

Case Study: Natural-Language-Processing (NLP) with Open Data for Drug Repositioning on Glioblastoma Therapy

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Education and research. graubynden

Agenda

- Introduction
- Methodology
- Results & Discussion
- Limitations & Further research



Speaker Introduction

Curdin Marxer

- BSc. Information Science
- MSc. in Business Administration: Information and Data Management
- Research assistant at the Centre for Data Analytics, Visualization and Simulation (DAViS) of the University of Applied Sciences of the Grisons in Chur, Switzerland





Background of our research

- Part of a collaborate research project between the DAViS Centre and two neurosurgeons of the Cantonal Hospital of Winterthur
- CUSP9v3 an innovative combined regimen of nine repurposed non-oncological drugs with metronomic temozolomide for the treatment of glioblastoma (malignant brain tumor)
- Our overarching research goal is to predict new possible drug candidates for repositioning by harvesting multiple different data sources using ML/DL techniques
- This research started as a master's thesis with the main research question:

How can unstructured text data be used to identify new drug repositioning candidates and how can they complement databases?



Drug development and the role of drug repositioning

- The development and discovery of new drugs is costly, risky and takes a lot of time
- The success rate of a newly developed drug to be clinically approved and to reach world-wide markets is below 10%
- Many newly developed medical compounds end up abandoned
- Drug repositioning/repurposing describes the process of identifying and developing new uses for already existing drugs or known active compounds
- Discover new use cases of known drugs by harvesting knowledge of previous research
- Highly beneficial (commercially and for patients), especially for rare diseases



Some strategies for drug repositioning

side-effect-based approaches

 based on the idea that therapeutically observed side effects of already developed drugs can also provide information about possible alternative uses

similarity-based approaches

- similarity between two drugs can be determined based on the culmination of multiple similarities in chemical structure, overlap of molecular target structures and side effects.
- similarities between diseases can be concluded through ontologies or shared treatment profiles



Challenges of working with drug data

- Highly complex and strongly interconnected data
- Amounts of biomedical data on drugs and the number of available repositories and databases are constantly increasing
- Data of these repositories or databases differ significantly in terms of scope, quality and reliability – causing inconsistencies
- Raise the challenge in selecting the adequate database(s) containing the required information



Examples of these inconsistencies based on our Case Study

Drugs used to treat Glioblastoma Multiforme

The following list of medications are in some way related to or used in the treatment of this condition.

All drug classes	~						≂ si	now filters
Drug name	Rating	Reviews	▼ Activity	?	Rx/OTC	Preg	CSA	Alcohol
✓ Avastin	8.3	7 reviews			Rx	C	N	
✓ Temodar	9.0	1 review			Rx	D	N	
✓ temozolomide	9.0	2 reviews			Rx	D	N	
➤ bevacizumab	8.5	8 reviews			Rx	C	N	
✓ Matulane	Rate	Add review	-		Rx	D	N	X
✓ hydroxyurea Off-label	Rate	Add review			Rx	D	N	
✓ BiCNU	Rate	Add review			Rx	D	N	
✓ Gliadel	Rate	Add review			Rx	D	N	
✓ carmustine	Rate	Add review	-		Rx	D	N	
✓ Mvasi	Rate	Add review	-		Rx	C	N	
✓ procarbazine	Rate	Add review	-		Rx	D	N	X
✓ Zirabev	Rate	Add review	-		Rx	C	N	
✓ Alymsys	Rate	Add review	-		Rx	C	N	

		Drug results:	7
DRUG $^{\uparrow \downarrow}$	DRUG NAME	<u>temozolomide</u>	Temozolomide is not directly active but undergoes rapid nonenzym DNA.
DB00262	Carmustine	<u>bevacizumab</u>	An anti-VEGF humanized murine monoclonal antibody. It inhibits VE
DB00762	Irinotecan	<u>carmustine</u>	a carcinogen according to the Fourth Annual Report on Carcinogen
DB06192	Nimotuzumab	Lomustine	An alkylating agent of value against both hematologic malignancies
DB00853	Temozolomide	vincristine	An antitumor alkaloid isolated from VINCA ROSEA. (Merck, 11th ed.)
Showing 1 to 4 of	4 entries		

procarbazine

Showing 1 to 4 of 4

FH GR drugs.com

go.drugbank.com (4 "drug" indications and 316 "drug trial" indications)

drugcentral.org

An antineoplastic agent used primarily in combination with mechlo

The potential of text data

- A huge amount of exclusive medical knowledge is hidden in various types of unstructured text data such as clinical reports, scientific research documents or journals
- Especially clinical reports provide new knowledge that is not yet recorded in standardized databases or summarized medical literature, e.g., on new side effects of individual drugs or drug-drug interactions
- Potential buried information on abandoned medical compounds



Goal of this research

- Test and evaluate different approaches and methods to predict new drug repositioning candidates using NLP on open and publicly available unstructured text data
- Determine the potential of unstructured text data to combat database inconsistencies by filling existing data gaps
- Development of two different workflows to identify drug repositioning candidates for possible therapeutic use for glioblastoma
 - Combined use of pre-trained biomedical Named Entity Recognition (NER) models to identify possible relationships between biomedical entities



Tools

- ScispaCy v0.5.1
- Provides fast, easy-to-use and robust biomedical NER-models
- Offers four different specialized biomedical NER models which enable a wide subject-specific scope of applications



Selection of open text data

- Extracted by using the term "Neuroectordermal Tumors" of the controlled vocabulary MeSH
- 6'741 clinical studies from ClinicalTrials.gov
- Supplemented with 3'259 abstracts from PubMed
- resulting test data set of 10'000 documents

Neoplasms Cysts Hamartoma Neoplasms by Histologic Type Histiocytic Disorders, Malignant 🗄 Leukemia Lymphatic Vessel Tumors Lymphoma Neoplasms, Complex and Mixed Neoplasms, Connective and Soft Tissue Neoplasms, Germ Cell and Embryonal Neoplasms, Glandular and Epithelial 🗄 Neoplasms, Gonadal Tissue Neoplasms, Nerve Tissue Meningioma Herve Sheath Neoplasms Neuroectodermal Tumors Craniopharyngioma Neoplasms, Neuroepithelial Ganglioneuroma Glioma Astrocytoma Glioblastoma Diffuse Intrinsic Pontine Glioma 🗄 Ependymoma Ganglioglioma Gliosarcoma Medulloblastoma Oligodendroglioma Optic Nerve Glioma Neurocytoma Neuroectodermal Tumors, Primitive Pinealoma Retinoblastoma Neuroectodermal Tumor, Melanotic Neuroendocrine Tumors



Method 1: Co-occurrence analysis

- Method 1: Co-occurrence analysis based on the "Guilt by Association (GBA)" principle
- Using the co-occurrence of NER-extracted biomedical entities to determine most similar document pairs
- Use these most similar document pairs to extract and associate new drug-disease pairs



"Guilt by Association" scheme for the discovery of new uses for known drugs (Chiang & Butte, 2009)



TABLE I

METHOD 1: VARIATIONS WITH THE RESPECTIVE USED LABELS OF DIFFERENT SCISPACY NER MODELS

ScispaCy	Variations and used labels					Variations and used labels				
NER	Biomedical	Genes,	Diseases,	Cell-						
Model	Entities	genomes,	symptoms,	types,						
		gene products	side-effects	lines,						
				components						
en_core_sci_lg	ENTITY									
en_ner_craft_md		GO, SO,		CL						
		GGP								
en_ner_jnlpba_md				CELL_TYPE,						
				CELL_LINE						
en_ner_bc5cdr_md			DISEASE							
en_ner_bionlp13cg_md		GENE_OR_	CANCER,	CELL,						
		GENE_PRO	PATHO	CELLULAR_						
		DUCT	LOGICAL_	COMPONENT						
			FORM							
			ATION							



Method 2: Chains of association

- Method 2: Chains of association using "Swanson's ABC-model"
- By building association chains to identify new possible transitive relations to determine new repurposing candidates
- Extraction of A-B relations from state-of-the-art biomedical databases
- Using extracted B-terms as search terms for the text data, identify hit documents, determine entity type C as possible repurposing candidate for A



"Swanson's ABC model" (Andronis et al., 2011)



TABLE II

METHOD 2: VARIATIONS OF CHAINS OF ASSOCIATION USING SWANSON'S ABC MODEL

Association chain Type	Entity relation type and used databases				
A-B-C-D	A-B	B- C			
"disease-gene-drug"	disease-gene				
	from OpenTargets [37]				
"disease-gene_variant-drug"	disease-gene_variant				
	from DisGeNET [38]				
"disease-symptom-drug"	disease-symptom from				
	Human Phenotype				
	Ontology (HPO) [39]				
"disease-drug-sideeffect-drug"	disease-drug	drug-sideeffect			
	from DrugBank [40]	from SIDER [41]			
"disease-drug-cell_lines-drug"	disease-drug	drug-cell_lines			
	from DrugBank [40]	from Genomics of			
		Drug Sensitivity in			
		Cancer (GDSC) [42]			



Results & Discussion

Our predicted candidates for repurposing

- Types and examples of results as predicted candidates for repurposing on glioblastoma therapy:
 - **Chemical elements:** calcium, indium
 - **Chemical compounds:** most observed type, e.g., O6-benzylguanine
 - **Experimental vaccines:** "DNX-2401" (tasadenoturev)
 - Hormones: estrogen, steroids
 - Various therapeutics: TT-Fields



Results & Discussion

Our evaluation of candidates

- Predicted repurposing candidates labeled in three categories for evaluation:
 - "Known in DrugBank"
 - "Potential unknown candidates"
 - > "Invalid"

Method 1: Co-occurrence Method 2: Chains of association





TABLE III

METHOD 1: SUMMARY OF RESULTS OF ALL EMPLOYED VARIATIONS

	Biomedical Entities	Genes, genomes, gene products	Diseases, symptoms, side-effects	Cell- types, lines, components
Maximum pairwise cosine distance between documents	< 0.35	< 0.2	< 0.2	< 0.2
Total number of predicted drug candidates	2734	6865	3898	22025
"Known in DrugBank" ratio	38.40%	60.13%	45.31%	39.21%
"Potential unknown candidates" ratio	20.56%	8.91%	16.47%	21.08%
"Invalid" ratio	41.04%	30.96%	38.22%	39.71%



TABLE IV

METHOD 2: SUMMARY OF RESULTS OF ALL EMPLOYED VARIATIONS

	"disease- gene- drug"	"disease- gene_variant- drug"	"disease- symptom- drug"	"disease- drug- sideeffect- drug"	"disease- drug- cell_line- drug"
Number of extracted search terms from the selected database	118	291	24	200	68
<i>Total number of predicted drug candidates</i>	2226	8	975	7021	47
"Known in DrugBank" ratio	38.63%	0%	39.90%	39.52%	44.68%
"Potential unknown candidates" ratio	20.44%	37.50%	24.51%	26.81%	14.89%
"Invalid" ratio	40.93%	62.50%	35.59%	33.67%	40.43%



Results & Discussion

Some conclusions

- The analysis of unstructured text data can enable a more comprehensive overview of potential repurposing candidates
- Case examples, like "Cixutumumab" and "Paracetamol" were identified as possible repurposing candidates. However, these compounds are currently not listed in DrugBank, although they have been part of clinical trials for the treatment of glioblastoma
- Using overlapping genes as markers showed most reliable potential candidates for repositioning through our methods and use case
- Rarely any gene variants or cell-lines were documented in our selected text data, so only symptoms, side-effects or genes seem suitable as possible embeddings for future analyses of text data



Limitations & Further research

Limitations

- Publicly available clinical text data are mostly only provided as short summaries or abstracts
- Lack of an objective qualitative assessment of our identified repositioning candidates
- Vague association approach, prone to false positives
 - most associations were not analyzed based on their exact semantic connections, such as their possible causalities and their positive or negative relationships
- Poor performance in precision and recall of ScispaCy NER-models in comparison to models from other biomedical NER-Taggers, e.g., "Stanza" (StanfordNLP) or "SparkNLP"



Limitations & Further research

Further research

- Use of better specialized NER models, continued training of available models on new data via Transfer Learning through SparkNLP
- Focus on the use of more full text data from PubMed-Central, scope not solely limited to "Neuroectodermal tumors" for "soft-repurposing"
- Extract drug combinations and regimen and profiling them with scores based on multiple data sources on side-effects, drug-drug interactions and drug-characteristics



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Thank you very for your attention. Feel free to ask any questions!

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