## Building CoronaWhy Knowledge Graph

FREYA Guest webinar

Slava Tykhonov Senior Information Scientist (DANS-KNAW, the Netherlands)

01.09.2020

## About me: DANS-KNAW projects (2016-2020)

- CLARIAH+ (ongoing)
- EOSC Synergy (ongoing)
- SSHOC Dataverse (ongoing)
- CESSDA DataverseEU 2018
- Time Machine Europe Supervisor at DANS-KNAW
- PARTHENOS Horizon 2020
- CESSDA PID (Personal Identifiers) Horizon 2020
- CLARIAH
- RDA (Research Data Alliance) PITTS Horizon 2020
- CESSDA SaW H2020-EU.1.4.1.1 Horizon 2020



## Motivation



### Slava Tykhonov 4:05 PM

Born in Kyiv, Ukraine but raised as a scientist in the Netherlands, during my career I saw a lot of cases where people refused to collaborate and work together due to own ambitions and wrong vision. I truly believe that dangerous things like coronavirus are possible in the modern society only because people are competing against each other and don't want to share their knowledge and competence, and work together in order to find a solution for a problem.

Stupidity, ignorance and limitness has no nationality, it's just a common thing that killing this world and COVID-19 is just one of the challenges. I'm here to open everything that should be open for the humanity, build the collaboration between people, speed up the innovation and start the development of the research infrastructure that will allow to bring Science back to the policy table, and quickly respond to the current and future challenges. I would say, we should be prepared for the technological future and don't afraid to disrupt the world. (edited)



### 7 weeks in lockdown in Spain



Resistere (I will resist)

## About CoronaWhy

#### www.coronawhy.org



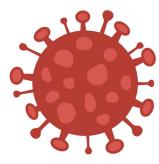
**Daily Progress** Calendar Home



#### FIGHTING CORONAVIRUS WITH ARTIFICIAL INTELLIGENCE

We are a globally distributed, volunteer-powered research organisation, trying to assist the medical community's ability to answer key questions related to COVID-19

JOIN THE FIGHT LEARN MORE



### Who we are?

Artur Kiulian started CoronaWhy because he realized that we are all in this together. Now CoronaWhy is an international group of 900+ volunteers whose mission is to improve global coordination and analysis of all available data pertinent to the COVID-19 outbreak and ensure all findings reach those who need

them.

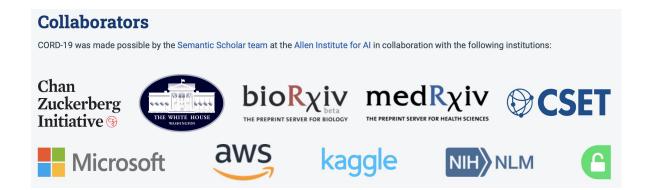
It's impossible to list everyone out but we will eventually.

1300+ people registered in the organization, more than 300 actively contributing!

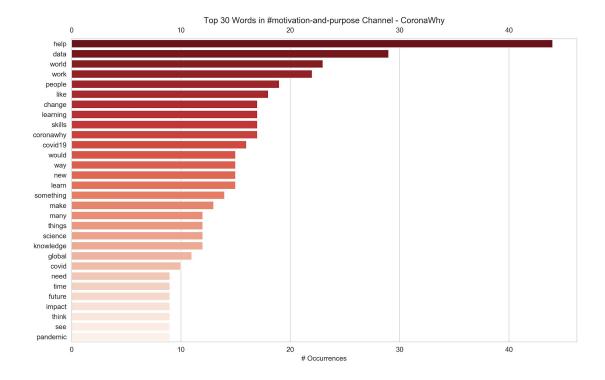
### COVID-19 Open Research Dataset Challenge (CORD-19)

It's all started from this (March, 2020):

"In response to the COVID-19 pandemic and with the view to boost research, the Allen Institute for AI together with CZI, MSR, Georgetown, NIH & The White House is collecting and making available for free the COVID-19 Open Research Dataset (CORD-19). This resource is updated weekly and contains over 52,000 scholarly articles, including 41,000 with full text, about COVID-19 and other viruses of the coronavirus family." (Kaggle)



## Motivation of CoronaWhy community members

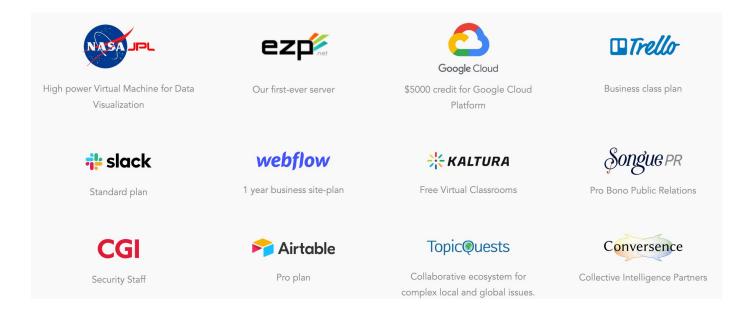


Credits: Andre Ye

# CoronaWhy Funding

Initial: \$5k from Google on GCP and \$4k from Amazon on AWS (April 2020)

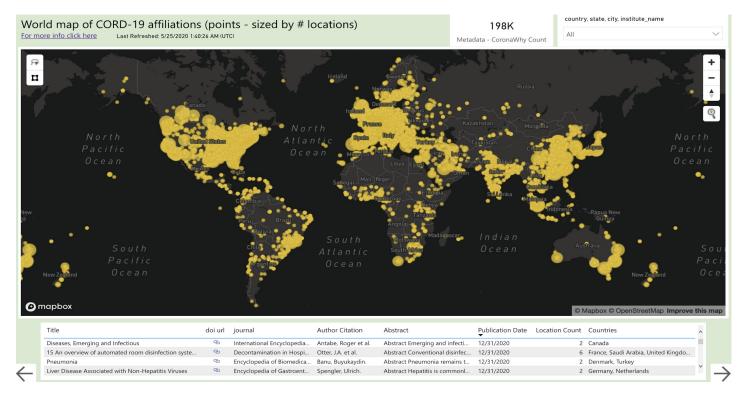
Donations: \$9k and 15k british pounds to sustain CoronaWhy infrastructure



# CoronaWhy Community Tasks (March-April)

- 1. Task-Risk helps to identify risk factors that can increase the chance of being infected, or affects the severity or the survival outcome of the infection
- 2. Task-Ties to explore transmission, incubation and environment stability
- 3. Match Clinical Trials allows exploration of the results from the COVID-19 International Clinical Trials dataset
- 4. COVID-19 Literature Visualization helps to explore the data behind the AI-powered literature review
- Named Entity Recognition across the entire corpus of CORD-19 papers with full text

## CORD-19 affiliations recognized with Deep Learning



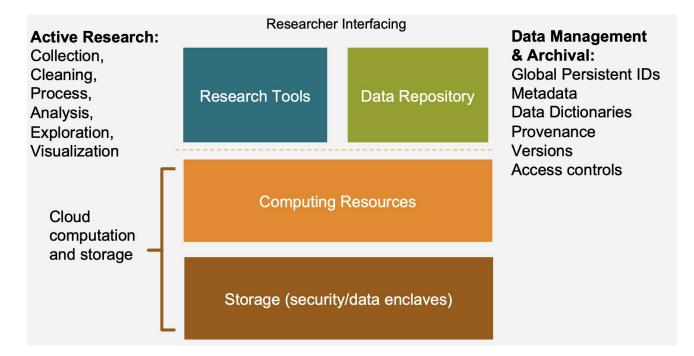
#### Source: CORD-19 map visualization and institution affiliation data

# Collaboration with other organizations

- Harvard Medical School, INDRA integration
- Helix Group, Stanford University
- NASA JPL, COVID-19 knowledge graph and GeoParser
- Kaggle, coronamed application
- Fraunhofer Institute for Intelligent Analysis and Information Systems IAIS, knowledge graph
- dcyphr, a platform for creating and engaging with distillations of academic articles
- CAMARADES (Collaborative Approach to Meta-Analysis and Review of Animal Data from Experimental Studies)

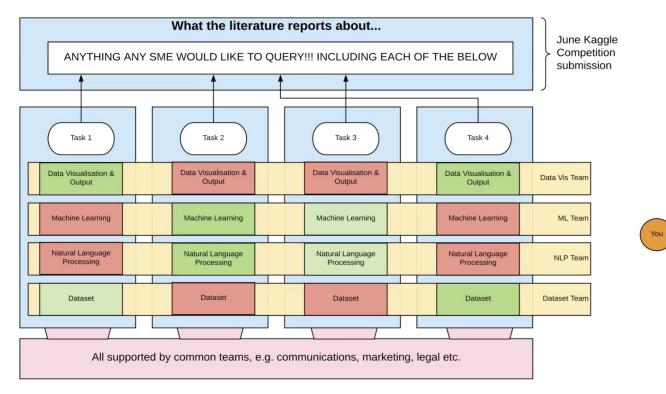
We've got almost endless data streams...

# Looking for Commons



Merce Crosas, "Harvard Data Commons"

## Building a horizontal platform to serve vertical teams



#### Source: CoronaWhy infrastructure introduction

## Turning FAIR into reality!

FM-F1B

FM-F3

### WHAT IS FAIR ?

### Findable:

F1 (meta)data are assigned a globally unique and persistent identifier; FM-F2

F2 data are described with rich metadata;

F3 metadata clearly and explicitly include the identifier of the data it describes; FM-F4

F4 (meta)data are registered or indexed in a searchable resource;

### Interoperable:

11 (meta)data use a formal, accessible, shared, and broadly applicable language for knowledge FM-11 representation.

12 (meta)data use vocabularies that follow FAIR principles.

I3 (meta)data include qualified references to other (meta)data; FM-I3

### Accessible:

A1 (meta)data are retrievable by their identifier using a standardized communications protocol;

A1.1 the protocol is open, free, and universally implementable;

A1.2 the protocol allows for an authentication and and authorization procedure, where necessary;

A2 metadata are accessible, even when the and are no longer available;

### **Reusable:**

R1 meta(data) are richly described with a plurality of accurate and relevant attributes;

R1.1 (meta)data are released with a clear and accessible data usage license; FM-R1.1

R1.2 (meta)data are associated with detailed provenance;

FM-R1.2

R1.3 (meta)data meet domain-relevant community standards;

FM-R1.3

Sci. Data 3:160018 doi: 10.1038/sdata.2016.18 (2016) http://fairmetrics.org

https://github.com/FAIRMetrics/Metrics/blob/master/ALL.pdf



DANS-KNAW is one of worldwide leaders in FAIR Data (FAIRsFAIR)

### Standing on the Shoulders of Giants: infrastructure







Horizon 2020 European Union Funding for Research & Innovation

Type of action & funding: Research and Innovation action (INFRAEOSC-04-2018)

Partners: 47 (20 beneficiaries + 27 LTPs) SH ESFRI Landmarks and Projects & international SSH data infrastructures Duration: 40 months (January 2019 – 30 April 2022) Duration: 40 months (January 2019 – 30 April 2022) Duration: 40 months (January 2019 – 30 April 2022)

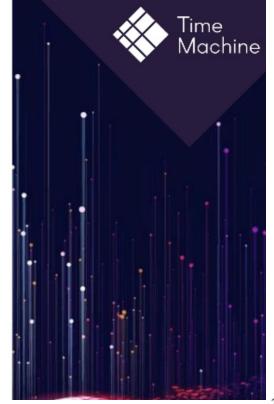
#### **Objectives:**

- · creating the social sciences and humanities (SSH) part of European Open Science Cloud (EOSC)
- maximising re-use through Open Science and FAIR principles (standards, common catalogue, access control, semantic techniques, training)
- · interconnecting existing and new infrastructures (clustered cloud infrastructure)
- · establishing appropriate governance model for SSH-EOSC

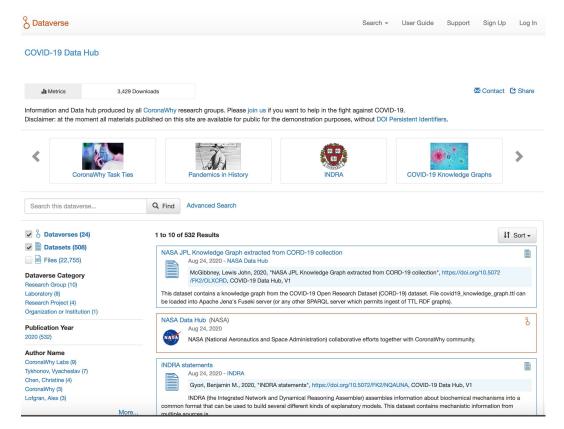
### Standing on the Shoulders of Giants: Big Data of the Past

# Time Machine is ...

- An international collaboration to bring 5000 years of European history to life
- Digitising millions of historical documents, painting and monuments
- The largest computer simulation ever developed
- An open access, interactive resource



## Dataverse as data integration point



- Available as a service for the community from April, 2020
  - Used by CoronaWhy vertical teams for the data exchange and share
- Intended to help researchers to make their data FAIR
- One of the biggest COVID-19 data archives in the world with 700k files
- New teams are getting own data containers and can reuse data collected and produced by others

#### http://datasets.coronawhy.org

## Dataset from CoronaWhy vertical teams

S Dataverse

Search - User Guide Support Sign Up Log In



CoronaWhy Task Risk (CoronaWhy)

COVID-19 Data Hub > CoronaWhy Task Risk >

### COVID-19 risk factors

Cite Dataset -



Mayya Lihovodov; Pranjalya Tiwari; Ansun Sujoe; Guillermo Blanco; Iason Konstantinidis; Kriti Mahajan; Robbie Edwards; Vijay Daita; Michael Wang; Lukasz Gagala; Brandon Eychaner; Mohammad Tanweer; Anrew Wood; Kevin Lee; Samtha Reddy; Mark Koranda; Ruslan Ollinyk, MD; Mike Honey; Randall Brown, MD; Artur Kiulian, 2020, "COVID-19 risk factors", https://doi.org/10.5072/FK2/3O2LV6, COVID-19 Data Hub, V1

Learn about Data Citation Standards.

Access Dataset -				
Contact Owner	Share			
Dataset Metrics 📀				
184 Downloads <table-cell></table-cell>				

Description 🔞

A major topic of interest among researchers is the study of the various risk factors related to COVID-19. A risk factor is anything that increases the chance of being infected, or affects the severity or the survival outcome of the infection. Many of the papers in the dataset are studies on the severity and outcome of the infection, without, however, any systematic documentation that would be easily searchable.

The focus of this study is to extract and present in a meaningful and easily accessible way scientific papers that are related to risk factors associated with viral diseases through a procedure that can be automated as much as possible.

At the current stage, a semi-automated approach is implemented using manual review of retrieved papers. It is important to note that through the proposed procedure a small subset of papers is manually reviewed, the ones that are identified as most probable to be relevant to a specific risk factor. This brings the volume of papers for review down to less than 100-200 instead of multiple thousands, rendering the review task feasible in much shorter timeframes.

Also, at the current stage the paper extraction is limited to the following factors:

Environmental: Pollution, Population Density, Humidity, Temperature Comorbidity: Heart diseases Demographics: Senior age Lifestyle: Smoking The above risk factors were identified as being the most important by the medical community. An extensive list of risk factors is provided under section 4 below and is subject of a future extension of this study.



## COVID-19 data files verification

8	Dataverse	Add Data 👻	Search -	User Guide	Support	Sign Up	Log In
	Description Image: coronavirus         Subject Image: Medicine, Health and Life Sciences         Files       Metadata         Terms       Versions						
	Change View Table Tree						
	Search this dataset Q Find						
	Filter by File Type: All + Access: All + File Tag: All +					It so	rt <del>+</del>
	1 to 10 of 17 Files					<b>⊥</b> Downlo	bad
	age-distribution-died-and-survivors.xlsx data/nospitalized/age-distribution-died-and-survivors.xlsx/ MS Excel Spreadsheet - 5.0 KB - May 30, 2020 - 0 Downloads MD5: 7343b286eat69ce86fac26e1a02342c1 Data snapshot from https://aw.githubusercontent.com/Sikerdebaard /dutchcovid19data/mostpitalcad/age-distribution-died-and-survivors.xlsx patients_deceased_dutchcovid19data_age_group_patients_recovered					Ł Downlo	bad
	age-distribution-status.xlsx data/nospitalized/age-distribution-status.xlsx/ MS Excel Spreadsheet - 5.1 KB - May 30, 2020 - 0 Downloads MD5: ea90cd071 e3597748ec185b19J956cc Data snapshot from https://raw.githubusercontent.com/Sikerdebaard /dutchcovid19data/master/data/hospitalized/age-distribution-status.xlsx patients_deceased_dutchcovid19data_patients_in_hospital_age_group patients_recovered					Ł Downlo	bad
	age-distribution-status.xlsx data/age-distribution-status.xlsx/ MS Excel Spreadsheet - 5.1 KB - May 30, 2020 - 0 Downloads MDFs: 9c9146x86b10f0aef2200885b5a4a3 Data snapshot from https://raw.githubusercontent.com/Sikerdebaard //dutchcovid19data/master/data/age-distribution-status.xlsx dutchcovid19data patients_in_hospital recovered_patients patients_in_icu deceased patients _ george					Ł Downlo	bad

We do a verification of every file by importing its contents to dataframe.

All column names (variables) extracted from tabular data available as labels in files metadata

We've enabled Dataverse data previewers to browse through the content of files without download!

We're starting internal challenges to build ML models for the metadata classification

## Dataverse content in Jupyter notebooks

Code	e + Text									~	RAM Disk	🖍 Editing	
Now	read the co	nten	t of first	file to dataframe	9								
	<pre>FILEID=pd<sup>+</sup> fileURL = df = pd.re df.head()</pre>	"%S	/api/ac	ccess/datafile,	<mark>∕%s"</mark> % (BASE_UR	L, FILEID)							
C*	Unname		Risk Factor	Title	Keyword/Ngram	No of keyword occurence in Paper	paper_id	URL	Sentences	Authors	Correlation	Design Methodology	
	0	0	age	Coronavirus-like particles in nonhuman primate	['older age group']	1	3cf9a172522a7db0df9e436029707bb6e3e0ff8c	['https://www.ncbi.nlm.nih.gov/pmc/articles/PM	['It might be assumed that coronaviruses are n	['Smith, G. C.; Lester, T. L.; Heberling, R. L	It might be assumed that coronaviruses are not	NaN	
	1	1	age	Estimates of the severity of coronavirus disea	['60 years and over', 'older age group']	7	ac2a1ba62fdf52eb276bf42b22ed3d927b5330b1	['https://doi.org/10.1016/s1473- 3099(20)30243	['Reported cases in Wuhan were more frequent i	['Verity, Robert; Okell, Lucy C; Dorigatti, II	Reported cases in Wuhan were more frequent in	In cases reported outside of mainland China ,	
	2	2	age	Infections in travellers returning to Turkey f	['65 years old']	3	f33e3be8c6ec1d348cf8983037dcf8adb25e7f94	['https://www.ncbi.nlm.nih.gov/pmc/articles/PM	['Seventy four (40 %) of them were ≥ 65 years	['Erdem, H.; Ak, O.; Elaldi, N.; Demirdal, T.;	A total of 185 Turkish patients were recruited	NaN	
	3	3	age	The use of corticosteroid as treatment in SARS	['patients older than']	1	5215440ec7a22706195be3c615e0ed2e940e4945	['https://doi.org/10.1016/j.jinf.2004.09.008',	['A total of 80 patients older than 18 years 0	['Auyeung, Tung Wai; Lee, Jenny S.W.; Lai, Win	NaN	NaN	
	4	4	age	Burden, seasonal pattern and symptomatology	['older age group']	5	0957f96f8188f65cc145464dc7882abd259e0f5f	['https://doi.org/10.1016/j.cmi.2015.05.027',	['On comparison of the two age groups ,	['Wei, L.; Chan, K H.; Ip, D.K.M.; Fang,	On comparison of the two age groups, viral	NaN	

Source: Dataverse examples on Google Colabs

## **COVID-19 Data Crowdsourcing**

#### Dataset in CoronaWhy Dataverse #579

New issue

en k-goncharova opened this issue 2 days ago · 4 comments

k-goncharova commented 2 days ago	c		Assignees No one assigned	
Hello,Your dataset was added to CoronaWhy (https://www.coronawhy.org/) Data Lake or as a piece of common COVID-19 dataframe https://datasets.coronawhy.org/dataset.xh persistentId=doi:10.5072/FK2/A20BEO? Would you be willing to help with maintenance of your dataset in Dataverse, e.g. adding	itml?	verse	Labels None yet	
relevant metadata and keeping the dataset up-to-date? That will help to make the data and accessible for medical science community.	-	lable	Projects None yet	
swsoyee commented 2 days ago	ier 😳	•••	Milestone No milestone	
Hi, @k-goncharova Sure, I will keep updating my dataset, and what should I do in Dataverse?			Linked pull requests Successfully merging may close this issue.	a pull request
k-goncharova commented 2 days ago	ior 😳		None yet	
Great, thank you. Please register in CoronaWhy Dataverse https://datasets.coronawhy.ogive you the Dataset creator permissions to your dataset. Then please add relevant me			Notifications	Customize
description and keywords to your dataset.	lauala	-	🗘 Subs	cribe
			You're not receiving n this thread.	otifications from
swsoyee commented 2 days ago	er 😳	•••	2 participants	
Okay, my user's name is swsoyee . I'm a little busy these days, so the progress maybe slow, please forgive me.			<b>(19)</b>	

CoronaWhy data management team does does the review of all harvested datasets and try to identify the important data.

We're approaching github owners by creating issues in their repos and inviting them to help us.

More than 20% of data owners joining CoronaWhy community or interested to curate their datasets.

Bottom-up data collection works!

## Challenge of data integration and various ontologies

CORD-19 collection processing with NLP pipeline:

- manual **annotation** and **labelling** of COVID-19 related papers
- automatic entity extraction and classification of text fragments
- statements extraction and curation
- linking papers to specific research questions with **relationships** extraction

Dataverse Data Lake streaming COVID-19 datasets from various sources:

- medical data
- socio-economic Data
- political data and statistics

#### The top five global concerns

55%	Coronavirus (Covid-19)
42%	Unemployment
31%	Poverty and social inequality
25%	Healthcare
24%	Financial/Political corruption

Research among adults aged 16-64 in 27 participating countries. c. 19,000 per month. (May 2020). Source: Global Advisor • Get the data • Created with Datawrapper

## The importance of standards and ontologies

Generic controlled vocabularies to link metadata in the bibliographic collections are well known: ORCID, GRID, GeoNames, Getty

Medical knowledge graphs powered by:

- Biological Expression Language (BEL)
- Medical Subject Headings (MeSH®) by U.S. National Library of Medicine (NIH)
- Wikidata (Open ontology) Wikipedia

Integration based on metadata standards:

• MARC21, Dublin Core (DC), Data Documentation Initiative (DDI)

## **Biological Expression Language (BEL)**

## **BEL Commons 3.0 Preview**

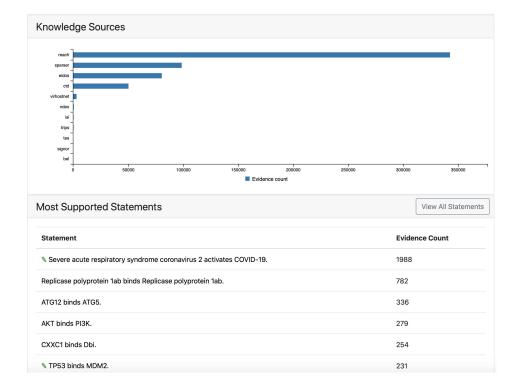
An environment for **curating**, **validating**, and **exploring** knowledge assemblies encoded in Biological Expression Language (BEL) to support **elucidating** disease-specific, mechanistic insight.



If you find BEL Commons useful in your work, please consider citing: Hoyt, C. T., Domingo-Fernández, D., & Hofmann-Apitius, M. (2018). BEL Commons: an environment for exploration and analysis of networks encoded in Biological Expression Language. *Database*, 2018(3), 1–11.

BEL was integrated in CoronaWhy infrastructure in April, 2020

## Statements extraction with INDRA



"INDRA (Integrated Network and Dynamical Reasoning Assembler) is an automated model assembly system, originally developed for molecular systems biology and currently being generalized to other domains."

Developed as a part of Harvard Program in Therapeutic Science and the Laboratory of Systems Pharmacology at Harvard Medical School.

http://indra.bio

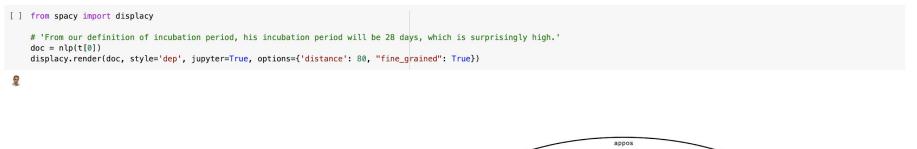
### Source: <u>EMMAA</u> (Ecosystem of Machine-maintained Models with Automated Assembly)

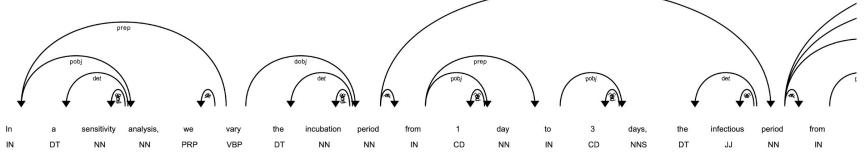
## Knowledge Graph curation in INDRA

Enector	activates	transcription, DNA-templated.	0/50 JSON
Phenob	arbital inc	reases the amount of CYP3A4.	0/50 JSON
Oseltan	nivir inhibi	ts Influenza, Human.	0/50 JSON
Arg-Val	activates	Asthma.	49/49 JSON
N reach		nknown if <b>RV</b> induces the development of wheeze and <b>asthma</b> or if <b>asthma</b> tics are more to <b>RV</b> infection.	18234348
<ul> <li>reach</li> <li>Correct</li> <li>Entity</li> <li>Ground</li> </ul>	ct Boundaries	nouse model of RV-induced asthma exacerbation. Optional description (240 chars)	24278777
<ul> <li>No Rel Wrong Activity Polarity</li> </ul>	lation Relation y vs. Amount y	e of immune responses as well as differential regulation of different innate and adaptive has been implicated in the increased susceptibility of asthmatics to RV and in RV - a and exacerbations.	18234348
Hypoti Agent	Conditions cation Site	th acute <b>RV</b> -induced <b>asthma</b> Wark et al., found that increased serum IP-10 levels but IR-8 was specifically associated with infection and correlated with the degree of ction (Wark et al., 2007).	18234348
♥ reach	(b)A mouse	model of RV-induced asthma exacerbation.	24278777
N reach		e the most common triggers of estimes exacerbations, it needs to be determined if 4 and IL-13 could be useful in preventing experimental RV-induced exacerbation of 50].	27088397
reach     r		igators have reported that RV-C caused more serious illness, especially wheezing and n of asthms, in some populations5, 9, 10, 11, 12, 13 compared with illnesses caused by RV	31389049

## Advanced Text Analysis (NLP pipeline)

We need a good understanding of all domain specific texts to make right statements:





Source: D.Shlepakov, How to Build Knowledge Graph, notebook

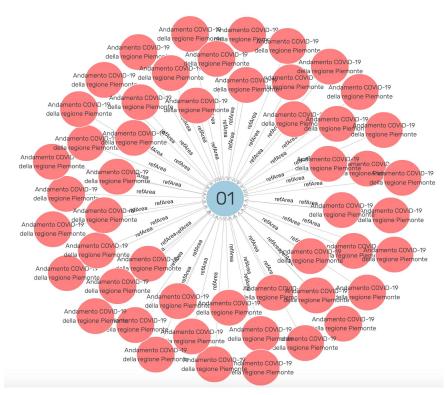
## Building domain specific knowledge graphs

- We're collecting all possible COVID-19 data and archiving in our Dataverse
- Looking for various related controlled vocabularies and ontologies
- Building and reusing conversion pipelines to get all data values linked in RDF format

<http://www.protezionecivile.gov.it/dataset/covid19/national-trend/observations/20200224> a gb:Observation ; rdfs:label "Andamento nazionale di giorno 24/02/2020"^^xsd:string ; gb:dataset <http://www.protezionecivile.gov.it/dataset/covid19/national-trend> ; sdmx-dimension:refArea <https://w3id.org/italia/controlled-vocabulary/territorial-classifications/countries/italy/ITA> sdmx-dimension:refTime "2020-02-24"^^xsd:date ; dpc:deads "7"^^xsd:int ; dpc:healed "1"^^xsd:int ; dpc:homeIsolation "94"^^xsd:int ; dpc:hospitalizedWithSymptoms "101"^^xsd:int ; dpc:intensiveCare "26"^^xsd:int ; dpc:newPositive "221"^^xsd:int ; dpc:swabs "4324"^^xsd:int ; dpc:totalCases "229"^^xsd:int ; dpc:totalHospitalized "127"^^xsd:int ; dpc:totalPositive "221"^^xsd:int ; dpc:totalPositiveVariation "0"^^xsd:int .

The ultimate goal is to automate the process of the Knowledge extraction by using the latest developments in Artificial Intelligence and Deep Learning.

## Visual graph of COVID-19 dataset



### Andamento COVID-19 della regione Piemonte 🔗

Andamento COVID-19 della regione Piemonte

Types:

qb:Observation

#### RDF rank:

0

Q Search instance properties

sdmx-dimension:refTime 2020-03-12

dpc:deads 26

dpc:healed

dpc:homelsolation
89

dpc:hospitalizedWithSymptoms 368

dpc:intensiveCare 97

dpc:newPositive **79** 

dpc:swabs 2879

#### Source: CoronaWhy GraphDB

## SPARQL endpoint for CoronaWhy KG

Query 眯

+

0	https://sparql.labs.coronawhy.org/sparql
1	PREFIX rdf: <http: 02="" 1999="" 22-rdf-syntax-ns#="" www.w3.org=""></http:>
2	PREFIX rdfs: <http: 01="" 2000="" rdf-schema#="" www.w3.org=""></http:>
3	PREFIX mesh: <http: id.nlm.nih.gov="" mesh=""></http:>
4	PREFIX grid: <https: institutes="" www.grid.ac=""></https:>
5	PREFIX bf: <http: bibframe="" id.loc.gov="" ontologies=""></http:>
e	PREFIX loc: <http: bibframe="" id.loc.gov="" ontologies="" source=""></http:>
7	PREFIX mads: <http: mads="" rdf="" v1#="" www.loc.gov=""></http:>
8	
9	<pre>select * from <http: coronawhy.org=""></http:> where</pre>
10	~ (
11	<pre>?cord rdfs:label "United States" .</pre>
12	mesh:C0243052 ?a ?b
13	

tesponse 🖻 Gallery 陆 Chart 🍳 Geo 🕼 Geo-3D 🎣 Geo events 🗖 Pivot 🚍 Timeline 10000 results in 3.051 seconds		Filter query results Page size: 50 🖸 🛓 😧
cord	¢ a	♦
ufind.apps.coronawhy.org/vufind/Record/03bwk538#Place651-7>	rdf:type	bf:Topic
ufind.apps.coronawhy.org/vufind/Record/094d0rn6#Place651-7>	rdf:type	bf:Topic
ufind.apps.coronawhy.org/vufind/Record/2egeyh0j#Place651-7>	rdf:type	bf:Topic
ufind.apps.coronawhy.org/vufind/Record/3p2rqavh#Place651-7>	rdf:type	bf:Topic
ufind.apps.coronawhy.org/vufind/Record/5kapn32k#Place651-7>	rdf:type	bf:Topic
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ufind.apps.coronawhy.org/vufind/Record/7bkf7wrs#Place651-7>	rdf:type	bf:Topic
ufind.apps.coronawhy.org/vufind/Record/7hcr406k#Place651-7>	rdf:type	bf:Topic
ufind.apps.coronawhy.org/vufind/Record/8pd6jdb5#Place651-7>	rdf:type	bf:Topic
	cord ufind.apps.coronawhy.org/vufind/Record/03bwk538#Place651-7> ufind.apps.coronawhy.org/vufind/Record/094d0rn6#Place651-7> ufind.apps.coronawhy.org/vufind/Record/2egeyh0j#Place651-7> ufind.apps.coronawhy.org/vufind/Record/3p2rqavh#Place651-7> ufind.apps.coronawhy.org/vufind/Record/3p2rqavh#Place651-7> ufind.apps.coronawhy.org/vufind/Record/5kapn32k#Place651-7> ufind.apps.coronawhy.org/vufind/Record/6g55l35h#Place651-7> ufind.apps.coronawhy.org/vufind/Record/6g55l35h#Place651-7> ufind.apps.coronawhy.org/vufind/Record/6g55l35h#Place651-7> ufind.apps.coronawhy.org/vufind/Record/7bkf7wrs#Place651-7>	cordaufind.apps.coronawhy.org/vufind/Record/03bwk538#Place651-7>rdf:typeufind.apps.coronawhy.org/vufind/Record/094d0rn6#Place651-7>rdf:typeufind.apps.coronawhy.org/vufind/Record/2egeyh0j#Place651-7>rdf:typeufind.apps.coronawhy.org/vufind/Record/3p2rqavh#Place651-7>rdf:typeufind.apps.coronawhy.org/vufind/Record/3p2rqavh#Place651-7>rdf:typeufind.apps.coronawhy.org/vufind/Record/3p2rqavh#Place651-7>rdf:typeufind.apps.coronawhy.org/vufind/Record/5kapn32k#Place651-7>rdf:typeufind.apps.coronawhy.org/vufind/Record/6g55l35h#Place651-7>rdf:typeufind.apps.coronawhy.org/vufind/Record/6g55l35h#Place651-7>rdf:typeufind.apps.coronawhy.org/vufind/Record/7bkf/Ywrs#Place651-7>rdf:typeufind.apps.coronawhy.org/vufind/Record/7bkf/Ywrs#Place651-7>rdf:typeufind.apps.coronawhy.org/vufind/Record/7bkf/Ywrs#Place651-7>rdf:typeufind.apps.coronawhy.org/vufind/Record/7bkf/Ywrs#Place651-7>rdf:typeufind.apps.coronawhy.org/vufind/Record/7bkf/Ywrs#Place651-7>rdf:typeufind.apps.coronawhy.org/vufind/Record/7bkf/Ywrs#Place651-7>rdf:typeufind.apps.coronawhy.org/vufind/Record/7bkf/Ywrs#Place651-7>rdf:typeufind.apps.coronawhy.org/vufind/Record/7bkf/Ymrs#Place651-7>rdf:typeufind.apps.coronawhy.org/vufind/Record/7bkf/Ymrs#Place651-7>rdf:typeufind.apps.coronawhy.org/vufind/Record/7bkf/Ymrs#Place651-7>rdf:typeufind.apps.coronawhy.org/vufind/Record/7bkf/Ymrs#Place651-7>rdf:typeufind.apps.coronawhy.org/vufind/Record/7bkf/Ymrs#Place651-7>rdf:typeufind.apps.c

### Source: <u>YASGUI</u>

## Do you know a lot of people that can use SPARQL?

PubChemRDF Use Cases: SPARQL query



Q: What adverse effects of chemicals that are oral acute toxic according to GHS statement have been reported in PubMed literature, annotated by MeSH indexing?

PREFIX cito: <http://purl.org/spar/cito/>
PREFIX fabio: <http://purl.org/spar/fabio/>
PREFIX skos: <http://www.w3.org/2004/02/skos/core#>
PREFIX sio: <http://semanticscience.org/resource/>
PREFIX dcterms: <http://purl.org/dc/terms/>
PREFIX meshv: <http://id.nlm.nih.gov/mesh/vocab#>
PREFIX mesh: <http://id.nlm.nih.gov/mesh/>

select distinct ?disease ?diseaselabel

#### where {

?compound sio:has-attribute/dcterms:subject/skos:broader/concept:Acute\_Toxicity\_Oral .

?syno sio:is-attribute-of ?compound .

?syno dcterms:subject ?meshconcept .

?pmid cito:discusses ?meshconcept .

?pmid fabio:hasSubjectTerm ?DQpair .

?DQpair meshv:hasQualifier mesh:Q000009 .

?pmid cito:discusses ?disease .

?disease rdf:type meshv:SCR\_Disease .

?disease rdfs:label ?diseaselabel .

Source: <u>Semantic annotation</u> of the Laboratory Chemical Safety Summary in PubChem

## **CLARIAH** conclusions



<sup>\*\*</sup>By developing these decentralised, yet controlled Knowledge Graph development practices we have contributed to increasing interoperability in the humanities and enabling new research opportunities to a wide range of scholars. However, we observe that users without Semantic Web knowledge find these technologies hard to use, and place high value in end-user tools that enable engagement. Therefore, for the future we emphasise the importance of tools to specifically target the goals of concrete communities – in our case, the analytical and quantitative answering of humanities research questions for humanities scholars. In this sense, usability is not just important in a tool context; in our view, we need to empower users in deciding under what models these tools operate." (CLARIAH: Enabling Interoperability Between Humanities Disciplines with Ontologies)

Chicken-egg problem: users are building tools without data models and ontologies but in reality they need to build a knowledge graph with common ontologies first!

## Linked Data integration challenges

- datasets are very heterogeneous and multilingual
- data usually lacks sufficient data quality control



Word Wide Web Consortium

- data providers using different modeling schemas and styles
- linked data cleansing and versioning is very difficult to track and maintain properly, web resources aren't persistent
- even modern data repositories providing only metadata records describing data without giving access to individual data items stored in files
- difficult to assign and manually keep up-to-date entity relationships in knowledge graph

CoronaWhy has too much information streams that seems to be impossible to integrate and give back to COVID-19 researchers. So, do we have a solution?

## Bibliographic Framework (BIBFRAME) as a Web of Data

"The Library of Congress officially launched its Bibliographic Framework Initiative in May 2011. The Initiative aims to re-envision and, in the long run, implement a new bibliographic environment for libraries that makes "the network" central and makes **interconnectedness commonplace**."

"Instead of thousands of catalogers repeatedly describing the same resources, the effort of one cataloger could be shared with many." (<u>Source</u>)

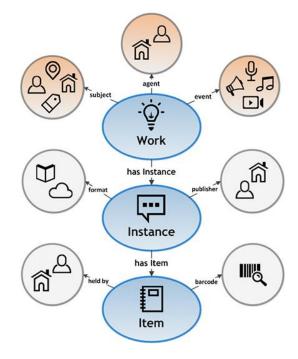
In 2019 BIBFRAME 2.0, the Library of Congress Pilot, was announced.

Let's take a journey and move from domain specific ontology to bibliographic!

## **BIBFRAME 2.0 concepts**

- **Work**. The highest level of abstraction, a Work, in the BIBFRAME context, reflects the conceptual essence of the cataloged resource: authors, languages, and what it is about (subjects).
- **Instance**. A Work may have one or more individual, material embodiments, for example, a particular published form. These are Instances of the Work. An Instance reflects information such as its publisher, place and date of publication, and format.
- **Item.** An item is an actual copy (physical or electronic) of an Instance. It reflects information such as its location (physical or virtual), shelf mark, and barcode.
- **Agents**: Agents are people, organizations, jurisdictions, etc., associated with a Work or Instance through roles such as author, editor, artist, photographer, composer, illustrator, etc.
- **Subjects**: A Work might be "about" one or more concepts. Such a concept is said to be a "subject" of the Work. Concepts that may be subjects include topics, places, temporal expressions, events, works, instances, items, agents, etc.
- **Events**: Occurrences, the recording of which may be the content of a Work.

### Source: the Library of Congress



## MARC as a foundation of the structured Data Hub



1999 Edition Update No. 1 (October 2000) through Update No. 30 (May 2020)

This online publication provides access to both the full and concise versions of the MARC 21 Format for Bibliographic Data. The "full" bibliographic format contains detailed descriptions of every data element, along with examples, input conventions, and history sections. The "concise" bibliographic format contains abridged descriptions of every data element, along with examples. The full and concise versions are identified in the header of each field description.

Changes to the MARC 21 Format for Bibliographic Data that resulted from Update No. 30 (May 2020) are displayed in red print. The date located in the header of the full version of each field indicates the last month and year of update.

#### Table of Contents

- Introduction [Full | Concise]
- Format Summary
- Leader [Full | Concise]
- <u>Directory</u>
- <u>00X: Control Fields</u>
- 01X-09X: Numbers and Code Fields
- Heading Fields General Information
- <u>1XX: Main Entry Fields</u>
- 20X-24X: Title and Title-Related Fields
   20X-24X: Fields
- <u>25X-28X: Edition, Imprint, Etc. Fields</u>
  3XX: Physical Description, Etc. Fields
- <u>3XX: Physical Description, Etc. Field</u>
   <u>4XX: Series Statement Fields</u>
- 4XX: Series Statement I
   5XX: Note Fields
- 6XX: Subject Access Fields
- 70X-75X: Added Entry Fields
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- 80X-83X: Series Added Entry Fields
- <u>841-88X: Holdings, Location, Alternate Graphics, Etc. Fields</u>
- · Appendix A: Control Subfields
- Appendix B: Full Level Record Examples
- <u>Appendix C: Minimal Level Record Examples</u>
- <u>Appendix D: Multiscript Records</u>
- Appendix E: Alphabetical List of Ambiguous Headings
- Appendix F: Initial Definite and Indefinite Articles
- <u>Appendix G: Format Changes for Update No. 30 (May 2020)</u>
- Appendix H: Local Data Elements

MARC standard was developed in the 1960s to create records that could be read by computers and shared among libraries. The term MARC is an abbreviation for MAchine Readable Cataloging.

The **MARC 21** bibliographic format was created for the international community. It's very rich, with **more** than 2,000 data elements defined!

It's identified by its ISO (International Standards Organization) number: ISO 2709

### Source: the Library of Congress, USA

## How to integrate data in the common KG?

- Use MARC 21 as a basis for all bibliographic and authority records
- All controlled vocabularies should be expressed in MARC 21 format for Authority Data, we need to build an authority linking process with the "human in the loop" approach that will allow to verify AI predicted links.
- Different MARC 21 fields could be linked to the different ontologies and/or even interlinked. For example, we can get some entities linked to both MeSH and Wikidata in the same bibliographic record to increase the interoperability of the Knowledge Graph.
- Every CORD-19 paper can get a metadata enrichment provided by any research team working on the NLP extraction of entities, relations or linking CV together.

# COVID-19 paper in MARC 21 representation

Holdings	Des	cription	n !	Comments Similar Items Staff View
LEAD	DER	0603	2cas a	2201165 4500
	001	o32e	9001	
	800	/////ca	as/////c	cc ////////chi///
	245	1	0	a The Transformation of Enterovirus Replication Structures: a Three-Dimensional Study of Single- and Double-Membrane Compartments
	856	4	0	<b> u</b> https://doi.org/10.1128/mbio.00166-11
	651			x coronavirus
	651		4	a Netherlands
	370			le Leiden, Netherlands
	852			a Department of Medical Microbiology, Molecular Virology Laboratory, Center of Infectious Diseases, Leiden University Medical Center, Leiden, The Netherlands
	650	1	2	a Act Relationship Type - transformation  x C1554215
	650	1	2	a Three-dimensional x C0450363
	650	1	2	a Induce (action) x C0205263
	650	1	2	<b> a</b> Membrane <b> x</b> C0596901
	650	1	2	<b> a</b> Cells <b> x</b> C0007634
	650	1	2	a Cell Microenvironment  x C1707328
	650	1	2	<b> a</b> RNA, Viral <b> x</b> C0035736
	650	1	2	Ja Anabolism Jx C0220781
	650	1	2	a structure  x C0678594
	650	1	2	a Enterovirus  x C0014383
	650	1	2	a Family Picornaviridae  x C0031886
	650	1	2	la Tissue membrane  x C0025255
	650	1	2	a Architecture as Topic  x C0003737

Structure of the bibliographic record:

- authority records contain information about authors and affiliation
- Medical entities extracted by NLP pipeline interlinked in 650x fields
- part of metadata fields generated and filled by Machine Learning models, part contributed by human experts
- provenance information kept in 833x fields indicating fully or partially machine-generated records
- Relations between entities stored in 730x fields

### Source: CoronaWhy CORD-19 portal

## Vufind discovery tool for libraries powered by MARC 21

CORONAV	VHY		Home	Daily Progress	Solutions 🗸	Data 🗸	Team JOIN	THE FIGHT!
Reset Filters Lang	All Fields 🗘 guage: English 🖾	Q Find Advance	<u>əd</u>				₽ <u>Login</u>	<u>Language</u> -
Search Results								
Suggested Topics with coronavirus 203,451	_	<u>COVID-19</u> 133,230	<u>C1880229</u> 4,507	DICOM Study 4,50		Nar	row Sea	arch
C0086418 4,317	Homo sapiens 4,317	more				Institut	ion	
Showing 1 - 20 results	of <b>203,461</b> for search ",	query time: 0.20s		Sort	Relevance	MyInstit	ution	203,461
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AVAILABLE	Pérez, I., Barragán Se	rrano, C., Álvarez Peña,	E., Díaz Domínguez,	<u>J.</u>		Univers	ity of Hong Kong	744

Source: CoronaWhy VuFind

# Landing page of publications from CORD-19

• CORONA <b>WHY</b>	Home	Daily Progress	Solutions 🗸	Data 🗸	Team	JOIN THE FIGHT!
All Fields						
Reset Filters Language: English 🛛 Suggested Topics: C1880229	9 🗙					
Search / The Transformation of Enterovi / Holdings						
★ Cite this □ Text this ■ Email this ➡ Print C <sup>*</sup> Export Record						
The Transformation of Enterovir	rus Replic	ation Stru	ctures: a	0.		14



#### The Transformation of Enterovirus Replication Structures: a Three-Dimensional Study of Single- and Double-Membrane Compartments

All positive-strand RNA viruses induce membrane structures in their host cells which are thought to serve as suitable microenvironments for viral RNA synthesis. The structures induced by enteroviruses, which are members of the family Picornaviridae, have so far been described as either single- or do...

#### Full description

		Pul
Main Authors:	Limpens, Ronald W. A. L., van der Schaar, Hilde M., Kumar, Darshan, Koster, Abraham J., Snijder, Eric J., van Kuppeveld, Frank J. M., Bårcena, Montserrat	and Str
Corporate Authors:	Leiden University Medical Center, Radboud University Nijmegen Medical Centre	Vir by:
Format:	Serial	Pul
Language:	English	Pos
Published:	mBio 2011	Viri by:
Subjects:	Act Relationship Type - transformation > C1554215 Three-dimensional > C0450363 Induce (action) > C0205263 Membrane > C0556901 Cells > C0007634 Cell Microenvironment > C1707328 RNA. Viral > C0035736	Pul Sei Co by: Pul
	Anabolism > C0220781	

### Source: CoronaWhy VuFind

#### **Similar Items**

SARS-Coronavi Supported by a Re Network of Modifie Reticulum by: Knoops, Kèvin, Published: (2008)	ticulovesicular d Endoplasmic
Three-Dimensionand Biogenesis of Structures Associa Virus Replication by: Romero-Brey, I Published: (2012)	<u>Membrane</u> ted with Hepatitis C
Packaging of Ge Positive-Sense Sin Viruses: A Comple by: Comas-Garcia, Published: (2019)	gle-Stranded RNA x Story

Role of Cellular Lipids in Positive-Sense RNA Virus Replication Complex Assembly and Function by: Stapleford, Kenneth A., et al. Published: (2010)

## **CORD-19 collection in BIBFRAME 2.0**

```
<br/><bf:Content rdf:about="http://id.loc.gov/vocabulary/contentTypes/txt">
         <rdfs:label>text</rdfs:label>
    </bf:Content>
</bf:content>
<bf:language>
    <bf:Language rdf:about="http://id.loc.gov/vocabulary/languages/%2Fch"/>
</bf:language>
<rdfs:label>The SARS Coronavirus S Glycoprotein Receptor Binding Domain: Fine Mapping and Functional Characterization</rdfs:label>
<bf:title>
    <bf:Title>
         <rdfs:label>The SARS Coronavirus S Glycoprotein Receptor Binding Domain: Fine Mapping and Functional Characterization</rdfs:label>
         <br/>

         <br/>
shf:mainTitle>The SARS Coronavirus S Glycoprotein Receptor Binding Domain: Fine Mapping and Functional Characterization</bf:mainTitle>
    </bf:Title>
</bf:title>
<bf:subject>
    <br/>

         <rdfs:label>coronavirus</rdfs:label>
         <madsrdf:authoritativeLabel>coronavirus</madsrdf:authoritativeLabel>
         <madsrdf:componentList rdf:parseType="Collection">
              <madsrdf:Topic>
                   <madsrdf:authoritativeLabel>coronavirus</madsrdf:authoritativeLabel>
              </madsrdf:Topic>
         </madsrdf:componentList>
    </bf:Place>
</bf:subject>
<bf:subject>
    <br/>bf:Place rdf:about="http://vufind.apps.coronawhy.org/vufind/Record/ofx0hvvs#Place651-7">
         <rdf:type rdf:resource="http://www.loc.gov/mads/rdf/v1#Geographic"/>
         <rdfs:label>United States</rdfs:label>
         <madsrdf:authoritativeLabel>United States</madsrdf:authoritativeLabel>
    </bf:Place>
</bf:subject>
<bf:subject>
    <bf:Topic rdf:about="http://id.nlm.nih.gov/mesh/C1175175">
         <rdf:type rdf:resource="http://www.loc.gov/mads/rdf/v1#ComplexSubject"/>
         <rdfs:label>Severe Acute Respiratory Syndrome--C1175175</rdfs:label>
         <madsrdf:authoritativeLabel>Severe Acute Respiratory Syndrome--C1175175</madsrdf:authoritativeLabel>
         <madsrdf:componentList rdf:parseType="Collection">
              <madsrdf:Topic>
                   <madsrdf:authoritativeLabel>Severe Acute Respiratory Syndrome</madsrdf:authoritativeLabel>
              </madsrdf:Topic>
              <madsrdf:Topic>
                    <madsrdf:authoritativeLabel>C1175175</madsrdf:authoritativeLabel>
              </madsrdf:Topic>
         </madsrdf:componentList>
         <bf:source>
              <bf:Source>
                    <bf:code>mesh</bf:code>
              </bf:Source>
         </bf:source>
    </bf:Topic>
</bf:subject>
<bf:subject>
    <br/><bf:Topic rdf:about="http://id.nlm.nih.gov/mesh/C1283195">
         <rdf:type rdf:resource="http://www.loc.gov/mads/rdf/v1#ComplexSubject"/>
         <rdfs:label>Mapping (action)--C1283195</rdfs:label>
         <madsrdf:authoritativeLabel>Mapping (action)--C1283195</madsrdf:authoritativeLabel>
         <madsrdf:componentList rdf:parseType="Collection">
              <madsrdf:Topic>
                   <madsrdf:authoritativeLabel>Mapping (action)</madsrdf:authoritativeLabel>
              </madsrdf:Topic>
```

## CoronaWhy Graph published as RDF



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COVID-19 Knowledge Graphs (CoronaWhy)

COVID-19 Data Hub > COVID-19 Knowledge Graphs >

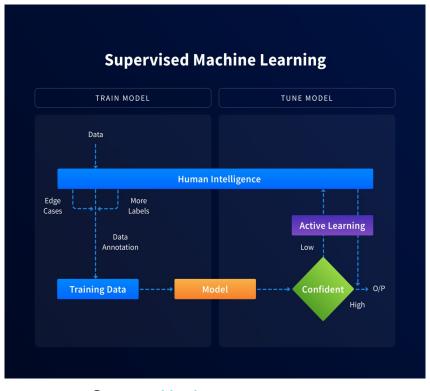
#### CORD-19 collection in RDF using MARC21 ontology

Version 5.3

Wheney, Vyacheslav, 2020, *CORD-19 collection in RDF using MARC21 ontology*, https://doi.org/10.5072/FK2/       Access Dataset *         DebDLV, COVID-19 Data Hub, V5       Learn about Data Cliation Standards.       Image: Contact Owner Ima					
Description ●       A sample from CORD-19 collection published in MARC21 standard and exposed as Resource Description Framework (RDF) for testing purposes. It's a first step to create a Knowledge Graph out of all COVID-19 papers. Sample data linked to: <ul> <li>Medical Subject Headings (MeSH) thesaurus</li> <li>GRID database of affiliations</li> <li>Geonames database of locations</li> </ul> <li>Download all files and put in /tmp/data folder, use isql-v to upload this RDF collection and query it in Virtuoso:         <ul> <li>Id_dir('tmp/data', '*.rdr', 'http://coronawhy.org/); rdf_loader_run (log_enable=&gt;3); checkpoint;</li> <li>Sample SPARQL query to access CoronaWhy COVID-19 Graph: PREFIX rdf: <http: 02="" 1999="" 22-rdf-syntax-ns#="" www.w3.org=""> PREFIX rdf: <http: 02="" 1999="" 22-rdf-syntax-ns#="" www.w3.org=""> PREFIX rdf: <http: 01="" 100="" rdf-schema#="" www.w3.org=""> PREFIX rdf: <http: 01="" 1090="" low.ww.go.org="" rdf-schema#=""> PREFIX rdf: <http: bibframe="" low.ww.go.org="" ontologies=""></http:> PREFIX bf: <http: bibframe="" low.ww.go.org="" ontologies=""></http:> PREFIX bf: <http: bibframe="" low.c.gov="" ontologies=""></http:></http:></http:></http:></http:></li> </ul> </li>			Access Dataset -		
Description ●       A sample from CORD-19 collection published in MARC21 standard and exposed as Resource Description Framework (RDF) for testing purposes. It's a first step to create a Knowledge Graph out of all COVID-19 papers. Sample data linked to: <ul> <li>Medical Subject Headings (MeSH) thesaurus</li> <li>GRID database of affiliations</li> <li>Geonames database of locations</li> </ul> <li>Download all files and put in /tmp/data folder, use isql-v to upload this RDF collection and query it in Virtuoso:         <ul> <li>Id_dir('tmp/data', '*.rdr', 'http://coronawhy.org/); rdf_loader_run (log_enable=&gt;3); checkpoint;</li> <li>Sample SPARQL query to access CoronaWhy COVID-19 Graph: PREFIX rdf: <http: 02="" 1999="" 22-rdf-syntax-ns#="" www.w3.org=""> PREFIX rdf: <http: 02="" 1999="" 22-rdf-syntax-ns#="" www.w3.org=""> PREFIX rdf: <http: 01="" 100="" rdf-schema#="" www.w3.org=""> PREFIX rdf: <http: 01="" 1090="" low.ww.go.org="" rdf-schema#=""> PREFIX rdf: <http: bibframe="" low.ww.go.org="" ontologies=""></http:> PREFIX bf: <http: bibframe="" low.ww.go.org="" ontologies=""></http:> PREFIX bf: <http: bibframe="" low.c.gov="" ontologies=""></http:></http:></http:></http:></http:></li> </ul> </li>		BOSDLV, COVID-19 Data Hub, V5	Contact Owner	Share	
Description ●       A sample from CORD-19 collection published in MARC21 standard and exposed as Resource Description Framework (RDF) for testing purposes. It's a first step to create a Knowledge Graph out of all COVID-19 papers. Sample data linked to: • Medical Subject Headings (MsSH) thesaurus • GRID database of affiliations • Geonames database of locations         Download all files and put in /tmp/data folder, use isql-v to upload this RDF collection and query it in Virtuoso: Id_dir('tmp/data',''.rdf','http://coronawhy.org/); rdf_loader_run (log_enable=>3); checkpoint;         Sample SPARQL query to access CoronaWhy COVID-19 Graph: PREFIX rdf: <http: 02="" 1999="" 22-rdf-syntax-ns#="" www.w3.org=""> PREFIX rdf: <http: 02="" 1999="" 20-rdf-syntax-ns#="" www.w3.org=""> PREFIX rdf: <http: 01="" 1000="" rdf-schema#="" www.w3.org=""> PREFIX rdf: <http: lid.nim.nih.gov="" mesh=""></http:> PREFIX rdf: <http: lid.nim.nih.gov="" mesh=""></http:> PREFIX rdf: <http: lid.nim.nih.gov="" mesh=""></http:> PREFIX bf: <http: bibframe="" lid.oc.gov="" ontologies=""></http:> PREFIX bf: &lt;</http:></http:></http:>		Cite Dataset - Learn about Data Citation Standards.	Dataset Metrics 📀		
<ul> <li>Description Framework (RDF) for testing purposes. It's a first step to create a Knowledge Graph out of all COVID-19 papers. Sample data linked to:</li> <li>Medical Subject Headings (MeSH) thesaurus</li> <li>GRID database of affiliations</li> <li>Geonames database of locations</li> </ul> Download all files and put in /tmp/data folder, use isql-v to upload this RDF collection and query it in Virtuoso: Id_dir('/tmp/data','*.rdf', 'http://coronawhy.org/'); rdf. Joader_run (log_enable=>3); checkpoint; Sample SPARQL query to access CoronaWhy COVID-19 Graph: PREFIX rdf: <http: 02="" 1999="" 22-rdf-syntax-ns#="" www.w3.org=""> PREFIX rdf: <http: di.ord.syntax-ns#=""> PREFIX rdf: <http: di.ord.syntax-ns#=""> PREFIX rdf: <http: di.ord.syntax-ns#=""> PREFIX rdf: <http: id.nim.nih.gov="" mesh=""></http:> PREFIX bf: <http: id.nim.nih.gov="" ords=""></http:> PREFIX bf: <http: bibframe="" id.log.gov="" ontologies=""></http:> PREFIX bf: <http: bibframe="" id.log.gov="" ontologies="" source=""> PREFIX mads: <http: bibframe="" id.log.gov="" ontologies="" source=""></http:></http:></http:></http:></http:></http:></http:></http:></http:></http:></http:></http:></http:></http:></http:></http:></http:></http:></http:>			345 Downloads 😨		
PREFIX rdf: <http: 02="" 1999="" 22-rdf-syntax-ns#="" www.w3.org=""> PREFIX rdfs: <http: 01="" 2000="" trschema#="" www.w3.org=""> PREFIX rdfs: <http: id.nim.nih.gov="" mesh=""></http:> PREFIX grid: <https: institutes="" www.grid.ac=""></https:> PREFIX grid: <https: institutes="" www.grid.ac=""></https:> PREFIX bf: <http: bibframe="" id.loc.gov="" ontologies=""></http:> PREFIX bf: <http: bibframe="" id.loc.gov="" ontologies="" source=""> PREFIX mads: <http: id.loc.gov="" mads="" rdf="" v1#=""></http:></http:></http:></http:>	Description 🕢	Description Framework (RDF) for testing purposes. It's a first step to create a Knowledge Graph out of all COVID-19 papers. Sample data linked to: • Medical Subject Headings (MeSH) thesaurus • GRID database of affiliations • Geonames database of locations Download all files and put in /tmp/data folder, use isql-v to upload this RDF collection and query it in Virtuoso: Id_clint'/tmp/data','*.rdf', 'http://coronawhy.org/'); rdf_joader_run (iog_enable=>3);			
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## Human-in-the-Loop for Machine Learning



"Computers are incredibly fast, accurate and stupid; humans are incredibly slow, inaccurate and brilliant; together they are powerful beyond imagination." Albert Einstein

"A combination of AI and Human Intelligence gives rise to an extremely high level of accuracy and intelligence (Super Intelligence)"

#### Source: <u>Hackernoon.com</u>

## CLARIAH and Network Digital Heritage (NDE) GraphiQL



CoronaWhy is running own instance of <u>NDE on Kubernetes</u> cluster and maintains the support of another ontologies (MeSH, ICD, NDF) available via their SPARQL endpoints!

## If you want to query API:

#### curl

"http://nde.dataverse-dev.coronawhy.org/nde/graphql?query=%20%7B%20terms(match%3A%22COVID%22%2Cdataset%3A%5B%22 wikidata%22%5D)%20%7B%20dataset%20terms%20%7Buri%2C%20altLabel%7D%20%7D%20%7D"



# Increasing Dataverse metadata interoperability

Subject \* 🕄

Keyword 🚱

Vocabulary 🕄	Term 😧	
wikidata	COVID-19	+
Vocabulary URL 🕢		
http://www.wikidata.org/entity/Q8106	389 <sup>.</sup>	
Vocabulary 🕢	Term 😧	
wikidata	covi	+
Vocabulary URL 😧	• COVID-19	
	<ul> <li>COVID-19 pandemic</li> <li>COVID-19 pandemic in India</li> </ul>	
	• Covi	
Citation 🕄	Covi     Covi	
	• SARS-CoV-2	+

Related Publication

External controlled vocabularies support contributed by <u>SSHOC project</u> (data infrastructure for the EOSC)

## Hypothes.is annotations as a peer review service

• 2 •						>	ų
CORONA <b>WHY</b>	н	ome	Hypothesis Test	Daily Progress	Calendar	0	
						•	
	Ensuring global	acces	ss to COVII	D-19 vacci	nes	1	4

AUTHORS: GAVIN YAMEY, MARCO SCHÄFERHOFF, RICHARD HATCHETT, MUHAMMAD PATE, FENG ZHAO, KACI KENNED

The current response to the coronavirus disease 2019 (COVID-19) pandemic involves aggressive implementation of suppressive involves aggressive involves aggressive involves aggressive implementation of suppressive involves aggressive involves aggressive involves as case identification, guarantine and isolation, contact tracing, and social distancing. However, models developed by the In COVID-19 Response Team suggest that "transmission will quickly rebound if interventions are relaxed".1 WHO warns of mu outbreaks of COVID-19 worldwide.2 The development of COVID-19 vaccines that can be used globally is therefore a priority pandemic.

This vaccine effort should be guided by three imperatives: speed, manufacture and deployment at scale, and global access. the World Bank and the Coalition for Epidemic Preparedness Innovations (CEPI), which funds development of epidemic global consultation on these goals.3 This consultation led to the launch of a COVID-19 Vaccine Development Taskforce that how to finance and manufacture vaccines for global access.

CEPI estimates that developing up to three vaccines in the next 12-18 months will require an investment of at least US\$2 2 includes phase 1 clinical trials of eight vaccine candidates, progression of up to six candidates through phase 2 and 3 trials, ( regulatory and quality requirements for at least three vaccines, and enhancing global manufacturing capacity for three vaccir does not include the costs of manufacture or delivery. Progress has been rapid. A phase 1 trial of a vaccine candidate, support National Institutes of Health and CEPI, began on March 16, 2020,5 and 2 days later a clinical trial began in China.6 Clinical t candidates will start soon.

Use of existing financing systems to support this work offers the benefits of speed and lower transaction costs than for not approaches. CEPI is supported by a World Bank financial intermediary fund that brings together public, philanthropic, and p respond to global priorities.7 Through this fund, CEPI can act as a global mechanism for funding vaccine development until licensed or used under emergency use provisions. Mobilising \$2 billion in funding will require funding from all sources. Give health, social, and economic consequences of COVID-19, there is a strong case for all governments to invest in vaccines.

- Q \$ 1 ? 8 ~ Public ~ 5 A F 4tykhonov (edited May 7) May 7 Public However, models developed by the Imperial College COVID-19 Response Team suggest that "transmission will quickly rebound if interventions are relaxed Trasmission to normal life COVID-19 response Imperial College COVID-19 Response Team ち 企 F cchen1111 May 7 @ Public the World Bank Host of a global consultation on vaccine development ふか下 cchen1111 May 7 Public 12-18 months time ふかす
- cchen1111 (edited May 7) May 7 US\$2 billion cost of vaccine development ふかて

Public

- 1. Al pipeline does domain specific entities extraction and ranking of relevant CORD-19 papers.
- 2 Automatic entities and statements will be added, important fragments should be highlighted.
- 3 Human annotators should verify results and validate all statements.

## **Doccano annotation with Machine Learning**

loccano 🛛 😰 Edit Data	Projects	Logout
Search document	1/1	
About 1 results (page 1 of 1) Sort by An atypical RNA pseudoknot stimulator and an upstream attenu	AMINO_ACID       a       CELL       c       CELLULAR_COMPONENT       C-c       CELL_LINE       S-c         CELL_TYPE       C-S-c       CHEBI       h       CHEMICAL       C-h       CL       1       DISEASE       d       DNA       C-d         GENE_OR_GENE_PRODUCT       g       GGP       C-g       GO       S-g       ORGANISM       o       PROTEIN       p         RNA       x       SIMPLE_CHEMICAL       s       SO       C-s       TAXON       t       UMLS       u	
	An atypical RNA pseudoknot * stimulator and an upstream attenuation signal for -1 ribosomal * -1 * ribosomal frameshifting of SARS * SARS coronavirus *. The -1 * -1 * ribosomal frameshifting requires the existence of an in cis RNA slippery sequence * cis RNA * RNA * slippery sequence * and is promoted by a downstream stimulator RNA An atypical RNA pseudoknot * RNA pseudoknot * pseudoknot * with an extra stem forme complementary sequences * complementary sequences * within loop 2 of an H-type pseudoknot * is characterized in the severe acute respiratory syndrome coronavirus coronavirus * (SARS * CoV) genome *. This pseudoknot * can serve as an efficient stimulator for -1 * -1 * frameshifting * in vitro. Mutational * analysis of the extra stem suggests frameshift * efficiency can be modulated via manipulation of the	ed by

#### Source: Doccano Labs

# Building an Operating System for Open Science

CoronaWhy Common Research and Data Infrastructure is distributed and robust enough to be scaled up and reused for other tasks like cancer research

All services are build from Open Source components

Data processed and published in FAIR way, the provenance information is the part of our Data Lake

Data evaluation and credibility is the top priority, we're providing tools for the expert community for the verification of our datasets

The transparency of data and services guarantees the reproducibility of all experiments and get bring new insights in COVID-19 research

## CoronaWhy Common Research and Data Infrastructure

Data preprocessing pipeline implemented on Jupyter notebook Docker with extra modules.

Dataverse as data repository to store data from automatic and curated workflows.

Elasticsearch has CORD-19 indexes on sections and sentences level with spacy enrichments. Other indexes: MeSH, Geonames, GRID.

Hypothesis and Doccano annotation services to annotate publications

Virtuoso and GraphDB with public SPARQL endpoints to query COVID-19 Knowledge Graph

Other services: Colab, MongoDB, Kibana, BEL Commons 3.0, INDRA, Geoparser, Tabula

https://github.com/CoronaWhy/covid-19-infrastructure

## 

/openapi.json

CoronaWhy is globally distributed, volunteer-powered research organisation. We're trying to assist the medical community's ability to answer key questions related to COVID-19.

COUTIERV	Put this citation in working papers and published papers that use this dataset: Guidotti et al., (2020). COVID-19 Data Hub. Journal of Open Source Software, 5(51), 2376, https://doi.org/10.21105 oss.02376	$\sim$
GET	/country/{item_id} Data Item	
dataverse	Dataverse integration by API. Available actions: [showfiles, getfile]	$\checkmark$
GET	/dataverse/{action} Dataverse	
cord Metadata	a by cord_id CORD-19 collection access by cord_id	$\sim$
GET	/cord/ Read Cord	
altmetrics	Altmetrics by DOI or cord_id CORD-19 papers Altmetrics	$\sim$
GET	/altmetrics/ Read Altmetrics	
search COF	ND-19 search CORD-19 papers search	$\sim$
GET	/cordsearch/ Search Cord	

## Source: CoronaWhy API built on FastAPI framework for Python

Thank you! Questions?

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