



# Development of a user-friendly and analytically strong platform to support near real-time surveillance of food animal diseases

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## Introduction

Swine diseases have shown an epidemic pattern globally over the years<sup>1</sup>, with a few examples being the emergency of highly pathogenic porcine reproductive and respiratory syndrome (PRRS) viruses<sup>2</sup>, porcine epidemic diarrhea virus<sup>3</sup>; and the Senecavirus A<sup>4</sup>.

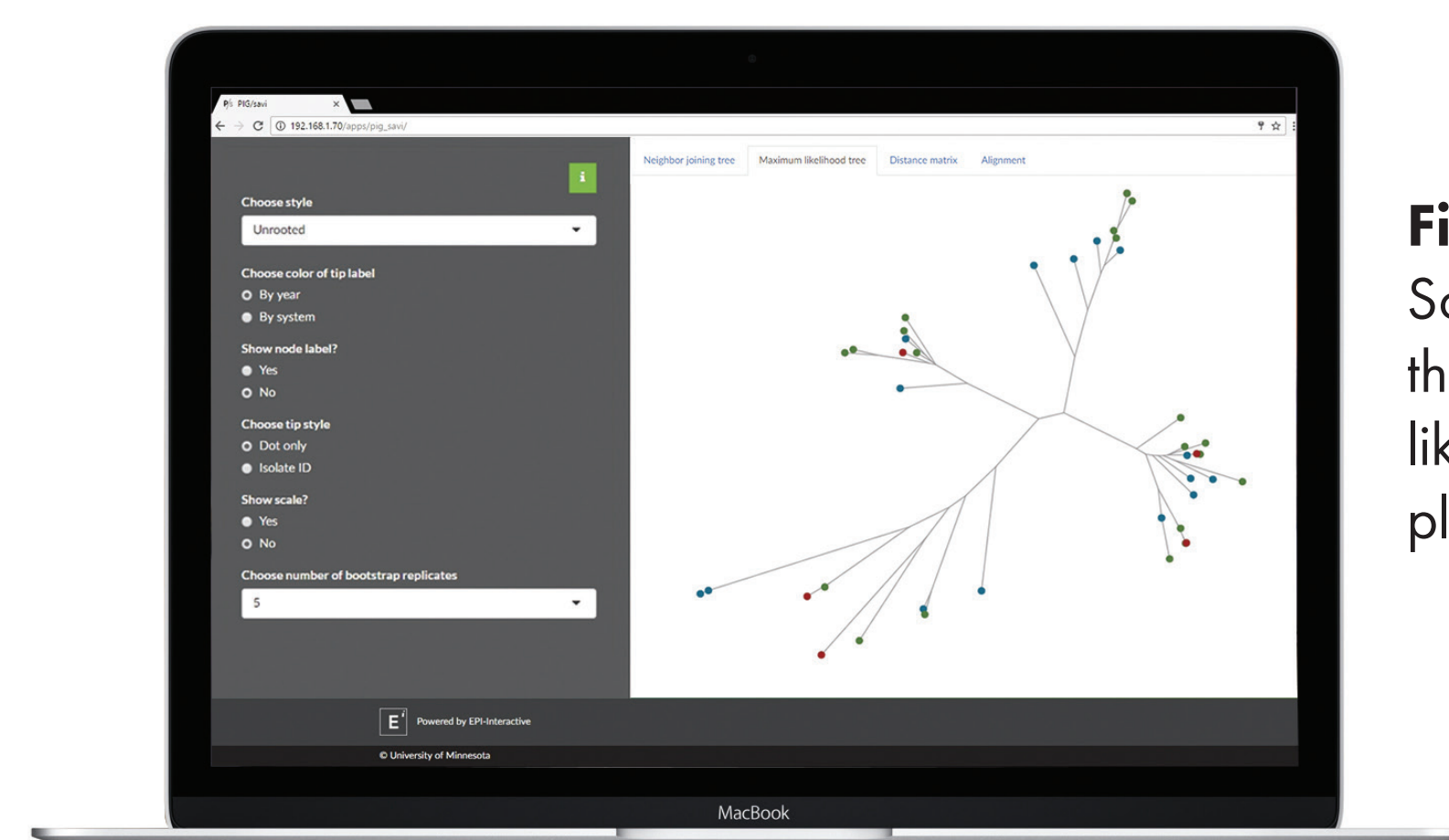
The Swine Health Monitoring Project (SHMP) is a national initiative to monitor and control swine pathogens in sow herds across the United States. As of March 2017, approximately 45% of the U.S. sow population was enrolled in the SHMP.

The **objective** of this project was to develop and demonstrate a platform to provide insights into food animal disease occurrence, spread and control, using PRRS and the SHMP as a model.

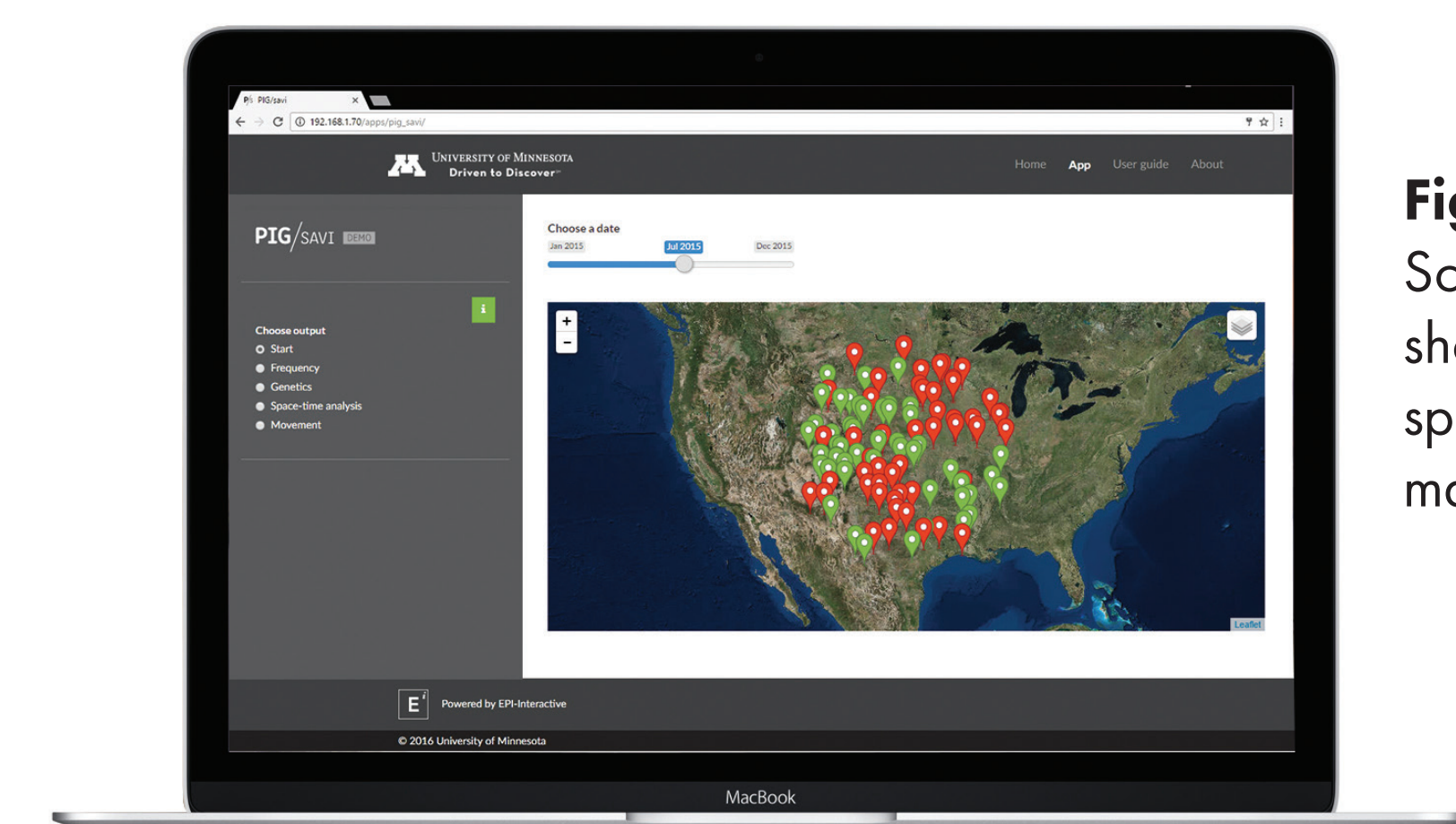
## Materials & Methods

**PIG/savi** was developed using the **Rstudio Shiny platform** (<http://shiny.rstudio.com>). It is composed of **four dashboards** that are demonstrated using fictitious SHMP-like data:

- 1. Disease frequency-** disease trends over time, including a cumulative incidence and an aggregate prevalence graph. Includes ability to filter by variables of interest (e.g. system)
- 2. Molecular characterization of PRRS virus isolates-** homology matrix and construction of two types of phylogenetic trees: neighbor-joining and maximum likelihood. Offers the ability to color tree nodes according to attributes of interest (Figure 1).
- 3. Space-time analysis-** visualization of swine farms in a satellite map with colors changing to represent status of disease over time, as well as construction of a kernel smoothed incidence risk map (Figure 2).
- 4. Network analysis-** visualization of animal movements in and out of each participating farm, as well as a data table option that show results of farm-level network statistics.



**Figure 1.** Screenshot showing the maximum likelihood phylogenetic tree.



**Figure 2.** Screenshot showing the space-time analysis map visualization.

## Results & Discussion

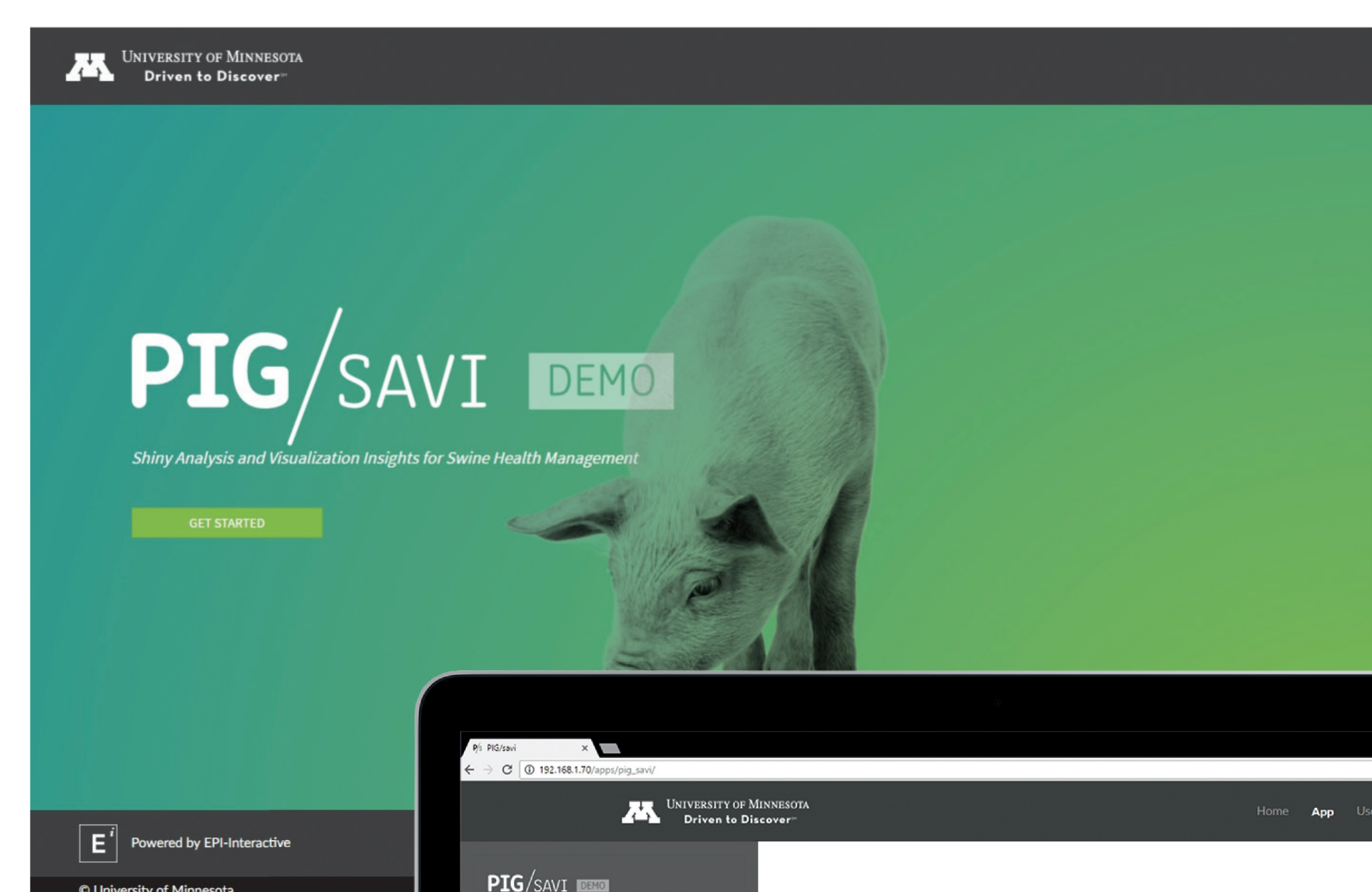
The tool developed herein is analytically strong and offers insights that cannot be provided by visualization-only available tools (Figures 3, 4).

The first dashboard allows for **monitoring of disease trends** over time and the identification of disease seasonality trends as well as of **potential epidemics**, which can serve as an early warning surveillance system.

The second dashboard presents a user-friendly view of methods that are commonly used at a local level to **discriminate between novel and preexisting PRRS virus strains** in order to infer spread patterns, which are the homology matrix and phylogenetic trees.

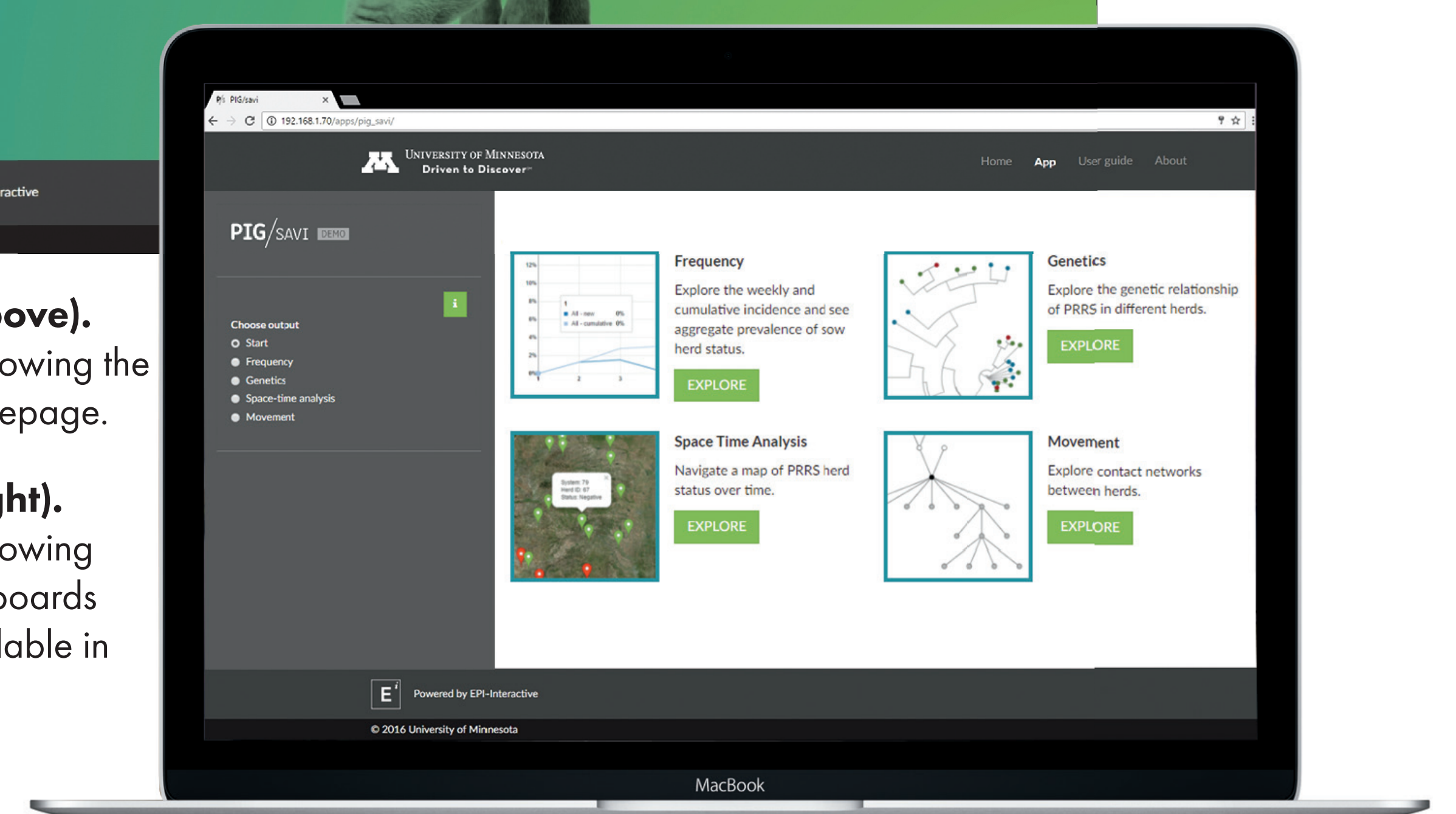
The spatial-temporal dashboard allows for the **identification of high-risk areas over time**, which can help characterize risk and provide insights on how PRRS is spreading across the country. It may additionally inform decisions such as movement of negative/ positive pigs to certain areas.

Finally, the animal movement dashboard allows for **rapid trace back**, which may be particularly useful not only for outbreak investigations when one wishes to rule out potential infection due to animal movement, but also when it is needed to **presume status** for other farms for the purposes, for example, of informing those who need to know during a control and eradication project.



**Figure 3 (above).** Screenshot showing the PIG/savi homepage.

**Figure 4 (right).** Screenshot showing the four dashboards currently available in PIG/savi.



## Conclusions & Future Directions

In conclusion, the platform developed in this project aims to centralize, integrate, and analyze surveillance information from multiple sources to provide immediate and eventually near real-time insights into specific diseases. The tool allows users to interact with the database and explore it in a flexible manner to improve their decision making process.

## Acknowledgments



## References

- <sup>1</sup>Meng, X. J. 2012. *Transb. Emerg. Dis.*, 59(1): 85-102;
- <sup>2</sup>Workman et al. 2016. *Genome Announc.*, 4(4): e00772-16;
- <sup>3</sup>Stevenson et al. 2013. *J. Vet. Diagn. Invest.* 25(5): 649-654;
- <sup>4</sup>Leme et al. 2015. *Transb. Emerg. Dis.*, 62 : 603-611.