Percent Removal for DBF and Chlorination (Phase 2)

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```
# clear environment
rm(list = ls())

# set working directory
setwd("C:/Users/wraseman/Hazen and Sawyer/Stanford, Benjamin - Loxahatchee DBF Evaluation/Data A
nalysis - Billy")
# load packages
library(tidyverse)  # ggplot2, dplyr for data wrangling and visualization

# read in percent removal data for DBF
data.dir <- "./data/"
filename <- "pct-rmv_dbf.rds"
data.path <- str_c(data.dir, filename)
dbf.df <- read_rds(path = data.path)

## print dataframe
print(dbf.df)
```

```
## # A tibble: 238 x 11
## # Groups:   DateCollected, Parameter [238]
##    DateCollected       Parameter FilterInfluent FilterEffluent
##    <dttm>              <chr>              <dbl>          <dbl>
##  1 2018-03-06 00:00:00 Acetamin~            110            110
##  2 2018-03-06 00:00:00 Bispheno~            200            160
##  3 2018-03-06 00:00:00 Caffeine            1200           1100
##  4 2018-03-06 00:00:00 Carbamaz~            270            230
##  5 2018-03-06 00:00:00 Cryptosp~            310             10
##  6 2018-03-06 00:00:00 Dilantin              45             98
##  7 2018-03-06 00:00:00 Gemfibro~           1800           1700
##  8 2018-03-06 00:00:00 Giardia             4260             10
##  9 2018-03-06 00:00:00 Ibuprofen            390             10
## 10 2018-03-06 00:00:00 Meprobam~             68             67
## # ... with 228 more rows, and 7 more variables: PostChlorination <dbl>,
## #   Biodeg <chr>, Sorption <chr>, ClOxidation <chr>, Units <chr>,
## #   PctRmvFilter <dbl>, PctRmvChlorination <dbl>
```

Visualize boxplots of percent removal for DBF

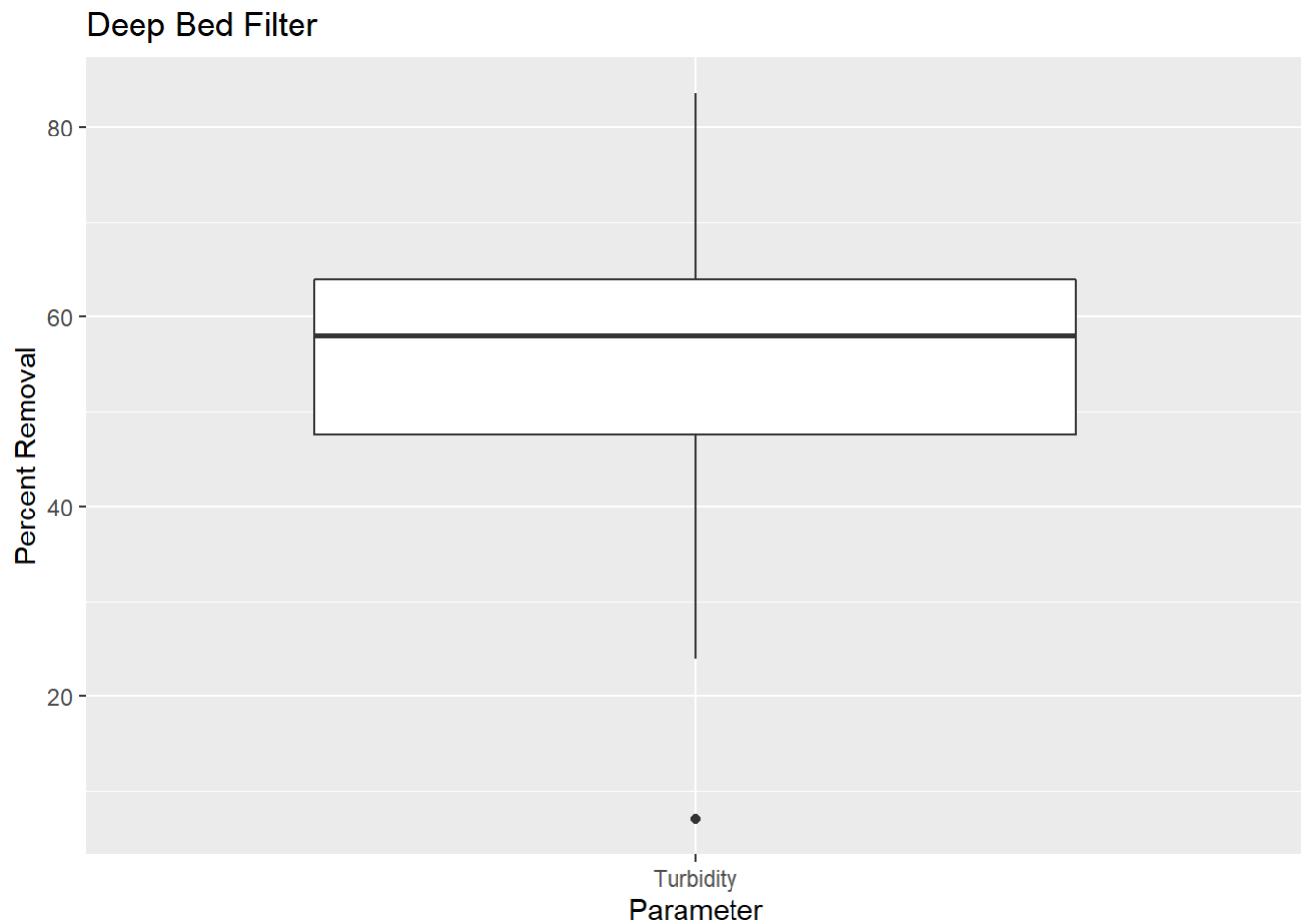# Giardia and Cryptosporidium

```
ggplot(data = filter(dbf.df, Parameter %in% c("Giardia", "Cryptosporidium")),
                aes(x=Parameter, y=PctRmvFilter)) +
   geom_boxplot() +
   ggtitle("Deep Bed Filter") +
   ylab("Percent Removal")
```
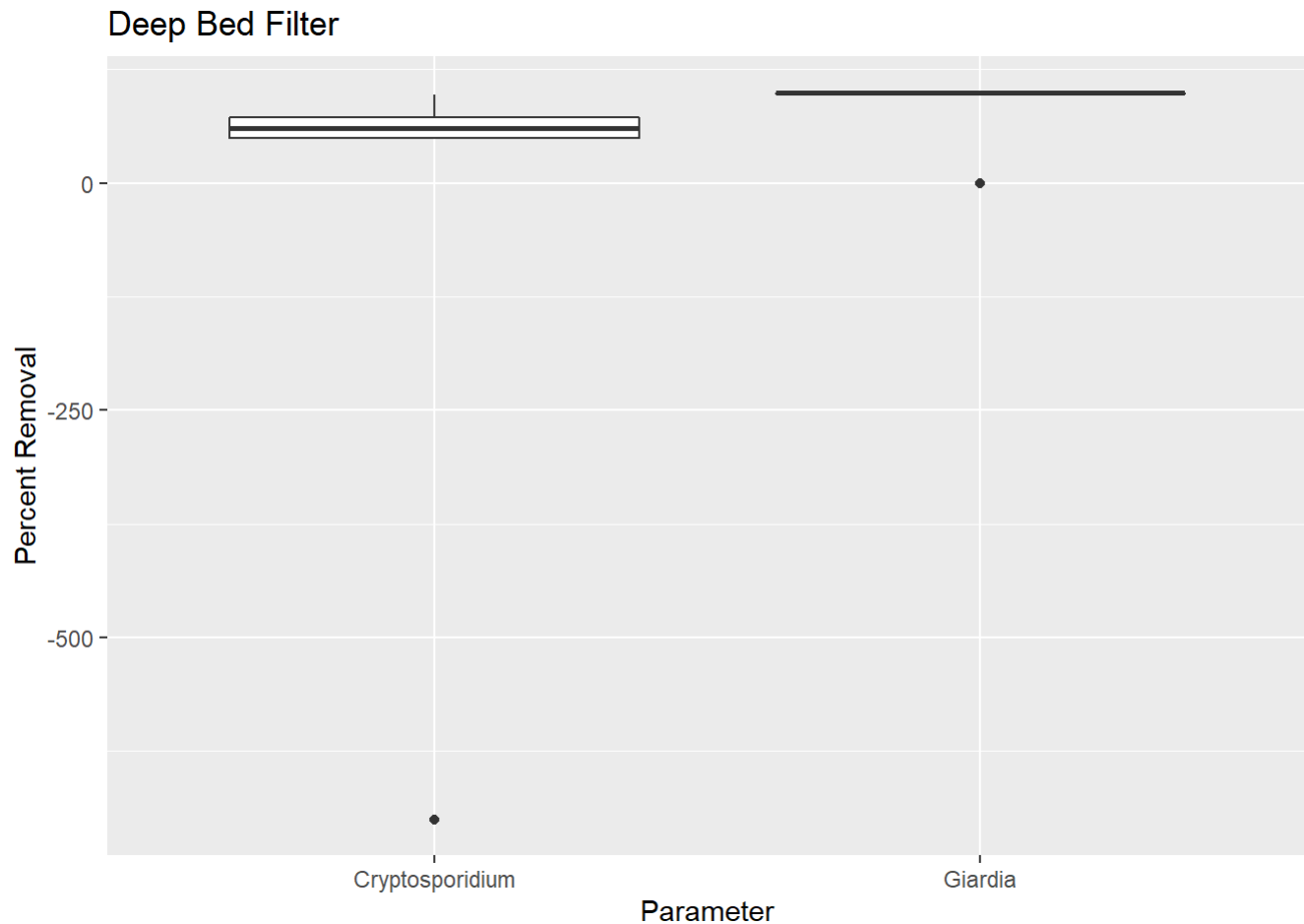
Deep Bed Filter
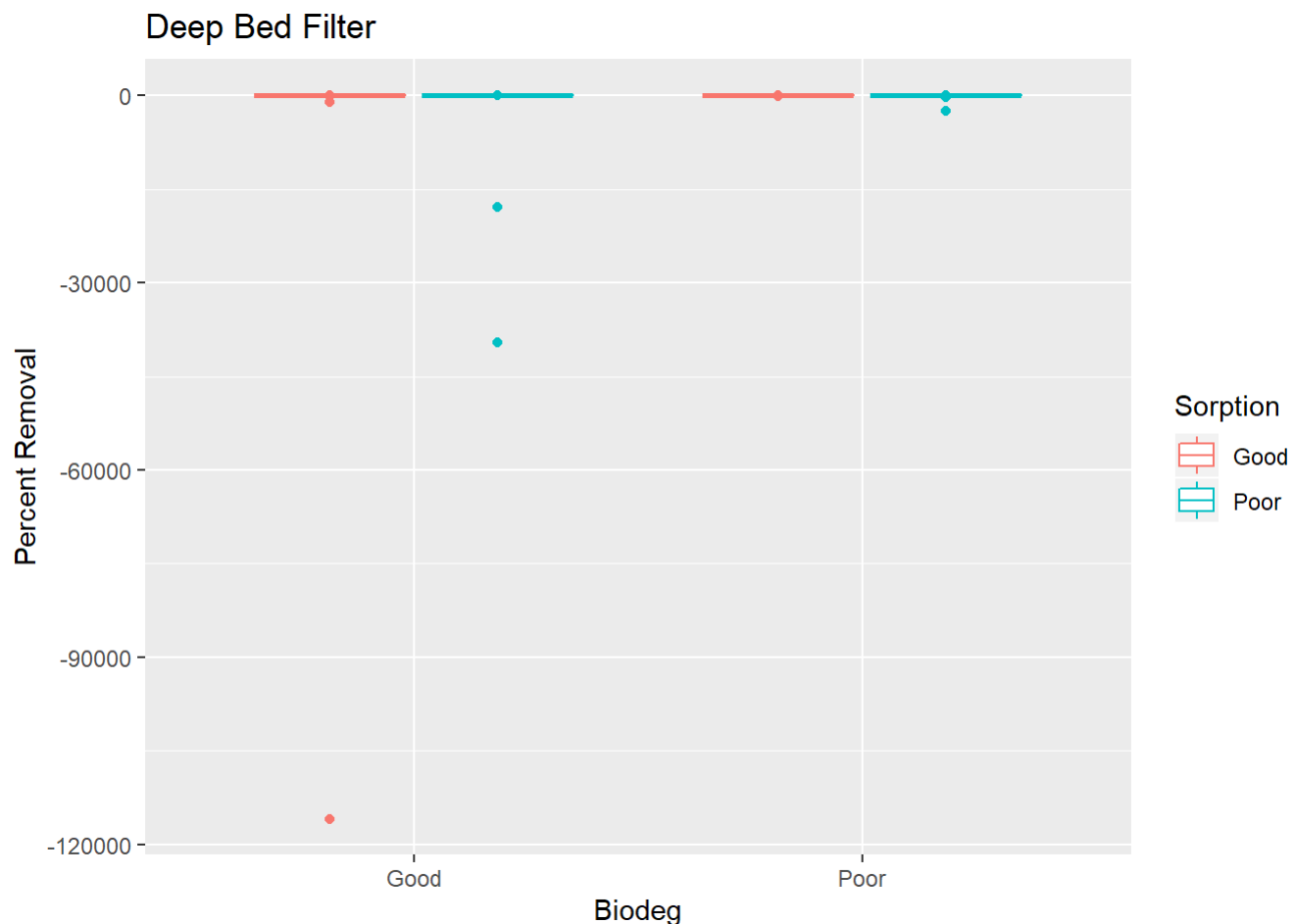

Turbidity

```
ggplot(data = filter(dbf.df, Parameter == "Turbidity"),
        aes(x=Parameter, y=PctRmvFilter)) +
   geom_boxplot() +
   ggtitle("Deep Bed Filter") +
   ylab("Percent Removal")
```

```
## Warning: Removed 1 rows containing non-finite values (stat_boxplot).
```

Deep Bed Filter

Contaminants of emerging concern (CEC)

```
ggplot(data = filter(dbf.df, !(Parameter %in% c("Giardia", "Cryptosporidium", "Turbidity"))),
       aes(x=Biodeg, y=PctRmvFilter, color=Sorption)) +
  geom_boxplot() +
  ggtitle("Deep Bed Filter") +
  ylab("Percent Removal")
```
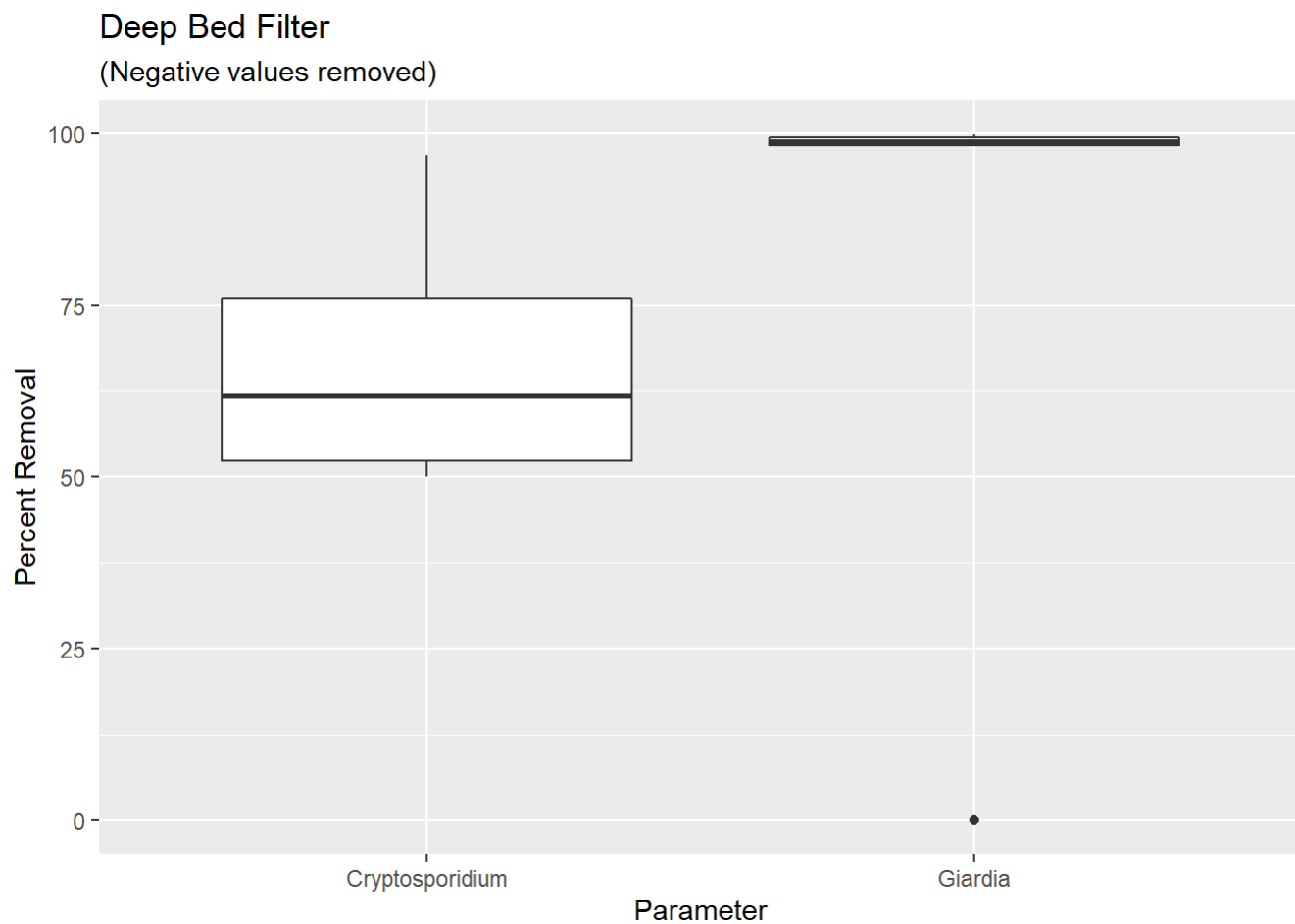
Deep Bed Filter

Visualize filter removal data without negative outliers

```
nonneg.filt <- filter(dbf.df, PctRmvFilter >= 0)
```

Giardia and Cryptosporidium

```
ggplot(data = filter(nonneg.filt, Parameter %in% c("Giardia", "Cryptosporidium")),
       aes(x=Parameter, y=PctRmvFilter)) +
  geom_boxplot() +
  ggtitle("Deep Bed Filter", "(Negative values removed)") +
  ylab("Percent Removal")
```

Deep Bed Filter

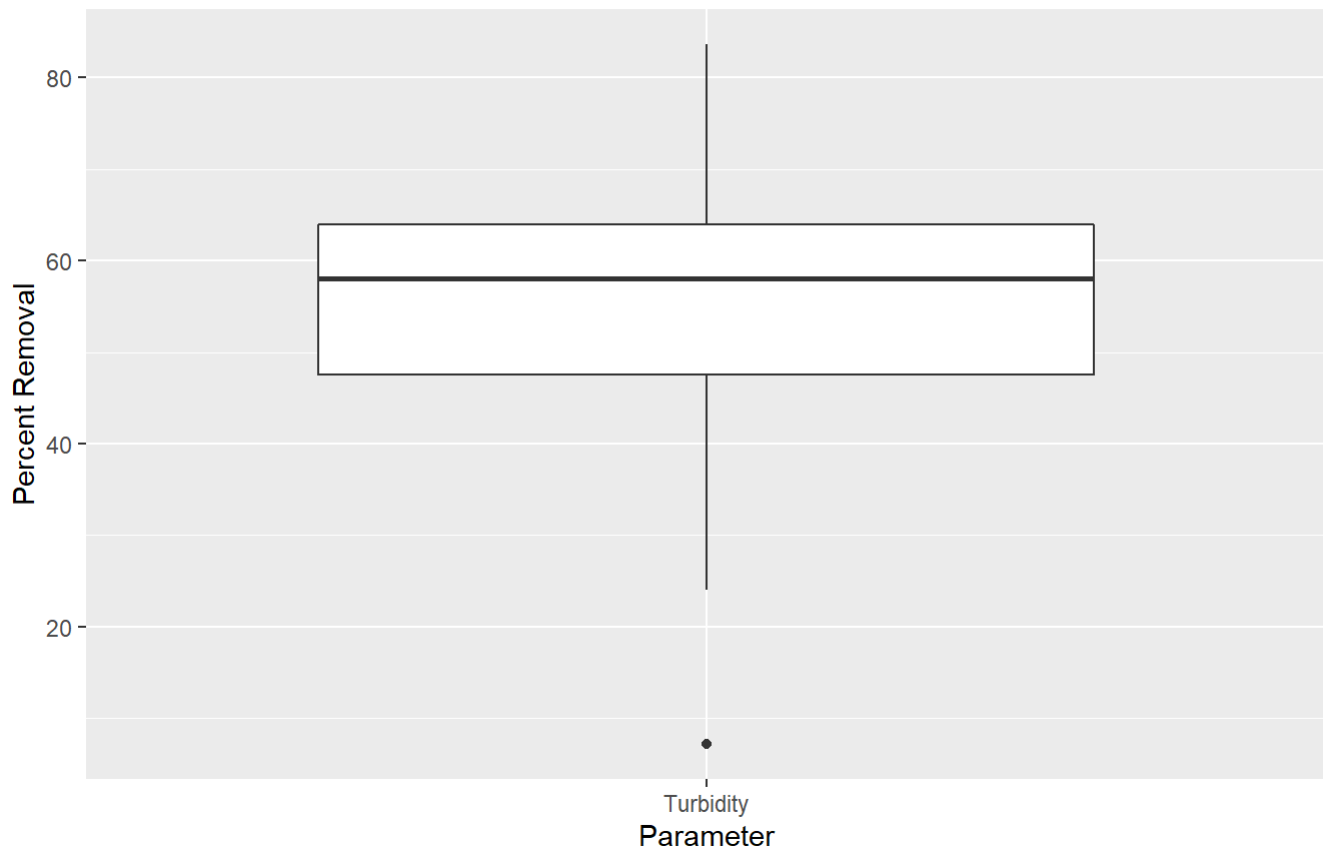(Negative values removed)

Turbidity

```
ggplot(data = filter(nonneg.filt, Parameter == "Turbidity"),
                aes(x=Parameter, y=PctRmvFilter)) +
  geom_boxplot() +
  ggtitle("Deep Bed Filter", "(Negative values removed)") +
  ylab("Percent Removal")
```
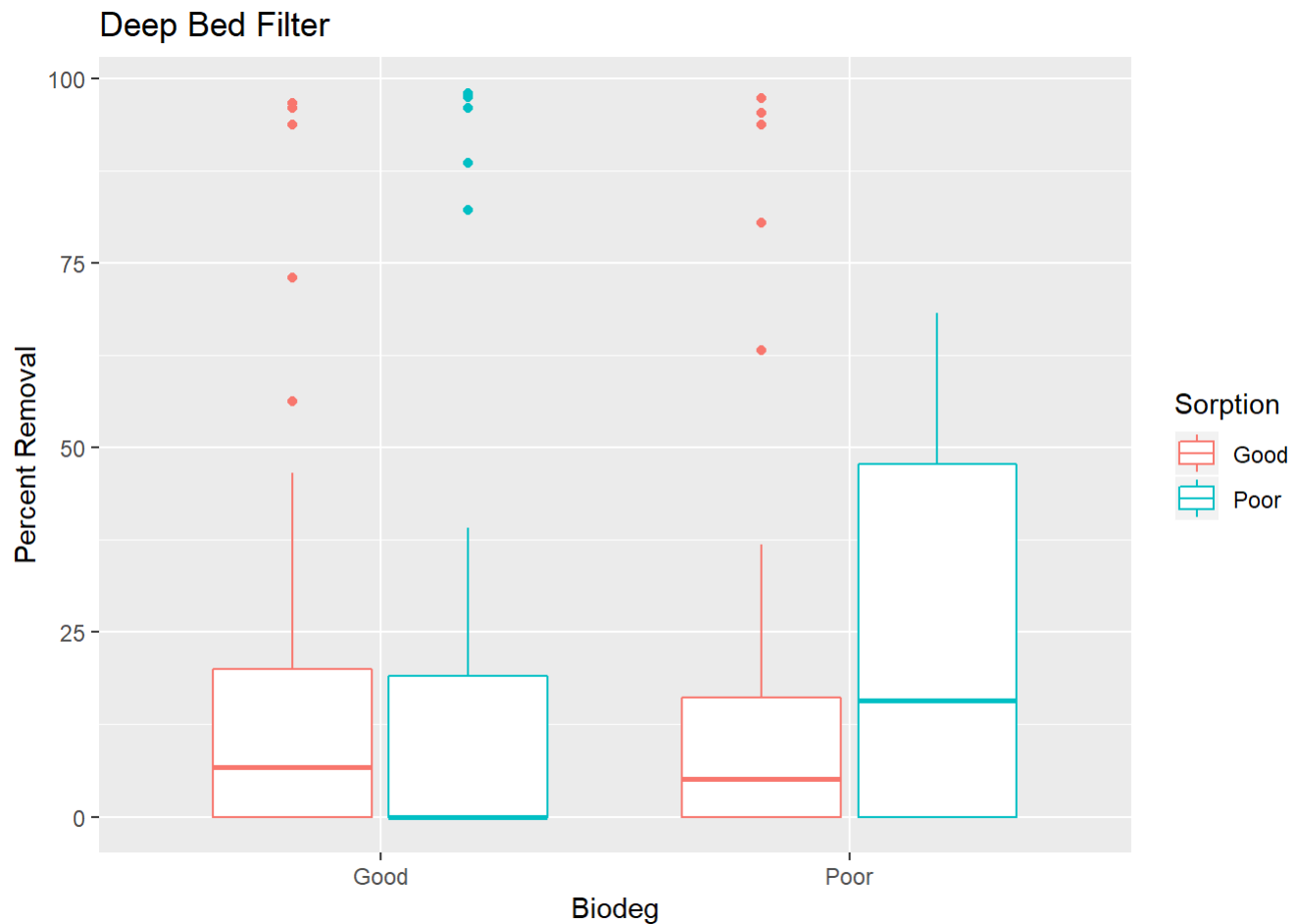
Deep Bed Filter
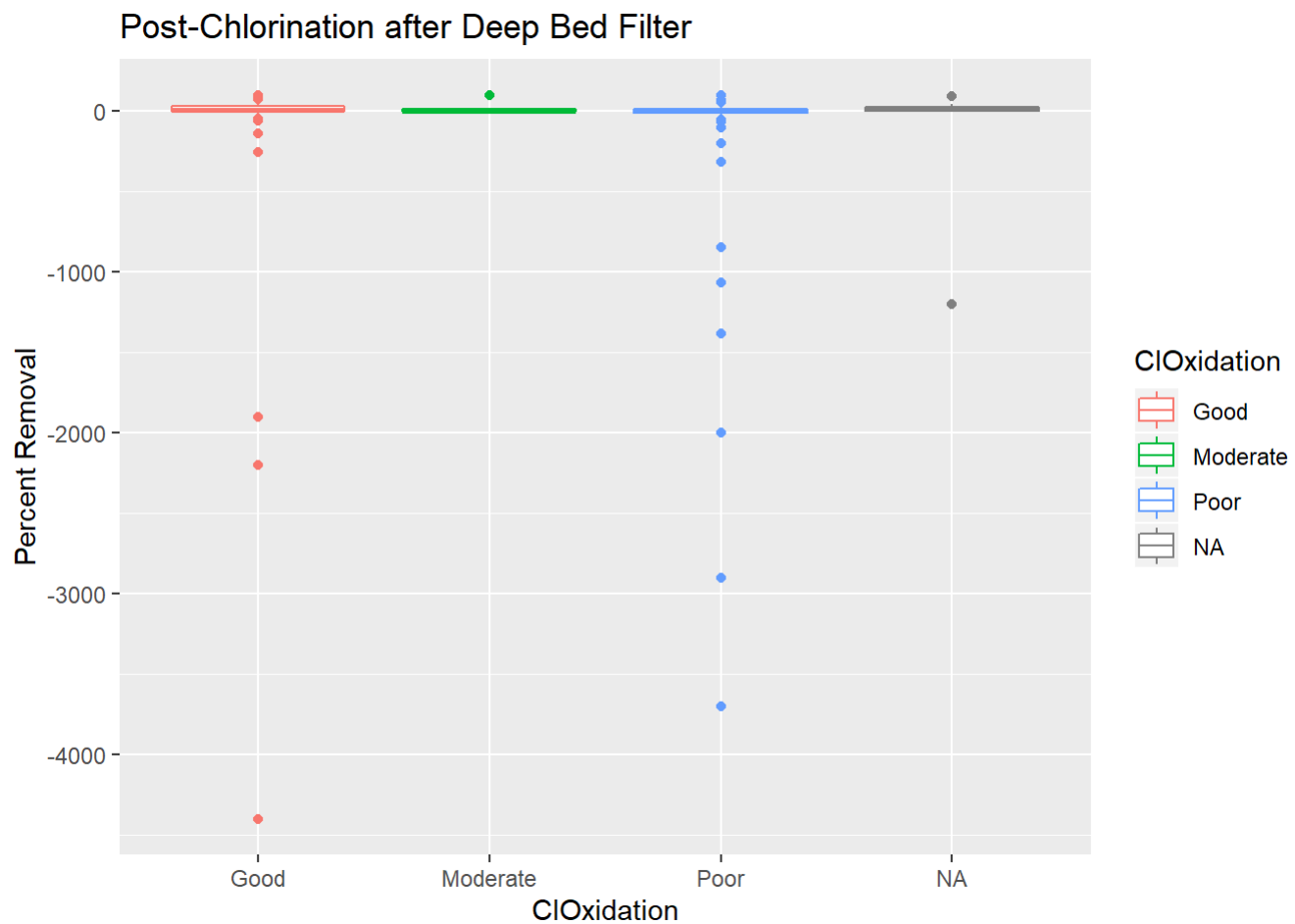(Negative values removed)

Contaminants of emerging concern (CEC)

```
ggplot(data = filter(nonneg.filt, !(Parameter %in% c("Giardia", "Cryptosporidium", "Turbidity"
))),
       aes(x=Biodeg, y=PctRmvFilter, color=Sorption)) +
  geom_boxplot() +
  ggtitle("Deep Bed Filter") +
  ylab("Percent Removal")
```

Deep Bed Filter

Visualize boxplots of percent removal for chlorination

```
## plot by chlorine oxidation category
ggplot(data = filter(dbf.df, !(Parameter %in% c("Giardia", "Cryptosporidium", "Turbidity"))),
       aes(x=ClOxidation, y=PctRmvChlorination, color=ClOxidation)) +
  geom_boxplot() +
  ggtitle("Post-Chlorination after Deep Bed Filter") +
  ylab("Percent Removal")
```

Post-Chlorination after Deep Bed Filter


```
## plot by chlorine oxidation category for only nonnegative values
nonneg.clox <- filter(dbf.df, PctRmvChlorination >= 0)
ggplot(data = filter(nonneg.clox, !(Parameter %in% c("Giardia", "Cryptosporidium", "Turbidity"
))),
       aes(x=ClOxidation, y=PctRmvChlorination, color=ClOxidation)) +
  geom_boxplot() +
  ggtitle("Post-Chlorination after Deep Bed Filter", "(Negative values removed)") +
  ylab("Percent Removal")
```

Post-Chlorination after Deep Bed Filter
(Negative values removed)