Phylodynamics of Ebola in West Africa

Luiz Max de Carvalho[1,a] & Andrew Rambaut[1]

[a] lm.carvalho@ed.ac.uk [1] Institute of Evolutionary Biology, University of Edinburgh, UK.

THE UNIVERSITY *of* EDINBURGH

Motivation

- The 2013-2016 West African Ebola virus disease (EVD) epidemic was the largest in history;
- A massive international collaboration produced the most comprehensive data set for an acute virus to date (over 5% sampling);
- Our challenge is to combine different sources of information (epidemiological, genetic, climatic, etc) to trace the epidemic and explain its mode and tempo.
- Investigate the role of particular mutations in disease severity;

Methods

In total 1610 genomes were sequenced so far. We take a Bayesian approach and estimate time-calibrated phylogenies with **BEAST**.

- We had viral load ($C(t)$ values) and outcome (death/survival) information for 236 patients $\rightarrow$ binomial GLM;
- Case counts ($\mathbf{Y}$) along climatic and socio-economic covariates ($\mathbf{X}$) for 56 locations $\rightarrow$ negative binomial GLM + SSVS:

$$Y_i \sim \text{NegBin}(p_i, r)$$
$$p_i = \frac{r}{(r + \lambda_i)}$$
$$\log(\lambda_i) = \alpha + \beta_1 \delta_1 x_{i1} + \ldots + \beta_P \delta_P x_{iP}$$

- Constructing outbreak clusters: every time a location receives a viral introduction that leads to >20 sampled cases, split the series before and after the introduction.

Results