

# Open source data tools: Goals, strategy, and examples

Jake Vander Laan

Utah Department of Environmental Quality

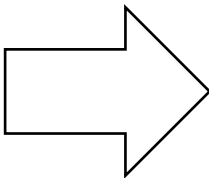
2021 ACWA Water Quality Modeling Workshop



# Utah's water quality assessment program

## Previous tools

- Mixture of:
  - Manual data downloads
  - Excel
  - Access queries
- Issues
  - Inefficient
  - Hard to replicate
  - Hard to document



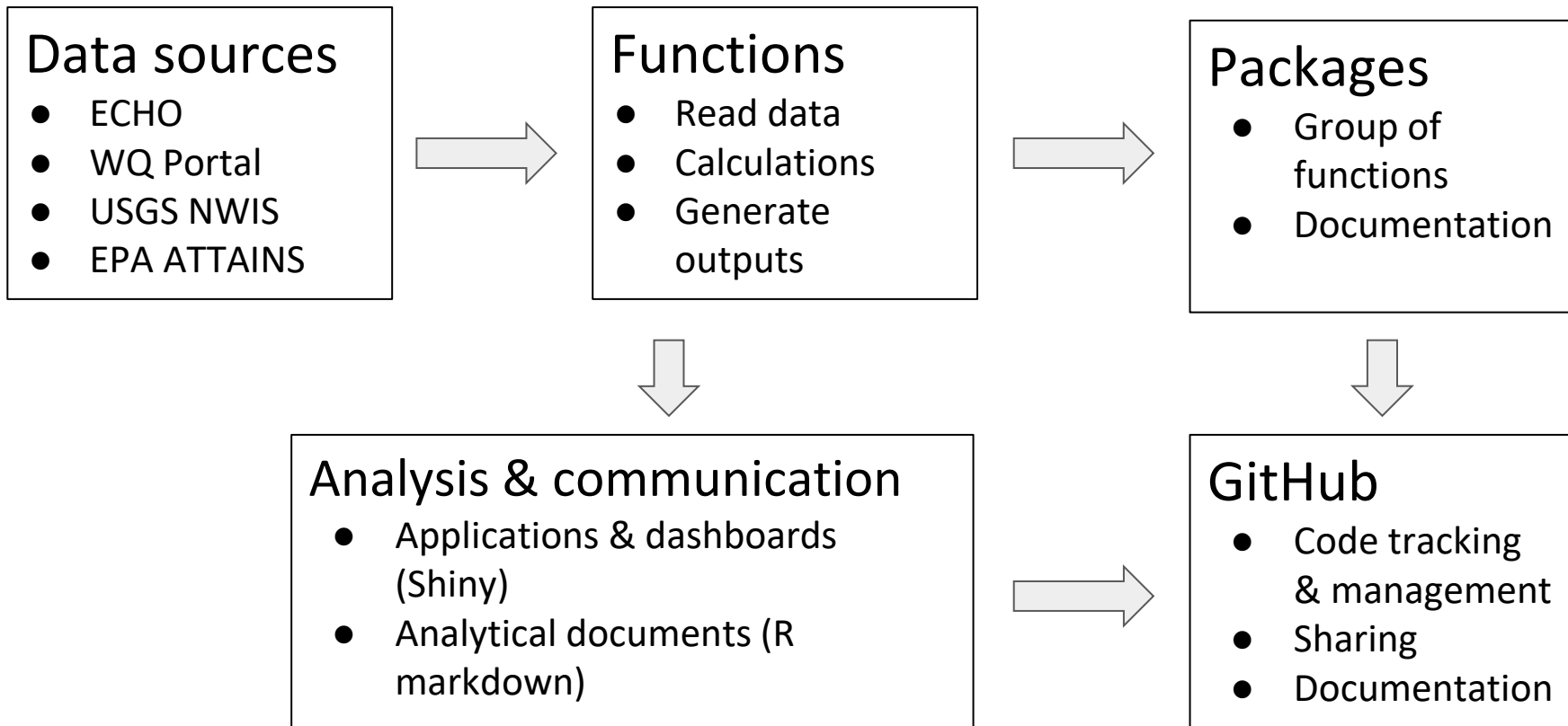
## R packages

- Recompilation of tools in R (functions & RMarkdown)
  - Flexible/adaptable
  - Quickly re-runnable
  - Fully documented
- Forced re-examination of process
- Had to build underlying structures & expertise
  - Digitizing criteria
  - Lookup/QAQC tables

# Tool development goals

1. Agency ownership
2. Accurate & efficient
3. Transparent & reproducible
4. Flexible
5. Shareable

# Hierarchical tools & workflow



# Functions & packages

NAMESPACE	documentation	5 months ago
readme.md	typo: compenents -> components	2 months ago
wqTools_0.0.0.9000.pdf	addMapResetButton	15 months ago

readme.md

## Utah DWQ's wqTools R-package

### Description

wqTools is a collection of R tools developed and designed for use by Utah Division of Water Quality staff. This includes functions for reading data from EPA's water quality portal & EPA ECHO, assigning spatial components of water quality standards to sample locations, generating study maps, performing unit conversions, generating plots, and other tools designed to support water quality analyses.

### Install

This package is in active development and can be installed via GitHub with `devtools::install_github("utah-dwq/wqTools")`.

### Manual

See [wqTools-manual.pdf](#) in GitHub for more information.

### Detailed examples

See the [wqTools Utah TDS vignette](#) for a detailed example of package usage to answer real water quality questions.

readECHO\_ec

*Read effluent chart data from EPA ECHO webservices*

### Description

This function extracts effluent chart data from EPA ECHO for multiple stations & combinations of parameters. All arguments are optional except p\_id. At least one p\_id must be specified.

### Usage

```
readECHO_ec(  
  ...,  
  print = TRUE,  
  stringsAsFactors = default.stringsAsFactors(),  
  progress = TRUE  
)
```

### Arguments

... additional arguments to be passed to ECHO query path. See [https://echo.epa.gov/tools/webservices/effluent-charts#!/Effluent\\_Charts/get\\_eff\\_rest\\_services\\_download\\_effluent\\_chart](https://echo.epa.gov/tools/webservices/effluent-charts#!/Effluent_Charts/get_eff_rest_services_download_effluent_chart) optional arguments for effluent chart data reads.

[github.com/utah-dwq/wqTools](https://github.com/utah-dwq/wqTools)

# RMarkdown documents

Reservoir analyses

Data imports

Subset & reshape data

Fill NDs

Site map

Stratification patterns

**Trophic indicators**

Data processing

Trophic summary stats

Time series

TSI comparison

TSI timeseries

TSI summary stats

Inflow TP & TN

## Trophic indicators

### Data processing

```
trophic_data=subset(grab_wq_data, CharacteristicName %in% c("Phosphate-phosphorus", "Chlorophyll a, uncorrected for pheophytin", "Nitrogen", "Depth, Secchi disk depth") & MonitoringLocationIdentifier %in% profiles$MonitoringLocationIdentifier)
trophic_data$ResultSampleFractionText[is.na(trophic_data$ResultSampleFractionText)]= "Total"

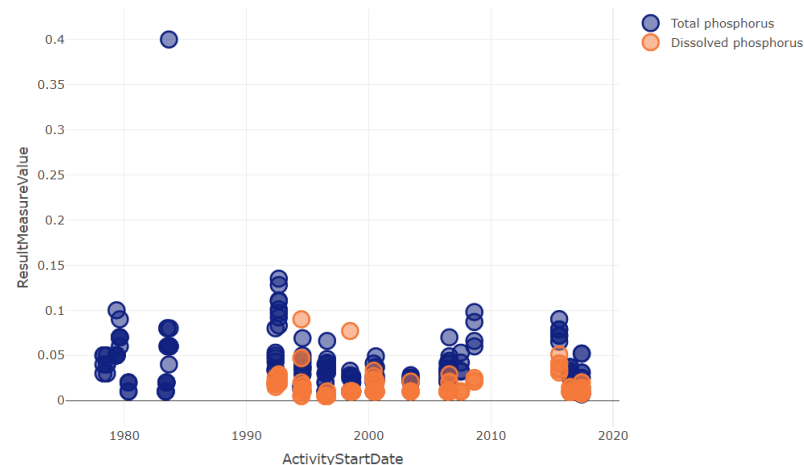
table(trophic_data$CharacteristicName, trophic_data$ResultSampleFractionText, exclude=NULL)
```

```
##
##                               Dissolved Total
## Chlorophyll a, uncorrected for pheophytin      0  52
## Depth, Secchi disk depth                       0  147
## Nitrogen                                       36  36
## Phosphate-phosphorus                         147 190
```

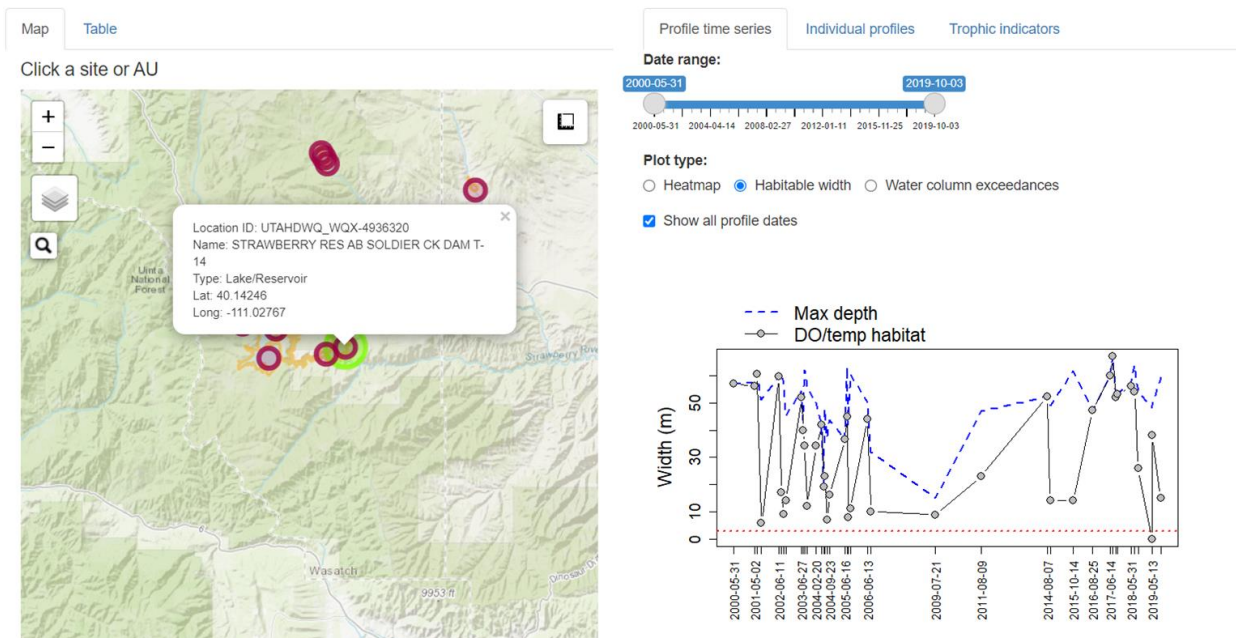
```
table(trophic_data$CharacteristicName, trophic_data$ResultMeasure.MeasureUnitCode, exclude=NULL)
```

```
##
##                               m mg/l ug/l
## Chlorophyll a, uncorrected for pheophytin      0  0  52
## Depth, Secchi disk depth                     147  0  0
## Nitrogen                                       0  72  0
## Phosphate-phosphorus                         0  337  0
```

### Phosphorus



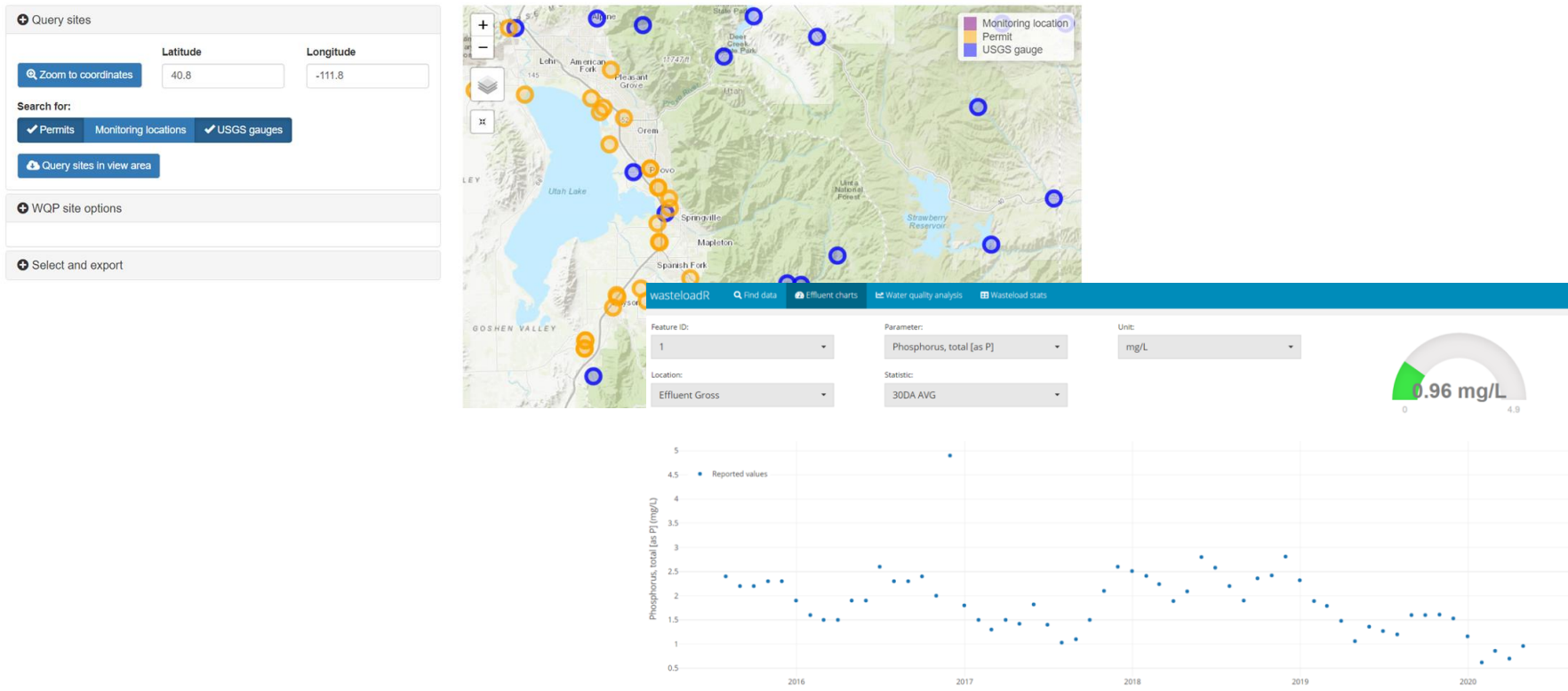
# Applications & dashboards



[udwq.shinyapps.io/lakedashboard](https://udwq.shinyapps.io/lakedashboard)

[github.com/utah-dwq/irTools/tree/master/inst/lakeDashboard](https://github.com/utah-dwq/irTools/tree/master/inst/lakeDashboard)

## Applications & dashboards





# Public communications



## SARS-CoV-2 Sewage Monitoring

SARS-CoV-2 (the virus that causes COVID-19, hereafter referred to as the virus) is shed in feces by infected individuals. Virus concentrations in sewage can be measured by collecting a sample at the inlet of sewage treatment plants. This information provides a pooled indicator of the status and trends of COVID-19 infections in communities served by the treatment plant (the sewershed).

Utah DEQ is collecting samples at 42 sewage treatment plants in Utah, representing approximately 80% of the state's population. The data from these samples provide a quantitative estimate of the average number of virus RNA gene copies entering the treatment plant and normalized to the number of people living in the sewershed. The data are updated regularly to provide additional information to public health partners regarding trends in virus prevalence in Utah's communities.



**COVID-19 information**  
For information regarding COVID-19 guidance and cases, see the Utah Department of Health COVID-19 information page.

[LEARN MORE](#)

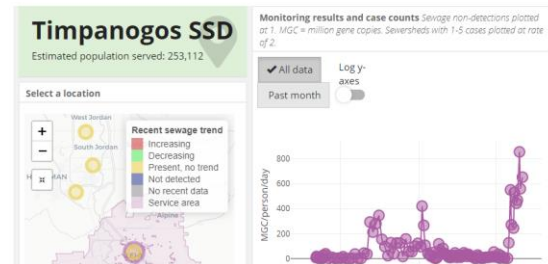
CURRENT DATA	BACKGROUND	RESOURCES	PILOT STUDY
--------------	------------	-----------	-------------

### Current Data

The interactive dashboard below shows results from ongoing SARS-CoV-2 sewage monitoring in Utah along with observed infection rates in each corresponding sewershed. Points on the map represent sewershed centroids and are color-coded by trends in gene copies in sewage over the four most recent samples. Areas without markers indicate unsampled locations. Select a location on the map to see monitoring results and infection rates for a desired sewershed.

### Important Note

On August 1, 2021, we moved all laboratory analyses associated with wastewater surveillance to the Utah Public Health Laboratory. There are a number of changes that could affect the end results displayed in this report, including sampling on different days, sample transportation times, RNA concentration/extraction methods, and the lab personnel running the analyses. It is extremely difficult to predict how these changes affect the results, though for at least some facilities the difference appears to be minimal. Results from some other facilities are now considerably higher. Ultimately, we expect the results post-change to be at least as accurate as previous data, if not more so.



[wastewatervirus.utah.gov](https://wastewatervirus.utah.gov)

# Questions

Jake Vander Laan  
jvander@utah.gov

