



Network analysis of cattle movements in Slovenia

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Introduction

Movement of animals between premises is one of the main factors contributing to the spread of infectious diseases in livestock. Network analysis enables the systematic investigation of animal trade and allows the evaluation of risk potential for disease spread.

Objective

The analysis of movement data to gain insight into the structure of cattle trade network in Slovenia.

Approach

Static network analysis of the directed graph

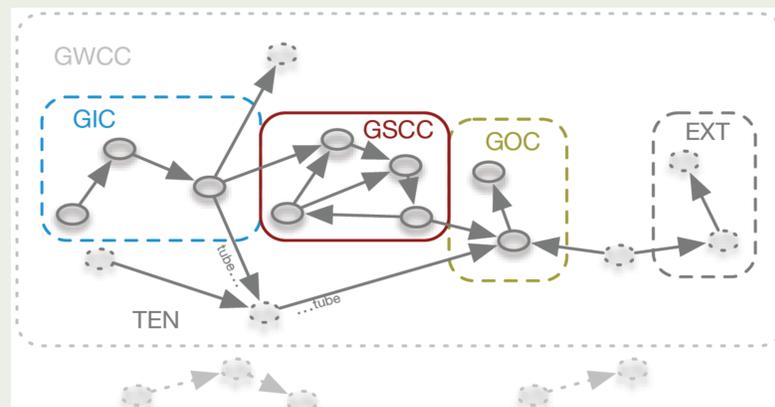
Nodes – farm holdings, pastures, slaughterhouses, animal waste processing centres, fairs.

Edges – movement of at least one animal from one premises to another with respect to link direction.

Unweighted static network – animal movements are aggregated if they connect the same two premises and have the same direction.

The time period from 1st Jan 2010 till 30th Nov 2015.

Component structure of directed graphs

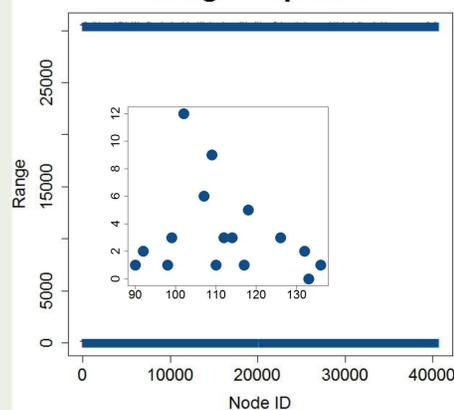


Legend: GWCC – giant weekly connected component, GSCC – giant strongly connected component, GIC – giant in component, GOC – giant out component, TEN – tendrils, EXT – external component.

(Lentz et al. 2016. arXiv:1602.09108v2 [physics.soc-ph])

Results

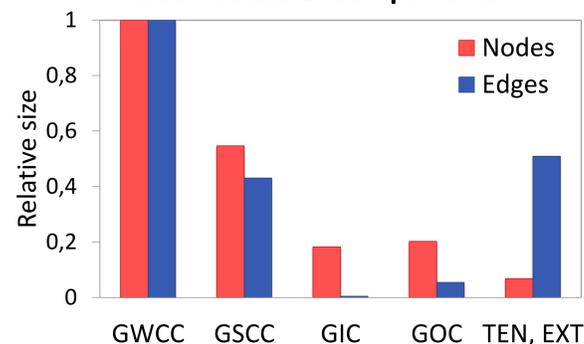
Range sequence



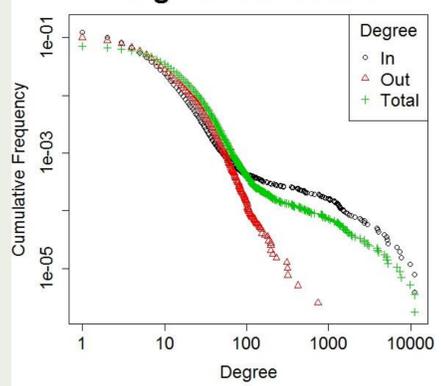
Standard network properties

Number of nodes	40,662
Number of edges	357,509
Size of GSCC	54.65 %
Average shortest path length	5.49
Diameter	16
Size of GWCC	99.995 %

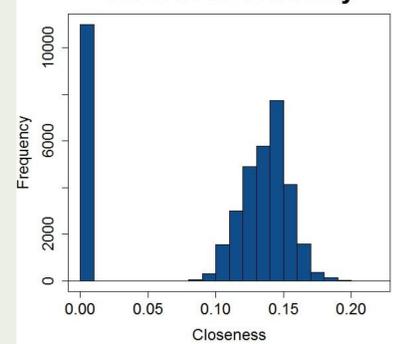
Relative sizes of components



Degree distribution



Closeness centrality



Diameter – the maximum value amongst shortest path lengths between node pairs in the GSCC.

Range – is the number of nodes within reach of a specified node by path of any length.

Degree – is the number of neighbors of a node:

in-degree – incoming neighbors,

out-degree – outgoing neighbors.

Closeness – the reciprocal average distance to all other nodes that can be reached from a specified node.

Component – is a set of nodes in which all nodes are connected to each other by path of any length.

Conclusions

- Around 73 % of the nodes have a long range and therefore represent a high risk for the spread of infectious diseases. Infection starting in one of these nodes could potentially spread to almost three quarters of the network.
- Centrality measures (degree and closeness centralities) demonstrate a strong hierarchical structure of the network. Nodes with higher centrality can be identified for targeted surveillance and control measures.
- Network analysis has proven to be particularly useful in terms of understanding the potential of spreading the infectious diseases.

Acknowledgements

The Society for Veterinary Epidemiology and Preventive Medicine is acknowledged for their contribution to the attendance of the Annual Conference SVEPM 2016, Elsinore.

Data were provided by the Administration of the Republic of Slovenia for Food Safety, Veterinary Sector and Plant Protection.

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