

# An interactive dashboarding tool for visualizing wastewater-based pathogen sequencing data



TEXAS  
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## Background

Wastewater-based epidemiology (WBE) is emerging as a cost-efficient and non-invasive pathogen surveillance tool that is capable of representing data not captured by clinical surveillance. Additionally, the application of next-generation sequencing (NGS) in WBE can allow for more comprehensive pathogen assessment. The data generated by this wastewater-based pathogen sequencing (WBPS) is underutilized even though it can provide crucial information about the emergence and spread of pathogen variants. Overall, the recent proliferation of WBE has resulted in a need for developing novel tools and strategies.

## Purpose

To develop a user-friendly R Shiny tool to effectively visualize WBPS data for public health use.

## Methods

Two **24-hour composite** influent wastewater samples are collected weekly at partnering municipalities and one international airport across the state.

Quantitative reverse transcription polymerase chain reaction (**RT-qPCR**) is employed to detect pathogens.

After RT-qPCR, pathogen genetic extracts are sent to the Texas DSHS Public Health Laboratory for **NGS**.

## About GenoWaste

GenoWaste is a solution to visualizing and examining WBPS data. This interactive R Shiny application was developed to track SARS-CoV-2 variants across participating sites of the Texas DSHS Wastewater Epidemiology & Surveillance Program.

GenoWaste can be employed as a **user-friendly visualization tool** to facilitate infectious disease surveillance across space-time and better inform public health action.

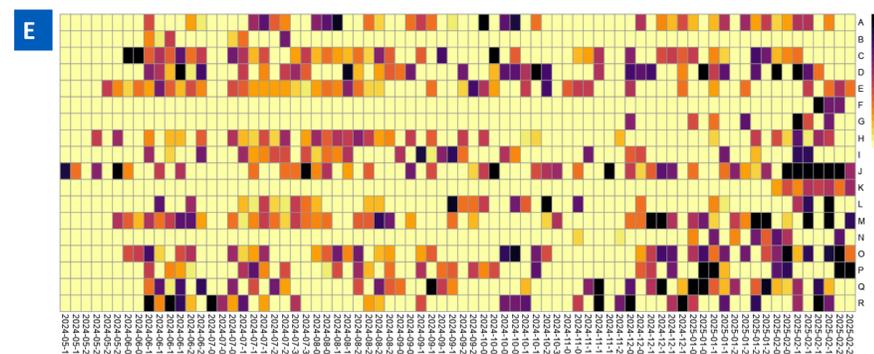
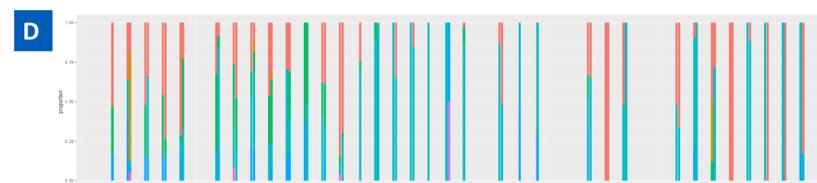
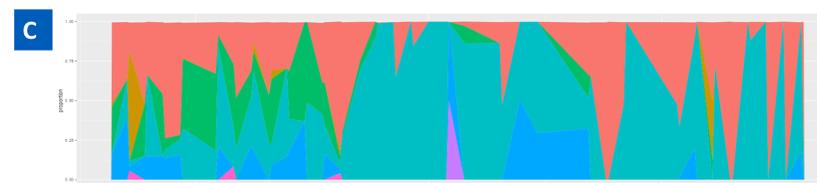
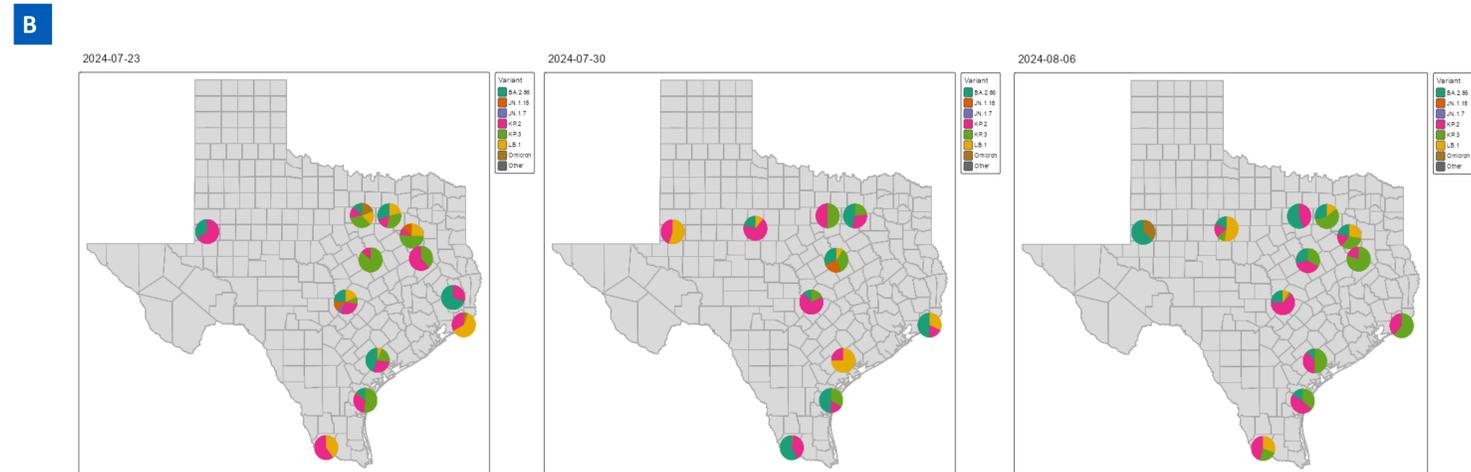
## Dashboard Preview



## Visualizing WBPS Data Using the Dashboarding Tool

There are two pages where a user can visualize WBPS data. The State Map page provides an interactive map, and the Data Visualization page allows the user to interactively explore the data.

On the **State Map page**, the user can select a date using a time-slider. When sequencing data is available, a map with pie charts depicting the proportion of variants at each sampling site is displayed (B). Due to the spatially discrete nature of wastewater data, this type of visualization is particularly useful. This state map visualization is provided to allow users to explore genomic trends across both space and time.



On the **Data Visualization page**, users can filter data by selecting a site, a variant, or both. The plot type options automatically update based on selections.

When **only a site is selected**, the plot type options are heatmaps, stacked area charts (C), and stacked bar charts (D).

When **only a variant is selected**, the plot type options are heatmaps (E) and variograms (A).

Additionally, when **both a variant and a site are selected** by the user, a line graph of the variant proportion over time for the selected site will be displayed.

## Next Steps

1. Publishing the dashboard
2. Develop replicable code and documentation for other programs
3. Publish a manuscript with the code