

```
species <- read.table("species.txt", header = T, colClasses = c("l", "n", "n"))
head(species)
  pH Biomass Species
high 0.4692972      30
high 1.7388704      39
high 2.0897785      44
high 3.9257871      35
high 4.3667927      25
high 5.4819747      29
species_mod2 <- glm(Species ~ Biomass * pH, poisson, data = species)
summary(species_mod2)
```

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Variance-Residuals:

```
  Min      1Q   Median      3Q      Max
4978 -0.7485 -0.0402  0.5575  3.2297
```

Coefficients:

```
              Estimate Std. Error z value Pr(>|z|)
(Intercept)   3.76812     0.06153   61.240 < 2e-16 ***
Biomass       -0.10713     0.01249  -8.577 < 2e-16 ***
low           -0.81557     0.10284  -7.935 2.18e-15 ***
mid           -0.33146     0.09217  -3.596 0.000272 ***
Biomass:pHlow -0.15503     0.04003  -3.873 0.0000774 ***
Biomass:pHmid -0.03189     0.02308  -1.382 0.166934
```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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```
Null deviance: 452.346 on 89 degrees of freedom
Residual deviance: 83.201 on 84 degrees of freedom
```



Number of Fisher Scoring iterations: 4

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Elinor Jones

University College London, UK

Simon Harden

University College London, UK

Michael J. Crawley

Imperial College London, UK

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