Phylodynamics Simulation of Phylogenetic Trees

Document type: Technical document

Software package: Mbindingavidity

Language: Matab

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Path: BindingAvidity/mat/Mbindingavidity:

Purpose: Phylodynamic simulation of viral infection using Individual-based model.

This document is the **software technical document** for software codes. For system architecture, please refer to ‘BindingSimX\_SystemFlow\_New.docx’. For system design, please refer to ‘BindingSimX\_ObjectDesign\_v2-3.docx’.

System Architecture (for modules developing)

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

BindingAvidity

mat

Mbindingavidity

Viruses

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

*Mbindingavidity*

main\_binding

tauleap\_singlesir\_ibm

dat\_x\_trans\_tmp.mat

virus\_traits.mat

DataTLSIR.mat

to other analysis

Output

sub Iterate (tau\_leap)

cal\_meanbding

mean\_binding.mat

plot\_simulation

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

1. main\_binding
2. Iterate (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

System produces 3 output objects:

1. dat\_x\_trans\_tmp.m

purpose: to reconstruct the transmission tree

produced by: output\_sir (Data)

variables:

* 1. dat\_viruses

Totally there are 5 columns. What are each columns corresponded to

1. DataTLSIR.mat: to store SIR dynamics

produced by: output\_sir(Data)

variables:

* 1. dat\_sir (t, Xt)
  2. params

1. virus\_traits.mat: to store virus traits
   1. dat\_VirusesArray
2. mean\_binding.mat
   1. meanBinding
   2. meanBindingFinal