Tutorial #5: Gaussian GLM - interaction

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5. Gaussian GLM

In the previous tutorials, we learned how to use a gaussian GLM when our predictor variable was either a single categorical (`site`) or continuous (`body_length`) variable, or a combination of both variables. However, these models do not allow us to determine whether the effect of our predictor variables are interactive. For example, what if we wanted to know not only whether `site`) and/or `body_length` affected insect `body_mass`, but whether the effect of `body_mass` differs between the different `sites` we sampled during our fieldwork.

We will still be considering the same hypothetical study where we measure the body mass of 20 insects (`body_mass`), their body lengths (`body_length`), at each of two sites (`site`).

```
head(data)
```

```
##    body_mass body_length site
## 1 18.7754002    15.28778    A
## 2 25.5245663    19.07157    A
## 3 23.4864950    14.49438    A
## 4 23.5963224    26.04058    A
## 5 28.9805369    11.87531    A
## 6  0.7743048    20.52689    A
```

5.1. Gaussian GLM - Interaction between predictors

Let's consider a model where we look at whether the body mass of an insect (`body_mass`) is correlated with insect `body_length` AND if insect `body_mass` differed between `site`, and also whether the effect of `body_mass` differs between the different `sites`.

H_0: Larger insects do not weigh more than smaller insects, and there is no difference in insect body mass between sites.

H_1: Larger insects weight more than smaller insects, and there is a difference in insect body mass between sites, and the effect of body length differs between sites.

Fitting the model

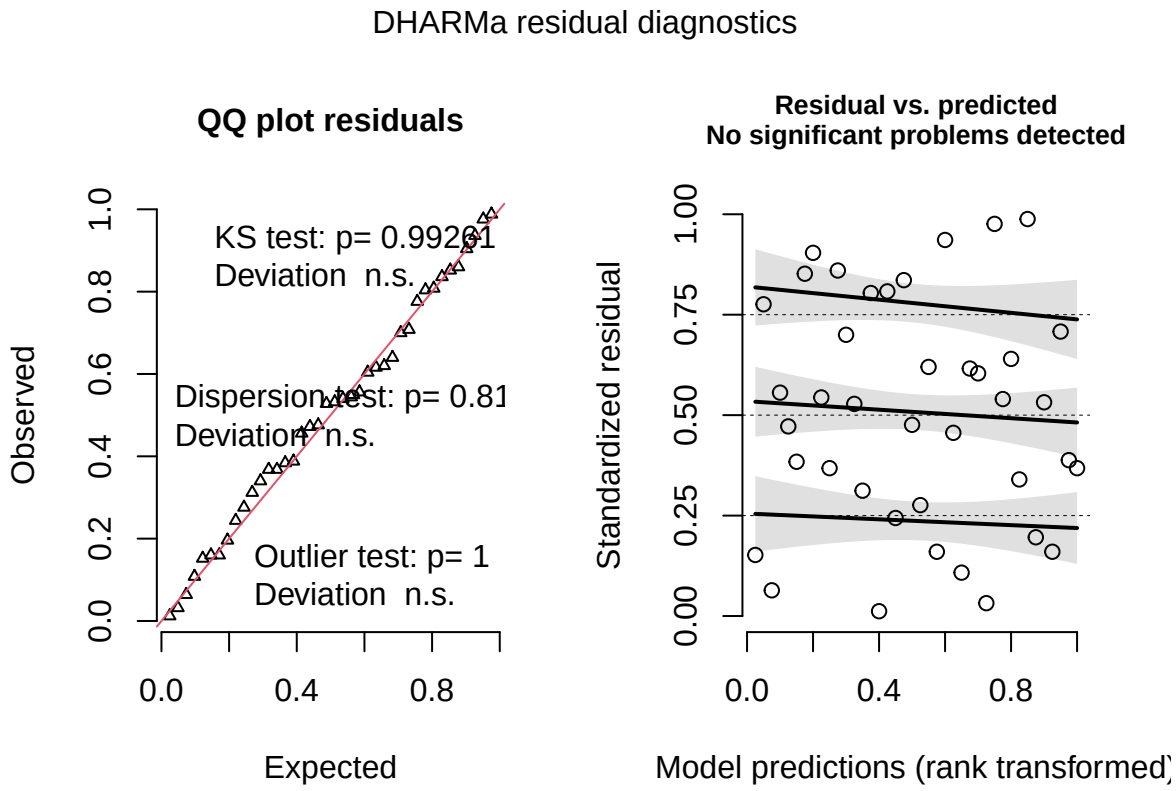
To allow the effects of our predictor variables to vary between each other, we have to change how we formulate our model, slightly. It is very easy though. All we need to do is replace the `+` between our predictors to a `*`.

```
mod1 <- glm(body_mass ~ body_length * site,
            data = data,
            family = gaussian(link = "identity"))
```

Evaluate model fit

Before we look at the results from our model, we must first check whether the GLM that we fit was an appropriate choice for our data.

```
mod1_diagnostis <- DHARMa::simulateResiduals(mod1)
plot(mod1_diagnostis)
```



LHS plot (QQplot): This plot tells us whether our data conforms to a normal (or gaussian) data distribution. If our GLM is a good fit to the data, the white triangles will fall approximately on the red 1:1 line and the KS test P-value will be greater than 0.05. The Kolmorogorov-Smirnoff test (KS test) evaluates whether our data follow the distribution we specified in the `family` argument in the GLM call above (remember: we said "family = gaussian").

- Interpreting this plot tells us that the gaussian data distribution seemed appropriate.

RHS plot (Fitted vs Residuals): This plot tells us whether there are issues with homogeneity of variances. GLM's, like ANOVA and linear regression, assume that the variance in the different groups, or across the range of x values, are approximately equal. We want to see the bold black lines for the different groups fall approximately at y = 0.50, and the range of the boxplots should be relatively similar.

- Interpreting this plot we can happily see that the bold black lines for the two boxplots are approximately at y = 0.50 and the range of the boxplots is almost equal.

Take home: The GLM that we fit seems like a good fit to the data. The inferences that we draw and results we obtain should be reasonable.

Results

Now we get to the bit we are interested in: assessing statistical significance and calculating p-values. To do this, we will use a Likelihood Ratio Test (LRT). When we have 2 or more predictor variables (here: `body_length` and `site`), and we fit an interaction term (`*`), we need to calculate p-values using type III sum-of-squares (SOS). SOS's are just different ways that we ask `R` to calculate p-values.

PLEASE DO NOT USE SUMMARY() - THIS WILL PRODUCE THE WRONG P-VALUES WHEN YOU HAVE MORE THAN 1 PREDICTOR VARIABLE

```
# Perform LRT  with type III sum-of-squares
car::Anova(mod1,
           # Specify we want a Likelihood Ratio Test
           test = "LR",
           # Specify that we want type III SOS
           type = "III")
```

```
## Analysis of Deviance Table (Type III tests)
##
## Response: body_mass
##                   LR Chisq Df Pr(>Chisq)
## body_length        1.1515  1     0.2832
## site               5.0800  1     0.0242 *
## body_length:site   2.2338  1     0.1350
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

So, the LRT tells us that there is no evidence for a statistical correlation between insect `body_length` and `body_mass` ($\chi^2 = 1.15$, d.f. $= 1$, P $= 0.283$), but insect `body_mass` is significantly different between `sites` ($\chi^2 = 5.08$, d.f. $= 1$, P $= 0.024$). There was no evidence for the effect of `body_length` to differ between sites (i.e. our interaction term) ($\chi^2 = 2.23$, d.f. $= 1$, P $= 0.135$). (This shouldn't come as a surprise because `body_length` was not significant).