

Imprecise Classification of the Gram Status of the Causal Pathogen of Clinical Mastitis

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Poster Abstract

Clinical Mastitis (CM) — a type of udder infection — is one of the most frequent and costly diseases in a dairy herd. Treating it effectively and quickly is therefore of economic importance. However, in order to select an optimal treatment, one needs to know the gram status of the causal pathogen. In principle, this information can be obtained by bacteriological culturing, but it typically takes too long to get the result of such tests, especially because CM needs treatment very soon after diagnosis. To solve this problem, classifiers are used to help farmers to decide on the gram status of the causal pathogen, allowing them to select an appropriate treatment before getting the result from bacteriological culturing.

Traditional classifiers only return the most probable gram status. However, in this particular context, when we are undecided about the pathogen's gram status — a situation we refer to by 'I don't know' — it is sometimes better to administer a broad-spectrum antibiotic treatment instead of a specific treatment that is tailored to the gram status. Van Der Gaag et al. (2009) took this aspect into account by using a stratifying classifier, which has 'I don't know' as one of its possible outputs. In the present contribution, we deal with this problem using the Naive Credal Classifier (NCC) (Zaffalon, 2002), and compare it with other methods. We also present a graphical method to compare classifiers with such 'imprecise' outputs, and use it to study the relationship between the size of the learning set and the performance of the classifiers.

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References

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