

WHO Outbreak Toolkit Virtual Assistant

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Outline

1. Overview
2. Input: Data dictionary, references and line lists
3. Score
4. Dimensionality reduction
5. Web application
6. Conclusion and outlook

1. Overview

Objective

Outbreak of **unknown origin**. . . Help formulating **hypotheses** on disease

Inspiration

Election online helper: Which party is closest to you?

Approach

Use expected answers for diseases of interest = **references**

Compare cases with expectations

Workflow

Input:

1. data dictionary
2. references
3. filled line lists

Output:

1. **2d visualisation** of cases and references
2. **scores** = similarity between cases and references

2. Input: Data dictionary, references and line lists

Data dictionary

Data dictionary = T0 and T1 questionnaires, i.e. **not** disease specific

Remove free text and other variables that can't be used here: 117 variables left

name	label	type	format	values	multiplicity
report_date	Date case was reported (DD, *)	date	YYYY-MM-DD	NA	0
notification_facility_type	Case reported by:	int_categorical	NA	0=unknown;1=mobileteam;2=ph	0
birth_date	Date of birth (DD/MM/YYYY):	date	YYYY-MM-DD	NA	0
age_year	Age at onset: years	int_ordinal	NA	0, 99	0
sex	Male Female	int_categorical	NA	1=male;2=female	0
occupation_hcw	Works in health facility:	int_categorical	NA	0=unknown;1=yes;2=no	0
gps_lat	GPS latitude:	float	point_decimal_no_grouping	-180, 180	0
gps_long	GPS longitude:	float	point_decimal_no_grouping	-180, 180	0
mass_gathering_yn	Did you participate in mass gathering?	int_categorical	NA	0=unknown;1=yes;2=no	0
mass_gathering_date	Date (DD/MM/YYYY):	date	YYYY-MM-DD	NA	1
no_hhd	How many household members?	int_ordinal	NA	0, 100	0
sick_hhd_yn	Do you have any household members who are sick?	int_categorical	NA	0=unknown;1=yes;2=no	0
sick_hhd_onset	date of onset (DD/MM/YYYY)	date	YYYY-MM-DD	NA	1
sick_comm_yn	Are you aware of people outside your household who are sick?	int_categorical	NA	0=unknown;1=yes;2=no	0
sick_comm_rel	Relationship	int_categorical	NA	1=friend;2=workmate;3=relative	1
sick_comm_onset	date of onset (DD/MM/YYYY)	date	YYYY-MM-DD	NA	0
contact_sym_yn	Did you have any contacts who are sick?	int_categorical	NA	0=unknown;1=yes;2=no	0
contact_sym_date	Date of last contact (DD/MM/YYYY)	date	YYYY-MM-DD	NA	0
travel_hist_yn	Did you travel, outside your region?	int_categorical	NA	0=unknown;1=yes;2=no	0
travel_hist_date	Traveling Date (DD/MM/YYYY)	date	YYYY-MM-DD	NA	1

References

For each disease: Reference = Variable *name*, *weight*, *observations*, *extension*

weight = how indicative of the disease

observations = range of expected answers

extension = expected 50% confidence interval of answers [optional]

name	weight	observations	extension
report_date	0	NA	252
notification_facility_type	0.5	1, 4	NA
birth_date	0	NA	9
age_year	1	49, 97	45
sex	0.5	1	NA
occupation_hcw	1	1	NA
gps_lat	1	2.78, 165.12	69.16
gps_long	1	91.61, 136.61	35.26
mass_gathering_yn	1	2	NA
mass_gathering_date	0	NA	344
no_hhd	0	32, 88	26

5 fake random references

Blue Fever, Danger Fever, Kleptospirosis, Viral Hepatitis Z, West Rhine Virus

5 real references: rough estimates

Hepatitis A, Hepatitis E, Leptospirosis, Mushroom, Yellow Fever

Line lists (events)

Generate synthetic events:

1. completely **random** cases
2. all cases drawn randomly from **1 disease** reference
3. all cases from **1 disease** but with **noise**
4. cases from **2 diseases** (half/half)
5. cases from **2 diseases** (half/half), with **noise**

with noise = 50% of variables of any one case are completely random

case_id	report_date	notification_fr	birth_date	age_year	sex	occupation_h	gps_lat	gps_long	mass_gatheri	mass_gatheri
danger_fever_event_1	2015-02-05	4	2018-08-20	54	2	1	-10.561609198	-118.40378069	2	2017-09-13
danger_fever_event_2	2019-09-01	4	2017-12-21	47	2	1	-16.694285074	-62.322222565	2	2015-08-08
danger_fever_event_3	2019-04-22	1	2015-02-11	44	2	1	6.1287991879	-102.70033583	2	2015-09-04, 20
danger_fever_event_4	2019-10-18	1	2015-06-10	44	2	1	1.6473386705	-100.35858407	2	2016-05-15, 20
danger_fever_event_5	2018-07-12	4	2017-12-24	43	2	1	-18.524208949	-40.380729289	2	2015-01-04, 20
danger_fever_event_6	2018-12-01	4	2018-10-24	58	2	1	-6.7130254994	-127.62705966	2	2017-01-02, 20
danger_fever_event_7	2017-05-14	1	2016-05-25	64	2	1	32.523126923	-140.13485732	2	2015-05-30, 20
danger_fever_event_8	2016-01-02	1	2017-05-17	44	2	1	-21.088938099	-19.647448508	2	2018-02-26
danger_fever_event_9	2018-01-03	1	2018-04-11	44	2	1	-7.3504254324	-112.05122689	2	2018-03-15, 20
danger_fever_event_10	2019-09-15	3	2015-10-15	59	2	1	-20.667682803	48.591987626	2	2015-10-22, 20
danger_fever_event_11	2015-08-23	4	2017-07-22	55	2	1	-15.869003509	-137.3709156	2	2016-03-16, 20
danger_fever_event_12	2015-05-25	3	2017-07-31	44	2	1	5.0164222981	-106.83533791	2	2015-07-01

3. Score

1 score for each case and each reference = how similar is this case to the reference?

For each variable:

- answer **within** range or set of reference *observations*: **+1**
- **missing** answer or “unknown”: **+0.5**
- answer **outside** of reference *observations*: **+0**

Score = weighted average over variables using the reference *weights*

(*extension* not used at the moment for scoring)

Case ~ reference \rightarrow score = 1

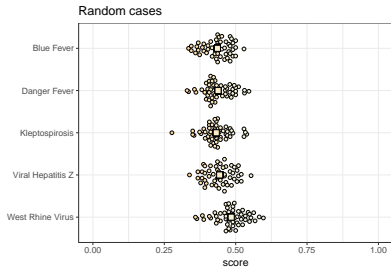
Case outside reference \rightarrow score = 0

Random case \rightarrow score \approx 0.5

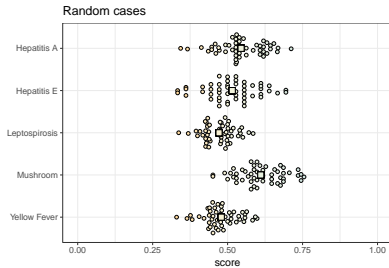
Tested 5 types of events for 2 sets of references = 10 scenarios

Scores: Random cases

fake references



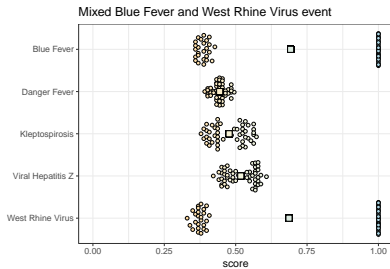
real references



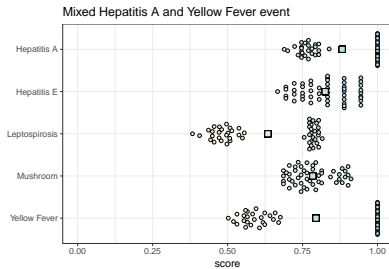
1 dot = 1 case / square = average

Scores: Cases from 2 diseases

fake references



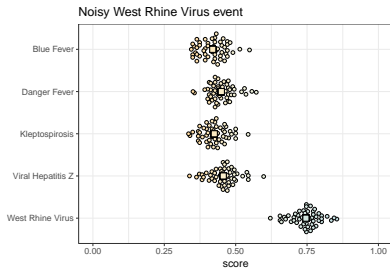
real references



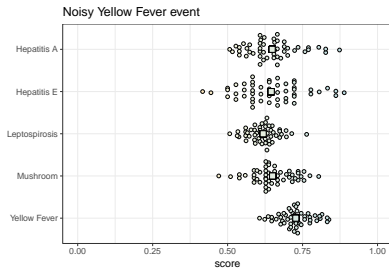
1 dot = 1 case / square = average

Scores: Cases from 1 disease with noise

fake references



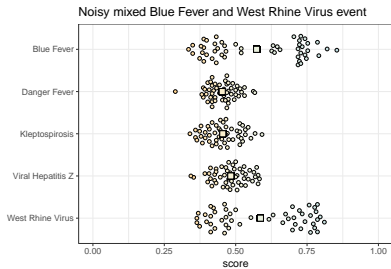
real references



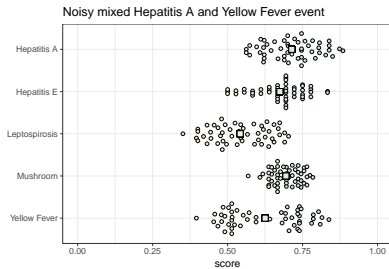
1 dot = 1 case / square = average

Scores: Cases from 2 diseases with noise

fake references



real references



1 dot = 1 case / square = average

4. Dimensionality reduction

Reduce dimensionality from 117 to 2 using the t-SNE algorithm

Needs a **distance** between cases:
similar approach and difficulties as for score

With d_{ij} the distance between case i and case j , and w_v the weight for variable v averaged over all references:

$$d_{ij} = \sqrt{\sum_v w_v d_{ijv}^2 / \sum_v w_v}$$

with

$d_{ijv} = \min_{m,n} |v_{im} - v_{jn}| / \max_{i,j} (\min_{m,n} |v_{im} - v_{jn}|)$ if variable is *int_ordinal*, *float* or *date*

$d_{ijv} = 1 - \delta(|\{v_{im}\}_m \cap \{v_{jn}\}_n|)$ if variable is *int_categorical*

$d_{ijv} = 0.5$ if any answer is missing

where v_{im} is the m -th observation of variable v for case i , and $\delta(x) = 0$ if $x = 0$, 1 else.

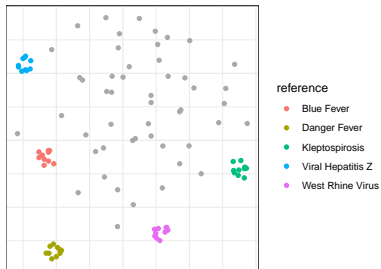
Smallest distance is 0 and largest distance is 1

Include **reference cases** for comparison

2d projection: Random cases

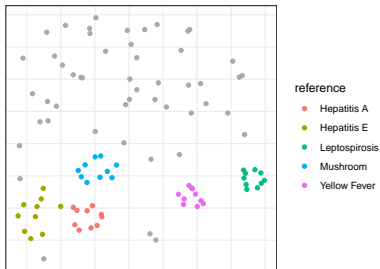
fake references

Random cases



real references

Random cases

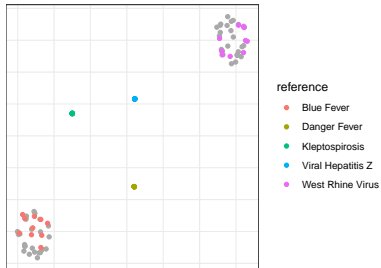


Caution: Cluster size doesn't mean anything

2d projection: Cases from 2 diseases

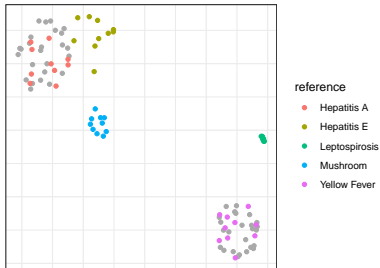
fake references

Mixed Blue Fever and West Rhine Virus event



real references

Mixed Hepatitis A and Yellow Fever event

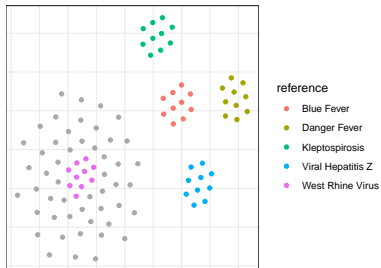


Caution: Cluster size doesn't mean anything

2d projection: Cases from 1 disease with noise

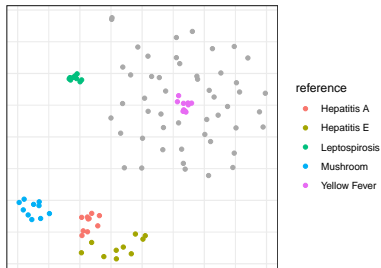
fake references

Noisy West Rhine Virus event



real references

Noisy Yellow Fever event

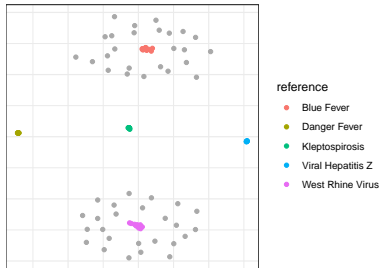


Caution: Cluster size doesn't mean anything

2d projection: Cases from 2 diseases with noise

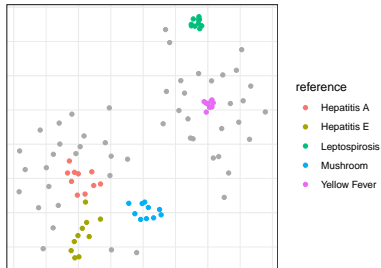
fake references

Noisy mixed Blue Fever and West Rhine Virus event



real references

Noisy mixed Hepatitis A and Yellow Fever event



Caution: Cluster size doesn't mean anything

5. Web application

R Shiny prototype

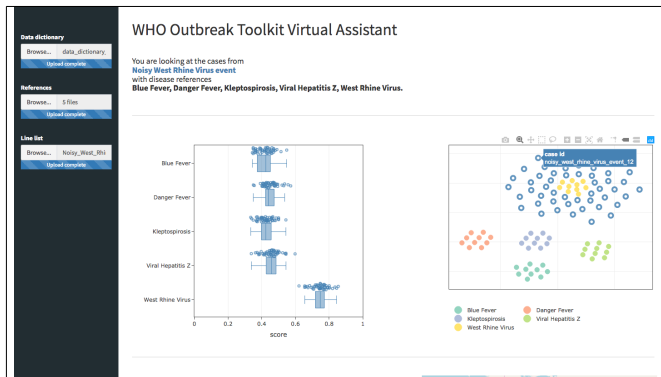
Input: upload data dictionary, set of references and 1 line list

Output: scores, 2d projection, epicurve, map, line list, pivot table

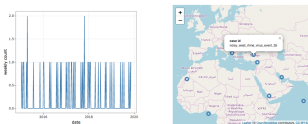
Installation:

local at the moment

WHO cloud (internal) or online (public) in the future



You are looking at the cases from
[Niley West Nile Virus event](#)
 with disease references
[Blue Fever](#), [Dengue Fever](#), [Kryptospirosis](#), [Viral Hepatitis E](#), [West Nile Virus](#)



History	cancel_year =	age_year =	total_amount =
Count	age_label_age =	sex =	

water_drinking_qty =	age_label_age	1	2	3	4	5	6	7	8	
	sex									Total
	water_drinking_qty	1	1	1	1	1	1	1	1	
	1									
	2	1	1	1	1	1	1	1	1	
	3									
	4	1	1	1	1	1	1	1	1	
	5									
	6									
	7									
	8									
	Total	1	1	1	1	1	1	1	1	

6. Conclusion and outlook

Conclusion

Already simple approaches are promising and deliver useful insights

2d visualisation: discriminates better
scores: single number per case / for the whole event

Usefulness for potential users can be probed: Are the *functionalities* interesting?

What's next? 2 possible directions

1. Improve and evaluate method

- computation time
- distinguish between suspected, confirmed and excluded cases
- find real line lists and convert to data-dictionary format
- evaluate the tool
- establish the reference for each epidemic prone disease
- machine learning (classification)

Resources needed: at least 1 data scientist & 1 medical expert

2. Prospective piloting

- build as software *or* integrate in other tools (Go.Data?)
- feasibility study needed

Resources needed: at least 1 software engineer

Ideas for collaborations:

- make an R package and share it with community, e.g. RECON
- Cambridge working group on same topic
- WHO Medical expert group, Antwerp (medical experts), READY project (USAIDS), RKI

Thank you!

Advertisement:

Anomaly detection for EIOS

Machine learning and natural language processing to detect signals in stream of articles

Signale team at the Robert Koch Institute
data science for infectious-disease epidemiology
rki.de/signale-project