Reproducibility review of: H-TFIDF: What makes areas specific over time in the massive flow of tweets related to the covid pandemic?

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2021-06-07



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Reviewed paper

Decoupes, R., Kafando, R., Roche, M., and Teisseire, M.: H-TFIDF: What makes areas specific over time in the massive flow of tweets related to the covid pandemic?, AGILE GIScience Ser., 2, 2, https://doi.org/10.5194/agile-giss-2-2-2021, 2021.

Summary

The authors provide a well documented workflow analysing a large number of Tweets over a considerable time span. Because of the data size, the authors provided instructions for a data subset, for which the code could be executed successfully and the created figures match the provided baseline, and also confirm that data can be created and the code is available for the results reported in the paper.

Reproducibility reviewer notes

Started with the anonymous repo at https://anonymous.4open.science/r/450b6e01-dbad-4ce4-a249-d53e88b6ff8c/README.md I went trough the pre-requisite steps as below; in the meantime, communication with the authors happened and the review was continued based on the code repository https://gitlab.irstea.fr/remy.decoupes/covid19-tweets-mood-tetis which is archived to https://doi.org/10.5281/zenodo.4742152.

[I also started applying for an academic Twitter project to handle the large number of requests, but did not follow though.]

```
git clone https://github.com/echen102/COVID-19-TweetIDs

mkvirtualenv agile-025
pip install —upgrade twarc
twarc configure

# The credentials for nordholmen have been saved to your configuration file at /home/daniel/.twarc

# following https://github.com/echen102/COVID-19-TweetIDs#hydrating-using-twarc-cli
pip3 install tgdm

# in ./COVID-19-TweetIDs
python3 hydrate.py
```

This ran for ~ 4 hours, then threw RecursionError: maximum recursion depth exceeded while calling a Python object, but luckily, hydrate.py skips existing files, so I just restarted the process. After several more hours, I reached out to the authors and asked for a smaller reproducible workflow.

Continue review based on de-anonymised repo gitlab.irstea.fr/remy.decoupes/covid19-tweets-mood-tetis.

```
git clone https://gitlab.irstea.fr/remy.decoupes/covid19-tweets-mood-tetis pip3 install -r covid19-tweets-mood-tetis/requirements.txt
```

Now, I try to run the "mini reproducible workflow" described in https://gitlab.irstea.fr/remy.decoupes/covid19-tweets-mood-tetis#run-a-mini-reproducibility-workflow-for-agile2021.

```
cd covid19-tweets-mood-tetis/
git checkout agile-reproducibility
export PWD-8(pwd)

cd experiments/agile21/echen_input_filtred/tweets/&& python3 hydrate.py
# takes just a few minutes

mkdir hydrating-and-extracting && find . —name '*.jsonl.gz' —exec cp —prv '{}' 'hydrating-and-extracting' ';'
gunzip hydrating-and-extracting/id.jsonl.gz
```

I run the indexing and geocoding in a container as follows. First I start Elasticsearch, following https://www.elastic.co/guide/en/elastic-stack-get-started/master/get-started-docker.html and adjusting paths and the host in logstash—config/{json.conf,twitter_template.json}. The local directories are mounted into the log01 container.

```
# configure Elasticsearch to not complain about only 40 GB left... https://stackoverflow.com/a/63881121/261210

curl -NTUT-H "Content-Type:_application/json" http://localhost:9200/_all/_settings -d '\[.\]'translocks.read_only_allow_delete":_null}'

# start a logstash container and connect it to the network with access to the required files
docker run -it —name log01 — network 025_clastic -v \$[pxd]\]/covid19-tweets-mood-tetis/experiments:/experiments/-v \$[pxd]\]/covid19-tweets-mood-tetis/experiments/-v \$[pxd]
```

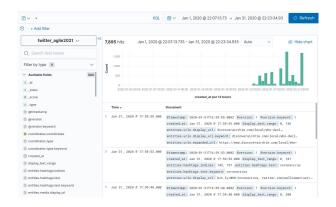


Figure 1: Screenshot of Kibana after loading Tweets

I let this run overnight and got 7985 tweets, as shown in the Figure below.

The geocoding seems to have worked:



Figure 2: Screenshot of Kibana: Tweet geolocation on map

Next, I try to run the main script:

python COVID-19-TweetIDS-ES-Analyse.py

The scripts seems to run successfully:

```
The scripts seems to run successfully:

//scm/daniel/virtualenvs/agile-025/lib/python3.8/site-packages/torch/cuda/_init__py:52: UserWarning: CIDA initialization: Found no NVID/pytorch/cl0/cuda/CUDAFunctions.cpp:100.)

return torch_C_cuda_getDeviceCount() > 0

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post-traitement flooding on: country

/home/daniel/.virtualenvs/agile-025/lib/python3.8/site-packages/tqdm/std.py:668: FutureWarning: The Panel class is removed from pandas. Accessing it from the top-level namespar from pandas import Panel

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The script also created some output files in experiments/agile21/results/jan_2weeks_week/, including some figures (see below), which match the ones mentioned in the README for the reduced workflow with small changes that can be explained due to the non-deterministic creation of the test dataset.

These figures resemble the ones in the paper using the full dataset. Therefore, I am confident the code and data underlying the analysis of the paper are available (or can be created) with the files shared in the repository. The authors provide detailed documentation for a pretty complex workflow.

The changes made to the configuration (e.g., to make it work with my container setup) using the agile—reproducibility branch of the repository are saved to a diff-file published alongside this document and the code is forked to the Reproducible AGILE GitLab organisation.

Comments to the authors

- Good job using anonymous.4open.science in the original submission!
- I don't really like the solution to put the small reproducible workflow into a branch this means that the example code will digress from the original workflow and will at some point be likely to

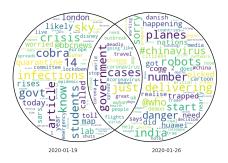
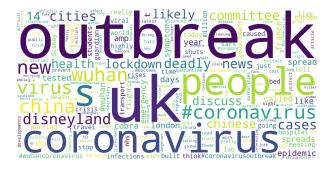


Figure 3: Venn diagramm per week for UK, file covid19-tweets-mood-tetis/experiments/agile21/results/jan_2weeks_week/venn/venn_United Kingdom.png



 $\label{lem:figure 4: Reproduction of Figure 3 (only one of two weeks). Wordcloud of H-TFIDF terms; file covid19-tweets-mood-tetis/experiments/agile21/results/jan_2weeks_week/country/wordcloud/United_Kingdom_2020-01-19.png \end{tabular}$

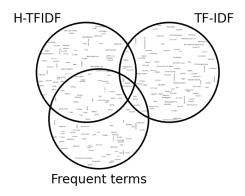


Figure 5: Reproduction of Figure 4. Common terms between H-TFIDF, TF-IDF and most frequent terms for United Kingdom in the last week of February; file covid19-tweets-mood-tetis/experiments/agile21/results/jan_2weeks_week/common/most_frequent_terms_by_country_United 0Kingdomvenn3.png

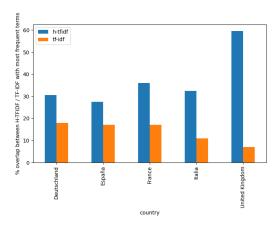
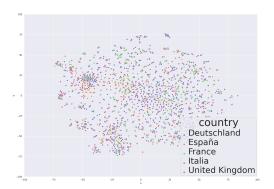


Figure 6: Reproduction of Figure 5 (only top 100 terms). Comparison of percentage of common words between H-TFIDF or TF-IDF with the most frequent terms per country; file covid19-tweets-mood-tetis/experiments/agile21/results/jan_2weeks_week/common/most_frequent_terms_by_country_100.png



 $\label{eq:figure 7} Figure~7: Reproduction~of~Figure~6a. Projection~of~H-TFIDF~representation~in~a~t-SNE~space;~file~covid19-tweets-mood-tetis/experiments/agile21/results/jan_2weeks_week/tsne/tsne_bert-embeddings_H-TFIDF.png$

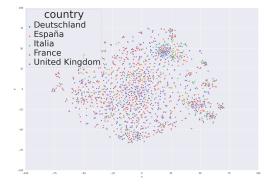


Figure 8: Reproduction of Figure 6b. Projection of TF-IDF representation in a t-SNE space; file covid19-tweets-mood-tetis/experiments/agile21/results/jan_2weeks_week/tsne/tsne_bert-embeddings_TF-IDF on corpus by Country.png

- break; I'd prefer to have a subdirectory, ideally you package the reusable parts of the workflow in a proper Python package
- Maybe the docker-compose configuration shared with this review is useful to you it would be great if you could come a bit closer to a "one click reproduction" with the help of containers, e.g., the steps that I did for logstash could also be automated with the help of a Dockerfile
- Please add information to the README regarding data sizes and expected runtimes! When I started cloning the Echen repo, I did not expect to download gigabytes of data. authors updated the README
- Please provide clear usage instructions in the README, including a list of table mapping scripts/commands to each figure in the manuscript (How can I recreate Figure x?) authors updated the README
- You can also add repository from GitHub in your own requirements.txt file and make installation of tware easier, see https://stackoverflow.com/a/35998253/261210 changed by authors
- A more suitable page for installing twarc would be https://twarc-project.readthedocs.io/en/latest/
- Please provide direct links to installation instructions for the ELK stack IMO a ready-to-use docker—compose configuration would be a good idea, the one I used is published in the reproduction material; also, specify the Elasticsearch version that you used.
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