

# Integrating genomic and epidemiologic data in enteric disease surveillance dashboard in Utah

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# Background

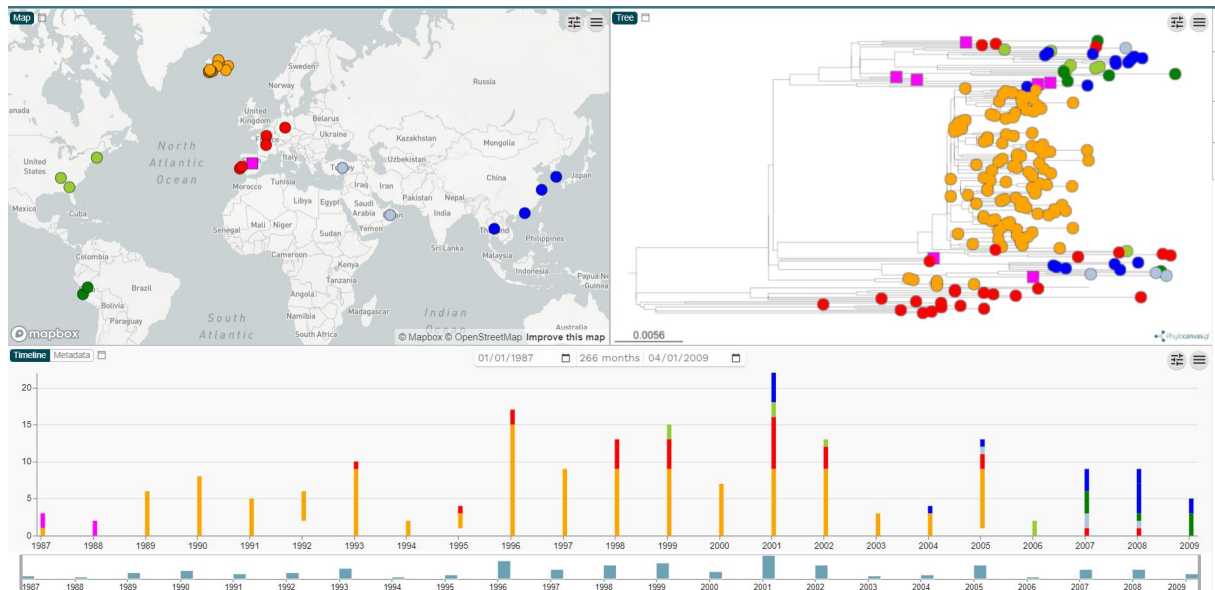
- Enteric disease is an important target for public health surveillance.
- Whole genome sequencing (WGS) data can provide key insights for disease surveillance.
- **Purpose:** Develop a dashboard to visualize genomic and epidemiologic data to facilitate disease surveillance.



# Goals

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- Visualize genomic relatedness.
- Filter on epidemiologically-relevant fields.
- Provide downloadable data.
- Access laboratory and epidemiologic data sources.



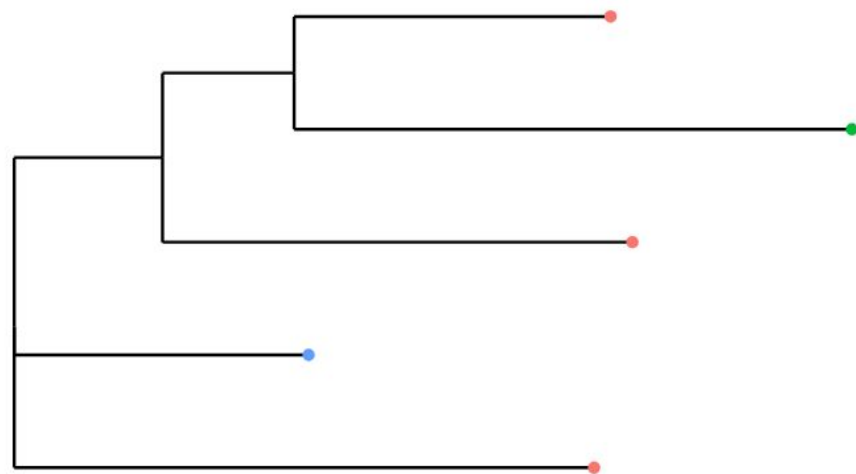
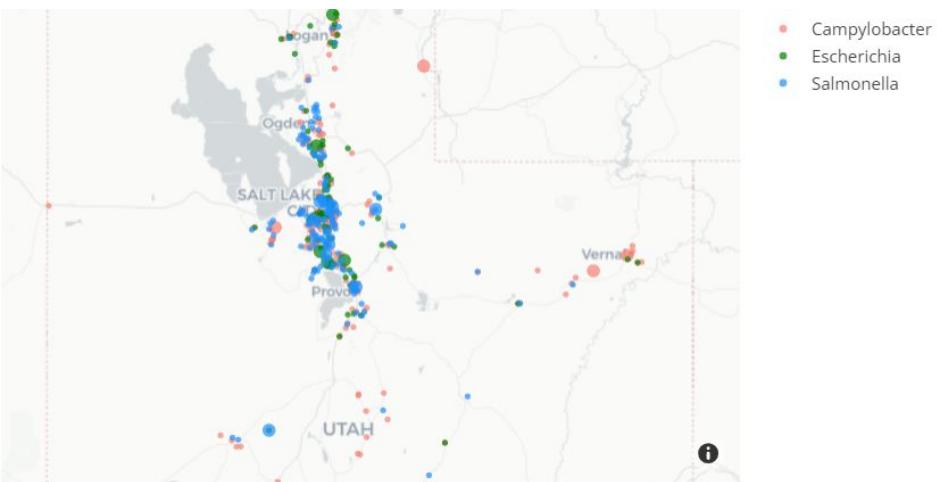
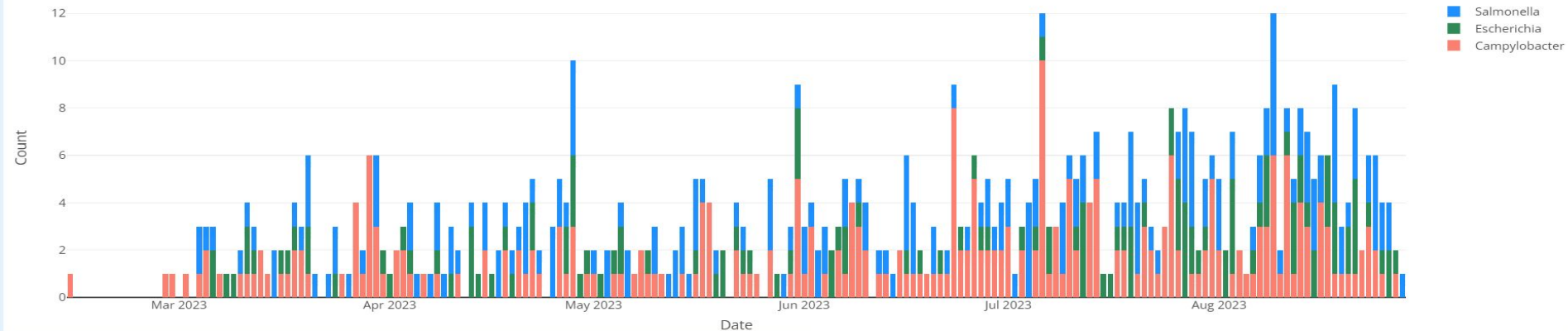
```

52 # Define UI
53 ui <- fluidPage(
54   tags$head(
55     tags$style(HTML('.container-fluid {
56       background-color: #e3f2fd;
57     }')),
58     tags$style(HTML('.title-panel {
59       background-color: #006666;
60       color: #FFFFFF;
61       text-align: left;
62       padding: 10px;
63       margin-bottom: 20px;
64     }'))
65   ),
66   titlePanel(
67     div(class = "title-panel",
68
69       # DHHS Logo
70       img(src = "Logo.png", alt = "Logo", height = 80,
71         style = "display: inline-block; margin-left: 10px;"),
72
73       # Title text
74       h1("Enteric Disease Genomic Surveillance Dashboard", style = "display
75
76     )
77   ),
78   fluidRow(
79
80     # Epi Curve
81     column(12, plotlyOutput("epi_curve")),
82
83
84     # Map and Phylogenetic Tree: one row
85     column(6,
86       h3("Map"),
87       plotlyOutput("enteric_map")),
88
89     column(6,
90       h3("Phylogenetic Tree"),
91       plotlyOutput("phylo_tree")),
92

```




# Dashboard visuals



# Dashboard visuals

|                      |     |          |             |             |      |                      |        |     |                |                   |
|----------------------|-----|----------|-------------|-------------|------|----------------------|--------|-----|----------------|-------------------|
| Key                  | CMR | Pathogen | Patient Sex | Patient Age | City | State                | County | Zip | Isolation Date | Lab Received Date |
| <input type="text"/> | All | All      | All         | /           | All  | <input type="text"/> | AI     | A   | AI             | All               |

### Metadata

 Reset Phylogenetic Tree Selection

CSV

Excel

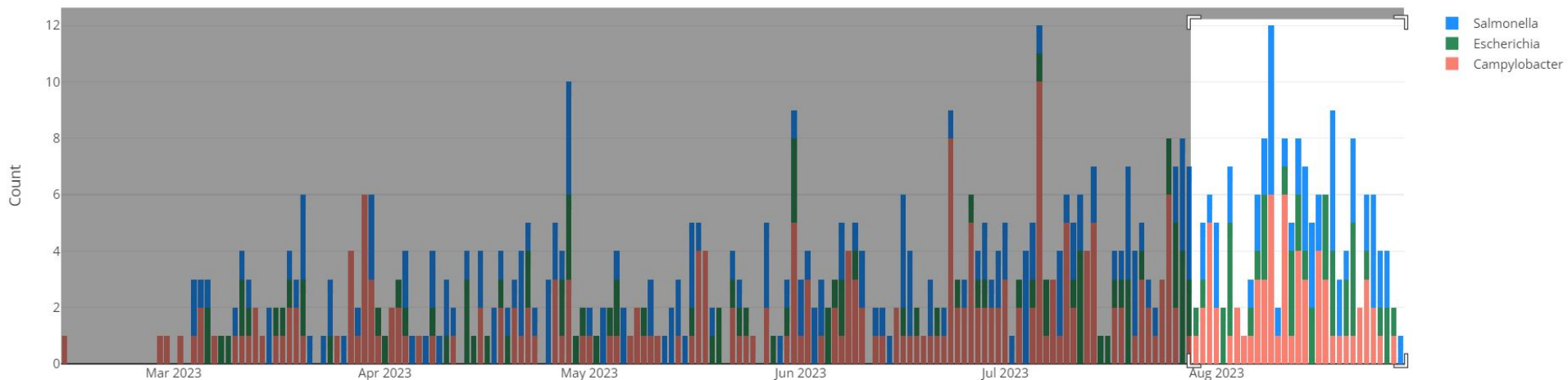
PDF

Showing 1 to 616 of 616 entries

|                      |                      |
|----------------------|----------------------|
| State                | County               |
| <input type="text"/> | <input type="text"/> |
| UT                   | BE                   |
| UT                   | BV                   |
| UT                   | CA                   |
| UT                   | CR                   |
| UT                   | DU                   |
| UT                   | DV                   |
| UT                   | EM                   |

|   |                   |     |
|---|-------------------|-----|
| Isolation Date  | Lab Received Date | All |
| AI  | All               | A   |
| <div><div>2023-02-13</div><div>2023-08-28</div></div> |                   |     |

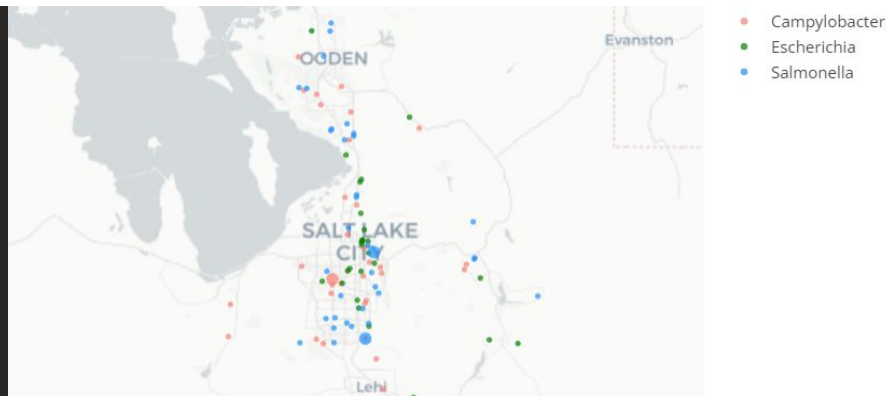
# Linked filtering



```
# Use relayout data from epicurve
relayout_data <- event_data("plotly_relayout", source = "epicurve_source")

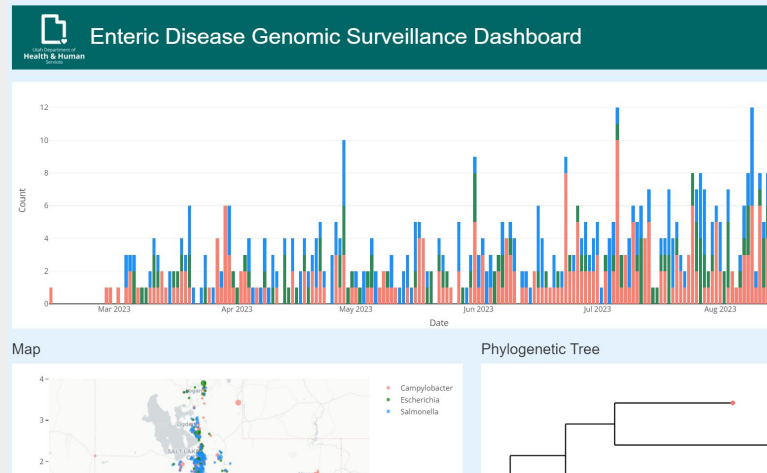
# Check if any points are selected
if (!is.null(relayout_data)) {
  # Check if x-axis range is available
  if (!is.null(relayout_data$xaxis.range[0]) && !is.null(relayout_data$xaxis.range[1])) {
    # Extract beginning and end range dates from event data
    date1 <- as.Date(relayout_data$xaxis.range[0])
    date2 <- as.Date(relayout_data$xaxis.range[1])

    # Filter data based on selected date range
    mapdata <- data[data$isolat_date >= date1 & data$isolat_date <= date2,]
  } else if (relayout_data$xaxis.autorange == TRUE && relayout_data$yaxis.autorange == TRUE) {
    # Reset to the full dataset if x and y autoranges are true
    mapdata <- data
  }
}
```





# Putting it all together



```
# JS code for event click reset
jsCodePhylo <- "ShinyJS.resetClickPhylo = function() { Shiny.onInputChange('plotly_click-phylo_source', 'null'); }"

# Define UI
ui <- fluidPage(
  tags$head(
    tags$style(HTML("<div class='container-fluid' { background-color: #e3f2fd; }")),
    tags$style(HTML("<div class='title-panel' { background-color: #006666; color: #FFFFFF; text-align: left; padding: 10px; margin-bottom: 20px; }"))
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  titlePanel(
    div(class = "title-panel",
      # DHHS Logo
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    # Epi Curve
    column(12, plotlyOutput("epi_curve")),

    # Map and Phylogenetic Tree: one row
    column(6,
      h3("Map"),
      plotlyOutput("enteric_map")),

    column(6,
      h3("Phylogenetic Tree"),
      plotlyOutput("enteric_phylo"))
  )
)
```

# Barriers and next steps

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- Hosting and sharing dashboard for continuous use.

# Conclusions

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- Enteric dashboard will meet a need for epidemiologists.
- Integration of genomic and epidemiologic data.

# **Acknowledgements**

- **Utah DHHS surveillance team and UPHL**
- **Utah state and local epidemiologists**
- **Utah DHHS informatics**

# Thank you

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