Modeling ASF in Poland

ASF-STOP COST

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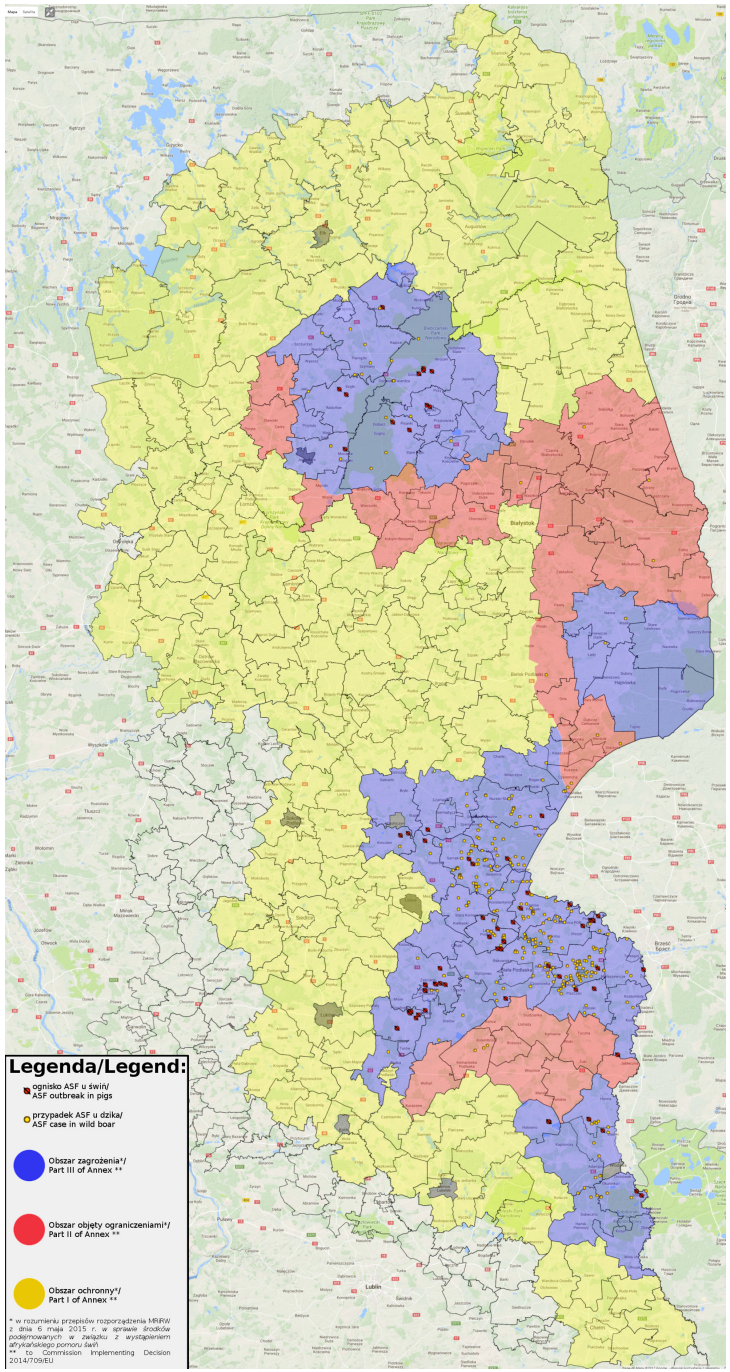
Problem

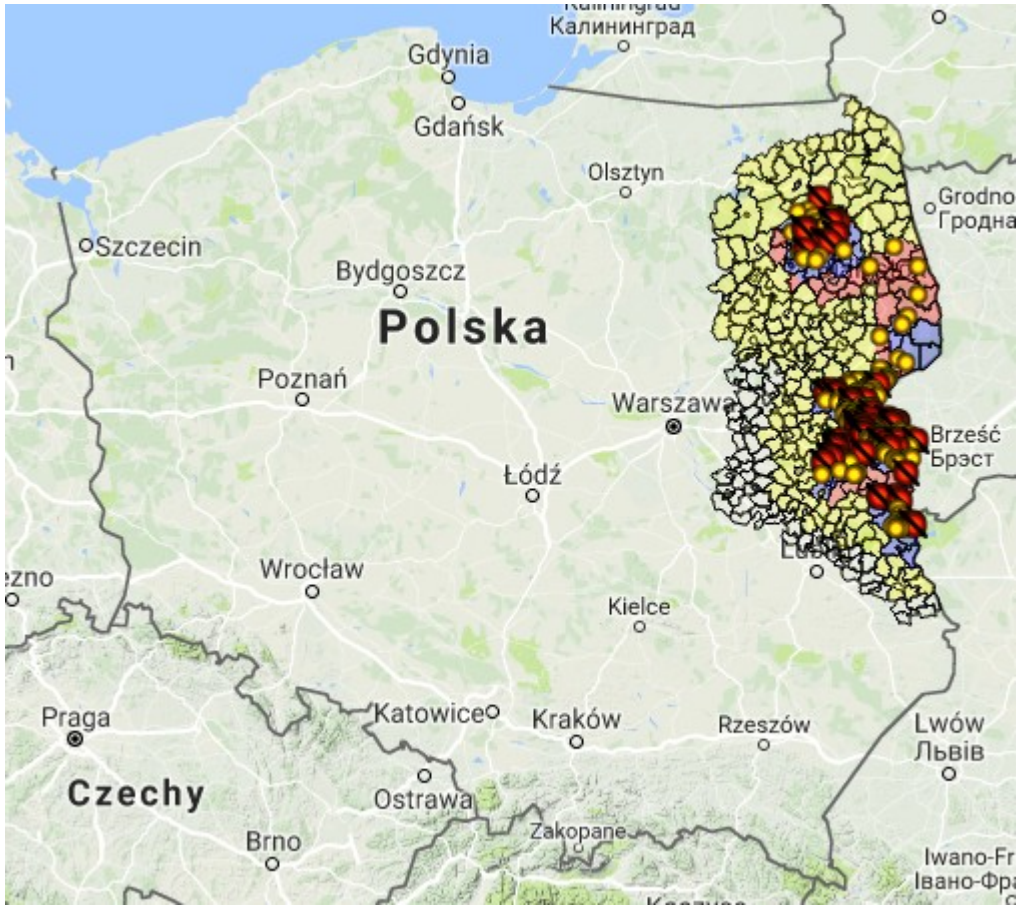
Recent rapid spread of the African Swine Fever (ASF) in the Northeast Poland during summer 2017 encourages us to prepare risk assessment for the whole country and predict future geographical transmission paths. African swine fever is viral infection which causes acute disease in domestic pigs and wild boar. Although the virus does not cause disease in humans, the impact it has on the economy, especially through trade and farming, is substantial.

Problem

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 model would be equipped with decision support systems as a tool for epidemiologists. In the preliminary setup, we perform outbeak investigation and simulate landscape-based propagation.

Problem





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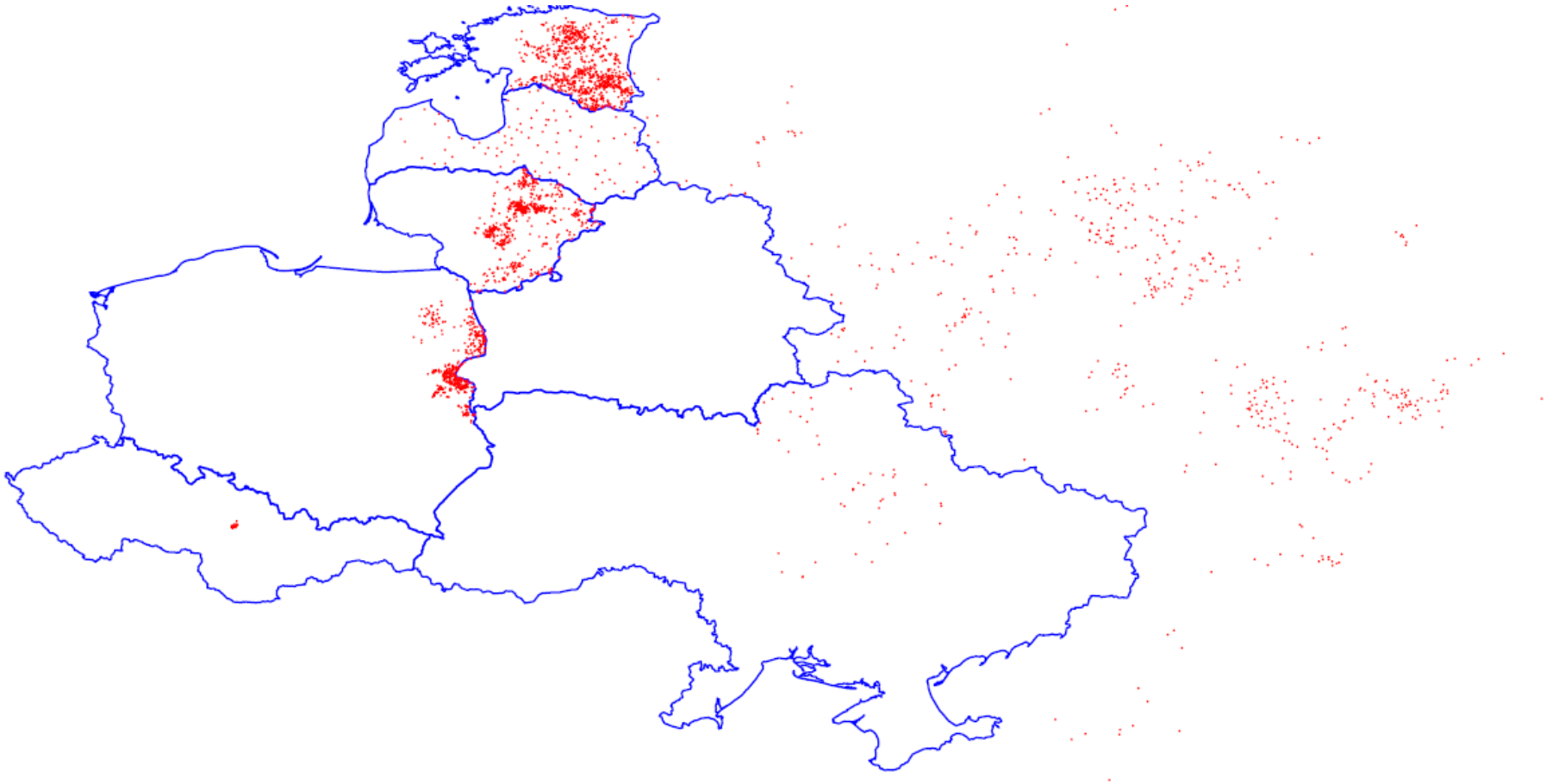
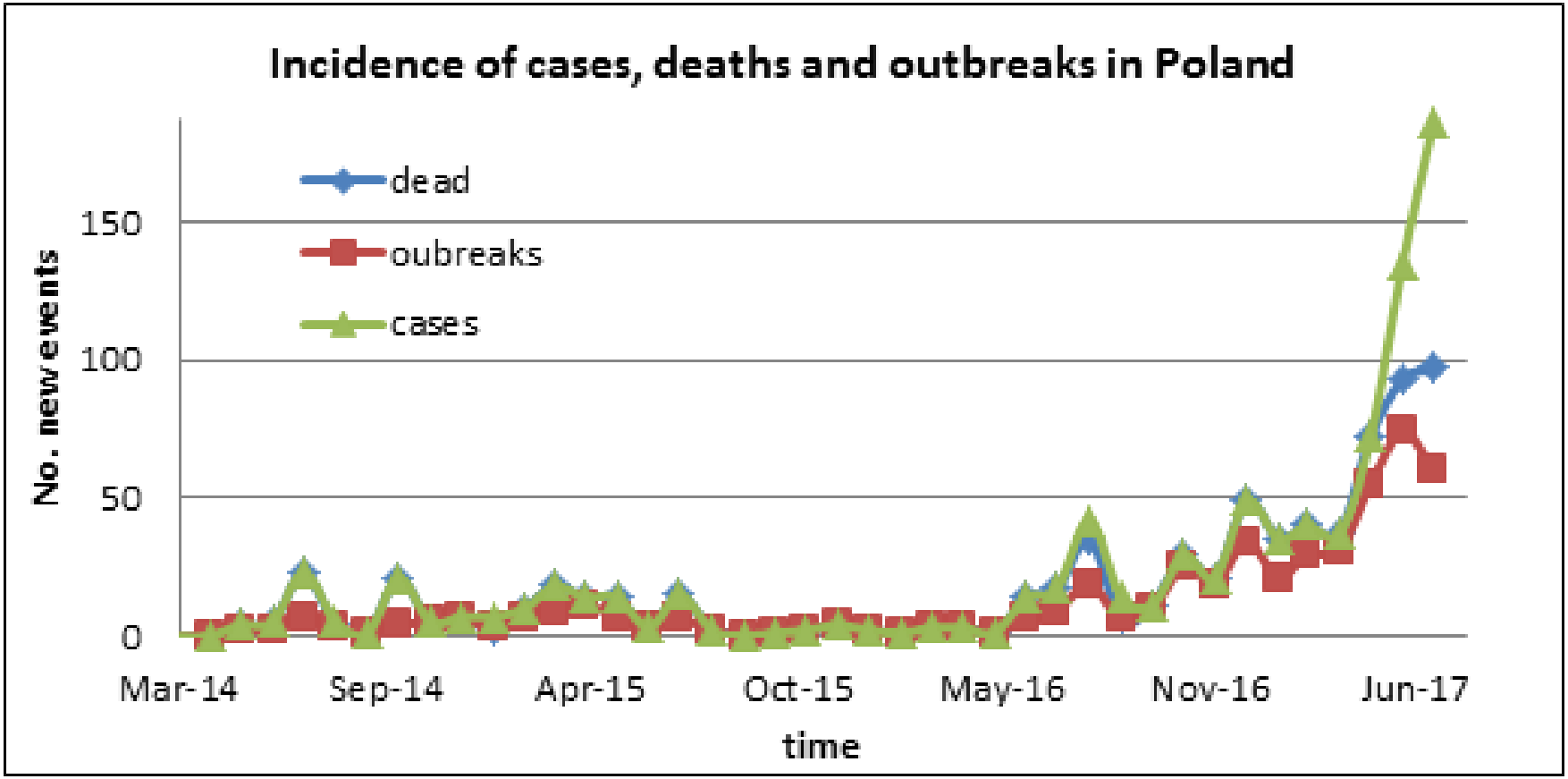
Problem



Data: OiE

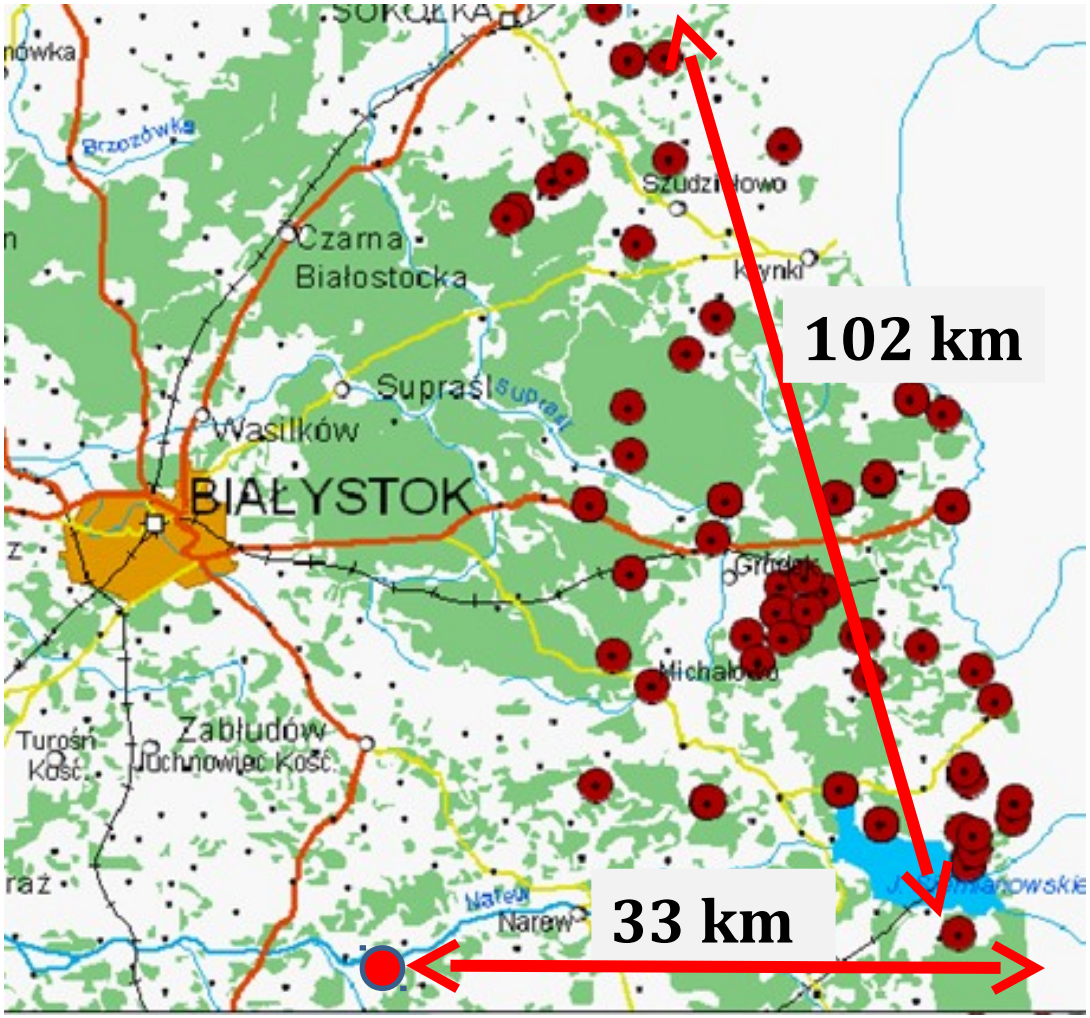
Problem



Wild boars

swines

Range 2014-2016



- Single genotype with 2 branches
- **Wild boars ~range 5-15km**
- **Human responsible for spread**

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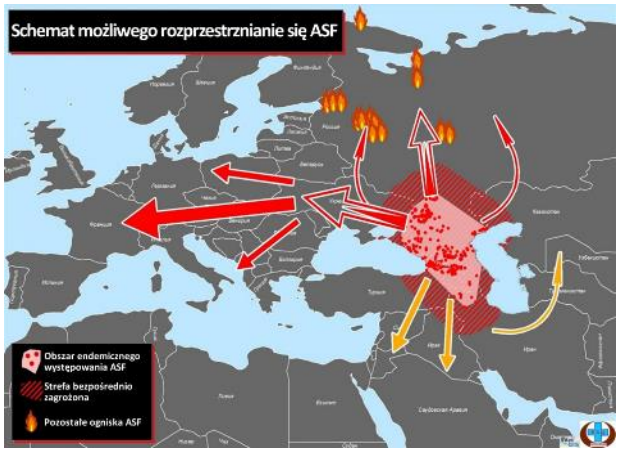
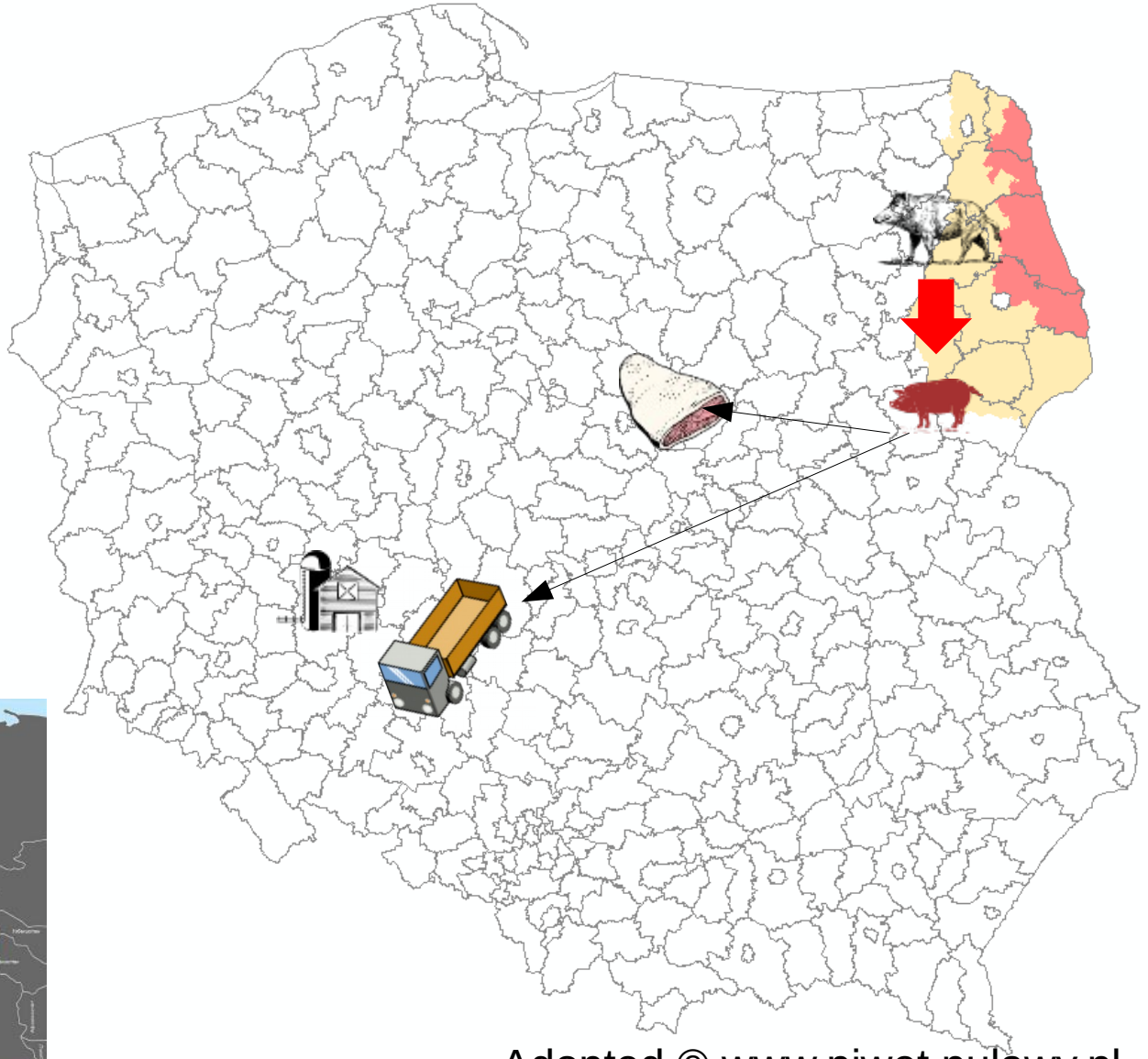
Risk





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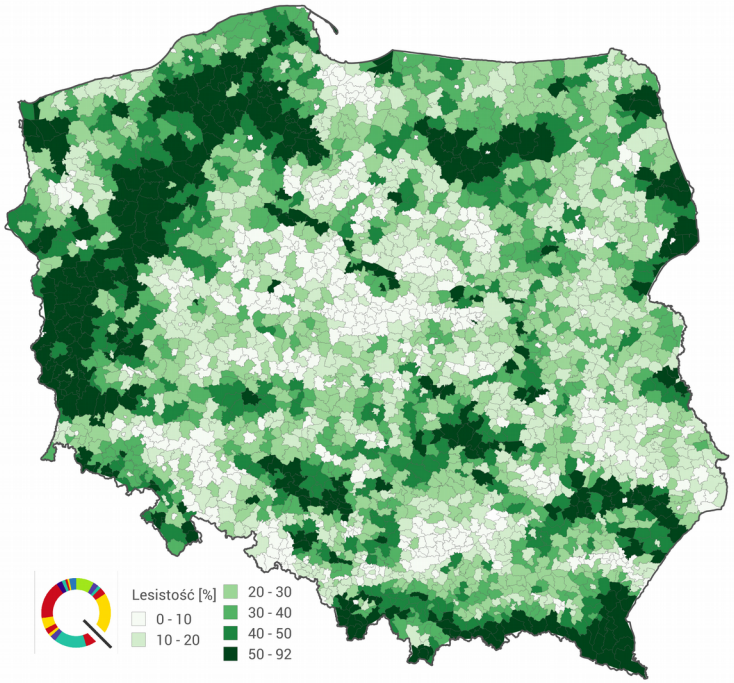
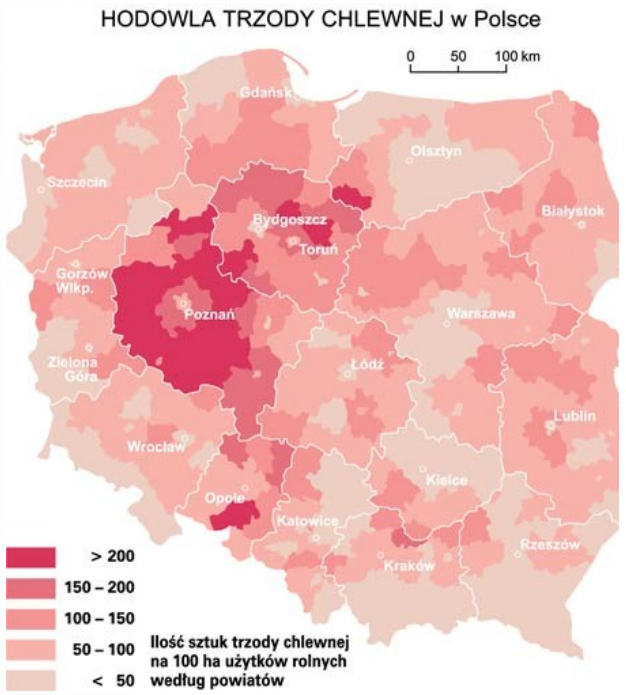
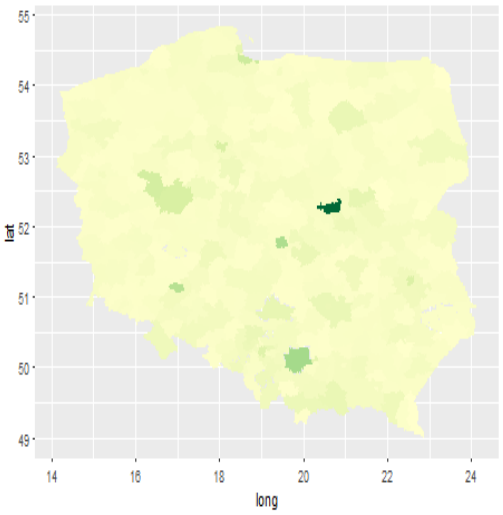
Data

- Forest density
- Swine population
- Human population

wild boars (vectors) swine (pathogen reservuar) people (human mob)







Reggresions

- 18 afected counties (poviats) from 380 in Poland
- 3,5 years of propagation
- ~ 100 oubeaks and ~600 cases

Dependent variable: arrival time of infections

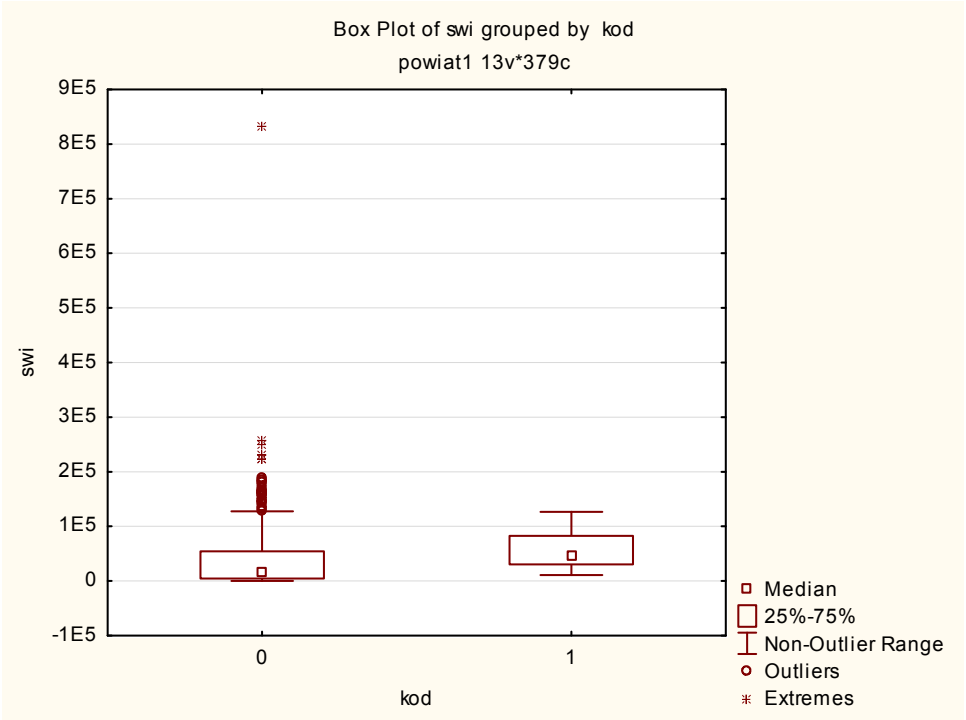
Effect	Univariate Tests of Significance for arrival_time		
	SS	F	p
dist to boarder	13405334	112.68	0.02
swine heads	41404	0.35	0.56
forest cov	386987	3.25	0.09
Error	1784447		

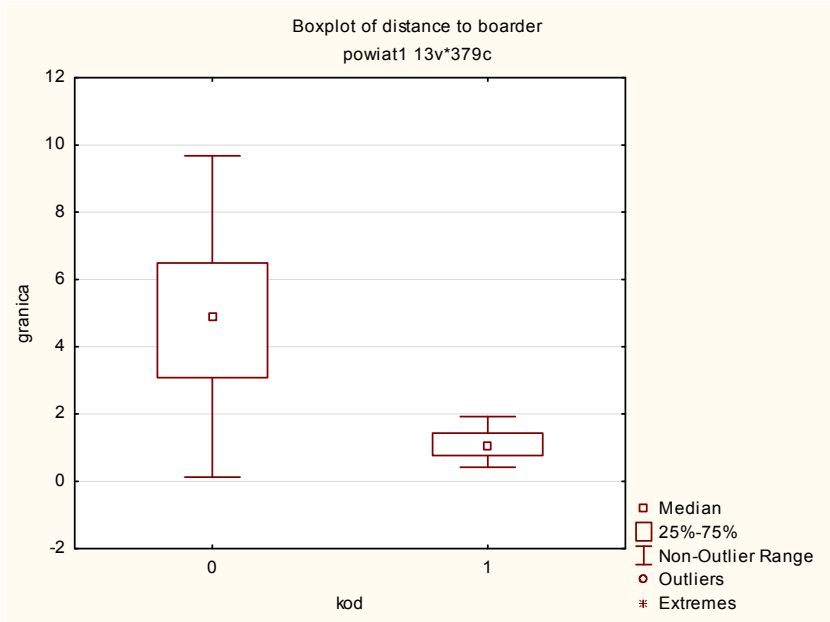
Dependent variable: infection in a county (0/1)

Effect	infection - Odds Ratios (powiat1) Distribution : BINOMIAL, Link function: LOGIT Modeled probability that kod = 1					
	Level of Effect	Column	Odds Ratio	Lower CL 95.0%	Upper CL 95.0%	p
Intercept		1				
boarder		2	0.104497	0.039902	0.273663	0.000004
swine		3	1.000016	1.000007	1.000025	0.000751
forest		4	1.030135	0.986176	1.076053	0.182094

Reggresions

Dependent variable: infection in a county (0/1)





Reggresions

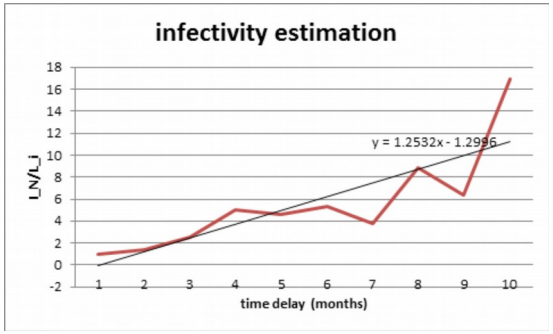
Dependent variable: number of cases in 2017

N=11	Regression Summary for Dependent Variable: number of cases) R= .73085690 R2= .53415180 Adjusted R2= .41768976 F(2,8)=4.5865 p<.04710 Std.Error of estimate: 31.978					
	b*	Std.Err. of b*	b	Std.Err. of b	t(8)	p-value
Intercept			-62.5642	40.79639	-1.53357	0.163678
swine	0.813589	0.268631	218.6065	72.17960	3.02865	0.016343
forest	0.353494	0.268631	1.4202	1.07927	1.31591	0.224660

Susceptible (S), Invectives (I), Detected (D)

Basic reproduction rate: $R_0 = inf * durat$
inf – infectivity
durat – detection time/elimination time

The early detection method in zeros approximation can be done by fitting the incidence curve to the exponential function, resulting estimation of the infectivity coefficient per month (*inf*~1.25).



According to simplified relation in SID (Susceptible, Infectious, Detected) model $R_0=inf*D$, we observe that detection and elimination time (D ~24 days) is critical to satisfy epidemic condition (R_0=1). It is enough to control epidemic with elimination time D shorter than 3 weeks (where two weeks are the time from infection to the first clinical symptoms).

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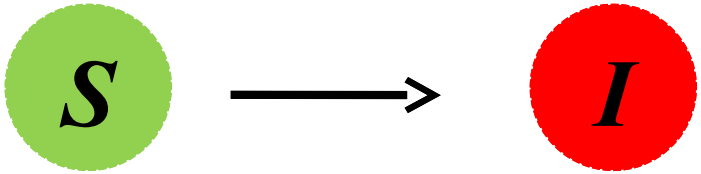


Susceptible (S), Invectives (I)

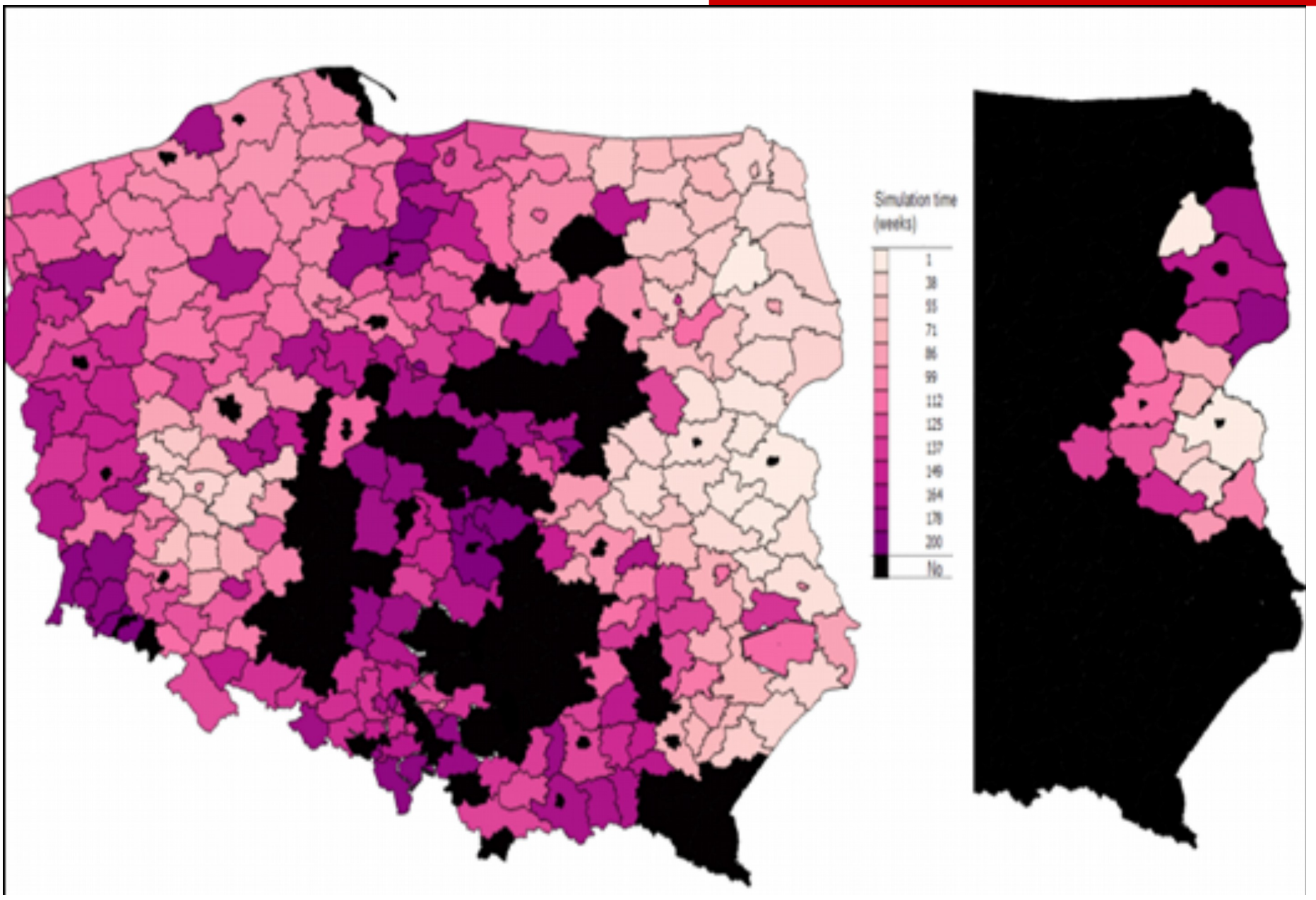
We run set of simulations for selected subspace of parameters *a*- swine amount significance, *b*- disease vectors (wild boars) significance, *c*- pork production chain significance.

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

Where: *a*, *b*, *c*, *d* – simulation parameters; *i*, *j* – poviats; *P* – normalized amount of pigs; *F* – coverage of forests; 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.

Some possible trajectories 2016-2020

Model – **spatial - based propagation**



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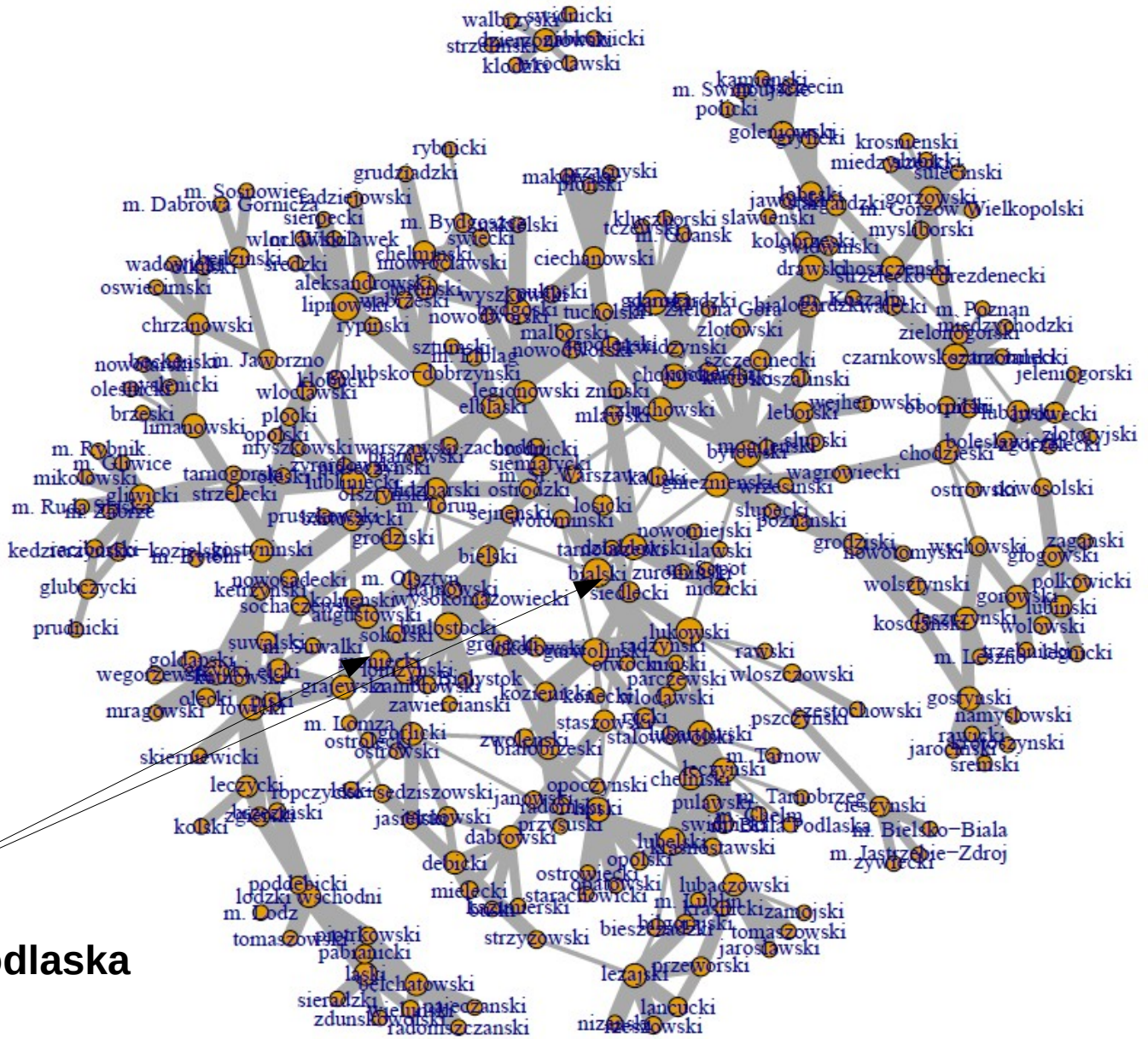
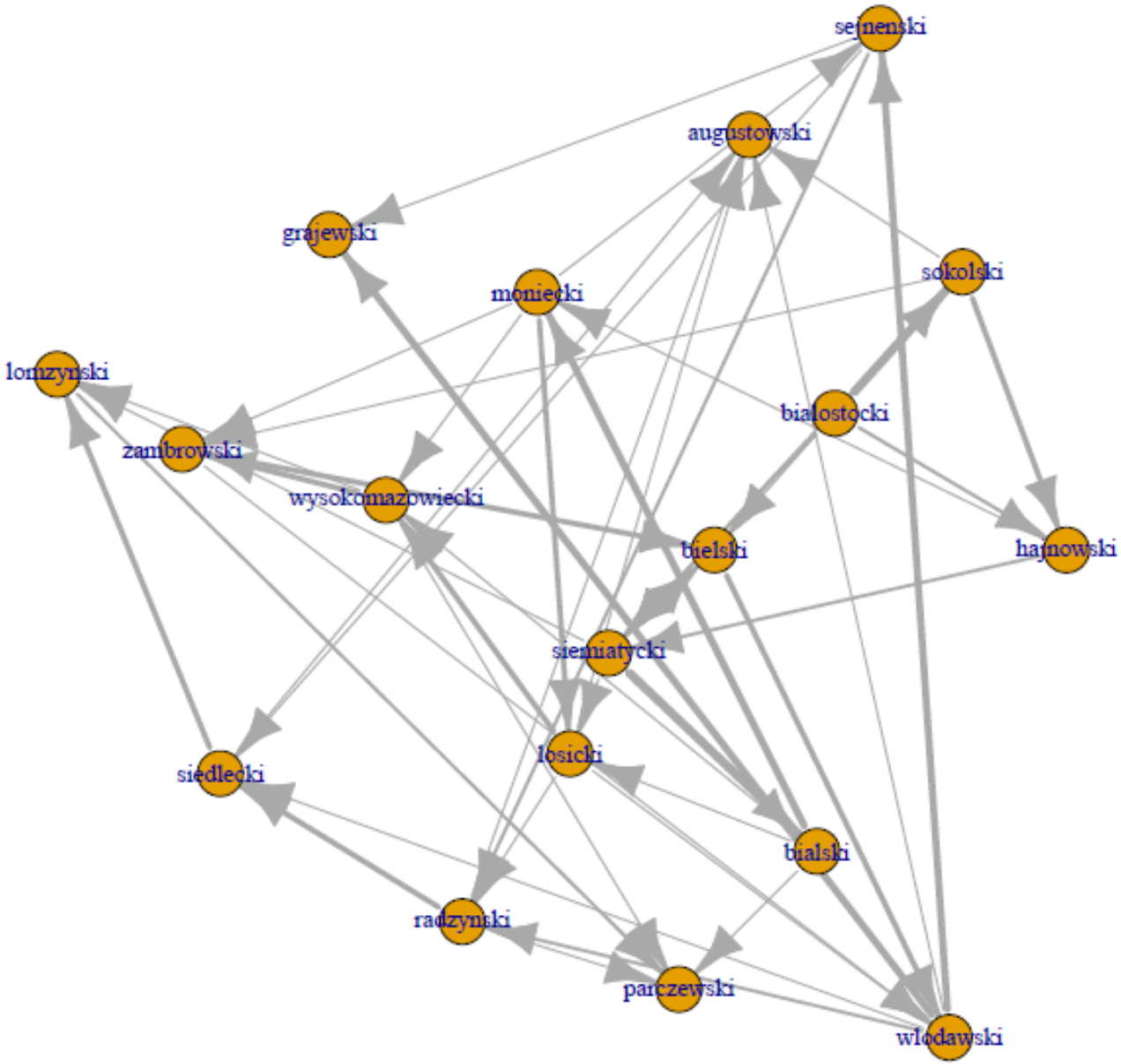


Sources:
Mońki i Biała Podlaska

Data – **spatial - based propagation**



Early epidemic growth estimation indicates that to keep the epidemiological status quo will require a very fast response from veterinary services (less than one week after detection to eliminate a single outbreak). Spatial modeling in a certain range of parameters proves the existence of a natural protective barrier within boarders of the ‘Congress Poland’. The spread of the disease to the ‘Greater Poland’ should result in the accelerated outbreak of ASF . In future analysis we will reconstruct the most likely _future paths of infection and classify regions into risk groups.