

SHORT TERM SCIENTIFIC MISSION (STSM) SCIENTIFIC REPORT

This report is submitted for approval by the STSM applicant to the STSM coordinator

Action number: CA15116

STSM title: Modelling spread of ASF in Poland

STSM start and end date: 30/09/2017 to 11/11/2017

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PURPOSE OF THE STSM:

Recent rapid spread of the African Swine Fever (ASF) in the Northeast Poland during summer 2017 encourages us to prepare risk assessment for the whole country and predict future geographical transmission paths.

We focus on a predictive stochastic ASF model based on empirical geographical data incorporating organizational network of regions, empirical forest, swine, and wild boar density as well as theoretical organizational structure of the pork production supply chain. This project should and as a decision support system as a tool for epidemiologists and veterinarians in chief.

We used available data on outbreak form O_iO and regional information from Statistics Poland (GUS). We use regression models and social network analysis to investigate the outbreak. We perform early epidemic growth estimation and simulate landscape-based propagation.

We also realize that up to our knowledge, there are is no scientific quantitative statistical studies to explain ASF for affected EU countries as Poland, Romania, Lithuania, Czech Republic and Latvia, and only for Estonia scientific analysis was performed (EFSA-Q-2017-00154).

The result of the cooperation gives novel interdisciplinary insights into understanding of the drivers of propagation of ASF in Poland as well as new computational and mathematical tools for reconstruction of the most likely future paths of infection and for the classification of regions into risk groups.

DESCRIPTION OF WORK CARRIED OUT DURING THE STSMS

Within around 3 week visit in Berlin (30.09-03.10, 9-19.10,1-11.10), we applied theoretical concepts of temporal networks to improve a computer-assisted ASF infection analyses and performed simulation assisted outbreak investigation.

During STSM, not only Veterinary Department FU-Berlin (Host Institution) was place of our research. We visited specialists from the field (experimental epidemiologists and inspectors) for providing us proxy of parameters:

- in Hamburg (German Infectious Diseases Federation) discussion on inferring genetic distances to validate our links (30.09.2017);

-in Greifswald (Friedrich-Loeffler-Institute) discussion on model and we gave presentation on our model (02.11.2017);

- in Berlin (Robert Koch Institute) discussion on model choice procedure (19.10.2017);

- in Berlin (Future Medicine Conference) discussion with Estonian researchers about similarity of our ASF outbreak (07.11.2017);

- in Berlin (German Federal Institute for Risk Assessment) with additionally some researchers from EFSA (Parma) and Hungary discussion on ASF model and we gave presentation on our model (10.11.2017).

We have lunched simulation on Soroban (computer cluster facility at FU-Berlin) due to computational complexity of inference algorithms.

I have personally learnt a lot from infectious disease veterinarians at FU. I have participated in One Health workshop on Tuberculosis (03.11.2017). I have been involved in food chain outbreaks investigation and *Camhylobacter* spread in poultry farms.

DESCRIPTION OF THE MAIN RESULTS OBTAINED

We analyze 380 Polish counties (poviats), where 18 have been affected.

1. Spatial Propagation (risk assessment for future)

We run set of simulations for selected subspace of parameters a- swine amount significance, b- disease vectors (wild boards) significance, c- pork production chain significance, d- human failure to restrictions.

$$p_{ij} \sim \frac{a(P_i * P_j)}{1 + d_{ij}} + \frac{b(F_i * F_j)}{1 + d_{ij}^2} + \frac{d(H_i * H_j)}{1 + d_{ij}}, \quad g_{ij} \sim p_{ij} * c$$

where

a, b, c, d – simulation parameters;

i, j – poviats;

P – normalized amount of pigs;

F – coverage of forests;

H – normalized human population;

p_{ij} – probability of infection from a neighbor;

g_{ij} – probability of infection from a whole networks;

d_{ij} – angular distance between centroids of poviats.

2. Network of outbreaks

We run simulation of artificial infection chain to understand real outbreak. We visualized the most probable infection paths for affected Polish counties.

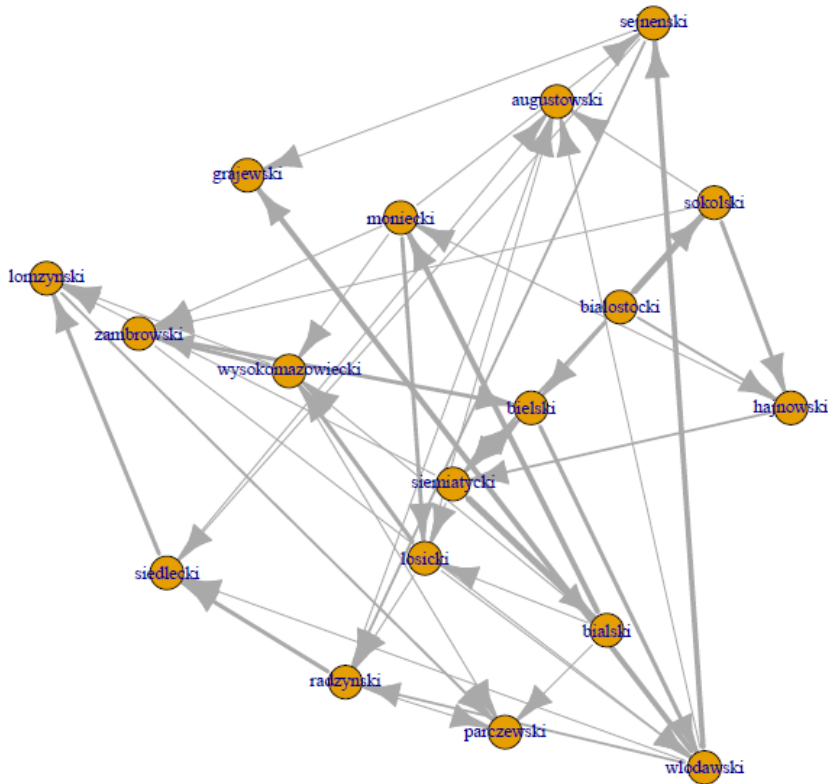


Fig. The most likely paths of infections, where nodes are counties and the links are transmission paths (thickness corresponds to likelihood of path)

3. Regressions

We cleaned the data registered by Polish Authorities (because of unacceptable amount of errors in registry 2014-2016, as wrong geocoding, etc.). We choose several regression models

For explained (dependent) variable:

- explained variable is 0/1 (infected/not infected county)
- explained variable is integer (number of events understood as sum of outbreaks and cases in county)
- explained variable is time (arrival time of ASF for given county)

For explaining variables:

- distance to the Belarus boarder;
- heads of pigs, coverage of forests, human population.

The most important conclusion is, that pig heads strongly explain both probability of introducing ASF as well as epidemic size (which is in contradiction to Estonian study). On the other hand, the forest coverage explains a little the arrival time of ASF (the same as in Estonian study).

FUTURE COLLABORATIONS (if applicable)

We are still waiting for results of simulation of our propagation study (algorithms are running at FU-supercomputer). I have external access to this supercomputer, so I will continue running and analyzing the results from Poland. Prof. Vitaly Belik will give a lecture at Berlin Statistical Colloquium on 05.12.2018. We are also working on the manuscript. Main aspects of the future analysis:

- Parameters a,b,c,d estimation according to minimization of a cost function (where cost is defined in two ways: as a difference between observed chains of infection events; as a difference in arrival times of infections);
- Moving to municipality resolution (pigs will be distributed randomly within a given county) and repeat the regression and outbreak network analysis;
- Add restriction rules in infected nodes;
- Involve Polish Veterinary Inspection and Veterinary Research Institute in the analysis;
- Extend model to other central European countries such as Hungary, Czech Republic, Slovakia and Romania.