Example Data Vignette

#Example data This data comes from our wastewater and case data merged together by site and date. Then filtered with by 3 sites; Green Bay, Janesville, and Mauston. Then a new column is added; geo_mean which is the geometric mean of N1 and N2. This gives roughly 500 rows to work with for examples across different sized sites over a large time frame.

```
library(DSIWastewater)
library(ggplot2)
```

```
data(Example_data, package = "DSIWastewater")
```

```
## Warning in data(Example_data, package = "DSIWastewater"): data set
## 'Example_data' not found
```

```
head(Example_data)
```

```
##          date      site tests prob_case conf_case prob_death conf_death
## 1 2020-08-23 Green Bay   365         0         2          0          0
## 2 2020-08-24 Green Bay   142         0        18          0          0
## 3 2020-08-30 Green Bay   290         0         0          0          0
## 4 2020-08-31 Green Bay   194         2        37          0          0
## 5 2020-09-06 Green Bay   187         0        13          0          0
## 6 2020-09-07 Green Bay   318         0         0          0          0
##        regions    county    pop      N1     N2 PMMoV hf183   flow tss  ph
## 1 Northeastern Green Bay 189000  7449.6 4464.0    NA    NA 18.363 300 7.6
## 2 Northeastern Green Bay 189000  7891.2 4732.8    NA    NA 22.004 398 7.1
## 3 Northeastern Green Bay 189000  5023.2 4586.4    NA    NA 19.903 272 7.3
## 4 Northeastern Green Bay 189000  8743.2 4524.0    NA    NA 22.663 186 7.4
## 5 Northeastern Green Bay 189000  8409.6 2736.0    NA    NA 16.496 408 7.1
## 6 Northeastern Green Bay 189000 12072.0 6146.4    NA    NA 17.660 534 7.5
##   conductivity temperature    epaid sample_id          pcr_type
## 1           NA          NA WI0065251       260 droplet digital PCR
## 2           NA          NA WI0065251       261 droplet digital PCR
## 3           NA          NA WI0065251       276 droplet digital PCR
## 4           NA          NA WI0065251       277 droplet digital PCR
## 5           NA          NA WI0065251       284 droplet digital PCR
## 6           NA          NA WI0065251       285 droplet digital PCR
##    n1_sars_cov2_units n1_sars_cov2_lod  n2_sars_cov2_units n2_sars_cov2_lod bod
## 1 copies/L wastewater            FALSE copies/L wastewater            FALSE 210
## 2 copies/L wastewater            FALSE copies/L wastewater            FALSE 310
## 3 copies/L wastewater            FALSE copies/L wastewater            FALSE 230
## 4 copies/L wastewater            FALSE copies/L wastewater            FALSE 210
## 5 copies/L wastewater            FALSE copies/L wastewater            FALSE 210
## 6 copies/L wastewater            FALSE copies/L wastewater            FALSE 240
##   do      created_on last_modified_on lab_submitter n1_lod n1_loq n2_lod n2_loq
```

```
## 1 NA 12/4/2020 17:38   1/7/2022 13:55        UWM 2236.8 7449.6 3724.8 6700.8
## 2 NA 12/4/2020 17:38   1/7/2022 13:55        UWM 2371.2 7891.2 3945.6 7104.0
## 3 NA 12/4/2020 17:38   1/7/2022 13:55        UWM 2337.6 7792.8 3895.2 7015.2
## 4 NA 12/4/2020 17:38   1/7/2022 13:55        UWM 2325.6 7764.0 3878.4 6986.4
## 5 NA 12/4/2020 17:38   1/7/2022 13:55        UWM 2068.8 6897.6 3448.8 6208.8
## 6 NA 12/4/2020 17:38   1/7/2022 13:55        UWM 2128.8 7089.6 3547.2 6384.0
##   bcov_rec_rate bcov_spike_conc zipcode state capacity_mgd sample_type
## 1            NA              NA      NA  <NA>           NA        <NA>
## 2            NA              NA      NA  <NA>           NA        <NA>
## 3            NA              NA      NA  <NA>           NA        <NA>
## 4            NA              NA      NA  <NA>           NA        <NA>
## 5            NA              NA      NA  <NA>           NA        <NA>
## 6            NA              NA      NA  <NA>           NA        <NA>
##   composite_freq sample_matrix sample_location sample_location_specify
## 1           <NA>          <NA>            <NA>                    <NA>
## 2           <NA>          <NA>            <NA>                    <NA>
## 3           <NA>          <NA>            <NA>                    <NA>
## 4           <NA>          <NA>            <NA>                    <NA>
## 5           <NA>          <NA>            <NA>                    <NA>
## 6           <NA>          <NA>            <NA>                    <NA>
##   wwtp_comments concentration_method extraction_method lod_ref quant_stan_type
## 1          <NA>                 <NA>              <NA>    <NA>            <NA>
## 2          <NA>                 <NA>              <NA>    <NA>            <NA>
## 3          <NA>                 <NA>              <NA>    <NA>            <NA>
## 4          <NA>                 <NA>              <NA>    <NA>            <NA>
## 5          <NA>                 <NA>              <NA>    <NA>            <NA>
## 6          <NA>                 <NA>              <NA>    <NA>            <NA>
##   quant_stan_ref inhibition_method n1_sars_cov2_error n1_ntc_amplify
## 1           <NA>              <NA>                 NA           <NA>
## 2           <NA>              <NA>                 NA           <NA>
## 3           <NA>              <NA>                 NA           <NA>
## 4           <NA>              <NA>                 NA           <NA>
## 5           <NA>              <NA>                 NA           <NA>
## 6           <NA>              <NA>                 NA           <NA>
##   n1_num_ntc_amplify n1_num_no_target_control n2_sars_cov2_error n2_ntc_amplify
## 1                 NA                       NA                 NA           <NA>
## 2                 NA                       NA                 NA           <NA>
## 3                 NA                       NA                 NA           <NA>
## 4                 NA                       NA                 NA           <NA>
## 5                 NA                       NA                 NA           <NA>
## 6                 NA                       NA                 NA           <NA>
##   n2_num_ntc_amplify n2_num_no_target_control avg_sars_cov2_conc
## 1                 NA                       NA                 NA
## 2                 NA                       NA                 NA
## 3                 NA                       NA                 NA
## 4                 NA                       NA                 NA
## 5                 NA                       NA                 NA
## 6                 NA                       NA                 NA
##   avg_sars_cov2_below_lod inhibition_detect inhibition_adjust
## 1                      NA              <NA>              <NA>
## 2                      NA              <NA>              <NA>
## 3                      NA              <NA>              <NA>
## 4                      NA              <NA>              <NA>
## 5                      NA              <NA>              <NA>
```

```
## 6                       NA             <NA>             <NA>
##   analytical_comments sample_collect_time test_result_date equiv_sewage_amt
## 1                <NA>             NA secs             <NA>               NA
## 2                <NA>             NA secs             <NA>               NA
## 3                <NA>             NA secs             <NA>               NA
## 4                <NA>             NA secs             <NA>               NA
## 5                <NA>             NA secs             <NA>               NA
## 6                <NA>             NA secs             <NA>               NA
##   geo_mean
## 1 5766.716
## 2 6111.258
## 3 4799.834
## 4 6289.216
## 5 4796.735
## 6 8613.904
```

```
ggplot(Example_data, aes(x=date, y=geo_mean, color = site)) +
  geom_point()
```

```
## Warning: Removed 24 rows containing missing values (`geom_point()`).
```