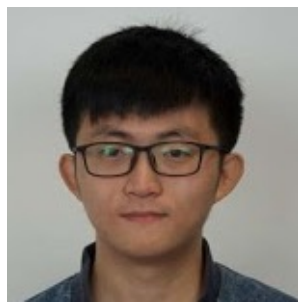


LREC 2022
Marseille

A Distant Supervision Corpus for Extracting Biomedical Relationships Between Chemicals, Diseases and Genes

Dongxu Zhang*,
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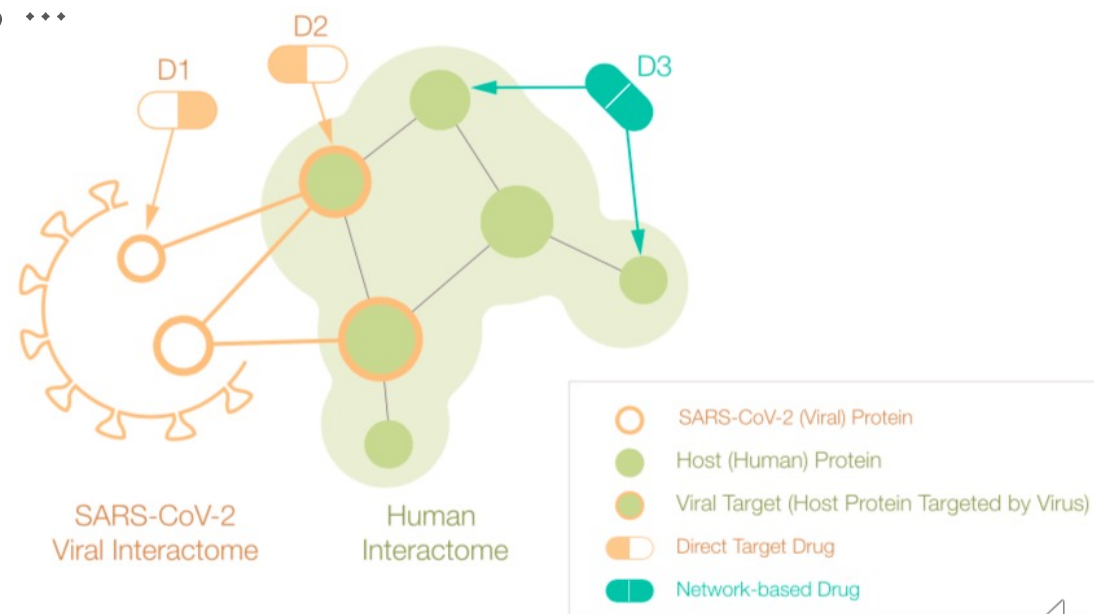
Andrew McCallum
UMass



Biomedical Relation Extraction: Motivation

- Assist curators of Biomedical KBs:
 - CTD, CMAP, ProteinDB, KEGG, ...
- Build Human Interactome Knowledge Graphs:
Drugs, Genes/Proteins, Diseases, Symptoms, ...
 - Understanding disease mechanisms (*Lee et al, 2019*)
 - Predict poly-pharmacy side-effects (*Zitnick et al, 2018*)
 - Drug re-purposing (*Morselli Gysi et al, 2020*)

Over 1M new papers p.a. !



Previous Biomedical RE Corpora

- Several labeled corpora, esp. since ~2006
- Limitations
 - Fewer documents
 - Fewer entity types, one or small number of relation types
 - Entity linking sometimes not included
- Curating Direct labeling of Entities and Relationships in text
 - Very useful for ML/NLP, but ...
 - Very time consuming
 - Curated corpora tend to be small



Introducing *ChemDisGene*

- New labeled dataset for Biomedical Relation Extraction
- Distant (document level) labels for
 - 18 relation types
 - Between 3 entity types (Chemicals, Diseases, Genes / Protein Gene-products)
- Two corpora
 - Large, automatically derived: ~80k abstracts
 - Manually curated: 523 abstracts

Outline

- Task definition
- ChemDisGene: Automated Derivation
- ChemDisGene: Manual Curation Process
- Dataset Statistics
- Benchmark Models



Task Definition

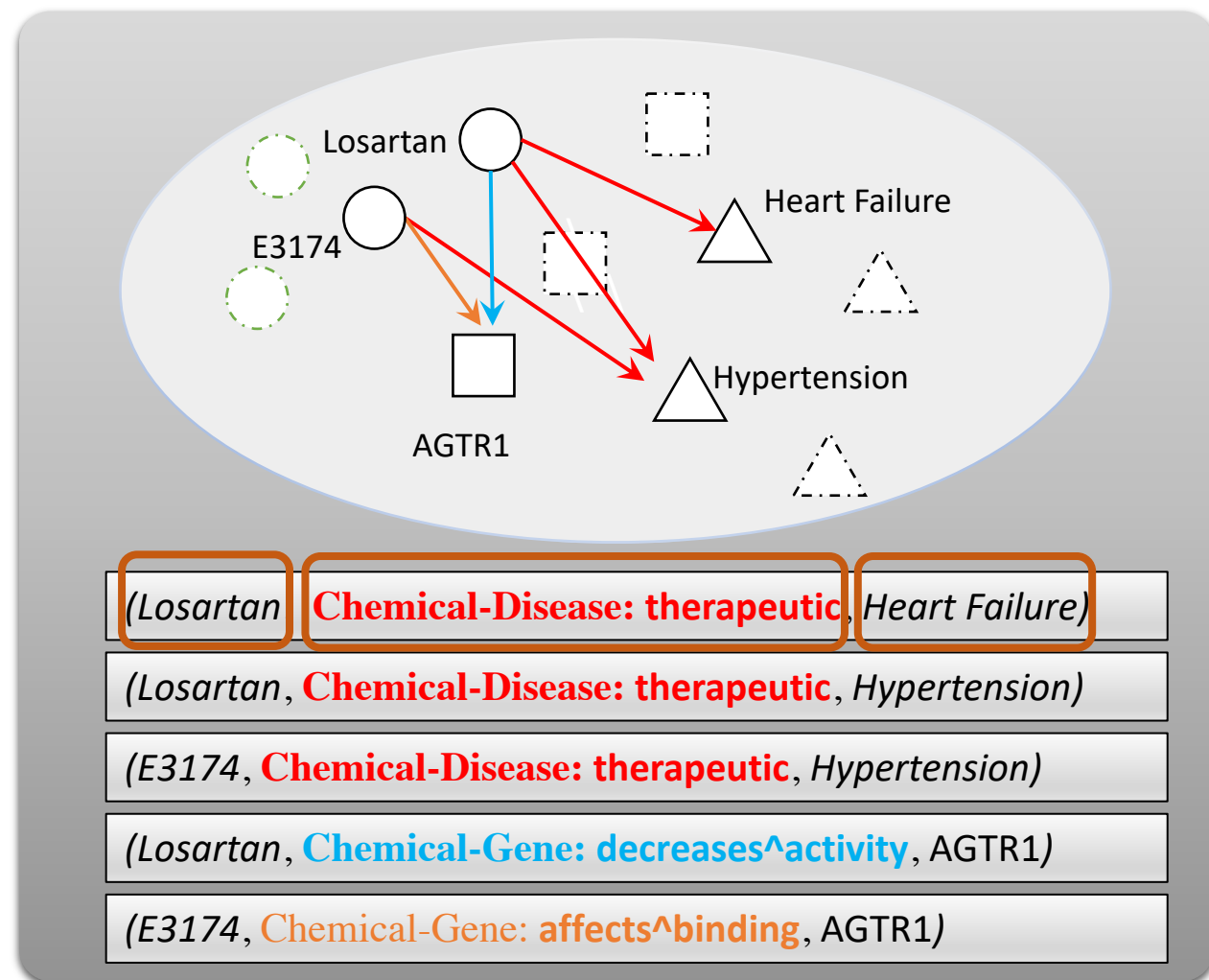
- Input
 - PubMed® Abstracts
 - Entity mentions linked: Chemicals, Diseases and Genes / Proteins.
- Output

Losartan: a selective angiotensin II type 1 (AT1) receptor antagonist for the treatment of heart failure

Losartan (COZAAR) is the prototype of a new class of potent and selective angiotensin II (AII) type 1 (AT(1)) receptor antagonists with the largest published preclinical and clinical data base. Losartan (parent compound), has moderate affinity for the AT(1) receptor (competitive inhibition). Losartan is well-absorbed orally as an active drug and is rapidly converted via oxidation in the human liver to a more potent metabolite (designated E3174) with an affinity 20- to 30-times greater for the AT(1) receptor (non-competitive inhibition). E3174 has a half-life of 6 - 9 h; elimination is via renal and hepatic routes. Antihyper-tensive and, in heart failure patients, haemodynamic activity is observed over a 24 h period with once daily dosing. Over 6 million patients have been treated for hypertension with continued excellent tolerability. Clinical experience in heart failure is growing, and ...

Task Definition (contd.)

- Input
 - PubMed® Abstracts
 - Entity mentions detected and linked.
- Output: Relationships
 - (Entity, Relation-type, Entity) triplets
 - Distant labels: Annotated at the Document Level



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Comparative Toxicogenomics Database (CTD)

<http://ctdbase.org>

- Expert curated KB of Relationships, between Chemicals, Diseases, Genes/Proteins, ...
- Primary contributions, extracted from research papers (*full text*)
- Distant Labels: Relationships associated with PubMed ID
- Relationship types:
 - Binary: “**lead acetate**_{Chemical} *results in decreased expression of* **14-3-3ZETA mRNA**_{Gene}”
 - Complex: **Quercetin**_{Disease} *inhibits the reaction*
[[**24-hydroxycholesterol**_{Chemical} *co-treated with*
27-hydroxycholesterol_{Chemical} *co-treated with*
cholest-5-en-3 beta,7 alpha-diol_{Chemical}]
results in increased expression of **ITGB1**_{Gene} mRNA]

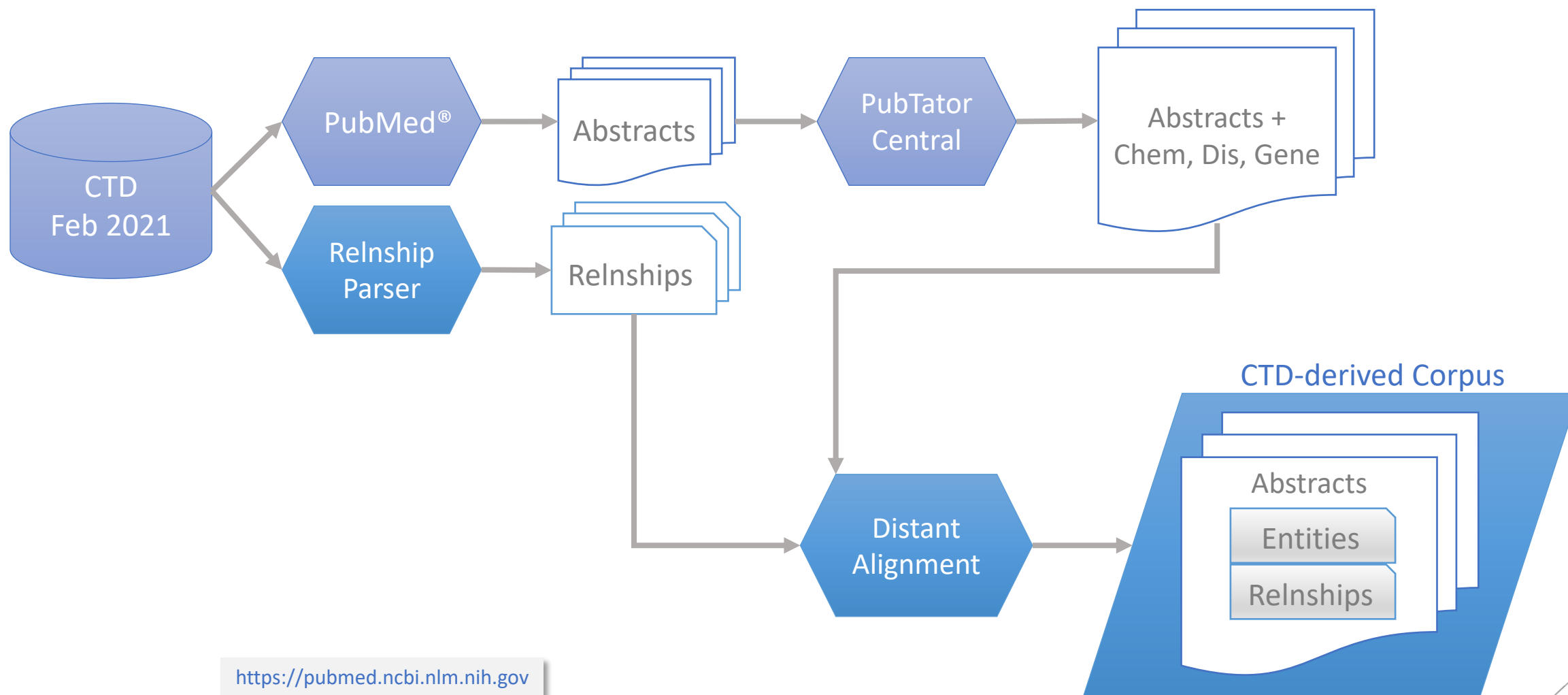


CTD Derivation Target: ChemDisGene

- Only Binary Relationships,
associated with Abstracts (not full-text)
- Reduced Relation Types:
 - Chemical – Disease: 2 types
 - Chemical – Gene: 6 types * (up to 3 degrees: *affects*, {*increases*, *decreases*})
 - Gene – Disease: 2 types
- Entities in Relationships:
Detect and link all mentions



Derivation from CTD



Relationship Parser

- Abstract fine-grained CTD relationships to reduced types
- Extract Binary relationships from complex and nested interactions in CTD

Complex nested interaction in CTD:

Quercetin_{Disease} *inhibits the reaction*

[[**24-hydroxycholesterol**_{Chemical} *co-treated with*
27-hydroxycholesterol_{Chemical} *co-treated with*
cholest-5-en-3 beta,7 alpha-diol_{Chemical}]
results in increased expression of **ITGB1**_{Gene} mRNA]

Extracted binary relationships:

expression-increases(**24-hydroxycholesterol**, **ITGB1**)
expression-increases(**27-hydroxycholesterol**, **ITGB1**)
expression-increases(**cholest-5-en-3 beta,7 alpha-diol**,
ITGB1)



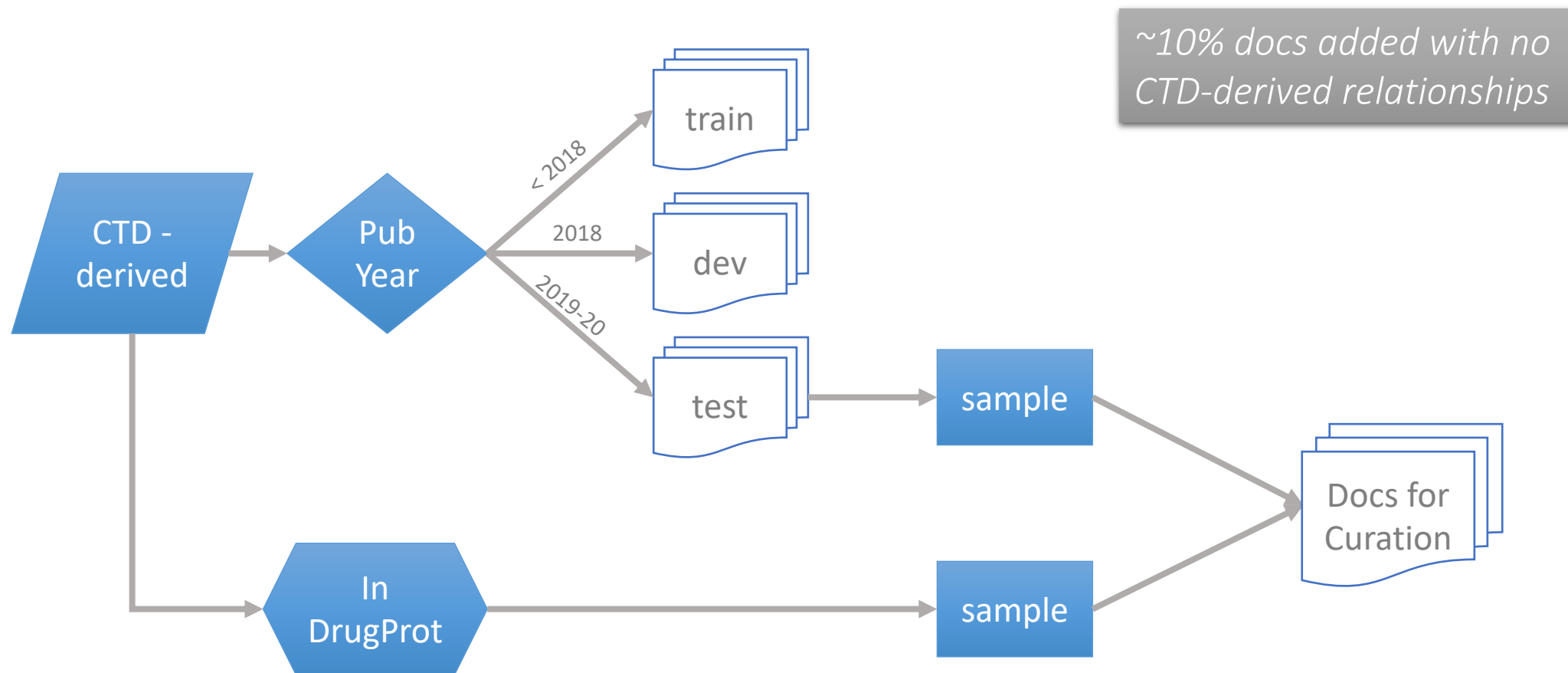
Entity Linking and Distant Alignment

- PubTator Central used to link mentions of
 - Chemicals (MeSH),
 - Diseases (MeSH and OMIM), and
 - Genes/Proteins (NCBI Gene)
- Alignment to extracted Relationships:
 - Reject relationships whose entities not detected in abstract
- *Noisy association: the abstract text may not actually express the relationship.*
 - 78% confidence based on curated sample

<https://www.ncbi.nlm.nih.gov/research/pubtator/>



Document Selection

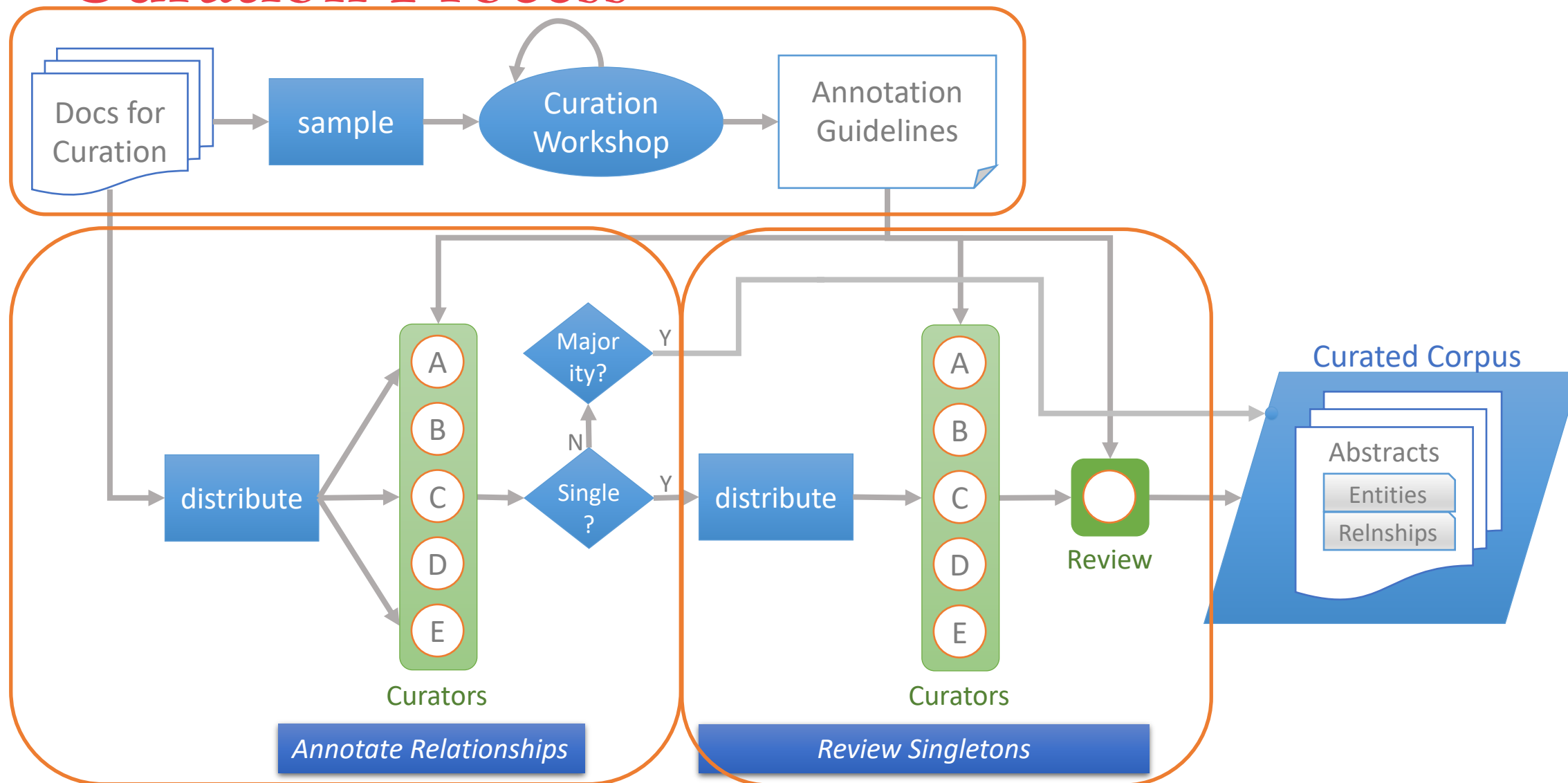


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Curation Process



Annotation Guideline examples

A: *Don't record investigated or motivating relationships that remain unknown and hypothetical.*

“Gene A is a therapeutic target for treatment of Disease X; it may therefore have a potential role in treatment of Disease Z.”

Record a relationship between Gene A and Disease X; but not between Gene A and Disease Z.

B: *Inferring a relationship across sentences.*

“We have previously identified a panel of fusion genes in aggressive prostate cancers. In this study, we showed that ... CCNH-C5orf30 and TRMT11-GRIK2 gene fusions were found in breast cancer, colon cancer, ...”

Record a ‘Gene-Disease: marker/mechanism’ relationship between C5orf30 and prostate cancers.



Annotator UI: Approve CTD-derived Reln

PMID = [30236862](#)

The PPARGC1A locus and CNS-specific PGC-1alpha isoforms are associated with Parkinson's Disease .

Parkinson's disease (PD) is the second most common neurodegenerative disease worldwide. PGC-1alpha, encoded by PPARGC1A, is a transcriptional co-activator that has been implicated in the pathogenesis of neurodegenerative discovered multiple new PPARGC1A transcripts that initiate from a novel promoter located far upstream of the reference gene promoter, are CNS-specific and are more abundant than reference gene transcripts in whole brain. These CNS-sp main full-length and several truncated isoforms via alternative splicing. Truncated CNS-isoforms include 17 kDa proteins that lack the second LXXLL motif serving as an interaction site for several nuclear receptors. We now determined expres reference gene transcripts in 5 brain regions of 21, 8, and 13 deceased subjects with idiopathic PD, Lewy body dementia and controls without neurodegenerative disorders, respectively. We observed reductions of CNS-specific transcript isoforms) only in the substantia nigra pars compacta of PD and Lewy body dementia. However, in the substantia nigra and globus pallidus of PD cases we found an up-regulation of transcripts encoding the 17 kDa proteins that inhibited transcription factors by full-length PGC-1alpha proteins in transfection assays. In two established animal models of PD, the PPARGC1A expression profiles differed from the profile in human PD in that the levels of CNS- and referen decreased in several brain regions. Furthermore, we identified haplotypes in the CNS-specific region of PPARGC1A that appeared protective for PD in a clinical cohort and a post-mortem sample ($P = .0002$). Thus, functional and genetic s CNS-specific PPARGC1A locus in PD.

Concepts in document

Genes

- ☐ 1. [10891](#): PPARG coactivator 1 alpha [PPARGC1A] (PPARGC1A, PGC-1alpha)

Diseases

- ☐ 1. [MESH:D010300](#): Parkinson Disease (PD, Parkinson's disease)
- ☐ 2. [MESH:D019636](#): Neurodegenerative Diseases (neurodegenerative disorders, neurodegenerative disease)
- ☐ 3. [MESH:D020961](#): Lewy Body Disease (Lewy body dementia)

Relations

Added by: CTD

Gene: [10891](#)

PPARG coactivator 1 alpha [PPARGC1A]

Disease: [MESH:D010300](#)

Parkinson Disease

Relation: **marker/mechanism**

Notes:

Delete this relation

Delete this relation

Added by: CTD

Gene: [10891](#)

PPARG coactivator 1 alpha [PPARGC1A]

Disease: [MESH:D020961](#)

Lewy Body Disease

Relation: **marker/mechanism**

Notes:

Delete this relation

Abstract, with
mentions underlined,
Types color-coded

Entities linked in
the abstract

Relationships derived
from CTD



Annotator UI: Add missing ('New') Relationships

Selecting
Entities will
highlight
mentions

PMID = [30236862](#)

The **PPARGC1A** locus and CNS-specific **PGC-1alpha** isoforms are associated with **Parkinson's Disease**.

Parkinson's disease (PD) is the second most common neurodegenerative disease worldwide. PGC-1alpha, encoded by PPARGC1A, is a transcriptional co-activator that has been implicated in the pathogenesis of neurodegenerative disorders. We recently discovered multiple new PPARGC1A transcripts that initiate from a novel promoter located far upstream of the reference gene promoter, are CNS-specific and are more abundant than reference gene transcripts in whole brain. These CNS-specific transcripts encode two main full-length and several truncated isoforms via alternative splicing. Truncated CNS-isoforms include 17 kDa proteins that lack the second LXXLL motif serving as an interaction site for several nuclear receptors. We now determined expression levels of CNS- and reference gene transcripts in 5 brain regions of 21, 8, and 13 deceased subjects with idiopathic PD, Lewy body dementia and controls without neurodegenerative disorders, respectively. We observed reductions of CNS-specific transcripts (encoding full-length isoforms) only in the substantia nigra pars compacta of PD and Lewy body dementia. However, in the substantia nigra and globus pallidus of PD cases we found an up-regulation of transcripts encoding the 17 kDa proteins that inhibited the co-activation of several transcription factors by full-length PGC-1alpha proteins in transfection assays. In two established animal models of PD, the PPARGC1A expression profiles differed from the profile in human PD in that the levels of CNS- and reference gene transcripts were decreased in several brain regions. Furthermore, we identified haplotypes in the CNS-specific region of PPARGC1A that appeared protective for PD in a clinical cohort and a post-mortem sample (P = .0002). Thus, functional and genetic studies support a role of the CNS-specific PPARGC1A locus in PD.

Concepts in document

Genes

- ☒ 10891: PPARG coactivator 1 alpha [PPARGC1A] (PPARGC1A, PGC-1alpha)

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- ☐ 1. MESH:D010300: Parkinson Disease (PD, Parkinson's disease)
- ☒ 2. MESH:D019636: Neurodegenerative Diseases (neurodegenerative disorders, neurodegenerative disease)
- ☐ 3. MESH:D020961: Lewy Body Disease (Lewy body dementia)

Relations

Added by: CTD

Gene: 10891 PPARG coactivator 1 alpha [PPARGC1A]	Disease: MESH:D010300 Parkinson Disease	Relation: marker/mechanism
---	--	----------------------------

Notes:

New Relation

Gene: 10891
PPARG coactivator 1 alpha [PPARGC1A]
Disease: MESH:D019636
Neurodegenerative Diseases

Notes:

-- Select a Relation Type --

- Chemical_Disease: marker/mechanism
- Chemical_Disease: therapeutic
- Chemical_Gene: increases expression
- Chemical_Gene: decreases expression
- Chemical_Gene: affects expression
- Chemical_Gene: increases activity
- Chemical_Gene: decreases activity
- Chemical_Gene: affects activity
- Chemical_Gene: increases metabolic_processing
- Chemical_Gene: decreases metabolic_processing
- Chemical_Gene: affects metabolic_processing
- Chemical_Gene: increases transport
- Chemical_Gene: decreases transport
- Chemical_Gene: affects transport
- Chemical_Gene: affects localization
- Chemical_Gene: affects binding
- Gene_Disease: marker/mechanism**
- Gene_Disease: therapeutic

Curator can select
Relation Type



Annotator UI: Singleton Review

PMID = [15078100](#)

Kinetic mechanism of [quinone oxidoreductase 2](#) and its inhibition by the antimalarial [quinolines](#) .

[Quinone oxidoreductase 2](#) ([QR2](#)) purified from human red blood cells was recently shown to be a potential target of the [quinoline](#) antimalarial compounds [Graves et al., (2002) Mol. Pharmacol. 62, 1364]. [QR2](#) catalyzes the two-electron reduction of [menadione](#) via the oxidation of [N-alkylated](#) or [N-ribosylated](#) [nicotinamides](#) . To investigate the mechanism and consequences of inhibition of [QR2](#) by the [quinolines](#) further, we have used steady-state and transient-state kinetics to define the mechanism of [QR2](#) . Importantly, we have shown that [QR2](#) when isolated from an overproducing strain of *E. coli* is kinetically equivalent to the enzyme from the native human red blood cell source. We observe ping-pong kinetics consistent with one substrate/inhibitor binding site that shows selectivity for the oxidation state of the FAD cofactor, suggesting that selective inhibition of the liver versus red blood cell forms of [malaria](#) may be possible. The reductant [N-methyldihydronicotinamide](#) and the inhibitor [primaquine](#) bind exclusively to the oxidized enzyme. In contrast, the inhibitors [quinacrine](#) and [chloroquine](#) bind exclusively to the reduced enzyme. The [quinone](#) substrate [menadione](#) , on the other hand, binds nonspecifically to both forms of the enzyme. Single-turnover kinetics of the reductive half-reaction are chemically and kinetically competent and confirm the inhibitor selectivity seen in the steady-state experiments. Our studies shed light on the possible in vivo potency of the [quinolines](#) and provide a foundation for future studies aimed at creating more potent [QR2](#) inhibitors and at understanding the physiological significance of [QR2](#) .

Approved Relations

Singleton Relations to Curate

Added by: Alison_Jee		
Chemical: MESH:D024483 Vitamin K 3	Gene: 4835 N-ribosyldihydronicotinamide:quinone reductase 2 [NQO2]	Relation: affects^binding
Creator's Notes:		
Notes: The quinone substrate menadione, on the other hand, binds nonspecifically to both forms of the enzyme.	☒ Accept this relation ☐ Reject this relation Reset review of this relation	✓

Added by: Parasvi_Patel		
Chemical: MESH:C037219 quinoline	Gene: 4835 N-ribosyldihydronicotinamide:quinone reductase 2 [NQO2]	Relation: affects^binding
Creator's Notes:		
Notes:	☐ Accept this relation ☒ Reject this relation Reset review of this relation	✗

Reviewer can Accept or Reject the singleton Relationship



Curation: Annotation Agreement

Relationships	Curators				
	A	B	C	D	E
All	0.85	0.84	0.83	0.88	0.88
CTD-derived	0.99	0.96	0.97	0.99	0.96
New	0.76	0.77	0.69	0.82	0.83

Agreement F1 scores for the 5 annotators against the ‘majority-approved’ reference subset.

Agreement for CTD-derived relationships (prompted in curation UI) is higher than for New relationships (curator has to enter the new relationship).



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- Task definition
- ChemDisGene: Automated Derivation
- ChemDisGene: Manual Curation Process
- Dataset Statistics
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Data Statistics: Highlights

- Distantly supervised *training* data:
76,942 abstracts with entity linking from PubTator
and 167k relation labels from CTD
- Manually curated *test* data: 523 abstracts (3,911 relationships).
- 18 relation types among Chemicals, Diseases, Genes/Gene products

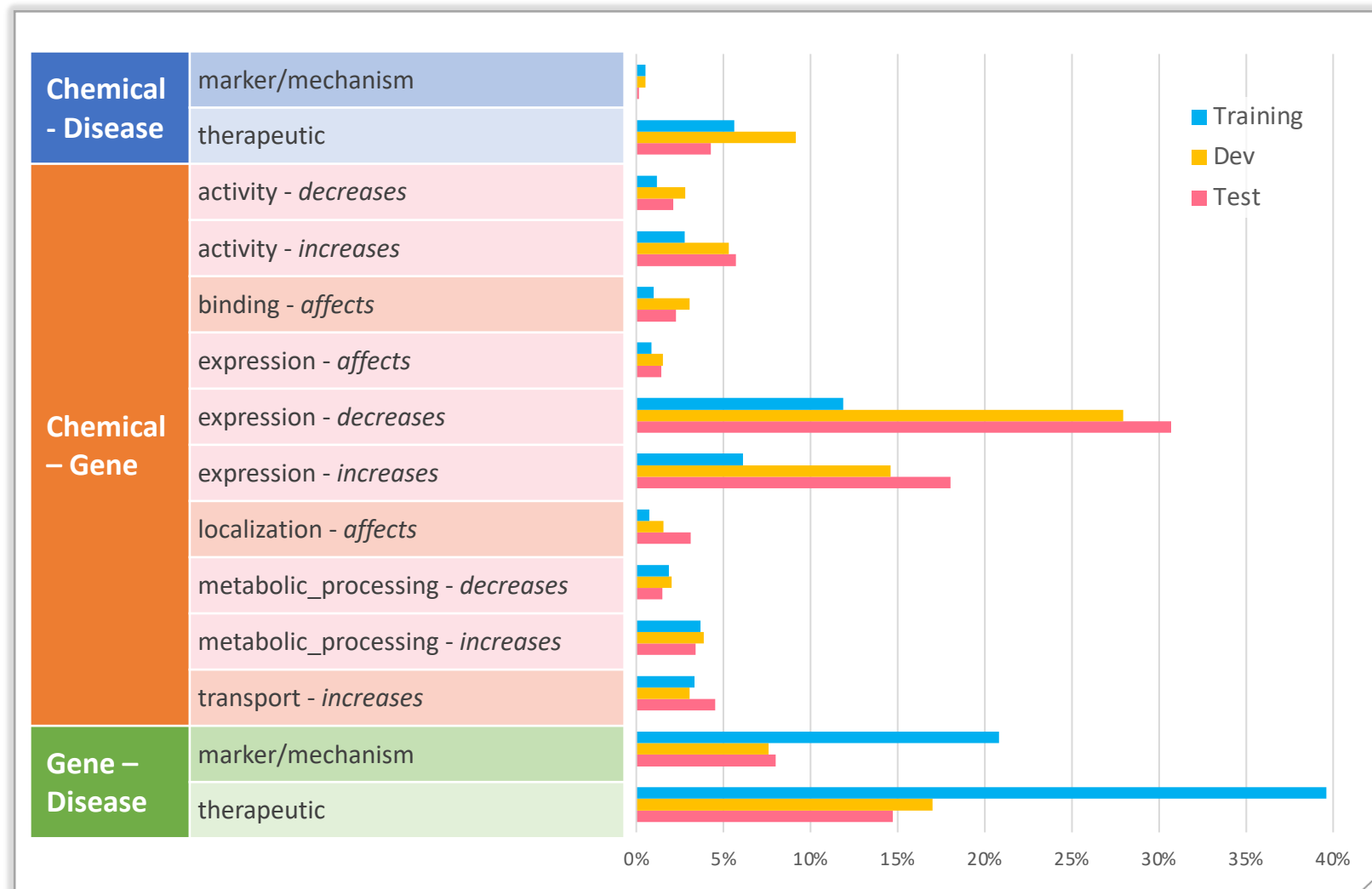
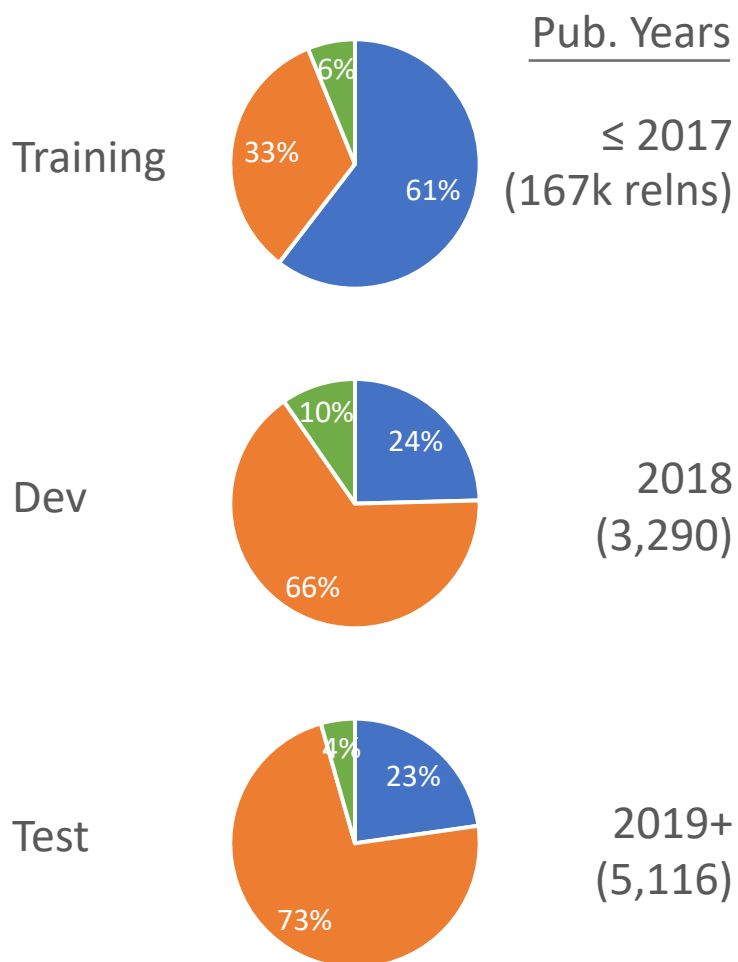


Corpus Statistics

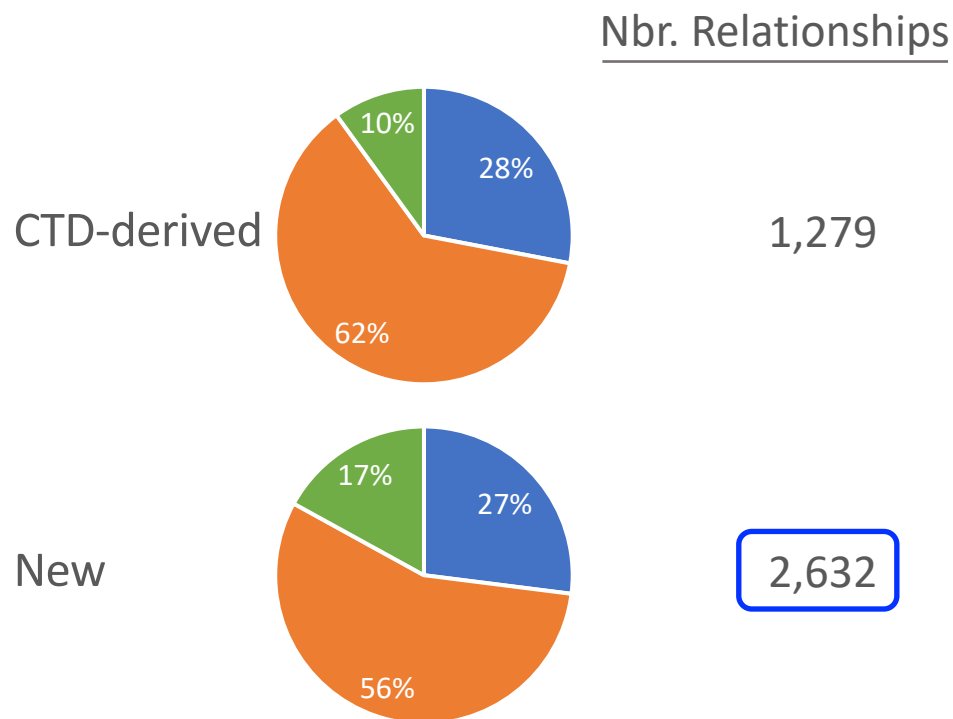
	CTD-derived Corpus			Curated Corpus
	Train	Dev	Test	
Nbr. abstracts	76,942	1,521	1,939	523
Abstracts w/o relations	7,244	397	436	5
Nbr. relationships	167,005	3,290	5,116	3,911
Unique relationships	93,801	3,127	4,801	3,806
Total entity mentions	1,532,117	36,114	49,839	14,248
Chemicals	686,102	13,986	19,895	5,739
Diseases	478,397	8,962	11,750	2,931
Genes	367,618	13,166	18,194	5,578
Unique entities in relationships	14,991	1,894	2,345	1,875
Chemicals	7,187	759	999	670
Diseases	2,413	283	287	318
Genes	5,391	852	1,059	887



Distr. Of Relationships, CTD-derived Corpus



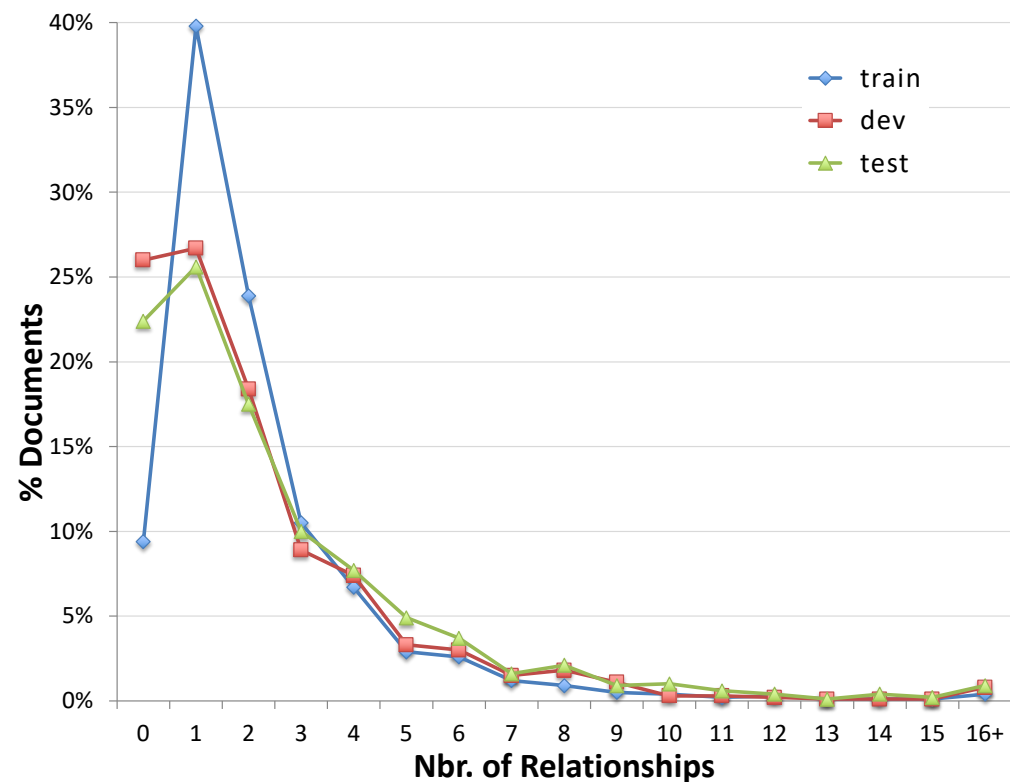
Distr. Of Relationships, Curated Corpus



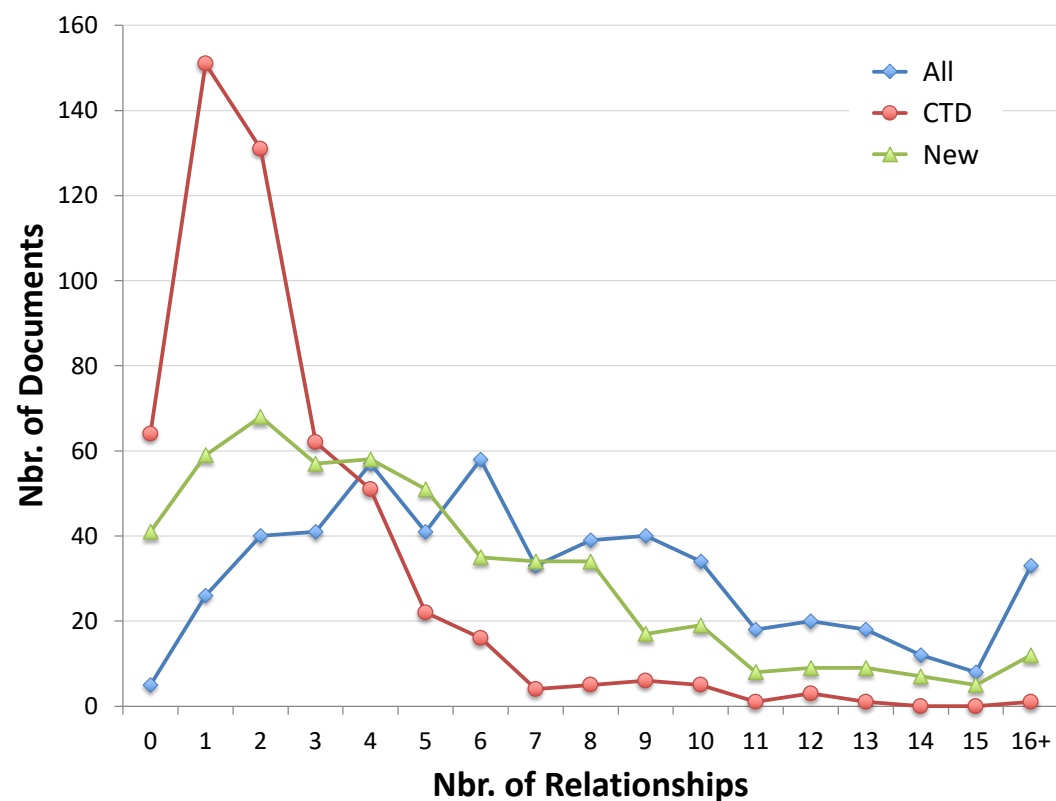
Chemical-Disease	CTD-... (%)	New (%)
marker/mechanism	16.4	16.6
therapeutic	12.0	10.4
Chemical-Gene	CTD-derived	New
activity - affects		1.2
activity - decreases	7.3	8.3
activity - increases	7.8	8.7
binding - affects	6.7	4.3
expression - affects	0.6	2.8
expression - decreases	13.1	10.4
expression - increases	18.4	11.8
localization - affects	1.5	0.8
metabolic_processing - affects		0.8
metabolic_processing - decreases	1.5	1.7
metabolic_processing - increases	4.0	3.0
transport - affects		0.8
transport - decreases		0.6
transport - increases	0.9	1.1
Gene-Disease	CTD-derived	New
marker/mechanism	9.3	14.1
therapeutic	0.5	2.9



Nbr. of Relationships per Document



CTD-derived Corpus



Curated Corpus

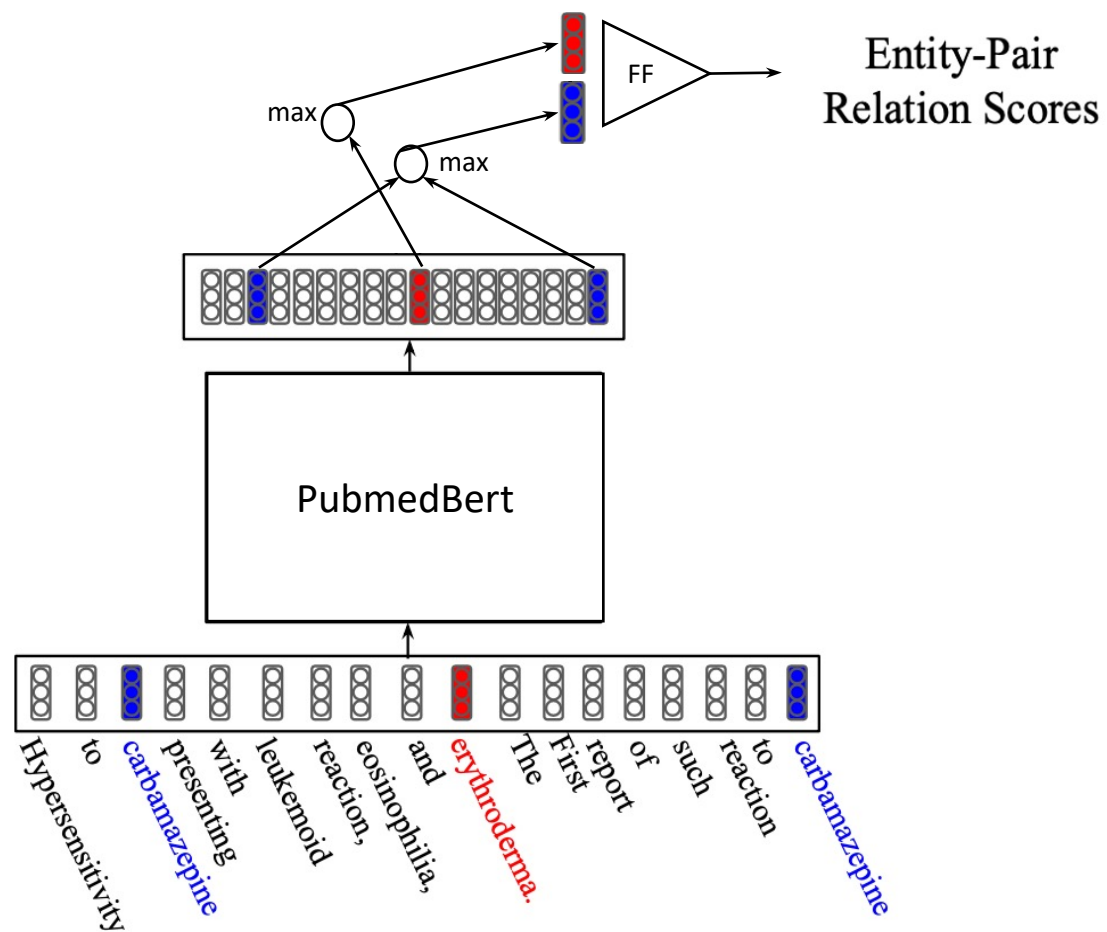


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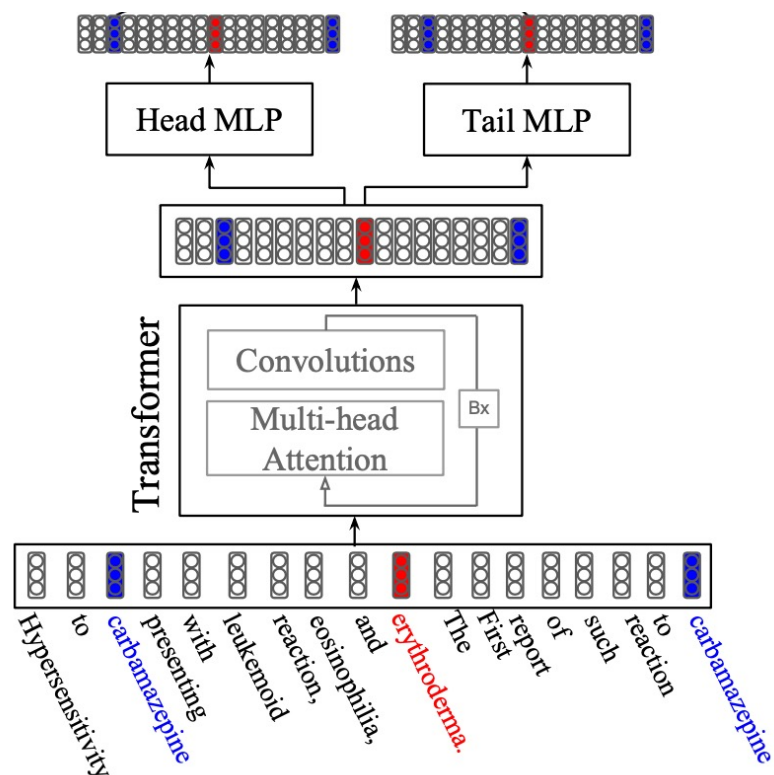
PubmedBert



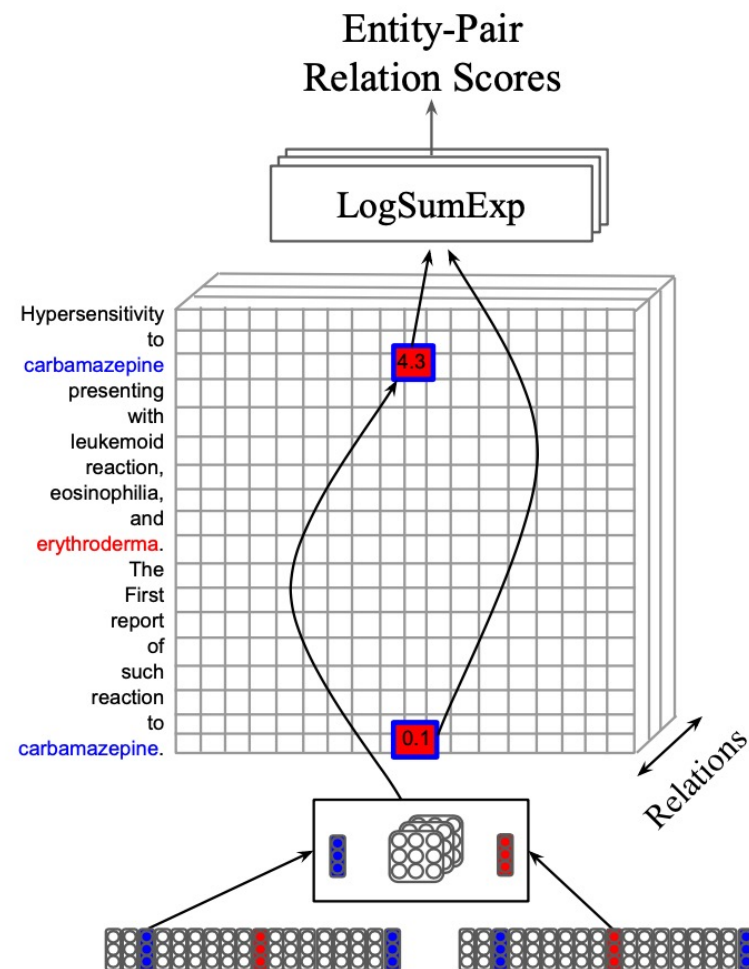
... (Gu et al, 2021)

Bi-Affine Relation Attention Networks (BRAN)

Transformer-based Text Encoder



Bilinear Relation Scorer

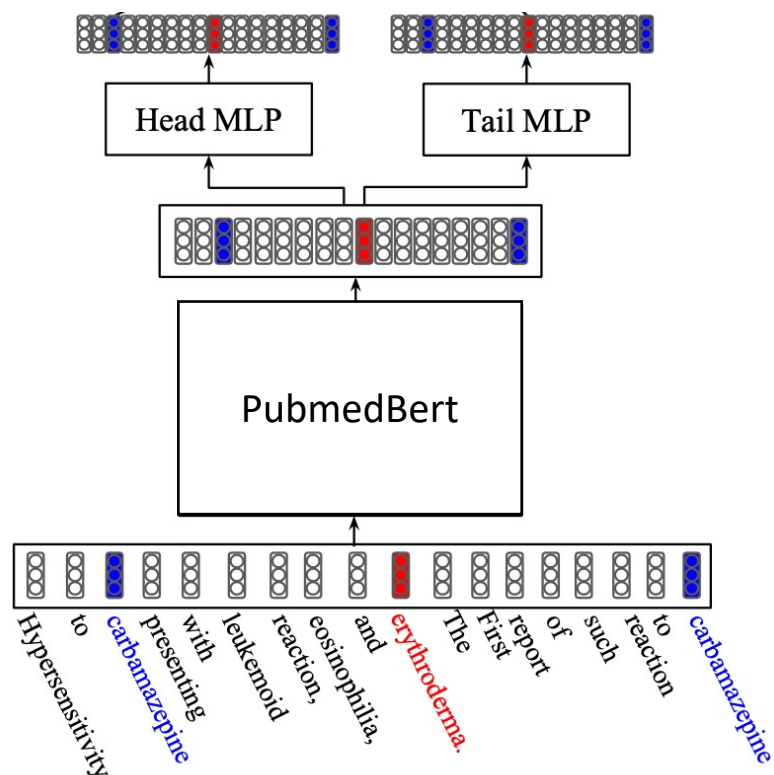


... (Verga et al, 2018)

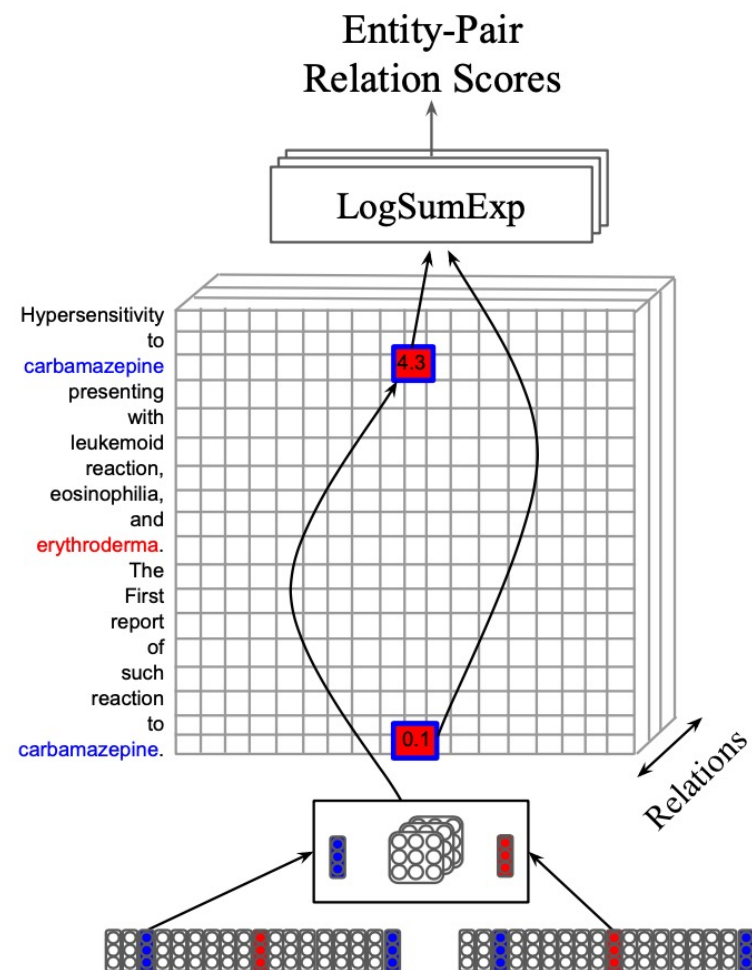


PubmedBert + BRAN

BERT-based Text Encoder



Bilinear Relation Scorer



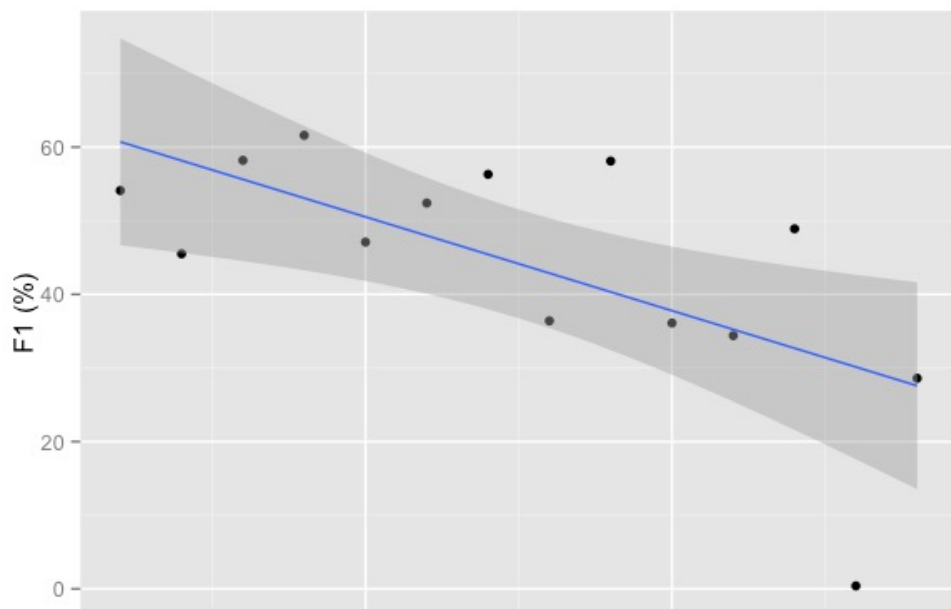
Benchmark RE Model Results

Model	Micro				Macro		
	P	R	F1	Avg. P	P	R	F1
<i>CTD-derived corpus: 'dev' split / 'test' split</i>							
BRAN	32.1 / 31.7	46.3 / 44.2	37.9 / 36.9	28.4 / 27.9	25.9 / 23.6	32.3 / 30.1	28.2 / 26.0
PubmedBert	50.3 / 49.6	59.3 / 56.1	54.5 / 52.6	50.3 / 50.1	43.6 / 39.0	50.3 / 48.4	44.9 / 41.7
PubmedBert + BRAN	53.9 / 53.9	61.0 / 57.3	57.3 / 55.6	54.0 / 54.3	45.0 / 42.7	54.1 / 50.4	48.7 / 44.4
<i>Curated corpus: CTD-derived relationships only / All relationships</i>							
BRAN	24.4 / 41.8	45.8 / 26.6	31.8 / 32.5	28.1 / 33.5	20.3 / 37.2	35.7 / 22.5	24.5 / 25.8
PubmedBert	43.0 / 64.3	61.7 / 31.3	50.7 / 42.1	50.7 / 46.9	34.7 / 53.7	53.4 / 32.0	39.6 / 37.0
PubmedBert + BRAN	46.5 / 70.9	61.1 / 31.6	52.8 / 43.8	53.0 / 50.6	45.8 / 69.8	59.0 / 32.5	47.0 / 40.5



Model Performance per Relation Type

Metrics for PubmedBert + BRAN
on the Curated Corpus,
sorted on decreasing relation
frequency in Training data.



Relation Type	F1
Chemical-Disease : marker/mechanism	54.1
Chemical-Disease : therapeutic	45.5
Chemical-Gene : expression - increases	58.2
Chemical-Gene : expression - decreases	61.6
Gene-Disease : marker/mechanism	47.1
Chemical-Gene : activity - increases	52.4
Chemical-Gene : activity - decreases	56.3
Chemical-Gene : metabolic_processing - increases	36.4
Chemical-Gene : binding - affects	58.1
Chemical-Gene : transport - increases	36.1
Chemical-Gene : metabolic_processing - decreases	34.4
Chemical-Gene : localization - affects	48.9
Chemical-Gene : expression - affects	0.4
Gene-Disease : therapeutic	28.6



Thankyou!

dataset:

<https://github.com/chanzuckerberg/ChemDisGene>

