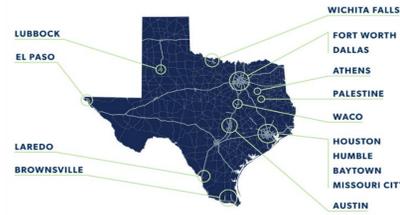


Maresso (Presenter)^{1,2,3,4*}, A., Tisza^{1,2}, M., Javornik-Cregeen^{1,2}, S., Hanson^{4,5}, B., Bauer^{4,5}, C., Piedra², P., Avadhanula², V., Wu⁵, F., Clark^{2,3}, J., Petrosino^{1,2}, J., Deegan^{4,5}, J., Boerwinkle^{4,5*}, E. *et al.*

THE PROGRAM

- Texas Wastewater and Environmental Biomonitoring (TexWEB)
- 15 Texas Cities
- ~ 40 sites
- ~ 7 million residents
- 6 working groups
- An early detection program of the Texas Epidemic Public Health Institute



THE PURPOSE

- Use **advanced sequencing technologies** to detect pathogens (“Every Sequence Everywhere All At Once”)
- Create an **operational process to notify** stakeholders and the public of the detection (“pathogen weather report”)
- **Innovate** around Methodology, Computational Biology, and Wastewater Science

THE PEOPLE

- **Science and Innovation Team** = Sequence wastewater and develop new innovative approaches and solutions
- **Computational and Analytics Team** = Analyze and validate sequencing data and develop new computational tools
- **Dashboard and Modeling** = Integrate data into public dashboard (SeqBoard), ensure accessibility, maintenance, predict
- **“Action!” Team** = Task force that advises on wastewater policy/practices, liaisons with Public Health Experts, develops SOPs
- **Communications Team** = develops best practices and materials to communicate findings, manages outreach, tracks use
- **Bioethics Team** = develops policy briefs around wastewater science, community surveys, develops data sharing plans

THE PERFORMANCE

- **3 Full Years** of weekly/biweekly sequencing analysis across most many sites
- **> 2,500 samples** processed and computationally analyzed
- **> 400 different viruses** detected
- **> 800 different strains** across 100 genera
- **> human/plant/animal** viruses
- **> 100 billion reads**
- **1 Dashboard (SeqBoard)** + website/video/tutorial
- **9 Manuscripts** published or in submission
- **> 60 viral level reports**
- **5 Alert Notifications** of very concerning viruses (+DSHS, CDC, White House)

THE PROCESS

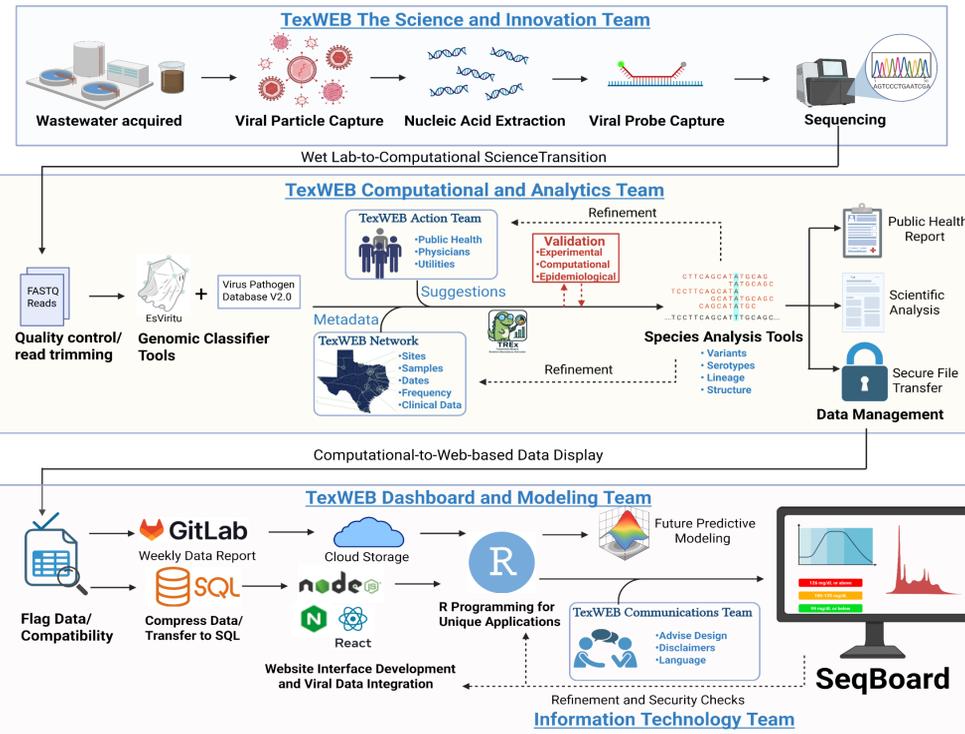
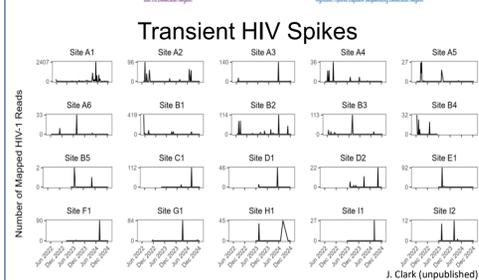
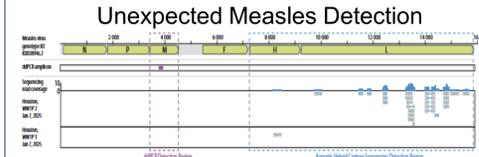
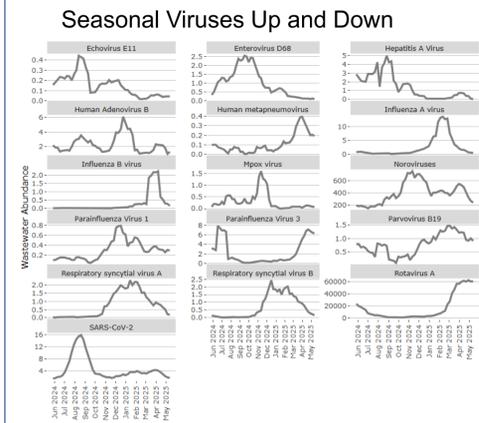


Figure: TexWEB Workflow, Team, and Processes. The team structure from Figure is overlaid with a general workflow following the acquisition of wastewater samples, the analysis of the viral species and variants present in them, and the conversion of sequencing data into an understandable and interactive dashboard termed **SeqBoard**. Note that at several points metadata and expertise inputs influence the data that is displayed and its format. At multiple steps there is refinement with iterative interactions improving workflow, knowledge, and display.

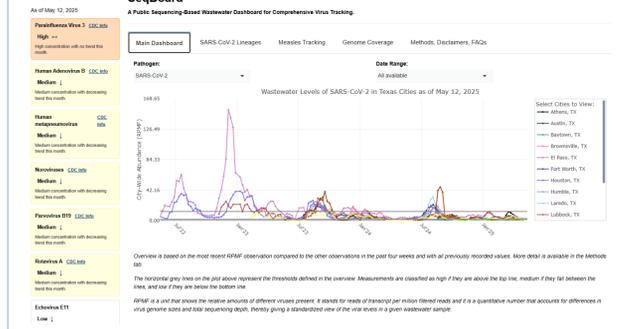
THE PLOT

Story 3: Outbreaks!

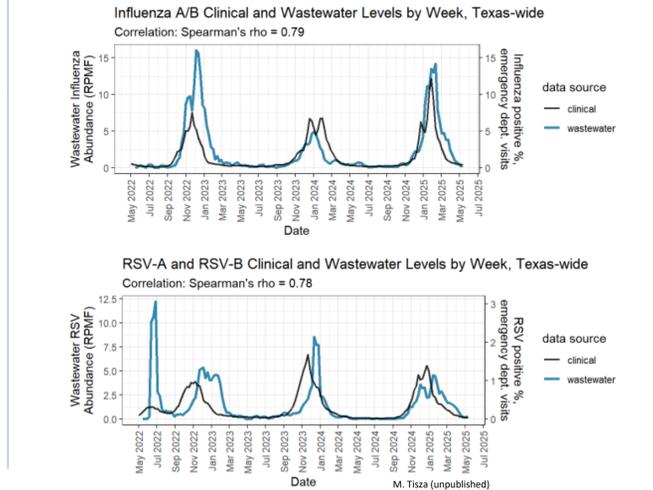


Story 4: SeqBoard

A sequencing-based dashboard

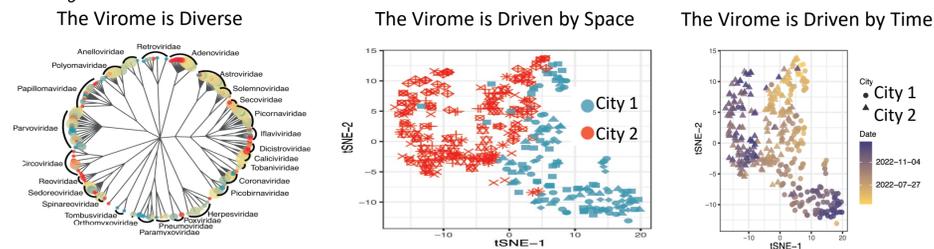


Story 5: Correlation to Clinical Data

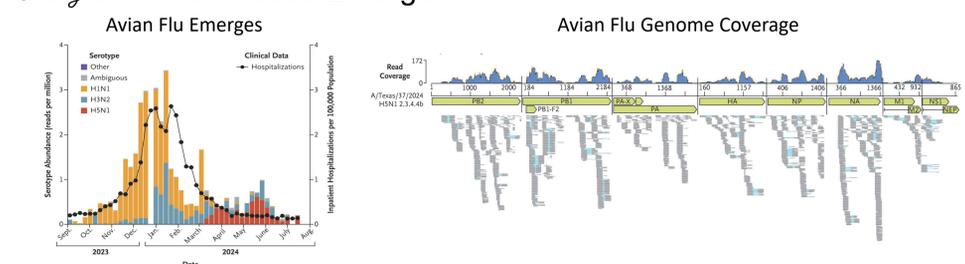


THE PLOT

Story 1: The Human Wastewater Virome!

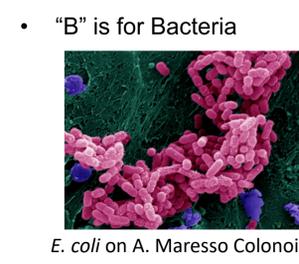
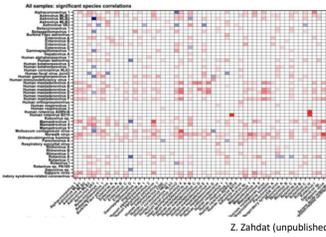


Story 2: Novel Viruses Emerge!



THE PROSPECTS

- Machine Learning to Associate and Predict “All by All”



Further Information, References, and Funding

TexWEB Website [QR Code]

SeqBoard [QR Code]

References
 PMID: 39259887
 PMID: 40340466
 PMID: 37026145
 PMID: 37898601
 PMID: 39341403
 PMID: 38076410

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