Supercharging laboratory data – from case to test to genetic tree in three clicks or less

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Summary

Diagnostic laboratories are a key data source for health information in both human and animal health. However, data application at the population or group level has been limited because reporting is primarily focused on individual cases or at a highly aggregated population level, allowing little opportunity for customised data exploration by end-users. While laboratory data will always be an opportunistic source of information for population health studies and interventions, advances in metadata collection and assembly will make laboratory data more usable in the future.

To address this challenge LAB SAVI provides a customer interface for laboratory testing results where the user can explore real-time test results in space and time, filter by specific criteria or compare genetic sequences of outbreaks. The first version of LAB SAVI was developed to monitor swine health and includes PCR and sequencing results for Porcine Respiratory and Reproductive Syndrome (PPRS) as well as antimicrobial susceptibility testing outputs.

Methodology & Results

Software used: R/Shiny, R Studio Connect and PostgreSQL

Stakeholder centric approach to design: we worked closely with stakeholders to aid better consumption of laboratory data on-the-job while improving routine use of specialist data.

High scalability: the application can easily be extended to include other animal species, procedures and analytics.

Secure access through dedicated user management system: allowing each user to see only farms they are affiliated with, safeguarding diagnostic data while allowing sharing of selected cases with affiliates or collaborators.

Application support: training and learning materials, such as video tutorials and a demo version with scrambled and anonymised data, are available within the app.

Features:

- instantaneous data visualisation
- map-driven access to both cases (reflecting farm visits) and procedures (reflecting specific laboratory tests)
- antimicrobial susceptibility profiling
- ability to save searches
- filter capability for a large number of variables, including specimen type, date, location and production flow
- genetic analysis (neighbour-joining trees and flexible sequence comparison including vaccine, reference and past outbreak strains); both tree-based and via homology maps

LAB SAVI allows users to explore aggregated laboratory results to support monitoring of animal health and improved response to disease events. Figures 1,2,3 and 4 illustrate key LAB SAVI functionalities.

Discussion

Recent advances in information technology and the (near) real-time processing of diagnostic results allow for improved access to for different stakeholders, in the case of veterinary diagnostic laboratories to provide guidance to veterinarians and producers about animal health status to support management of disease, productivity and welfare. LAB SAVI provides improved investigation of disease events, but also an enhanced capacity for contextual analyses such as group-level antimicrobial susceptibility trends, spatial or temporal exploration of the data. Furthermore, it creates improved accessibility to specialist analysis, such as the assessment of genetic relatedness or exploration of susceptibility trends.

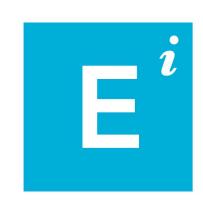
A demo video of LAB SAVI is available at: https://vimeo.com/359697105

Acknowledgements

Morrison Swine Health Monitoring Programme (MSHMP), Minnesota Department of Agriculture, UMN Drive

University of Minnesota Veterinary Diagnostic Laboratory team

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We connect data with people



Figure 1: Dedicated log-in page controlling user access for LAB SAVI.

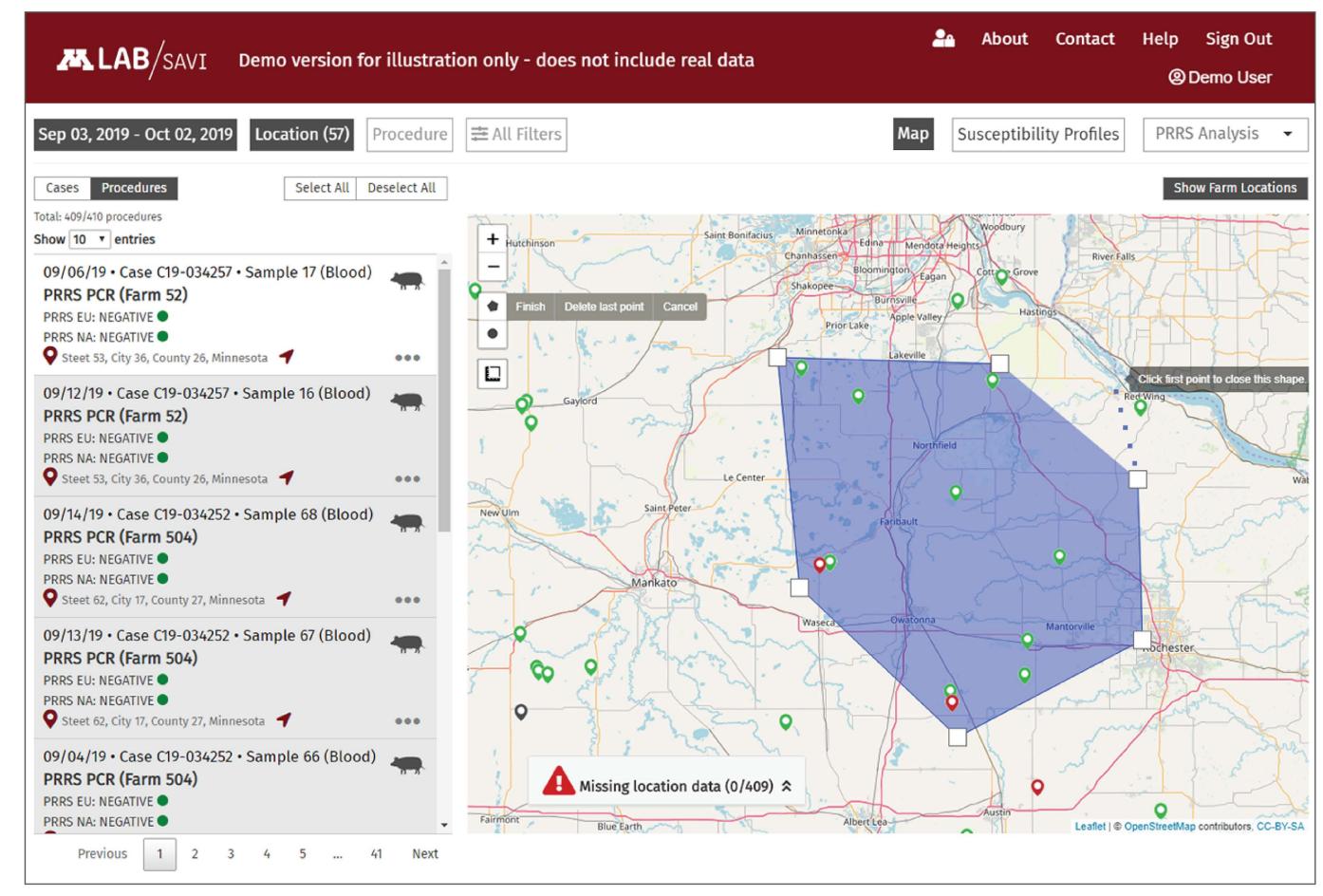


Figure 2: Map-driven access to cases and procedures.

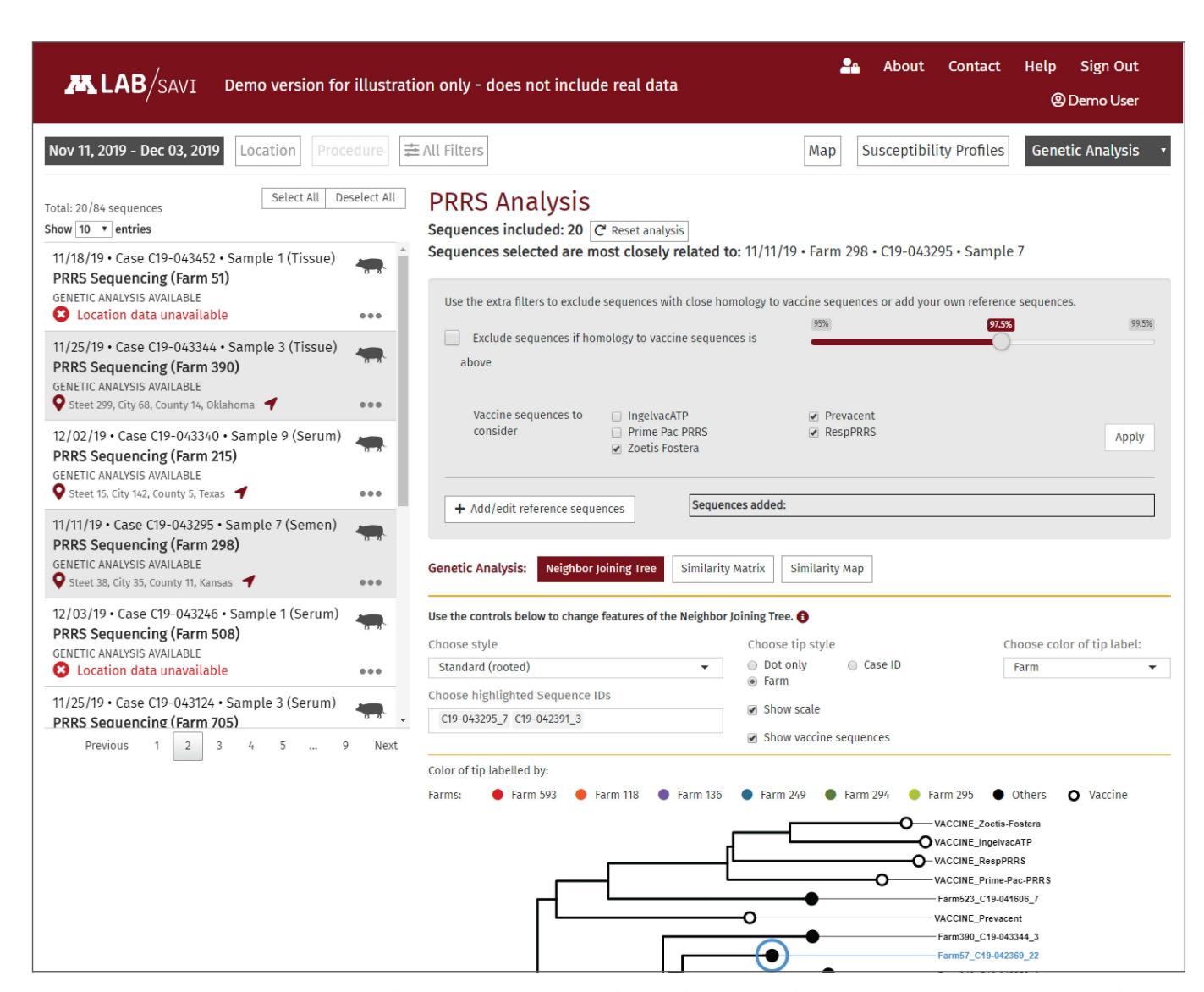


Figure 3: Users can explore genetic relatedness of PRRS sequences in the form of highly customisable neighbour-joining trees.

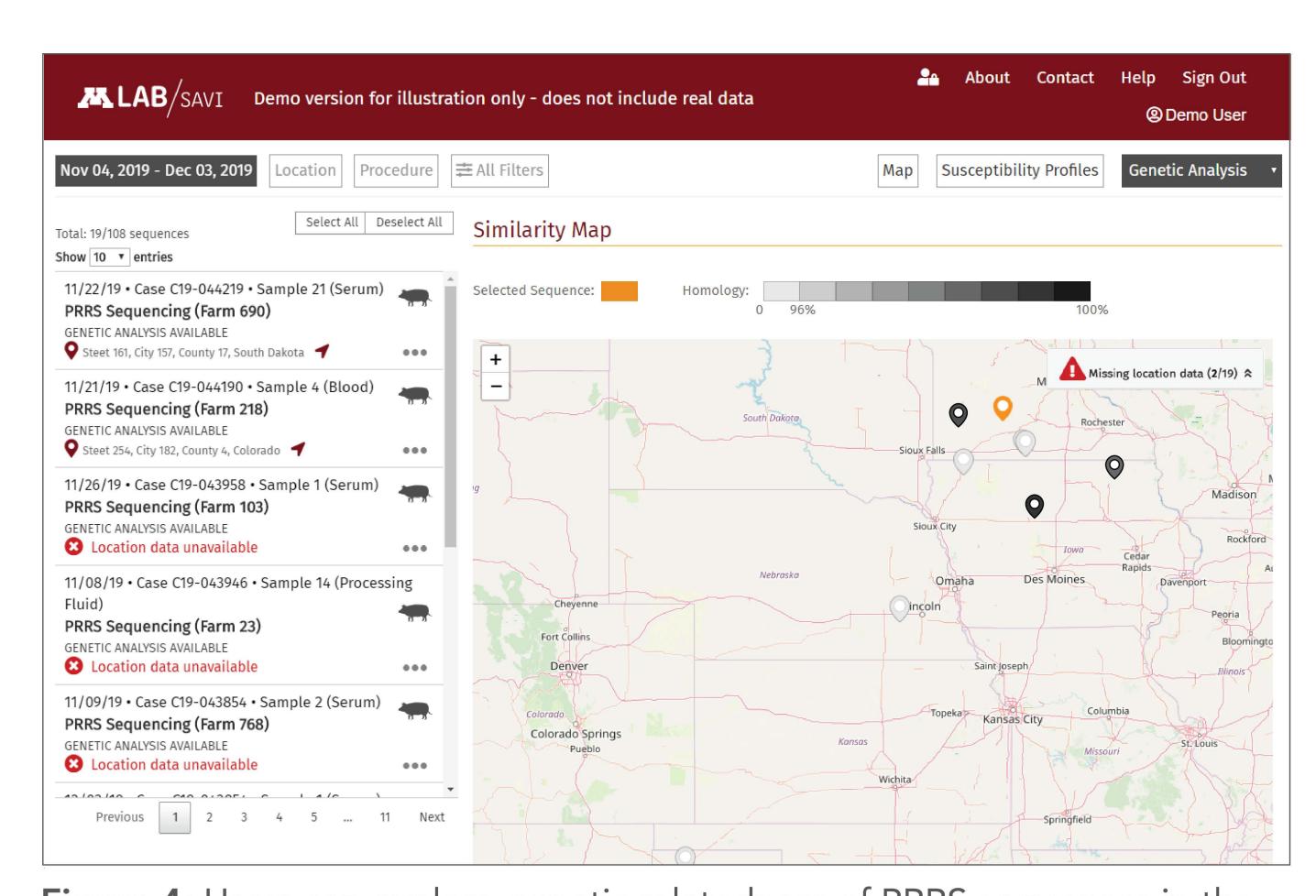


Figure 4: Users can explore genetic relatedness of PRRS sequences in the form of a customisable similarity map.