

Computational Scenario Testing of Infectious Diseases

Siew Ann CHEONG



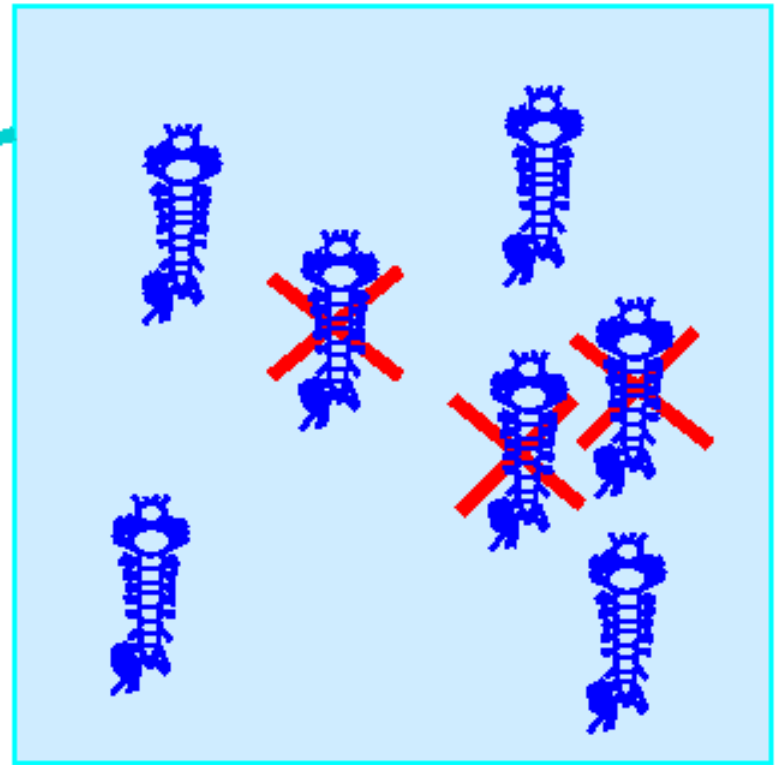
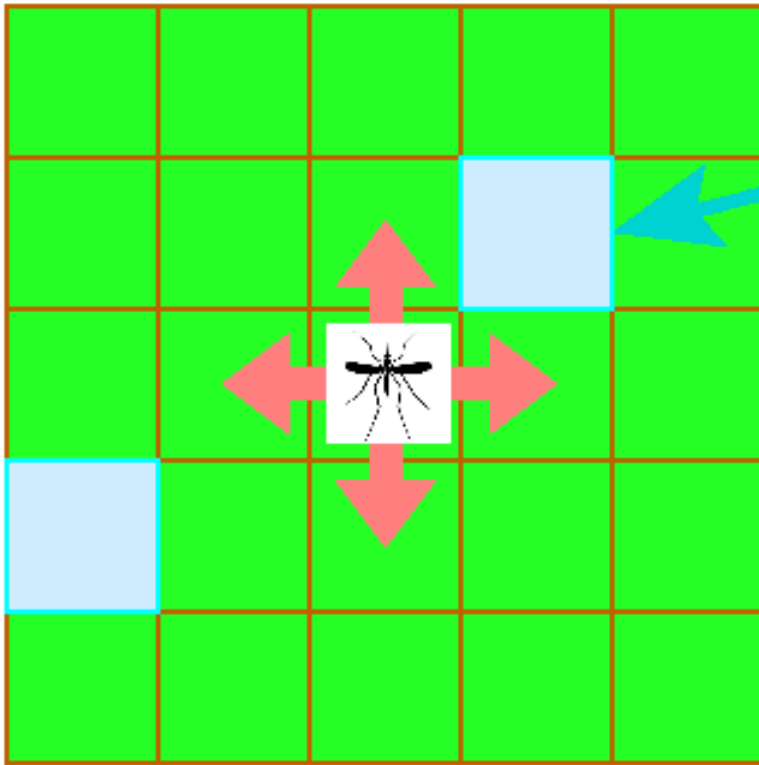
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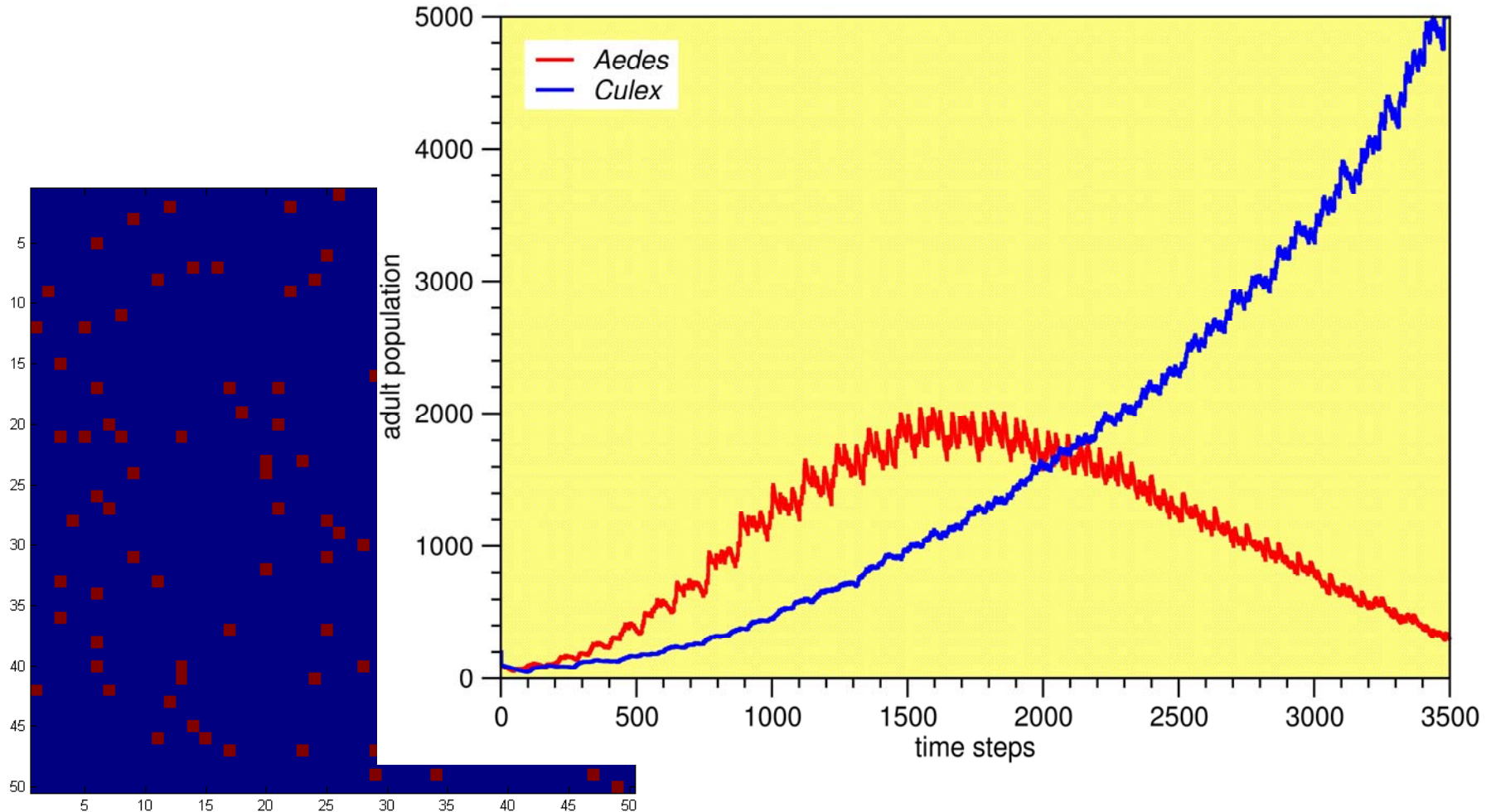
Acknowledgments

- Competitive breeding between *Aedes* and *Culex*
 - Hui Rong Amanda TEO (NTU)
 - Choon Siang TANG (NEA)
- Human-vector interaction
 - Whei Yeap SUEN (NTU)
- Viral integration into *Aedes* genome
 - Michael Kia Liang THAN (NTU)
- Evolutionary model of dengue epidemics
 - Dr Khoa TD THAI (Amsterdam Medical Center)
 - David HALIM (NTU)

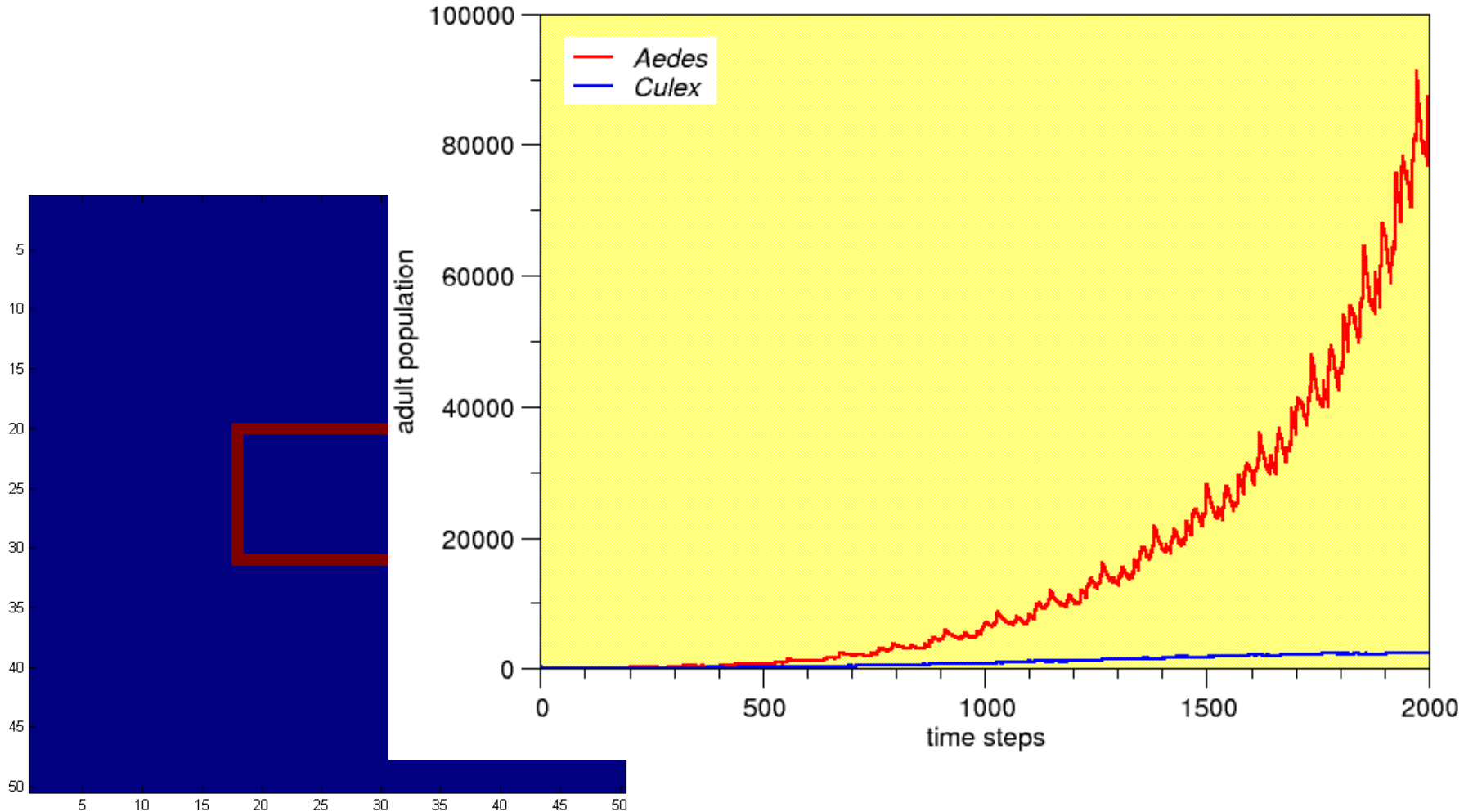
Competitive Breeding Between *Aedes* and *Culex*



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Density	2%	3%	5%
Benchmark	0.0%	5.0%	9.0%
Straight line	33.3%	47.5%	80.0%
Three branch	23.3%	43.3%	60.0%
Closed loop	23.3%	33.3%	43.3%
Four branch	13.3%	26.7%	36.7%

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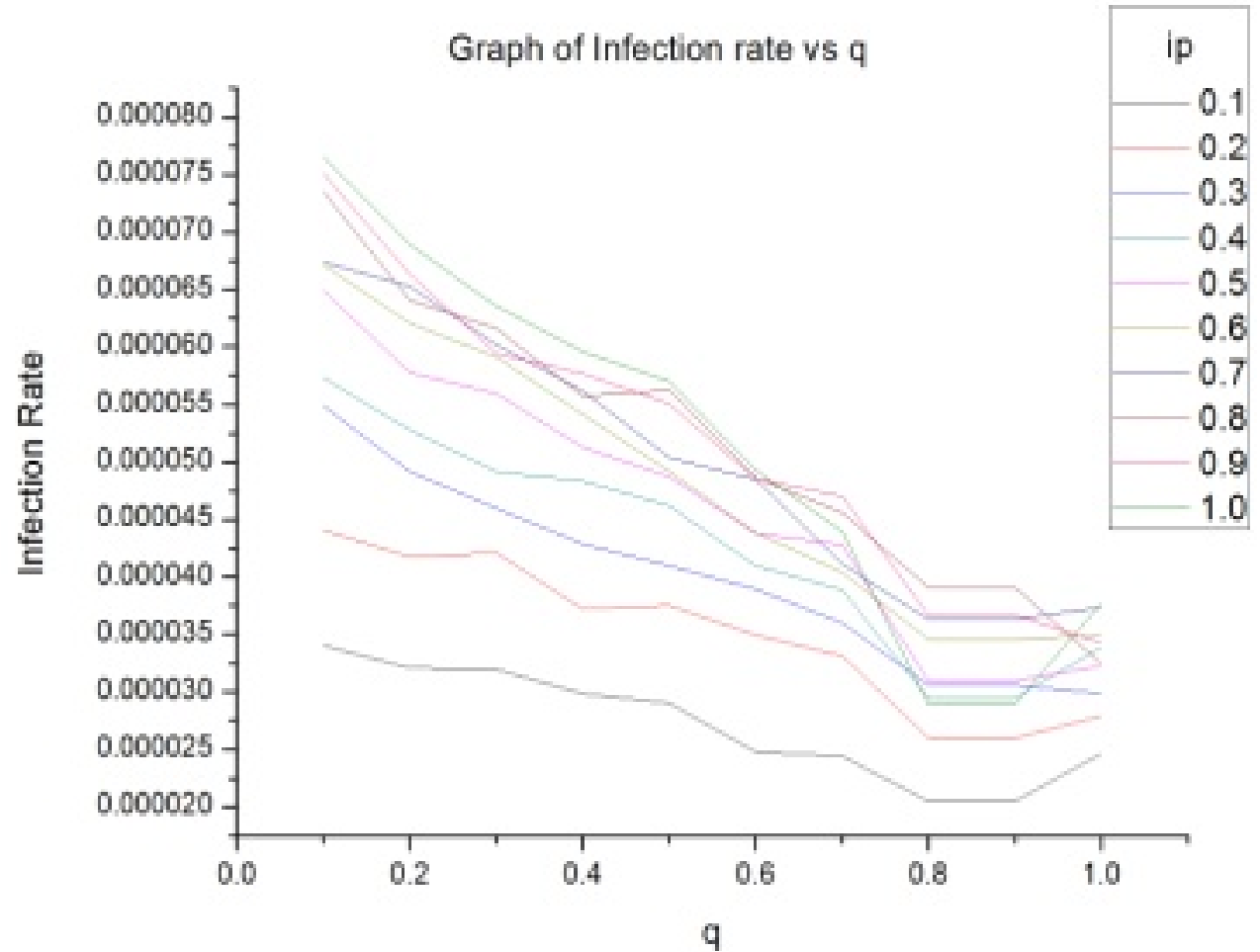
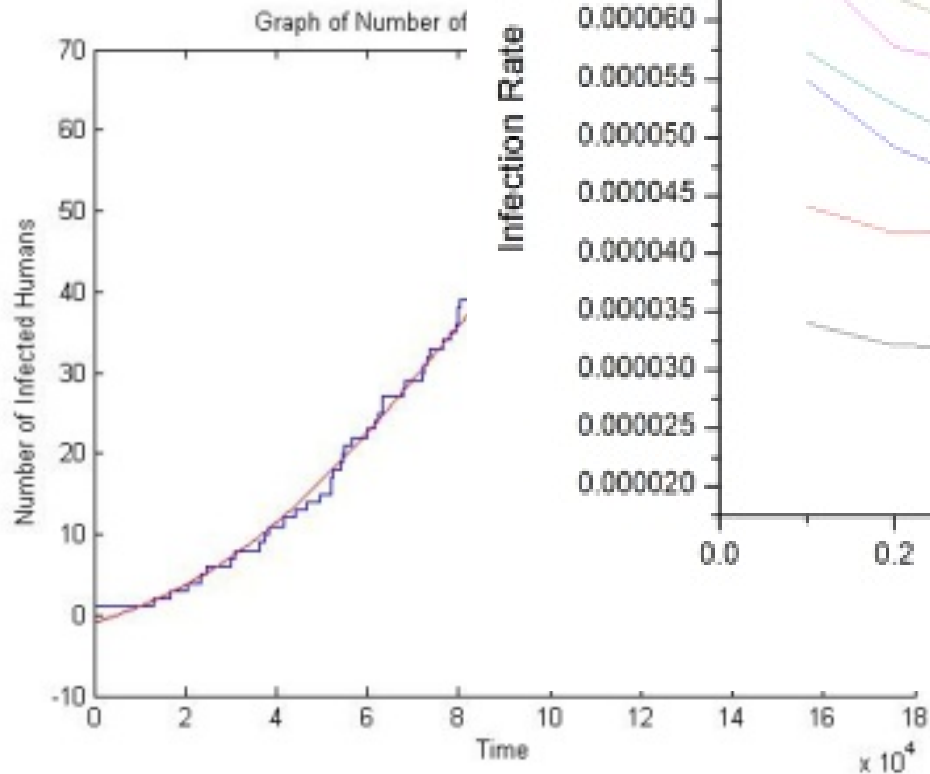


Human-Vector Interaction

- $10 \times 10 \text{ km}^2$ town = 1024×1024 grid
- 100 humans + 5000 mosquitoes
- Slower mosquito, $0 < q < 1$
- Same cross-infection probability ip
- Epidemiological models
 - Susceptible-Infected (SI)
 - Susceptible-Infected-Recovered (SIR)
 - Susceptible-Subclinical-Infected-Recovered (SsIR)

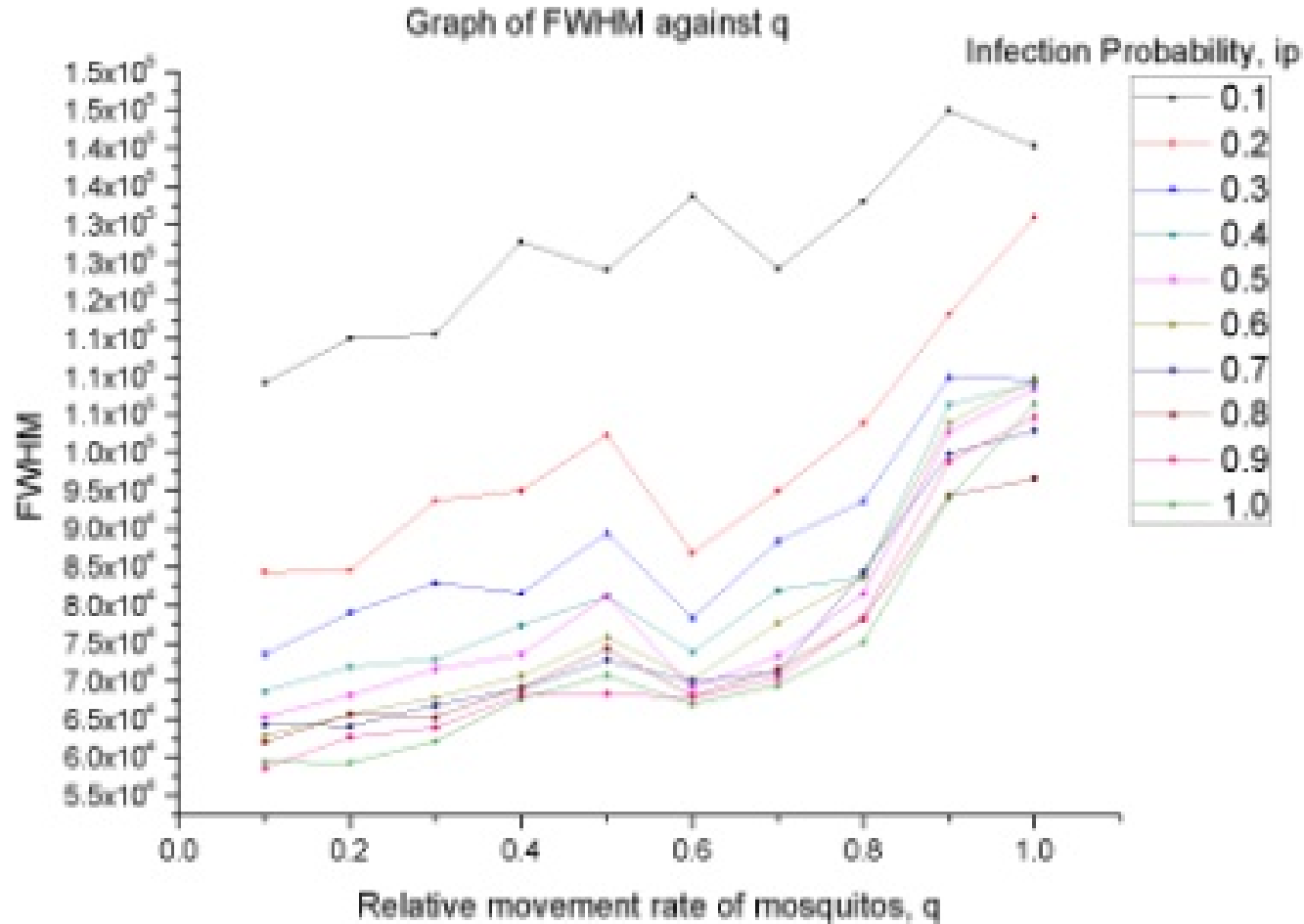
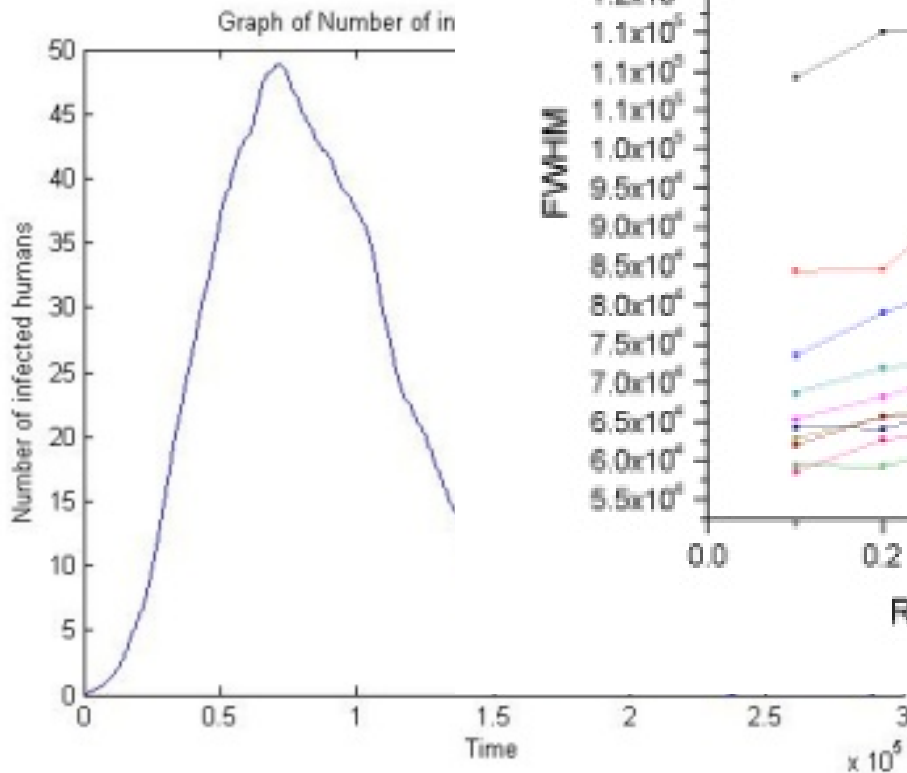
Human-Vector Interaction

SI Epidemic



Human-Vector Interaction

SIR/SsIR Epidemic





Human-Vector Interaction

- Partially completed
 - Structured human mobility
 - infection rate increases 10–100 times
- To start soon
 - 80% subclinical, 20% clinical
 - Quarantine
 - Social distancing



Viral Integration into Mosquito Genome

○ Facts

- DENV
 - Endemic strain
- DENV vectors
 - *Aedes aegypti* & *Aedes albopictus*
 - Habitat segregation
- Low rate of vertical transmission

○ Puzzle

- Long inter-epidemic periods
 - Dengue should be extinct!



Viral Integration into Mosquito Genome

○ Facts

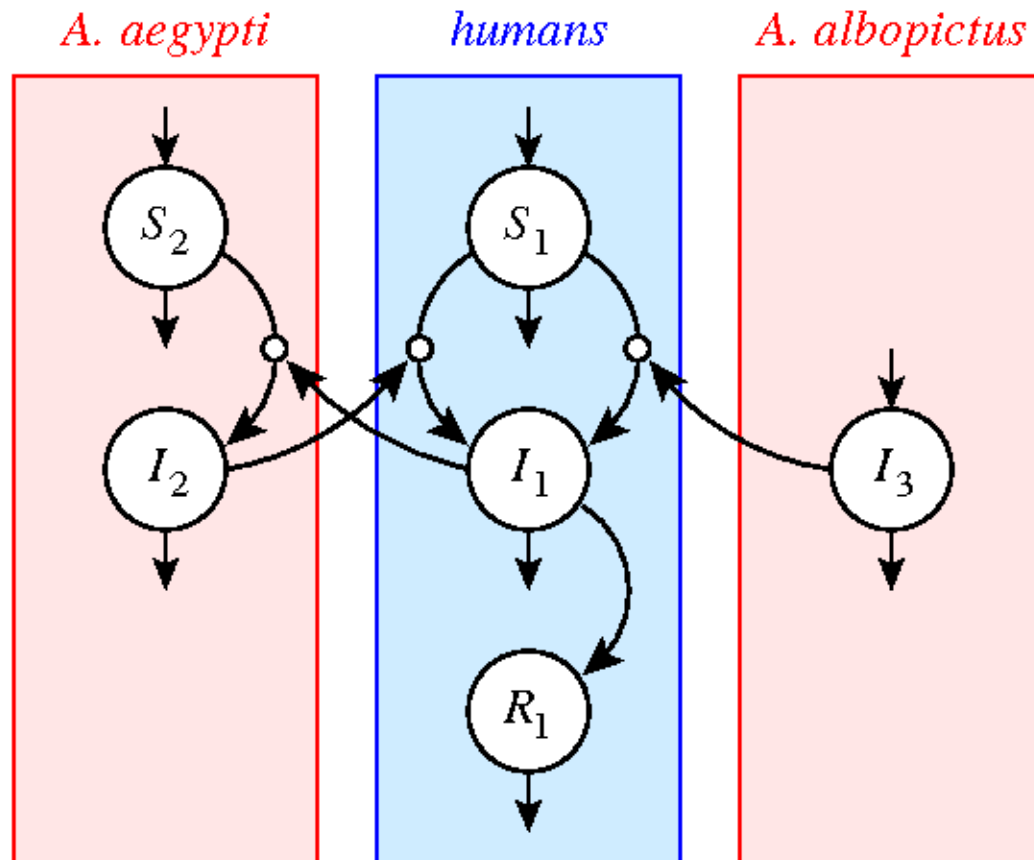
- Viral integration into host genome
- Crochu *et al*, 2004. *J. Gen. Virol.* **85**, 1971.
- Roiz *et al*, 2009. *Viol. J.* **6**, 93.

○ Scenario

- DENV integrated into *Aedes albopictus* genome
- Temperature-driven release (*El Nino*?)
- *Aedes albopictus* seeds epidemic
- *Aedes aegypti* spreads epidemic

Viral Integration into Mosquito Genome

- Coupled SIR Model





Viral Integration into Mosquito Genome

- Future plans

- Periodic driving

- *Aedes albopictus* population
 - *Aedes albopictus* infectivity

- Spatial extension

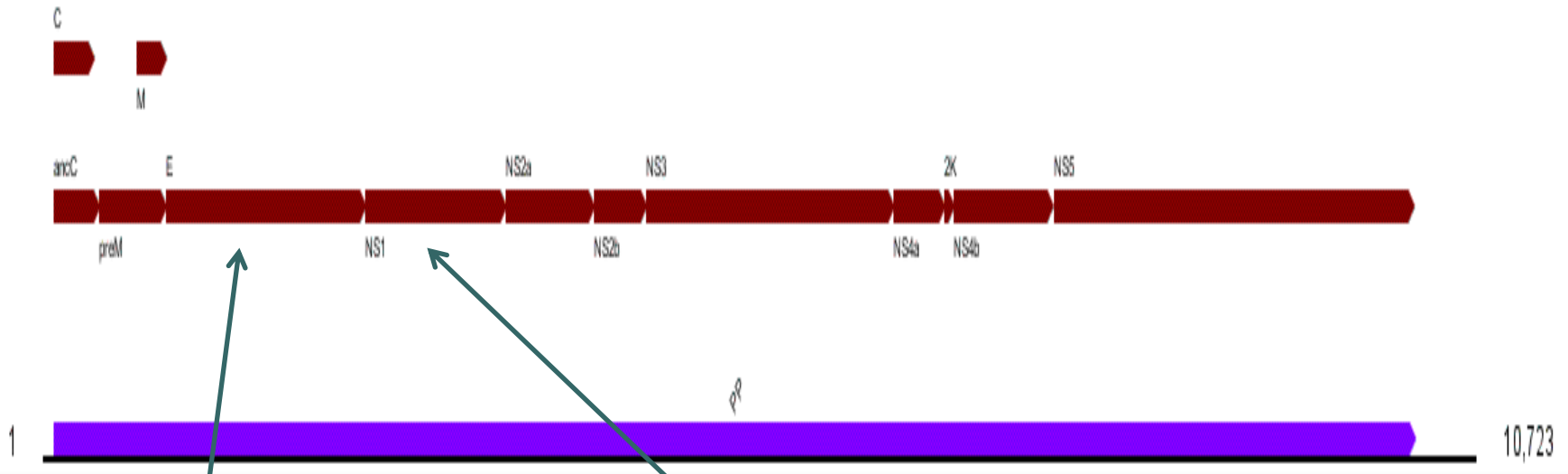
- Urban *Aedes aegypti*
 - Rural *Aedes albopictus*



DENV Evolution & Epidemiology

- Exciting interface between evolution and epidemiology
 - Advances in phylogenetic techniques
 - Growing interest in past decade
- DENV evolution
 - Accelerated during epidemic
 - Ecological competition between strains

DENV Evolution & Epidemiology



infectivity →
infection probability

severity → virus
copy number



DENV Evolution & Epidemiology

- Simulate $N = 10,000$ sequences
 - SIR dynamics for each sequence
 - Fitness driven substitution
 - Point mutations
- Each sequence consists of
 - E subsequence
 - Different infectivity
 - $NS1$ subsequence
 - Different reproductive rate



The Next Step...

- Complete present studies
 - Compare with empirical data
- Collaborations with regional partners
 - Modeling + simulation to understand clinical data
 - Test experimentally inaccessible scenarios



Thank You!

Contact Information

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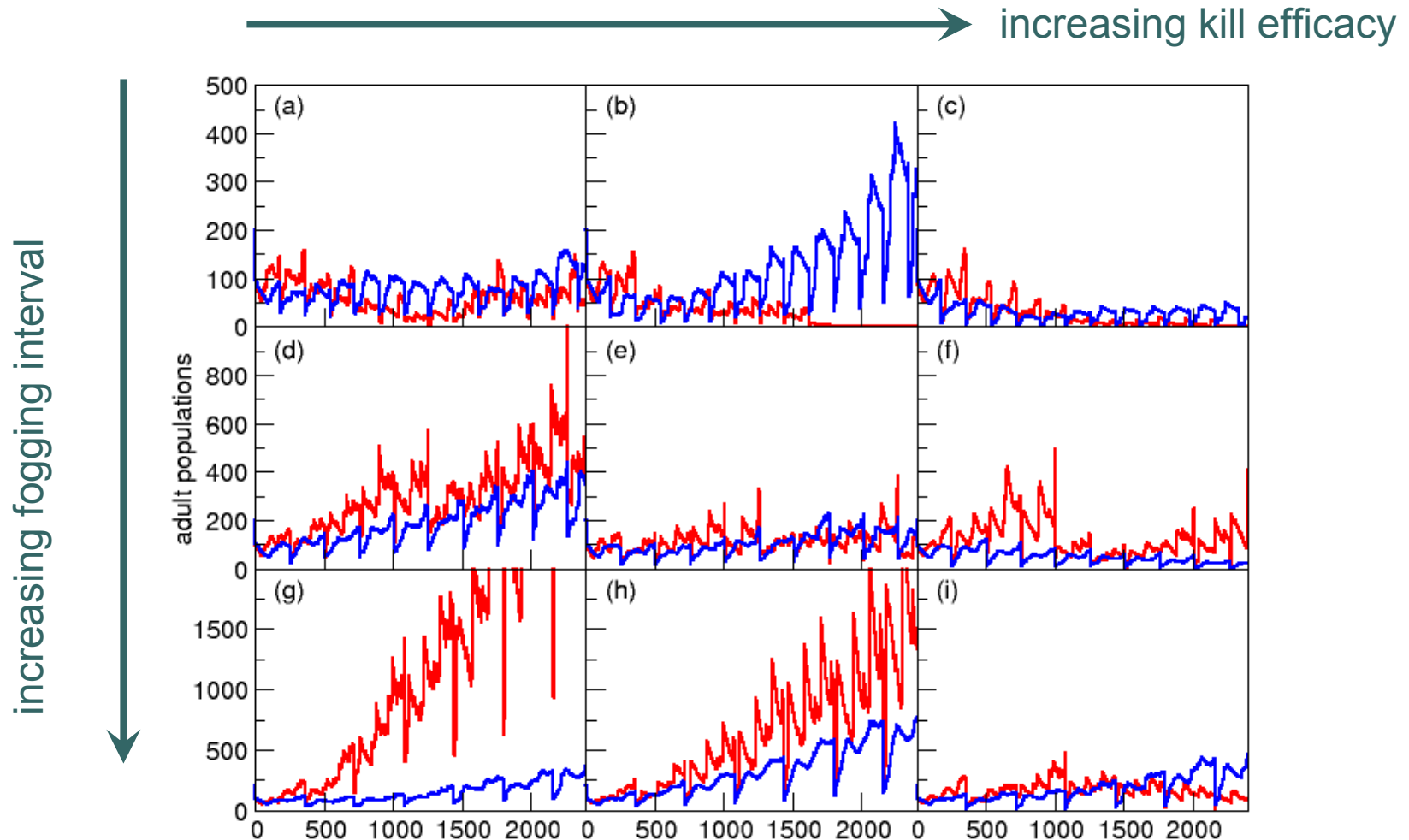
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