**Generating Data**

**BASIC CASE:**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Parameter** | **Outbreaker paper** | **Ebola** | **SARS** |  |
| **S** | **200** | **200** | **200** | Still first stages of an outbreak  Look at first few sequences |
| **R0** | **1.5** | **1.5** | **3.5[[1]](#footnote-1)** |  |
| **Mu** | **1e-4** |  | Outbreaker |  |
| **Pi** | **1** | **1** | **1** |  |
| **w.dens** | **gamma(2,0.7)** |  |  |  |
| **f.dens** | **gamma(2,0.7)** |  |  |  |
| **Imports** | **0.05** | **0** | **0** |  |
| **DNA Length** | **10,000** | Rambaut | Outbreaker |  |
| **Eps** |  |  |  |  |
| **Xi** |  |  |  |  |
| **Superspreader** |  | **5x/10%** | **10x/5%** |  |

**EXPLORING ACROSS EPS AND XI:**

* Eps
  + 0 – 1 is feasible
* Xi
  + 0 – ?
  + We should explore > 1 (more misinformative than informative)
  + We should explore p(non-infectious) = 1 (Xi = Eps = 1)
  + However focus should probably be at lower ranges (0-0.?)
* Resolution?
  + move kappa = move pi = FALSE
  + init = 1
* Find.import = FALSE
* Runs = 50

**SARS**

* SARS has a strong genetic signature
* So can maybe get away with lower eps
* Superspreader (10x larger) (5%)
* Weighted average = R0

**Ebola**

* Andrew Rambaut
* Set up superspreaders
* Superspreader (5x larger) (10%)
* Weighted average = R0

**SPECIAL SCENARIOS:**

* Basic Case
  + Information
    - Timing
    - Timing, genetic
    - Timing, contact
    - Timing, contact, genetic
  + Super-spreaders = TRUE
* How much contact do we need to improve situational awareness
* Small vs. large outbreak
* High vs. low R0
  + single analysis
* Broad generation distribution
  + single analysis
* High imports (?)

**R OUTPUT**

**storage.SARS**

* data
  + parameter.set1
    - param
      * S
      * n
      * R0
      * Mu
      * Pi
      * w.dens
      * f.dens
      * Imports
      * DNA length
      * Eps
      * Xi
    - outbreak
      * 50 simOutbreak objects
    - CTD
      * 50 simCTD objects
    - outbreaker.output
      * [50x timing – tc for eps= 0]
      * [50x timing, genetic –tgc =0]
      * 50x timing, contact
      * 50x timing, contact, genetic
    - analysis
      * tc.accuracy
      * tgc.accuracy
      * tc.confidence
      * tgc.confidence
      * tgc.entropy
      * tc.entropy
      * tc.time
      * tgc.time
    - plot
      * violinplot comparing accuracy, confidence, entropy and time
  + parameter.set.2
  + parameter.set.3
  + …
  + time.noDNA.noCTD (occurs on tc eps=0)
  + time.DNA.noCTD (occurs on tgc eps=0)
* plots
  + abs.plot
  + rel.plot
  + smooth.plot

**storage.ebola**

**Things to do**

-envelope colour

-plot points

-add unit tests

-Rich on Tuesday

-Documentation on cluster stuff

-Run simCTD on cluster

1. Lipsich et al. 2003 [↑](#footnote-ref-1)