Automated screening of COVID-19 preprints: Can we help authors to improve transparency and reproducibility?

Peter Eckmann, Nico Riedel, Halil Kilicoglu, Gerben ter Riet, Cyril Labbé, Jennifer Byrne, Guillaume Cabanac, Amanda Capes-Davis, Bertrand Favier, Shyam Saladi, et al.

Automated screening of COVID-19 preprints: Can we help authors to improve transparency & reproducibility?

Peter Eckmann[1], Nico Riedel[2], Halil Kilicoglu[4], Cyril Labbé[5], Gerben ter Riet[6,7], Jennifer Byrne[8], Guillaume Cabanac[9], Amanda Capes-Davis[8,10], Bertrand Favier[11], Shyam Saladi[12], Peter Grabitz[2,3], Alexandra Bannach-Brown[2], Robert Schulz[2,3], Sarah McCann[2,3], Rene Bernard[2,3], Anita Bandrowski[1], Tracey Weissgerber[2,3]

[1]UC San Diego, La Jolla, CA, USA, [2]Berlin Institute of Health, Germany, [3]Charité, Berlin, Germany, [4]Univ. of Illinois at Urbana-Champaign, IL, USA, [5]Univ. Grenoble Alpes, France, [6]Univ. of Amsterdam, Netherlands, [7]Amsterdam Univ. of Applied Sciences, Netherlands, [8]Univ. of Sydney, Westmead, New South Wales, Australia, [9]Univ. de Toulouse, France, [10]CellBank Australia, [11]Univ. Greonble Alpes, La Tronche, France, [12]California Institute of Technology, CA, USA

Background

- Preprints have grown in popularity since COVID-19 emerged
- Rapid publication is useful during a pandemic, but the lack of peer review has concerned many scientists
- Can we evaluate preprints at scale without relying on authors or the knowledge of readers?

Evaluation

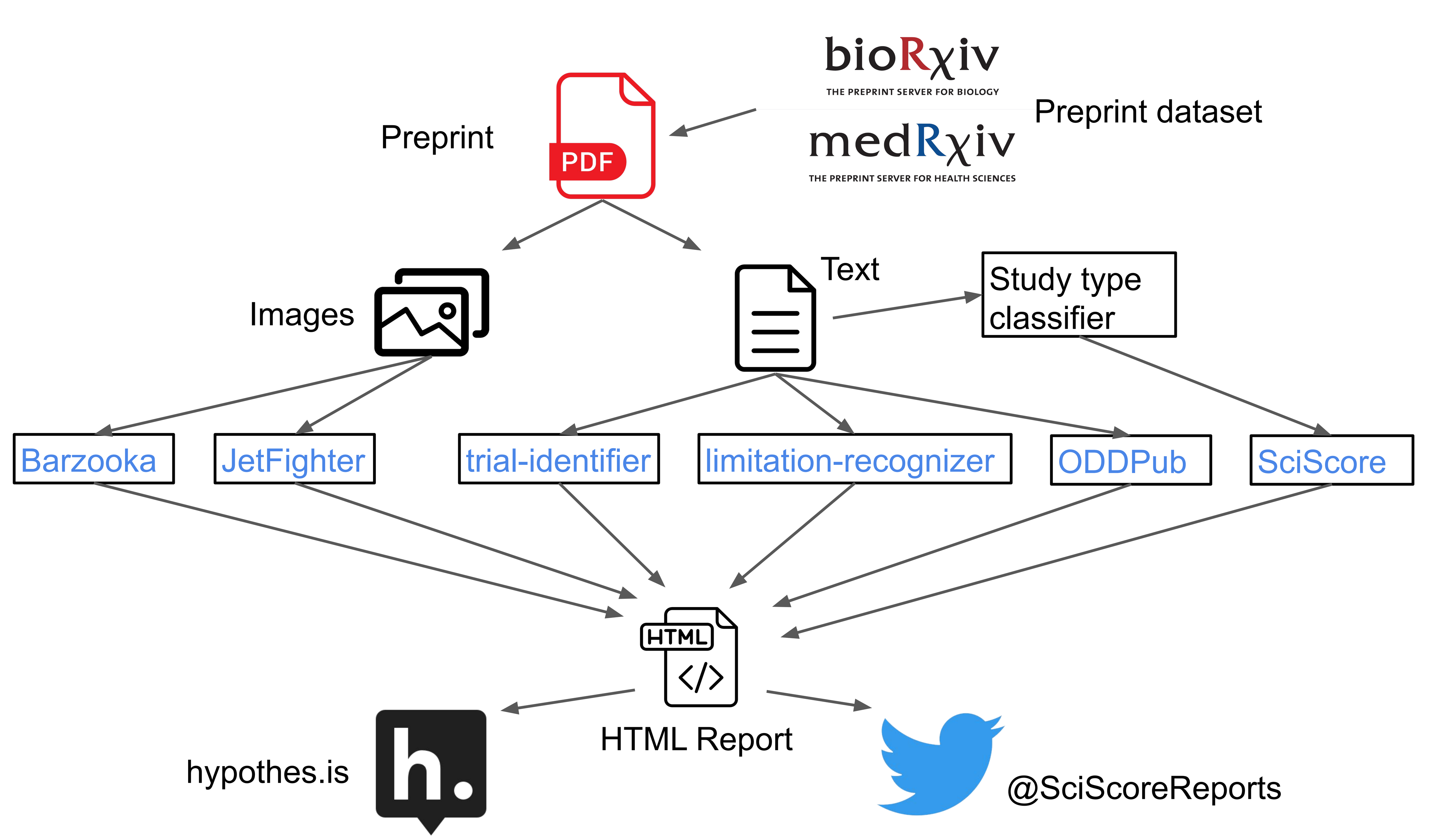
- Goal to automatically evaluate COVID-19 preprints for reproducibility criteria
- Each preprint is downloaded, parsed, and analyzed by a set of tools:
  - SciScore screens for rigor criteria defined by NIH and resources used (software tools, cell lines, etc.)
  - ODDPub screens for the presence of open data and code
  - Limitation-recognizer screens for study limitation statements
  - Barzooka screens for bar graphs used for continuous data
  - JetFighter screens for rainbow color maps
  - Seek&Blastn screens for correctly identified nucleotide sequences
  - Trial-identifier screens for and verifies clinical trial numbers

Visit us at

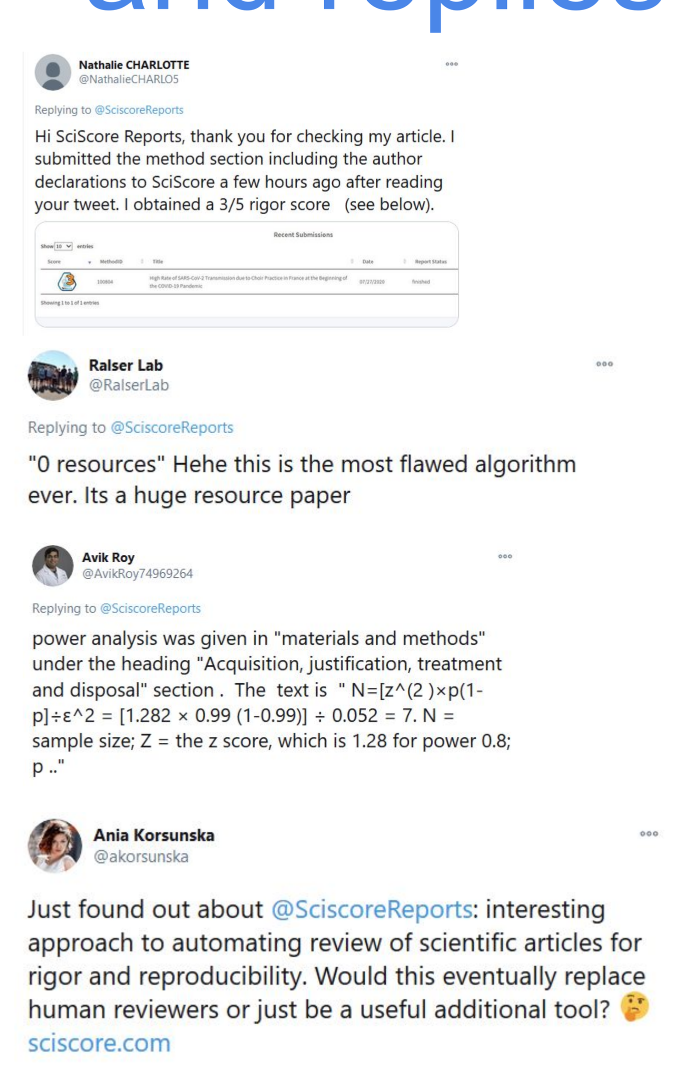
https://scicrunch.org/ASWG

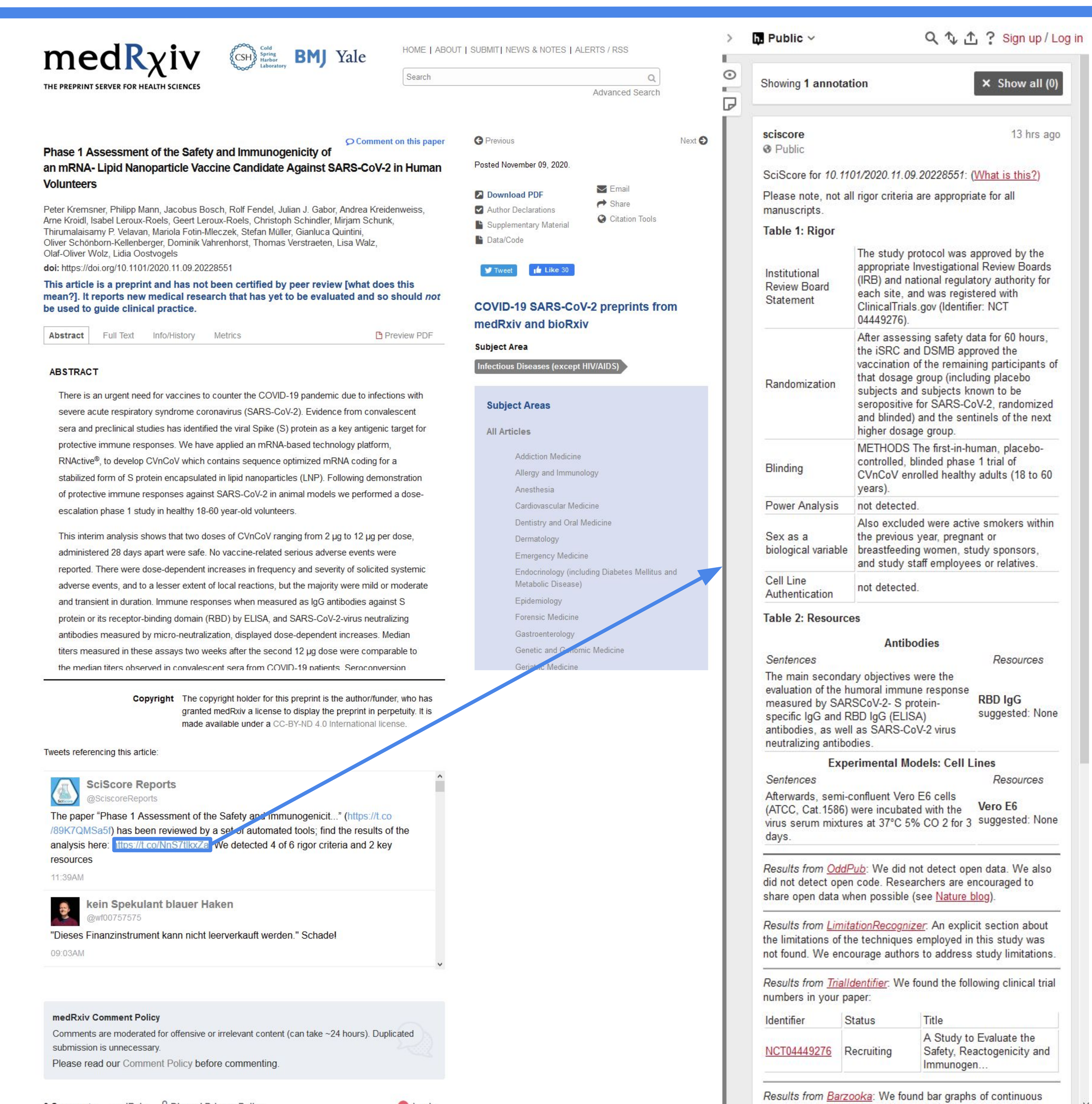
https://twitter.com/SciscoreReports

Pipeline overview



Sample report and replies





Results

- Study design features
  - 75% of analyzed preprints are secondary analyses, modeling studies, or cell line studies
  - 20% addressed sex as a biological variable, despite known sex differences in COVID-19
  - 6.1% used model organisms, mainly mice
- Transparency
  - 34.4% included self-acknowledged study limitations
  - 14.3% shared open code
  - 13.6% of preprints shared open data
- Data presentation
  - 7.6% used rainbow colormaps, which are not colorblind safe and can create visual artifacts for viewers with normal color vision
  - 7.3% used bar graphs for continuous data, which can lead to misleading figures

- Combined, the automated Tweets have been viewed about 380,000 times
- Current average of ~1,000 views and ~10 link clicks per day
- The account has accumulated a total of
  - 2459 link clicks
  - 98 retweets
  - 42 replies

Conclusions

- It is feasible to conduct large-scale automated screening of preprints for common quality criteria and provide feedback to study authors and readers before publication
- Reports can publicly raise awareness of factors that affect study quality and reproducibility, while helping authors to present their research in a more transparent and reproducible manner.