## HW4 fish data

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First load package and data.

```
library(readr)
library(reshape2)
library(tidyverse)
library(directlabels)

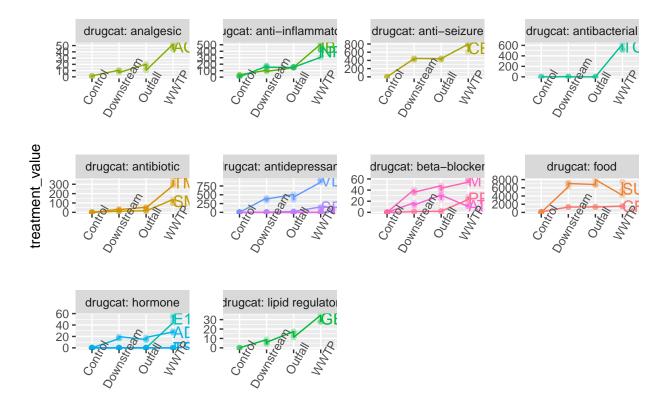
fish_data<-read_csv("fish.csv",col_names = TRUE)
colnames(fish_data)[3]<-"SampleID"
fish_name<-read_csv("fish_names.csv",col_names = TRUE)</pre>
```

switch wide format to long format, and merge 2 data set together. Now the full data has all the information for plotting.

```
#wide format to long format
fish_long<-melt(fish_data, id.vars = c("SampleID", "Site", "MetCode", "SamplerType"),
        variable.name = "treatment_variable",
        value.name = "treatment_value")

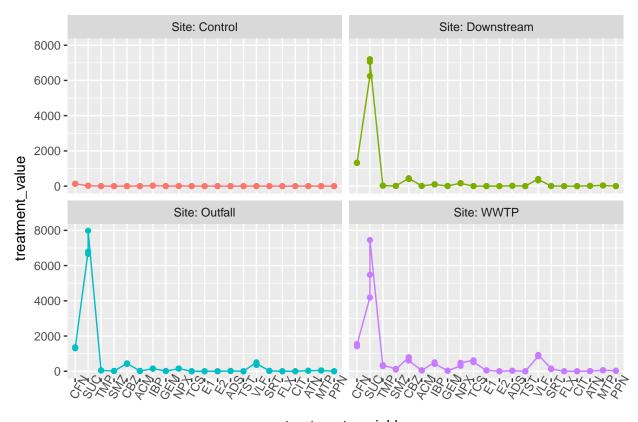
#merge name data with long format data.
fish_name$treatment_variable<- fish_name$abbr
full<-merge(fish_long, fish_name)
(full%>%select(-abbr))->full
```

First plot showing under same drugcat, how drug changes with Site. Like under drugcat is food, SUC always have higher value for each Site than CFN, same happen to antidepressant, and antibiotic. However, like with drugcate is beta-blocker, ATN has higher value than PPN fot both Site: Downstream and Outfall, but PPN higher than ATN for site:WWTP.

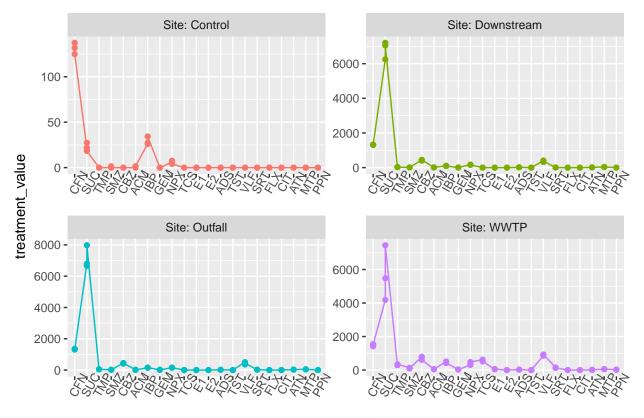


## Site

Second plot is drug's value for each Site. SUC has much higher value for each Site except Control. Compared to onther Site, control almost has fewer changes for each drug.



## treatment\_variable



treatment\_variable