



# On the Dynamical Behavior of the Epidemiological Processes on Bipartite Networks

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## Vector-Borne Diseases

A **vector-borne** disease is an illness where the pathogen is transmitted from an infected individual to another individual by a blood-sucking, arthropod or other, called **vector**.

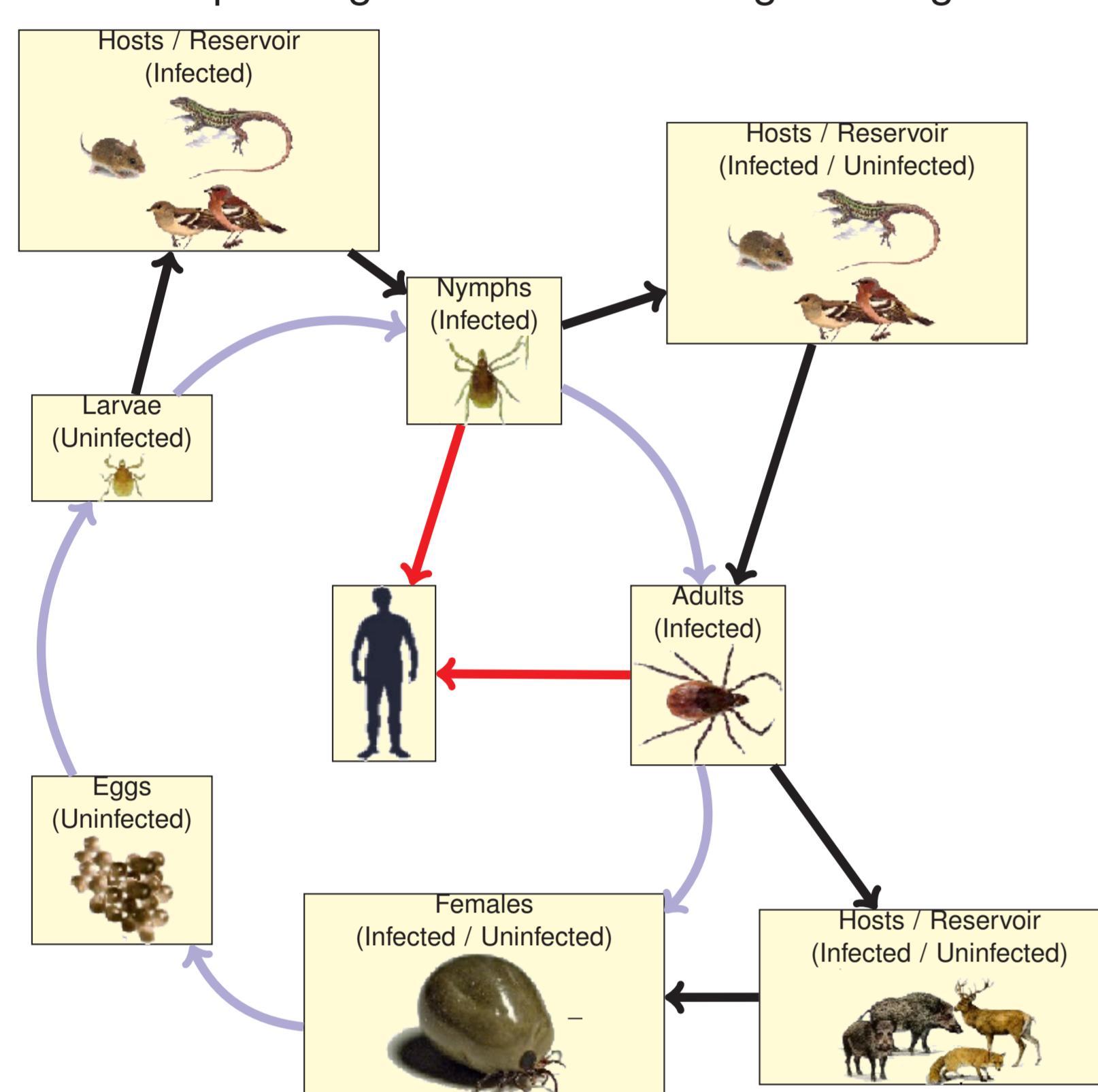
These diseases depend upon three different classes of actors:

- the **pathogens**, either viruses, bacteria, protozoa, or helminths (worm);
- the **vectors**, commonly arthropods such as ticks or mosquitoes;
- the **hosts**, usually vertebrate, which could be infected by vectors, thus becoming source of infection for vectors successively feeding on them.

## An Example: Lyme Borreliosis

Lyme Borreliosis (LB) is the most common vector borne disease of humans in temperate climates. It can affect at different threat levels several tissues in the human body: skin, heart, nervous system, eyes, kidneys and liver.

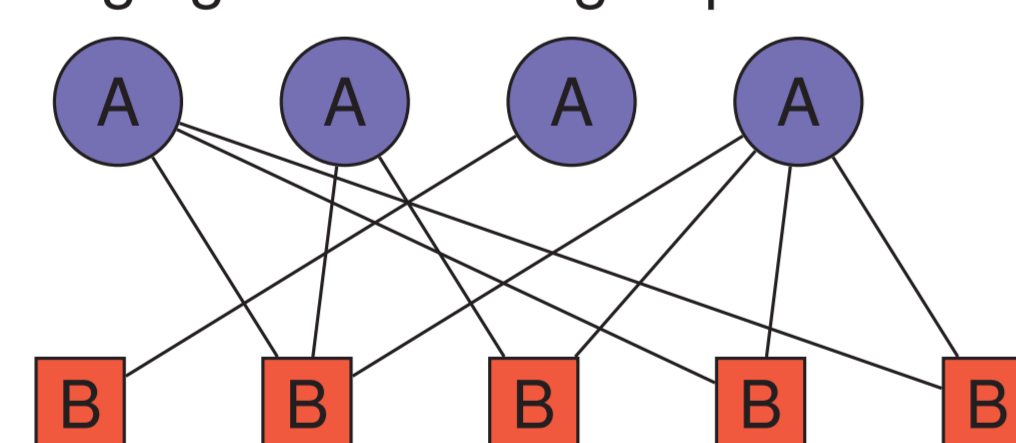
LB pathologic agent are spirochetal bacteria belonging to the Borrelia genus. Vectors are hard ticks of the genus Ixodes (in Europe I. ricinus), while hosts are small-medium vertebrate such as reptiles, birds and mammals depending on the host-seeking tick stage.



## Networks in Vector-Borne Disease Modelling

For the **heterogeneous** nature of the transmission dynamics between vectors and hosts the use of homogeneous mixing models is not appropriate, while a network approach is highly motivated. The dynamic network approach is a non-reductionist approach enabling analysis of systems as a whole, which makes it an ideal tool for epidemiological systems.

The transmission network of a number of important vector-borne diseases could be naturally described by a **bipartite network**, structure where nodes are divided in two groups and edges are allowed only between nodes belonging to different groups.



In order for this model to faithfully describe those epidemiological systems, pathogen transmission may occur only between hosts and vectors or, in other words, the transmission between individuals of the same family does not happen or at least it is negligible.

Examples that satisfy such constraints are pathogens like those responsible for **Tick Borne Encephalitis** or **Lyme disease**, two of the most reported diseases transmitted by ticks.

## Transmission over Bipartite Networks

The transmission of pathogens over a bipartite networks was firstly analyzed by Gomez-Gardenes and colleagues for **heterosexually transmitted diseases**.

Those results were generalized by Bisanzio and coauthors and applied to **vector-borne diseases**. In that paper an important result was proven: if until then the aggregative behavior of vectors on hosts was usually described by **negative-binomial** distributions, they showed on different datasets that the best fitting was **power law** with exponents around 2.5.

This implies an important consequence: the epidemic threshold vanishes in the limit of large network sizes. In other terms, the condition for an endemic behavior, observed in several countries around the world, seems to be well supported by field data.

## Essential bibliography

- Pastor-Satorras, R., Vespignani, A. - **Epidemic Spreading in Scale-Free Networks** - Phys. Rev. Lett., **86**,14, 3200–3203 (2001)
- Gómez-Gardeñes, J., Latora, V., Moreno, Y., Profumo, E.: - **Spreading of sexually transmitted disease in heterosexually populations** - PNAS, **105**, 5, 1399–1404 (2008)
- Bisanzio, Bertolotti, Tommasone, Amore, Ragagli, Mannelli, Giacobini, Provero: - **Modeling the Spread of Vector-Borne Diseases on Bipartite Networks** - PLoS ONE, **5**, 10, 2010
- Ferreri L., Venturino E., Giacobini M. - **Do Disease Spreading on Bipartite Networks Have Some Evolutionary Advantages?** - LNCS 6623 - 2011

## The Importance of Being Bipartite

Moreover, in a recent manuscript we showed that a pathogen agent spreading on a bipartite scale-free network can have some **evolutionary benefits** with respect to its diffusion on classical scale-free unipartite networks.

We say that a pathogen spreading over a peculiar network structure has some **evolutionary benefits** if the endemic situation is satisfied for transmission probabilities smaller than those needed on the other network structures. Moreover, in the following, we choose an harder definition:

★ a pathogen has some evolutionary advantages spreading over a peculiar network structure if with the same transmission probability the endemic situation is reached over the peculiar network structure but not over others ★

In particular we are interested to find under what conditions a pathogens benefits of spreading over a bipartite network. In other words we are interested to derive the conditions for which a vector-borne disease, despite its more complex behavior, in some cases benefits by it.

## Comparing the Spreading in Bipartite and Unipartite Networks

In order to compare the endemic conditions for the spreading in bipartite and unipartite networks we evaluate the main characteristics of bipartite networks in which the bipartite structure is not taken into account.

In a bipartite network in which we do not care about its bipartite structure the probability for a node to have a node with  $k$  degree is given by the probability for a node of the first family to have  $k$  connections knowing that we are in the first family plus the probability for a node of the second family to have  $k$  connections knowing that we are in the second family:

$$\mathbb{P}(k) = \mathbb{P}(k/A)\mathbb{P}(A) + \mathbb{P}(k/B)\mathbb{P}(B)$$

Moreover, after few steps, we can found

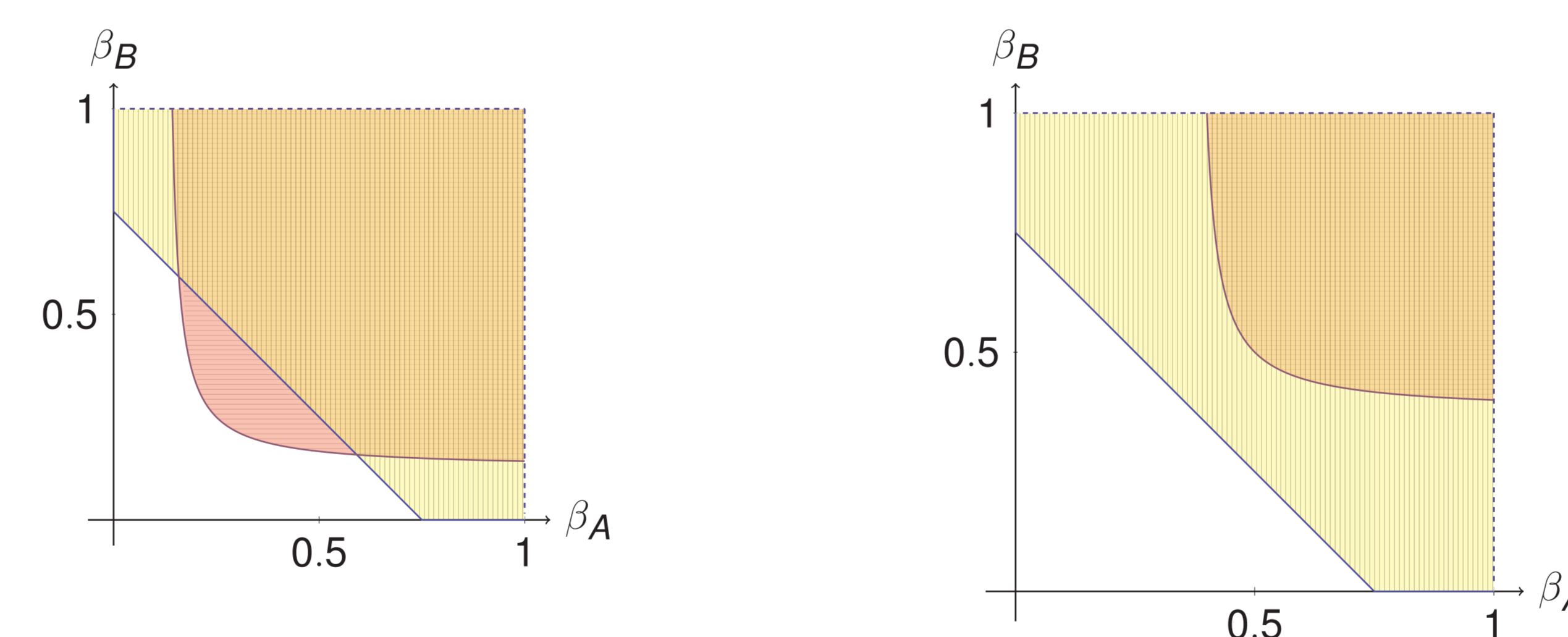
$$\frac{\beta}{\mu} = \frac{\beta_A \langle k \rangle_A + \beta_B \langle k \rangle_B}{\mu_A \langle k \rangle_A + \mu_B \langle k \rangle_B}$$

where we have used the useful equation that binds the number of nodes in each population and the average number of contacts

$$N_A \langle k \rangle_A = N_B \langle k \rangle_B$$

## The Evolutionary Advantage

For the sake of simplicity we assume that the recovery rates  $\mu_A$  and  $\mu_B$  are equal to 1. Below we show for what couples of transmission probability  $(\beta_A, \beta_B)$  the endemic scenario is reached in bipartite networks (pink) and in unipartite networks in which the bipartite structure is not take into account (yellow) in two different networks.



Now there exists an ensembles of network for which with a couple of transmission probability  $(\beta_A, \beta_B)$  the endemic state is reached in the bipartite network but not in the unipartite if the following are hold:

$$\begin{cases} \beta_A \beta_B \geq \frac{\langle k \rangle_A \langle k \rangle_B}{\langle k^2 \rangle_A \langle k^2 \rangle_B} \\ \frac{\beta_A \langle k \rangle_A + \beta_B \langle k \rangle_B}{\langle k \rangle_A + \langle k \rangle_B} < \frac{2 \langle k \rangle_A \langle k \rangle_B}{\langle k \rangle_A \langle k^2 \rangle_B + \langle k^2 \rangle_A \langle k \rangle_B} \end{cases} \quad (1)$$

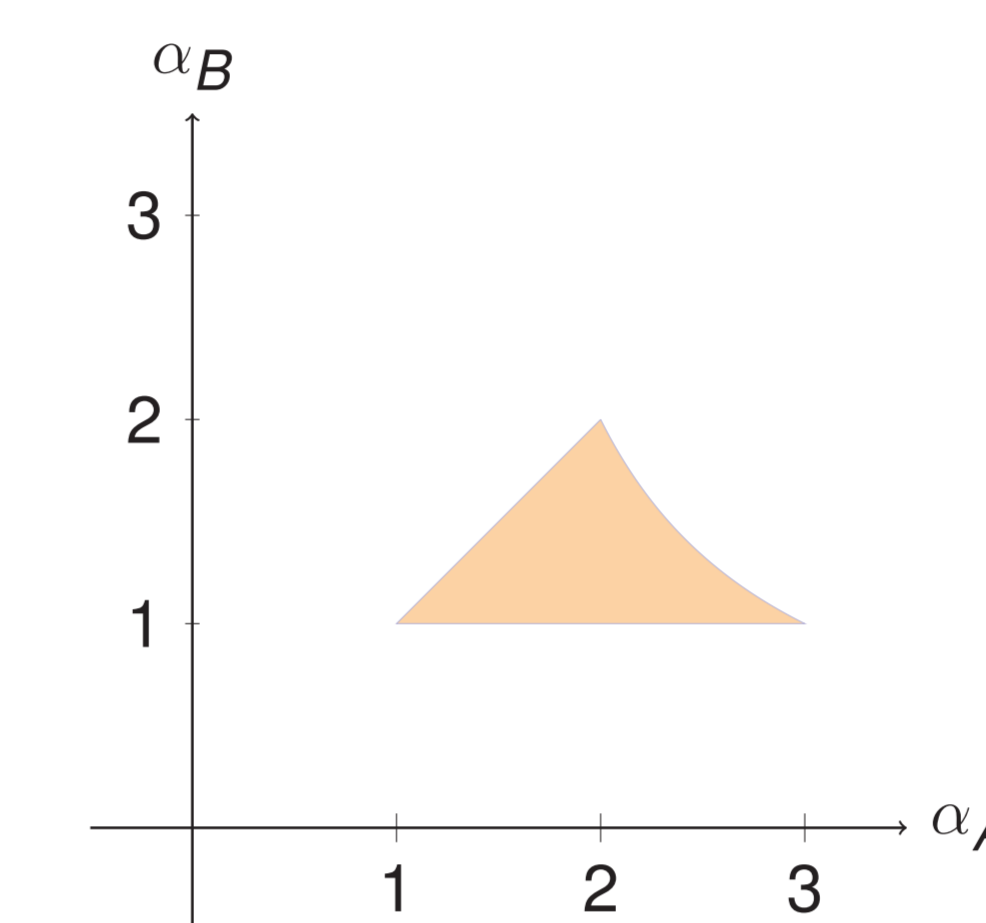
## Asymptotic Behavior for Contacts Distributed as Power Law

We investigate under what conditions the system of inequalities (1) is verified for two populations with degree distributed as power law.

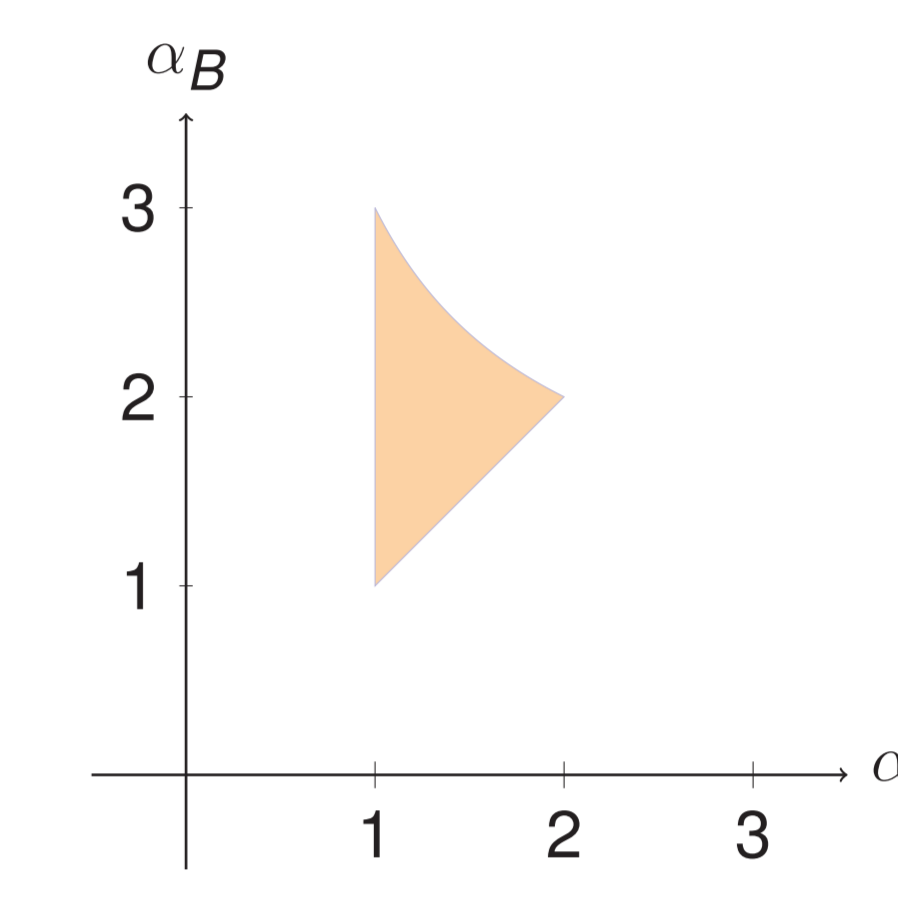
In order to consider the **asymptotic behavior** in the limit of large size network we bind the maximum degree of the network with its size:

$$k_n \simeq k_0 N_n^{\frac{1}{\alpha}}, \quad n = A, B$$

Using this equation we found that the systems of inequalities in the limit of large size network is verified for exponents verifying the following:



$$1 < \alpha_B < \alpha_A < 2 \text{ united with } 2 < \alpha_A < 3 \wedge 1 < \alpha_B < \frac{2}{\alpha_A - 1}$$

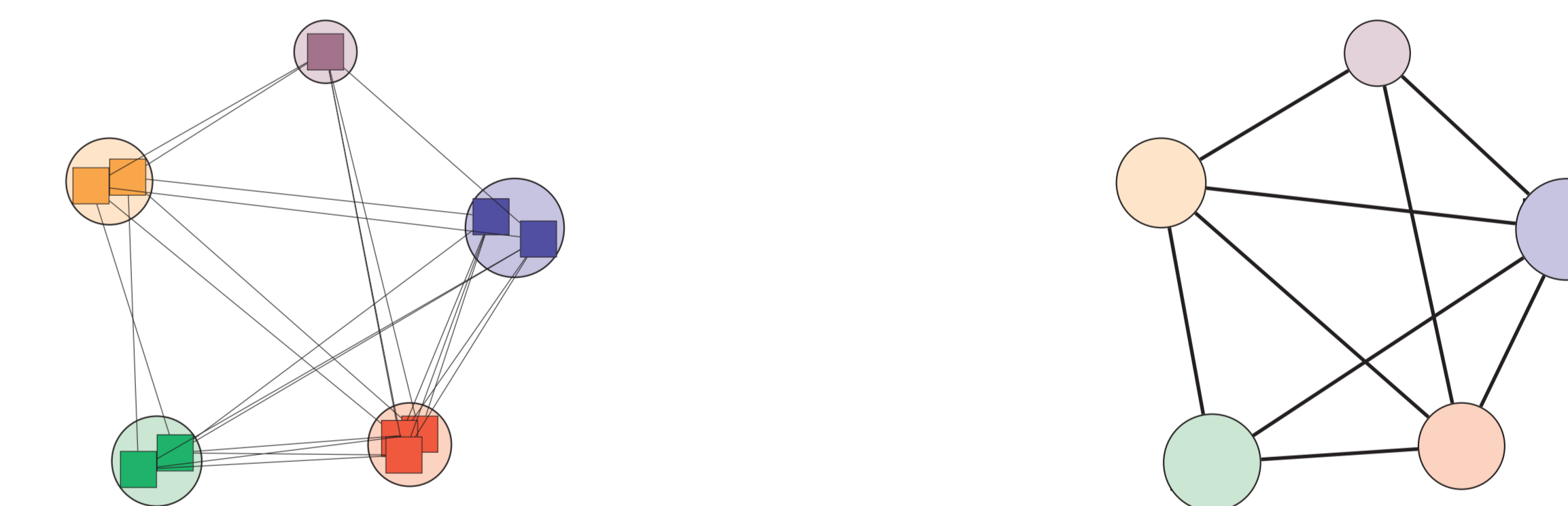


$$1 < \alpha_A < \alpha_B < 2 \text{ united with } 1 < \alpha_A < 2 \wedge 2 < \alpha_B < \frac{\alpha_A + 2}{\alpha_A}$$

## A Multipartite Graph

A multipartite graph is defined to have the vertex set partitioned into  $N$  parts and edges are allowed only between nodes belonging to different parts.

We define the **metastructure** of a graph the graph of its vertices parts. Edges among two different parts are hold if at least a couple of vertices of those parts are connected:

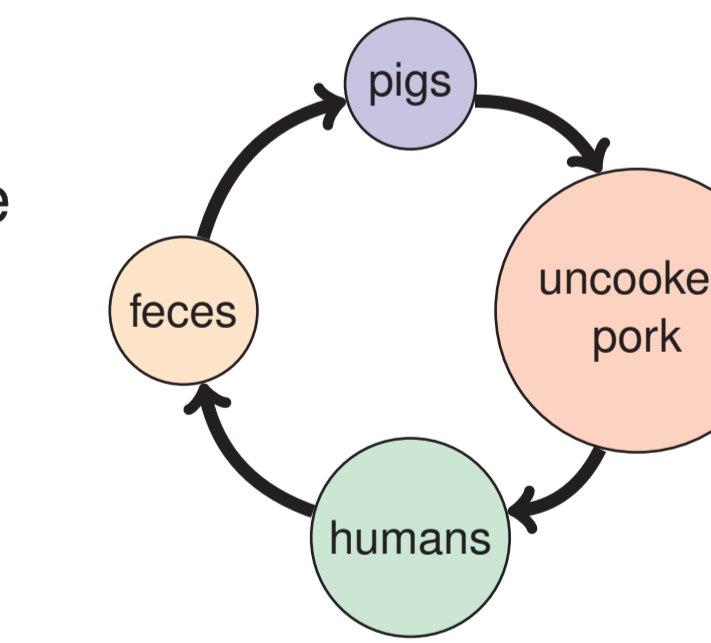


## Epidemic Dynamics on Multipartite Graphs

In some eco-epidemiological systems different species of vectors are competent only for different species of hosts. A natural description of such kind of transmission may be done by a particular class of multipartite graphs: graphs whose metastructure is a cyclic graph. As a simple example consider the metastructure of the transmission network of *Taenia Solium*.

We found that the epidemic threshold for a  $N$ -partite network with cyclic metastructure is given by:

$$\frac{\beta_1}{\mu_1} \dots \frac{\beta_N}{\mu_N} > \frac{\langle k \rangle_1}{\langle k^2 \rangle_1} \dots \frac{\langle k \rangle_N}{\langle k^2 \rangle_N}$$



## Conclusions

We have demonstrated that:

- pathogens, such as sexually transmitted diseases in heterosexual populations or vector-host pathogens like tick-borne encephalitis or Lyme borreliosis, can have some advantage if spreading on a bipartite network instead of spreading on the same network without the bipartite constraint;
- the epidemic threshold in a multipartite graph with cyclic metastructure is nothing but the product of the epidemic threshold of each parts. Therefore for the epidemic threshold vanish asymptotically in the large population size is sufficient that at least the second moment of one class diverges faster than the first moment of one class which diverges more rapidly.

## Future Works

These results are only one of the first step we plan to do in the understanding of the pathogens transmission in vector-borne diseases.

Therefore in the future we are going to:

- carry out simulations to confirm our theoretical results,
- examine the effective structure of the contacts between vectors and hosts,
- examine the role of cofeeding transmission in vector-borne diseases, and more extensively to implement an individual-based model for the vector-borne disease transmission.