GST酶活

Dependencies

```
library(ggplot2)
library(tidyverse)
```

Load data

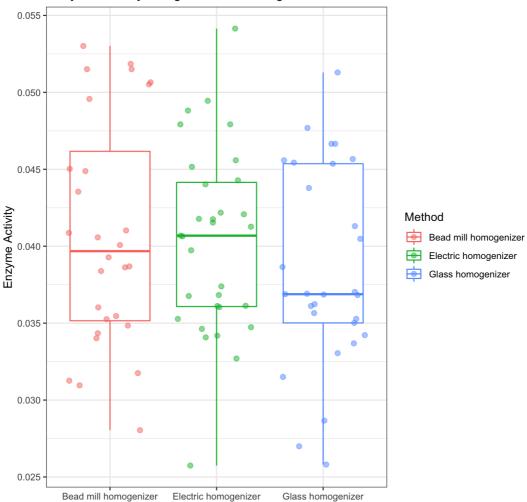
```
enzyme_activity_data <- read.csv("./result-Total.csv")
DT::datatable(enzyme_activity_data)
```

```
homogenizer <- enzyme_activity_data %>% filter(Method_Group == 0
)
DT::datatable(homogenizer)
```

```
pH <- enzyme_activity_data %>% filter(Method_Group == 1
)
DT::datatable(pH)
```

Plot and ANOVA

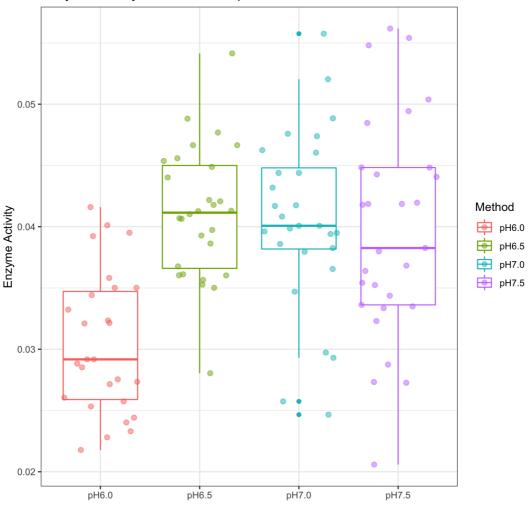
Enzyme activity using different homogenizer method



summary(aov(Enzyme_Activity_avg ~ Method, data = homogenizer))

```
Df Sum Sq Mean Sq F value Pr(>F)
Method 2 0.000086 4.321e-05 0.985 0.378
Residuals 85 0.003729 4.387e-05
```

Enzyme activity under different pH



```
summary(aov(Enzyme_Activity_avg ~ Method, data = pH))
```

```
Df Sum Sq Mean Sq F value Pr(>F)

Method 3 0.002077 0.0006923 14.28 6.69e-08 ***

Residuals 108 0.005238 0.0000485
---

Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
```

Using the normalized data

```
ggplot(homogenizer, aes(x = Method, y = Enzyme_Activity_avg_norm, color = Method))

# geom_boxplot()

# geom_jitter(size = 2, alpha = 0.5)

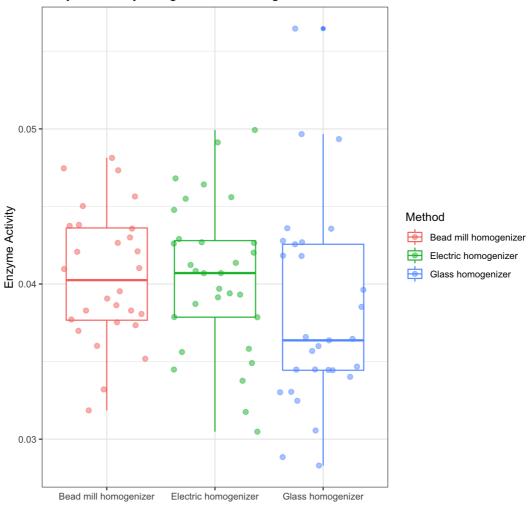
# labs(x = "", y = "Enzyme Activity", title = "Enzyme activity using different homogenizer normalize"

# theme_bw()

# theme

( axis.title.x = element_text(angle = -25, vjust = 0.5)
)
```

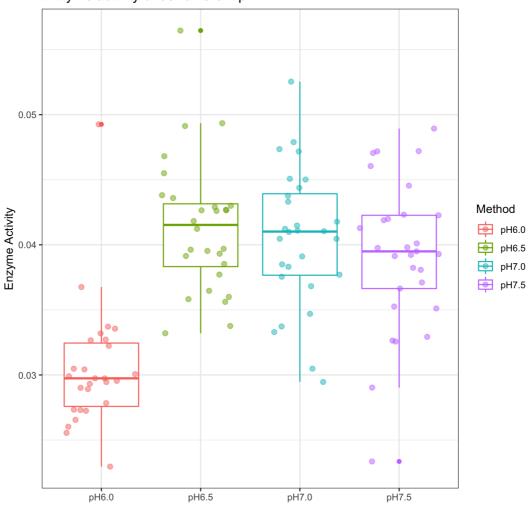
Enzyme activity using different homogenizer normalized



```
summary(aov(Enzyme_Activity_avg_norm ~ Method, data = homogenizer))
```

```
Df Sum Sq Mean Sq F value Pr(>F)
Method 2 0.0001064 5.321e-05 1.929 0.152
Residuals 85 0.0023449 2.759e-05
```

Enzyme activity under different pH



summary(aov(Enzyme_Activity_avg_norm ~ Method, data = pH))

```
Df Sum Sq Mean Sq F value Pr(>F)

Method 3 0.002093 0.0006978 25.22 1.92e-12 ***

Residuals 108 0.002988 0.0000277

---

Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
```