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

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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. [[5]] collected and sequenced data from 72 patients in Sierra Leone and analyzed their basic reproductive number (R_0), 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 [[3]] from 78 individuals contracted with Ebova virus. [[5]] 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. There are many studies conducted to understand the evolution of Ebola virus (EBOV). It is crucial for gathering how the virus is maintained from one outbreak to another, how it creates such devastation, and how we can lessen the outbreaks in the future [[2]]. My main goal in this final project is to a phylogenetic tree with birth-death process Bayesian model [[5]] and skyline plot [[4]]

2 Methods

Birth-death models. To model the spread, I assume several parameters: a transmission rate, a becoming-noninfectious rate, and a samplng probability which all be used in the birth-death model. These parameters could change in a piece-wise constant fashion. 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]].

The priors.

- Assume a constant reproductive number R_0 (the ratio of the transmission rate over the becoming-noninfectious rate) for initialization. The prior then be a LogNormal(0, 0.125).

- The time of origin be a uniform distributed random variable.

Birth-death skyline plot.

3   Results

(working on it)

4   Discussion

(working on it)

References

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

[2]   C. J. Brown et al. "New Perspectives on Ebola Virus Evolution". In: *PLoS ONE* 11 (8): e0160410 (2016). DOI: `10.1371/journal.pone.0160410`.

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

[4]   T. Stadler et al. "Birth-death skyline plot reveals temporal changes of epidemic spread in HIV and hepatitis C virus (HCV)". In: *PNAS* 110 (2013). DOI: `10.1073/pnas.1207965110`.

[5]   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`.