

SHORT TERM SCIENTIFIC MISSION (STSM) SCIENTIFIC REPORT

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

Action number: **CA 17110**

STSM title: **WG3 | STSM3 Review and ranking of methods for the estimation of a probability of freedom from infection from data generated by disease control programmes**

STSM start and end date: **25/11/2019 to 13/12/2019**

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PURPOSE OF THE STSM:

This STSM aimed to review and rank the output-based surveillance methods for the estimation of freedom from infection, in this case from Bovine Viral Diarrhea Virus (BVDV) infection in cattle, produced in previous STSMs, respectively the Scenario Tree model and Bayesian Hierarchical model, and the design and data collection matrix. During the mission is expected from the researcher, to define the advantages and disadvantages of the risk-based methods assessed

DESCRIPTION OF WORK CARRIED OUT DURING THE STSMS

The STSM3 of WG3 was hosted at Oniris, Ecole Nationale Vétérinaire, Agroalimentaire et de l'Alimentation de Nantes-Atlantique in the BIOEPAR research unit under the coordination of Dr. Aurélien Madouasse. The tasks carried out were based on individual work under the guidance and coordination of the group leader.

The activities were to:

- introduction in the types of surveillance proposed for models to estimate the probability of disease freedom;
- descriptions of the main methods used for output-based surveillance methods: scenario tree model, Bayesian hierarchical models and the STOC free model focusing on their application in BVDV control programmes at the herd level or country level, assessing the alternative design of them, from low to high complexity;
- exploration of output generated by the STOC free model;
- describing the outputs of scenario trees and Bayesian methods for output based surveillance.

During the period, there was one Skype meeting with the WG3 leader and co-leader as well as with the researcher from previous STSM. During this meeting details from the work done were discussed and guidance regarding the current STSM was provided. There was another Skype meeting with the rest of WG3 during which we discussed the summary from previous meeting, the current status and the proposed directions for future work.

DESCRIPTION OF THE MAIN RESULTS OBTAINED

After reviewing of the methods for outcome-based surveillance, it was possible to identify criteria for the choice of a type of model adequate for each country, region and herd considering the country status regarding disease (likely free vs. endemic disease) and the type of data (survey vs. longitudinal data).

The type of outputs generated by scenario trees was then considered. The first generation of outcome-based standards described for the scenario tree methodology is the sensitivity of surveillance (SSe) and quantifies the probability of detecting the disease if it is present at the design prevalence.

The second generation of outcome-based standards generated by scenario trees is the probability of freedom Pr(free) (Negative Predictive Value). The probability of freedom from infection is given by negative test results. This surveillance quantifies if the disease is being below the design prevalence given a surveillance system and a number of negative test results.

The STOC free model (Surveillance Tool for Outcome-based Comparison of FREEdom from infection) is dedicated to estimating the confidence of freedom of control programmes of both non-regulated and regulated diseases in EU from longitudinal data and is applicable to identify units likely free from infection when infection is present in the region / country. It is designed to use risk factors and test result data.

All models offer the possibility to include multiple types of inputs for assessing. In order to weight the risk factors, scenario trees rely on expert opinion while the STOC free model estimates these weights from data and prior. Scenario trees generate a surveillance system sensitivity if the disease were present at the design prevalence given that no test has been confirmed positive or a probability of absence of infection which is a negative predictive value. For Bayesian models, further work is needed in order to categorise units (herds, regions...) as free from infection from distributions of posterior probabilities of infection generated by such models.

FUTURE COLLABORATIONS (if applicable)

The valuable expertise of the scientists from the BIOEPAR unit can be very useful in sharing the experience with the scientist from Romania, particularly for the personnel from the Institute of Diagnosis and animal Health, Bucharest. Any further cooperation will be with interest.