SISMID Reconstructing transmission with genomic data: resources list

A (by no means exhaustive) list of publications, websites, relevant for 'Reconstructing transmission with genomic data' at SISMID. 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

Declaring a tuberculosis outbreak over with genomic epidemiology, Hatherell et al 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

Genome-based transmission modelling separates imported tuberculosis from recent transmission within an immigrant population, Ayabina et al 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

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

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

Reconstructing foot-and-mouth disease outbreaks: a methods comparison of transmission
network models, Firestone et al 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

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

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 SISMID 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**