Analysis of Ebola data from HealthMap

true

12 December, 2017

Introduction

Parameters for Ebola and Reproduction Number Estimation

Culled from literature

Gravity model parameters

Wide Data load

Read in cleaned-up and wide formatted data.

We now use the incidence count to estimate reproduction number.

```
## [[1]]
## NULL
##
## [[2]]
## NULL
##
## [[3]]
## NULL
```

We assume that the reproduction number remains unchanged for the time period over which we wish to project. For each location, distribution of r_t at t.proj is r_t over the next n.days.sim.

Determine the flow matrix for the countries of interest only.

At this point, all the pieces are in place. by.location_incid contains the incidence count r.j.t contains the estimates of reproduction numbers. p.movement conatins the probabilities. SI_Distr is the serial interval distribution. The model is: lambda.j.t = p.movement * (incidence * r_t) * serial_interval taking care of the dimensions of course. Now divide the dataset into training and validation sets.

We will now split our data into training and validation sets.