

100,000+ visitors
 17,000+ analyses
 14,000+ stored type strain genomes
 2,600+ active users
 9,7M+ genome comparisons
 260+ citations so far

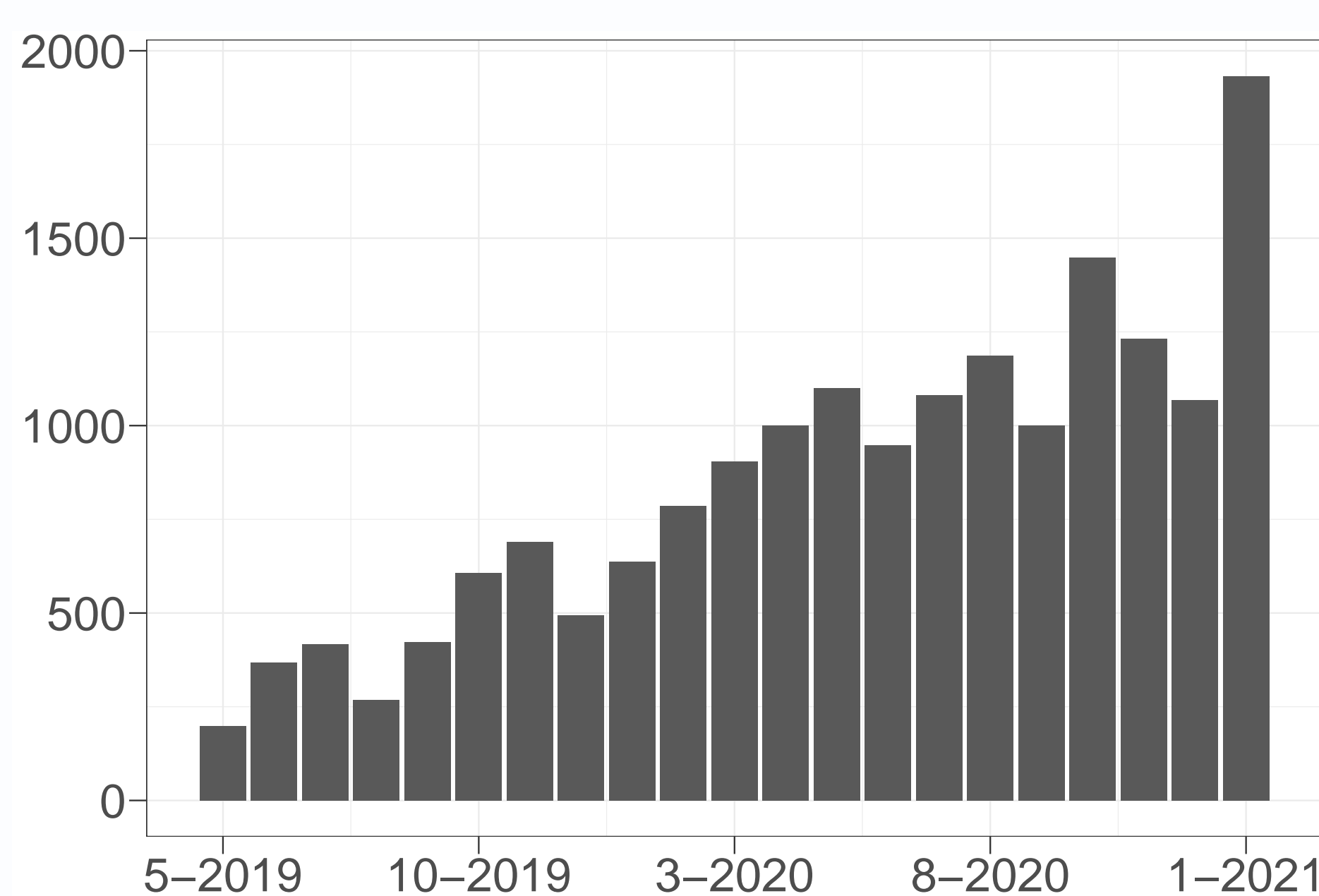


TYGS 2020 Year in Review

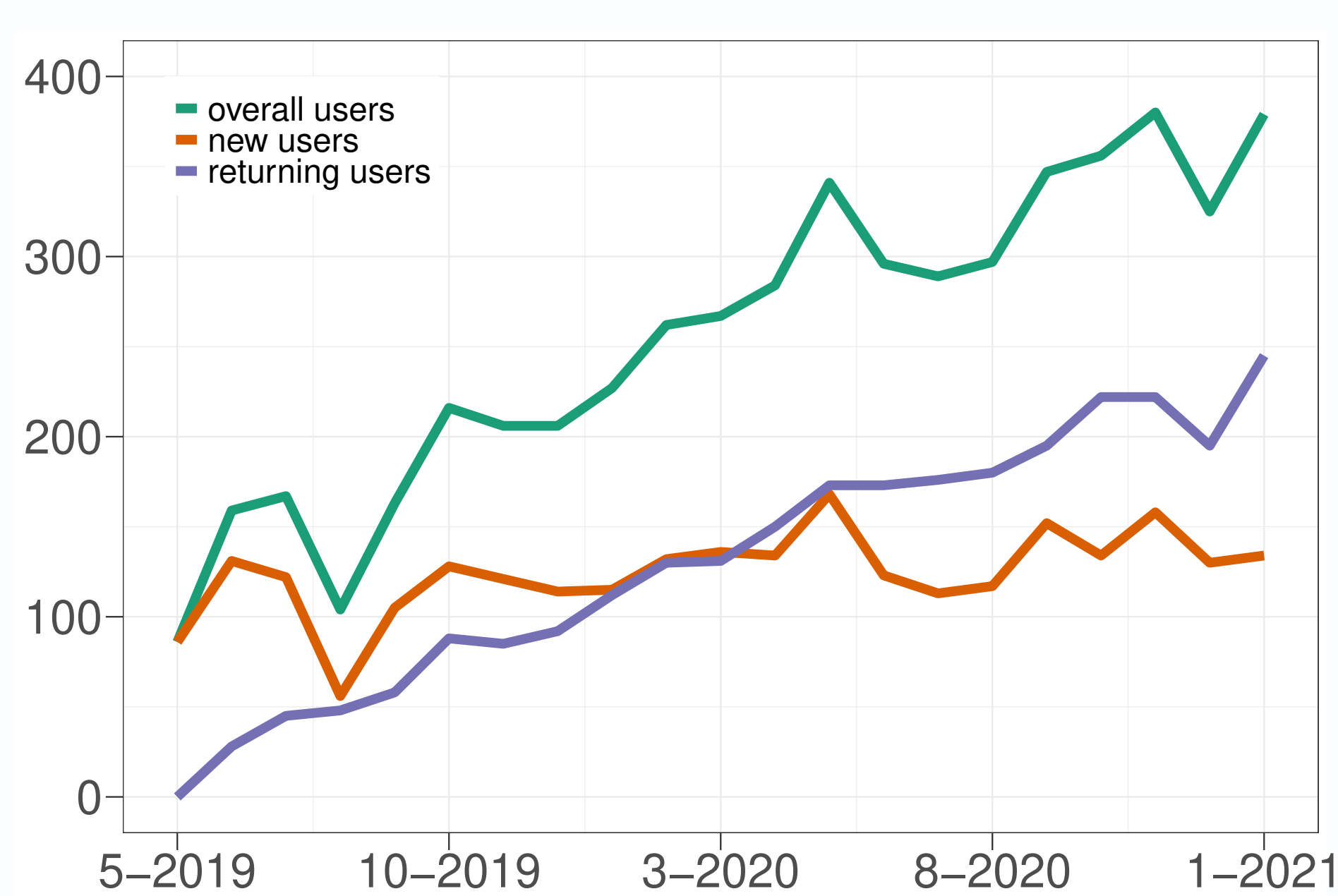
DSMZ platform for automated genome-based taxonomy in numbers

Jan Meier-Kolthoff

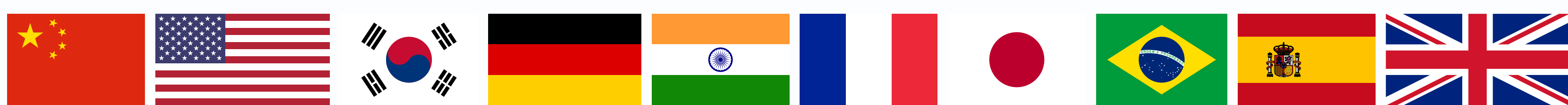
Monthly job submissions



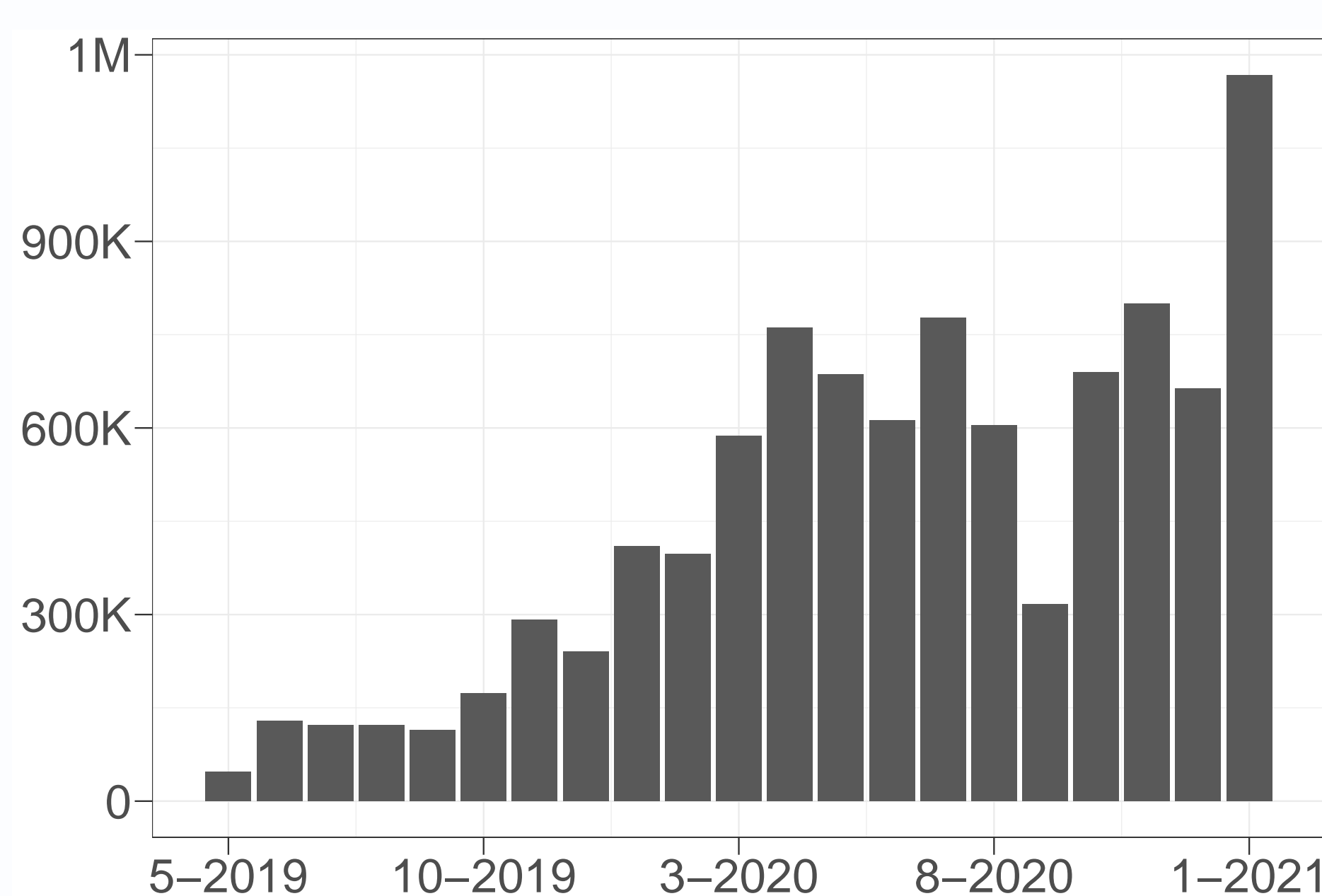
New vs. returning users



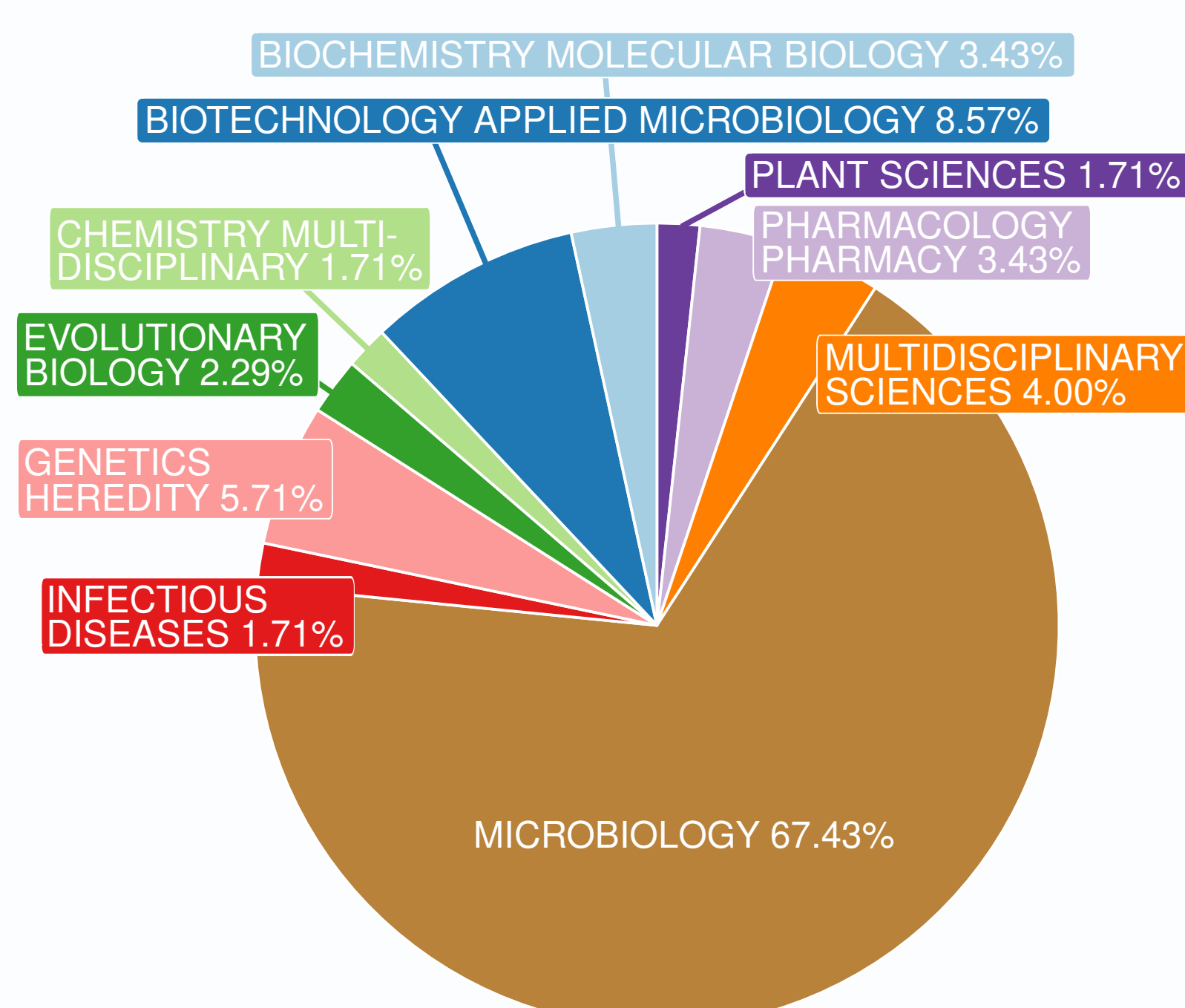
Ten most frequent locations of TYGS users



Genome comparisons



Analysis of citations



Major achievements and updates in 2020

- As of July/August 2020, the TYGS paper is placed in the top 1% of the academic field of Microbiology based on the Web of Science (tm) 'highly cited' threshold.
- LPSN-TYGS interface: TYGS analyses of species and entire genera can now be easily triggered from within LPSN
- option to download a publication-ready PDF report on each TYGS job
- fast, complementary genome-only-based determination of closest type strains
- extended API access

Feedback

"Congratulations to this great tool! It's better and much faster than everything I tried before to get complete information about taxonomy (phylogenomics) of novel genome sequences."

TYGS user from Humboldt University of Berlin, Germany

"Thank you for developing TYGS. It seems a very valuable resource for promoting the transition to proper genome-based taxonomy."

TYGS user from University of York, UK

"I just wanted to tell you how much I appreciate using TYGS, and how much my students love it as a tool that starts each of their taxonomy projects."

TYGS user from Midwestern University, USA

"It is a very good platform and convenience for users."

TYGS user from Shenzhen University, China

"I think that the pipelines you guys have developed are awesome and SO helpful, thank you!"

TYGS user from University of North Carolina at Charlotte, USA

"Vielen Dank für die Arbeit mit TYGS, was eine sehr praktische Ergänzung zu meiner taxonomischen Arbeit bietet."

TYGS user from Institut f. Med. Mikrobiologie, Rostock

"What a great step-up from GGDC to the TYGS server!"

TYGS user from some Biotech Company, Denmark

"Congrats for your outstanding website."

TYGS user from Public Health Ontario, Canada

"Thank you for recommending TYGS the other day. This is a very useful tool and we are currently working on further analysis."

TYGS user from Tokyo University, Japan

"I am very thankful for devising such a wonderful online tool for phylogenetic analysis. It is very user friendly and comprehensible"

TYGS user from University of Hyderabad, India

"I am really grateful for your work and the possibility of using TYGS."

TYGS user from Max Rubner-Institute, Germany

"TYGS is always very helpful in doing our researches. Thank you very much for running such a convenient site."

TYGS user from National Agriculture and Food Research Org., Japan

"Congratulations on putting together this great server."

TYGS user from California Institute of Technology, USA

"Thank you very much for TYGS, very useful for a beginner like me."

TYGS user from Okayama University, Japan

"I am using the TYGS server and so excited about the user-friendly interface and the output."

TYGS user from AIST, Japan

"Congratulations on creating the TYGS tool, it helped a lot in my research. I loved the tree graphic design"

TYGS user from Universidade Federal do Paraná, Brazil

"I am impressed by how good the TYGS server works. Congratulations!"

TYGS user from Max Planck Institute of Biochemistry, Germany

"Thanks a lot to all of the TYGS team for TYGS! It's definitely much easier to use TYGS than to manually collect all the type strains"

TYGS user from Justus Liebig University Giessen, Germany

"I have been using your website for analysing taxonomy of a bacteria species, and it has provided me very useful information."

TYGS user from UNSW Sydney, Australia



TYPE (STRAIN)
GENOME SERVER

<https://tygs.dsmz.de>
Nat. Commun. 10, 2182 (2019)

Questions? Contact us via
<https://tygs.dsmz.de/feedback/new>

