

# Calculated Info

Marlin

2023-06-15

This package contains a couple tools to create useful views of the data not by default in the dataframe. These mostly come in the form of the default case and wastewater dataframe augment function.

## Wastewater augmeanting function

The wastewater function does three things. first it replaces Concentrations below the level of detection (LOD) with  $\text{LOD} / 2$  which is considered best practice. Second it calculates a geometric average of the two gene concentrations. Finally it gets a flow and population normalized logged version of the data which previous work has shown the best results.

```
library(DSIWastewater)
```

```
## Registered S3 method overwritten by 'quantmod':  
##   method      from  
##   as.zoo.data.frame zoo
```

```
data(WasteWater_data, package = "DSIWastewater")  
head(buildWasteAnalysisDF(WasteWater_data))
```

```
## # A tibble: 6 x 9  
##   site   date      pop    N1    N2  flow geoMean sars_cov2_adj_load_l~1    n  
##   <chr> <date>    <dbl> <dbl> <dbl> <dbl>   <dbl>         <dbl> <int>  
## 1 Algoma 2020-10-06  3171 10000    NA 0.498    NA             NA      34  
## 2 Algoma 2020-10-13  3171 10000 16500 0.499 12845.         0.306     34  
## 3 Algoma 2020-10-20  3171 10000 16500 0.402 12845.         0.212     34  
## 4 Algoma 2020-10-27  3171 10000 16500 0.67  12845.         0.434     34  
## 5 Algoma 2020-11-03  3171 10000 16500 0.489 12845.         0.297     34  
## 6 Algoma 2020-11-10  3171 10000 16500 0.463 12845.         0.273     34  
## # i abbreviated name: 1: sars_cov2_adj_load_log10
```

## Case augmeanting function

The case function does two things. first it normalizes the data by population. Second it calculates a rolling sum and average of the data. This needs the population data contained in its own data frame.

```
data(Case_data, package = "DSIWastewater")  
data("pop_data", package = "DSIWastewater")#need to fix pop_data  
#head(buildCaseAnalysisDF(left_join(Case_data, pop_data, by = "site")))
```

These functions are slightly out of date and not used in many new analysis projects

*#TODO work on comparing the output of these methods*