

# Does ZVI lower microbial diversity?

*TBD*

*2018-01-24*

## 1 Objective

Determine if ZVI filtration lowers microbial diversity.

## 2 Approach

- 16S Alpha diversity analysis - compare the diversity between ZVI filtered and reclaimed water. Test for differences using appropriate paired two sample test (may need to account for temporal sampling)
- Total abundance - if E. coli dominant, use E. coli MPN as abundance measurement

## 3 Results

### 3.0.1 Alpha Diversity Analysis

```
ggplot(rw_v_zw) +  
  geom_pointrange(aes(x = Sample_Code, y = est,  
                      ymin = lower, ymax = upper)) +  
  scale_y_log10() +  
  theme_bw() + facet_wrap(~Collection_Date) +  
  labs(y = "Richness Estimate", x = "Sample Type")
```

### 3.0.2 Alpha Diversity Significance Test

```
sample_code <- rw_v_zw$Sample_Code  
  
design_mat <- model.matrix(~ sample_code + 1)  
  
colnames(design_mat) <- colnames(design_mat) %>% str_replace("sample_code", "")  
rw_v_zw_betta <- betta_random(chats = rw_v_zw$est, ses = rw_v_zw$seest,  
                             X = design_mat, groups = rw_v_zw$Collection_Date)  
rw_rich <- rw_v_zw_betta$table[1,1] %>% round(0)  
rw_se <- rw_v_zw_betta$table[1,2] %>% round(0)  
zw_rich <- rw_rich + rw_v_zw_betta$table[2,1] %>% round(0)  
zw_se <- rw_v_zw_betta$table[2,2] %>% round(0)  
p_val <- rw_v_zw_betta$table[2,3]  
rw_v_zw_betta$table
```

##	Estimates	Standard Errors	p-values
## (Intercept)	761.5960	111.5134	0.000
## ZW	-190.7677	152.9253	0.212

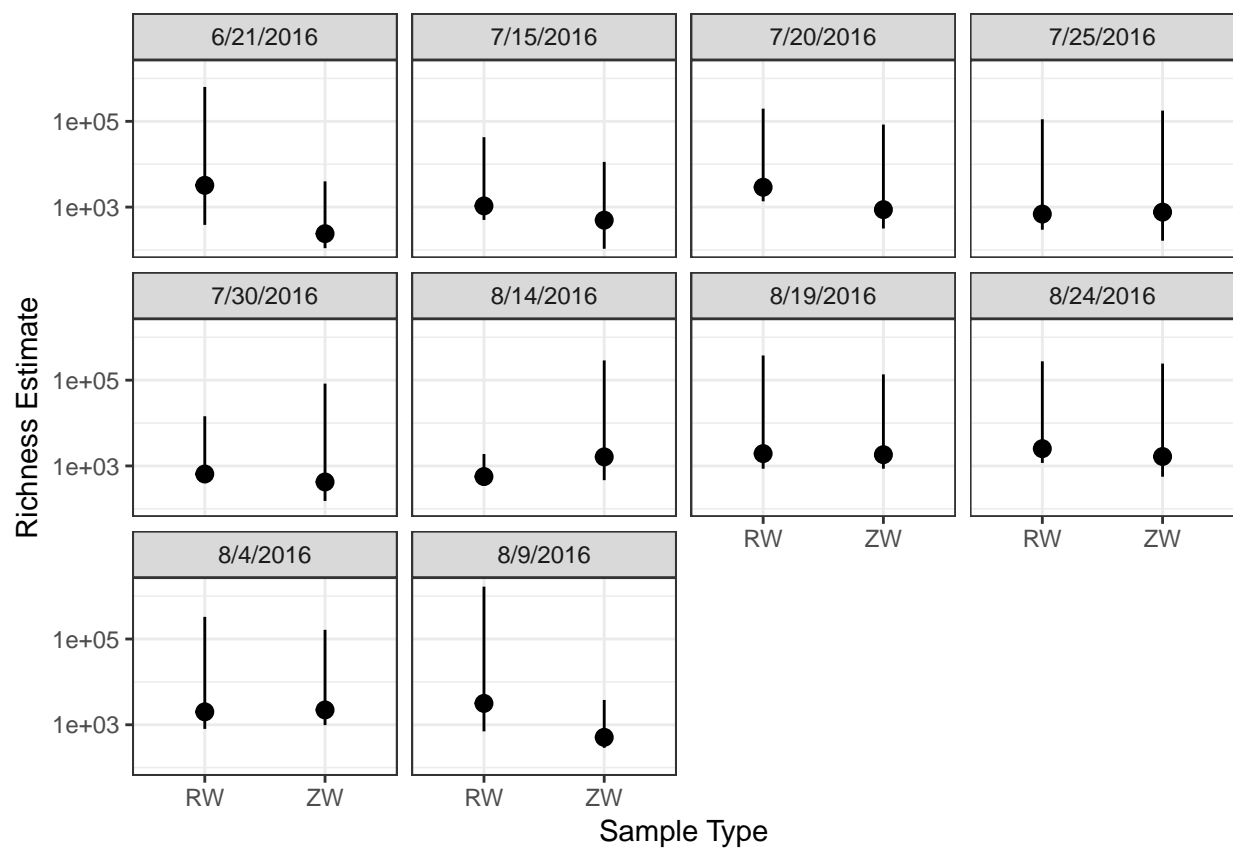


Figure 1: Comparison of richness estimates between samples collected before and after ZVI filtration, RW and ZW sample types respectively.

## 4 Summary

Using breakaway betta model to test for differences in richness in samples collected before and after ZVI filtration. The `betta_random` model with collection date as a random effects to account for paired samples. While richness decreased after ZVI filtration (RW -  $762 \pm 112$ , ZW -  $571 \pm 153$  ), the change in richness was not statistically significant,  $p = 0.212$ .

## 5 Session information

### 5.1 Git repo commit information

```
repo <- repository(path = "../")
last_commit <- commits(repo)[[1]]
```

The current git commit of this file is 26a4191af8ece3261c241445f9a5fbbad16e16fc, which is on the master branch and was made by Nate Olson on 2018-01-12 13:36:17. The current commit message is added beta div example code. The repository is online at <https://github.com/nate-d-olson/mgtst-pub>

### 5.2 Platform Information

```
s_info <- devtools::session_info()
print(s_info$platform)

## setting value
## version R version 3.4.3 (2017-11-30)
## system x86_64, darwin16.7.0
## ui unknown
## language (EN)
## collate en_US.UTF-8
## tz America/New_York
## date 2018-01-24
```

### 5.3 Package Versions

```
s_info$packages %>% filter(`*` == "*") %>% select(-`*`) %>%
  knitr::kable()
```

package	version	date	source
base	3.4.3	2017-11-30	local
bindrepp	0.2	2017-06-17	CRAN (R 3.4.0)
breakaway	3.0	2016-03-30	CRAN (R 3.4.2)
datasets	3.4.3	2017-11-30	local
devtools	1.13.4	2017-11-09	CRAN (R 3.4.3)
dplyr	0.7.4	2017-09-28	CRAN (R 3.4.2)
forcats	0.2.0	2017-01-23	CRAN (R 3.4.0)
ggplot2	2.2.1	2016-12-30	CRAN (R 3.4.0)
git2r	0.21.0	2018-01-04	CRAN (R 3.4.3)
graphics	3.4.3	2017-11-30	local
grDevices	3.4.3	2017-11-30	local
knitr	1.18	2017-12-27	cran (@1.18)
methods	3.4.3	2017-11-30	local
purrr	0.2.4	2017-10-18	CRAN (R 3.4.3)
readr	1.1.1	2017-05-16	CRAN (R 3.4.0)
stats	3.4.3	2017-11-30	local
stringr	1.2.0	2017-02-18	CRAN (R 3.4.0)
tibble	1.4.1	2017-12-25	CRAN (R 3.4.3)
tidyr	0.7.2	2017-10-16	CRAN (R 3.4.2)
tidyverse	1.2.1	2017-11-14	CRAN (R 3.4.3)
utils	3.4.3	2017-11-30	local