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Modelling the spread of *Mycoplasmopsis bovis* in Sweden using the SimInf framework

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Mycoplasmopsis bovis (previously *Mycoplasma bovis*) causes severe infections in cattle, which impact animal welfare and induce production losses (Maunsell et al., 2011). Since the prevalence is increasing in Sweden (Hurri et al., 2022) and because treatment is difficult and efficient vaccines lacking, there is a need to identify strategies to control the spread of *M. bovis* and protect free herds.

To better understand the epidemiology of *M. bovis* on a regional and national level and to propose control strategies, a data-driven within- and between-herd spread model will be developed in SimInf (Widgren et al., 2019). To account for the dynamic herd sizes and spread by animal movements, all registered cattle events (births, deaths, and between-herd movements) since 2005 will be included. To include livestock data in the model, a novel flow-based technique, was developed to find the longest plausible path, 'location change pattern', of the reported events for each animal. Additionally, the geographical location of each holding will be included to capture local spread and spatial properties, e.g., temperature. Longitudinal samples of *M. bovis* antibodies in bulk tank milk (BTM) exist and to match this data in simulations, a sex- and age structured compartment model will be used for the within-herd spread. Parametrisation will be done using Approximate Bayesian Computation (ABC), to find the model and parameters that best match the observed BTM data.

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