

Calculated Info

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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 $LOD / 2$ 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These functions are slightly out of date and not used in many new analysis projects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