JAMES RENNIE BEQUEST

REPORT ON EXPEDITION/PROJECT/CONFERENCE

Expedition/Project/ Conference Title:	Network Modelling of Epidemics
Travel Dates:	14-22 June 2014
Location:	Seattle, USA
Group member(s):	Manon Ragonnet
Aims:	To learn how to model networks and perform network simulations in R

OUTCOME (not less than 300 words):-

I am grateful for the funding provided by the James Rennie Bequest, as it made it possible for me to attend the Network Modelling of Epidemics workshop in Seattle (http://statnet.csde.washington.edu/EpiModel/nme/2014/index.html).

The workshop was incredibly instructive: I learned how to model and simulate contact networks and how to simulate the transmission of epidemics through networks. We studied both static networks and dynamic networks, allowing for the simulation of epidemics across contact networks that change over time. The workshop was conducted in R using packages developed by the instructors (Martina Morris, Stephen Goodreau and Sam Jenness). The newest package, EpiModel, was launched for the first time during the workshop. I will be using these tools for the analysis of HIV phylogenetic data towards the completion of my PhD. Such an analysis has never been done before; in fact few people know how to use these tools at present. I was able to discuss my planned work with the instructors and they had helpful suggestions on many points. Beyond my PhD, they suggested I may want to collaborate with people collecting sexual contact data in the UK, something I had not thought about and will now definitely consider.

During the workshop, I met researchers working on a wide range of fascinating topics and diseases. This includes two PhD students working on Hepatitis C and Brucella, respectively, who have sequence data for their pathogens but no expertise in phylogenetics. I have accepted to help them conduct their analyses as it is a good opportunity for me to work collaboratively on diseases other than HIV and build a professional network of my own.

While I was in Seattle, I gave a seminar at the University of Washington Department of Microbiology, hosted by Jim Mullins. This is the first seminar I have given, and it was a great opportunity for me to practice my presentations skills. Over 30 people attended, including Trevor Bedford and Josh Herbeck, both acclaimed viral evolution researchers. The talk seemed to have been well received as it stimulated many questions and discussion. I spent some time with one of Jim's postdoctoral researchers helping him set up analyses in BEAST (a computer program for evolutionary analyses developed by Andrew Rambaut from the University of Edinburgh, which I use regularly in my work).

Overall, I felt that my trip was extremely worthwhile: the skills learned at the workshop will be helpful in my PhD and beyond, I received advice from leaders in their field and expanded my professional network.