A little study on the origin of Ebola virus in the 2014 Sierra Leone outbreak

Contents

1 Background

There was an outbreak of Ebola disease in West Africa during 2014, which at least began spreading in December 2013. One of the huge hits occured in Sierra Leone. [3] collected and sequenced data from 72 patients in Sierra Leone and analyzed their basic reproductive number ($R0$), estimated the lengths of incubation and infectious periods, and used phylogenetic trees to study how the virus population structure affected the epidemic. The data itself were first introduced in [2] from 78 individuals contracted with Ebova virus. [3] classified the outbreak in Sierra Leone as a larger outbreak (with 72 patients) and a smaller outbreak (6 patients) then decided to focus on the larger one. My main goal in this final project is to contruct a model transmission using Poisson regreesion and a phylogenetic tree with Bayesian approach, then compare the results to [3] which modeled using birth-death process Bayesian model.

2 The pipeline

Data exploration and transmission model The first case of EBOV in Sierra Leone was found on May 25. The epidemic happened since then until June 02. Modeling the transmission rate can be done using MCMC simulation ([1]).

Phylogenetic tree using Bayesian approach

- Determine all priors needed

- Build the model (?)

References

[1] J. Asher. "Forecasting Ebola with a regression transmission model". In: *Epidemics* 22 (2017).

[2] S. K. Gire et al. "Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak". In: *Science* 345 (6202 2014).

[3] T. Stadler et al. "Insights into the Early Epidemic Spread of Ebola in Sierra Leone Provided by Viral Sequence Data". In: *PLOS Currents Outbreaks* Edition 1 (2014). DOI: `10.1371/currents.outbreaks.02bc6d927ecee7bbd33532ec8ba6a25f`.