

Sri Lankan Water Project

Deformities_Replication_1

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```
library(tidyverse)
```

```
## -- Attaching packages ----- tidyverse 1.3.0 --
```

```
## v ggplot2 3.3.3    v purrr  0.3.4
## v tibble  3.0.5    v dplyr  1.0.3
## v tidyr   1.1.2    v stringr 1.4.0
## v readr   1.4.0    v forcats 0.5.0
```

```
## -- Conflicts ----- tidyverse_conflicts() --
```

```
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(broom)
```

```
Deformities_ForR_Replication_1 <- subset(Deformities_ForR_Replication_1, `Total Number` != 0)
```

```
Deformities_ForR_Replication_1 %>%
  mutate(Deformities_ForR_Replication_1,
    deformed = `Total Number` - `Number Normal`,
    percentage_deformed = deformed / `Total Number`) %>%
  ggplot(aes(x = Glyphosate, y = percentage_deformed)) +
  geom_point() +
  geom_smooth(method=lm, se=TRUE) +
  labs(x = "Glyphosate concentration", y = "Percentage Deformed")
```

```
Deformities_ForR_Replication_1_New <- Deformities_ForR_Replication_1 %>%
```

```
  mutate(Deformities_ForR_Replication_1,
    deformed = `Total Number` - `Number Normal`,
    percentage_deformed = deformed / `Total Number`)
```

```
model_replicate_1_deformities <- lm(percentage_deformed ~ Glyphosate, data = Deformities_ForR_Replication_1_New)
tidy(model_replicate_1_deformities)
```

$$\widehat{Replicate1Deformities} = 0.956 + 0.00360 \text{ Glyphosate}$$

```

Deformities_ForR_Replication_1_New %>%
  group_by(`Sample Type`) %>%
  summarize(mean_percentage_deformed = mean(percentage_deformed), sd = sd(percentage_deformed)) %>%
  ggplot(aes(x = `Sample Type`, y = mean_percentage_deformed)) +
  geom_bar(stat = "identity") +
  geom_errorbar(aes(ymin=mean_percentage_deformed - sd, ymax=mean_percentage_deformed + sd))

```

```

Deformities_ForR_Replication_1_New %>%
  group_by(`Sample Type`) %>%
  summarize(mean_percentage_deformed = mean(percentage_deformed), sd = sd(percentage_deformed)) %>%
  ggplot(aes(x = `Sample Type`, y = mean_percentage_deformed)) +
  geom_violin()
#doesn't work as data points insufficient (https://stackoverflow.com/questions/60549030/geom-violin-using)

```

```

ggplot(data = Deformities_ForR_Replication_1_New, mapping = aes(x = Glyphosate, y = percentage_deformed)) +
  geom_point() +
  facet_wrap(~ `Sample ID`)

```