

“Design and Analysis of Infectious Disease Studies”

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Abstract The sixth workshop on this theme has a primary focus on mathematical and statistical methods for analysing genomic data in the context of infectious disease transmission dynamics. A secondary focus area is the development and application of network theory for epidemiology. Motivated by new and emerging technologies that enable routine collection of high-resolution genomic data during outbreaks of infectious disease, and by new problems posed by the covid-19 pandemic, these areas bring considerable challenges requiring novel mathematical models and new methods for statistical analysis. The problems involve genomic data from small-scale disease outbreaks where the focus is on inferring transmission routes and for large-scale scenarios where pathogen evolution is of key interest. Despite recent advances, most of which are motivated by specific data sets or specific pathogens, many challenges remain. From a mathematical point of view, models that include a genomic component are inherently more complex than standard epidemic models and the underlying theory for such models remains under-developed. From a statistical point of view, challenges arise because high-resolution genomic data are typically very high-dimensional, which renders many standard approaches to analysis infeasible. An associated challenge is the need to develop computationally efficient algorithms that can be used for statistical analysis. The covid-19 pandemic has brought more challenges as the number of genomic sequences has far outstripped the algorithm efficiency of computation. Widespread testing, trace, isolation, lockdowns and quarantine for covid-19 have raised novel questions for network theory. This workshop will be based around the broad area of design and analysis of infectious disease studies, but with a special focus on mathematical models and statistical methods for genomic data, transmission networks, and pathogen evolution.

Mathematics Subject Classification 2020 Primary 62P10 Applications of statistics to biology and medical sciences, meta-analysis; Secondary 05C82 Small world graphs, complex networks; 92-08 Computational methods for problems pertaining to biology; 92D20 Protein sequences, DNA sequences; 92D30 Epidemiology