Phylodynamics Simulation of Phylogenetic Trees - Mbindingavidity

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Version: 1

Date: May 26, 2015

Packages for modules developing:

* BindingAvidity/mat/Mbindingavidity: Phylodynamic simulation of viral infection using Individual-based model.
* System Architecture
* System Design
* Program Flow

System Architecture (for modules developing)

This shows the file structures for the BindingAvidity package. The package simulate disease antigenic change while keep tracking individual viruses binding avidity.

BindingAvidity

mat

Mbindingavidity

Viruses

System produces 3 objects into ‘out’ folder:

1. dat\_x\_trans\_tmp.mat: to reconstruct the transmission tree
2. DataTLSIR.mat: to store SIR dynamics
3. virus\_traits.mat: to store virus traits

To run the code:

Go to the Mbindingavidity folder and run main\_binding.m.

System Design

The folder contains the following mat files. main\_binding.m is the main function which initialize the parameters and initial status then calls the tauleap function.

main\_binding.m

tauleap\_singlesir\_ibm\_matrix.m

readparams.m

get\_beta.m

get\_beta\_list.m

cal\_meanbding.m

plot\_simulation\_log\_i.m

main\_binding.m

*Mbindingavidity*

dat\_x\_trans\_tmp.mat

virus\_traits.mat

DataTLSIR.mat

to other analysis

viruses

tau\_leap

cal\_meanbding

mean\_binding.mat

plot\_simulation

Program Flow for generating virus transmission, SIR, and their traits

1. main\_binding
2. Tau-leap
   1. Update virus binding avidity v and transmission rate beta
   2. Calculate number of events happened
   3. Update the epidemiological status
   4. Updating transmission for each viral strain
      1. insert new viruses into CurrentViruses
      2. insert new viruses into VirusesArray
   5. Update the death and recovery for current viruses
3. Produce output files
   1. output\_virus\_transmission(VirusesArray)
   2. output\_sir(DataXt);
   3. output\_traits(CurrTime);
   4. Produce output files
4. calculate mean binding and plot\_simulation