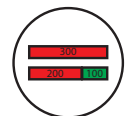


a.

Virus Structure



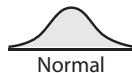
two segments
600 bp total

■ regular mutation rate

■ high mutation rate

Parameters

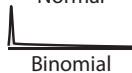
of
progeny



$$\mu=1.2$$

$$\sigma^2=0.5$$

of mutations
(regular)



$$n=300 \text{ or } 200$$

$$p=0.008$$

of mutations
(high)



$$\text{min}=20$$

$$\text{max}=60$$

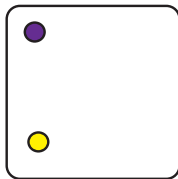
of starting viruses
total # of viruses

1 to 4

20 to 50

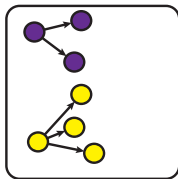
Simulation Process

initialize

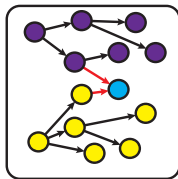


t=0

replicate, reassort, and mutate



t=1



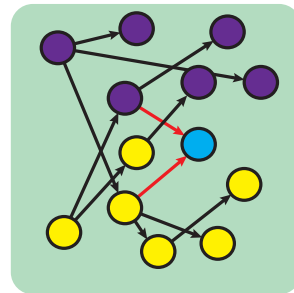
t=2

● different viral lineages
● reassortant virus
→ reassortment

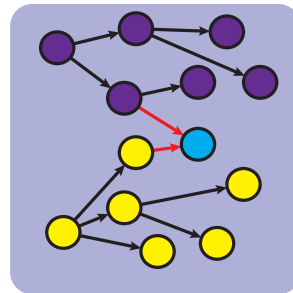
...

b.

Null Model

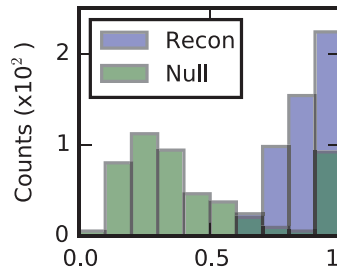


Reconstruction



c.

Clonal Descent



Reassortment

