

SHORT TERM SCIENTIFIC MISSION (STSM) SCIENTIFIC REPORT

Action number: 17110

STSM start and end date: 13/10/2019 to 02/11/2019

Grantee name: ELEFThERIOS MELETIS

STSM title WG3 | STSM1

Evaluation of statistical methods for the estimation of a probability of freedom from infection from data generated by disease control programmes

PURPOSE OF THE STSM:

The objective of WG3 STSM1 was the evaluation of statistical methods that could be used in order to demonstrate freedom from infection and estimate a probability of freedom from infection for non-regulated diseases control programmes. In addition, the aim of this STSM was the presentation of these methods in a workshop in Zurich, Switzerland. The goal was to tackle each method's strengths and limitations.

DESCRIPTION OF WORK CARRIED OUT DURING THE STSMS

During the STSM, the first two weeks were dedicated to literature review of the existing statistical methods. Overall 25 publications were read. The reference method is considered to be scenario tree modelling, and all other methods were compared to the reference standard. Other methods in order to demonstrate country or zone freedom from infection are hierarchical models applied in a Bayesian framework and a Bayesian statistical model that was developed under the STOC free project, that incorporates all available information generated by different control programmes. Furthermore, use of Bayesian Networks is another method that was extracted by the literature, in order to estimate the probability of freedom from infection. The third week was devoted to the preparation of the workshop. Concepts such as output-based surveillance standards and probability of freedom from infection were addressed, since those values are of greater importance, rather than Specificity and Sensitivity. The objective was to present each method, point out the advantages and disadvantages of each one and provide a hands-on example of a scenario tree analysis. A dataset for the surveillance of BVDV infection in cattle was available and simulations in order to estimate the probability of freedom from infection using Bayesian Networks were undertaken with alterations on the dataset.

DESCRIPTION OF THE MAIN RESULTS OBTAINED

Scenario tree analysis is the current statistical method that is adopted in order to prove freedom from infection and estimate the probability of freedom from infection. Main limitation of scenario tree modelling is that it can only be applied to populations free from infection, because it is a methodology that performs quantitative analysis of multiple complex data sources to support claim of freedom from infection. However, basic advantage of scenario trees is that they divide the population into homogenous sub-populations, where each unit (i.e. animal, herd) has the same probability of being infected and detected, given that infection is present. On the other hand, the other models can be applied to both infected and uninfected populations or populations with unknown infection status. Bayesian hierarchical models assess the

probability that an animal population in a country is free from a specific pathogen (“infection”). In order to come to that conclusion the country-level infection status, region-level infection status, and herd-level infection status are modelled. That model allows level of inference when the country is infected. Basically the model proceeds from higher levels of the hierarchy to the lowest, asking if infection is present and thus estimates the probability of infection at the animal-level. The STOC-free model describes a statistical framework that estimates the probability of infection incorporating all the available information generated by different control programmes for the estimation, including context, information on the control programmes, test results and risk factors. Lastly, Bayesian networks can be applied to estimate the probability of freedom from infection. Main advantage is that these models take into consideration the conditional probabilities between the variables decreasing the number of independent parameters. Prior knowledge can be very helpful for the all of the above methods.

FUTURE COLLABORATIONS (if applicable)

The WG3 STSM 2 “evaluation of machine learning methods for the estimation of a probability of freedom from infection from data generated by disease control programmes”, will expand the results from this STSM.

A more thorough report will be drafted in order to present the state of the art on the methods used to demonstrate freedom from infection for non-regulated disease control programmes.