

SISMID Module 4: resources list

A (by no means exhaustive) list of publications, websites, relevant for module 4 of SISMID 2021 - reconstructing transmission with genomic data. None of this reading is required for the course - but these are resources we cite during the lectures or that we have found interesting and think you might enjoy too.

Papers:

TransPhylo:

Genomic Infectious Disease Epidemiology in Partially Sampled and Ongoing Outbreaks, Didelot et al <https://doi.org/10.1093/molbev/msw275>

A Snapshot of SARS-CoV-2 Genome Availability up to April 2020 and its Implications: Data Analysis, Mavian et al [10.2196/19170](https://doi.org/10.2196/19170)

Declaring a tuberculosis outbreak over with genomic epidemiology, Hatherell et al [10.1099/mgen.0.000060](https://doi.org/10.1099/mgen.0.000060)

Evaluating the use of whole genome sequencing for the investigation of a large mumps outbreak in Ontario, Canada, Stapleton et al [10.1038/s41598-019-47740-1](https://doi.org/10.1038/s41598-019-47740-1)

Genome-based transmission modelling separates imported tuberculosis from recent transmission within an immigrant population, Ayabina et al [10.1099/mgen.0.000219](https://doi.org/10.1099/mgen.0.000219)

High-resolution mapping of tuberculosis transmission: Whole genome sequencing and phylogenetic modelling of a cohort from Valencia Region, Spain, Xu et al <https://doi.org/10.1371/journal.pmed.1002961>

Transmission Trees on a Known Pathogen Phylogeny: Enumeration and Sampling, Hall and Colijn <https://doi.org/10.1093/molbev/msz058>

Transmission analysis of a large TB outbreak in London: mathematical modelling study using genomic data, Xu et al <https://doi.org/10.1099/mgen.0.000450>

Assessing the extent of community spread caused by mink-derived SARS-CoV-2 variants, Wang et al <https://doi.org/10.1016/j.xinn.2021.100128>

Outbreaker(2):

outbreaker2: a modular platform for outbreak reconstruction, Campbell et al
[10.1186/s12859-018-2330-z](https://doi.org/10.1186/s12859-018-2330-z)

Bayesian inference of transmission chains using timing of symptoms, pathogen genomes and contact data, Campbell et al <https://doi.org/10.1371/journal.pcbi.1006930>
When are pathogen genome sequences informative of transmission events? Campbell et al [10.1371/journal.ppat.1006885](https://doi.org/10.1371/journal.ppat.1006885)

Real-time outbreak analysis: Ebola as a case study
<https://www.reconlearn.org/post/real-time-response-3.html>

Other mentioned papers:

Tracking the COVID-19 pandemic in Australia using genomics, Seeman et al
<https://doi.org/10.1038/s41467-020-18314-x>

Beyond the SNP threshold, Stimson et al <https://doi.org/10.1093/molbev/msy242>

Near real-time monitoring of HIV transmission hotspots from routine HIV genotyping: an implementation case study, Poon et al, [10.1016/S2352-3018\(16\)00046-1](https://doi.org/10.1016/S2352-3018(16)00046-1)

Reconstructing foot-and-mouth disease outbreaks: a methods comparison of transmission network models, Firestone et al [10.1038/s41598-019-41103-6](https://doi.org/10.1038/s41598-019-41103-6)

Integrating genetic and epidemiological data to determine transmission pathways of foot-and-mouth disease virus, Cottam et al, <https://doi.org/10.1098/rspb.2007.1442>

Reconstructing disease outbreaks from genetic data: a graph approach, Jombart et al, [10.1038/hdy.2010.78](https://doi.org/10.1038/hdy.2010.78)

Unravelling transmission trees of infectious diseases by combining genetic and epidemiological data, Ypma et al., <https://doi.org/10.1098/rspb.2011.0913>

A Bayesian inference framework to reconstruct transmission trees using epidemiological and genetic data, Morelli et al, <https://doi.org/10.1371/journal.pcbi.1002768>

Molecular phylogenetics: principles and practice, Yang et al, <https://doi.org/10.1038/nrg3186>

Inferring Phylogenies, Felsenstein,
<https://www.sinauer.com/media/wysiwyg/tocs/InferringPhylogenies.pdf>

Neighbour joining revealed, Gascuel and Steel,
<https://academic.oup.com/mbe/article/23/11/1997/1322446>

Additional papers:

Evidence for transmission of COVID-19 prior to symptom onset, Tindale, Stockdale et al
[10.7554/eLife.57149](https://doi.org/10.7554/eLife.57149)

Simultaneous inference of phylogenetic and transmission trees in infectious disease outbreaks, Klinkenberg et al <https://doi.org/10.1371/journal.pcbi.1005495>

Random forests for genomic data analysis, Chen and Ishwaran,
<https://doi.org/10.1016/j.ygeno.2012.04.003>

Web resources:

Phylogenetics: An introduction
<https://www.ebi.ac.uk/training/online/courses/introduction-to-phylogenetics/>

BEAST: Bayesian evolutionary analysis by sampling trees <https://beast.community/>

BEAST2 <https://www.beast2.org/> (many good tutorials on this site)

A Practical Guide to MCMC Part 1: MCMC Basics
<https://jellis18.github.io/post/2018-01-02-mcmc-part1/>

Microreact - Open data visualization and sharing for genomic epidemiology:
<https://microreact.org/showcase>

Nextstrain - Real-time tracking of pathogen evolution <https://nextstrain.org/>

Books:

Modeling infectious diseases in humans and animals, Matt J. Keeling and Pejman Rohani.
Mathematical models for communicable diseases, Fred Brauer and Carlos Castillo-Chavez.
Phylogenetic trees made easy : a how-to manual, Barry G. Hall.
Mathematics of evolution and phylogeny, Olivier Gascuel.
Life: The Science of Biology, Purves et al (different editions have different authors)
Analysis of infectious disease data, N.G. Becker
Stochastic epidemic models and their statistical analysis, H. Andersson and T Britton
Infectious diseases of humans R.M. Anderson and R.M. May.
Handbook of Infectious Disease Data Analysis, Edited By Leonhard Held, Niel Hens, Philip D O'Neill, Jacco Wallinga (inc. chapter Methods for Outbreaks Using Genomic Data, Don Klinkenberg, Caroline Colijn, Xavier Didelot)

And the other SIS MID modules of course!

We also have a list of recommended books and online resources listed on our research group website: <https://www.sfu.ca/magpie/resources.html>