

# Biehler et al

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## load libraries

```
library(ggplot2)
library(dplyr)
library(betareg)
library(emmeans)
```

## Import CSV

```
data <- read.csv("../datafiles/BiehlerDataBKA.csv", header = TRUE, sep = ",")

# Convert 'Sex', 'Month', 'Year', and 'Species' to factors
data$Sex <- factor(data$Sex)
data$Species <- factor(data$Species)
data$Year <- factor(data$Year)
data$Month <- factor(data$Month)
```

## Mean and Standard Deviation for BKA

```
# Calculate mean and SD for each species
summary_stats <- data %>%
  group_by(Species) %>%
  summarise(
    Mean = mean(Bacterial_Killing_Percentage, na.rm = TRUE),
    SD = sd(Bacterial_Killing_Percentage, na.rm = TRUE)
  )

# Print the summary statistics
print(summary_stats)
```

```
## # A tibble: 4 x 3
##   Species Mean  SD
##   <fct>   <dbl> <dbl>
## 1 AMGO    26.3  4.76
```

```
## 2 HOFI      60.1  5.56
## 3 LEGO      27.6  6.12
## 4 PISI      33.4  7.38
```

## Transformation of data

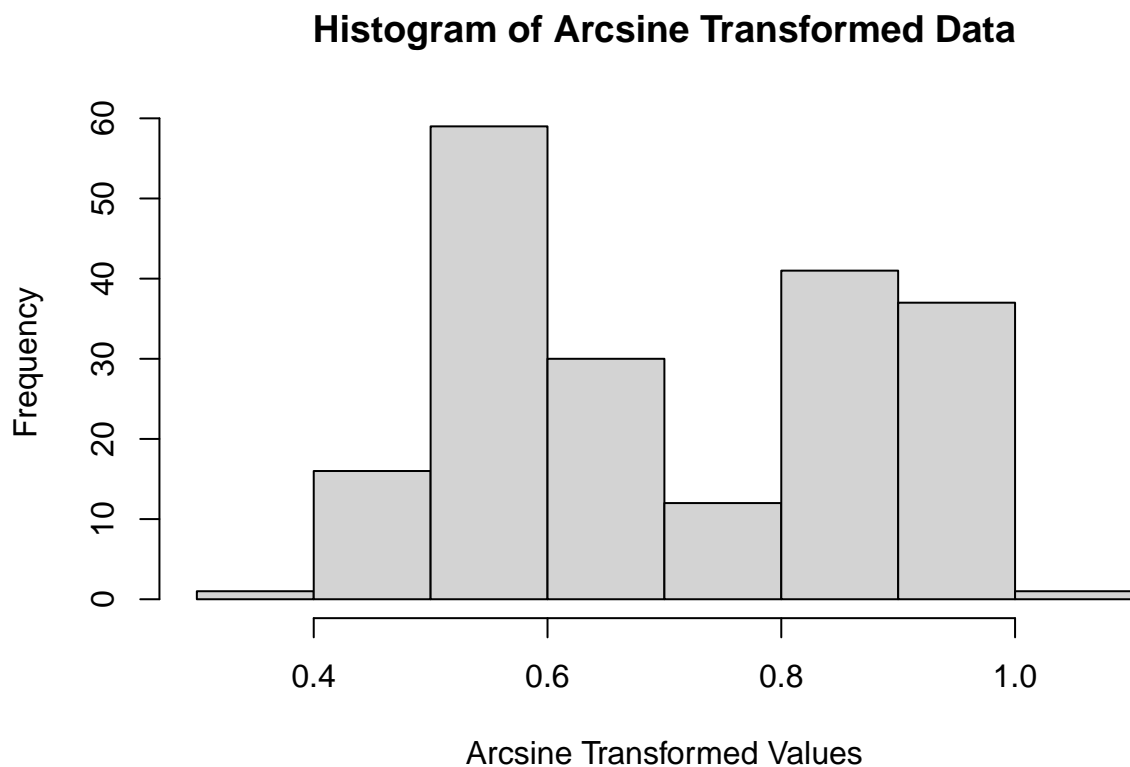
```
# Convert percentage to proportion
data$Bacterial_Killing_Proportion <- data$Bacterial_Killing_Percentage / 100

# Apply arcsine square root transformation
data$Bacterial_Killing_Arcsine <- asin(sqrt(data$Bacterial_Killing_Proportion))

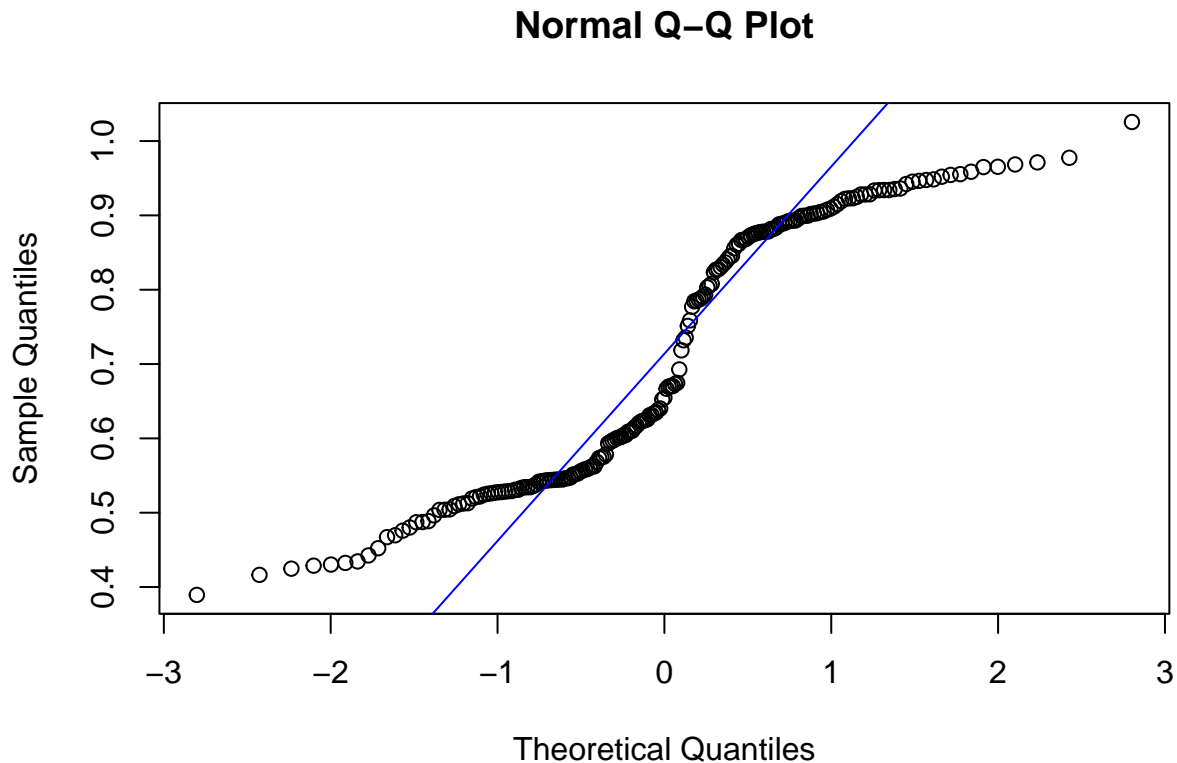
# Shapiro-Wilk test for normality
shapiro.test(data$Bacterial_Killing_Arcsine)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  data$Bacterial_Killing_Arcsine
## W = 0.89719, p-value = 2.093e-10
```

```
# Visual inspection with histogram and Q-Q plot
hist(data$Bacterial_Killing_Arcsine, main="Histogram of Arcsine Transformed Data", xlab="Arcsine Transf
```



```
qqnorm(data$Bacterial_Killing_Arcsine)
qqline(data$Bacterial_Killing_Arcsine, col="blue")
```



Beta regression as data are not normally distributed after arcsin transformation

```
# Fit a beta regression model for the proportion data
beta_bka_species <- betareg(Bacterial_Killing_Proportion ~ Species, data = data)

# View the summary of the model
summary(beta_bka_species)
```

```
##
## Call:
## betareg(formula = Bacterial_Killing_Proportion ~ Species, data = data)
##
## Quantile residuals:
##      Min       1Q   Median       3Q      Max
## -3.1051 -0.4407  0.0222  0.6436  2.8471
##
## Coefficients (mean model with logit link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.02429    0.05124 -19.989  < 2e-16 ***
## SpeciesHOFI  1.43335    0.05803  24.701  < 2e-16 ***
## SpeciesLEGO  0.05717    0.06338   0.902   0.367
## SpeciesPISI  0.32771    0.07343   4.463 8.09e-06 ***
```

```
##
## Phi coefficients (precision model with identity link):
##      Estimate Std. Error z value Pr(>|z|)
## (phi)   63.794      6.383   9.994   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Type of estimator: ML (maximum likelihood)
## Log-likelihood: 281.8 on 5 Df
## Pseudo R-squared: 0.8618
## Number of iterations: 12 (BFGS) + 2 (Fisher scoring)
```

## Post Hoc Comparison

```
# Obtain estimated marginal means for Species from the beta regression model
emmeans_species <- emmeans(beta_bka_species, ~ Species)

# Perform pairwise comparisons between all species
pairwise_comparisons <- pairs(emmeans_species, adjust = "fdr")

# Print pairwise comparisons with more significant digits
print(pairwise_comparisons)
```

```
## contrast      estimate      SE df z.ratio p.value
## AMGO - HOFI  -0.3367 0.01190 Inf -28.268 <.0001
## AMGO - LEGO  -0.0113 0.01240 Inf  -0.906 0.3651
## AMGO - PISI  -0.0684 0.01530 Inf  -4.455 <.0001
## HOFI - LEGO   0.3254 0.00991 Inf  32.823 <.0001
## HOFI - PISI   0.2683 0.01340 Inf  20.046 <.0001
## LEGO - PISI  -0.0571 0.01390 Inf  -4.122 <.0001
##
## P value adjustment: fdr method for 6 tests
```

```
# Convert pairwise comparisons to a data frame
pairwise_results_df <- as.data.frame(pairwise_comparisons)

# View the results
pairwise_results_df
```

```
## contrast      estimate      SE df z.ratio p.value
## AMGO - HOFI -0.3366701 0.011910018 Inf -28.268 <.0001
## AMGO - LEGO -0.0112617 0.012435274 Inf  -0.906 0.3651
## AMGO - PISI -0.0683771 0.015347939 Inf  -4.455 <.0001
## HOFI - LEGO  0.3254084 0.009914167 Inf  32.823 <.0001
## HOFI - PISI  0.2682929 0.013383544 Inf  20.046 <.0001
## LEGO - PISI -0.0571154 0.013856993 Inf  -4.122 <.0001
##
## P value adjustment: fdr method for 6 tests
```

## Model Testing

```
# Fit a model with main effects only
main_effects_model <- betareg(Bacterial_Killing_Proportion ~ Species + Sex + Year + Season, data = data)
model_A <- betareg(Bacterial_Killing_Proportion ~ Species + Season, data = data)
model_B <- betareg(Bacterial_Killing_Proportion ~ Species + Year, data = data)
model_C <- betareg(Bacterial_Killing_Proportion ~ Species + Sex * Season + Year, data = data)
model_D <- betareg(Bacterial_Killing_Proportion ~ Species + Season + Year, data = data)
model_E <- betareg(Bacterial_Killing_Proportion ~ Species, data = data)
model_F <- betareg(Bacterial_Killing_Proportion ~ Species * Sex + Year, data = data)
model_G <- betareg(Bacterial_Killing_Proportion ~ Species * Sex + Season, data = data)
model_H <- betareg(Bacterial_Killing_Proportion ~ Species + Sex * Season, data = data)
model_I <- betareg(Bacterial_Killing_Proportion ~ Species + Sex * Year, data = data)
model_J <- betareg(Bacterial_Killing_Proportion ~ Sex, data = data)
model_K <- betareg(Bacterial_Killing_Proportion ~ Year, data = data)
model_L <- betareg(Bacterial_Killing_Proportion ~ Season, data = data)
# Example for comparing models using AIC
AIC(main_effects_model, model_A, model_B, model_C, model_D, model_E, model_F, model_G, model_H, model_I,
```

```
##           df      AIC
## main_effects_model  9 -559.8485
## model_A             6 -554.1383
## model_B             7 -561.7371
## model_C            10 -558.0144
## model_D             8 -563.4248
## model_E             5 -553.6223
## model_F            11 -553.1538
## model_G            10 -544.9225
## model_H             8 -548.4218
## model_I            10 -559.7015
## model_J             3 -160.8675
## model_K             4 -293.2483
## model_L             3 -431.9622
```

## Summarize AIC models

```
summary(main_effects_model)
```

```
##
## Call:
## betareg(formula = Bacterial_Killing_Proportion ~ Species + Sex + Year +
##   Season, data = data)
##
## Quantile residuals:
##      Min       1Q   Median       3Q      Max
## -3.1474 -0.5828  0.0807   0.6198  2.4004
##
## Coefficients (mean model with logit link):
##              Estimate Std. Error z value Pr(>|z|)
```

```
## (Intercept) -0.875709 0.167426 -5.230 1.69e-07 ***
## SpeciesHOFI 1.462259 0.141884 10.306 < 2e-16 ***
## SpeciesLEGO 0.026942 0.062362 0.432 0.665730
## SpeciesPISI 0.204804 0.096681 2.118 0.034146 *
## SexMale -0.003919 0.038914 -0.101 0.919787
## YearThree -0.402639 0.109250 -3.685 0.000228 ***
## YearTwo -0.197386 0.083270 -2.370 0.017767 *
## SeasonWinter 0.234765 0.119693 1.961 0.049833 *
##
## Phi coefficients (precision model with identity link):
## Estimate Std. Error z value Pr(>|z|)
## (phi) 69.654 6.992 9.963 <2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Type of estimator: ML (maximum likelihood)
## Log-likelihood: 288.9 on 9 Df
## Pseudo R-squared: 0.8735
## Number of iterations: 19 (BFGS) + 2 (Fisher scoring)
```

```
summary(model_A)
```

```
##
## Call:
## betareg(formula = Bacterial_Killing_Proportion ~ Species + Season, data = data)
##
## Quantile residuals:
##      Min       1Q   Median       3Q      Max
## -3.1252 -0.4436  0.0103  0.7090  2.8518
##
## Coefficients (mean model with logit link):
## Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.21270 0.13148 -9.223 < 2e-16 ***
## SpeciesHOFI 1.62184 0.13424 12.081 < 2e-16 ***
## SpeciesLEGO 0.06119 0.06302 0.971 0.332
## SpeciesPISI 0.36463 0.07654 4.764 1.9e-06 ***
## SeasonWinter 0.18816 0.12121 1.552 0.121
##
## Phi coefficients (precision model with identity link):
## Estimate Std. Error z value Pr(>|z|)
## (phi) 64.613 6.466 9.993 <2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Type of estimator: ML (maximum likelihood)
## Log-likelihood: 283.1 on 6 Df
## Pseudo R-squared: 0.8637
## Number of iterations: 14 (BFGS) + 2 (Fisher scoring)
```

```
summary(model_B)
```

```
##
## Call:
```

```
## betareg(formula = Bacterial_Killing_Proportion ~ Species + Year, data = data)
##
## Quantile residuals:
##      Min      1Q  Median      3Q      Max
## -3.1127 -0.5797  0.1057  0.6045  2.4373
##
## Coefficients (mean model with logit link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.65661    0.11679  -5.622 1.88e-08 ***
## SpeciesHOFI  1.24014    0.08568  14.475 < 2e-16 ***
## SpeciesLEGO  0.02367    0.06288   0.376 0.706652
## SpeciesPISI  0.15602    0.09572   1.630 0.103120
## YearThree   -0.38743    0.11050  -3.506 0.000455 ***
## YearTwo     -0.19670    0.08416  -2.337 0.019433 *
##
## Phi coefficients (precision model with identity link):
##              Estimate Std. Error z value Pr(>|z|)
## (phi)      67.847      6.792    9.99 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Type of estimator: ML (maximum likelihood)
## Log-likelihood: 287.9 on 7 Df
## Pseudo R-squared: 0.87
## Number of iterations: 30 (BFGS) + 2 (Fisher scoring)
```

```
summary(model_C)
```

```
##
## Call:
## betareg(formula = Bacterial_Killing_Proportion ~ Species + Sex * Season +
##      Year, data = data)
##
## Quantile residuals:
##      Min      1Q  Median      3Q      Max
## -3.1223 -0.5408  0.0716  0.6321  2.4411
##
## Coefficients (mean model with logit link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -0.85952    0.17189  -5.000 5.73e-07 ***
## SpeciesHOFI    1.45648    0.14253  10.219 < 2e-16 ***
## SpeciesLEGO    0.02439    0.06266   0.389 0.69710
## SpeciesPISI    0.20625    0.09669   2.133 0.03292 *
## SexMale       -0.01857    0.05287  -0.351 0.72543
## SeasonWinter   0.21278    0.13097   1.625 0.10423
## YearThree     -0.40792    0.11006  -3.706 0.00021 ***
## YearTwo       -0.19963    0.08339  -2.394 0.01667 *
## SexMale:SeasonWinter 0.03171    0.07812   0.406 0.68476
##
## Phi coefficients (precision model with identity link):
##              Estimate Std. Error z value Pr(>|z|)
## (phi)      69.712      6.997    9.963 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Type of estimator: ML (maximum likelihood)
## Log-likelihood: 289 on 10 Df
## Pseudo R-squared: 0.8737
## Number of iterations: 21 (BFGS) + 2 (Fisher scoring)
```

```
summary(model_D)
```

```
##
## Call:
## betareg(formula = Bacterial_Killing_Proportion ~ Species + Season + Year,
## data = data)
##
## Quantile residuals:
##      Min      1Q  Median      3Q      Max
## -3.1424 -0.5730  0.0783  0.6100  2.4041
##
## Coefficients (mean model with logit link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -0.86498    0.16128  -5.363 8.17e-08 ***
## SpeciesHOFI   1.44868    0.14081  10.288 < 2e-16 ***
## SpeciesLEGO   0.02618    0.06231   0.420 0.674391
## SpeciesPISI   0.18623    0.09633   1.933 0.053207 .
## SeasonWinter  0.22082    0.11749   1.879 0.060181 .
## YearThree    -0.40172    0.10963  -3.664 0.000248 ***
## YearTwo      -0.19676    0.08340  -2.359 0.018305 *
##
## Phi coefficients (precision model with identity link):
##              Estimate Std. Error z value Pr(>|z|)
## (phi)      69.129      6.921   9.988 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Type of estimator: ML (maximum likelihood)
## Log-likelihood: 289.7 on 8 Df
## Pseudo R-squared: 0.8726
## Number of iterations: 17 (BFGS) + 2 (Fisher scoring)
```

```
summary(model_E)
```

```
##
## Call:
## betareg(formula = Bacterial_Killing_Proportion ~ Species, data = data)
##
## Quantile residuals:
##      Min      1Q  Median      3Q      Max
## -3.1051 -0.4407  0.0222  0.6436  2.8471
##
## Coefficients (mean model with logit link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -1.02429    0.05124 -19.989 < 2e-16 ***
## SpeciesHOFI   1.43335    0.05803  24.701 < 2e-16 ***
## SpeciesLEGO   0.05717    0.06338   0.902  0.367
```



```
## SpeciesPISI 0.32771 0.07343 4.463 8.09e-06 ***
##
## Phi coefficients (precision model with identity link):
## Estimate Std. Error z value Pr(>|z|)
## (phi) 63.794 6.383 9.994 <2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Type of estimator: ML (maximum likelihood)
## Log-likelihood: 281.8 on 5 Df
## Pseudo R-squared: 0.8618
## Number of iterations: 12 (BFGS) + 2 (Fisher scoring)
```

```
summary(model_F)
```

```
##
## Call:
## betareg(formula = Bacterial_Killing_Proportion ~ Species * Sex + Year,
## data = data)
##
## Quantile residuals:
## Min 1Q Median 3Q Max
## -3.0994 -0.5729 0.0859 0.6276 2.4510
##
## Coefficients (mean model with logit link):
## Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.68474 0.13464 -5.086 3.66e-07 ***
## SpeciesHOFI 1.28157 0.11286 11.356 < 2e-16 ***
## SpeciesLEGO 0.05501 0.11377 0.484 0.628716
## SpeciesPISI 0.25900 0.12776 2.027 0.042637 *
## SexMale 0.04757 0.10285 0.463 0.643698
## YearThree -0.38956 0.11119 -3.504 0.000459 ***
## YearTwo -0.19958 0.08399 -2.376 0.017491 *
## SpeciesHOFI:SexMale -0.06613 0.11581 -0.571 0.567978
## SpeciesLEGO:SexMale -0.04899 0.13446 -0.364 0.715577
## SpeciesPISI:SexMale -0.16257 0.14585 -1.115 0.264994
##
## Phi coefficients (precision model with identity link):
## Estimate Std. Error z value Pr(>|z|)
## (phi) 68.704 6.896 9.964 <2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Type of estimator: ML (maximum likelihood)
## Log-likelihood: 287.6 on 11 Df
## Pseudo R-squared: 0.8716
## Number of iterations: 20 (BFGS) + 2 (Fisher scoring)
```

```
summary(model_G)
```

```
##
## Call:
## betareg(formula = Bacterial_Killing_Proportion ~ Species * Sex + Season,
```

```
##      data = data)
##
## Quantile residuals:
##      Min      1Q  Median      3Q      Max
## -3.1296 -0.4613 -0.0136  0.6618  2.7703
##
## Coefficients (mean model with logit link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -1.24004    0.16032  -7.735 1.03e-14 ***
## SpeciesHOFI      1.65268    0.16555   9.983 < 2e-16 ***
## SpeciesLEGO      0.12142    0.11318   1.073 0.283349
## SpeciesPISI      0.43296    0.11240   3.852 0.000117 ***
## SexMale          0.05221    0.10549   0.495 0.620659
## SeasonWinter     0.18228    0.13633   1.337 0.181233
## SpeciesHOFI:SexMale -0.05820    0.11869  -0.490 0.623872
## SpeciesLEGO:SexMale -0.08794    0.13650  -0.644 0.519415
## SpeciesPISI:SexMale -0.09276    0.15933  -0.582 0.560424
##
## Phi coefficients (precision model with identity link):
##              Estimate Std. Error z value Pr(>|z|)
## (phi)    65.202      6.542   9.967  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Type of estimator: ML (maximum likelihood)
## Log-likelihood: 282.5 on 10 Df
## Pseudo R-squared: 0.865
## Number of iterations: 20 (BFGS) + 2 (Fisher scoring)
```

```
summary(model_H)
```

```
##
## Call:
## betareg(formula = Bacterial_Killing_Proportion ~ Species + Sex * Season,
##      data = data)
##
## Quantile residuals:
##      Min      1Q  Median      3Q      Max
## -3.1255 -0.4416 -0.0106  0.6987  2.8353
##
## Coefficients (mean model with logit link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -1.221321    0.142792  -8.553 < 2e-16 ***
## SpeciesHOFI      1.633948    0.136703  11.953 < 2e-16 ***
## SpeciesLEGO      0.062733    0.063220   0.992  0.321
## SpeciesPISI      0.381892    0.078644   4.856 1.2e-06 ***
## SexMale          -0.005991    0.054458  -0.110  0.912
## SeasonWinter     0.202624    0.135407   1.496  0.135
## SexMale:SeasonWinter -0.003522    0.080115  -0.044  0.965
##
## Phi coefficients (precision model with identity link):
##              Estimate Std. Error z value Pr(>|z|)
## (phi)    65.035      6.525   9.967  <2e-16 ***
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Type of estimator: ML (maximum likelihood)
## Log-likelihood: 282.2 on 8 Df
## Pseudo R-squared: 0.8646
## Number of iterations: 16 (BFGS) + 2 (Fisher scoring)
```

```
summary(model_I)
```

```
##
## Call:
## betareg(formula = Bacterial_Killing_Proportion ~ Species + Sex * Year,
##   data = data)
##
## Quantile residuals:
##      Min       1Q   Median       3Q      Max
## -3.0593 -0.5194  0.0603  0.5828  2.3826
##
## Coefficients (mean model with logit link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -0.744026   0.164117  -4.534  5.8e-06 ***
## SpeciesHOFI    1.219247   0.084854  14.369 < 2e-16 ***
## SpeciesLEGO    0.004104   0.063085   0.065  0.9481
## SpeciesPISI    0.144567   0.095270   1.517  0.1292
## SexMale        0.155158   0.168951   0.918  0.3584
## YearThree     -0.376571   0.171093  -2.201  0.0277 *
## YearTwo       -0.043684   0.145399  -0.300  0.7638
## SexMale:YearThree -0.037773  0.186023  -0.203  0.8391
## SexMale:YearTwo -0.234566  0.174926  -1.341  0.1799
##
## Phi coefficients (precision model with identity link):
##              Estimate Std. Error z value Pr(>|z|)
## (phi)    70.316      7.058   9.962 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Type of estimator: ML (maximum likelihood)
## Log-likelihood: 289.9 on 10 Df
## Pseudo R-squared: 0.8748
## Number of iterations: 20 (BFGS) + 2 (Fisher scoring)
```

```
summary(model_J)
```

```
##
## Call:
## betareg(formula = Bacterial_Killing_Proportion ~ Sex, data = data)
##
## Quantile residuals:
##      Min       1Q   Median       3Q      Max
## -2.0585 -0.8762 -0.2497  0.9821  1.9359
##
## Coefficients (mean model with logit link):
##              Estimate Std. Error z value Pr(>|z|)
```

```
## (Intercept) -0.19860    0.07601  -2.613  0.00898 **
## SexMale     -0.15832    0.09622  -1.645  0.09988 .
##
## Phi coefficients (precision model with identity link):
##      Estimate Std. Error z value Pr(>|z|)
## (phi)   8.4850    0.8124   10.45  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Type of estimator: ML (maximum likelihood)
## Log-likelihood: 83.43 on 3 Df
## Pseudo R-squared: 0.01405
## Number of iterations: 12 (BFGS) + 2 (Fisher scoring)
```

```
summary(model_K)
```

```
##
## Call:
## betareg(formula = Bacterial_Killing_Proportion ~ Year, data = data)
##
## Quantile residuals:
##      Min      1Q  Median      3Q      Max
## -3.0871 -0.4960  0.0873  0.7849  1.6154
##
## Coefficients (mean model with logit link):
##      Estimate Std. Error z value Pr(>|z|)
## (Intercept)   0.5563    0.1550   3.589 0.000332 ***
## YearThree     -1.5331    0.1679  -9.129 < 2e-16 ***
## YearTwo       -0.5777    0.1609  -3.590 0.000331 ***
##
## Phi coefficients (precision model with identity link):
##      Estimate Std. Error z value Pr(>|z|)
## (phi)   16.764    1.645   10.19  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Type of estimator: ML (maximum likelihood)
## Log-likelihood: 150.6 on 4 Df
## Pseudo R-squared: 0.516
## Number of iterations: 10 (BFGS) + 2 (Fisher scoring)
```

```
summary(model_L)
```

```
##
## Call:
## betareg(formula = Bacterial_Killing_Proportion ~ Season, data = data)
##
## Quantile residuals:
##      Min      1Q  Median      3Q      Max
## -5.2527 -0.3970  0.0791  0.6391  2.2376
##
## Coefficients (mean model with logit link):
##      Estimate Std. Error z value Pr(>|z|)
```

```
## (Intercept)    0.31951    0.03565    8.962    <2e-16 ***
## SeasonWinter -1.22697    0.05121   -23.961    <2e-16 ***
##
## Phi coefficients (precision model with identity link):
##      Estimate Std. Error z value Pr(>|z|)
## (phi)   33.659     3.347   10.06   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Type of estimator: ML (maximum likelihood)
## Log-likelihood:   219 on 3 Df
## Pseudo R-squared: 0.7495
## Number of iterations: 15 (BFGS) + 2 (Fisher scoring)
```

## Boxplot of BKA

```
# Reorder the species factor levels
data$Species <- factor(data$Species, levels = c("AMGO", "LEGO", "PISI", "HOFI"))

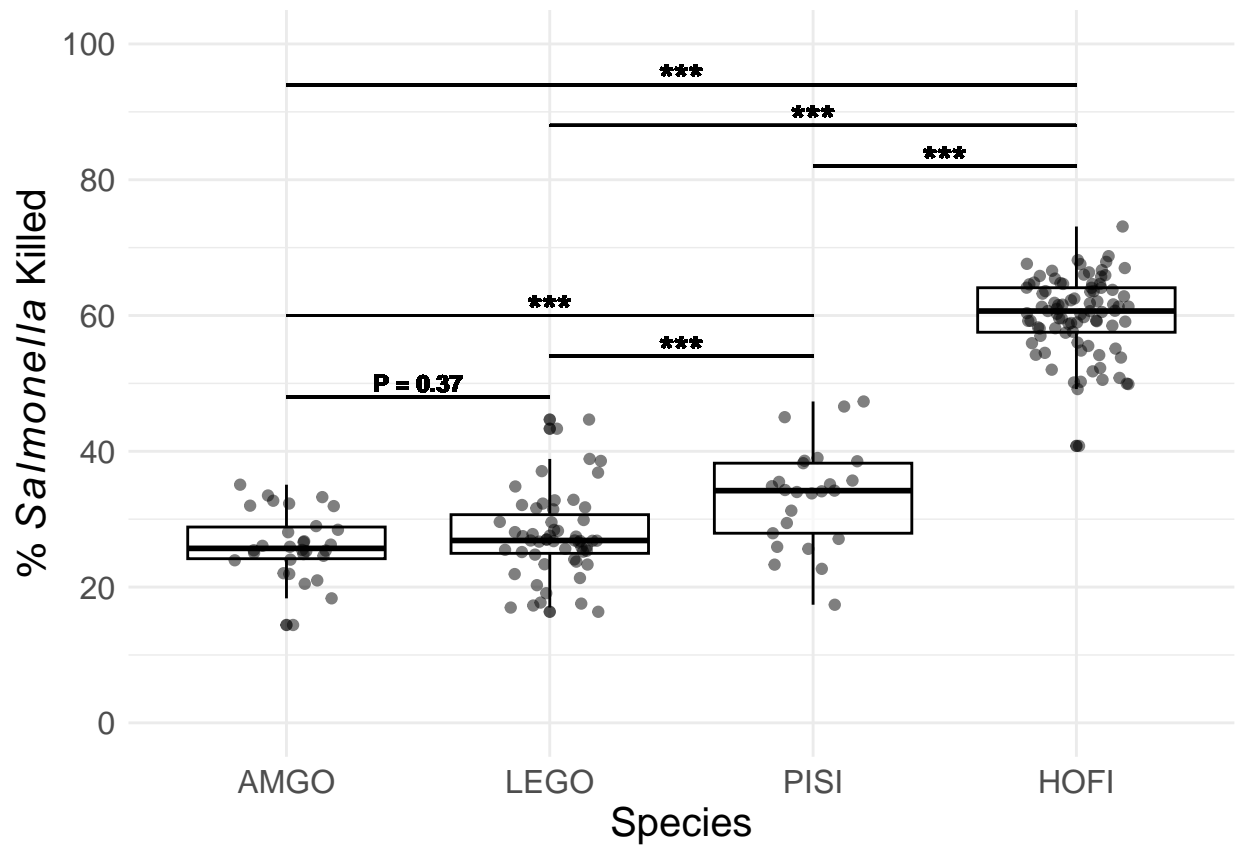
# Create box plot with individual points
BKAAssay <- ggplot(data, aes(x=Species, y=Bacterial_Killing_Percentage)) +
  geom_boxplot(color="black", alpha=0.7) + # Box plot
  geom_jitter(width=0.2, size=1.5, alpha=0.5) + # Jittered points
  labs(x="Species",
       y=expression("% " * italic(Salmonella) * " Killed")) +
  scale_y_continuous(limits = c(0, 100), breaks = seq(0, 100, by = 20)) +
  theme_minimal() +
  theme(plot.title = element_text(hjust = 0.5, face = "bold", size = 15),
        axis.title.x = element_text(size = 15),
        axis.title.y = element_text(size = 15),
        axis.text.x = element_text(size = 12), # Bold x-axis labels
        axis.text.y = element_text(size = 12) # Bold y-axis numbers
  ) +
  # Add line for significance between AMGO and HOFI
  geom_segment(aes(x=1, xend=4, y=94, yend=94), color="black", linewidth=.5) +
  # Add text for significance label "****"
  geom_text(aes(x=2.5, y=95, label="****"), color="black", size=5, fontface="bold") +
  # Add line for significance between LEGO and HOFI
  geom_segment(aes(x=2, xend=4, y=88, yend=88), color="black", linewidth=.5) +
  # Add text for significance label "****"
  geom_text(aes(x=3, y=89, label="****"), color="black", size=5, fontface="bold") +
  # Add line for significance between PISI and HOFI
  geom_segment(aes(x=3, xend=4, y=82, yend=82), color="black", linewidth=.5) +
  # Add text for significance label "****"
  geom_text(aes(x=3.5, y=83, label="****"), color="black", size=5, fontface="bold") +
  # Add line for significance between PISI and AMGO
  geom_segment(aes(x=1, xend=3, y=60, yend=60), color="black", linewidth=.5) +
  # Add text for significance label "****"
  geom_text(aes(x=2, y=61, label="****"), color="black", size=5, fontface="bold") +
  # Add line for significance between PISI and LEGO
  geom_segment(aes(x=2, xend=3, y=54, yend=54), color="black", linewidth=.5) +
```

```

# Add text for significance label "***"
geom_text(aes(x=2.5, y=55, label="***"), color="black", size=5, fontface="bold") +
# Add line for significance between AMGO and LEGO
geom_segment(aes(x=1, xend=2, y=48, yend=48), color="black", linewidth=.5) +
# Add text for significance label "***"
geom_text(aes(x=1.5, y=50, label="P = 0.37"), color="black", size=3, fontface="bold")

print(BKAAssay)

```



```
# export tiff with 300dpi
```

```

ggsave(
  filename="../figures/BKAAssay.tiff",
  plot = BKAAssay,
  width = 200,
  height = 200,
  units = c("mm"),
  dpi = 300,
  bg = "white"
)

```

## Import Growth Curve Data

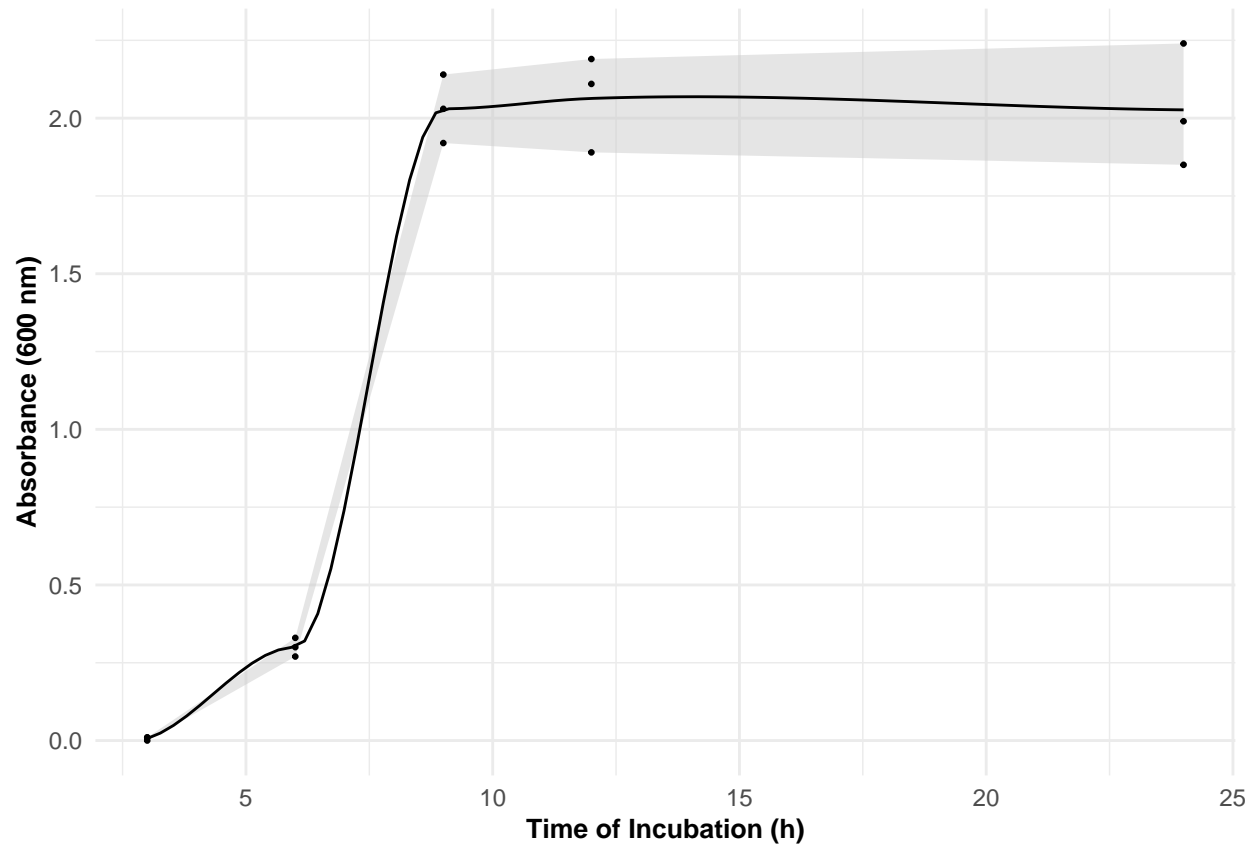
```
growthcurvedata <- read.csv("../datafiles/GrowthCurve.csv", header = TRUE, sep = ",")
```

## Growth Curve

```
# Calculate mean absorbance for each time point
average_data <- growthcurvedata %>%
  group_by(Time.h.) %>%
  summarise(
    Mean = mean(A600),
    SD = sd(A600),
    Min = min(A600),
    Max = max(A600)
  )

# Plot with smoothed line and shaded area representing the standard deviation
growthcurve <- ggplot() +
  geom_ribbon(data = average_data, aes(x = Time.h., y = Mean, ymin = Min, ymax = Max),
    fill = "grey80", alpha = 0.5) +
  geom_smooth(data = average_data, aes(x = Time.h., y = Mean), method = "loess",
    formula = y ~ x, color = "black", se = FALSE,
    size = 0.5) +
  geom_point(data = growthcurvedata, aes(x = Time.h., y = A600), color = "black", size = 0.5) +
  labs(x = "Time of Incubation (h)",
    y = "Absorbance (600 nm)") +
  theme_minimal() +
  theme(
    plot.title = element_text(hjust = 0.5, face = "bold", size = 10),
    axis.title.x = element_text(face = "bold", size = 10),
    axis.title.y = element_text(face = "bold", size = 10)
  )

print(growthcurve)
```



export tiff with 300dpi

```
ggsave(  
  filename="../figures/growthcurve.tiff",  
  plot = growthcurve,  
  width = 200,  
  height = 100,  
  units = c("mm"),  
  dpi = 300,  
  bg = "white"  
)
```