Sri Lankan Water Project

Survival wrt Replication 1

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May 25, 2022

```
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)
```

```
Fish_Data_ForR_Excel_Modified_Replicate1 <- subset(Fish_Data_ForR_Excel_Modified_Replicate1,`48_surv`!=
```

```
Fish_Data_ForR_Excel_Modified_Replicate1 %>%
  mutate(Fish_Data_ForR_Excel_Modified_Replicate1, percentagesurvival = `96_surv` / Initial_total) %>%
  ggplot(aes(x = Glyphosate, y = percentagesurvival)) +
  geom_point() +
  geom_smooth(method=lm, se=FALSE) +
  labs (x = "Glyphosate concentration", y = "Percentage Survival")
```

```
Fish_Data_ForR_Excel_Modified_Replicate2 <- Fish_Data_ForR_Excel_Modified_Replicate1 %>%
  mutate(percentagesurvival = `96_surv` / Initial_total)
model_replicate_1_survival <- lm(percentagesurvival ~ Glyphosate, data = Fish_Data_ForR_Excel_Modified_
tidy(model_replicate_1_survival)
```

$$\widehat{Replicate1Survival} = 0.969 - 0.00647\ Glyphosate$$

```
Fish_Data_ForR_Excel_Modified_Replicate1 %>%
  group_by(`Sample Type`) %>%
  summarize(mean_percentage_survival = mean(percentagesurvival), sd = sd(percentagesurvival)) %>%
  ggplot(aes(x = `Sample Type`, y = mean_percentage_survival)) +
  geom_bar(stat = "identity") +
  geom_errorbar(aes(ymin=mean_percentage_survival-sd, ymax=mean_percentage_survival+sd))
```