

**Next-generation molecular & evolutionary epidemiology of infectious disease**

Date: 14<sup>th</sup> & 15<sup>th</sup> May 2012

Organised by: Oliver Pybus, Christophe Fraser & Andrew Rambaut

DAY 1				DAY 2			
SESSION 1 <b>Spatial molecular epidemiology</b> Chair: Andrew Rambaut		SESSION 2 <b>Host immunity &amp; genetics and pathogen evolution</b> Chair: Oliver Pybus		SESSION 3 <b>Integrating epidemiology &amp; molecular evolution</b> Chair: Christophe Fraser		SESSION 4 <b>New data and technologies for epidemic surveillance and public health</b> Chair: Brian Spratt CBE FRS	
<b>09.00</b>	Welcome by Julie Maxton & Christophe Fraser						
<b>09.05</b>	<b>Leslie Real</b> Spatial Phylodynamics of Emerging Infectious Disease: Rabies as a Model System	<b>13.30</b>	<b>Paul Kellam</b> High-throughput sequencing reveals host-virus interactions during epidemics	<b>09.00</b>	<b>Maciej Boni</b> Epidemiology and population genetics of influenza in a tropical setting	<b>13.30</b>	<b>Larry Brilliant</b> The future of disease surveillance: from "feet on the street" to "clues from the cloud"
<b>09.30</b>	Discussion	<b>14.00</b>	Discussion	<b>09.30</b>	Discussion	<b>14.00</b>	Discussion
<b>09.45</b>	<b>Dan Haydon</b> The application of short read next-generation-sequencing to Foot & Mouth Disease Virus	<b>14.15</b>	<b>Sebastian Bonhoeffer</b> Recovering transmission structure and dynamics from viral sequence data	<b>09.45</b>	<b>William Hanage</b> Phylogenomics and phylodynamics of <i>Streptococcus pneumoniae</i>	<b>14.15</b>	<b>Sharon Peacock</b> Microbial whole genome sequencing in diagnostic and public health microbiology
<b>10.15</b>	Discussion	<b>14.45</b>	Discussion	<b>10.15</b>	Discussion	<b>14.45</b>	Discussion
<b>10.30</b>	Coffee	<b>15.00</b>	Tea	<b>10.30</b>	Coffee	<b>15.00</b>	Tea
<b>11.00</b>	<b>Marc Suchard</b> Next-generation computational statistics for infectious diseases	<b>15.30</b>	<b>Cecile Viboud</b> Comparative spatial dynamics of acute viral infections	<b>11.00</b>	<b>Simon Frost</b> HIV as a model phylodynamic system	<b>15.30</b>	<b>Simon Hay</b> Mapping the global distribution of infectious diseases: past, present and future
<b>11.30</b>	Discussion	<b>16.00</b>	Discussion	<b>11.30</b>	Discussion	<b>16.00</b>	Discussion
<b>11.45</b>	<b>Philippe Lemey</b> Integrating ecological and evolutionary dynamics in spatial analysis of infectious diseases	<b>16.15</b>	<b>Sunetra Gupta</b> Evolution of influenza: antigenic drift or thrift?	<b>11.45</b>	<b>Katia Koelle</b> The use of viral sequence data to evaluate the degree of disease superspreading, with an application to influenza H1N1pdm	<b>16.15</b>	<b>Panel Discussion</b>
<b>12.15</b>	Discussion	<b>16.45</b>	Discussion	<b>12.15</b>	Discussion	<b>17.00</b>	CLOSE
<b>12.30</b>	LUNCH	<b>17.00</b>	CLOSE	<b>12.30</b>	LUNCH		