Phylodynamics Simulation of Phylogenetic Trees

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Folder: antigenic\_drift

Spec: System Design

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Background:

This document describes the system design and program flow of the new project based on the previous project entitled *critical analysis of binding avidity hypothesis*. The previous project ends in early, 2014. The files are located in ‘BindingSim’ and ‘binding\_v3’.

System Design

There are 3 packages will be developed and stored in 3 different folders. The functions of each packages are described here:

* BindingAvidity/mat/Mbindingavidity: Phylodynamic simulation of viral infection using Individual-based model.
* InferPhylo/make\_infection\_tree: Inferring phylogenetic trees based on finding MRCA in each lineage.
* tradeoff: Show the viral within host fitness

There will be 3 packages maintained in 3 separate folders. Once the packages are done, integrate them into a release version which can run on PC or server.

antigenic\_drift

BindingSim

tradeoff package

InferPhylo

package

BindingAvidity

package

plot transmission diagrams

make infection tree

stochastic simulation

Charts

trees

Viruses

Supplementary

The original files are stored in the following directories, G:\MyPC2015\working\Projects.Duke\Projects\_2014

There are two folders.

1. BindingSim
2. release

‘BindingSim’ stores the original functions for each module, which should be run on each PC.

‘release’ stores the integrated version of the code which can be run on the DSCR server.

Integrated Version for server (Packages for release version):

Mainly we add *main* and *mainout* folders to save main scripts and output files.

* binding\_v3
  + binding\_ode: ODE to quickly calculate stationary status
  + main
    - calbinding: calculate binding avidity on the transmission tree
    - infertree: infer the transmission tree
    - job: script for job submitting on clusters
    - plotfig: plot simulated lineages
    - main\_simulation.m
  + mainout
    - ibms: output of stochastic simulation
    - ode: output of deterministic simulation
    - tree: output of transmission tree
  + make\_infection\_tree: resample and generate the transmission tree. Packaged is distributed from “InferPhylo/make\_infection\_tree/”
  + Mbindingavidity: The packaged is distributed from “BindingAvidity/mat/Mbindingavidity/”
  + tradeoff