

Dynamics of infectious diseases on trade networks

1. Introduction

Concerning the introduction and the dissemination of livestock infectious diseases, the trade of animals is an important risk factor. Data on the movement of animals between animal holdings in Germany, which are recorded in the HI-Tier database, are investigated. Network analysis tools are used for the investigation. In addition an infection model is introduced for a sample of the network.

2. Network description

A network (also graph) $G = (V, E)$ is a set consisting of vertices (also nodes) V and edges E . Small networks can easily be understood without a complicated mathematical description. Large and complex networks, such as trade networks, need a mathematical representation.

Adjacency matrix. The trade network is represented by an adjacency matrix A , which determines whether two nodes (here holdings) i and j are connected with each other. A connection from i to j does not imply that there's a connection from j to i , hence our network is a directed graph (also digraph). The elements of the adjacency matrix a_{ij} are 1, if there is a connection from i to j , and 0 otherwise.

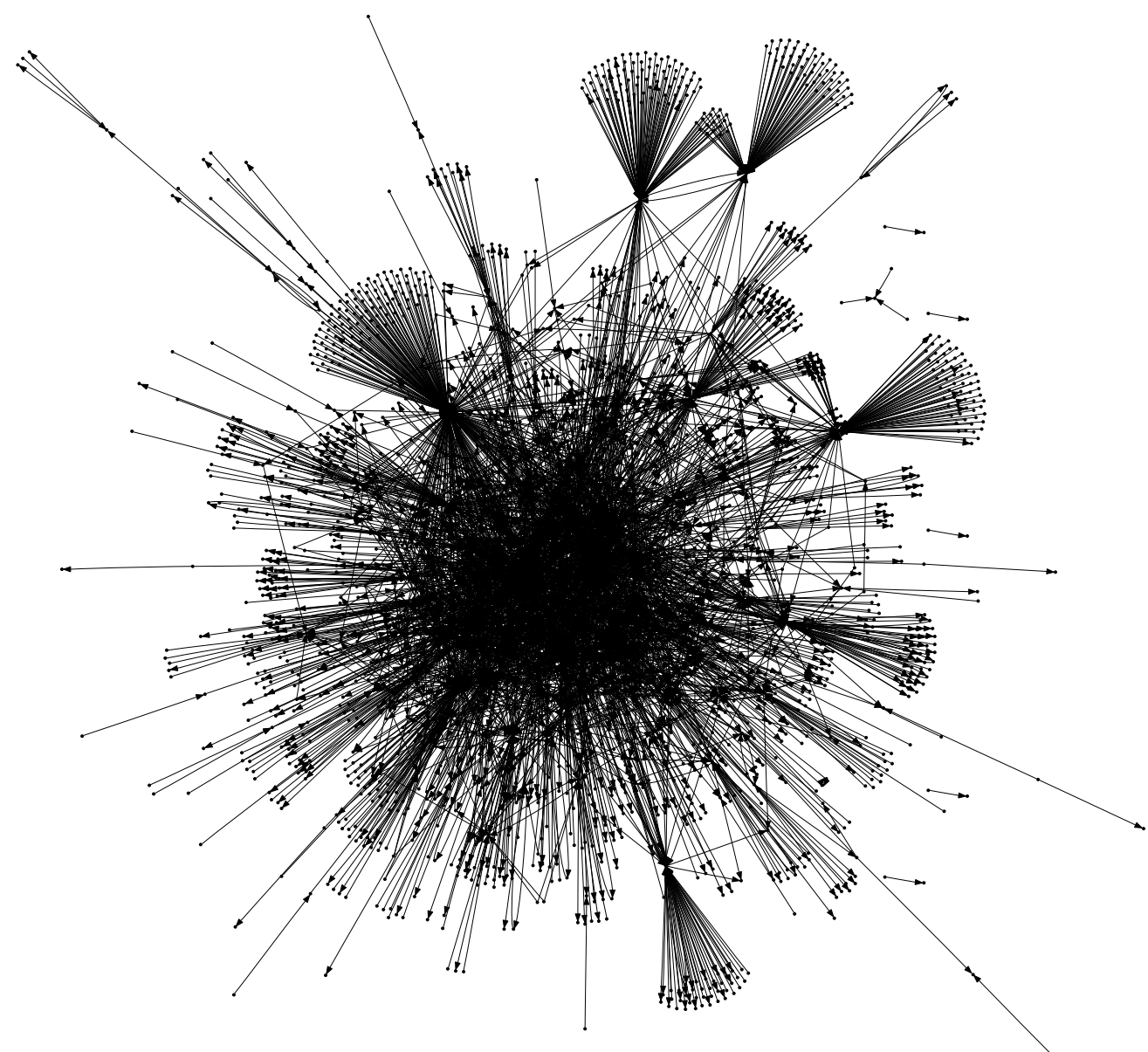


Figure 1: Livestock trade network of a German county. The nodes represent the holdings and the edges represent the trade connections between the holdings. The position of the nodes doesn't correspond to the geographical position of the holdings.

3. Centrality measures

The relevance of single nodes can be expressed in terms of centrality measures.

Degree. The simplest centrality measure is the degree d of a node, which is the number of nodes a node is connected to. In a directed network each node has an in-degree d^- and an out-degree d^+ . The out degree of a holding i corresponds to the number of holdings it exports animals to. The in degree of i corresponds to the number of holdings i imports from. The degree of a node can be calculated from the adjacency matrix

$$d^+(i) = \sum_{j=1}^n a_{ij}, \quad d^-(i) = \sum_{j=1}^n a_{ji}$$

Degree distribution. After the computation of the degrees of a network it is useful to compute their distribution. Basically this distribution can be classified by one of the following types:

- an exponential distribution ($p(d) \sim \exp(-d)$) which is found in random graphs.
- a power law distribution ($p(d) \sim d^{-\gamma}$) which is found in most networks in nature.

In the latter case the network is called scale free. In that case the epidemic threshold decreases. Consequently an infection can spread also for small values of the epidemic parameters.

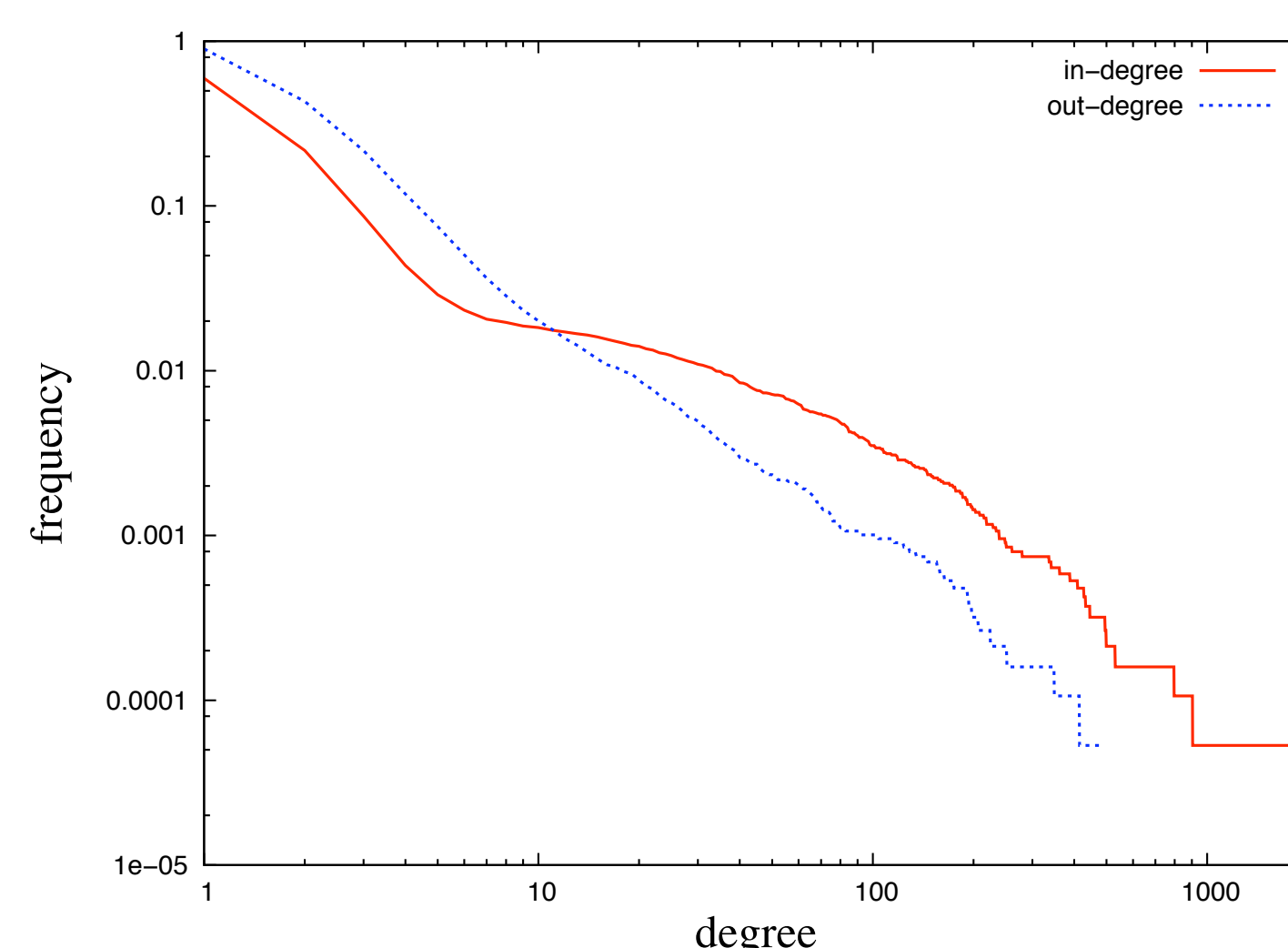


Figure 2: In and out degree distribution of the German livestock trade network.

Closeness. The closeness of a node i is defined as its reciprocal average shortest distance to all other reachable nodes. A feature of nodes with high closeness is that other nodes can be reached within only few steps. The closeness of the trade network has a typical value, which corresponds to the average shortest path length in the network.

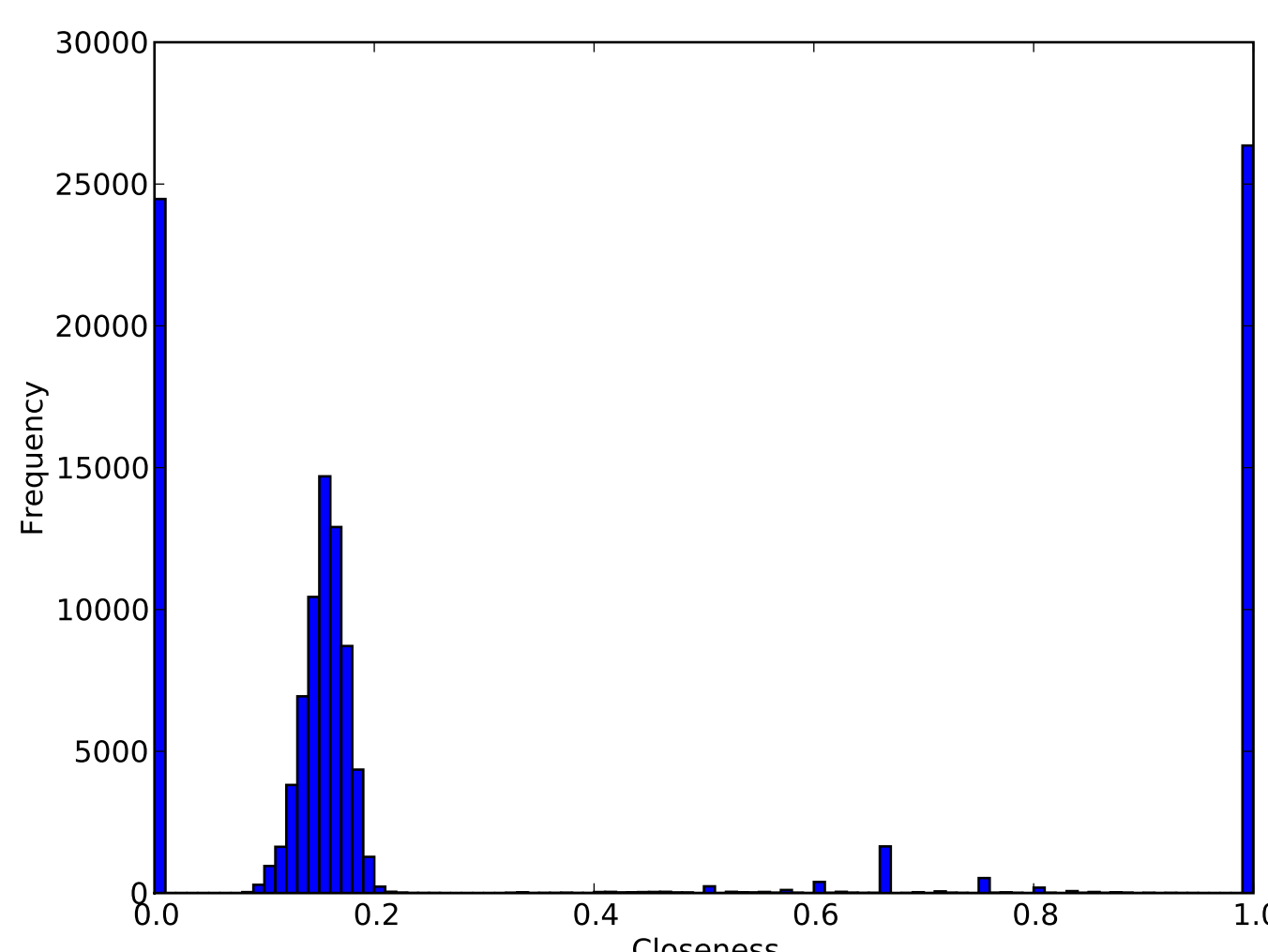


Figure 3: Closeness distribution of the German livestock trade network.

Range. The starting node is essential for the spread of an epidemic. Some nodes are only able to reach very few other nodes at all. The *range* of a node i is defined by the total number of distinct nodes that can be reached using every possible path starting from node i . Only nodes of long range are important for the effective spread of the epidemic. The distribution of ranges within the trade network has a very special structure. About half of the nodes have a range of only up to 100. The other nodes can reach about half of the whole network (about 55,000).

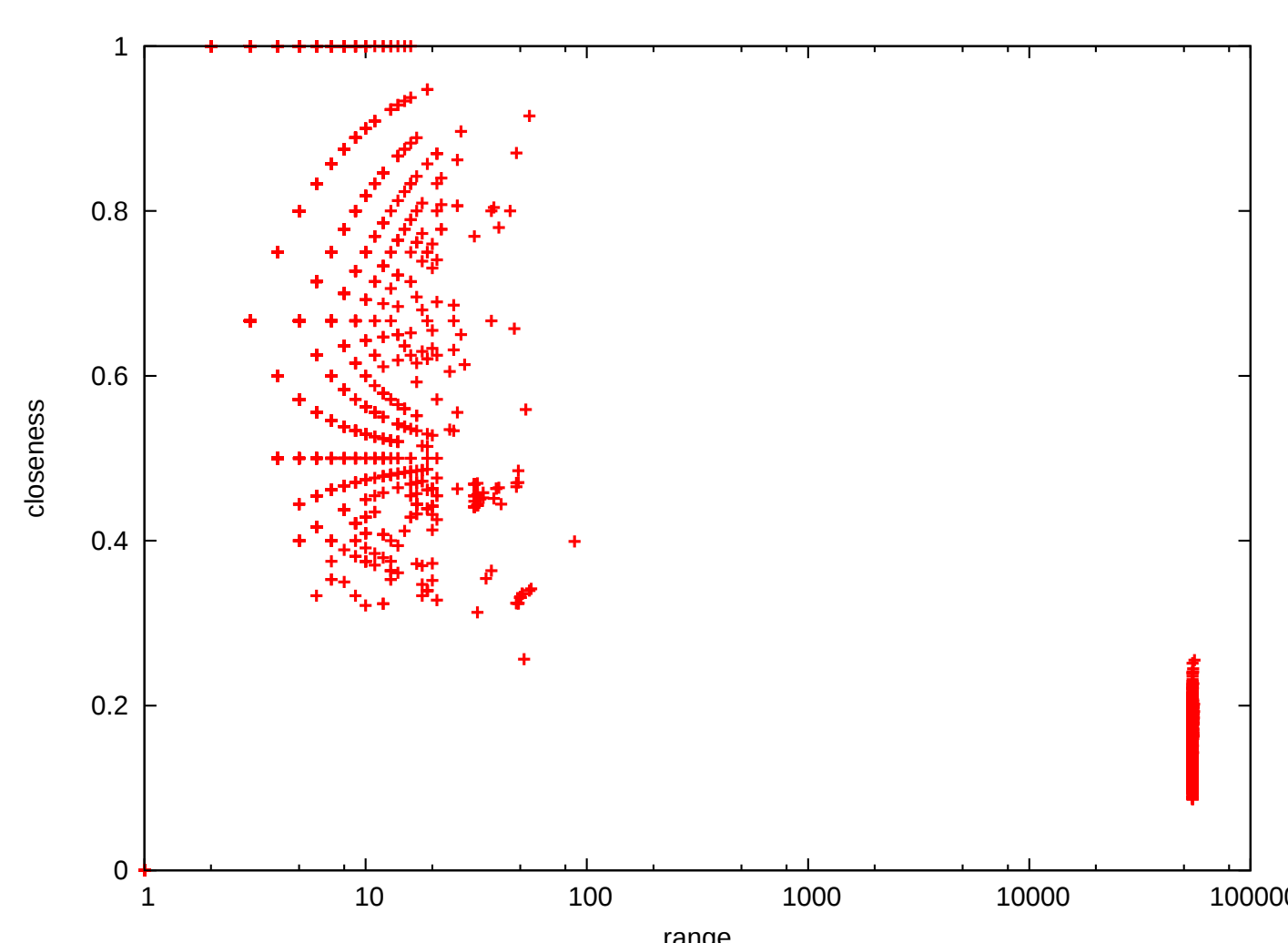


Figure 4: Range vs. closeness of the holdings in the investigated area.

4. Infection dynamics

Understanding the dynamics. The dynamics of the infection can easily be understood by introducing two new variables. The first is the total number of infected ($\sum_k i_k$). To measure the distribution of the infection we introduce the variable participation $u = 1 - \phi$, where

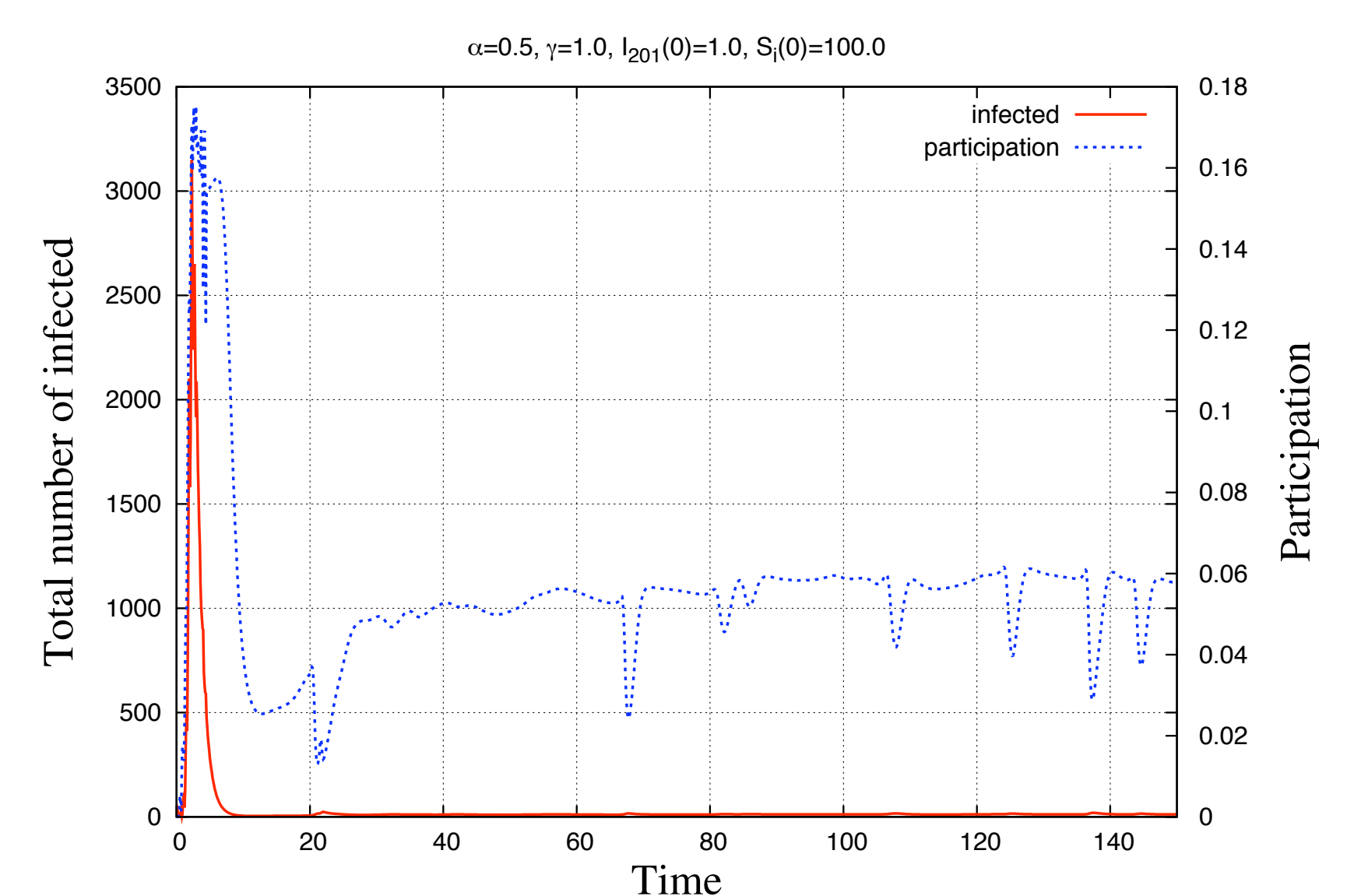
$$\phi = \arccos \frac{\mathbf{i} \cdot \mathbf{b}}{|\mathbf{i}| |\mathbf{b}|} = \arccos \sqrt{\frac{1}{\dim}}$$

is the angle between the infection vector and the bisectrix $\mathbf{b}$. If the infection is localized at only one holding, the participation is 0. For a uniformly distributed infection the participation is 1.

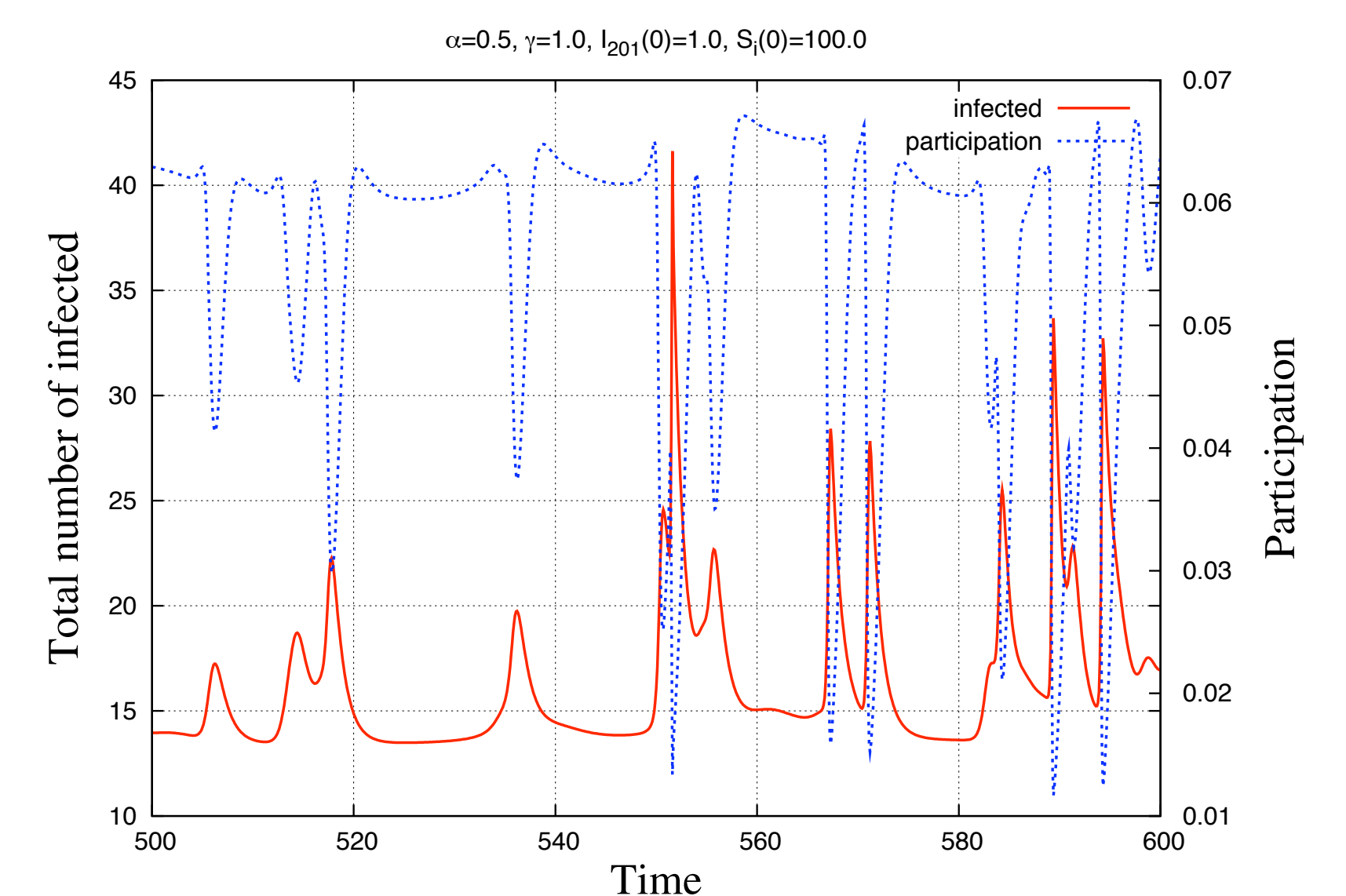
SIR model. The basic idea is a SIR-model containing interaction *between* holdings and *within* holdings.

$$\begin{aligned} \Delta s &= -\alpha [(M^T s) * i + (M^T i) * s - s * i] + M^T s - M s \\ \Delta i &= \alpha [(M^T s) * i + (M^T i) * s + s * i] + M^T i - M i - \gamma i \\ \Delta r &= M^T r - M r + \gamma i \end{aligned}$$

The solutions of the SIR equations depend on the initial infected node. Since only half of all nodes have a sufficient large range, the number of potentially initial infected nodes is extremely reduced. Then the shape of the solution only depends on the disease parameters.



(a) Short time behaviour.



(b) Long time behaviour.

Figure 5: Solutions of the SIR model in the trade dominated regime.

5. Outlook

Further work will be focused on the investigation of the parameter space. For the understanding of the whole livestock infectious disease dynamics other networks have to be considered. These might be the animal feed network, the veterinarian network or the wild animal contact network. Furthermore the decomposition of the network into smaller communities will be considered.