

# Network Models of Phage- Bacteria Coevolution

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# The question

Statistical,  
Nonlinear and  
Soft Matter  
Physics

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## Network models of phage-bacteria coevolution

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- How the **interactions** between bacteria, virulent phages, and temperate phages might affect the **diversity** of these groups

# **PART I**

## **Interactions between bacteria and phages**

# Phage-bacterial ecosystems

- Virulent phages
  - lytic life cycle
- Temperate phages
  - lytic life cycle
  - lysogenic life cycle
    - prophage
    - immunity to lytic infection

# Horizontal transfer of genes

- Evolution of new phage strains
  - gain genes from other phages shared common hosts
  - **infect** new hosts
- Evolution of new bacteria strains
  - gain genes from phages or bacteria
  - **resistant** to previous phages

## **PART II**

# **Stochastic network models**

# Evolutionary dynamics of networks

- “The rules for **adding** or **removing** nodes and links use only **the structural properties of the network** at that time”
- **Feedback** and **regulate** according to a set of parameters which control the network topology, modularity or density.
- Emphasis on **holistic** properties of the system

# Elements of the network models: basic concepts

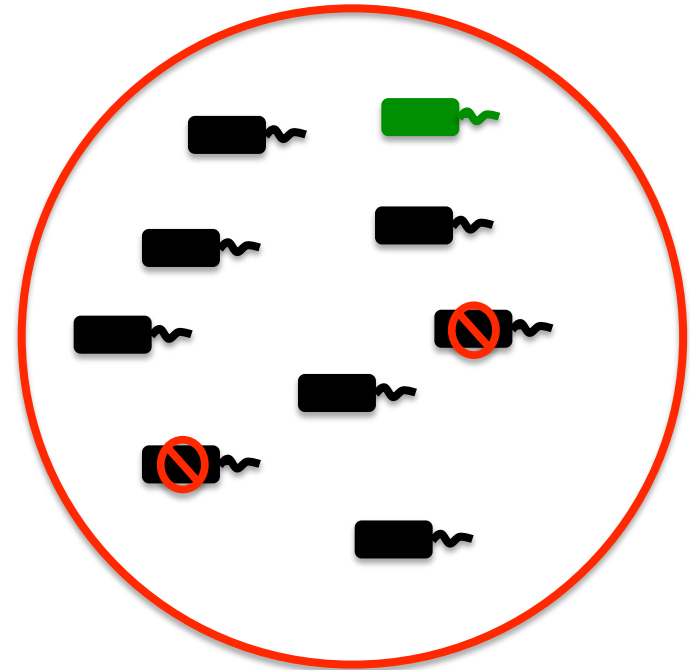
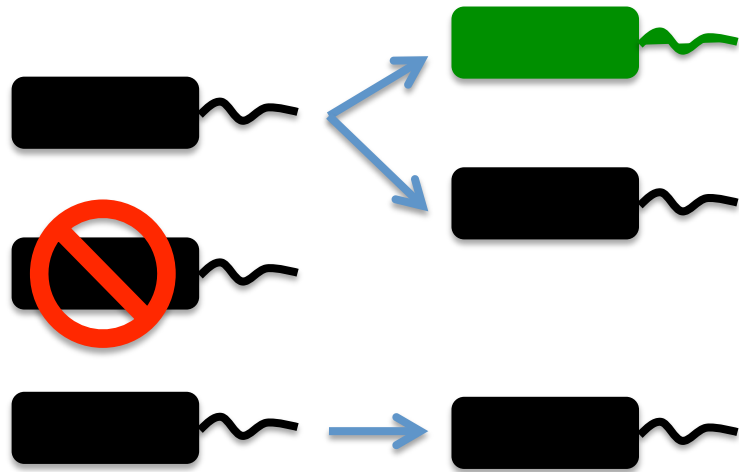
- **Nodes**
  - represent species (bacteria or phages)
- **Links**
  - represent interactions
  - host-parasite relationships (virulent phage)
  - prophage-encoded resistance (temperate phage)
- **Dynamics**
  - rules of network evolution
  - speciation (duplication of nodes, increase the fitness)
  - extinction (removal of nodes according to loads)
  - horizontal transfer of genetic information



# Elements of the network models: basic quantities

- “Trophic layer” of bacteria
  - number of different bacterial species/strains ( $N_B$ )
  - bacteria are independent
- Time steps of network evolution
  - bacteria speciation rate ( $t$ )
- Quantitative rules of the dynamic process
  - *speciation rate*
  - *extinction rate*

# Model A



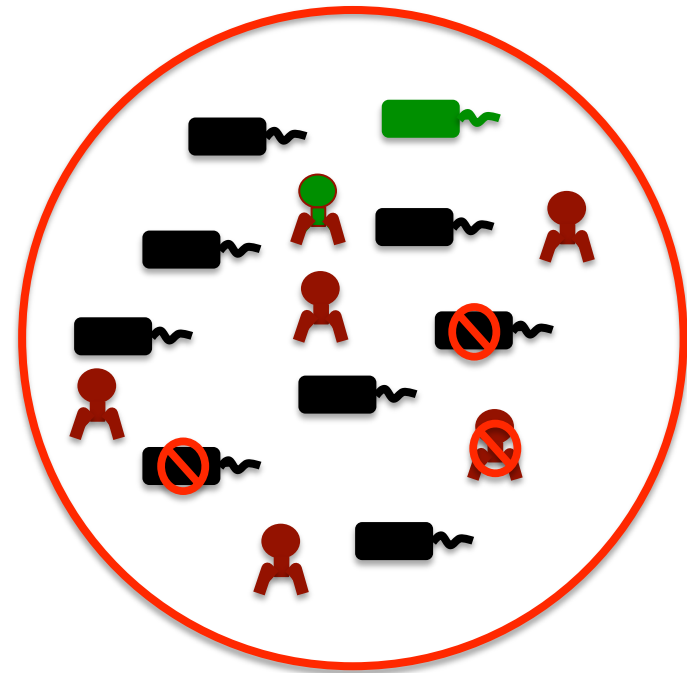
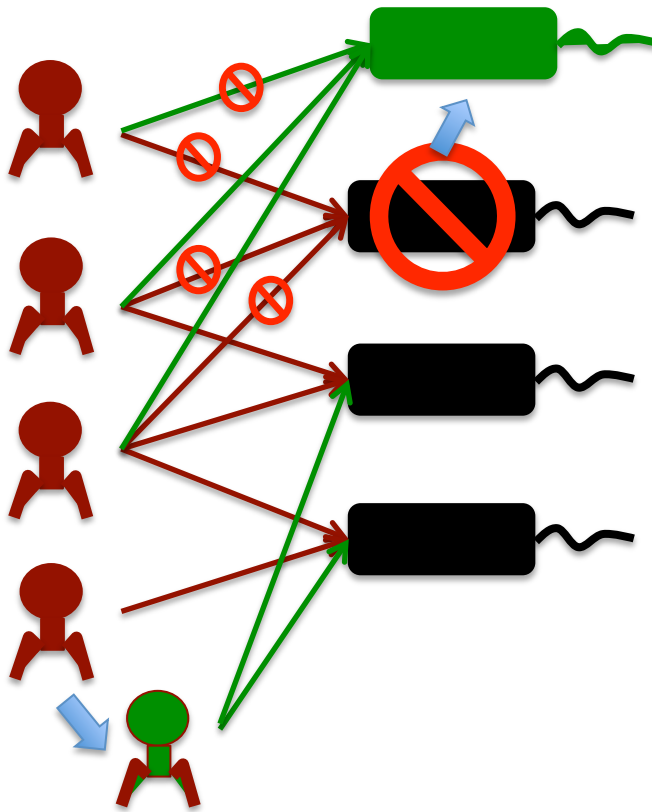
 **speciation**

 **extinction**

# Model A

- At every time  $t$ , two types of events occur
  - bacteria speciation
    - select a random strain and duplicate it
    - $N_B(t) = N_B(t-1) + 1$
  - bacteria extinction
    - strain was removed according to a probability
    - $P(i) = N_B / (N_o * N_o)$ ,  $i = 1, 2, \dots, N_B(t)$
    - random extinction associated with environmental loads common to all strains
    - $N_o$  represents the carrying capacity of the ecosystem

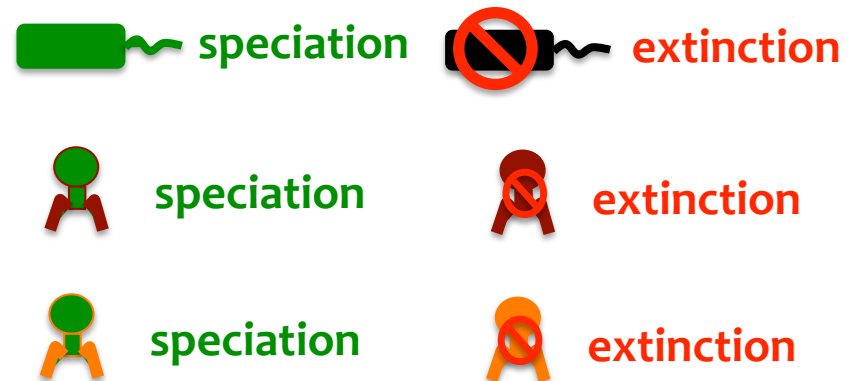
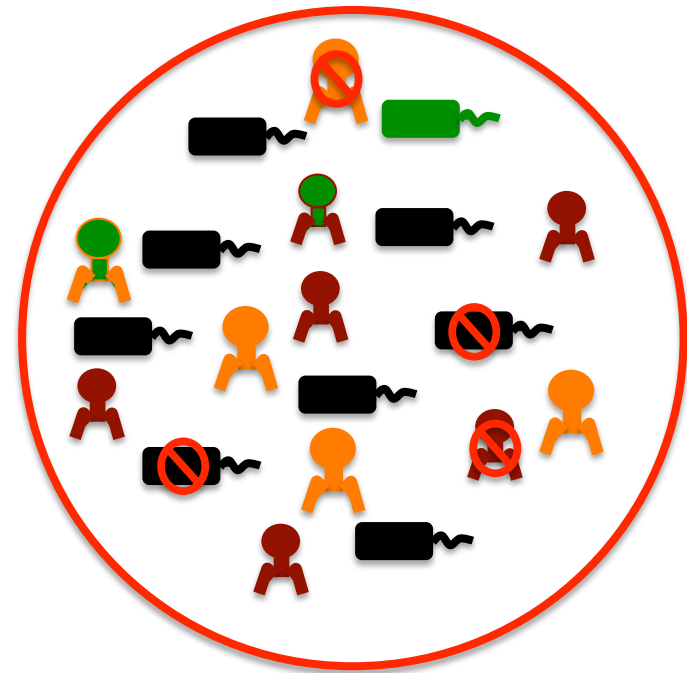
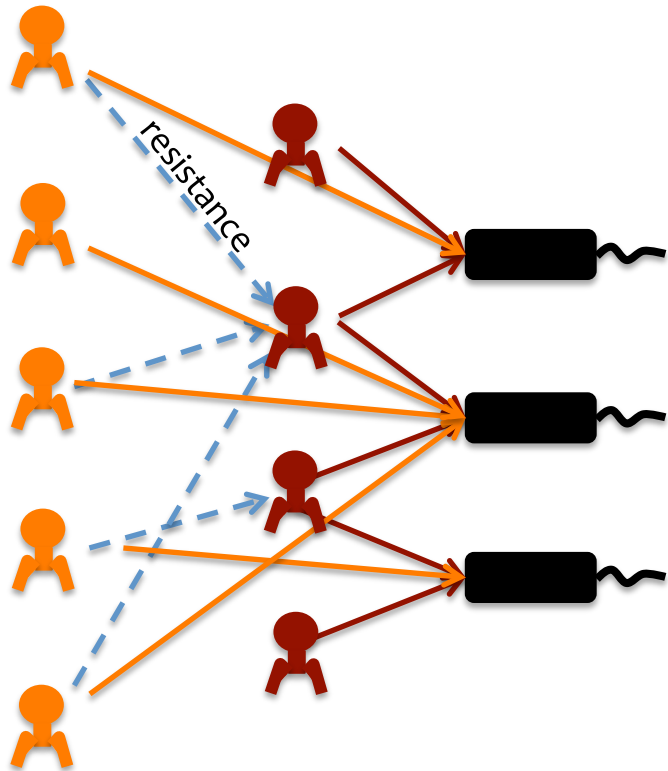
# Model B



# Model B

- Based on Model A
- Adding
  - $N_V$  of virulent phage strains
  - links between phage and bacterial strains
- At every time  $t$ , two types of events occur
  - *Bacterial speciation*
    - duplicate with its original links, and remove a random link, if possible
  - *Phage speciation*
    - duplicate a number of phage strains (Poisson distribution with mean  $\mu$ )
    - adding a link to a single bacterial strain (locally or randomly)
  - *Bacterial extinction*
    - common extinction rate:  $n/N_0^2$ , with  $n = \sum_{i=1}^{N_B} e^{-\beta b_i}$
    - number of links:  $\beta/N_0$
  - *Phage extinction*
    - load of infections (link density):  $\sigma/N_0$

# Model C



# Model C

- At every time  $t$ , two types of events occur
  - *Bacterial speciation*
    - duplicate with its original links, and remove a random link, if possible (priority to strong links)
  - *Phage speciation*
    - virulent
      - duplicate a number of phage strains (Poisson distribution with mean  $\mu$ )
      - adding a link to a single bacterial strain (locally or randomly), or remove a link from temperate phage
    - temperate
      - similar to virulent except links manipulation
  - *Bacterial extinction*
    - common extinction rate
    - **strong** links ( $\beta$ ) and **weak** links ( $\sigma$ )
  - *Phage extinction*
    - load of infections (link density)
    - same for virulent and temperate

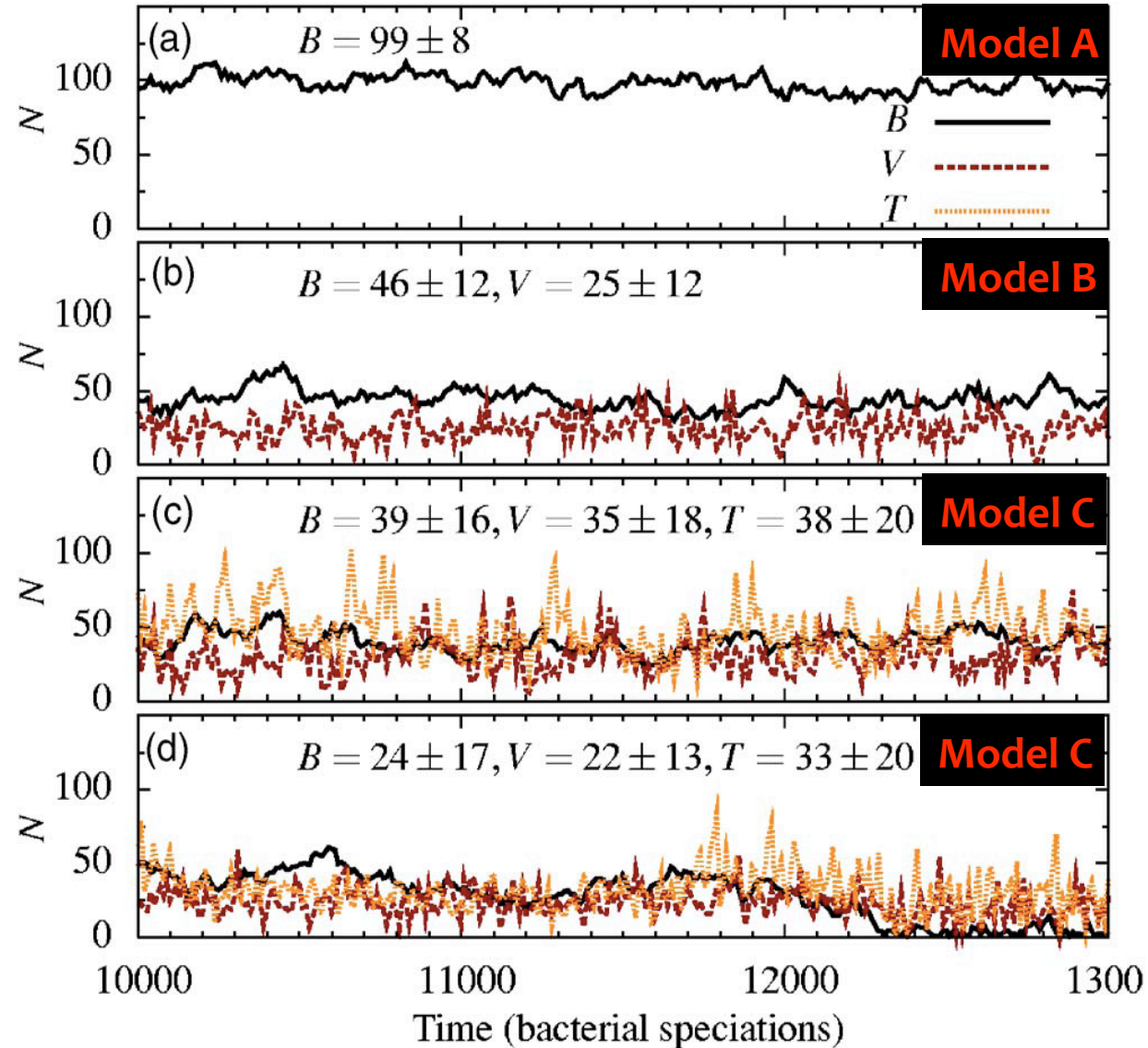
# **PART III**

## **Results and conclusions**



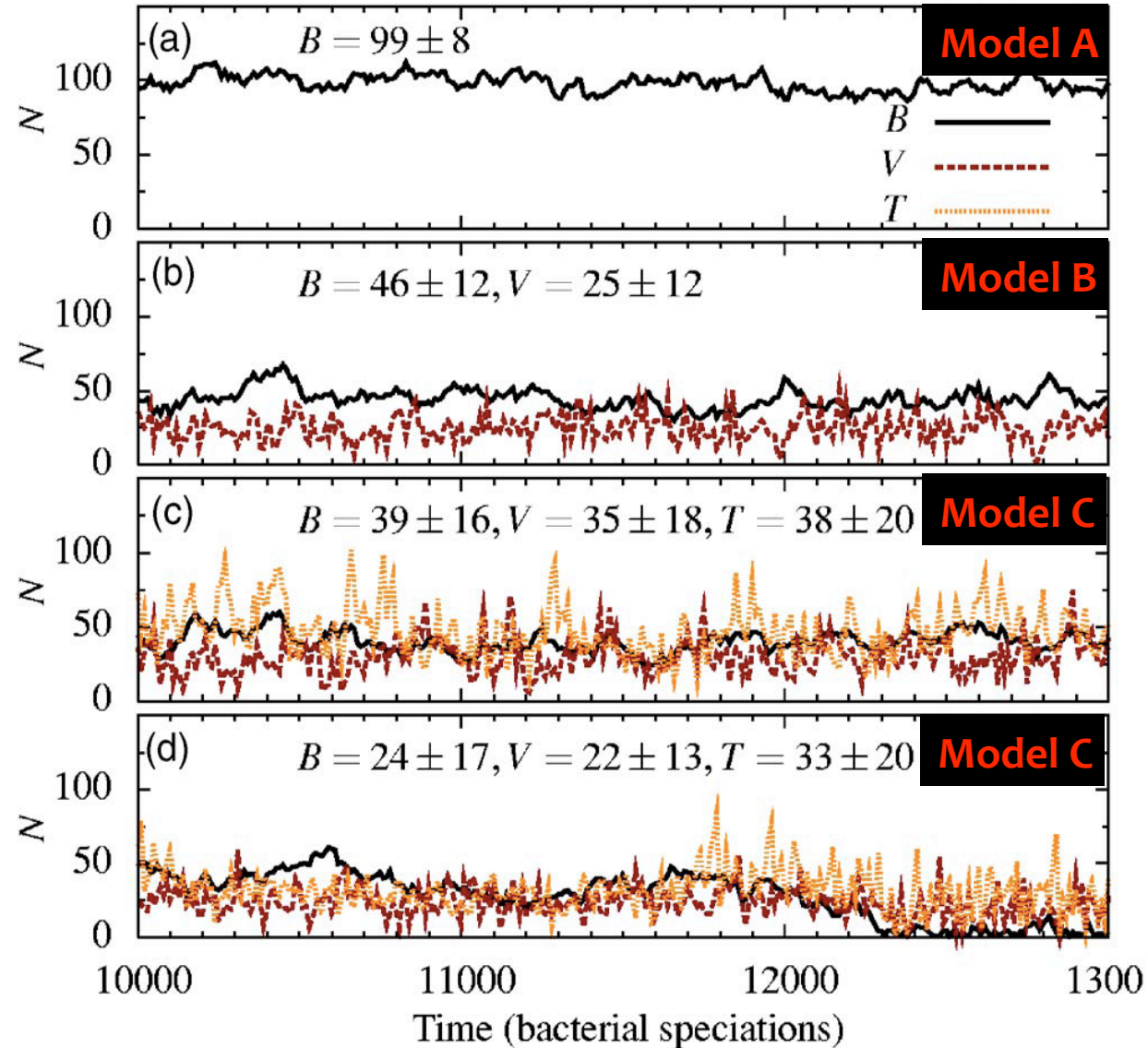
# Dynamics of models

- Parameters
  - $N_0=100$
  - sets the scale for number of bacterial strains,
  - $\mu=2.5$
  - number of phage duplications per bacterial duplication
  - $\beta=2.0$ , and  $\sigma=0.2$
  - the strong and weak loads



# Dynamics of models

- Model A
  - $N_B$  fluctuates around  $N_0$
- Model B
  - fluctuates relatively more than for model A
  - reduce independence of  $N_B$
  - positive feedback
- Model C
  - increase fluctuations
  - more virulent strains
  - more bacteria than no resistance

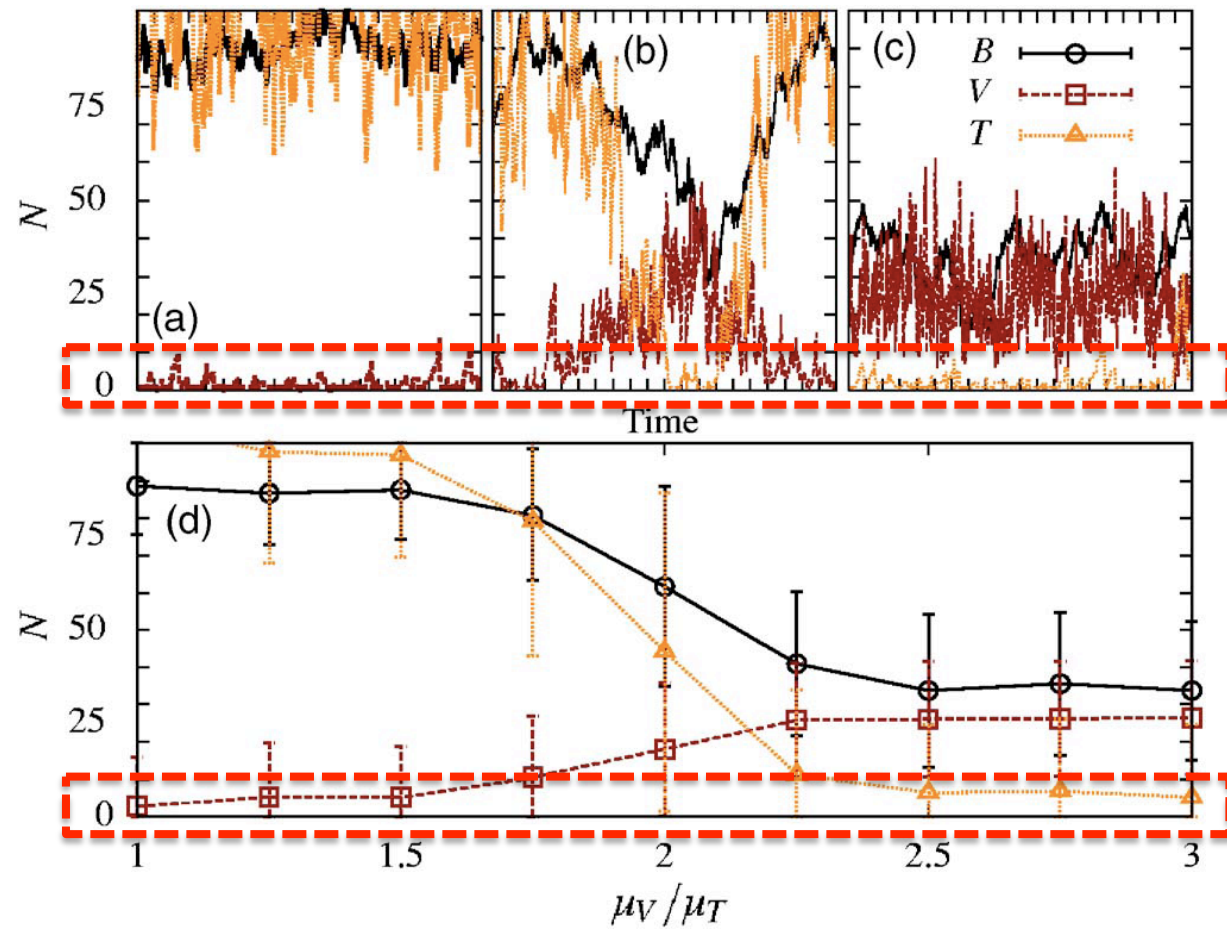


# When try to model the natural eco-systems

- The fact
  - high diversity and coexistence of temperate and virulent phage strains in nature ecological systems
- The models
  - difficult to produce viable and diverse ecosystems where many different species and strategies coexist
  - winner-take-all” situation

# Coexistence of temperate, virulent phage and bacteria

- Model D
  - similar to Model C
  - modify the speciation rate of phage
  - a) proportional to diversity
  - b)  $\mu_V = 2\mu_T$
  - c)  $\mu_V = 3\mu_T$
- Collapse of virulent or temperate phage



 Collapse "zone"

# The success of Model C

- “phage **speciation rule** was a major determinant of the viability of coexistence of temperate and virulent phages”
- succeeded where the speciation rate of each phage group is **independent of its diversity**

# Conclusion

- “Diversity could be stably maintained in the model only if the probability of speciation was independent of the diversity”
- “could be achieved in real ecosystems if the speciation rate is primarily set by the availability of ecological niches”

**Thanks for your attention :)**