



PHYLODYNAMICS OF EBOLA IN WEST AFRICA

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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 → binomial GLM;

§ Case counts (Y) along climatic and socio-economic covariates (X) for 56 locations → negative binomial GLM + SSVS:

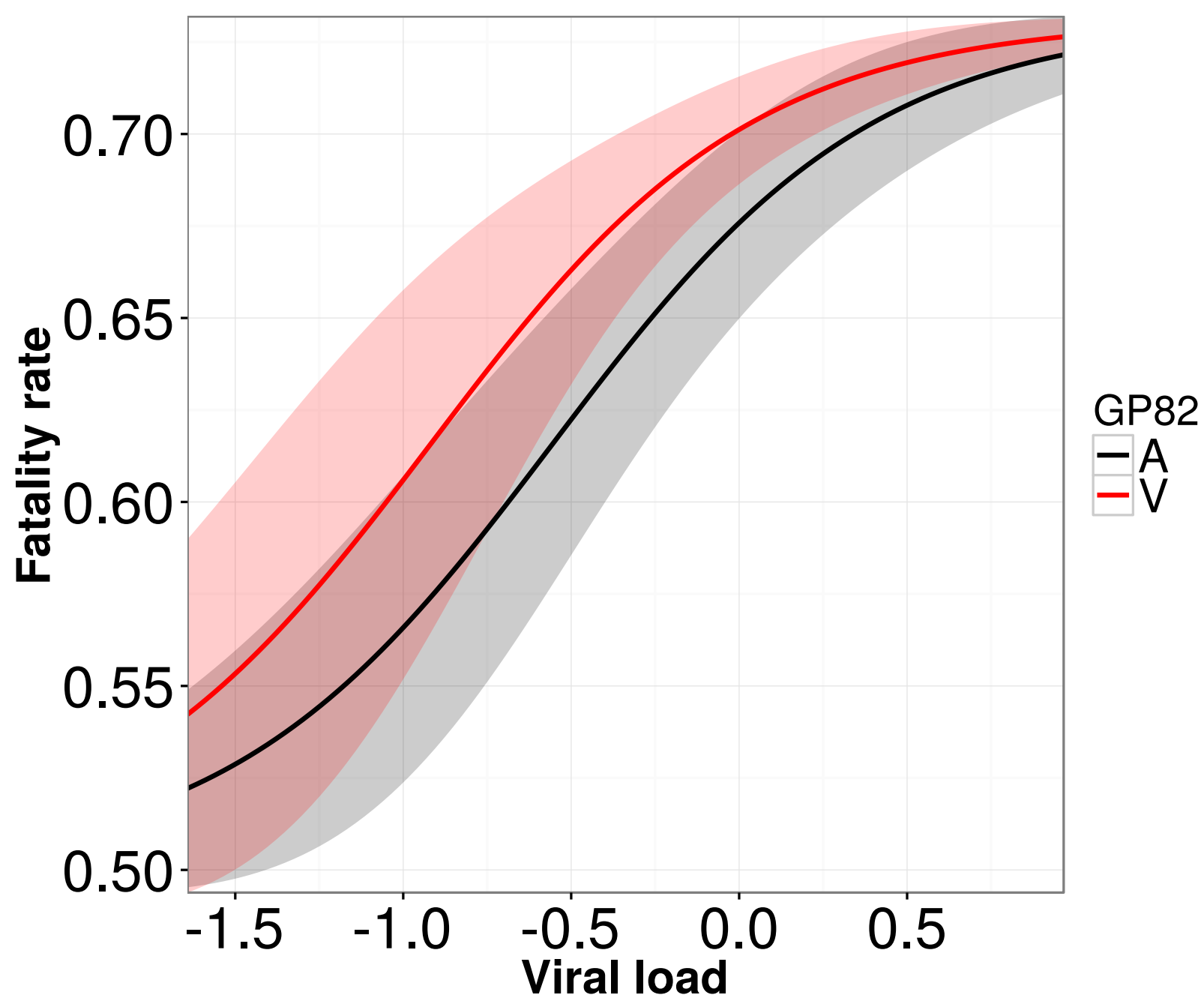
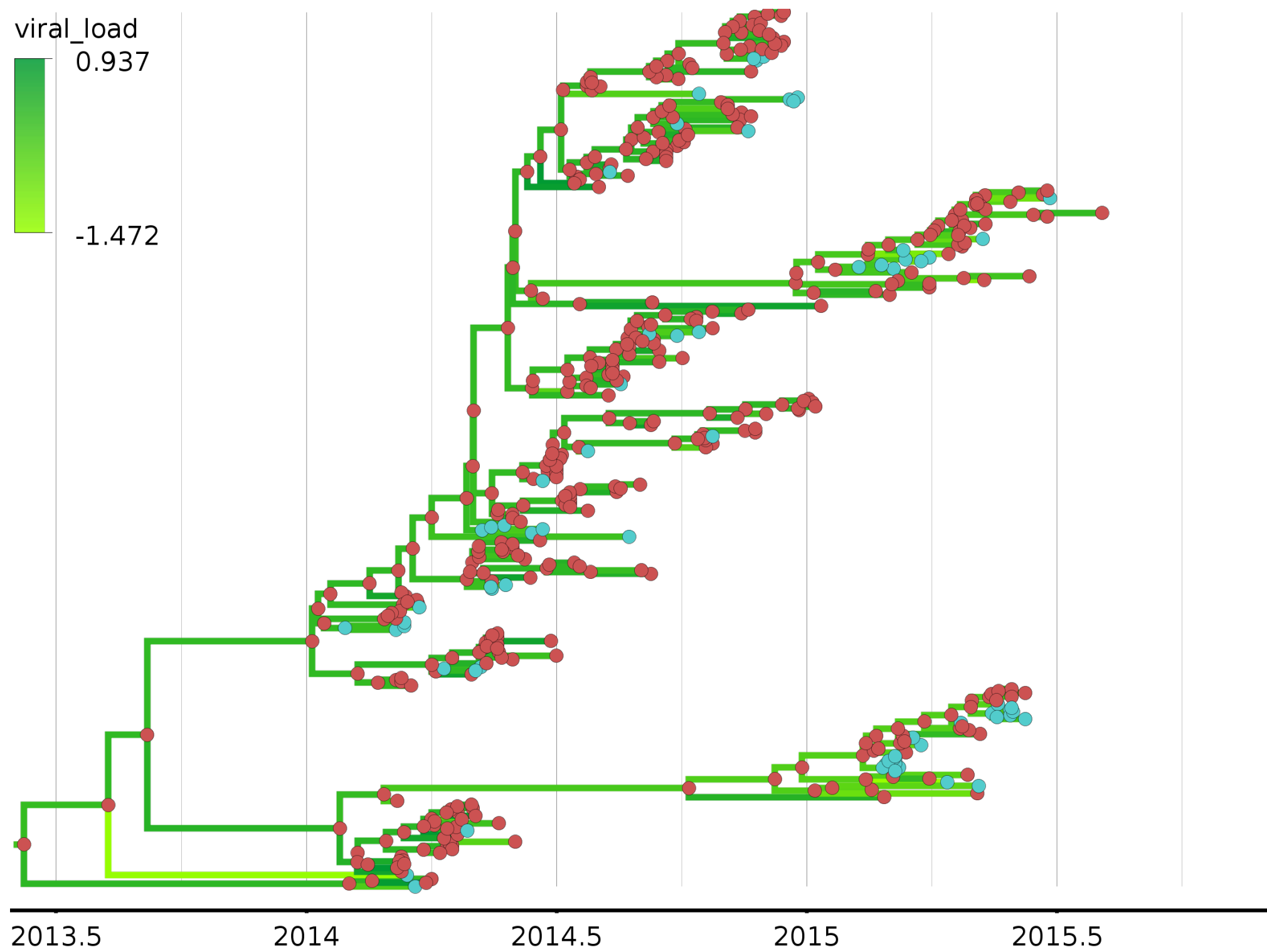
$$Y_i \sim \text{NegBin}(p_i, r)$$

$$p_i = \frac{r}{(r + \lambda_i)}$$

$$\log(\lambda_i) = \alpha + \beta_1 \delta_1 x_{i1} + \dots + \beta_P \delta_P x_{iP}$$

§ 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



Predictor	Description	Coefficient				Inclusion probability	B.F.	
		-1	0	1	mean [95% C.I.]	0.0	1.0	
TempSS	Temperature seasonality				-1.1 [-1.6, -0.5]			>50
tt50K	Time to travel to a population centre of 50,000 people				-0.9 [-1.4, -0.4]			32.4
PopSize	Population size				0.9 [0.3, 1.6]			29.6
Precip	Precipitation				0.8 [0.2, 1.3]			4.4
tt100K	Time to travel to a population centre of 0.1 million people				-0.8 [-1.7, -0.1]			3.8
		-1	0	1		3	15	50
		B.F. Threshold						

