CGS698
Assignment-4

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Part 1:A simple linear regression: Power posing and testosterone

```
> library(readr)
> library(dplyr)
> library(brms)
> library(rstudioapi)
> # Load the observed data
> df_powerpose <- read.csv("F:/Study
Material/Summer/CGS698/Assignment/df_powerpose.csv", sep = ",", header = TRUE)
> df_powerpose$hptreat <- as.factor(df_powerpose$hptreat)
> # Convert the gender variable to numeric (0 = Female, 1 = Male)
> df_powerpose$female <- ifelse(df_powerpose$female == "Female", 1, 0)
> # Define the formula for the linear model
> formula <- testm2 ~ hptreat + female + age
> # Define weakly informative priors
> priors <- c(
+  set_prior("normal(0, 1)", class = "b"),   # Priors for the regression
coefficients
+  set_prior("normal(0, 1)", class = "Intercept")  # Prior for the intercept
+ )
> model <- brm(
+  formula = formula,
+  data = df_powerpose,
+  family = gaussian(),
+  prior = priors,
+  iter = 2000,
+  chains = 4,
+  cores = 4
+ )
Compiling Stan program...
Start sampling
> summary(model)
```

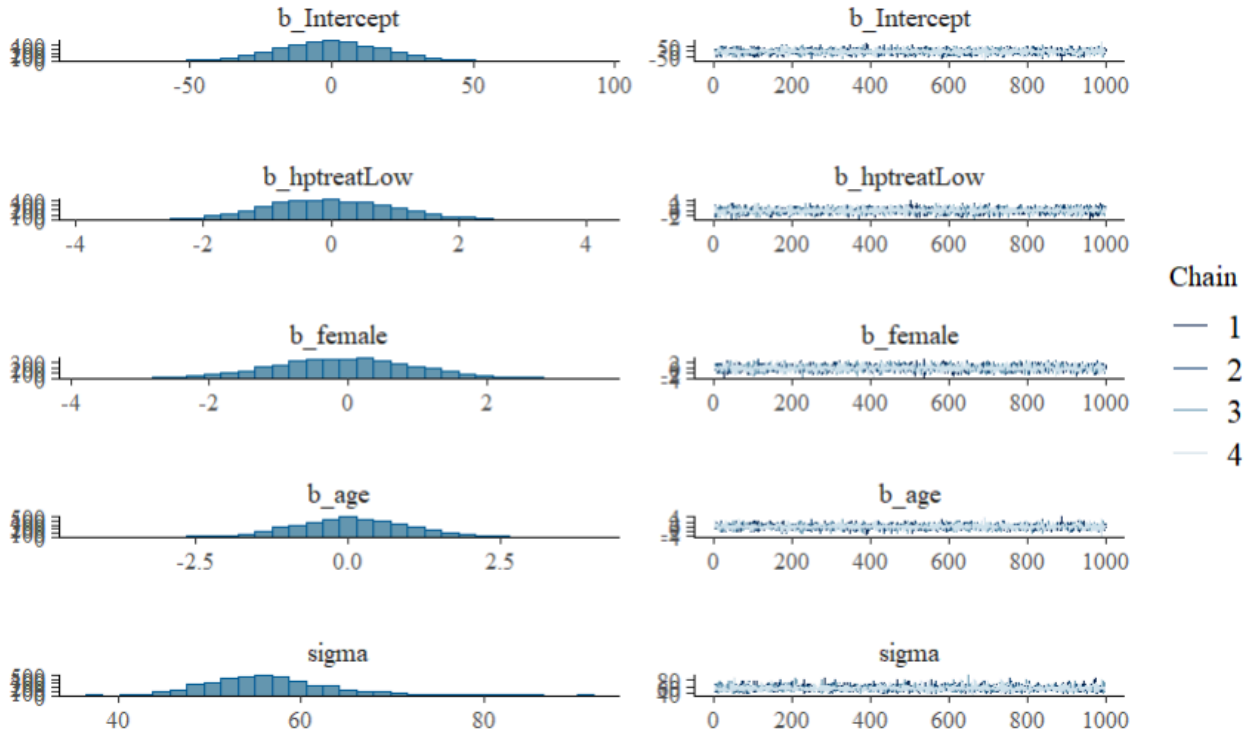
Summary of Model:

```
 Family: gaussian
  Links: mu = identity; sigma = identity
Formula: testm2 ~ hptreat + female + age
   Data: df_powerpose (Number of observations: 39)
```

```
  Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
         total post-warmup draws = 4000

Regression Coefficients:
           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept     -0.14     19.87   -39.87    39.09 1.00     5256     2830
hptreatLow    -0.03      1.00    -2.02     1.93 1.00     4707     3065
female        -0.06      1.01    -2.02     1.90 1.00     4960     3132
age            0.04      0.93    -1.78     1.88 1.00     5277     2949

Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma    56.45      6.62    45.42    71.58 1.00     5040     3010

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
```

Plot:

```
> plot(model)
```



Part 2:Poisson regression models and hypothesis testing

2.1)

```
> library(MASS)
> # Function to predict the number of crossing dependencies
> predict_crossings <- function(sentence_length, alpha, beta) {
+  # Compute the log of the expected rate
+  log_lambda <- alpha + beta * sentence_length
+
+  # Convert to the expected rate
+  lambda <- exp(log_lambda)
+
+  # Generate the number of crossing dependencies from the Poisson distribution
+  crossings <- rpois(1, lambda)
+
+  return(crossings)
+ }
> # Example usage
> set.seed(123)  # Set seed for reproducibility
> sentence_length <- 15
> alpha <- 1
> beta <- 0.1
> predicted_crossings <- predict_crossings(sentence_length, alpha, beta)
> cat("Predicted number of crossing dependencies:", predicted_crossings, "\n")
```

Output:

```
Predicted number of crossing dependencies: 10
```

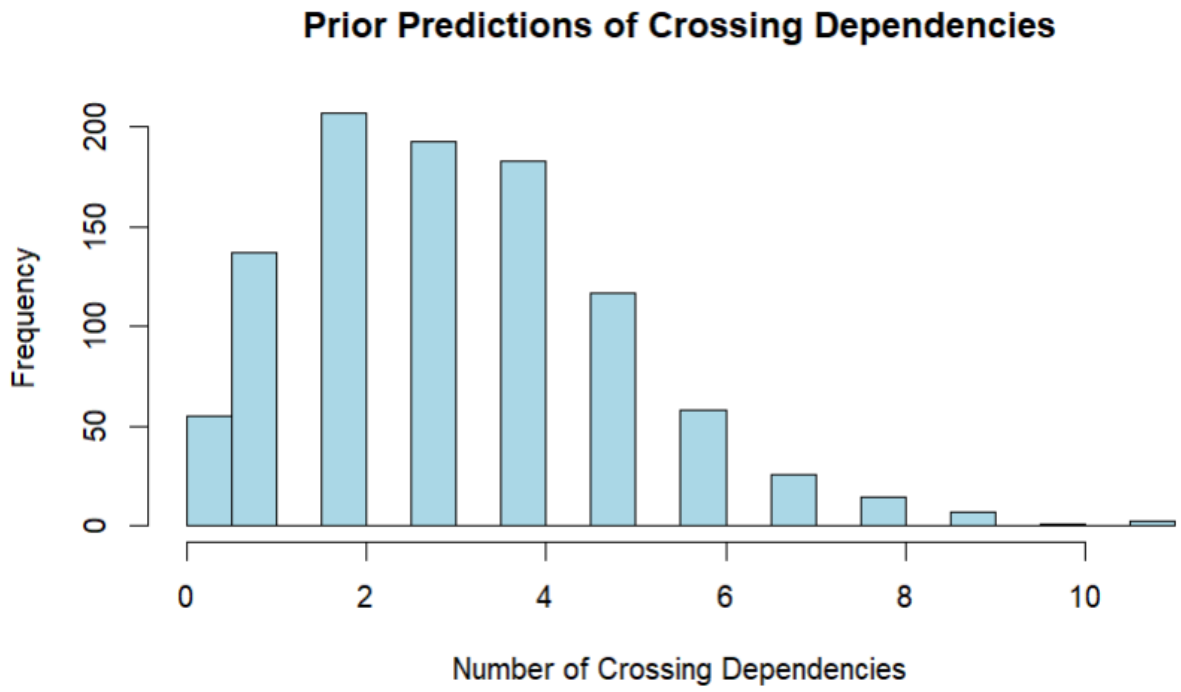
2.2)

```
> library(MASS)
> # Function to generate prior predictions
> generate_prior_predictions <- function(sentence_length, n_samples = 1000) {
+  # Sample from the priors
+  alpha_samples <- rnorm(n_samples, mean = 0.15, sd = 0.1)
+  beta_samples <- rnorm(n_samples, mean = 0.25, sd = 0.05)
+
+  # Compute the log of the expected rate for each sample
+  log_lambda_samples <- alpha_samples + beta_samples * sentence_length
+
+  # Convert to the expected rate
+  lambda_samples <- exp(log_lambda_samples)
+
+  # Generate the number of crossing dependencies for each sample
+  crossing_samples <- rpois(n_samples, lambda_samples)
+
+  return(crossing_samples)
+ }
> # Generate prior predictions for sentence length of 4
> set.seed(123)  # Set seed for reproducibility
```

```
> sentence_length <- 4
> n_samples <- 1000
> prior_predictions <- generate_prior_predictions(sentence_length, n_samples)
> # Summarize and plot the prior predictions
> summary(prior_predictions)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  0.000   2.000   3.000   3.184   4.000  11.000
> hist(prior_predictions, breaks = 30, main = "Prior Predictions of Crossing
Dependencies",
+     xlab = "Number of Crossing Dependencies", col = "lightblue", border =
"black")
```

Result:

```
 Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.000   2.000   3.000   3.184   4.000  11.000
```



2.3)

```
> library(brms)
> # Set the working directory
> setwd("F:\\Study Material\\Summer\\CGS698\\Assignment")
> # Load the data
> crossings_data <- read.csv("crossings.csv")
> # Inspect the data
> head(crossings_data)
  Language s.id s.length nCross
1   German    1        2      0
2   German    2        2      1
3   German    3        2      0
4   German    4        2      0
5   German    5        2      2
6   German    6        2      1
> str(crossings_data)
'data.frame':     1900 obs. of  4 variables:
 $ Language: chr  "German" "German" "German" "German" ...
 $ s.id    : int  1 2 3 4 5 6 7 8 9 10 ...
 $ s.length: int  2 2 2 2 2 2 2 2 2 2 ...
 $ nCross  : int  0 1 0 0 2 1 1 0 0 0 ...
> summary(crossings_data)
   Language             s.id          s.length      nCross
 Length:1900        Min.   :  1.0   Min.   : 2   Min.   : 0.000
 Class :character   1st Qu.:238.0   1st Qu.: 6   1st Qu.: 0.000
 Mode  :character   Median :475.5   Median :11   Median : 1.000
                    Mean   :475.5   Mean   :11   Mean   : 1.674
                    3rd Qu.:713.0   3rd Qu.:16   3rd Qu.: 2.000
                    Max.   :950.0   Max.   :20   Max.   :12.000
> # Define Model M1 formula
> formula_M1 <- bf(nCross ~ s.length + (1 | Language), family = poisson())
> # Prior for Model M1
> priors_M1 <- c(
+  prior(normal(0.15, 0.1), class = "Intercept"),  # alpha
+  prior(normal(0, 0.15), class = "b")             # beta
+ )
> # Define Model M2 formula
> formula_M2 <- bf(nCross ~ s.length * Language + (1 | Language), family =
poisson())
> # Prior for Model M2
> priors_M2 <- c(
+  prior(normal(0.15, 0.1), class = "Intercept"),   # alpha
+  prior(normal(0, 0.15), class = "b"),             # beta
+  prior(normal(0, 0.15), class = "b", coef = "LanguageGerman"),  # beta for
languageGerman
+  prior(normal(0, 0.15), class = "b", coef = "s.length:LanguageGerman")  #
beta for interaction term
+ )
> # Fit Model M1
```

```
> fit_M1 <- brm(formula_M1, data = crossings_data, prior = priors_M1, iter =
2000, chains = 4)
Compiling Stan program...
Start sampling

SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 1).
Chain 1:
Chain 1: Gradient evaluation took 0.000442 seconds
Chain 1: 1000 transitions using 10 leapfrog steps per transition would take
4.42 seconds.
Chain 1: Adjust your expectations accordingly!
Chain 1:
Chain 1:
Chain 1: Iteration:    1 / 2000 [  0%]  (Warmup)
Chain 1: Iteration:  200 / 2000 [ 10%]  (Warmup) .... (and so on)

> # Fit Model M2
> fit_M2 <- brm(formula_M2, data = crossings_data, prior = priors_M2, iter =
2000, chains = 4)
Compiling Stan program...
Start sampling

SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 1).
Chain 1:
Chain 1: Gradient evaluation took 0.000403 seconds
Chain 1: 1000 transitions using 10 leapfrog steps per transition would take
4.03 seconds.
Chain 1: Adjust your expectations accordingly!
Chain 1:
Chain 1:
Chain 1: Iteration:    1 / 2000 [  0%]  (Warmup)
Chain 1: Iteration:  200 / 2000 [ 10%]  (Warmup)
Chain 1: Iteration:  400 / 2000 [ 20%]  (Warmup)
Chain 1: Iteration:  600 / 2000 [ 30%]  (Warmup)...(and so on)


> # Summarize Model M1
> summary(fit_M1)
> # Summarize Model M2
> summary(fit_M2)
```

Summary of Model M1:

```
Family: poisson
  Links: mu = log
Formula: nCross ~ s.length + (1 | Language)
   Data: crossings_data (Number of observations: 1900)
  Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
         total post-warmup draws = 4000
```

```
Multilevel Hyperparameters:
~Language (Number of levels: 2)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.60      0.48     0.13     1.69 1.32       10       17

Regression Coefficients:
          Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept    -1.49      0.09    -1.68    -1.31 1.05      814     1354
s.length      0.15      0.00     0.14     0.16 1.09       29     1353

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
```

Summary of Model M2:

```
 Family: poisson
  Links: mu = log
Formula: nCross ~ s.length * Language + (1 | Language)
   Data: crossings_data (Number of observations: 1900)
  Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
         total post-warmup draws = 4000

Multilevel Hyperparameters:
~Language (Number of levels: 2)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.94      0.56     0.27     2.41 1.00      710      584

Regression Coefficients:
                      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS
Tail_ESS
Intercept                -1.43      0.13    -1.69    -1.17 1.00     2380
2012
s.length                  0.10      0.01     0.09     0.11 1.00     2256
2212
LanguageGerman           -0.03      0.15    -0.34     0.27 1.00     1934
2234
s.length:LanguageGerman   0.09      0.01     0.08     0.11 1.00     2038
2053
Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
```

2.4)

```
> library(brms)
> library(dplyr)
> library(ggplot2)
> # Load the dataset
> observed <- read.csv("F:/Study
Material/Summer/CGS698/Assignment/crossings.csv", sep = ",", header = TRUE)
>
> # Visualize average rate of crossings
> observed %>%
+  group_by(Language, s.length) %>%
+  summarise(mean.crossings = mean(nCross)) %>%
+  ggplot(aes(x = s.length, y = mean.crossings, group = Language, color =
Language)) +
+  geom_point() + geom_line()
`summarise()` has grouped output by 'Language'. You can override using the
`.groups` argument.
> # Center the predictors
> observed$s.length <- observed$s.length - mean(observed$s.length)
>
> # Create indicator variable for language
> observed$lang <- ifelse(observed$Language == "German", 1, 0)
> # Initialize vectors to store log predictive densities in each fold
> lpds.m1 <- c()
> lpds.m2 <- c()
>
> # Initialize untested data
> untested <- observed
>
> # Perform k-fold cross-validation (assuming k = 4)
> for (k in 1:4) {
+  # Prepare test data and training data
+  ytest <- sample_n(untested, size = nrow(observed) / 5)
+  ytrain <- setdiff(observed, ytest)
+  untested <- setdiff(untested, ytest)
+
+  # Fit model M1 on training data
+  fit.m1 <- brm(
+    nCross ~ 1 + s.length,
+    data = ytrain,
```

```
+    family = poisson(link = "log"),
+    prior = c(
+      prior(normal(0.15, 0.1), class = Intercept),
+      prior(normal(0, 0.15), class = b)
+    ),
+    cores = 4
+  )
+
+  # Fit model M2 on training data
+  fit.m2 <- brm(
+    nCross ~ 1 + s.length + lang + s.length * lang,
+    data = ytrain,
+    family = poisson(link = "log"),
+    prior = c(
+      prior(normal(0.15, 0.1), class = Intercept),
+      prior(normal(0, 0.15), class = b)
+    ),
+    cores = 4
+  )
+
+  # Retrieve posterior samples
+  post.m1 <- posterior_samples(fit.m1)
+  post.m2 <- posterior_samples(fit.m2)
+
+  # Calculate log pointwise predictive density using test data for model M1
+  lppd.m1 <- 0
+  for (i in 1:nrow(ytest)) {
+    lpd_im1 <- log(mean(dpois(ytest[i, ]$nCross,
+                              lambda = exp(post.m1[, 1] +
+                                             post.m1[, 2] * ytest[i,
]$s.length))))
+    lppd.m1 <- lppd.m1 + lpd_im1
+  }
+
+  # Calculate log pointwise predictive density using test data for model M2
+  lppd.m2 <- 0
+  for (i in 1:nrow(ytest)) {
+    lpd_im2 <- log(mean(dpois(ytest[i, ]$nCross,
+                              lambda = exp(post.m2[, 1] +
+                                             post.m2[, 2] * ytest[i,
]$s.length +
+                                             post.m2[, 3] * ytest[i, ]$lang +
+                                             post.m2[, 4] * ytest[i,
]$s.length * ytest[i, ]$lang))))
+    lppd.m2 <- lppd.m2 + lpd_im2
+  }
+
+  # Store log predictive densities
+  lpds.m1 <- c(lpds.m1, lppd.m1)
```

```
+  lpds.m2 <- c(lpds.m2, lppd.m2)
+ }
Compiling Stan program...
Start sampling
Compiling Stan program...
Start sampling
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Start sampling
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Start sampling
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Start sampling
Compiling Stan program...
Start sampling
Compiling Stan program...
Start sampling
Warning messages:
1: Method 'posterior_samples' is deprecated. Please see ?as_draws for
recommended alternatives.
2: Method 'posterior_samples' is deprecated. Please see ?as_draws for
recommended alternatives.
3: Method 'posterior_samples' is deprecated. Please see ?as_draws for
recommended alternatives.
4: Method 'posterior_samples' is deprecated. Please see ?as_draws for
recommended alternatives.
5: Method 'posterior_samples' is deprecated. Please see ?as_draws for
recommended alternatives.
6: Method 'posterior_samples' is deprecated. Please see ?as_draws for
recommended alternatives.
7: Method 'posterior_samples' is deprecated. Please see ?as_draws for
recommended alternatives.
8: Method 'posterior_samples' is deprecated. Please see ?as_draws for
recommended alternatives.
>
> # Calculate expected log predictive density (elpd) for model M1 and M2
> elpd.m1 <- sum(lpds.m1)
> elpd.m2 <- sum(lpds.m2)
>
> # Calculate evidence in favor of M2 over M1
> difference_elpd <- elpd.m2 - elpd.m1
>
> # Print results
```
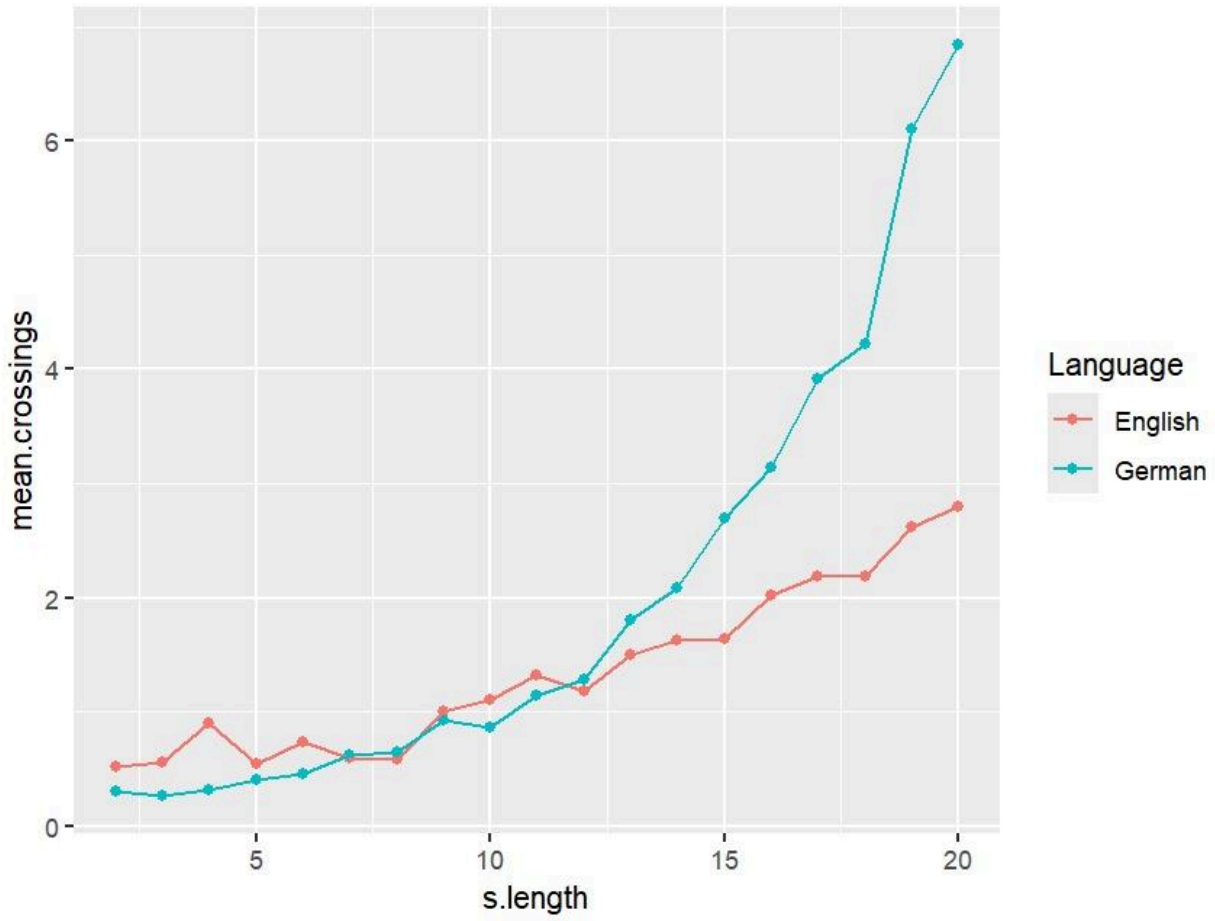

Output:

```
> cat("Predictive accuracy of model M1 (elpd):", elpd.m1, "\n")
Predictive accuracy of model M1 (elpd): -2224
> cat("Predictive accuracy of model M2 (elpd):", elpd.m2, "\n")
Predictive accuracy of model M2 (elpd): -2131.142
> cat("Difference in elpd (M2 - M1):", difference_elpd, "\n")
Difference in elpd (M2 - M1): 92.85859
```

Plot:



>