Phylodynamics Simulation of Phylogenetic Trees

Author: Hsiang-Yu Yuan

Folder: antigenic\_drift

Spec: Object Design

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The design of individual based model

The document of Object Design describes the flow of algorithms at the object level. Also, it describes the design of the object, array or the relationship of the objects.

**Data Objects:**

**Output Objects:**

|  |  |
| --- | --- |
| **params** | Required parameters |
| **VirusesArray** | Every virus strains |
| **CurrentVirus** | Current virus strains |
| **metadata** | Column name of viruses |

1.vid

2.birth

3.death

4.parent

5.infectionK

**dat\_viruses**

1.iso\_date

2-301. Ik=1-300

**dat\_sir**

vid

birth

death

parent (sourceVirus)

infectionK (*k*)

beta (beta(*v*,*k*))

initialV

currentV

**CurrentVirus**

**Beta:**[k x 1]

vid

birth

death

parent (sourceVirus)

infectionK (*k*)

beta (beta(*v*,*k*))

initialV

currentV

**VirusArray**

**Some setting for params and metadata**

params.filename = 'params.dat';

params.out\_dir = out\_dir;

metadata.ibms.proj = ['std'];

metadata.ibms.parameterFile = ['dat/' params.filename];

metadata.ibms.initVirusFlag = true;

metadata.ibms.out\_dir = out\_dir;

**Rate properties**

|  |  |
| --- | --- |
| Rate\_Birth | Birth rate |
| Rate\_Death\_S | Death rate for S |
| Rate\_Death\_I | Death rate for I |
| Rate\_Death\_R | Death rate for R |
| Rate\_Recovery | Recovery rate for I |
| Rate\_Wanning | Wanning rate for R |