STOC free: WP3, Deliverable 3.2.2

Results of each of the case studies

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September 2020

GA/EFSA/AFSCO/2016/01-03

This study was awarded a grant by EFSA and was co-financed by public organisations in the countries participating in the study

Content

Conclusions

- The two versions of the model (i.e. animal level and herd level) can efficiently capture data from different BVDV control programs.
- Risk factors estimates were available and successfully incorporated in some of the case studies.
- The STOC free model can be used for assessment of probability of freedom from BVDV when disease is still present in the population to some degree. When the disease is completely absent in the population, other methods (e.g. scenario tree models) are more suitable.
- The model and input formats need to be further refined to avoid disproportionate influence of priors on model outputs.
- Translation of model output into conclusions about BVD status of individual herds in a user-friendly format require further work.

Background

For endemic infections in cattle that are not regulated at European Union (EU) level, such as bovine viral diarrhoea virus (BVDV), European Member States (MS) have implemented control or eradication programs (hereafter "CPs") tailored to their specific situations. Safe trade would be facilitated with an output-based framework that enables a transparent and standardized comparison of confidence of freedom for CPs across herds, regions or countries. In the STOC free project, we have taken the first steps towards development of such a framework by developing a tool for data collection, and models that can be used to analyse data and estimate the probability that disease is truly absent in a herd given the control programme that is in place in the herd or region.

To test and illustrate the developed tools/models, a number of case studies based on actual data from ongoing programs in five different countries (DE, FR, IE, NL, SE, UK) have been performed. This deliverable includes a description of these case studies, and recommendations for further improvement of the STOC free model.

Discussion

The case studies have highlighted a number of points where the STOC free model needs further development. The results of the case studies presented in this deliverable report should not be considered real values for freedom of BVDV in the respective countries. In some cases there have been problems with convergence or a very strong influence of prior distributions on the results. Different solutions have been tried to handle this, and work is ongoing to identify if adjustments to the model or data is required.

The cases also highlight the complexity of BVD and different control programs for this disease. Delayed removal of persistently infected animals, combination of different types of tests representing different types of outcomes i.e. direct (diagnosing virus) or indirect (diagnosing antibodies) indication of BVDV in the herd, and confirmatory testing are all example of real life scenarios that may result in heterogeneous data that is difficult to include in the model without risking misleading results. In some cases, a low number of test occasions per year or time period seemed to not generate enough data to inform the model and lead to convergence. However, some test results could be considered valid also in subsequent time periods and could thus potentially be included more than once. For example, when tissue tag tests are carried out in all newborn calves and no virus is detected, then in a month when no calves are born, virus is still absent as proved by the previous test results. This needs to be further investigated.

Additionally, we experienced problems to run the model with large datasets, which was due to memory limits of the computer or R giving errors ("R encountered a fatal error"). The session was then terminated. In the Dutch case study, adding multiple years of data also lead to convergence problems.

Another identified challenge is to understand what priors to use in the model. More guidance or instructions may be needed to make sure priors are correctly used in the model and conclusions about model outputs are correctly drawn. This is ongoing work within the project for which for example a workshop is organized.

Some sampling schemes for BVD are based on animal testing, while others are based on herd testing. To facilitate modelling of both types of data, two versions of the model were developed, one on animal level and one on herd level. Results from testing of animals were combined with herd level testing by aggregating the results to herd level. The aggregation may require more work, e.g. to certify that the correct priors for test sensitivity and specificity are used.

Data from populations with very low prevalence or freedom of BVD is not suitable for the STOC free model. In particular, this was illustrated in the Swedish case, where data could not give any additional information about test sensitivity given that there are no positive test results that could be included, and subsequently a small proportion of herds were incorrectly concluded to be infected. Also, when BVD is successfully eradicated in a population, the control programme will be transformed into a surveillance programme with less frequent sampling. Too few observations from some herds turned out to be a problem in the Swedish case. We conclude that when disease is completely absent in the population, other methods are more suitable.

Based on for example the Scottish case, we also conclude that it may be necessary to model test results from different subpopulations within the same programme separately. For example, given the differences in management and production systems between beef and dairy cattle, these two subpopulations may have very different probability of successfully removing BVDV from the herd.

To meet the overall purpose, i.e. to analyse data and estimate the probability that disease is truly absent in a herd which is considered free of BVD according to the CP in place, a standardised and user-friendly way to summarise the model output is need. This should include translation of model output into conclusions about BVD status in individual herds.