Predicting bacteria shedding patterns of cattle with Johne's Disease

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1 Summary of short-term visit May 25 - June 07

The main objectives of this visit were to develop a mathematical modeling framework that uses a deterministic or a stochastic model or a hybrid model (deterministic + stochastic) to predict the bacteria shedding patterns of cattle infected with *Mycobacterium avium* subp. *paratuberculosis* (MAP) and determine immune response markers that correlate with disease progression (bacterial shedding). During the two week period, we identified techniques to test our models with longitudinal data (immune response and bacteria/colony forming units (CFU) data) from 58 cattle that were naturally exposed to MAP. We managed to categorize our animals into three distinct groups based on the immune response and CFU data. We performed preliminary statistical data analysis to establish the correlation between shedding (and disease progression) and immune response markers. We also devised three mechanistic models that are appropriate to capture the cattle MAP shedding dynamics, and the observed Th1 and Th2 immune response kinetics. Model parameters derived from fitting these models will help explain whether shedding patterns observed in these animals are a result of errors in measurement or sampling errors, whether the mechanistic process linking immune markers and shedding patterns is appropriate to capture the process and whether there is intrinsic noise (or an inherent stochastic process) in the Th1 and Th2 immune responses that lead to the observed MAP shedding fluctuations. We have started confronting our models with the cattle infection data.

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