Winter 2021, Schedule of papers

The topic this quarter is "Statistical genetics and its application to Covid-19/SARS-Cov-2". I have chosen a selection of papers on Covid-19 published in 2020-2021, or still in BioRxiv.

Week 1 (January 5). Everyone. Overview of the general topic, and some background.

Come prepared to provide at least one comment about what you know about on topics related to Covid-19 (the disease) or SARS-Cov-2 (the virus).

Week 2 (January 12). Alan Min, leader. GWAS and single-gene association analyses.

GWAS studies

Ellinghaus, D. et al. (2020). Genomewide Association Study of Severe Covid-19 with Respiratory Failure. New England Journal of Medicine 383, 1522-1534. (Ellinghaus uses a clinical phenotype and nominates two regions including ABO)

Zeberg, H., and Paabo, S. (2020). The major genetic risk factor for severe COVID-19 is inherited from Neanderthals. Nature 587, 610-612. (Zeberg uses Covid hospitalizations and nominates 1 region in common with Ellinghaus)

ABO:

May, J.E., et al. (2020) Questioning the association between ABO type and outcomes in patients with COVID-19. Annals of Hematology. (online). (A quick paper to read: May raises questions about the ABO association, but the sample size isn't huge - results in small samples are mixed.)

Week 3 (January 19). Seth: BEAST (phylodynamic estimation of a viral tree)

Gill MS et al (2020) Online Bayesian phylodynamic inference in BEAST with application to epidemic reconstruction. Molecular Biology and Evolution 37(6):1832 - 1842. doi: 10.1093/molbev/msaa047.

Suchard MA et al (2018) Bayesian phylogenetic and phylodynamic data integration using BEAST 1.10. Virus Evolution 4(1):vey016. doi: 10.1093/ve/vey016.

It will be helpful, first, to look at an analysis approach that permeates a lot of the work related to our understanding of the SARS-Cov-2 virus and its epidemiological spread. A challenge is the tremendous literature on estimating and using data on phylogenies. In the current context, the paper by Gill is likely to be the more useful, so that should be the focus of our discussion. The paper by Suchard lists some of the current features of BEAST that may be relevant, so a quick read would be useful.

Week 4 (January 26). Nasif & Sanne: Initial spread of Covid-19 in WA.

Bedford T et al. (2020) Cryptic transmission of SARS-CoV-2 in Washington state. Science 370:571-575. doi: 10.1126/science.abc0523.

This is the work that indicated (to the world) very early in the pandemic that there was community spread of the virus, either by people who were not recognized as being sick with Covid-19, or by asymptomatic people.

Week 5 (February 2). Hanley & Lily. Origin of the SARS-CoV-2 virus.

Hu et al (2020). Characteristics of SARS-CoV-2 and COVID-19. Nature Reviews Microbiology (Oct. 6, 2020 online) - the first 5.5 pages, which summarizes the issues with determining the source of the virus (skip the biochemistry part in the second half).

Latinne et al (2020) Origin and cross-species transmission of bat coronaviruses in China. Nature Communications 11. (The main paper).

Ul-Rahman et al (2020) A comparative phylogenomic analysis of SARS-CoV-2 strains reported from non-human mammalian species and environmental samples. Molecular Biology Reports 47:9207-9217 (for their clustering of viral sequences taken from animals together with humans).

Week 6 (February 9). Nandana. Spread of Covid-19 in Europe & N. America

Worobey M et al (2020) The emergence of SARS-CoV-2 in Europe and North America. Science 370:564-570.

Week 7 (February 16). Nobu. Complications of combined samples.

Turakhia et al. (2020) Stability of SARS-CoV-2 phylogenies. PLoS Genetics 16(11) e1009175. doi: 10.1371/journal.pgen.1009175. [This is the main paper]

Gaudin & Desnues (2018) Hybrid capture-based next generation sequencing and its application to human infectious diseases. Frontiers in Microbiology 9 art. 2924. doi:10.3389/fmicb.2018.02924. [Short review of sequencing techniques for small organisms. Also useful is the wikipedia page on Exome Sequencing: https://en.wikipedia.org/wiki/Exome_sequencing (Links to an external site.) (up to but not beyond the section on Ethical issues), and the page on DNA Sequencing: https://en.wikipedia.org/wiki/DNA_sequencing, (Links to an external site.) especially some information in section 6 on high-throughput methods]

Week 8 (February 23). Ruoyi & Jacob. Deep mutational scanning: mutation interpretation and potential.

Starr et al (2020) Deep Mutational Scanning of SARS-CoV-2 Receptor Binding Domain Reveals Constraints on Folding and ACE2 Binding Cell 182 (5):1295 [the main Covid-19 paper]

Fowler and Fields (2014) Deep mutational scanning: a new style of protein science. Nature Methods 11(8):801-807. [This paper outlines the principles underlying the methods used by Starr et al. Also, some of the issues mentioned in the Week7 Wikipedia articles may be useful and relevant].

Week 9 (March 2). Zorian. Evolution of the virus.

Tasakis et al (2021) SARS-CoV-2 variant evolution in the United States: High accumulation of viral mutations over time likely through serial Founder Events and mutational bursts. bioRxiv preprint, doi: https://doi.org/10.1101/2021.02.19.431311; this version posted February 19, 2021. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. [This is not peer reviewed, so keep that in mind when reading it]

and

Choi et al (2020) Persistence and Evolution of SARS-CoV-2
in an Immunocompromised Host. New England Journal of Medicine. 383:2291-2293.

Week 10 (March 9). Yunqi. New SARS-CoV-2 variants: which ones are of concern?

To set the stage, read the short report by Rambaut at the following link:
https://virological.org/t/preliminary-genomic-characterisation-of-an-emergent-sars-cov-2-lineage-in-the-uk-defined-by-a-novel-set-of-spike-mutations/563 (Links to an external site.)

Starr TN et al. (2021) Prospective mapping of viral mutations that escape antibodies used to treat COVID-19. Science 371(6531):850-854. [Main paper - This paper is a followup of the previous Starr et al paper on deep mutational scanning, and uses in-vitro methods to evaluate what allows escape from antibodies].

Wang P et al. (2021) Antibody resistance of SARS-CoV-2 variants B.1.351 and B.1.1.7. BioRxiv preprint doi: https://doi.org/10.1101 (Links to an external site.)/2021.01.25.428137; this version posted February 12, 2021. [Secondary paper, focus on the section starting on line 178, where they evaluate evidence of viral escape in-vivo rather than in-vitro.]

Note: this paper by Wang et al is online at Nature as of March 8, 2021. An accelerated preview is available in the Files folder on this website, and at: https://doi.org/10.1038/s41586-021-03398-2 (Links to an external site.).

There are multiple terminologies to describe the virus strains.
The UK variant/strain is B.1.1.7
The South African variant/strain is B.1.351
The Brazilian variant/strain is B.1.1.28(plus modifiers) or P.1 or 501Y.V3