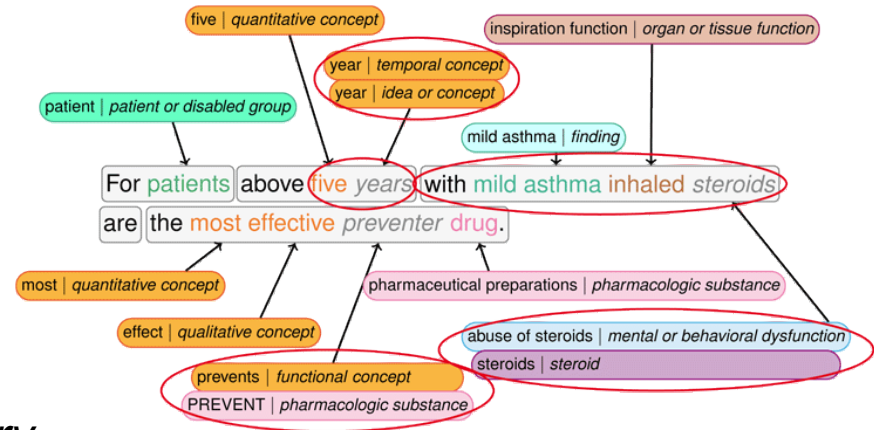
Bridging the Gap

Concepts

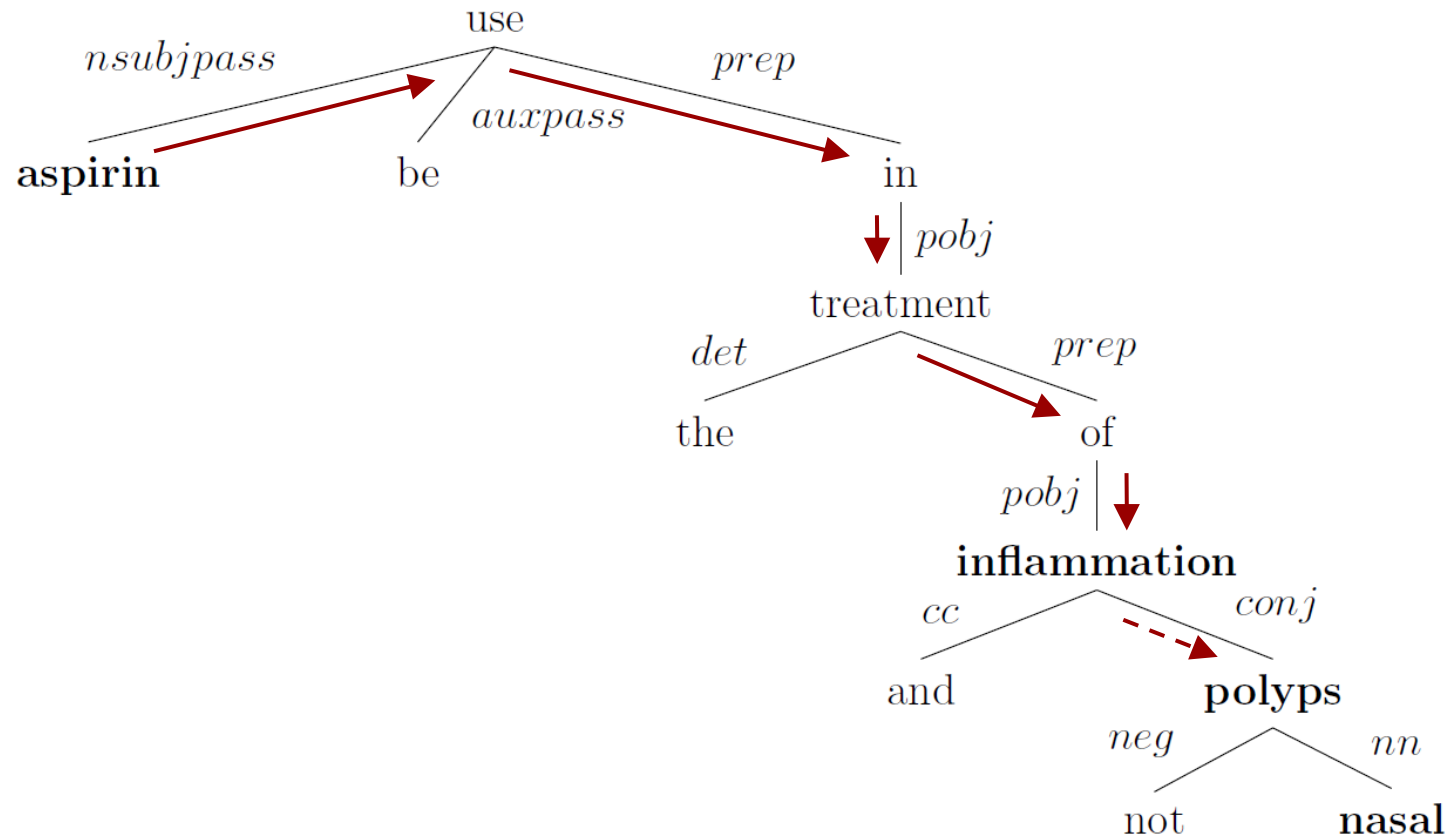
- concept annotation of natural language text with *MetaMap*

Relations

- problem: reliable relation annotation *not possible* or *very restricted*
- suggested solution: use plain textual relation between annotated concepts → *dependency paths*



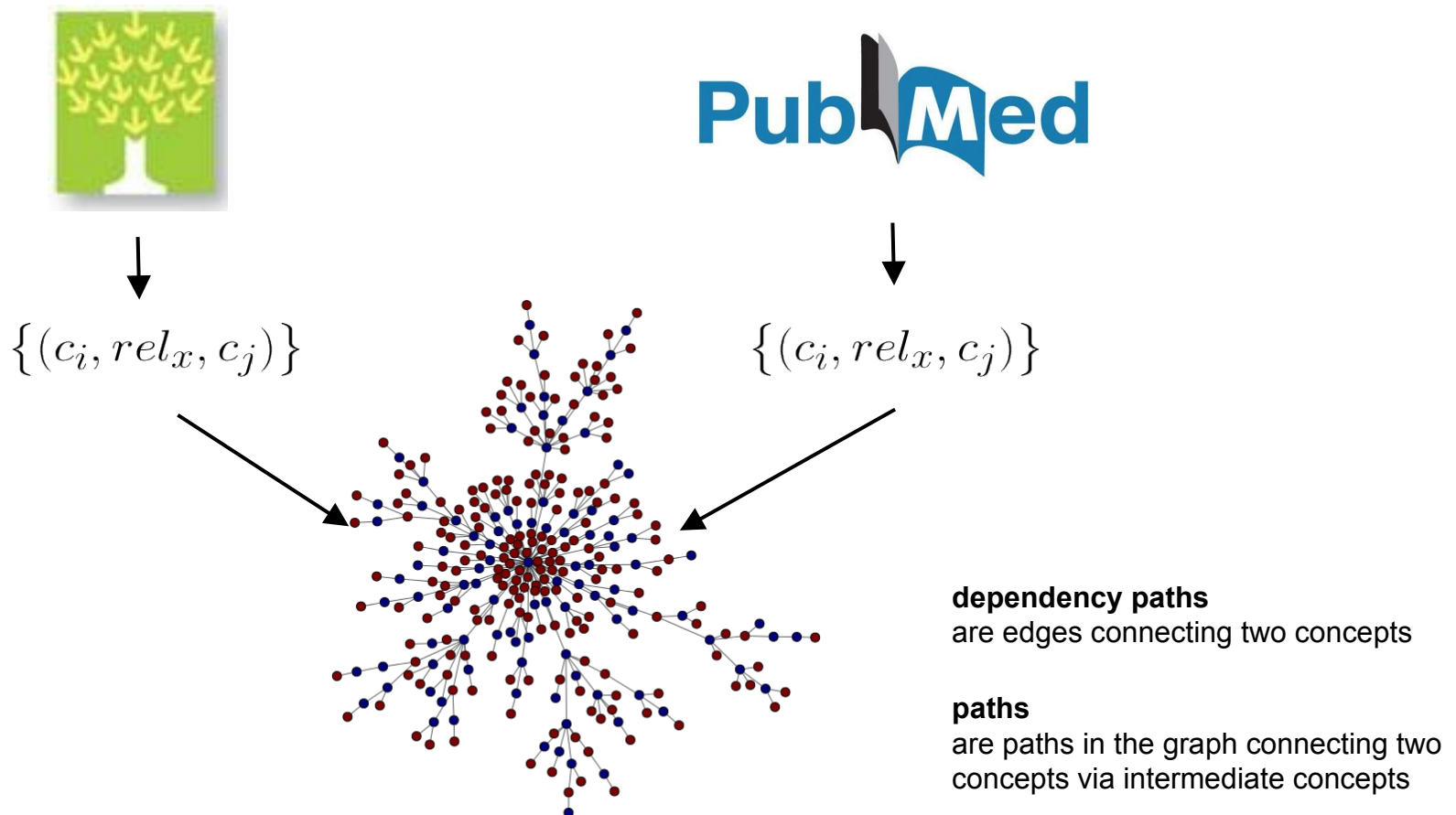
Textual Relations



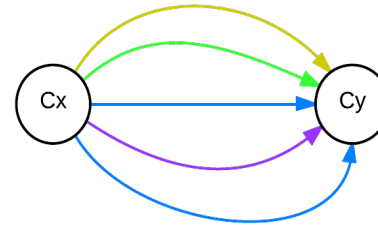
(aspirin, $\xrightarrow{nsubjpass}$ use \xleftarrow{prep} in \xleftarrow{pobj} treatment \xleftarrow{prep} of \xleftarrow{pobj} , inflammation)

(aspirin, $neg_ \xrightarrow{nsubjpass}$ use \xleftarrow{prep} in \xleftarrow{pobj} treatment \xleftarrow{prep} of \xleftarrow{pobj} , nasal polyps)

Combining knowledge



Representing Relations



- simple model: **one-in-N** encoding
 - feature vector of a relation is a vector with only one 1 in the respective dimension
 - feature space is as large as there are relations
- some relations are semantically similar or even synonymous to each other
- simple model assumes all relations to be semantically dissimilar to each other
- need to encode relations semantically
- new model: **semantic** encoding
 - apply **LDA** to extract semantic vectors of much lower dimensionality for relations, ensuring semantically similar relations to have similar vectors
 - directly applicable by denoting a **pair of concepts** as a **document** with its **relations** (textual and structured) as **words**

Does LDA extract semantic vectors?

relation	most similar relations
has_target	$\xrightarrow{dobj} form \xleftarrow{prep} with \xleftarrow{pobj}$
	$\xrightarrow{nsubjpass} degrade \xleftarrow{agent} by \xleftarrow{pobj}$
	$\xrightarrow{nn} activity \xrightarrow{nsubjpass} inhibit \xleftarrow{agent} by \xleftarrow{pobj}$
	$\xrightarrow{nsubj} inhibit \xleftarrow{dobj} phosphorylation \xleftarrow{prep} of \xleftarrow{pobj}$
	$\xrightarrow{nsubj} show \xleftarrow{dobj} affinity \xleftarrow{prep} for \xleftarrow{pobj}$
	$\xrightarrow{nsubjpass} show \xleftarrow{xcomp} interact \xleftarrow{prep} with \xleftarrow{pobj}$
	$\xrightarrow{dep} form \xleftarrow{dobj}$
	$\xrightarrow{nsubj} inhibit \xleftarrow{prep} in \xleftarrow{pobj} presence \xleftarrow{prep} of \xleftarrow{pobj}$
	$\xrightarrow{nsubjpass} cross - linked \xleftarrow{prep} to \xleftarrow{pobj}$
	$\xrightarrow{dep} form \xleftarrow{nsubjpass}$
	$\xrightarrow{dobj} inhibit \xleftarrow{prep} with \xleftarrow{pobj}$
	$\xrightarrow{nsubj} potentiate \xleftarrow{dobj} activity \xleftarrow{prep} of \xleftarrow{pobj}$
	$\xrightarrow{nsubjpass} prepare \xleftarrow{agent} by \xleftarrow{pobj} reaction \xleftarrow{prep} of \xleftarrow{pobj}$
	$\xrightarrow{nn} substrate \xleftarrow{prep} include \xleftarrow{pobj}$
	$\xrightarrow{nsubj} act \xleftarrow{prep} by \xleftarrow{pobj}$

Does LDA extract semantic vectors?

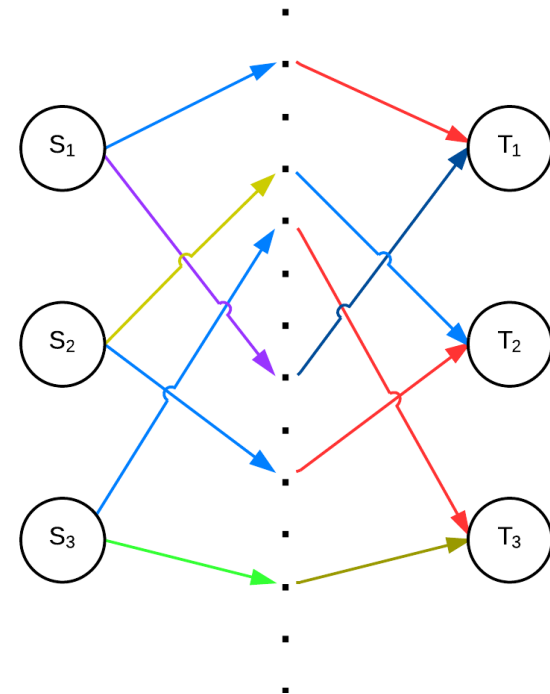
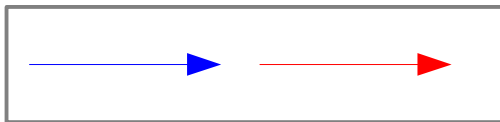
relation	most similar relations
may_treat	$\xrightarrow{pobj} \text{with} \xrightarrow{prep} \text{patient} \xrightarrow{nsbjpass} \text{treat} \xleftarrow{prep} \text{with} \xleftarrow{pobj}$
	$\xrightarrow{nsbj} \text{be} \xleftarrow{prep} \text{in} \xleftarrow{pobj} \text{treatment} \xleftarrow{prep} \text{of} \xleftarrow{pobj}$
	$\xrightarrow{nsbj} \text{be} \xleftarrow{attr} \text{treatment} \xleftarrow{prep} \text{for} \xleftarrow{pobj}$
	$\xrightarrow{nn} \text{patient} \xleftarrow{partmod} \text{treat} \xleftarrow{prep} \text{with} \xleftarrow{pobj}$
	$\xrightarrow{nsbjpass} \text{use} \xleftarrow{prep} \text{in} \xleftarrow{pobj} \text{treatment} \xleftarrow{prep} \text{of} \xleftarrow{pobj}$
	$\xrightarrow{nsbjpass} \text{use} \xleftarrow{prep} \text{for} \xleftarrow{pobj} \text{treatment} \xleftarrow{prep} \text{of} \xleftarrow{pobj}$
	$\xrightarrow{pobj} \text{with} \xrightarrow{prep} \text{treat} \xleftarrow{prep} \text{for} \xleftarrow{pobj}$
	$\xrightarrow{dobj} \text{receive} \xleftarrow{prep} \text{for} \xleftarrow{pobj}$
	$\xrightarrow{attr} \text{be} \xleftarrow{prep} \text{in} \xleftarrow{pobj} \text{treatment} \xleftarrow{prep} \text{of} \xleftarrow{pobj}$
	$\xrightarrow{pobj} \text{with} \xrightarrow{prep} \text{patient} \xleftarrow{rcmod} \text{treat} \xleftarrow{prep} \text{with} \xleftarrow{pobj}$
	$\xrightarrow{nsbjpass} \text{administer} \xleftarrow{prep} \text{to} \xleftarrow{pobj} \text{patient} \xleftarrow{prep} \text{with} \xleftarrow{pobj}$
	$\xrightarrow{nsbjpass} \text{use} \xleftarrow{prep} \text{in} \xleftarrow{pobj} \text{patient} \xleftarrow{prep} \text{with} \xleftarrow{pobj}$
	$\xrightarrow{dobj} \text{use} \xleftarrow{prep} \text{in} \xleftarrow{pobj} \text{patient} \xleftarrow{prep} \text{with} \xleftarrow{pobj}$
	$\xrightarrow{nsbj} \text{improve} \xleftarrow{prep} \text{in} \xleftarrow{pobj} \text{patient} \xleftarrow{prep} \text{with} \xleftarrow{pobj}$
	$\xrightarrow{nsbj} \text{have} \xleftarrow{prep} \text{in} \xleftarrow{pobj} \text{patient} \xleftarrow{prep} \text{with} \xleftarrow{pobj}$

Task

Find characteristic (path-)patterns for relations in the knowledge graph

$$R_l = \{(S1, T1), (S2, T2), (S3, T3)\}$$

Does this relation have a characteristic path pattern?

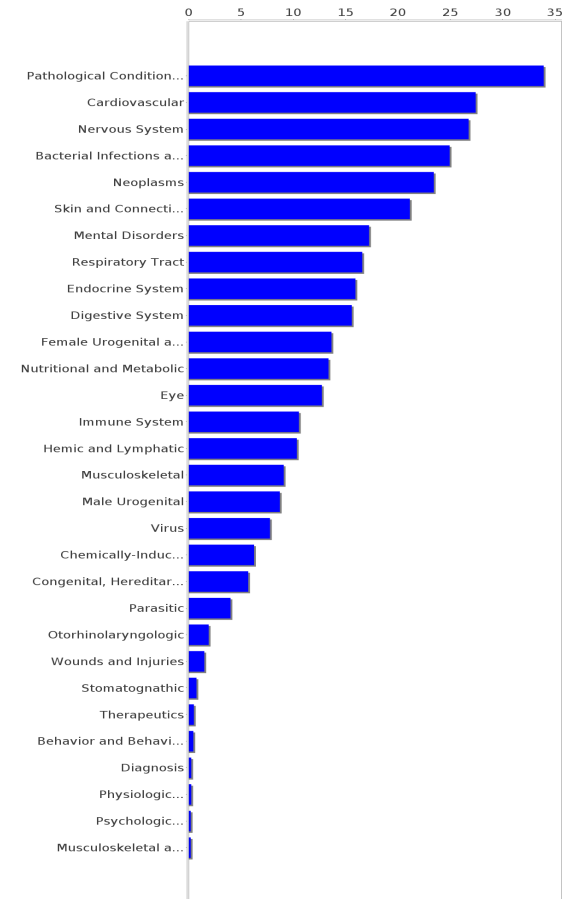


Paths found in knowledge graph

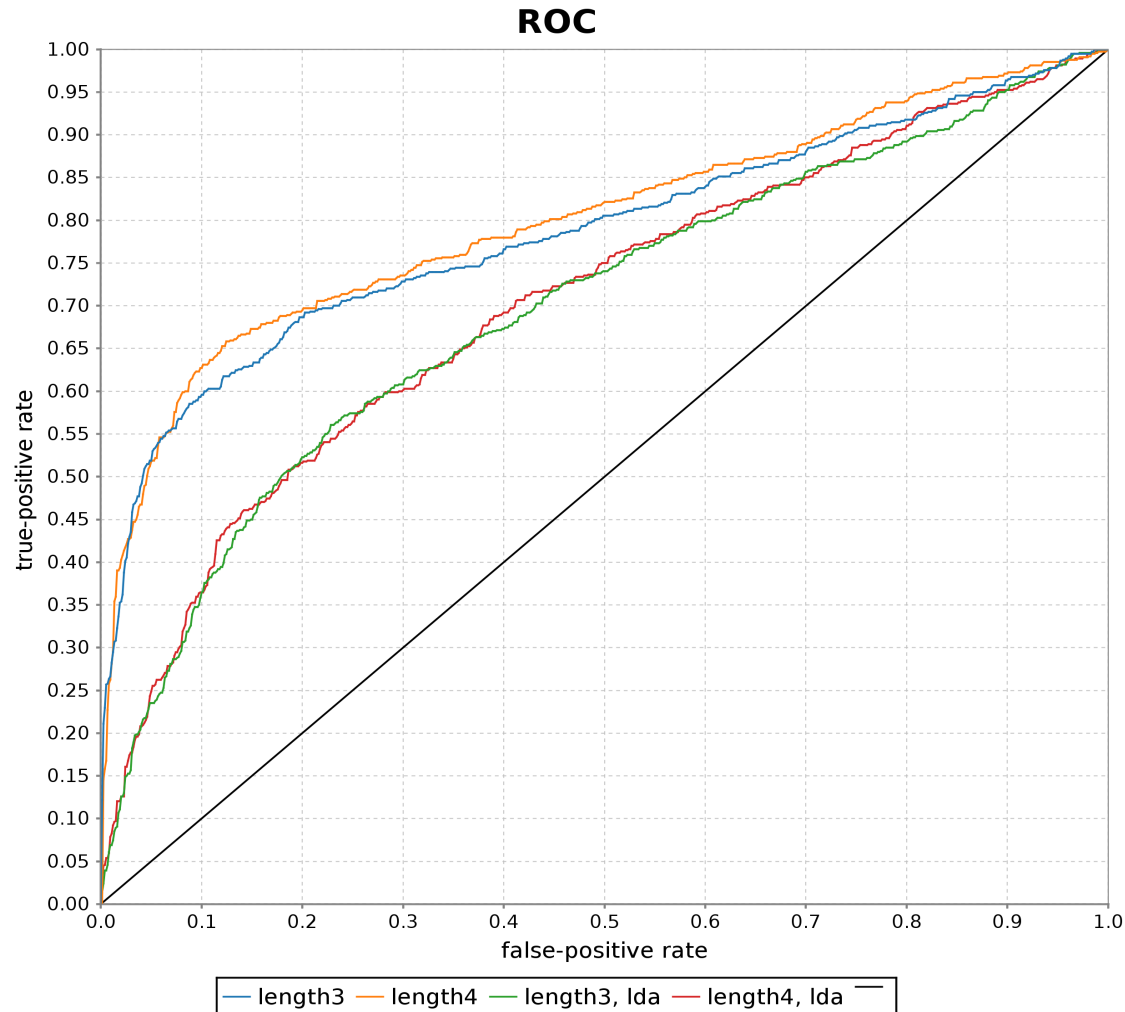
Experiments

- extraction of datasets
 - *may treat* (410 pairs from UMLS)
 - *has target* (740 pairs from DrugBank)
- construction of negative pairs for specific relation
- extraction of paths in knowledge graph for all pairs of the positive and negative examples
- training of logistic regression classifier with both *one-in-N* and *LDA* features
- evaluations focusing on high precision

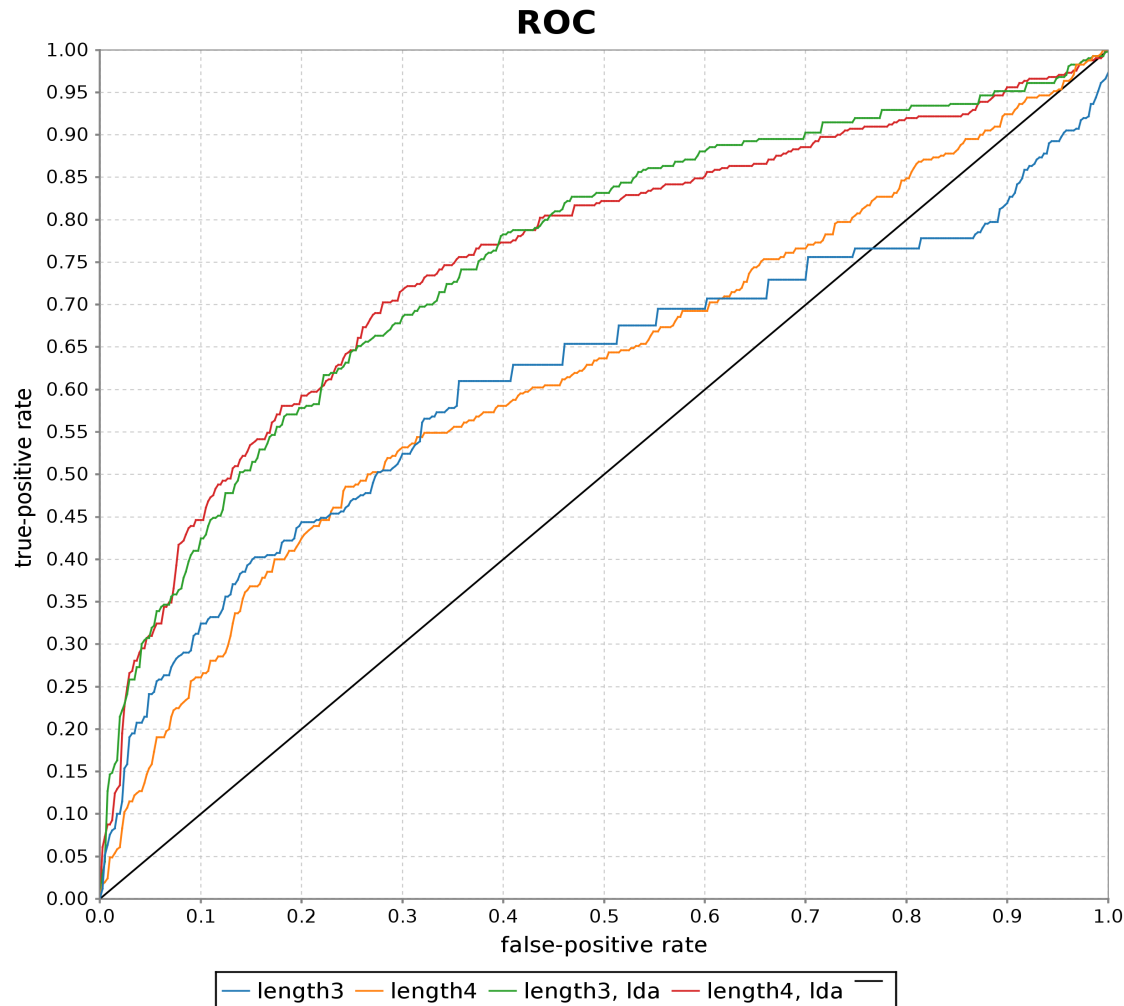
diseases type distribution



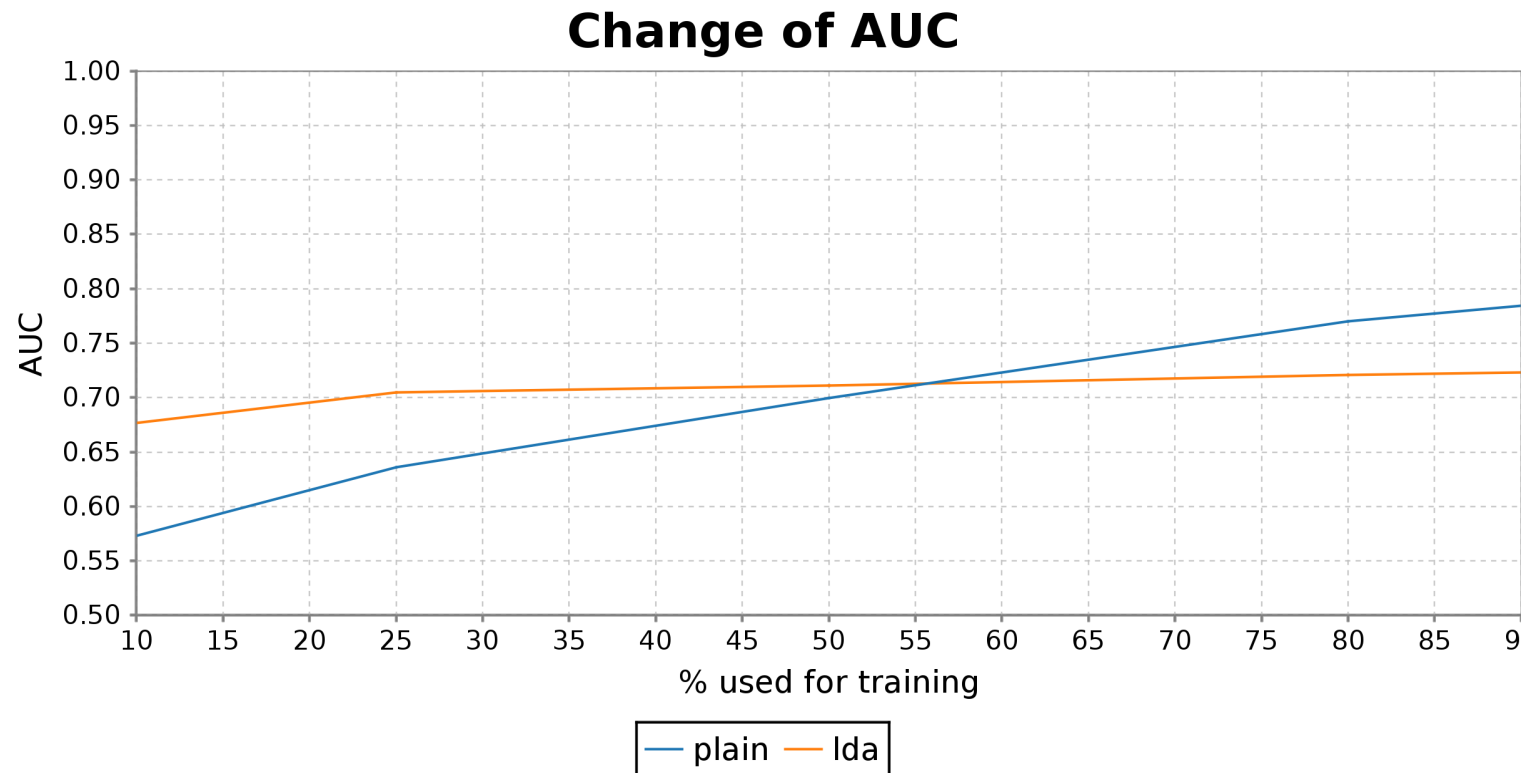
Impact of lengths and feature types, *has target*



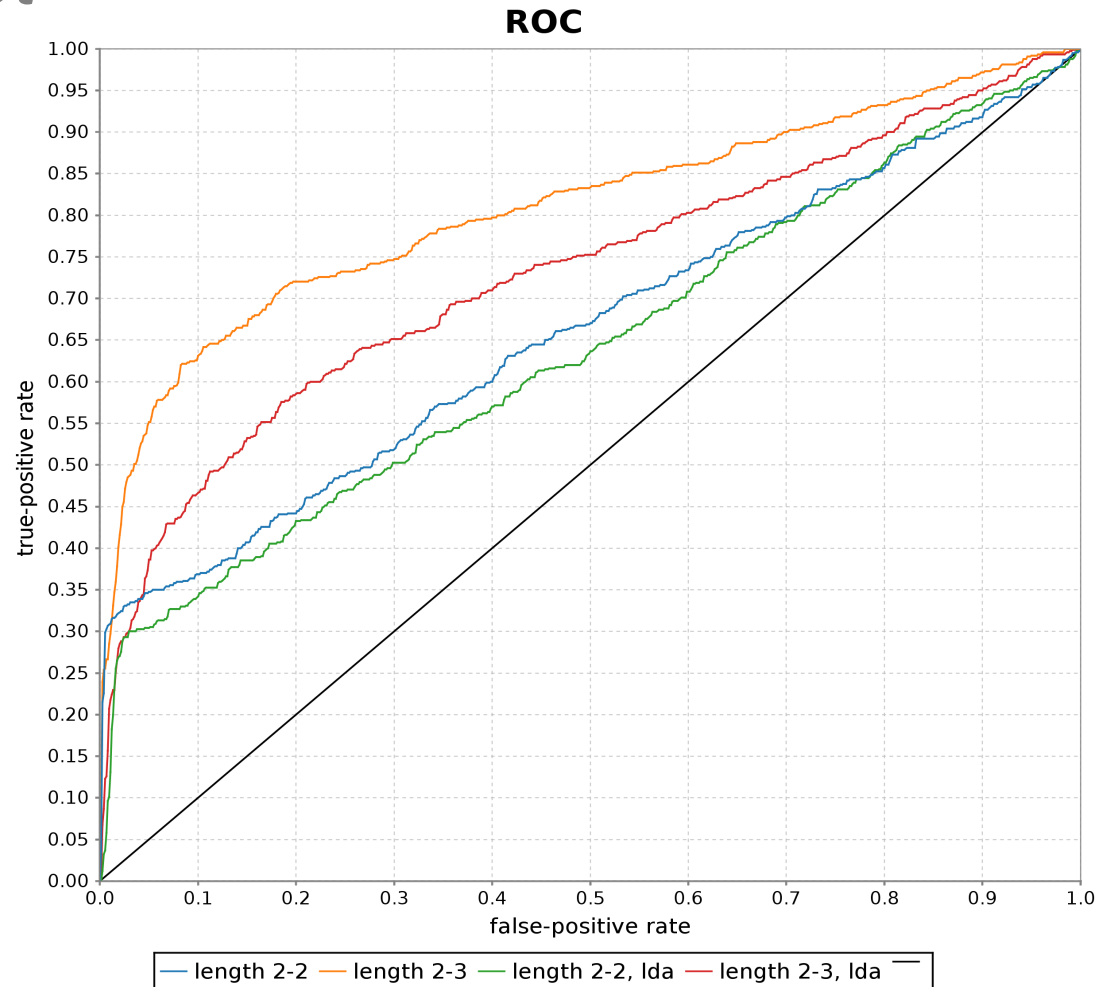
Impact of lengths and feature types, *may treat*



One-in-N vs. LDA features, has target



Direct vs. Direct + Indirect Connections, *has target*



Summary of Results

dataset	length	AUC		accuracy (precision, recall)	
		<i>plain</i>	<i>lda</i>	<i>plain</i>	<i>lda</i>
<i>may_treat</i>	3-3	0.61	0.73	0.63 (0.63, 0.61)	0.69 (0.76, 0.63)
	3-4	0.62	0.75	0.62 (0.67, 0.49)	0.70 (0.71, 0.69)
<i>has_target</i>	3-3	0.78	0.72	0.75 (0.87, 0.59)	0.68 (0.74, 0.60)
	3-4	0.80	0.70	0.77 (0.84, 0.66)	0.66 (0.70, 0.58)

Example Paths

highly weighted feature	explanation
$\left(\xrightarrow{dep} induce \xleftarrow{prep} in \xleftarrow{pobj} \right), \left(\xrightarrow{pobj} in \xrightarrow{prep} express \xleftarrow{nsubjpass} \right)$	<p>The substance is induced into something, in which the target (gene/protein) is expressed.</p>
$\left(\xrightarrow{pobj} by \xrightarrow{agent} suppress \xleftarrow{nsubjpass} \right), \left(\xrightarrow{nsubj} increase \xleftarrow{prep} at \xleftarrow{pobj} \right)$	<p>The drug suppresses something that is increased by the disease.</p>

Conclusions

- ***automatic discovery*** of relations using only ***indirect knowledge*** is ***possible***
- using not only direct but also ***indirect knowledge*** to ***discover relations*** between concepts is ***very useful***
- ***semantic (LDA)*** encoding ***help***, when data is ***sparse***

Thank you for your attention!
Questions?



Statistics

Textual part of the graph after pruning

Concepts/Vertices: ~ 95,000

Avg. degree: ~ 410.5

Connected Pairs: ~ 9 million

Most common concepts:

cell, rat, mouse, disease, proteins, ...

Edges: ~ 39 million

Textual relation labels: ~ 105,000

Avg. occurrence: ~ 371.27

Most frequently occurring textual relation labels:

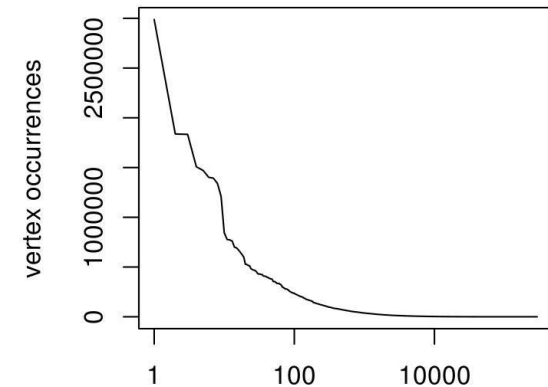
hmod → treat *amod* →

hmod → induce *amod* →

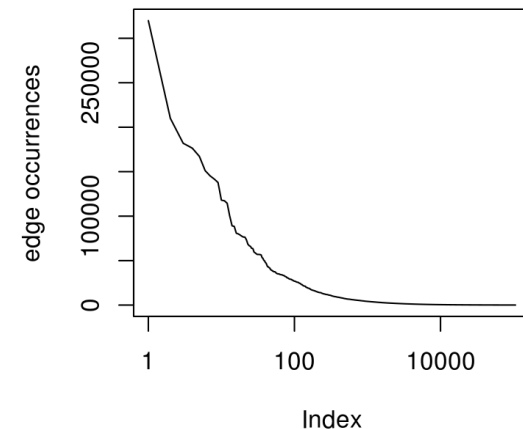
←*prep* include ←*pobj*

nsubj → be ←*prep* in ←*pobj*

Vertex Occurences

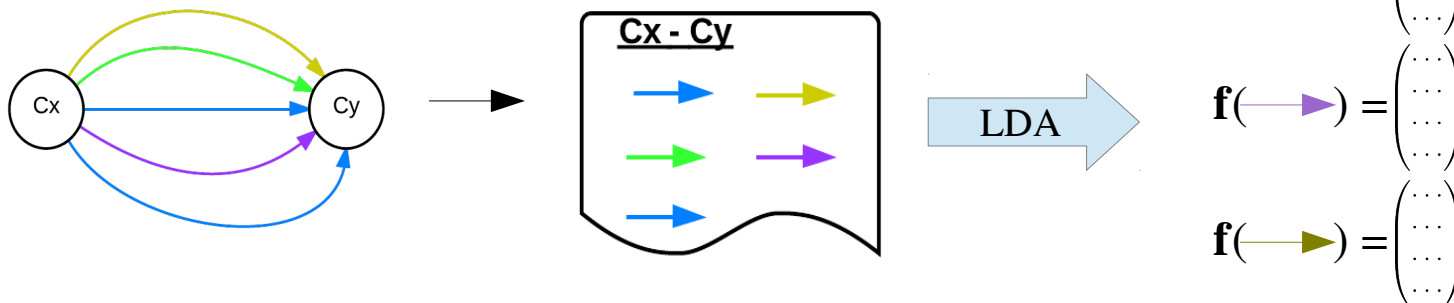


Edge Occurences



From Word- to Relation-Spaces

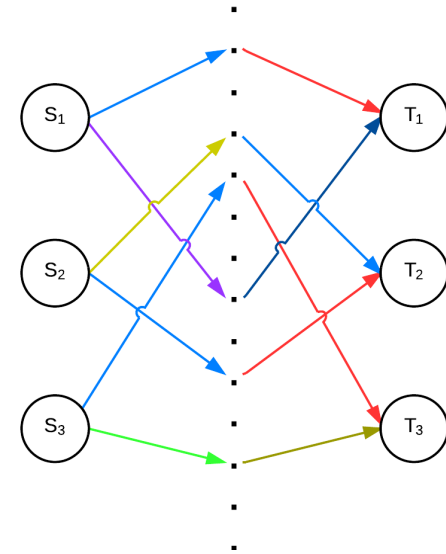
- numerous co-occurrence based algorithms computing semantic vectors for words co-occurring in a set of documents, e.g.,
 - latent semantic analysis (LSA)
 - reflective random indexing (RRI)
 - generalization of principle component analysis (gPCA)
 - **latent dirichlet allocation (LDA)**
- directly applicable by denoting a **pair of concepts** as a **document** with its **relations** (textual and structured) as **words**



Overview

$$R_l = \{(S_1, T_1), (S_2, T_2), (S_3, T_3), \dots\}$$

1. Extract Paths



2. Encode pairs as feature vectors

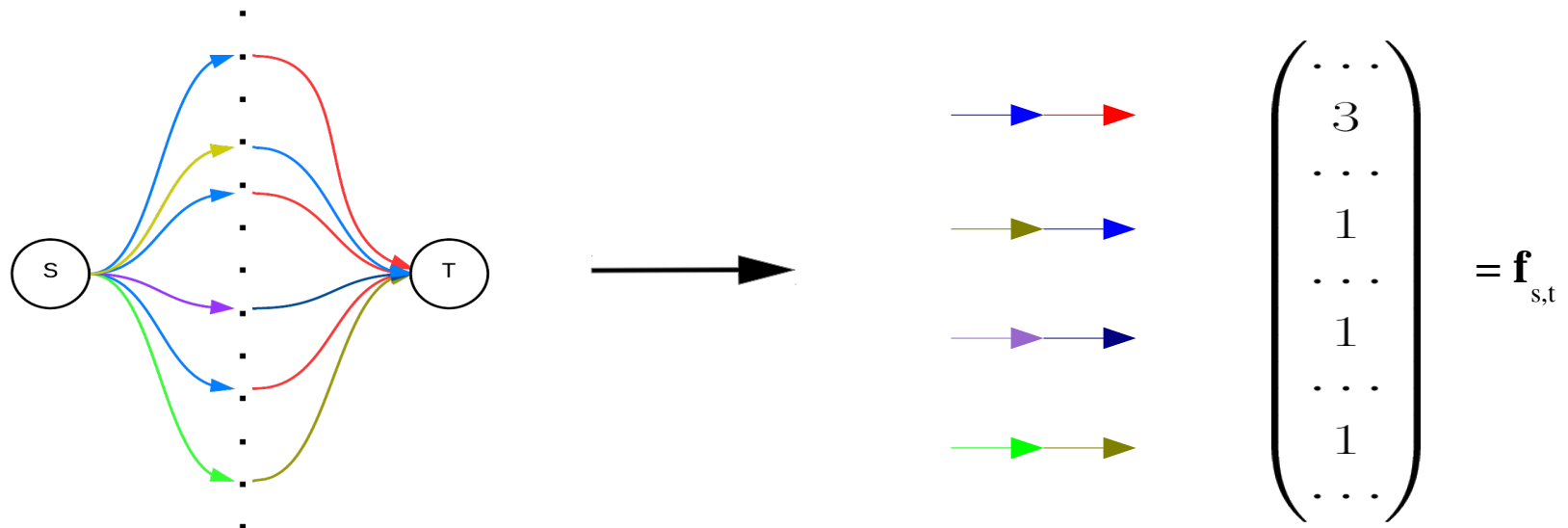
$$\{\mathbf{f}_{S_1, T_1}, \mathbf{f}_{S_2, T_2}, \mathbf{f}_{S_3, T_3}, \dots\}$$

3. Train Classifier

$$(S, T) \in R_l \Leftrightarrow c_l(\mathbf{f}_{S, T}) > \theta$$

Modeling

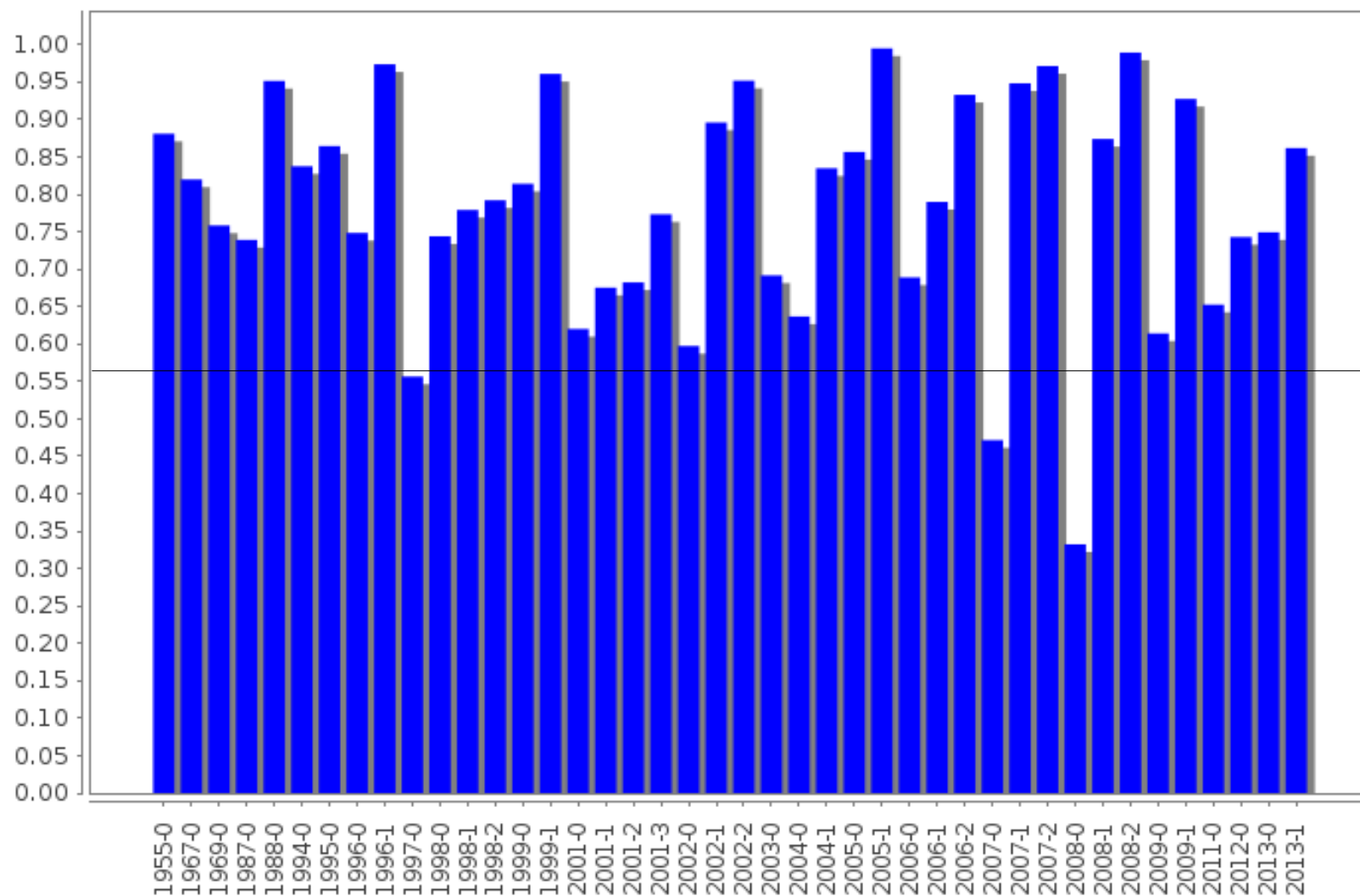
- How to represent a pair of concepts as a feature vector?
- *concept pair* = **multiset of paths** in the knowledge graph
- each path pattern (i.e., sequence of relations) between the source and target concept becomes a feature



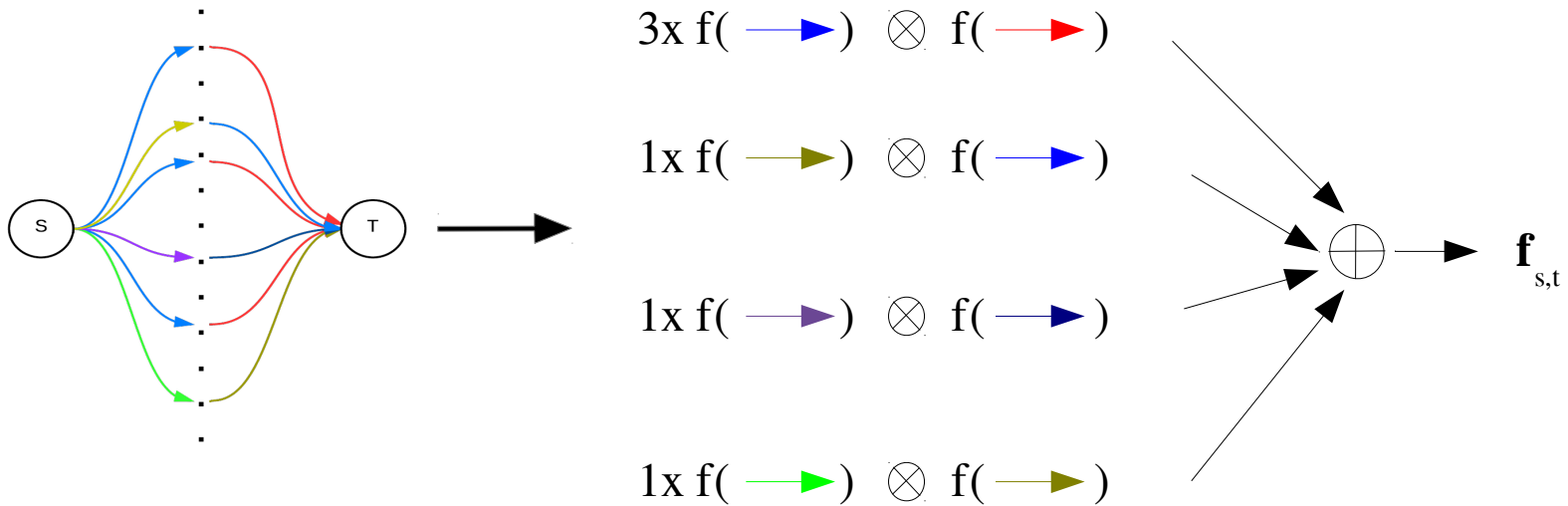
Some problems with this approach

- text mining error at every stage:
 - concept annotation, e.g. the “IMPACT gene”, Retinoic Acid Response Element abbreviated as “RARE”, the “Household gene”, etc.
 - POS tagging + dependency parsing more error prone on scientific text
- dependency paths neglect context of the assertions being made
- attributes of nouns or verbs neglected, e.g., *level* occurs in dependency path, but not the quality of the mentioned *level* (*high*, *low*, ...)
- no co-reference resolution → missing knowledge

Classification scores of repositioned drug-disease pairs

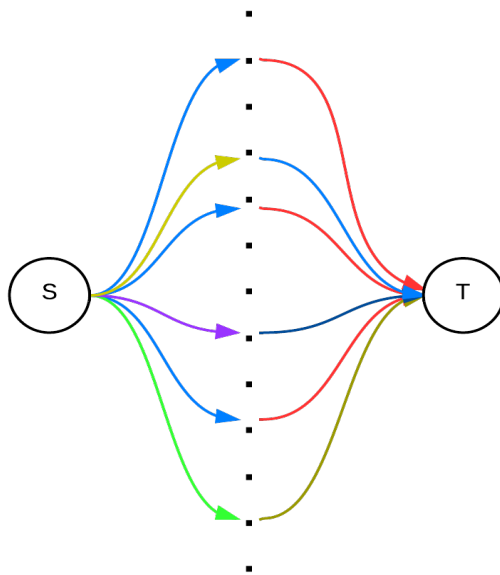


General Modeling



$$\mathbf{u} \otimes \mathbf{v} = \mathbf{u}\mathbf{v}^T = \begin{bmatrix} u_1 \\ u_2 \\ u_3 \\ u_4 \end{bmatrix} \begin{bmatrix} v_1 & v_2 & v_3 \end{bmatrix} = \begin{bmatrix} u_1 v_1 & u_1 v_2 & u_1 v_3 \\ u_2 v_1 & u_2 v_2 & u_2 v_3 \\ u_3 v_1 & u_3 v_2 & u_3 v_3 \\ u_4 v_1 & u_4 v_2 & u_4 v_3 \end{bmatrix}.$$

Modeling



Simple

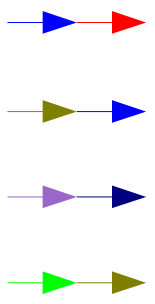


Diagram showing four pairs of colored arrows representing features:

- Blue arrow pointing right, followed by a red arrow pointing right.
- Yellow arrow pointing right, followed by a blue arrow pointing right.
- Purple arrow pointing right, followed by a blue arrow pointing right.
- Green arrow pointing right, followed by a yellow arrow pointing right.

$$\begin{pmatrix} \dots \\ 3 \\ \dots \\ 1 \\ \dots \\ 1 \\ \dots \\ 1 \\ \dots \end{pmatrix} = \mathbf{f}_{s,t}$$

LDA

$$\begin{aligned} & 3x f(\text{blue arrow}) \otimes f(\text{red arrow}) \\ & 1x f(\text{yellow arrow}) \otimes f(\text{blue arrow}) \\ & 1x f(\text{purple arrow}) \otimes f(\text{blue arrow}) \\ & 1x f(\text{green arrow}) \otimes f(\text{yellow arrow}) \end{aligned}$$

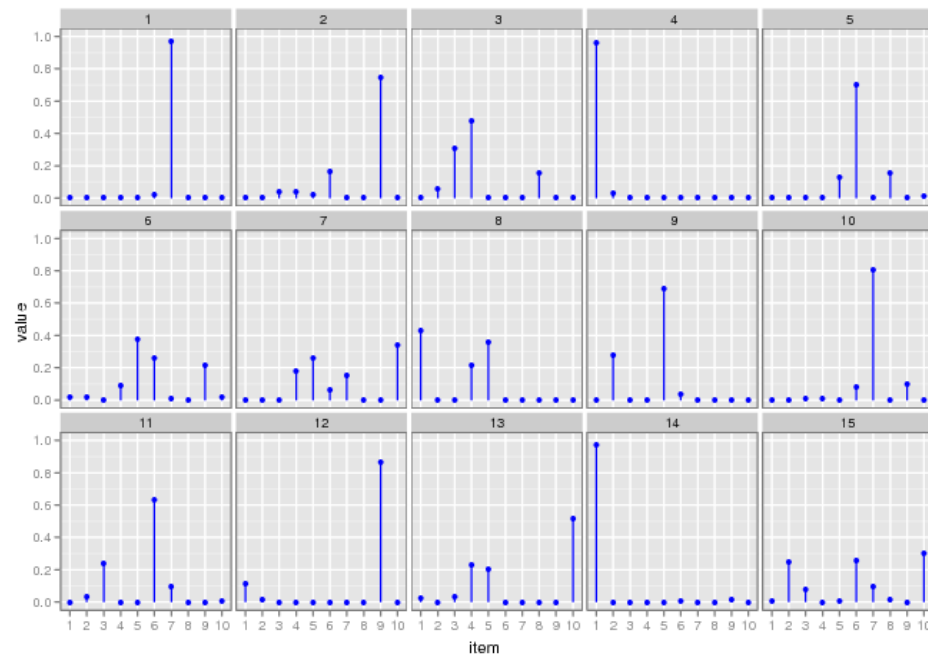
Diagram showing the LDA process. The four feature pairs are combined into a single vector $\mathbf{f}_{s,t}$ using a summation operation (\oplus).

$$\oplus = \mathbf{f}_{s,t}$$

LDA modeling relations between concepts

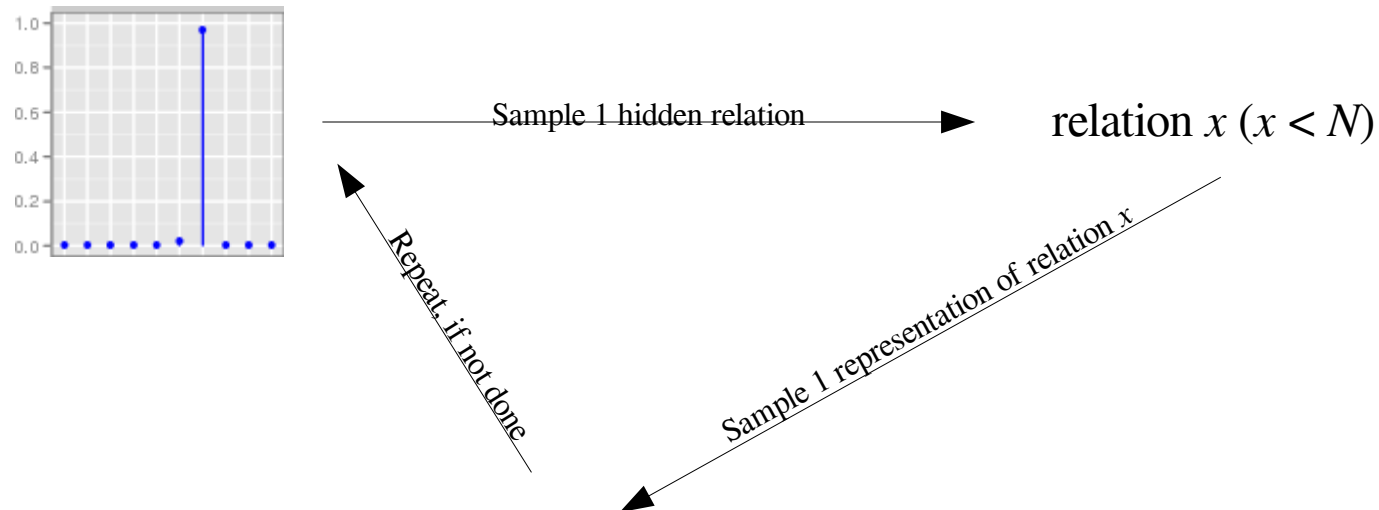
- pair of concepts = probability distribution of N real, but hidden relations (topics of LDA)

$$\alpha = 0.1$$



LDA modeling relations between concepts

- given: 1 pair of concepts = distribution of hidden but real relations



E.g.:

$hmod \rightarrow treat$ $amod \rightarrow$ (from Medline)

$hmod \rightarrow induce$ $amod \rightarrow$ (from Medline)

$may_prevent$ (from UMLS)