Computational Scenario Testing of Infectious Diseases

Siew Ann CHEONG
Acknowledgments

- **Competitive breeding between *Aedes* and *Culex***
  - Hui Rong Amanda TEO (NTU)
  - Choon Siang TANG (NEA)
- **Human-vector interaction**
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- **Viral integration into *Aedes* genome**
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- **Evolutionary model of dengue epidemics**
  - Dr Khoa TD THAI (Amsterdam Medical Center)
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Competitive Breeding Between *Aedes* and *Culex*
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## Competitive Breeding Between *Aedes* and *Culex*

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Human-Vector Interaction

- 10 × 10 km² 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

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

![Diagram showing the coupled SIR model for A. aegypti, humans, and A. albopictus with nodes S2, I2, S1, I1, R1, I3, and arrows indicating the flow between compartments.]
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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