



Phylogenetics and Networks for Generalised HIV Epidemics in Africa (PANGAEA-HIV)

Phylogenetic Methods Comparison Exercise – call for participation

PANGAEA-HIV is a major new initiative funded by the Bill and Melinda Gates Foundation to generate a large volume of next generation sequence data from African HIV cohorts to facilitate the phylodynamic characterization of generalized HIV epidemics. The *PANGAEA-HIV Methods Milestone 1* aims to evaluate existing phylogenetic methods in their ability to identify recent changes in HIV incidence in order to inform HIV prevention efforts in sub-Saharan Africa.

Research groups are invited to participate in a blinded methods comparison exercise on simulated sequence data sets that capture different HIV transmission dynamics in generalized HIV-1 epidemics. Secondary aims of the exercise are to evaluate the merits of full genome sequence data, and the impact of changing sequence coverage. Full information and simulated data sets are available from <http://bit.ly/PANGEAHIVsim>.

Key Dates

- Nov-7th : Deadline for preliminary, freeform research reports by participating groups.
- Dec-2nd : workshop to compare and consolidate initial results in London, where we will also begin to plan a publication. Attendance of participating research groups will be covered by PANGAEA-HIV.

The PANGAEA methods comparison working group

Anne Cori [¶], Christophe Fraser [¶],
Matthew Hall ^{*}, Emma Hodcroft ^{*},
Andrew Leigh Brown ^{*}, Mike Pickles [¶],
Andrew Rambaut ^{*}, Manon Ragonnet-Cronin ^{*}, Oliver Ratmann [¶]

The PANGAEA Consortium Executive group

Deenan Pillay [§], Christophe Fraser [¶],
Paul Kellam [°], Andrew Leigh Brown ^{*},
Tulio de Oliveira [§]

[§]Africa Centre for Health and Population Studies, University of KwaZulu-Natal, Durban, SA; [¶]Imperial College London, UK; [°]Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, UK; ^{*}University of Edinburgh, UK