"Yersina, Variola, Vibrio oh my! Using genetics to help uncover the origins of pandemics past"

Pandemics occur at the crossroads of a complex interplay between biological, ecological and social factors (to name a few). At various points in our history (and our pre-history) favourable ecological conditions have set the stage for the emergence, re-emergence or re-surgence of infectious microbes to play out their (sometimes), final acts. Unravelling the where, what, why and how of our recent (Virbrio in North America) and not so recent (Yersinia and Variola in Medieval Europe) pandemics, helps build frameworks for a better understanding of ‘plagues’ in the present and future. An accurate genomic identification of our infectious companions from such times is a small, yet important part of the overall work. I will discuss the benefits of genetic ‘time-travel’, that is the processes we use to glean small but significant stretches of genetic information, that when pieced together, begin to address questions about the origins, timing and spread of these plagues and how together in meaningful collaboration with other disciplines such as history, ecology, archaeology etc, we can come to a more consilient approach to the study of ancient disease.

* Reception to follow in SGIS Atrium