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Risk of introduction of African swine fever to Denmark through animal movements, trucks and imported meat

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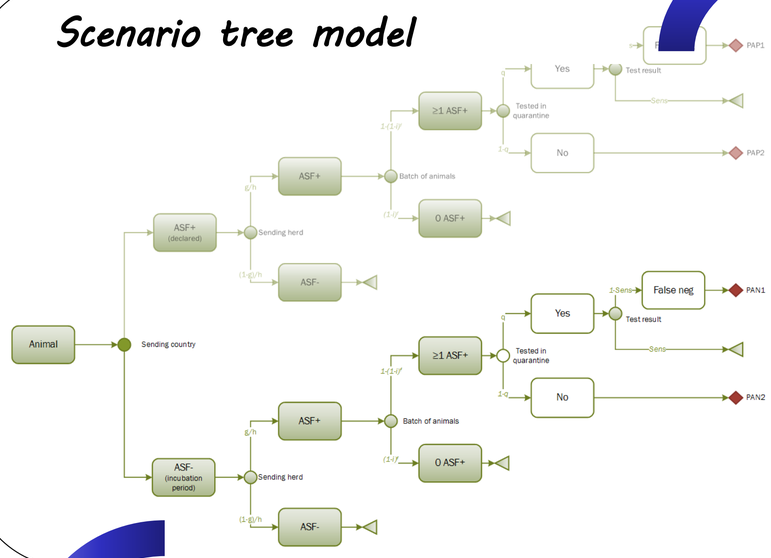
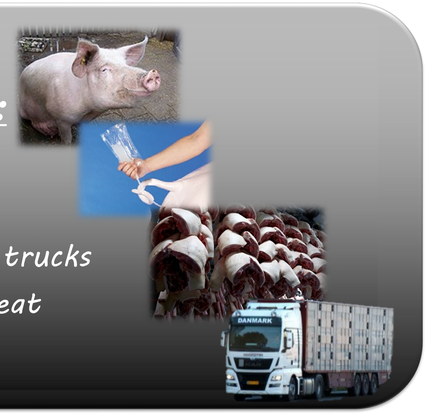
Scenario tree model



Pathways included:

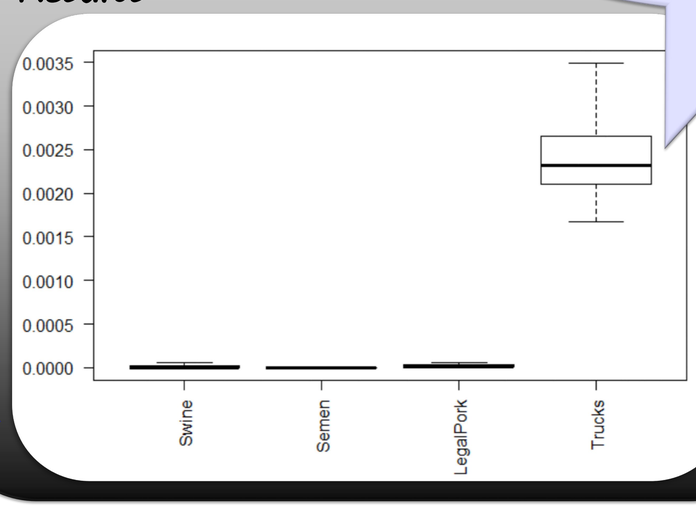
- Import of animals
- Import of semen
- Returning livestock trucks
- Legally imported meat



Input data

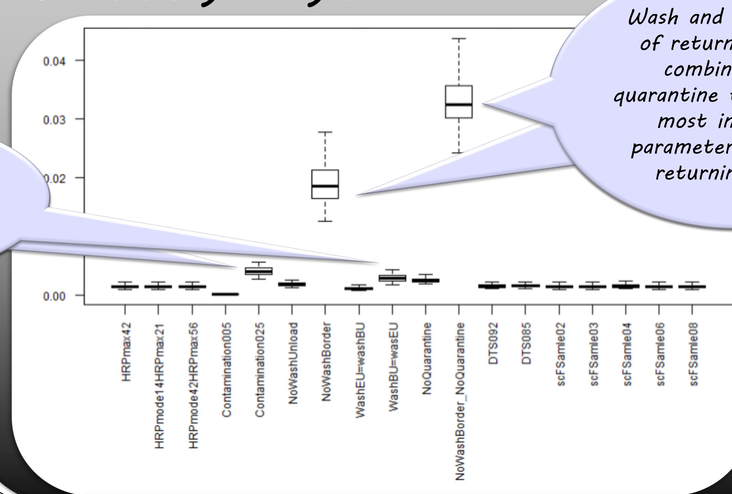
- Danish statistics
  - Legeally import of meat and meat products
- Traces
  - Imports of live pigs and semen
- Eurostat and OIE
  - Numbers of herds in countries of origin
- Nigsch et al. 2013
  - Numbers of infected herds within HRP in EU countries
- Mur et al., 2012
  - Risk of introduction to free EU countries
- DANISH
  - Probability of wash and disinfection at border
- Veterinary and Food Administration
  - Effect of wash and disinfection

Results



The probability of introduction is highest from trucks returning after export of pigs
- Despite the extra control measures implemented
- Due to the high numbers of returning trucks

Sensitivity analysis



Probability of contamination and effect of wash and disinfection are also influential

Wash and disinfection of returning trucks combined with quarantine time are the most influential parameters regarding returning trucks

Conslusion/Perspectives

- Focus on returning trucks must be continued
- Further research on contamination of vehicles and virus survival time in trucks is needed
- Other patways needs to be investigate
  - Illegal imports, hunters and vets travelling to infected areas, farm employees from other countries – maybe in a qualitative analyses as data is limited

Transport vehicle being washed and disinfected at the Danish border

Pigs experimentally infected with ASF

Materials and methods:

The risk of introduction via imported pigs or boar semen was calculated based on:

$$p_{intro,swine,c} = 1 - \prod_c (1 - p_{batch_c})^{\#batch_c * HRP/time},$$

whereas c is the country of origin, p_{batch_c} is the probability that a batch from county c is infected, $\#batch_c$ is the number of batches imported from country c, HRP is the length of the high risk period as estimated based on Nigsch et al. 2013 and time is the time period in which data was extracted. Futhermore, $p_{batch,c}$ is calculated as

$$p_{batch,c} = P_c * (1 - (1 - p_{an_c})^{batchSize_c}) * p\_surv * (1 - p\_detect) + P_c * (1 - (1 - p_{an_c})^{batchSize_c}) * (1 - p\_surv),$$

whereas P_c is the probability that country c is infected, p_{an_c} is the probability of selecting an infected animal from a randomly chosen herd in country c, $batchSize_c$ is the number of animals in a batch from country c, p_surv is the probability that an exported batch of animals is clinically surveyed before export, and p_{detect} is the probability of detection of ASF at surveillance. Eah scenario was run in 200 iterations.

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