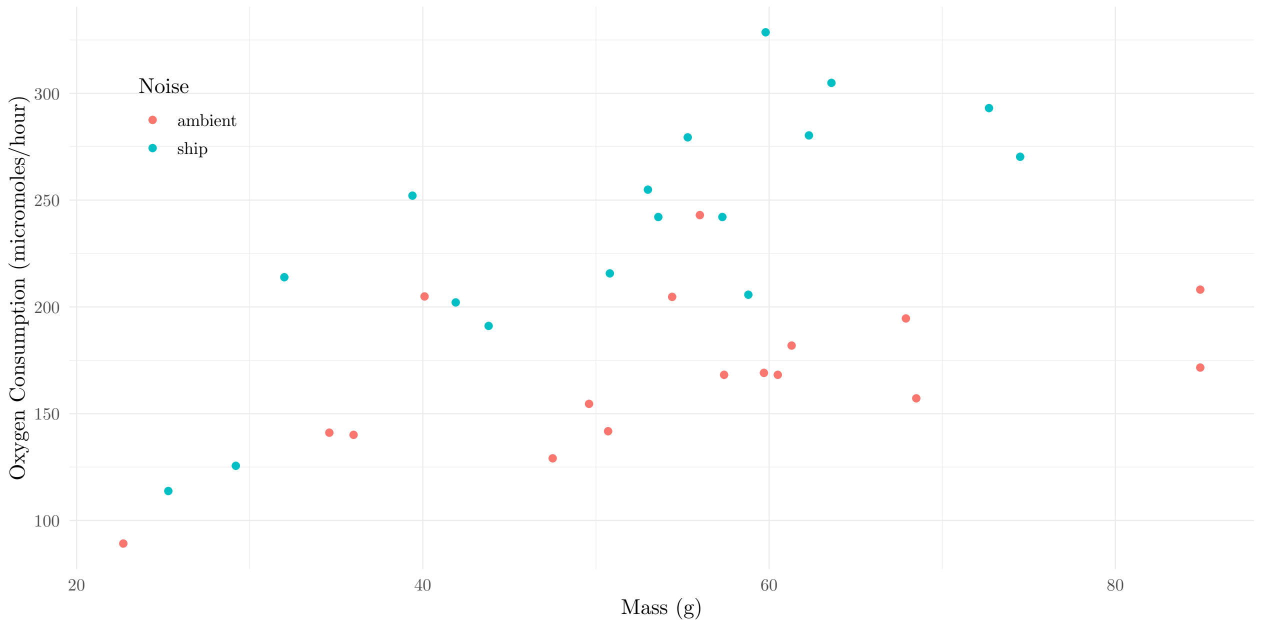
Over-dispersion and Quasi-likelihood, Marginal Effects, the Delta Method, and Survival Analysis

Statistics 516, Homework 4 (Solutions)

Physiological Responses of Shore Crabs to Ship Noise

The data in the data frame `CrabShip` in the **Stat2Data** package are from an experiment that investigated physiological responses of shore crabs (*Carcinus maenas*) to ship noise.[1] Captive crabs were randomly assigned to one of two treatment groups. One group of crabs was exposed to a recording of 7.5 minutes of ship noise. The other group was exposed to a recording of 7.5 minutes of ambient harbor noise. The researchers observed the rate of oxygen consumption of each crab as well as its mass.[2] The plot below shows the data.

```r
library(ggplot2)
library(Stat2Data)
data(CrabShip)
p <- ggplot(CrabShip, aes(x = Mass, y = Oxygen, color = Noise)) +
  geom_point() + theme_minimal() + theme(legend.position = c(0.1, 0.8)) +
  labs(y = "Oxygen Consumption (micromoles/hour)", x = "Mass (g)")
plot(p)
```



From the plot it appears that ship noise tends to increase oxygen consumption rate, and that larger crabs tend to have higher oxygen consumption rates. Assume that the goal is to model how ship noise affects oxygen consumption rate and how this depends on the mass of the crab. Suppose we model the data using

[1]Source: Wale, M. A., Simpson, S. D., Radford, A. N. (2013). Size-dependent physiological responses of shore crabs to single and repeated playback of ship noise, *Biology Letters*, *9*, 20121194.

[2]The help file for the `CrabShip` data frame, view-able using either `help(CrabShip)` or `?CrabShip` once the **Stat2Data** package is loaded, labels the `Mass` variable incorrectly as oxygen uptake. This should be labeled as mass of the crab in grams.

the nonlinear regression model

$$E(O_i) = \begin{cases} \beta_a m_i^\gamma, & \text{if the noise source is ambient,} \\ \beta_s m_i^\gamma, & \text{if the noise source is ship,} \end{cases}$$

where O_i and m_i are the oxygen consumption and mass for the i-th observation, respectively, and β_a, β_s, and γ are the parameters of the model. The model specifies that the expected oxygen consumption is proportional to a power transformation of mass, with the constant of proportionality depending on the treatment condition (i.e., noise source). To estimate this nonlinear model we can first estimate a linear model with $\gamma = 0.5$ to get starting values for β_a and β_s, and then use these estimates as starting values in the nonlinear model.[3]

```
library(dplyr)
m_start <- nls(Oxygen ~ case_when(
    Noise == "ambient" ~ beta_a * Mass,
    Noise == "ship"    ~ beta_s * Mass,
  ), start = list(beta_a = 1, beta_s = 1), data = CrabShip)
summary(m_start)$coefficients
```

```
       Estimate Std. Error t value  Pr(>|t|)
beta_a    2.914     0.1739   16.76 2.093e-17
beta_s    4.507     0.1875   24.04 4.746e-22
```

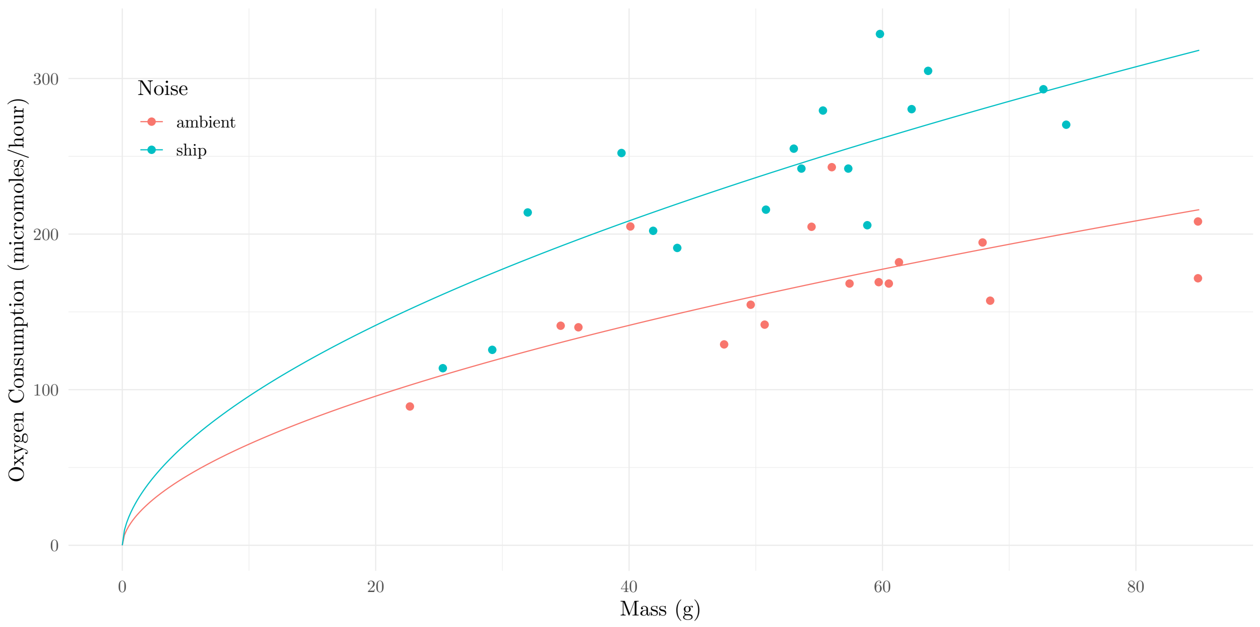
```
m_final <- nls(Oxygen ~ case_when(
    Noise == "ambient" ~ beta_a * Mass^gamma,
    Noise == "ship"    ~ beta_s * Mass^gamma
  ), start = list(beta_a = 2.9, beta_s = 4.5, gamma = 0.5),
  data = CrabShip)
summary(m_final)$coefficients
```

```
       Estimate Std. Error t value  Pr(>|t|)
beta_a  17.8658     7.5707   2.360 2.476e-02
beta_s  26.3527    10.9220   2.413 2.193e-02
gamma    0.5607     0.1036   5.411 6.615e-06
```

Here is a plot of the estimated model.

```
d <- expand.grid(Noise = c("ambient","ship"),
  Mass = seq(0, 85, length = 500))
d$yhat <- predict(m_final, newdata = d)
p <- p + geom_line(aes(y = yhat), data = d)
plot(p)
```

[3]To find a good initial value of γ you can try estimating different linear models by specifying (not estimating) the value of gamma and then plotting the model with the data or the residuals against the predicted values until you get what looks like a good fit. Also note that $\gamma^{0.5} = \sqrt{\gamma}$ so this is essentially a square root transformation of mass.



The model looks reasonable, but it is not easy to interpret in terms of the individual model parameters. But it may be useful to interpret the model in terms of linear and nonlinear *functions* of the model parameters. In what follows be sure you use the final model with the estimated γ parameter (i.e., `m_final`) and not the first model (i.e., `m_start`) which was just a working model used to obtain starting values for the parameters.

1. For the noise source to affect the expected oxygen consumption we need $\beta_s \neq \beta_a$ or, equivalently, $\beta_s - \beta_a = 0$. So rejecting the null hypothesis that $\beta_s - \beta_a = 0$ will conclude a statistically significant effect of the noise treatment. This can be done several ways. The quantity $\beta_s - \beta_a$ is a linear function of the model parameters, so by estimating it with `lincon` you will get a test statistic for the test of the null hypothesis above. You can also estimate $\beta_s - \beta_a$ using the `dmethod` function which will provide the same inferences.[4] Report output given by these two functions to verify that they give the same result. Another approach is to use a F test statistic by using the `anova` function and specifying a null model. This is very similar to the likelihood ratio test but uses a different test statistic (the `test = "LRT"` is not needed for `anova` here as it will default to using the F test statistic when applied to a `nls` object). The null model can be written as

$$E(O_i) = \beta m^{\gamma},$$

since if $\beta_s = \beta_a$ then we can remove the subscript and just call the common parameter β. Note that for your starting value of β you could use the average of the estimates of β_s and β_a. Report the test statistic and p-value for this test.

Solution: Here are the tests of the null hypothesis that $\beta_s - \beta_a = 0$ using `lincon` and `dmethod`. First I will convert the `Noise` variable to a character variable and re-estimate the model to avoid bug in `margeff` that will be fixed soon.

```r
CrabShip$Noise <- as.character(CrabShip$Noise)
m_final <- nls(Oxygen ~ case_when(
    Noise == "ambient" ~ beta_a * Mass^gamma,
    Noise == "ship"    ~ beta_s * Mass^gamma
  ), start = list(beta_a = 2.9, beta_s = 4.5, gamma = 0.5),
  data = CrabShip)
```

[4]While the `dmethod` function is designed for situations where we want to make inferences about a *nonlinear* function of the model parameters, it does not require that the function be nonlinear. And one might argue that using the `dmethod` function is easier since the user only needs to specify an expression rather than work out the coefficients for a linear function of the model parameters.

```
library(trtools)
lincon(m_final, a = c(-1, 1, 0))
```

```
           estimate    se lower upper tvalue df  pvalue
(-1,1,0),0    8.487 3.584 1.177  15.8  2.368 31 0.02431
```

```
dmethod(m_final, pfunc = "beta_s - beta_a",
  pname = c("beta_a", "beta_s", "gamma"))
```

```
 estimate    se lower upper tvalue  df  pvalue
    8.487 3.584 1.462 15.51  2.368 Inf 0.01789
```

To make the test and confidence interval from `dmethod` agree with that from `lincon` we can manually set the degrees of freedom as follows.

```
dmethod(m_final, pfunc = "beta_s - beta_a",
  pname = c("beta_a", "beta_s", "gamma"), df = 31)
```

```
 estimate    se lower upper tvalue df  pvalue
    8.487 3.584 1.177  15.8  2.368 31 0.01789
```

Unfortunately there is a bug in `dmethod` that only applies the specified degrees of freedom to the confidence interval and not the p-value calculation. That will be fixed soon in an update. Next I will specify F test of the same null hypothesis.

```
m_null <- nls(Oxygen ~ beta * Mass^gamma,
  start = list(beta = 22, gamma = 0.6), data = CrabShip)
summary(m_null)$coefficients
```

```
      Estimate Std. Error t value Pr(>|t|)
beta   34.5804    21.5239   1.607  0.11797
gamma   0.4476     0.1549   2.890  0.00687
```

```
anova(m_null, m_final)
```

```
Analysis of Variance Table

Model 1: Oxygen ~ beta * Mass^gamma
Model 2: Oxygen ~ case_when(Noise == "ambient" ~ beta_a * Mass^gamma, Noise == "ship" ~ beta_s * Ma
  Res.Df Res.Sum Sq Df Sum Sq F value  Pr(>F)
1     32      86452
2     31      34998  1  51454    45.6 1.5e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

In a linear model this test would give the same p-value as the test based on the t test statistic as reported by `lincon`. But this is not the case in a nonlinear regression model. There is evidence that in these cases the F test is more accurate, although frequently the two tests will give the same result.

2. Suppose we want to estimate the difference in the expected oxygen consumption between the two treatment conditions. This can be written as $\beta_s m^\gamma - \beta_a m^\gamma$ or $(\beta_s - \beta_a)m^\gamma$. Since this depends on the mass of the crab (m), a useful approach might be to estimate the difference for an average crab. The mean crab mass in this study is about $m = 53$ grams. There are a couple of ways that you can estimate this difference in R. One would be to estimate it as a discrete marginal effect using the `margeff` function, and another is to use the delta method with the `dmethod` function. Estimate this difference using both functions, being sure to report the estimate, standard error, and confidence interval. You should obtain the same result using these two functions.

   Solution: Here is the marginal effect estimated using the `margeff` function.

```
margeff(m_final,
  a = list(Noise = "ship", Mass = 53),
  b = list(Noise = "ambient", Mass = 53))
```

```
 estimate    se lower upper tvalue df    pvalue
    78.62 11.53  55.1 102.1  6.816 31 1.232e-07
```

And here is the marginal effect estimated using `dmethod`.

```
dmethod(m_final, pfunc = "(beta_s - beta_a) * 53^gamma",
  pname = c("beta_a", "beta_s", "gamma"))
```

```
 estimate    se lower upper tvalue  df    pvalue
    78.62 11.53 56.01 101.2  6.816 Inf 9.335e-12
```

3. The marginal effect discussed in the previous problem can also be framed as a percent change or difference. This is defined as
$$\frac{\beta_s m^\gamma - \beta_a m^\gamma}{\beta_a m^\gamma} \times 100\%$$
which will tell us what percent larger the expected oxygen consumption is for a crab in the ship noise condition versus the ambient noise condition. Estimate this marginal effect for an average crab with a mass of 53 grams using the `margeff` function, and also estimate it using the `dmethod` function, being sure to report the estimate, standard error, and confidence interval from each function. You should obtain the same results using these two functions.

   Solution: Here are the estimates of the percent difference in the expected oxygen consumption from the `margeff` and `dmethod` functions.

```
margeff(m_final, type = "percent",
  a = list(Noise = "ship", Mass = 53),
  b = list(Noise = "ambient", Mass = 53))
```

```
 estimate   se lower upper tvalue df    pvalue
     47.5 8.75 29.66 65.35  5.429 31 6.273e-06
```

```
dmethod(m_final,
  pfunc = "100 * (beta_s*53^gamma - beta_a*53^gamma) / (beta_a*53^gamma)",
  pname = c("beta_a", "beta_s", "gamma"))
```

```
 estimate   se lower upper tvalue  df    pvalue
     47.5 8.75 30.35 64.65  5.429 Inf 5.661e-08
```

4. Suppose a researcher was interested in how quickly the expected oxygen consumption increases with mass. The relationship is not linear so this rate of change depends on the mass of the crab. But we could estimate the rate of change for an average crab with a mass of $m = 53$ grams. This is the "instantaneous" marginal effect of mass at a mass of $m = 53$ grams. Estimate this quantity using the `margeff` function for each of the two treatment conditions. Report the estimates, standard errors, and confidence interval. Also estimate these quantities using the `dmethod` function by using the fact that the instantaneous marginal effects for mass for the ship and ambient conditions can be shown to be equal to $\beta_s \gamma m^{\gamma-1}$ and $\beta_a \gamma m^{\gamma-1}$, respectively.[5]

   Solution: The "instantaneous" marginal effects can be estimated as follows using the `margeff` and `dmethod` functions.

[5]These are derivatives. Note that, for example,
$$\frac{d}{dm}\beta_s m^\gamma = \beta_s \gamma m^{\gamma-1}.$$

```r
margeff(m_final, delta = 0.001,
  a = list(Noise = c("ship","ambient"), Mass = 53 + 0.001),
  b = list(Noise = c("ship","ambient"), Mass = 53))
```

```
 estimate     se lower upper tvalue df    pvalue
    2.583 0.4811 1.601 3.564  5.368 31 7.478e-06
    1.751 0.3181 1.102 2.400  5.504 31 5.065e-06
```

```r
dmethod(m_final, pfunc = "beta_s*gamma*53^(gamma-1)",
  pname = c("beta_a", "beta_s", "gamma"))
```

```
 estimate     se lower upper tvalue  df    pvalue
    2.583 0.4811  1.64 3.526  5.368 Inf 7.965e-08
```

```r
dmethod(m_final, pfunc = "beta_a*gamma*53^(gamma-1)",
  pname = c("beta_a", "beta_s", "gamma"))
```

```
 estimate     se lower upper tvalue  df    pvalue
    1.751 0.3181 1.127 2.374  5.504 Inf 3.716e-08
```

You can use the `dmethod` function to estimate both marginal effects at the same time by creating an expression that returns both values.

```r
dmethod(m_final, pfunc = "c(beta_s,beta_a)*gamma*53^(gamma-1)",
  pname = c("beta_a", "beta_s", "gamma"),
  fname = c("ship","ambient"))
```

```
        estimate     se lower upper tvalue  df    pvalue
ship       2.583 0.4811 1.640 3.526  5.368 Inf 7.965e-08
ambient    1.751 0.3181 1.127 2.374  5.504 Inf 3.716e-08
```

The `dmethod` function has an optional argument `fname` which works like the `cname` argument for the `contrast` function.

Swedish Speed Limit Study — Revisited

Recall the Swedish speed limit study from the previous homework assignment. As in the previous homework the following will format the data for modeling.

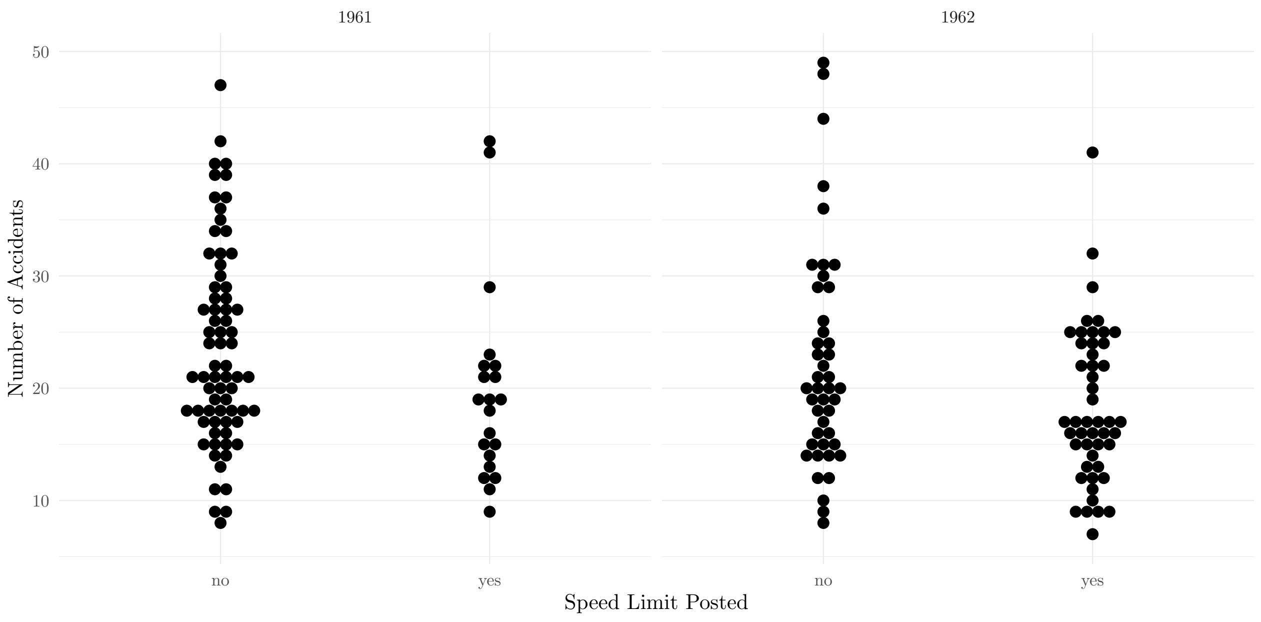
```r
library(SMPracticals)
library(dplyr)
library(tidyr)
data(limits)

limitstudy <- limits %>%
  rename(limit_1961 = lim1, limit_1962 = lim2, y_1961 = y1, y_1962 = y2) %>%
  pivot_longer(cols = -day, names_to = c(".value", "year"), names_sep = "_") %>%
  mutate(limit = factor(limit, levels = c(0,1), labels = c("no","yes")))
head(limitstudy)
```

```
# A tibble: 6 x 4
  day   year  limit     y
  <fct> <chr> <fct> <int>
1 1     1961  no        9
2 1     1962  no        9
3 2     1961  no       11
4 2     1962  no       20
5 3     1961  no        9
```

```
6 3     1962  no       15
```

Here is another way to visualize the data using a dot plot.

```r
p <- ggplot(limitstudy, aes(x = limit, y = y)) +
  theme_minimal() + geom_dotplot(binaxis = "y", binwidth = 1,
    stackdir = "center", position = position_dodge()) +
  labs(x = "Speed Limit Posted", y = "Number of Accidents") +
  facet_wrap(~ year)
plot(p)
```



Here is the Poisson regression model you used in the previous homework assignment.

```r
m <- glm(y ~ limit + year, family = poisson, data = limitstudy)
summary(m)$coefficients
```

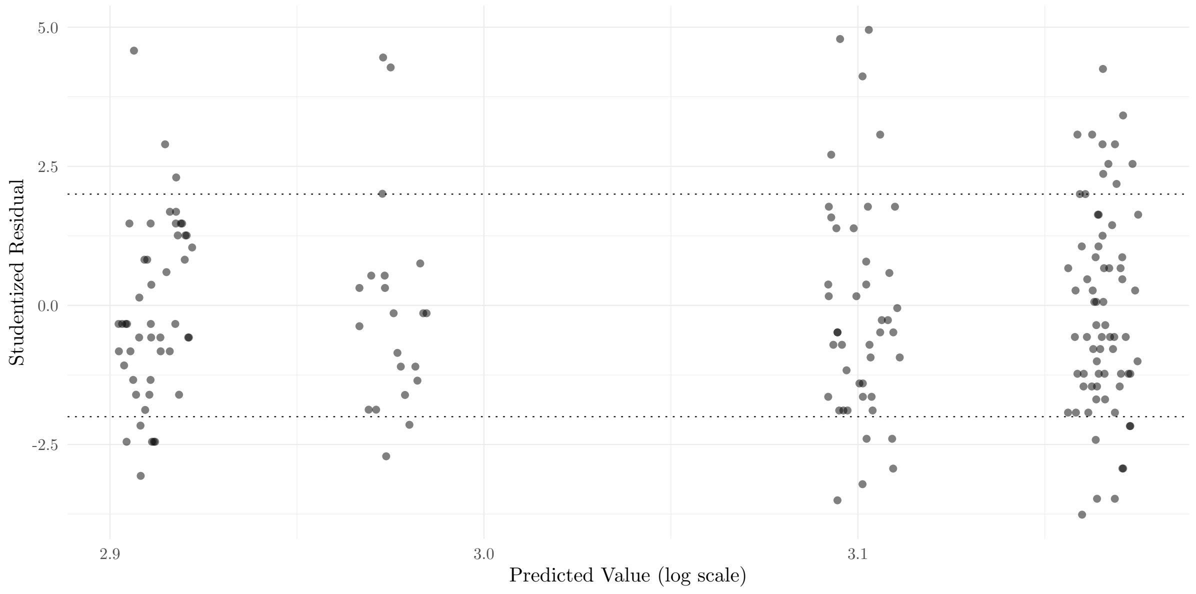
```
            Estimate Std. Error z value  Pr(>|z|)
(Intercept)  3.16513    0.02294 137.977 0.0000000
limityes    -0.18893    0.03547  -5.327 0.0000001
year1962    -0.06394    0.03335  -1.917 0.0551916
```

In what follows you will consider inferences based on this model while also dealing with possible over-dispersion.

1. Explain why the Poisson regression model specified above exhibits over-dispersion based on (a) a residual plot and (b) the residual deviance. Be sure to include the residual plot and the residual deviance in your answer.

   Solution: First consider the residual plot. Mine might be a bit more fancy than yours.

   ```r
   set.seed(123)
   d <- data.frame(p = predict(m), r = rstudent(m))
   p <- ggplot(d, aes(x = p, y = r)) + theme_minimal() +
     geom_jitter(height = 0, width = 0.01, alpha = 0.5) +
     labs(x = "Predicted Value (log scale)",
       y = "Studentized Residual") +
     geom_hline(yintercept = c(-2, 2), linetype = 3)
   plot(p)
   ```



Note that you could also use something simple like `plot(predict(m), rstudent(m))`. It looks like there are more residuals larger than two in absolute value than we would expect if there was no over-dispersion. Here is how we could compute the proportion of residuals with absolute values greater than two.

```r
mean(abs(rstudent(m)) > 2)
```

```
[1] 0.2391
```

So almost 24% of the residuals have absolute values of more than two. The residual deviance is also a bit larger (relative to the degrees of freedom) than we like to see.

```r
summary(m)
```

```

Call:
glm(formula = y ~ limit + year, family = poisson, data = limitstudy)

Deviance Residuals:
   Min      1Q  Median      3Q     Max
-3.743  -1.391  -0.361   1.037   4.892

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   3.1651     0.0229  137.98   <2e-16 ***
limityes     -0.1889     0.0355   -5.33    1e-07 ***
year1962     -0.0639     0.0333   -1.92    0.055 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 624.98  on 183  degrees of freedom
Residual deviance: 582.39  on 181  degrees of freedom
AIC: 1478

Number of Fisher Scoring iterations: 4
```

The residual deviance is more than three times the residual degrees of freedom.

2. Poisson regression assumes that $\text{Var}(Y_i) = E(Y_i)$. This is a property of the Poisson distribution. Over-dispersion is when $\text{Var}(Y_i) > E(Y_i)$. As we discussed in class, one approach to dealing with over-dispersion for Poisson regression is to use quasi-likelihood and relax the variance structure to $\text{Var}(Y_i) = \phi E(Y_i)$ where ϕ is a dispersion parameter which allows for some patterns of over-dispersion.[6] Estimate the model above using this quasi-likelihood approach. Create a residual plot like you did in the previous problem and comment briefly if you think this quasi-likelihood approach was effective at dealing with over-dispersion. Report the estimates, standard errors, and confidence intervals for the model parameters. Compare these to what you obtained in the previous homework and discuss briefly what has (or has not) changed and how.

   Solution: Here is how we can estimate the model using quasi-likelihood with the variance structure specified above.

```
m.quasi <- glm(y ~ limit + year, family = quasipoisson, data = limitstudy)
cbind(summary(m.quasi)$coefficients, confint(m.quasi))
```

```
            Estimate Std. Error t value   Pr(>|t|)   2.5 %   97.5 %
(Intercept)  3.16513    0.04209  75.207 1.815e-138  3.0816  3.24659
limityes    -0.18893    0.06507  -2.903  4.150e-03 -0.3173 -0.06212
year1962    -0.06394    0.06118  -1.045  2.974e-01 -0.1840  0.05583
```

   For comparison here are the estimates, standard errors, and confidence intervals without using quasi-likelihood.

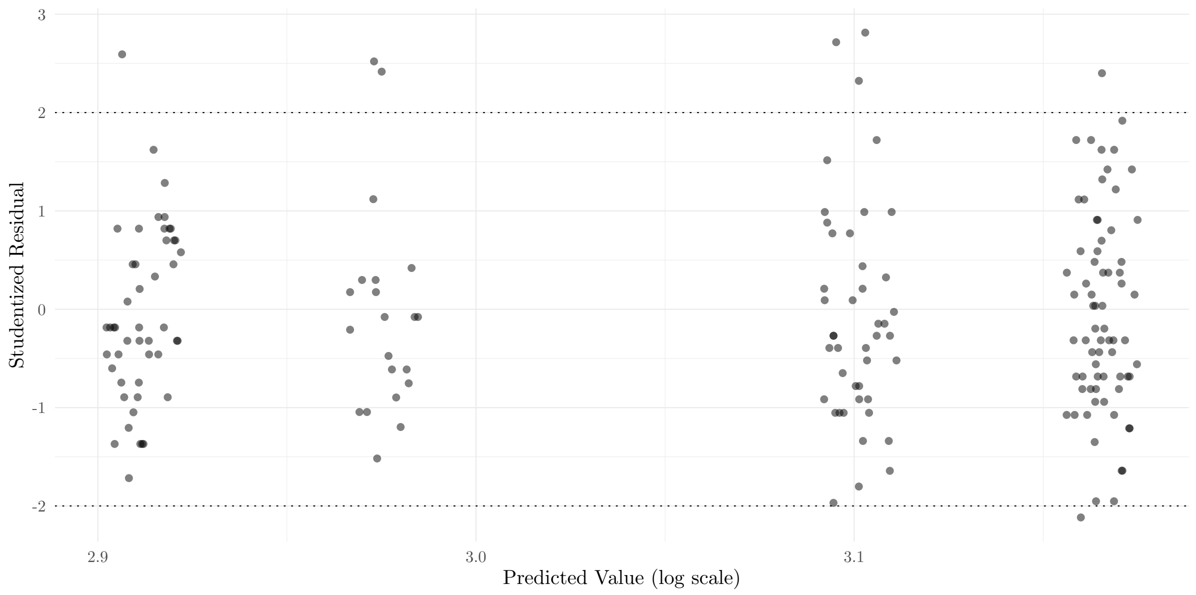
```
cbind(summary(m)$coefficients, confint(m))
```

```
            Estimate Std. Error z value  Pr(>|z|)   2.5 %    97.5 %
(Intercept)  3.16513    0.02294 137.977 0.0000000  3.1199  3.209786
limityes    -0.18893    0.03547  -5.327 0.0000001 -0.2587 -0.119636
year1962    -0.06394    0.03335  -1.917 0.0551916 -0.1294  0.001376
```

   Note that the estimates are the same, but when using quasi-likelihood the standard errors are larger resulting in wider confidence intervals. This also affects the values of the test statistics (they are smaller in absolute value when using quasi-likelihood) which reduces the p-values. When we fail to account for over-dispersion this usually causes the standard errors to be underestimated, so we might assume that this is the case here when not using quasi-likelihood. Here is the residual plot when using quasi-likelihood.

```
set.seed(123)
d <- data.frame(p = predict(m.quasi), r = rstudent(m.quasi))
p <- ggplot(d, aes(x = p, y = r)) + theme_minimal() +
  geom_jitter(height = 0, width = 0.01, alpha = 0.5) +
  labs(x = "Predicted Value (log scale)",
    y = "Studentized Residual") +
  geom_hline(yintercept = c(-2, 2), linetype = 3)
plot(p)
```

[6]Note that this is not the only way to use quasi-likelihood to deal with over-dispersion in Poisson regression. Another common approach is to specify the variance structure $\text{Var}(Y_i) = \phi E(Y_i)^p$ where p is some specified value. We can view the variance structure $\text{Var}(Y_i) = \phi E(Y_i)^p$ as a special case where $p = 1$. Recall that this can be specified when using the `glm` function with `family = quasipoisson`.



This is a significant improvement. The proportion of residuals with absolute values is much less.

```
mean(abs(rstudent(m.quasi)) > 2)
```

```
[1] 0.04348
```

It is difficult to see if there is any clear trend in the residuals. There might be a bit more variability for higher predicted values, but the trend is not very pronounced.

3. In the previous homework assignment you estimated (a) the expected number of accidents with and without a posted speed limit each year and (b) the rate ratio for describing the relationship between whether or not a limit was posted and the expected number of accidents. Do this again but using the model you estimated in the previous problem using quasi-likelihood. Compare these estimates to what you obtained in the previous homework and discuss briefly what has (or has not) changed and how.

   Solution: First the estimated expected number of accidents when using quasi-likelihood and when not using quasi-likelihood.

```
library(emmeans)
emmeans(m, ~limit*year, type = "response")
```

```
 limit year rate    SE  df asymp.LCL asymp.UCL
 no    1961 23.7 0.543 Inf      22.6      24.8
 yes   1961 19.6 0.704 Inf      18.3      21.0
 no    1962 22.2 0.637 Inf      21.0      23.5
 yes   1962 18.4 0.547 Inf      17.4      19.5

Confidence level used: 0.95
Intervals are back-transformed from the log scale
```

```
emmeans(m.quasi, ~limit*year, type = "response")
```

```
 limit year rate    SE  df asymp.LCL asymp.UCL
 no    1961 23.7 0.997 Inf      21.8      25.7
 yes   1961 19.6 1.292 Inf      17.2      22.3
 no    1962 22.2 1.168 Inf      20.0      24.6
 yes   1962 18.4 1.004 Inf      16.5      20.5

Confidence level used: 0.95
```

```
Intervals are back-transformed from the log scale
```

And next the rate ratios for the effect of limits.

```
pairs(emmeans(m, ~limit|year, type = "response"),
  infer = TRUE, reverse = TRUE)
```

```
year = 1961:
 contrast ratio     SE  df asymp.LCL asymp.UCL null z.ratio p.value
 yes / no 0.828 0.0294 Inf     0.772     0.887    1  -5.327  <.0001

year = 1962:
 contrast ratio     SE  df asymp.LCL asymp.UCL null z.ratio p.value
 yes / no 0.828 0.0294 Inf     0.772     0.887    1  -5.327  <.0001

Confidence level used: 0.95
Intervals are back-transformed from the log scale
Tests are performed on the log scale
```

```
pairs(emmeans(m.quasi, ~limit|year, type = "response"),
  infer = TRUE, reverse = TRUE)
```

```
year = 1961:
 contrast ratio     SE  df asymp.LCL asymp.UCL null z.ratio p.value
 yes / no 0.828 0.0539 Inf     0.729     0.941    1  -2.903  0.0037

year = 1962:
 contrast ratio     SE  df asymp.LCL asymp.UCL null z.ratio p.value
 yes / no 0.828 0.0539 Inf     0.729     0.941    1  -2.903  0.0037

Confidence level used: 0.95
Intervals are back-transformed from the log scale
Tests are performed on the log scale
```

Note that the estimates of the expected rates and rate ratios are the same, but the standard errors are larger when using quasi-likelihood resulting in wider confidence intervals, test statistics that are smaller in absolute value, and thus larger p-values (similar to what we saw in the last problem). Again, failing to account for over-dispersion frequently results in underestimation of the standard errors.

Typically when using quasi-likelihood for a Poisson or logistic regression model we use a finite degrees of freedom based on the residual degrees of freedom. This is what is done by default by `summary` as well as `contrast`, but not by functions from the **emmeans** package. But you can manually specify the degrees of freedom using the `df` argument. Here is how you would do it here.

```
emmeans(m.quasi, ~limit*year, type = "response", df = 181)
```

```
 limit year rate    SE  df lower.CL upper.CL
 no    1961 23.7 0.997 181     21.8     25.7
 yes   1961 19.6 1.292 181     17.2     22.3
 no    1962 22.2 1.168 181     20.0     24.7
 yes   1962 18.4 1.004 181     16.5     20.5

Degrees-of-freedom method: user-specified
Confidence level used: 0.95
Intervals are back-transformed from the log scale
```

```
pairs(emmeans(m.quasi, ~limit|year, type = "response"),
  infer = TRUE, reverse = TRUE, df = 181)
```

```
year = 1961:
 contrast ratio     SE  df lower.CL upper.CL null t.ratio p.value
 yes / no 0.828 0.0539 181    0.728    0.941    1  -2.903  0.0042

year = 1962:
 contrast ratio     SE  df lower.CL upper.CL null t.ratio p.value
 yes / no 0.828 0.0539 181    0.728    0.941    1  -2.903  0.0042

Degrees-of-freedom method: user-specified
Confidence level used: 0.95
Intervals are back-transformed from the log scale
Tests are performed on the log scale
```

4. The model can be written as

$$\log E(Y_i) = \beta_0 + \beta_1 l_i + \beta_2 y_i,$$

where l_i and y_i are indicator variables for when a limit is posted and for when the year is 1962. The model can be written case-wise as

$$\log E(Y_i) = \begin{cases} \beta_0, & \text{if there is no limit and the year is 1961,} \\ \beta_0 + \beta_1, & \text{if there is a limit and the year is 1961,} \\ \beta_0 + \beta_2, & \text{if there is no limit and the year is 1962,} \\ \beta_0 + \beta_1 + \beta_2, & \text{if there is a limit and the year is 1962.} \end{cases}$$

We can also write the model case-wise as

$$E(Y_i) = \begin{cases} e^{\beta_0}, & \text{if there is no limit and the year is 1961,} \\ e^{\beta_0}e^{\beta_1}, & \text{if there is a limit and the year is 1961,} \\ e^{\beta_0}e^{\beta_2}, & \text{if there is no limit and the year is 1962,} \\ e^{\beta_0}e^{\beta_1}e^{\beta_2}, & \text{if there is a limit and the year is 1962.} \end{cases}$$

Let $\mu_{l,61}$ and $\mu_{n,61}$ denote the expected number of accidents in 1961 when a limit was posted and when a limit was not posted, respectively. Similarly let $\mu_{l,62}$, and $\mu_{n,62}$ be the same expectations but for 1962. We can see from the above that, for example, $\mu_{l,61} = e^{\beta_0}e^{\beta_1}$. Earlier in the course we discussed marginal means and main effects for linear models. We can also define these for a nonlinear model such as this model. The marginal means for the expected number of accidents for when limits are posted and when they are not posted are defined as

$$\mu_l = \frac{\mu_{l,61} + \mu_{l,62}}{2} \quad \text{and} \quad \mu_n = \frac{\mu_{n,61} + \mu_{n,62}}{2},$$

respectively. These are the average expected number of accidents for each limit condition. We can then define the main effect of the limit condition as

$$\mu_l - \mu_n = \frac{\mu_{l,61} + \mu_{l,62}}{2} - \frac{\mu_{n,61} + \mu_{n,62}}{2} = (\mu_{l,61} + \mu_{l,62} - \mu_{n,61} - \mu_{n,62})/2.$$

Estimate the two marginal means and the main effect for the limit condition using the `dmethod` function after writing them as functions of the model parameters β_0, β_1, and β_2.[7] Be sure to report the estimates, standard errors, and confidence intervals for the two marginal means and for the main effect. **Note**: This problem is *extra credit* for students in Stat 436, but is *required* for students in Stat 516.

Solution: First I will estimate the marginal means. I will use the model estimated using quasi-likelihood here.

[7]Remember that the exponential function has the property that $e^a e^b = e^{a+b}$ which can also be written as $\exp(a+b)$. You might find this useful when using the `exp` function in R.

```r
dmethod(m.quasi, pfunc = "(exp(b0+b1) + exp(b0+b1+b2))/2",
  pname = c("b0","b1","b2")) # for limit
```

```
 estimate     se lower upper tvalue  df    pvalue
    19.01 0.9959 17.05 20.96  19.08 Inf 3.435e-81
```

```r
dmethod(m.quasi, pfunc = "(exp(b0) + exp(b0+b2))/2",
  pname = c("b0","b1","b2")) # for no limit
```

```
 estimate     se lower upper tvalue  df     pvalue
    22.96 0.8329 21.33 24.59  27.57 Inf 2.923e-167
```

Next I will estimate the difference in the marginal means or the "main effect" of the limit.

```r
dmethod(m.quasi, pfunc = "(exp(b0+b1) + exp(b0+b1+b2) - exp(b0) - exp(b0+b2))/2",
  pname = c("b0","b1","b2"))
```

```
 estimate    se  lower  upper tvalue  df   pvalue
   -3.952 1.327 -6.553 -1.352 -2.979 Inf 0.002896
```

Interestingly these can be done using the `contrast` function with a custom transformation function. It also uses the delta method.

```r
trtools::contrast(m.quasi,
  a = list(limit = "yes", year = c("1961","1962")),
  tf = function(x) mean(exp(x)))
```

```
 estimate     se lower upper tvalue  df    pvalue
    19.01 0.9959 17.04 20.97  19.08 181 3.318e-45
```

```r
trtools::contrast(m.quasi,
  a = list(limit = "yes", year = c("1961","1962")),
  tf = function(x) mean(exp(x)))
```

```
 estimate     se lower upper tvalue  df    pvalue
    19.01 0.9959 17.04 20.97  19.08 181 3.318e-45
```

```r
trtools::contrast(m.quasi,
  a = list(limit = c("yes","yes","no","no"), year = c("1961","1962","1961","1962")),
  tf = function(x) (exp(x[1]) + exp(x[2]) - exp(x[3]) - exp(x[4]))/2)
```

```
 estimate    se  lower  upper tvalue  df   pvalue
   -3.952 1.327 -6.571 -1.334 -2.979 181 0.003293
```

This functionality of the `contrast` function is still a bit experimental.

Presence-Absence of Little Owls in Nest Boxes

The data frame `anoctua` in the **blmeco** package is from a study that investigated the placement of nest boxes for little owls (*Athene noctua*) in central Germany.[8]

```r
library(blmeco)
data(anoctua)
head(anoctua)
```

```
  Id PA elevation
1  1  1       223
2  2  1       260
```

[8]Gottschalk, T. K., Ekschmitt, K., & Wolters, V. (2011). Efficient placement of nest boxes for the little owl (*Athene noctua*). *Journal of Raptor Research*, *45(1)*, 1–14.

```
3  3  1       243
4  4  1       246
5  5  1       176
6  6  1       160
```

The variables that concern us are `PA` (an indicator variable for the presence of an owl in a given nest box) and elevation (in meters above sea level).[9] The `Id` variable is just an integer identifier for each nest box. Assume that the owls tend to prefer nests at an elevation that is not too low and not too high. To model this we might use a polynomial logistic regression model.

```
m <- glm(PA ~ elevation + I(elevation^2), family = binomial, data = anoctua)
summary(m)$coefficients
```

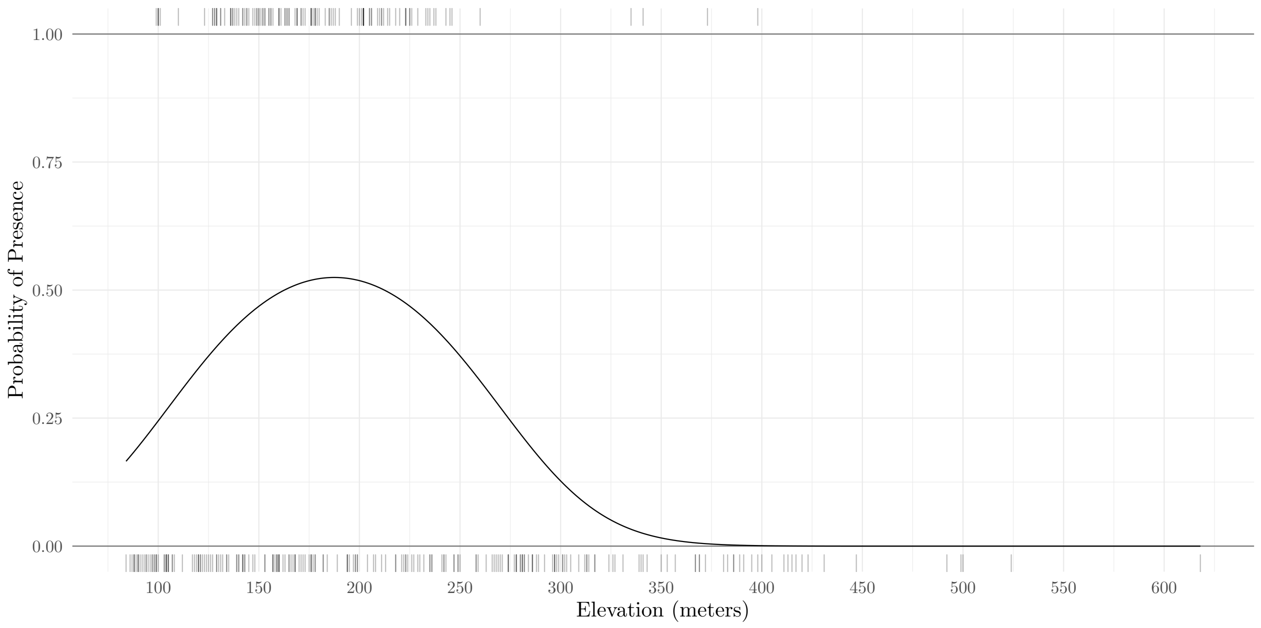
```
               Estimate Std. Error z value  Pr(>|z|)
(Intercept)    -5.52928  1.194e+00  -4.631 3.645e-06
elevation       0.06002  1.287e-02   4.664 3.103e-06
I(elevation^2) -0.00016  3.276e-05  -4.886 1.031e-06
```

Such a model allows for the probability of a nest box being used to peak at a certain elevation and decrease as the elevation moves below and above that value. This can be seen in a plot of the model with the data, using what is called a rug plot to show the raw data.[10]

```
d <- data.frame(elevation = seq(84, 618, length = 1000))
d$yhat <- predict(m, newdata = d, type = "response")

p <- ggplot(anoctua, aes(x = elevation, y = PA)) + theme_minimal() +
  geom_rug(data = subset(anoctua, PA == 0), alpha = 0.25, sides = "b") +
  geom_rug(data = subset(anoctua, PA == 1), alpha = 0.25, sides = "t") +
  geom_hline(yintercept = c(0, 1), alpha = 0.5) +
  labs(x = "Elevation (meters)", y = "Probability of Presence") +
  scale_x_continuous(breaks = seq(100, 700, by = 50)) +
  geom_line(aes(y = yhat), data = d)
plot(p)
```

[9]A model for these data based on just elevation will be a considerable oversimplification because the locations of the nest boxes varied in terms of several other important environmental variables.

[10]Plotting data with a binary response can be a bit tricky. One approach I sometimes use is to plot the binary responses using what is sometimes called a "rug plot" where each point is shown as a short line segment, with a "rug" at the top indicating the elevations of nest boxes with owls present, and another at the bottom indicating the elevations of nest boxes with no owl present. This works relatively well if there are not too many overlapping observations. Note how I use `subset` to select which observations to put into the top and bottom rugs.



The "rugs" at the top and bottom of the plot show the elevations of nest boxes where owls were present and absent, respectively. In what follows you will use the delta method to obtain estimates of meaningful nonlinear functions of the parameters of this model. When specifying these functions, make use of parentheses to enforce the proper order of operations, use `exp` and `sqrt` for the functions $\exp(x)$ and $\sqrt{x}$, respectively, and remember to use `*` for multiplication and `^` for exponentiation (other than e^x). Also note that you can check your results against the figure to see if they look reasonable. This is a good way to catch some errors.

1. The logistic regression model estimated above can be written as

$$E(Y) = \frac{e^{\eta}}{1+e^{\eta}},$$

where

$$\eta = \beta_0 + \beta_1 x + \beta_2 x^2,$$

and where x is elevation and Y is the binary response variable so that $E(Y)$ is the probability that a nest box at a given elevation would be occupied.[11] Let x_m be the elevation at which the probability of presence is *maximized*. In lecture on April 4th there was an example where we found the percent hardwood that would maximize the expected tensile strength. Applying a similar argument we can show that the elevation that would maximize presence probability would also maximize η. The argument is that x_m solves the equation

$$\frac{d(\beta_0 + \beta_1 x + \beta_2 x^2)}{dx} = 0$$

for x. The solution is

$$x_m = \frac{-\beta_1}{2\beta_2},$$

just like the example from lecture. The fact that this is a logistic regression model does not change this result since $E(Y)$ is a monotonic function of η (i.e., η is the log of the odds of presence, so whatever maximizes this will also maximize the probability of presence). Use the `dmethod` function to obtain estimate, standard error, and confidence interval for x_m.

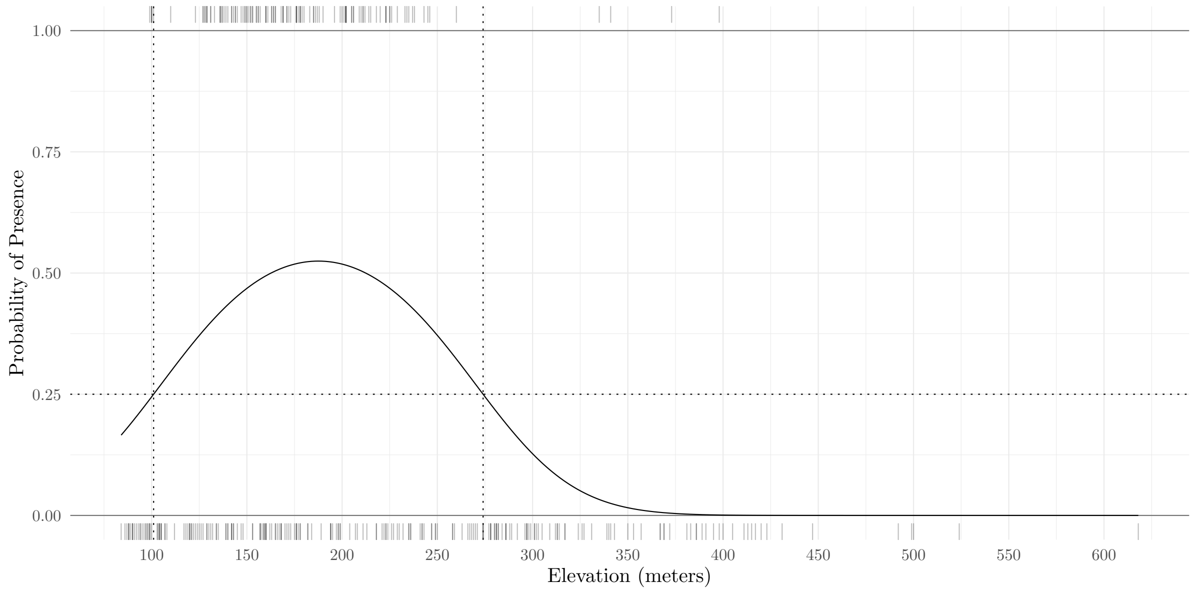
Solution: The value of x_m can be estimated as follows.

```
dmethod(m, pfunc = "-b1/(2*b2)", pname = c("b0","b1","b2"))
```

[11] Recall that for a binary response variable $E(Y) = P(Y = 1)$.

```
 estimate    se lower upper tvalue  df     pvalue
    187.5 6.853 174.1   201  27.36 Inf 7.317e-165
```

2. Suppose we want to find the *two* values of elevation, x_l and x_h, such that the probability of presence is *at least* 0.25 for elevations between x_l and x_h. The figure below depicts these two values for the estimated model.



We can see that x_l and x_h are approximately 100 and 275 meters, respectively, but we need to express them as functions of the model parameters to obtain exact estimates as well as standard errors. This can be done by solving

$$\log\left[\frac{0.25}{1-0.25}\right] = \beta_0 + \beta_1 x + \beta_2 x^2$$

for x, but note that there should be *two* values of x that solve this equation: x_l and x_h.[12] This is basically the problem of solving the quadratic equation

$$ax^2 + bx + c = 0$$

where $a = \beta_2$, $b = \beta_1$, and $c = \beta_0 - \log(1/3)$. The solution is given by the quadratic formula

$$x = \frac{-b \pm \sqrt{b^2 - 4ac}}{2a}.$$

Substituting $a = \beta_2$, $b = \beta_1$, and $c = \beta_0 - \log(1/3)$ we get

$$x = \frac{-\beta_1 \pm \sqrt{\beta_1^2 - 4\beta_2[\beta_0 - \log(1/3)]}}{2\beta_2}.$$

Note that this equation gives *two* solutions for x, x_l and x_h, by interpreting the operator "±" as "+" for one value and "−" for the other value. Use the `dmethod` function to obtain estimates, standard errors, and confidence intervals for x_l and x_h.

Solution: The values of x_l and x_h can be estimated as follows.

```r
dmethod(m, pfunc = "(-b1 + sqrt(b1^2 - 4*b2*(b0 - log(1/3))))/(2*b2)",
  pname = c("b0","b1","b2"))
```

[12]Note that you can easily generalize this approach to probabilities other than 0.25.

```
 estimate    se lower upper tvalue  df    pvalue
      101 9.815  81.8 120.3  10.29 Inf 7.465e-25
```

```
dmethod(m, pfunc = "(-b1 - sqrt(b1^2 - 4*b2*(b0 - log(1/3))))/(2*b2)",
  pname = c("b0","b1","b2"))
```

```
 estimate    se lower upper tvalue  df     pvalue
      274 9.317 255.8 292.3  29.41 Inf 3.919e-190
```

3. A quadratic logistic regression model will have a better fit to the data if we apply a logarithmic transformation to elevation so that

$$\eta = \beta_0 + \beta_1 \log(x) + \beta_2 \log(x)^2.$$

This can be seen by looking at the residual deviance of this model versus that without the transformation. This model can be estimated as follows.

```
m <- glm(PA ~ log(elevation) + I(log(elevation)^2), family = binomial, data = anoctua)
summary(m)$coefficients
```

```
                    Estimate Std. Error z value  Pr(>|z|)
(Intercept)         -190.528     30.643  -6.218 5.044e-10
log(elevation)        74.294     11.878   6.255 3.979e-10
I(log(elevation)^2)   -7.232      1.149  -6.295 3.067e-10
```

Some algebra will show that for this model we have that

$$x_m = \exp\left(\frac{-\beta_1}{2\beta_2}\right)$$

and the solutions to x_l and x_m are given by

$$x = \exp\left(\frac{-\beta_1 \pm \sqrt{\beta_1^2 - 4\beta_2[\beta_0 - \log(1/3)]}}{2\beta_2}\right).$$

Produce a plot of this new model like that shown in the previous problem. You do not need to include the horizontal and vertical dotted lines.[13] Then use the `dmethod` function to obtain estimates, standard errors, and confidence intervals for x_m, x_l, and x_h. **Note**: This problem is *extra credit* for students in Stat 436, but is *required* for students in Stat 516.

Solution: Here is how to find the estimates of x_m, x_l, and x_h for this model.

```
dmethod(m, pfunc = "exp(-b1/(2*b2))", pname = c("b0","b1","b2"))
```

```
 estimate    se lower upper tvalue  df    pvalue
    170.1 4.979 160.4 179.9  34.16 Inf 8.57e-256
```

```
dmethod(m, pfunc = "exp((-b1 + sqrt(b1^2 - 4*b2*(b0 - log(1/3))))/(2*b2))",
  pname = c("b0","b1","b2"))
```

```
 estimate    se lower upper tvalue  df     pvalue
      110 4.795 100.6 119.4  22.94 Inf 1.806e-116
```

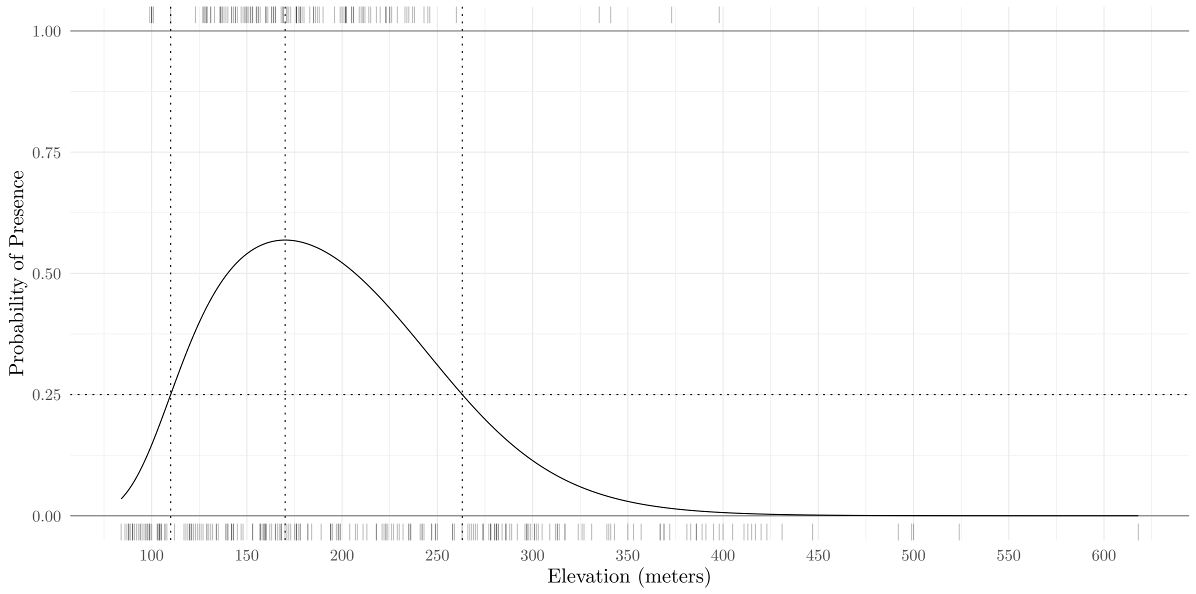
```
dmethod(m, pfunc = "exp((-b1 - sqrt(b1^2 - 4*b2*(b0 - log(1/3))))/(2*b2))",
  pname = c("b0","b1","b2"))
```

```
 estimate    se lower upper tvalue  df     pvalue
    263.1 9.524 244.4 281.8  27.62 Inf 5.713e-168
```

[13] If you are curious, the horizontal line is drawn using `geom_hline(yintercept = 0.25, linetype = 3)` and the vertical lines are drawn using `geom_vline(xintercept = c(xl,xu), linetype = 3)` where `xl` and `xu` are the estimates of x_l and x_h, respectively.

Here is a plot of the model with annotations showing the estimates of x_m, x_l, and x_h.

```r
d <- data.frame(elevation = seq(84, 618, length = 1000))
d$yhat <- predict(m, newdata = d, type = "response")

p <- ggplot(anoctua, aes(x = elevation, y = PA)) + theme_minimal() +
  geom_rug(data = subset(anoctua, PA == 0), alpha = 0.25, sides = "b") +
  geom_rug(data = subset(anoctua, PA == 1), alpha = 0.25, sides = "t") +
  geom_hline(yintercept = c(0, 1), alpha = 0.5) +
  labs(x = "Elevation (meters)", y = "Probability of Presence") +
  scale_x_continuous(breaks = seq(100, 700, by = 50)) +
  geom_line(aes(y = yhat), data = d) +
  geom_hline(yintercept = 0.25, linetype = 3) +
  geom_vline(xintercept = c(170.1, 110, 263.1), linetype = 3)
plot(p)
```



Reactions of Lizards to Fire Ants

The data in the data frame `FireAnts` in the **Lock5Data** are from a study of the reactions of eastern fence lizards (*Sceloporus undulatus*) to red imported fire ants (*Solenopsis invicta*).[14] The ants are native to South America but were unintentionally introduced to the southern United States and are considered an invasive species. These ants are a challenge for the native lizards because they compete for the same nesting habitats, prey on lizard eggs, and their venom is toxic to the lizards. Studies like this one have shown that lizards that have been exposed to the ants have developed escape responses. In this study lizards were exposed to fire ants under controlled conditions, and the researchers observed two behavioral responses: number of twitches and how many seconds elapsed before the lizard would flee from the area. The lizards used in the study came from two different habitats: a habitat that had been invaded by fire ants and another that had not been invaded. One purpose of the study was to determine if prior exposure to fire ants resulted in behavioral changes in the lizards.

Flee times recorded as 61 seconds in the data frame are actually right-censored at 60 seconds (i.e., the researcher did not wait more than one minute for the lizard to flee, so if the lizard did not flee after one minute we assume that the unrealized flee time would be more than one minute). For analysis it is useful

[14]Langkilde, T. (2009). Invasive fire ants alter behavior and morphology of native lizards. *Ecology*, *90(1)*, 208–217.

to create variables to (a) indicate if an observation is censored or not and (b) show the actual flee time or 60 seconds if the flee time was right-censored. The following will create the new variables `censored` and `fleetime`.

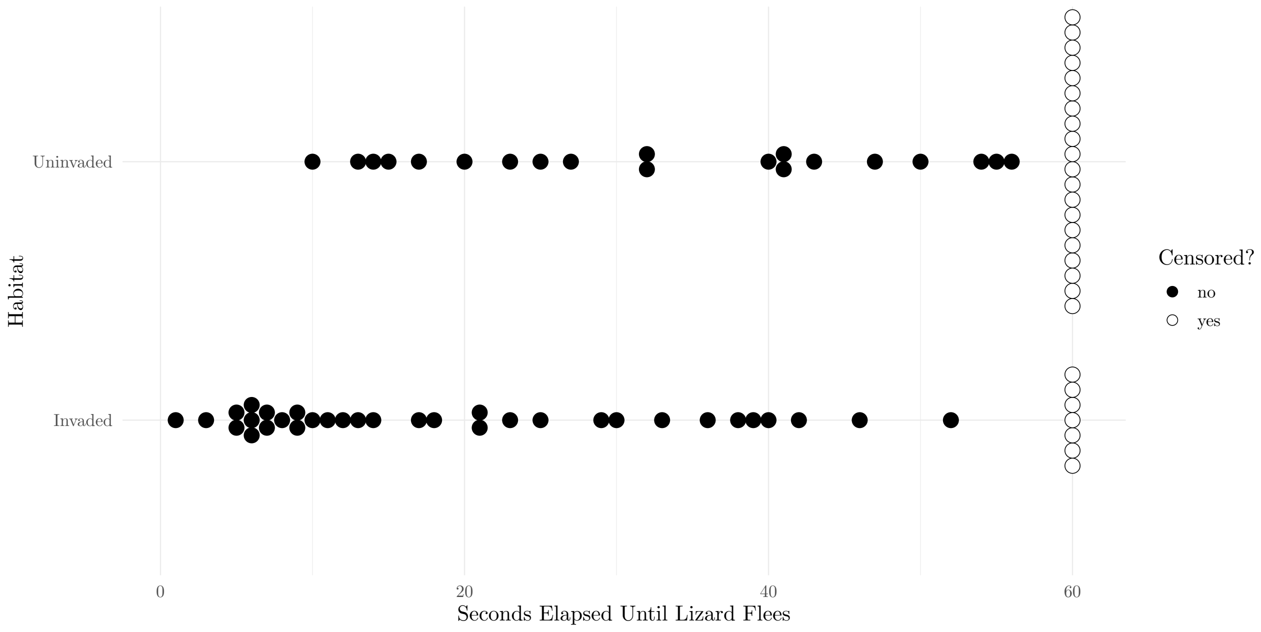
```r
library(Lock5Data)
FireAnts$censored <- ifelse(FireAnts$Flee == 61, "yes", "no")
FireAnts$fleetime <- ifelse(FireAnts$Flee == 61, 60, FireAnts$Flee)
```

You have often seen me use the `dplyr` and `tidyr` packages for data manipulation. Here is another way you can create the new variables.

```r
library(dplyr)
FireAnts <- FireAnts %>%
  mutate(censored = ifelse(Flee == 61, "yes", "no")) %>%
  mutate(fleetime = ifelse(Flee == 61, 60, Flee))
```

We can visualize the data as follows.

```r
library(ggplot2)
p <- ggplot(FireAnts, aes(x = Habitat, y = fleetime, fill = censored)) +
  geom_dotplot(aes(fill = censored), binwidth = 1, binaxis = "y",
    stackdir = "center", method = "histodot") +
  scale_fill_manual(values = c("black", "white")) +
  theme_minimal() + coord_flip() +
  labs(y = "Seconds Elapsed Until Lizard Flees", fill = "Censored?")
plot(p)
```



Note that the open points at 60 seconds are all right-censored times and do not represent actual flee times.

1. Estimate an accelerated failure time model with time until the lizard flees (i.e., `fleetime`) as the response variable. Specify a Weibull distribution for the flee time, and be sure that you properly specify the right-censoring in the data by either creating a "status" variable or by using a logical statement with `==` in the `Surv` function.[15] Use the `flexsurvreg` function from the **flexsurv** package. Report the

[15]You will need to create this variable, noting that it should assume a value of one if the observation is *not* censored, and zero if the observation *is* censored. One way to do this would be to use the `ifelse` function. But another approach is to use the fact that `censored == "no"` will evaluate to one if the statement is true for an observation, and zero if the statement is false for an

parameter estimates, standard errors, and confidence intervals by using the `print` function with the model object created by `flexsurvreg` (recall that `summary` does not work the same with `flexsurvreg` objects as it does with `lm`, `nls`, and `glm` objects).

Solution: Here is the estimated accelerated failure time model.

```
library(flexsurv)
m <- flexsurvreg(Surv(fleetime, censored == "no") ~ Habitat,
  dist = "Weibull", data = FireAnts)
print(m)
```

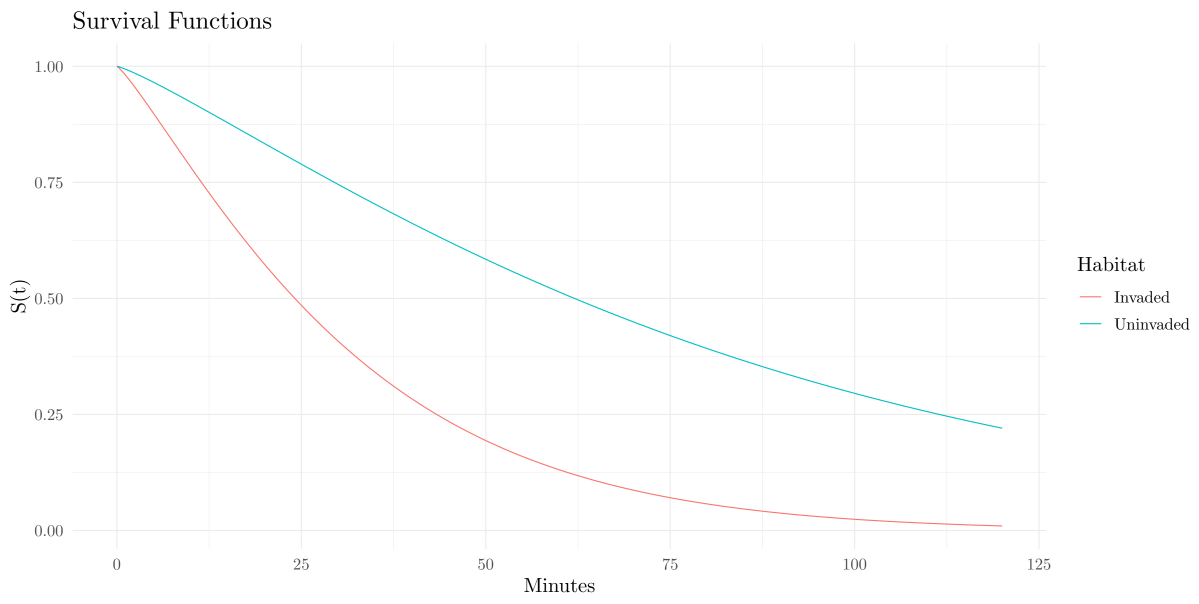
```
Call:
flexsurvreg(formula = Surv(fleetime, censored == "no") ~ Habitat,
    data = FireAnts, dist = "Weibull")

Estimates:
                  data mean  est     L95%    U95%    se      exp(est)  L95%    U95%
shape                 NA      1.182   0.939   1.488   0.139      NA        NA      NA
scale                 NA     32.881  24.584  43.979   4.879      NA        NA      NA
HabitatUninvaded   0.500      0.945   0.451   1.438   0.252   2.572     1.571   4.212

N = 80,  Events: 53,  Censored: 27
Total time at risk: 2917
Log-likelihood = -257.2, df = 3
AIC = 520.4
```

2. Plot two estimated survival functions and two estimated hazard functions — one for each habitat — based on the model you estimated above. Plot this function over two minutes (120 seconds) starting at zero. You can use the option `B = 0` in the `summary` function to turn off calculation of the standard errors which can be computationally intensive and not necessary for your plots.

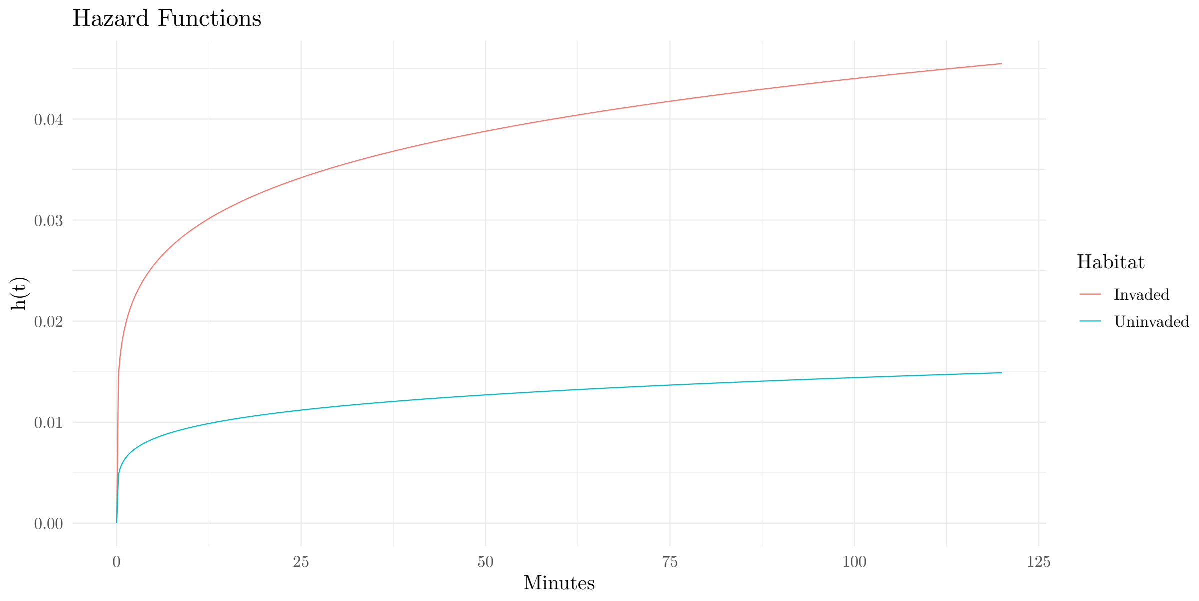
   Solution: Here are the estimated survival and hazard functions functions.

```
d <- data.frame(Habitat = c("Invaded","Uninvaded"))
d <- summary(m, newdata = d, t = seq(0, 120, length = 500),
  type = "survival", B = 0, tidy = TRUE)
p <- ggplot(d, aes(x = time, y = est, color = Habitat)) + theme_minimal() +
  geom_line() + labs(x = "Minutes", y = "S(t)", title = "Survival Functions")
plot(p)
```

observation.



```r
d <- data.frame(Habitat = c("Invaded","Uninvaded"))
d <- summary(m, newdata = d, t = seq(0, 120, length = 500),
  type = "hazard", B = 0, tidy = TRUE)
p <- ggplot(d, aes(x = time, y = est, color = Habitat)) + theme_minimal() +
  geom_line() + labs(x = "Minutes", y = "h(t)", title = "Hazard Functions")
plot(p)
```



Note that for any given time point, the survival probability of a lizard from the invaded habitat is smaller (i.e., they are less likely to wait at least that long to flee) and the hazard rate is higher (i.e., they are more likely to flee in the next moment if they have not done so already). This is consistent with the hypothesis that lizards from the invaded habitat have learned to avoid the fire ants.

3. The accelerated failure time model you estimated in the previous problem can be written as

$$\log T_i = \beta_0 + \beta_1 x_i + \sigma\epsilon_i$$

or

$$T_i = e^{\beta_0} e^{\beta_1 x_i} e^{\sigma \epsilon_i},$$

where T_i and x_i are time until the lizard flees and an indicator variable for the habitat, respectively, for the i-th observation. Report an estimate and confidence interval for e^{β_1}, and explain briefly how you would interpret its value in terms of time until the lizard flees for one habitat versus the other.

Solution: We can see from the output that the estimate is about 2.572 and the confidence interval is (1.571,4.212). This means that for lizards from an uninvaded habitat their time until fleeing is about 2.6 times longer than lizards from the invaded habitat (on average). Note that you can estimate the expected time until fleeing as follows.

```
d <- data.frame(Habitat = c("Invaded","Uninvaded"))
d <- summary(m, newdata = d, type = "mean", tidy = TRUE)
d
```

```
    est   lcl    ucl   Habitat
1 31.05 23.59  42.01   Invaded
2 79.87 53.39 124.03 Uninvaded
```

4. As we discussed in class, an accelerated failure time model that specifies a Weibull distribution for time is also a proportional hazards model. However the parameterization for the proportional hazards model is different. A Weibull proportional hazards model can be estimated using `flexsurvreg` with `dist = "weibullPH"`. Estimate this model and report the parameter estimates, standard errors, and confidence intervals using the `print` function. Also give the hazard ratio for the effect of habitat and briefly interpret this hazard ratio in terms of how it characterizes the relationship between the hazard functions for the two habitats.

   Solution: Here is how to estimate the proportional hazards model.

```
m <- flexsurvreg(Surv(fleetime, censored == "no") ~ Habitat,
  dist = "WeibullPH", data = FireAnts)
print(m)
```

```
Call:
flexsurvreg(formula = Surv(fleetime, censored == "no") ~ Habitat,
    data = FireAnts, dist = "WeibullPH")

Estimates:
                  data mean  est       L95%      U95%      se        exp(est)  L95%
shape                   NA    1.18190   0.93867   1.48816   0.13894        NA        NA
scale                   NA    0.01611   0.00564   0.04603   0.00863        NA        NA
HabitatUninvaded   0.50000   -1.11648  -1.67764  -0.55532   0.28631   0.32743   0.18681
                  U95%
shape                   NA
scale                   NA
HabitatUninvaded   0.57389

N = 80,  Events: 53,  Censored: 27
Total time at risk: 2917
Log-likelihood = -257.2, df = 3
AIC = 520.4
```

   The estimate of the hazard ratio is about 0.33, showing that the hazard rate for lizards from the uninvaded habitat is about a third that of lizards from the invaded habitat. This is consistent with the plot of the hazard functions.

5. Estimate a Poisson regression model with the number of twitches as the response variable and habitat as the explanatory variable. Estimate a rate ratio for habitat and write a sentence that properly interprets

the value of this rate ratio in terms of the expected number of twitches.

Solution: This is a bit of a review problem since you've already had some experience with Poisson regression.

```r
m <- glm(Twitches ~ Habitat, family = poisson, data = FireAnts)
summary(m)$coefficients
```

```
                 Estimate Std. Error z value  Pr(>|z|)
(Intercept)        1.0116    0.09535  10.610 2.684e-26
HabitatUninvaded  -0.9163    0.17838  -5.137 2.794e-07
```

```r
trtools::contrast(m, tf = exp,
  a = list(Habitat = c("Uninvaded","Invaded")),
  b = list(Habitat = c("Invaded","Uninvaded")),
  cname = c("Uninvaded/Invaded","Invaded/Uninvaded"))
```

```
                  estimate lower  upper
Uninvaded/Invaded      0.4 0.282 0.5674
Invaded/Uninvaded      2.5 1.762 3.5463
```

The expected number of twitches for lizards from the uninvaded habitat is about 0.4 times that of lizards from the invaded habitat (i.e., about 60% less). Also, the expected number of twitches for lizards from the invaded habitat is about 2.5 times that of lizard from the univaded habitat (i.e., about 150% more).