Vaccine Safety Signals in VAERS 1990-2022

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Abstract

The aim of this study was to detect safety signals for the 98 vaccines recorded in the VAERS dataset from 1990 to 2022 – a period of over 32 years. The metric used to detect safety signals was the Proportional Reporting Ratio (PRR). A single dataset was created by concatenating the datasets for each year from 1990 to 2022. The resulting dataset had 8.7 million rows, each row consisting of three columns – ID, vaccine and symptom. There were 2 million unique VAERS-IDs, 98 unique vaccines and 16575 unique symptoms. The dataset was then grouped by vaccine and grouped by symptom. Then the Proportional Reporting Ratios were calculated for each symptom associated with each vaccine. The resulting data shows the safety signals for each vaccine.

This data is of critical interest to the public, so has been made accessible through downloadable CSV files and through an online interface (interface) that enables users to read off the symptoms for each vaccine, sorted by PRR, and read off the vaccines for each symptom, sorted by PRR. See Appendix for downloadable CSVs.

The dataset can also be used as a basis for identifying which features (symptoms) are most predictive of any particular target variable (symptom) – and so aide in diagnosis. It can also be used to determine if there is a high incidence of biomarkers for an illness, and consequently predict the likelihood of that illness following medication..

Significant safety signals were detected for the COVID-19 vaccine for different symptoms including cardiac disorder, thrombosis, cancer, menstrual disorder, and amyloidosis.

The purpose and utility of this project lies in its usefulness to anyone thinking about taking any vaccine, or wanting to find out more about vaccines on their child's vaccine schedule. The interface enables users to see which adverse effects are disproportionately associated with any vaccine.

Quick Access

Interface :	interface
CSV raw :	raw
CSV Symptom count	count
CSV Grouped by vaccine :	vax
CSV Grouped by symptom :	sym
Coding :	code

Introduction

What is Proportional Reporting Ratio?

An important method for detecting drug safety signals is Proportional Reporting Ratio . This method was created in 2001 by **S.J.W Evans et al, "Use of Proportional Reporting Ratios (PRRs) for Signal Generation from Spontaneous Drug Reaction Reports"** [1].

Cases	Drug of interest	Comparator
Event of interest	a	c
Other events	b	d

$$PRR = \frac{a/(a+b)}{c/(c+d)}$$

PRR calculates the percentage of reports where a particular symptom is recorded following administration of a drug A, and sees if this varies significantly from the percentage of reports where the same symptom is recorded after administration of drug B.

> *"The PRR is defined as the ratio between the frequency with which a specific adverse event is reported for the drug of interest (relative to all adverse events reported for the drug) and the frequency with which the same adverse event is reported for all drugs in the comparison group."*
>
> *"For example, suppose that nausea was reported 83 times for a given drug of interest, out of 1356 adverse events reported for the drug. Thus the proportion of adverse events of nausea for this drug is 83/1356 = 0.061. Suppose that we wish to compare the drug of interest to a class of drugs, for which nausea was reported as an adverse event 1489 times, out of 53789 total adverse events reported for drugs in the class. Thus, nausea was reported with proportion 1489 / 53789 = 0.028 for the class of drugs. The PRR in this case is 0.061 / 0.028 = 2.18. This tells us that nausea was reported more than twice as frequently (among all adverse event reports) for the drug of interest compared to drugs in the comparison group. "* **Wikipedia, (2023), "Proportional Reporting Ratio"** [2]

Usage of PRR by the European Medical Association (EMA)

PRR is used for the detection of serious drug reactions (SDRs) by “the European Medical Association (EMA) in their EudraVigilance Data Analysis System

> *“Different statistical methods to generate SDRs are in use. In the EudraVigilance Data Analysis System, the* ***Proportional Reporting Ratio (PRR)*** *has been implemented in the first release. Other methods will be considered for future implementation*.**”**
>
> **European Medicines Agency,(2006), "Guideline on the Use of Statistical Signal Detection Methods in the Eudravigilance Data Analysis System" [3]**

Usage of PRR by the Center for Disease Control (CDC)

This method is also used by the Center for Disease Control (CDC) in the USA. On January 29th of 2021 the CDC released a document titled 'Vaccine Adverse Event Reporting System (VAERS) Standard Operating Procedures for COVID-19' (for official use only) which announced the CDC's intention:

> "*CDC will perform* ***Proportional Reporting Ratio (PRR)*** *analysis [...], excluding laboratory results, to identify AEs that are disproportionately reported relative to other AEs. [...] To determine if results need further clinical review, consider if clinically important, unexpected findings, seriousness, specific syndrome or diagnosis rather than non-specific symptoms"*
>
> **Centers for Disease Control and Prevention, (2021), "Vaccine Adverse Event Reporting System (VAERS) Standard Operating Procedures for COVID-19 (as of 29 January 2021) [4]**

Defining a Strong Signal

A strong signal is where **PRR > 2**, in other words where the frequency of the symptom for the drug of interest is twice as high as the frequency of that symptom for the comparator drug/s. When PRR > 2, then there is a disproportionate occurrence of the symptom for the drug of interest compared to the comparator drugs.

A strong signal is also defined by the confidence we can have in it. We can have more confidence in a signal if –

1. the datasets of both the target and comparator drugs are large **(a + b > 1000)** and **(c + d > 1000).**
2. if the PRR remains consistent across multiple different samples.
3. if the symptom count is large **(a > 10**) and **(c > 10)**

Strong Signal Criteria used by CDC

The CDC uses the following criteria –

1. (**Symptom events >= 3)**
2. **(PRR >= 2)**
3. **(Chi-Square >= 4**)

See **Ref : Excel spread sheets released by CDC through Freedom of Information request**

These are exactly the same criteria that were used by Evans in 2001 **[1]**. However, in study by **van Puijenbroek E.P, et al, (2002), "A comparison of measures of disproportionality for signal detection in spontaneous reporting systems for adverse drug reactions"** **[5]** , a comparison was made between the proportionality scores obtained by different methods, and the scores were found to become consistent when a > 10 and c > 10.

A Technical Note on PRR

PRR >= 2, is the level used by the CDC to detect a safety signal. However, to be exact we should say that the lower confidence limit of PRR >= 2

The lower and upper confidence limits are given by the equations here –

Lower Confidence Limit = $\mathbf{PRR/e^{1.96 \times s}}$

Upper Confidence Limit = $\mathbf{PRR \times e^{1.96 \times s}}$

s is the standard deviation, and is given by the formula -

$$s = \sqrt{\frac{1}{a} + \frac{1}{c} - \frac{1}{a+b} - \frac{1}{c+d}}$$

Ref : "Proportional Reporting Ratio",(May 2021), https://www.rxmd.com **[6]**

Multiple samples : Sample variation is a possible cause of a high PRR. To rule this out, multiple samples of equal size should be taken to ensure that there is consistency in the PRR across samples. In this way we can know if the difference in PRR is due to random variation or due to a significant difference between the drug reactions.

Large samples : Biased reporting might occur if one individual were inputting all the records. However if records are input by a large population of independent individuals then the effects of individual reporting bias would be lessened.

The Need for Big Data : Because of the need for multiple, large, independent samples, it is important to gather as much data as possible. In the study that follows, pharmacovigilance data is gathered from 32 years of VAERS records (1990 to 2022). This provides far stronger assessment of signals than relying on a single year of data.

5 Preliminary Studies

2 CDC (VAERS) Studies

PRR for death (1990 - 2022) : **Paardekooper C., (2023), "Proportional Reporting Ratio - signal detection in pharmacovigilance"** [7]

PRR for COVID vs FLU vaccine : **Paardekooper C.,(2023), "Major Differences between Effects of COVID and FLU Vaccines"** [8]

2 WHO (Vigiaccess) Studies

PRR for COVID vs FLU vaccine : **Paardekooper C., (2023), "Comparing COVID Vaccine with INFLUENZA Vaccine using Vigiaccess.org database (WHO database)"** [9]

PRR for COVID vs 7 other vaccines **: Paardekooper C., (2023), "Not the Same - comparing COVID jabs with other vaccines"** [10]

COVID vs FLU (cardiac symptoms) : **Paardekooper C., (2023), "Comparing COVID19 and Flu Vaccines Using WHO Data"** [11]

Method

1. **Raw Dataset**

   All of the vaccine adverse events records over the last 32 years were compiled into a single dataset.

   The dataset contained 2 columns

   1 Vaccine name
   2 Symptom

   The dataset had 8,685,997 rows, each row recording a symptom and the associated vaccine. There were a total of 16575 unique symptoms and 98 different vaccines

   This dataset can be downloaded here – **Raw Data** [12] (67.3 Mb)

2. **Grouped Datasets**

   By Vaccine : This dataset was then grouped by vaccine, so you can select a vaccine column and see every symptom ranked by PRR.

   This dataset can be downloaded here – **Grouped by Vaccine** [13] (1.6 Mb)

   By Symptom : This dataset was then grouped by symptom, so you can select a symptom column, and see every vaccine ranked by PRR.

   This dataset can be downloaded here – **Grouped by Symptom** [14] (1.2M)

3. **Technical Details**

   Full technical details of how the dataset was read, pre-processed and grouped can be found in the Appendix or online here – **Technical Details** [15]

4. **Metric**

   The metric used to compare vaccines is PROPORTION. This metric is called the PRR ratio.

   1. A symptom occurs with a frequency that is disproportionately high for one vaccine compared to another
   2. disproportion is consistent across many samples

5. **User Interface**

   This data is of critical interest to the public, so has been made accessible through downloadable CSV files, and through an online interface ([16]) that enables users to read off the symptoms for each vaccine, sorted by PRR, and read off the vaccines for each symptom, sorted by PRR.

   The purpose and utility of this project lies in its usefulness to anyone thinking about taking any vaccine, or wanting to find out more about vaccines on their child's vaccine schedule. The interface enables users to see which adverse effects are disproportionately associated with any vaccine.

Results

The resulting dataset of PRR scores enables users to read off the symptoms for each vaccine, sorted by PRR, and read off the vac cines for each symptom, sorted by PRR.

A user can input a vaccine name, and see what symptoms are associated with it, and the PRR scores for each symptom. A symptom with a PRR score greater than 2 would be a safety signal, since it would be occurring with a disproportiona tely high frequency for that vaccine. Here is an example for COVID 19 vaccines.

Venous thrombosis limb	66.89373648
Cerebral venous sinus thrombosis	41.76091303
Retinal vascular thrombosis	39.66333292
Superior sagittal sinus thrombosis	33.1799035
Cerebral artery thrombosis	32.7985253
Superficial vein thrombosis	32.48071013
Peripheral artery thrombosis	29.74749969
Jugular vein thrombosis	29.55681059
Aortic thrombosis	28.98474329
Ophthalmic vein thrombosis	25.29808734
Pulmonary artery thrombosis	22.11993567
Mesenteric vein thrombosis	18.59218731
Deep vein thrombosis	17.01287674
Transverse sinus thrombosis	14.49237164
Atrial thrombosis	14.11099344
Coronary artery thrombosis	13.88216652
Pulmonary thrombosis	13.46123799
Cerebral thrombosis	12.88210813
Arterial thrombosis	12.20410244
Portal vein thrombosis	12.16172708
Retinal vein thrombosis	11.11445043
Carotid artery thrombosis	11.05996783
Cerebral venous thrombosis	10.15052751
Vascular stent thrombosis	9.91583323
Basilar artery thrombosis	9.72514413

The user can also input a symptom name to see to see the vaccines associated with it in rank order. Here is an example –

VAX_TYPE	Thrombosis
COVID19	9.317497532
EBZR	4.56214126
MER	1.846060997
6VAX-F	0.993500753
UNK	0.828471506
HPV4	0.572608238
COVID19-2	0.403862872
HEPAB	0.372547745
ANTH	0.323189654
RUB	0.284667046
FLUR4	0.282654115
FLUX(H1N1)	0.265041887
FLUC3	0.251455147
IPV	0.223397944
HPV9	0.206571735
FLUN(H1N1)	0.199931516
FLUA3	0.18970467
FLUA4	0.181061455
HPVX	0.177651495
HPV2	0.173925755
FLUN4	0.160721795
FLUX	0.132490444
MEN	0.131828239
LYME	0.131352749

The purpose of the interface and the CSV files is to enable users carry out their own searches. However, here are some examples of strong safety signals for the COVID19 vaccine compared to other vaccines. A strong signal is where the PRR > 2.

Thrombosis Safety Signals

VAX_TYPE	Thrombosis
COVID19	9.317497532
EBZR	4.56214126
MER	1.846060997
6VAX-F	0.993500753
UNK	0.828471506
HPV4	0.572608238
COVID19-2	0.403862872
HEPAB	0.372547745
ANTH	0.323189654
RUB	0.284667046
FLUR4	0.282654115
FLUX(H1N1)	0.265041887
FLUC3	0.251455147
IPV	0.223397944
HPV9	0.206571735
FLUN(H1N1)	0.199931516
FLUA3	0.18970467
FLUA4	0.181061455
HPVX	0.177651495
HPV2	0.173925755
FLUN4	0.160721795
FLUX	0.132490444
MEN	0.131828239
LYME	0.131352749

Myocarditis Safety Signals

VAX_TYPE	Myocarditis
COVID19	13.92251651
SMALL	4.725110996
TDAPIPV	1.64830256
MU	1.496781596
UNK	0.443571099
MEN	0.325243213
IPV	0.27555316
HEPAB	0.262518369
MEA	0.258785342
HPV9	0.183994471
COVID19-2	0.181026698
FLUA3	0.175484449
SMALLMNK	0.155111915
FLUC3	0.155067119
FLUX	0.153239547
RAB	0.140250169
FLUC4	0.119123186
MNQ	0.113208013
DTAPIPV	0.104256187
FLUR4	0.087144691
TDAP	0.086689036
HEP	0.085538545
YF	0.07271262
ANTH	0.072415019
TD	0.071405039

Menstrual Safety Signals

VAX_TYPE	Menstrual disorder
COVID19	7.318829289
EBZR	6.309896501
HPV2	2.464954068
HPVX	1.722903412
HPV4	1.372762112
UNK	0.870207831
DF	0.638894509
COVID19-2	0.609682119
HPV9	0.444882506
HEP	0.122855805
ANTH	0.12182156
HEPAB	0.073565792
FLUC4	0.066780554
FLUX	0.057210424
MNQ	0.042304433
FLU4	0.033502684
HEPA	0.033438355
MMR	0.025426071
PPV	0.014571839
VARCEL	0.01171032
FLU3	0.004340007

Cancer Safety Signals

VAX_TYPE	Breast cancer
COVID19	4.327175744
HEPAB	3.324066846
LYME	2.04561382
HPV2	1.81068161
HEP	1.231101244
HPV4	0.692089416
FLUX	0.516723113
FLU3	0.494911902
PPV	0.329168241
VARZOS	0.075650007

Symptoms can be filtered to identify all symptoms related to a particular disorder – for example Thrombosis.

Thrombosis Safety Signals for COVID 19 vaccines only

SYMPTOM	COVID19
Venous thrombosis limb	66.89373648
Cerebral venous sinus thrombosis	41.76091303
Retinal vascular thrombosis	39.66333292
Superior sagittal sinus thrombosis	33.1799035
Cerebral artery thrombosis	32.7985253
Superficial vein thrombosis	32.48071013
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Retinal vein thrombosis	11.11445043
Carotid artery thrombosis	11.05996783
Cerebral venous thrombosis	10.15052751
Vascular stent thrombosis	9.91583323
Basilar artery thrombosis	9.72514413

Myocarditis Safety Signals for COVID 19 vaccines only

SYMPTOM	COVID19
Myocarditis	13.92251651
Viral myocarditis	6.025775578
Myocarditis infectious	3.051025609
Myocarditis septic	1.144134603
Chronic myocarditis	0.762756402
Eosinophilic myocarditis	0.520061183

Menstrual Safety Signals for COVID 19 vaccines only

SYMPTOM	COVID19
Abnormal menstrual clots	inf
Menstrual headache	inf
Heavy menstrual bleeding	60.09849895
Intermenstrual bleeding	53.61895006
Premenstrual pain	49.76985525
Premenstrual syndrome	24.72024158
Menstrual discomfort	16.20857355
Menstrual cycle management	9.91583323
Menstrual disorder	7.318829289
Premenstrual dysphoric disorder	4.004471112
Premenstrual headache	1.906891006

Cancer Safety Signals for COVID 19 vaccines only

SYMPTOM	COVID19
Breast cancer recurrent	10.67858963
Breast cancer metastatic	6.864807621
Hepatic cancer	6.67411852
Triple negative breast cancer	6.48342942
Lung cancer metastatic	5.911362118
Cancer screening	5.720673017
Colon cancer metastatic	5.720673017
Colorectal cancer	5.339294816
Breast cancer	4.327175744
Renal cancer	4.32228628
Testis cancer	4.004471112
Endometrial cancer	3.623092911
Prostate cancer metastatic	3.051025609
Recurrent cancer	2.860336509
Colon cancer	2.593371768
Papillary thyroid cancer	2.542521341
Bone cancer	2.415395274
Prostate cancer	2.288269207
Non-small cell lung cancer stage IV	2.288269207
Renal cancer metastatic	2.288269207
Hepatic cancer metastatic	2.288269207
Bladder cancer	1.906891006
Rectal cancer	1.652638872
Cancer pain	1.525512805
Fallopian tube cancer	1.144134603
Oesophageal cancer metastatic	1.144134603

Predicting the Incidence of an Illness from the Incidence of Bio-markers

COVID 19 vaccines have been associated with the formation of amyloid clots within the circulatory system. These amyloid clots have been reported extensively – see **Paardekooper C., (2023), "Undertakers provide evidence of Amyloid Clots in COVID Vaccinated"** [17]

A search of the dataset reveals that COVID19 vaccines generate a safety signal for amyloidosis – with a PRR of 3.55

Vaccine	Proportional Reporting Ratio
HEPAB	17.67295539791259
HPV2	9.626790560078296
COVID19	3.5595298774693047
HEP	1.8407894793622024

COVID19 vaccines also generates a safety signal for cerebral amyloid angiopathy. This is a condition where amyloid builds up on the walls of the arteries of the brain – with a PRR of 6.1

Vaccine	Proportional Reporting Ratio
COVID19	6.102051218518808
VARZOS	1.5130001480092752

Referring to the medical literature, **"Blood Tests for Amyloidosis"** [18], there are a number of biomarkers associated with amyloidosis. These include –

- Paraproteinemia
- Monoclonal Gammopathy
- Serum amyloid A protein
- Light Chain analysis
- Blood alkaline phosphatase
- Troponin T
- Brain Natriuretic peptide
- Blood Fibrinogen

On the following pages are the PRR scores for each of these biomarkers. These PRR scores show that there is a disproportionately high incidence of these biomarkers with COVID-19 vaccines.

Paraproteinaemia

Vaccine	Proportional Reporting Ratio
FLU4	20.11556984225236
COVID19	1.525512804629702

Monoclonal Gammopathy

Vaccine	Proportional Reporting Ratio
TYP	17.07988759929582
HEPA	5.8778102733387065
COVID19	2.2882692069445527
FLUX	2.010178939554817
FLU3	1.563921611618159
PPV	1.2805447436912094

Serum Amyloid A Protein

Vaccine	Proportional Reporting Ratio
MENB	34.7775853478205
COVID19	3.051025609259404

Light Chain Analysis

Vaccine	Proportional Reporting Ratio
COVID19	6.737681553781184
HIBV	4.062174864110247
FLUX	0.7424985272229503
FLU3	0.5686987678611486
PPV	0.4729940044264827
VARZOS	0.2180901114247603

Troponin T

Vaccine	Proportional Reporting Ratio
COVID19	25.049613666930902
SMALLMNK	1.7102517000022457
FLUC3	1.709757781460605

Brain Natriuretic Peptide

Vaccine	Proportional Reporting Ratio
COVID19	24.850603587417847
COVID19-2	0.6643356341233816
SMALL	0.3136329672239526
FLU4	0.1950600711975986

Blood Fibrinogen

Vaccine	Proportional Reporting Ratio
COVID19	33.34335130119206
IPV	1.8014622268444425
HIBV	0.4861470726859703
FLUX(H1N1)	0.4743907055947873
RV1	0.4549481444458328
RV5	0.3086812459172663
MMRV	0.2128849245257205

Blood Alkaline Phosphatase

Vaccine	Proportional Reporting Ratio
COVID19	19.610221053062457
FLUN(H1N1)	0.6135213727716133
HPV2	0.3558887452894009
HPV9	0.2817080140440851
RV1	0.259830298013245
COVID19-2	0.2251268743714497
UNK	0.1874511076105688
RV5	0.1762942460518869
FLU(H1N1)	0.1752992581673529
MENB	0.171318154422761

Given the high incidence of bio-markers that indicate amyloidosis, we can predict that amyloidosis will be an effect of the COVID-19 vaccine, in the same way that a high incidence of Troponin and Brain Natriuretic Peptide are indicative of heart damage.

Clotting Biomarkers

A high incidence of Fibrin D-Dimer, Coagulation Factor, Coagulation Factor V, and Coagulation Factor VII are indicative of clotting.

Fibrin D-Dimer

Vaccine	Proportional Reporting Ratio
COVID19	29.018575225163787
EBZR	4.757838887190797
DTIPV	3.2339423888170296

Abnormal Clotting Factor

Vaccine	Proportional Reporting Ratio
HEPAB	26.50943309686888
COVID19	3.6230929109955423
HEP	2.761184219043304

Here are the PRRs for coagulation related adverse reactions following COVID-19 vaccination

Coagulation factor	28.98474329
Coagulation time	18.68753186
Hypercoagulation	10.67858963
Coagulation test	10.27337529
Coagulation factor VII level	8.771698627
Anticoagulant therapy	8.556635731
Coagulation factor V level	6.769463071
Coagulation factor VIII level increased	5.339294816
Anticoagulation drug level above therapeuti	3.686655945
Coagulation factor increased	3.43240381
Circulating anticoagulant	3.21447341
Coagulation test abnormal	2.923899542
Anticoagulation drug level	2.669647408
Anticoagulation drug level below therapeuti	2.288269207
Coagulation factor inhibitor assay	2.288269207

So if we know the biomarkers for a particular illness, then we can use the database to see the degree to which those biomarkers are over represented with a particular vaccine, and hence determine whether the illness will be associated with the vaccine.

Conversely, this dataset can be used with a classification algorithm to predict the occurrence of a target variable (e.g. myocarditis) based on the PRR values for the 16575 symptoms. In this way, those symptoms most predictive of the target variable can be isolated, so the dataset has diagnostic value.

Do Clinical Studies Support an Association Between COVID Vaccines and High PRR Scores

The safety signals found for COVID 19 vaccines have been confirmed by clinical studies.

See here –

1. **[19]** Published Science Database - React19
2. **[20]** 1000 peer reviewed articles on "Vaccine" injuries (drtrozzi.org)
3. **[21]** Data from Autopsies

Confirmation of PRRs by CDC FOI Request

Ref : **[22]** CDC Finds Hundreds of Safety Signals for Pfizer and Moderna COVID-19 Vaccines

Here are the excel files released by the CDC -

7.29.22 Table 5 PRR of PTs for COVID19 mRNA Compared to Non-COVID

7.22.29 Table 5 PRR of PTs for COVID19 mRNA Compared to Non-COVID

7.15.29 Table 5 PRR of PTs for COVID19 mRNA Compared to Non-COVID

The PRRs are >> 2 and are comparable to the magnitude of PRR found in my study. Differences arise due to the period over which data was collected. The CDC data for non-COVID19 was collected from 1st January 1st 2009 until 29th July 2022. The data for COVID 19 mRNA was collected from 14th December 2020 till 29th July 2022. In comparison, I gathered all VAERS data from 1990 till November 2022.

Screenshot of CDC data

MedDRA Codes ALL Reports (SERIOUS 18+)	12/14/2020-07/29/2022 COVID19 mRNA N=73178	01/01/2009-07/29/2022 NON-COVID19 N=13287	12/14-07/29 Chi-Square	12/14-07/29 PRR
THROMBOSIS	1449	60	152.33	4.38
PULMONARY THROMBOSIS	579	3	98.23	35.04
PORTAL VEIN THROMBOSIS	75	2	8.70	6.81
PERIPHERAL ARTERY THROMBOSIS	72	2	8.18	6.54
MESENTERIC VEIN THROMBOSIS	55	1	6.94	9.99
JUGULAR VEIN THROMBOSIS	49	1	5.88	8.90
DEEP VEIN THROMBOSIS	1441	122	69.39	2.14
CORONARY ARTERY THROMBOSIS	65	3	5.47	3.93

MedDRA Codes ALL Reports (SERIOUS 18+)	12/14/2020-07/29/2022 COVID19 mRNA N=73178	01/01/2009-07/29/2022 NON-COVID19 N=13287	12/14-07/29 Chi-Square	12/14-07/29 PRR
MYOCARDIAL STRAIN	59	1	7.64	10.71
MYOCARDIAL FIBROSIS	52	2	4.79	4.72
INFARCTION	1458	111	83.84	2.38

MedDRA Codes ALL Reports (SERIOUS 18+)	12/14/2020-07/29/2022 COVID19 mRNA N=73178	01/01/2009-07/29/2022 NON-COVID19 N=13287	12/14-07/29 Chi-Square	12/14-07/29 PRR
ISCHAEMIC STROKE	465	32	29.95	2.64
INTERNAL HAEMORRHAGE	56	2	5.46	5.08
HAEMOFILTRATION	76	1	10.67	13.80

MedDRA Codes ALL Reports (SERIOUS 18+)	12/14/2020-07/29/2022 COVID19 mRNA N=73178	01/01/2009-07/29/2022 NON-COVID19 N=13287	12/14-07/29 Chi-Square	12/14-07/29 PRR
VENTRICULAR HYPOKINESIA	160	8	13.75	3.63
VASCULAR DEMENTIA	42	1	4.67	7.63
TROPONIN INCREASED	404	24	30.75	3.06
THALAMIC INFARCTION	66	4	4.30	3.00
DYSFUNCTION	94	1	13.90	17.07
DILATATION	76	1	10.67	13.80
RETINAL ARTERY OCCLUSION	87	6	5.02	2.63
PULMONARY THROMBOSIS	579	3	98.23	35.04
PULMONARY INFARCTION	122	4	13.50	5.54
PULMONARY EMBOLISM	2794	120	292.51	4.23
PORTAL VEIN THROMBOSIS	75	2	8.70	6.81
PERIPHERAL ARTERY THROMBOSIS	72	2	8.18	6.54
OCCLUSION	40	1	4.32	7.26
INTERVENTION	91	2	11.51	8.26
INCREASED	43	1	4.84	7.81
NIH STROKE SCALE ABNORMAL	57	1	7.29	10.35
NIH STROKE SCALE	65	1	8.71	11.80
MYOCARDIAL STRAIN	59	1	7.64	10.71
MYOCARDIAL FIBROSIS	52	2	4.79	4.72
DYSFUNCTION SYNDROME	317	21	21.16	2.74
LEFT VENTRICULAR FAILURE	252	7	31.07	6.54
JUGULAR VEIN THROMBOSIS	49	1	5.88	8.90
ISCHAEMIC STROKE	465	32	29.95	2.64
INTRACARDIAC THROMBUS	91	2	11.51	8.26
INTERNAL HAEMORRHAGE	56	2	5.46	5.08
IMPLANTABLE CARDIAC MONITOR INSERTION	61	1	8.00	11.08
EMBOLIC STROKE	94	5	7.34	3.41
SEGMENT ELEVATION	236	19	11.72	2.26
DEEP VEIN THROMBOSIS	1441	122	69.39	2.14
DEATH	10169	618	879.39	2.99
CORONARY ARTERY THROMBOSIS	65	3	5.47	3.93
CORONARY ARTERY OCCLUSION	194	12	13.73	2.94
CORONARY ARTERY DISSECTION	51	1	6.23	9.26
INSERTION	273	17	19.49	2.92
CORONARY ANGIOPLASTY	44	1	5.01	7.99
COR PULMONALE ACUTE	46	1	5.36	8.35
CHRONIC LEFT VENTRICULAR FAILURE	163	7	15.72	4.23
CEREBRAL INFARCTION	422	37	18.38	2.07
CEREBRAL ARTERY OCCLUSION	105	2	13.99	9.53
CEREBELLAR STROKE	82	1	11.75	14.89
CARDIO-RESPIRATORY ARREST	761	67	33.46	2.06
CARDIOGENIC SHOCK	273	24	11.61	2.07
CARDIAC FAILURE ACUTE	349	13	37.86	4.87
CARDIAC FAILURE	647	50	35.64	2.35
CARDIAC ASSISTANCE DEVICE USER	85	2	10.45	7.72

APPENDIX : TECHNICAL DETAILS OF METHODOLOGY

Source Data and Files

[23] VAERS Nov 11th Downloadable files (vaersaware.com)

Reading the VAERSVAX Files

```
import pandas as pd
import matplotlib.pyplot as plt
import folium
import os, re
from sklearn.preprocessing import StandardScaler
from sklearn.preprocessing import normalize
from IPython.display import IFrame
from sklearn.cluster import AgglomerativeClustering
import scipy.cluster.hierarchy as shc
%matplotlib inline
import warnings
warnings.filterwarnings('ignore')
```

```
dfList2=[]


for root,dirs,files in os.walk(r"C:\Users\User\Downloads\AllVAERSDataCSVS"):
    for fname in files:


        if "VAERSVAX" in fname:
            try:

                frame = pd.read_csv(r"C:\Users\User\Downloads\AllVAERSDataCSVS\\" + fname, encoding='windows-1252')
                frame1 = frame[['VAERS_ID','VAX_TYPE']]

                dfList2.append(frame1)
            except:
                print(fname)

datasetvax = pd.concat(dfList2)
```

Stats on the Data

2352562 unique VAERS IDs [**datasetvax**['VAERS_ID'].nunique()]

2856247 total number of VAERS Ids [**datasetvax**['VAERS_ID'].count()]

503685 are VAERS Ids are duplicated

Removing Duplicates

Why are they duplicated? Because they represent two or more different vaccines that a person had at the same time. Taking multiple medicines makes it hard to attribute adverse effects to a particular medicine, so these records are removed. When they are dropped, we have 2049804 unique VAERS IDs and 2049804 VAERS IDs in total. So now we just have one of each VAERS ID. This means that we have 2049804 records where each person took one vaccine and had one set of adverse symptoms. This is ideal for pharmacovigilance.

```
datasetvax = datasetvax.drop_duplicates(subset=['VAERS_ID'],keep=False)
datasetvax['VAERS_ID'].count()
```

[This could be further refined selecting those on no medications at the time of vaccination, and those with no pre-existing illnesses – which would require looking at the VAERSDATA table]

Removing Vaccines with Too Few Reports

Here are the number of reports for each vaccine in VAERSVAX. If we are doing a statistical analysis, those vaccines that have fewer than 100 reports will generate unreliable scores, so should be dropped. I haven't done this in the current analysis.

[**datasetvax**['VAX_TYPE'].value_counts()]

COVID19	1391183	FLUN4	3815	RV	184
VARZOS	98254	HEPAB	3504	DTPPVHBHPB	150
FLU3	71582	DTAPIPV	3367	MU	121
HEP	42877	DTP	2899	DTAPH	117
PPV	42262	FLUN(H1N1)	2607	MER	107
VARCEL	40604	FLUA3	2437	CHOL	107
HPV4	36590	DTAPIPVHIB	2414	PER	69
FLU4	29085	TTOX	2383	ADEN_4_7	61
MMR	26953	LYME	2188	MM	56
FLUX	23054	FLUX(H1N1)	2150	DPP	53
TDAP	20383	IPV	2134	TDAPIPV	50
UNK	15168	FLUR4	2081	EBZR	44
PNC13	13973	HPVX	2043	DTPIPV	37
HPV9	12957	YF	1553	TBE	34
HEPA	12618	MEN	1543	PNC15	30
TD	11715	FLUA4	1467	CEE	30
RV5	11673	SMALLMNK	1227	DTPHEP	28
DTAP	10456	DT	1221	DTIPV	26
MMRV	9443	DTAPHEPBIP	1138	JEVX	25
MNQ	8620	FLUC3	1083	DTPPHIB	21
MENB	8030	DTPHIB	836	HBPV	20
FLU(H1N1)	7735	RUB	825	PLAGUE	20
COVID19-2	6641	MEA	522	PNC10	20
HIBV	6520	PNC20	465	DTPIHI	19
ANTH	6148	RVX	448	DTOX	18
FLUN3	5269	HBHEPB	338	HEPATYP	16
FLUC4	5037	JEV	290	MUR	9
RAB	4596	BCG	284	MENHIB	6
HPV2	4580	FLUR3	225	H5N1	4
PNC	4210	DF	217	MNC	4
RV1	4062	OPV	192	SSEV	3
TYP	3908	JEV1	191	MNQHIB	3
SMALL	3851	6VAX-F	188		

Symptoms

There are 5 symptoms columns in VAERS – labelled SYMPTOM1, SYMPTOM2, SYMPTOM3, SYMPTOM4, SYMPTOM5. There can be more than one row of symptoms for each VAERS ID

Reading the VAERSSYMPTOMS Files

```
dfList3=[]

for root,dirs,files in os.walk(r"C:\Users\User\Downloads\AllVAERSDataCSVS"):
    for fname in files:

        if "VAERSSYMPTOMS" in fname:
            try:

                frameY = pd.read_csv(r"C:\Users\User\Downloads\AllVAERSDataCSVS\\" + fname, encoding='windows-1252')

                frame1 = frameY[['VAERS_ID','SYMPTOM1']]
                frame2 = frameY[['VAERS_ID','SYMPTOM2']]
                frame3 = frameY[['VAERS_ID','SYMPTOM3']]
                frame4 = frameY[['VAERS_ID','SYMPTOM4']]
                frame5 = frameY[['VAERS_ID','SYMPTOM5']]


                frame2 = frame2.rename(columns={'SYMPTOM2': 'SYMPTOM1'})
                frame3 = frame3.rename(columns={'SYMPTOM3': 'SYMPTOM1'})
                frame4 = frame4.rename(columns={'SYMPTOM4': 'SYMPTOM1'})
                frame5 = frame5.rename(columns={'SYMPTOM5': 'SYMPTOM1'})
                concatenated = pd.concat([frame1, frame2, frame3, frame4, frame5])
                dfList3.append(concatenated)

            except:
                print(fname)
datasetsymptoms = pd.concat(dfList3)
```

Removal of Null Values from SYMPTOM1 Column

There are a total count of 15682620 records in **datasetsymptoms** found by counting the VAERS-IDs. However this is comprised o f comprised of 9959381 symptoms and 5723239 null values.

- 15682620 symptom records
- 9959381 symptoms
- 5723239 nulls

These null values were removed leaving –

- 9959381 symptom records where there were
- 9959381 symptoms
- 2352303 VAERS-IDs

```
datasetsymptoms = datasetsymptoms.dropna(how='any')
```

These are the symptoms for 2352303 unique VAERS-IDs, which closely corresponds to the original number of VAERS-IDs in the V AERSVAX table before duplicates were removed.

Counting the Frequency of Each Symptom and Exporting to a Dataframe

```
countdf = datasetsymptoms['SYMPTOM1'].value_counts().rename_axis('unique_values').reset_index(name='counts')
```

unique_values	counts
Pyrexia	318381
Headache	277176
SARS-CoV-2 test	227363
Fatigue	223902
Pain	199188
COVID-19	189505
Chills	168428
Nausea	160436
Dizziness	155965
Pain in extremity	155492
Injection site erythema	118251
Myalgia	118157
Injection site pain	118016
Rash	111443
Dyspnoea	108718
Arthralgia	106531
No adverse event	106449
Vomiting	90657

Merging

The **datsetvax** table was then merged with the **datasetsymptoms** table on the common field of VAERS-ID, so we end up with -

- 8685997 records
- 2049647 unique (VAERS_ID)
- 16575 unique (SYMPTOM1)
- 98 unique vaccines (VAX_TYPE)
- averaging 4.237 symptoms per report (VAERS_ID).

```
vaxsym = datasetvax.merge(datasetsymptoms[['VAERS_ID', 'SYMPTOM1']])
```

The VAXSYM dataset is the raw data, listing every symptom and its associated vaccine. It can be downloaded here, as a csv file. Unfortunately it has 8.7 million rows so cannot be opened in excel (Excel has a limit of 1 million rows). However, you will be able to read it with Python into a Jupyter Notebook, and carry out any analysis there.

[12] https://howbad.info/vaxsym.zip (67.3 Mb)

Symptoms per Record

It is interesting to look at number of symptoms recorded for each vaccine-type and divide this by the number of VAERS_IDs for t hat type to get the average number of symptoms per record. It is hypothesised that some vaccines may have a greater number o f symptoms per record because their toxicity is more intense, more distributed or more persistent.

This result can then be compared with the number of symptoms per record for other vaccines to get a PRR score.

The raw data for vaccines may show that a greater number of symptoms are reported for each COVID report compared to other vaccines. This could be because the vaccine was causing more ailments because –

1. it's bio distribution was greater ,
2. it's permeation of cells was greater,
3. it's duration of effect more prolonged and
4. it's effects more intense owing to the biologically active nature of the spike antigen which is a proven toxin.

In comparison a short lived, local, non-toxic , biologically inactive antigen would be expected to generate fewer symptoms.

What is the maximum and minimum number of symptoms recorded per record, what is the average and standard deviation ?

Grouping by Pivot Table

```
fsym = vaxsym.pivot_table(index='SYMPTOM1', columns='VAX_TYPE',
aggfunc=len, fill_value=0)

fsym.to_csv(r"C:\Users\User\Downloads\vaccine-symptoms2.csv")
```

The FSYM dataset is useful for seeing the frequency of occurrence of each symptom for each vaccine – so you can see how many datapoints analysis is based upon. This file can be opened I Excel.

[24] https://howbad.info/fsym.zip (0.35 Mb)

Converting Raw Counts to a PRR Ratio

The PRR ratio is calculated by

1. Counting the frequency of symptom S for vaccine V
2. Dividing this by the total symptom count for vaccine V

   [This gives the % of symptoms for vaccine V that are symptom S]
3. Counting the frequency of symptom S for all other vaccines
4. Dividing this by the total symptom count for all other vaccines

   [This gives the % of symptoms for all other vaccines that are symptom S]
5. PRR = % of symptoms for vaccine V that are symptom S divided by % of symptoms for all other vaccines that are sympto m S

```
df1 = fsym.apply(lambda x: x/sum(x), axis=0)
df2 = fsym.apply(lambda x: sum(x) - x, axis = 1)
df3 = fsym.apply(lambda x: 8685997 - sum(x), axis=0)
dfA = df1.div(df2.values)
dfB = pd.DataFrame(dfA.values*df3.values, columns=fsym.columns, index=fsym.index)
```

```
dfB.to_csv(r"C:\Users\User\Downloads\all-sym-vax-safety2.csv")
```

Each vaccine is shown as a separate column, and each row is a separate symptom. You can use this dataset to quickly see which symptoms are disproportionately associated with each vaccine.

You can download the dataset here -

[13] https://howbad.info/grouped-by-vaccine.zip (1.6 Mb)

Transposing Data

```
tdf = dfB.T
tdf.head()
```

```
tdf.to_csv(r"C:\Users\User\Downloads\prr-ratios-all-vaccines.csv")
```

This dataset has a separate column for each symptom, and a separate row for each vaccine. It is useful for quickly seeing which vaccines are worst for any chosen symptom, since you can sort each column by PRR ratio.

Please note that because this dataset has 16575 columns, it may not fully load into Excel.

You can download this dataset here – **[14]** https://howbad.info/grouped-by-symptoms.zip (1.2 Mb)

Generating Random Samples for Different Vaccines

```
Covid = vaxsym.loc[vaxsym['VAX_TYPE'] == 'COVID19']
Flu = vaxsym.loc[vaxsym['VAX_TYPE'] == 'FLU3']

for i in range(0,100):
    Cov = Covid.sample(n = 20000)
    Fov = Flu.sample(n= 20000)
    p = Cov.loc[Cov['SYMPTOM1'] == 'Thrombosis']
    q = Fov.loc[Fov['SYMPTOM1'] == 'Thrombosis']
    num = p['VAERS_ID'].count()/q['VAERS_ID'].count()
    print('{:4.2f}'.format(num) , "   Counts = " , p['VAERS_ID'].count(), " | " , q['VAERS_ID'].count())
```

Full Code File

Here you can find the complete Python code that was used to carry out this analysis.

[25] Python Code for Vaccine Analysis

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