**R Questions**

* In the MCMC, is the movement of mu based on previous position in MCMC?
  + or is it random?
  + No, new mu = old mu + rnorm(1,0,sd.mu)
* Is the order of the moves random or what?
* How did you choose c(0.1,8,0.1) for weighting of moving infection dates?
* Do we consider imports?
  + We can’t use them in the analysis because we don’t have a pair!
* How to re-factorise our log likelihood for efficiency?
* How does contact work for find.imports?
* Speed
  + 42 seconds vs 45 for one try
* Inference
  + When genetic data is lacking
    - one try: 18% -> 94%, only one not found is an import
* Use the same simulation
  + but different simCTD
* Analysis output
  + Mean support for the true ancestry (ie percent of posterior)
  + And calculate entropy
* Figures and methods
* Writing up
  + description of model
    - likelihoods etc
  + bullet point draft of introduction
* test that and design of tests
  + data processing
  + giving the right errors
  + trivial mistakes
    - ie indices outside of dataset
* Contact tracing and ebola paper
* Look at burnin and see if there are any trends
* coda package to analysis mcmc chain
* Looking at superspreaders in the paper with heterogeneity
  + does contact tracing work to identify this
* Inferring minimum contact coverage required for a given situation
* Timed contacts

Things to ADD to outbreaker.2

* Add simulated data to fake.outbreak
  + And therefore add CTD=x$CTD to roxgyen example of outbreaker.data
* There seem to be two descriptions of move.pi in outbreaker.config