

Integrating pathogen genomic data with contact information to identify possible causes for emergent disease scenarios

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Recent analyses have already shown both that existing infectious diseases have been exacerbated by landscape level changes over the past few decades, and that future emergence of novel infectious are likely to be similarly exacerbated. However, identifying the signatures of those changes can be challenging.

The generation of pathogen sequence data provides us with an unprecedented level of detail about transmission processes. By combing these with epidemiological and demographic information, we can gain insights into drivers of emergent infection scenarios that are otherwise impossible to obtain. Here, I use a combination of analytical methods, to show that the combination of changes in wildlife distributions and changes in farm management have likely contributed in emergent bovine Tuberculosis problems and discuss how this provide some insights into potential problems for the future.