Basic statistical modelling in R
GLMs (Generalised Linear Models)

Clarke van Steenderen
Department of Zoology and Entomology
Rhodes University
South Africa

Clarke.vansteenderen@ru.ac.za

Generalised Linear Models (GLMs)

Linear models assume normality in residuals/error terms → i.e. a constant relationship between mean and variance. But what if this is not met?

We can apply different error structures to a linear model to account for deviations from normality. This means that we can use a GLM, and specify the "family" type depending on the type of data in question

Common families are:

- **Binomial → two-state data**
- **Negative binomial → count data that is overdispersed**
- **Poisson → count data**
- **Gaussian → normally-distributed; essentially a LM or ANOVA**
- **Exponential/beta → proportions**

An ANOVA is a LM or GLM (Gaussian)
ANOVAs have one or more categorical predictors (1 or 2-way) and a continuous response variable

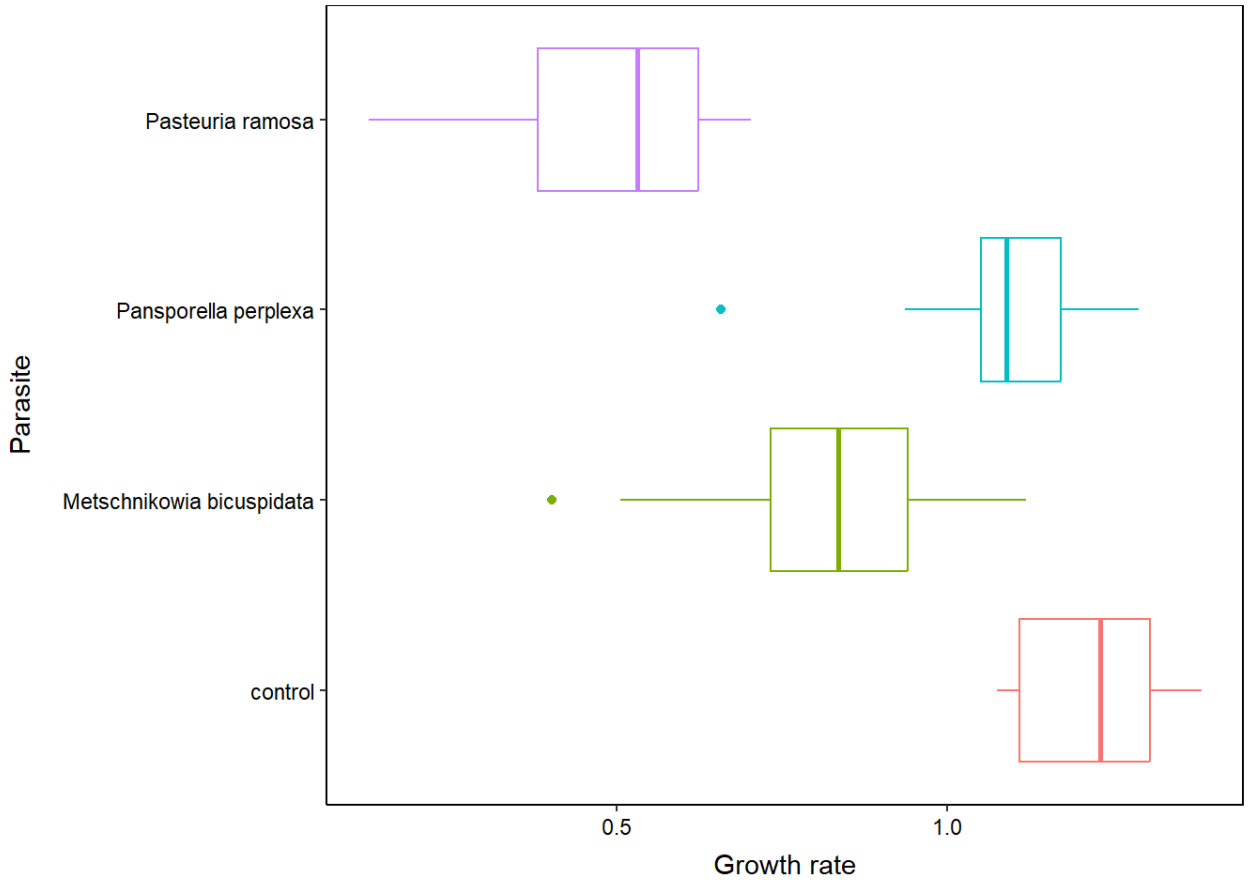
NB: offsets in GLMS → factors that are not strictly predictors, but are used to correct the model (e.g. sampling effort, population size and structure)

Sum-of-square tests assess the significance of each parameter in the model → use `anova(model)` **or** `car::Anova(model, type = x)`

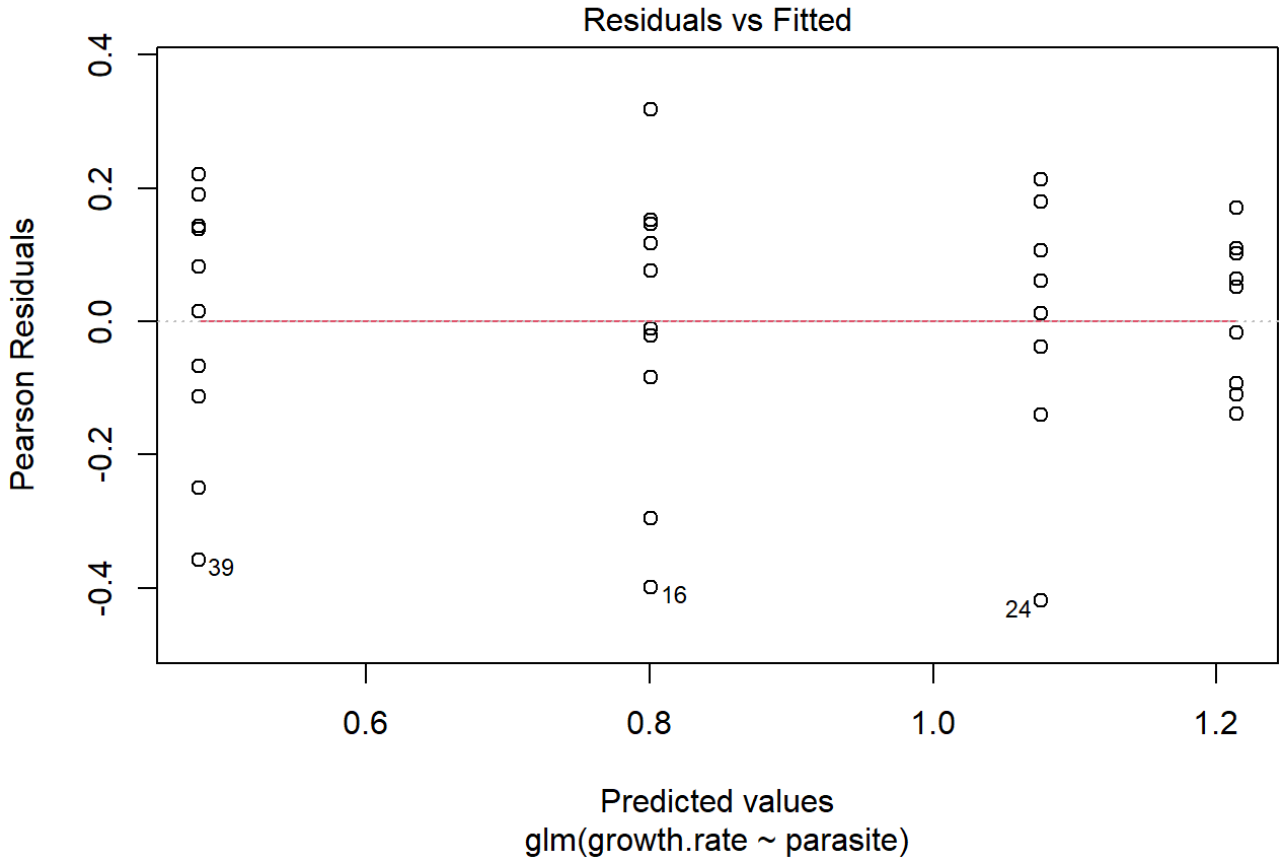
Where `type = I, II, or III`
I: One predictor variable
II: Two or more predictors with no interaction terms
III: Two or more predictors with interaction terms

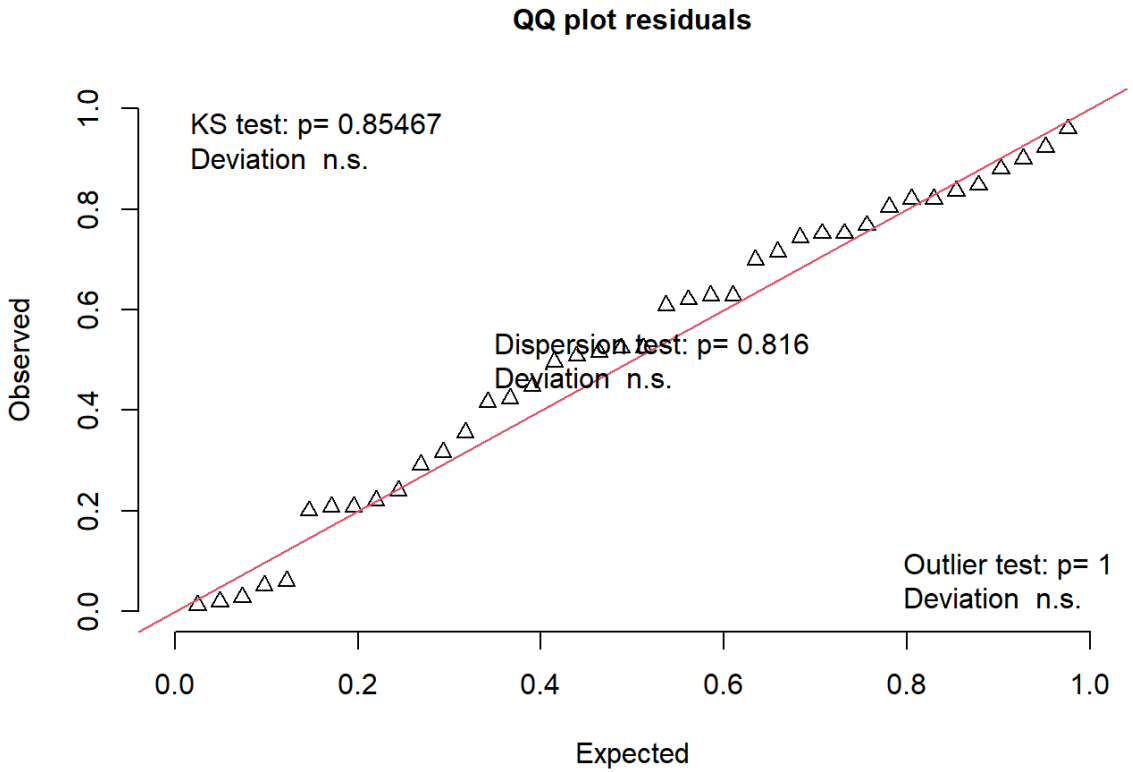
GLM: Gaussian

Growth rates (continuous) across different parasite species (categorical)
GLMs with a Beta distribution are sometimes used for rate data, but a Gaussian GLM is simpler, if it meets all the assumptions



```
daphnia.glm.gaus = glm(data = daphnia.data,
growth.rate ~ parasite,
family = gaussian)
```

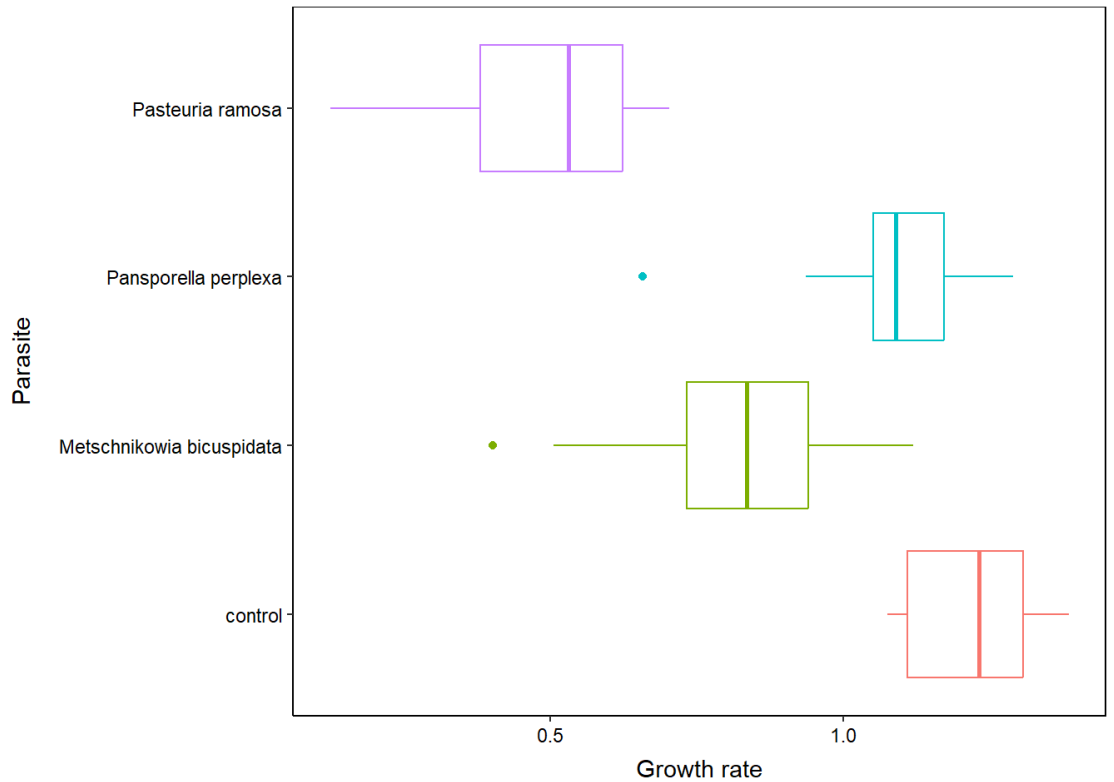




```
anova(daphnia.glm.gaus, test = "LR")
```

```
Analysis of Deviance Table

Model: gaussian, link: identity

Response: growth.rate

Terms added sequentially (first to last)


          Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
NULL                         39     4.3028
parasite  3   3.1379         36     1.1649 < 2.2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
> daphnia.means = Rmisc::summarySE(daphnia.data, measurevar = "growth.rate",
+                                  groupvars = "parasite")
> daphnia.means
                   parasite  N growth.rate        sd         se        ci
1                    control 10   1.2139088 0.1141824 0.03610766 0.0816812
2 Metschnikowia bicuspidata 10   0.8011541 0.2158424 0.06825535 0.1544043
3      Pansporella perplexa 10   1.0763551 0.1795313 0.05677277 0.1284289
4          Pasteuria ramosa 10   0.4822030 0.1938393 0.06129737 0.1386643
```

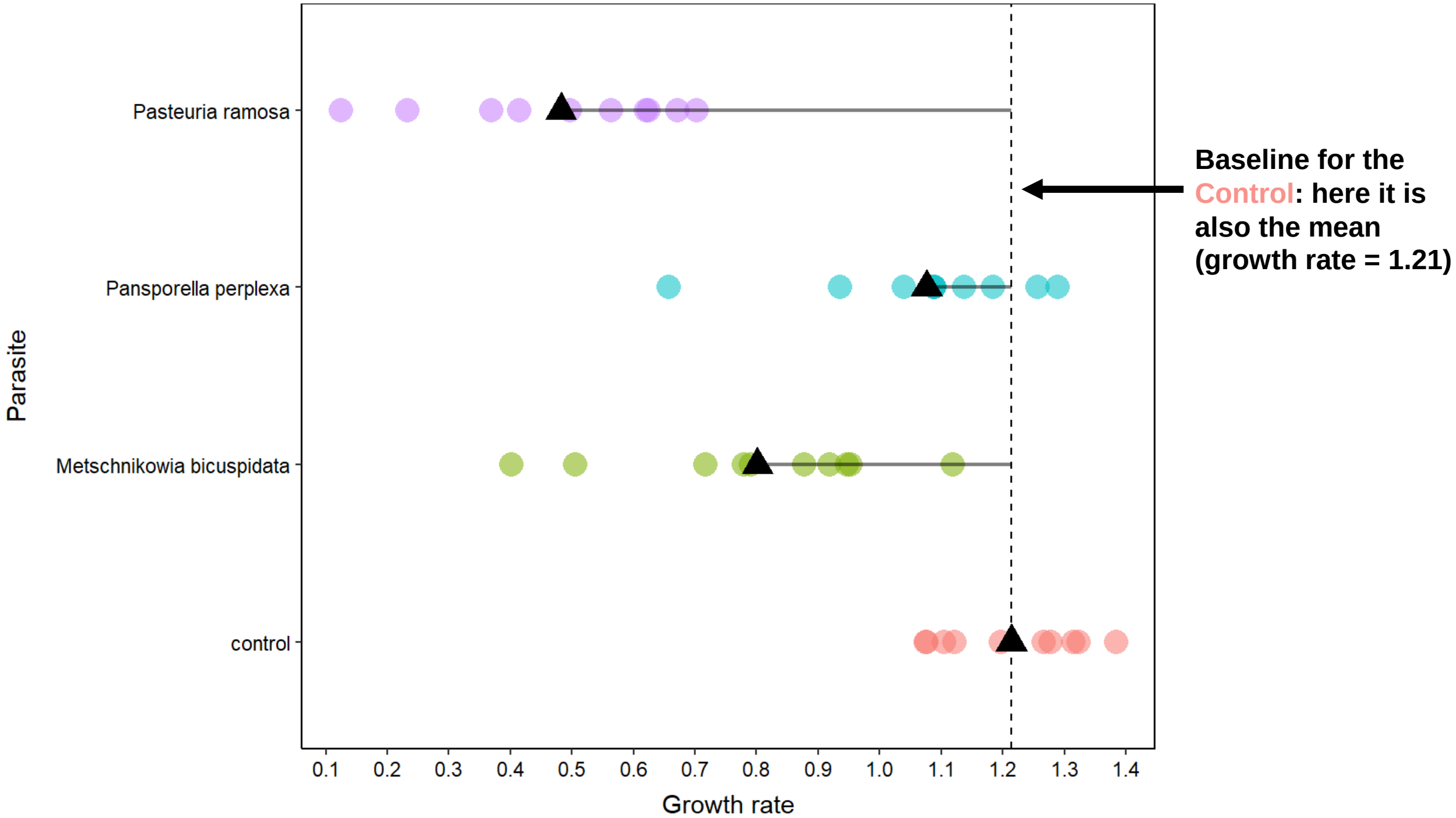


- **The control group is the first "level" alphabetically, and is used as the base category for comparison → this is the (Intercept), and represents the baseline level for the control (1.21391). This is only the case when there is a single categorical predictor, and here, this value is then also the mean**
- **The other Estimate values show how far each other category is from the Control, relative to the baseline level of the Control category**

```
Call:
glm(formula = growth.rate ~ parasite, family = gaussian, data = daphnia.data)

Coefficients:
                                Estimate Std. Error t value Pr(>|t|)
(Intercept)                      1.21391    0.05688  21.340  < 2e-16 ***
parasiteMetschnikowia bicuspidata -0.41275    0.08045  -5.131 1.01e-05 ***
parasitePansporella perplexa      -0.13755    0.08045  -1.710   0.0959 .
parasitePasteuria ramosa          -0.73171    0.08045  -9.096 7.34e-11 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- *M. bicuspidata* is 0.41275 units less than the control: i.e. 1.21391 – 0.41275 = 0.80116, which is significant ($p < 0.001$)

```
Call:
glm(formula = growth.rate ~ parasite, family = gaussian, data = daphnia.data)

Coefficients:
                                 Estimate Std. Error t value Pr(>|t|)
(Intercept)                       1.21391    0.05688  21.340  < 2e-16 ***
parasiteMetschnikowia bicuspidata -0.41275    0.08045  -5.131 1.01e-05 ***
parasitePansporella perplexa      -0.13755    0.08045  -1.710   0.0959 .
parasitePasteuria ramosa          -0.73171    0.08045  -9.096 7.34e-11 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 0.03235768)

    Null deviance: 4.3028  on 39  degrees of freedom
Residual deviance: 1.1649  on 36  degrees of freedom
AIC: -17.935
```


Pasteuria ramosa
Pansporella perplexa
Metschnikowia bicuspidata
control
Parasite
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
1.1
1.2
1.3
1.4
Growth rate
Baseline for the Control: here it is also the mean (growth rate = 1.21)

What if we had another variable, in addition to parasite?

```
glm(formula = growth.rate ~ parasite + temperature,
family = gaussian, data = daphnia.data)
```

Hypothetical output:

```
Coefficients:
                                Estimate Std. Error t value Pr(>|t|)
(Intercept)                      1.50000    0.20000   7.500   < 2e-16 ***
parasiteMetschnikowia bicuspidata -0.30000    0.08000  -3.750   0.0002 ***
parasitePansporella perplexa      -0.10000    0.08500  -1.176   0.2417
parasitePasteuria ramosa          -0.50000    0.09000  -5.556   < 2e-16 ***
temperature                       0.05000    0.01000   5.000   5.6e-06 ***
```

Here, the baseline for the Control would be a mean growth rate of 1.5 when temperature = 0

***M. bicuspidata*, at 0 degrees, would have a growth rate 0.3 units less → i.e. 1.5 – 0.3 = 1.2**

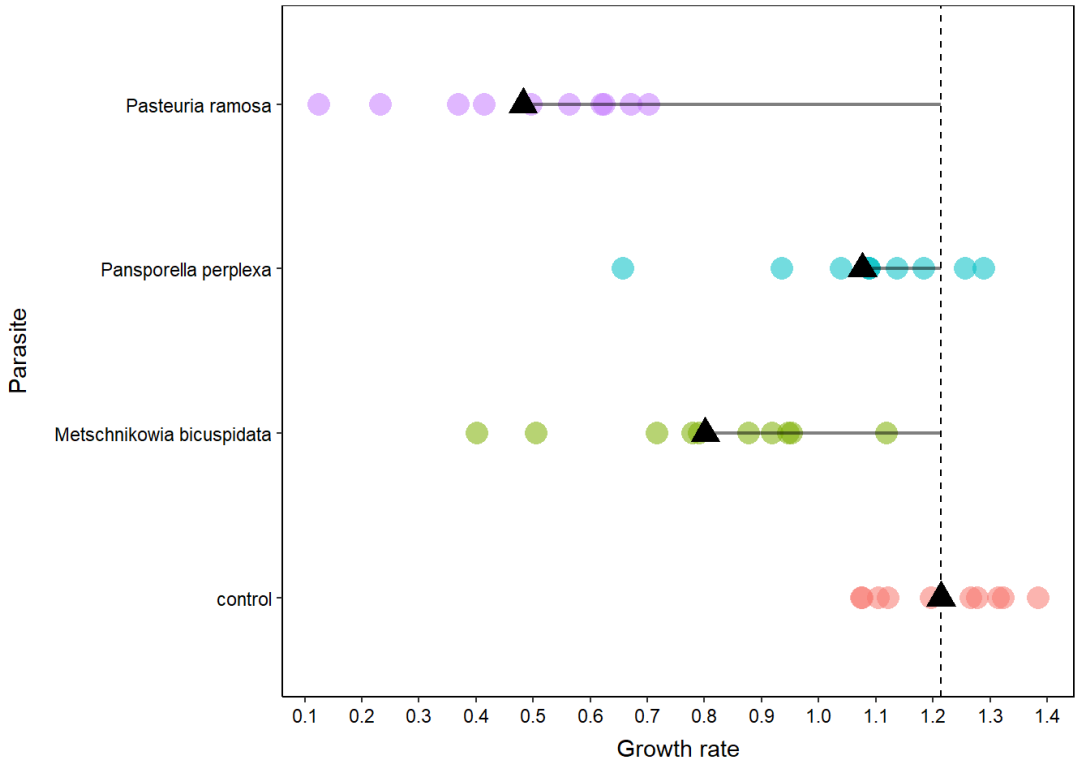
The temperature coefficient ($\beta_1 = 0.05$) means that for every 1 degree increase, growth rate increases by 0.05 across all parasites

We know that growth rates vary significantly across parasites, but which parasites exactly?

Post-hoc tests show comparisons between all our variables, and highlight which ones are significant. The Tukey test is a very popular choice

```
posthoc.daphnia = emmeans::emmeans(daphnia.glm.gaus, pairwise ~ parasite, adjust
= "tukey")
```

```
contrast                                          estimate     SE df lower.CL upper.CL t.ratio p.value
 control - Metschnikowia bicuspidata                 0.413 0.0804 36   0.1961   0.6294   5.131  0.0001
 control - Pansporella perplexa                      0.138 0.0804 36  -0.0791   0.3542   1.710  0.3335
 control - Pasteuria ramosa                          0.732 0.0804 36   0.5150   0.9484   9.096  <.0001
 Metschnikowia bicuspidata - Pansporella perplexa   -0.275 0.0804 36  -0.4919  -0.0585  -3.421  0.0082
 Metschnikowia bicuspidata - Pasteuria ramosa        0.319 0.0804 36   0.1023   0.5356   3.965  0.0018
 Pansporella perplexa - Pasteuria ramosa             0.594 0.0804 36   0.3775   0.8108   7.386  <.0001

Confidence level used: 0.95
Conf-level adjustment: tukey method for comparing a family of 4 estimates
P value adjustment: tukey method for comparing a family of 4 estimates
```



The estimate values (magnitude and sign) indicate differences in size – compare to the plot

contrast	estimate	SE	df	lower.CL	upper.CL	t.ratio	p.value
control - Metschnikowia bicuspidata	0.413	0.0804	36	0.1961	0.6294	5.131	0.0001
control - Pansporella perplexa	0.138	0.0804	36	-0.0791	0.3542	1.710	0.3335
control - Pasteuria ramosa	0.732	0.0804	36	0.5150	0.9484	9.096	<.0001
Metschnikowia bicuspidata - Pansporella perplexa	-0.275	0.0804	36	-0.4919	-0.0585	-3.421	0.0082
Metschnikowia bicuspidata - Pasteuria ramosa	0.319	0.0804	36	0.1023	0.5356	3.965	0.0018
Pansporella perplexa - Pasteuria ramosa	0.594	0.0804	36	0.3775	0.8108	7.386	<.0001

Confidence level used: 0.95
Conf-level adjustment: tukey method for comparing a family of 4 estimates
P value adjustment: tukey method for comparing a family of 4 estimates

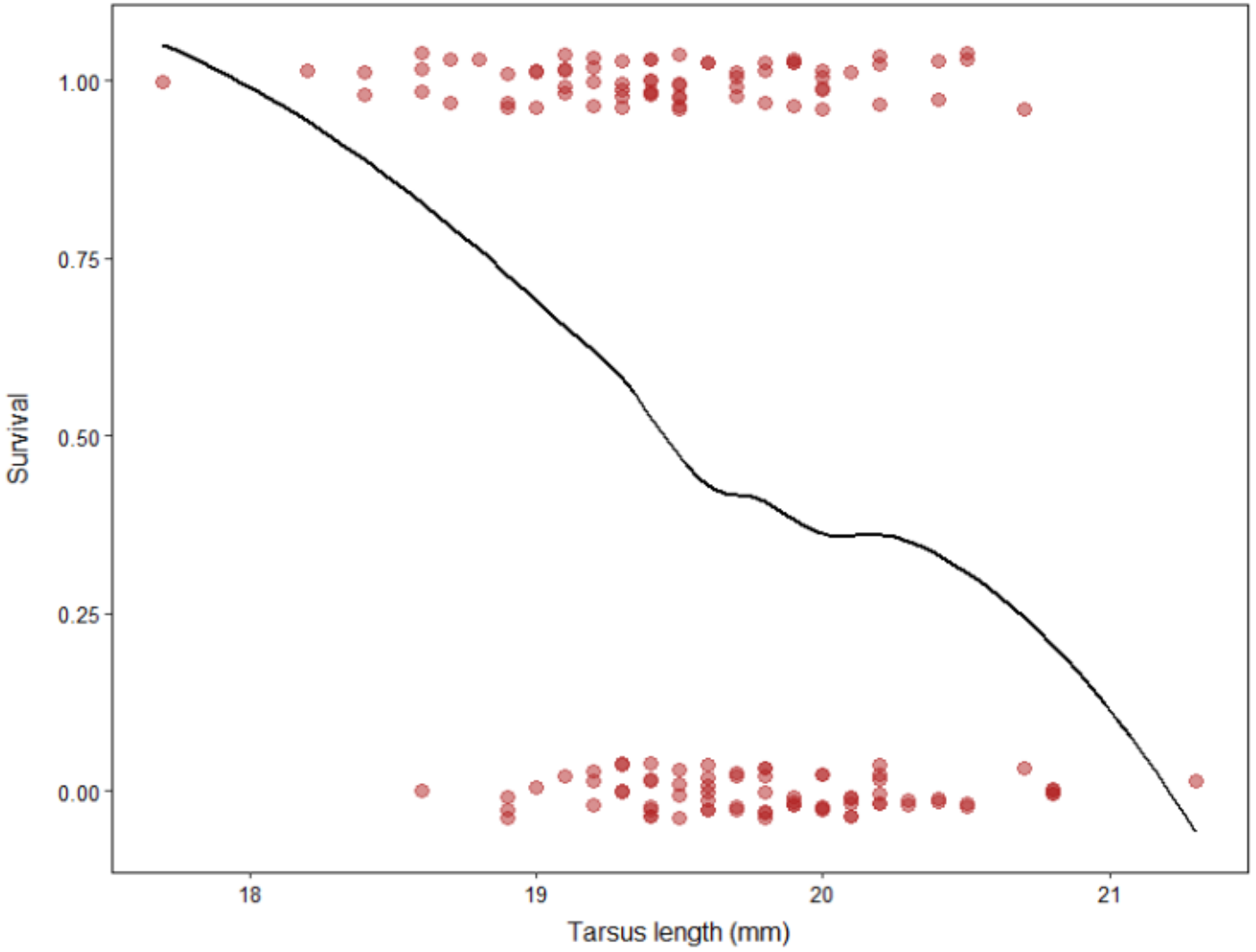
GLM: binomial

Schluter & Smith (1986) had a look at whether different morphological traits of song sparrows had an effect on survival. We'll focus on tarsal length:

```
> head(sparrow.data)
  mass wing tarsus blength bdepth bwidth year sex survival predictions
1 23.7 67.0   17.7     9.1    5.9    6.8 1978   f        1   0.9147634
2 23.1 65.0   19.5     9.5    5.9    7.0 1978   f        0   0.5272762
3 21.8 65.2   19.6     8.7    6.0    6.7 1978   f        0   0.4958586
4 21.7 66.0   18.2     8.4    6.2    6.8 1978   f        1   0.8512375
```

What relationship do you notice?

Is it good for these sparrows to have small or large feet? Why?



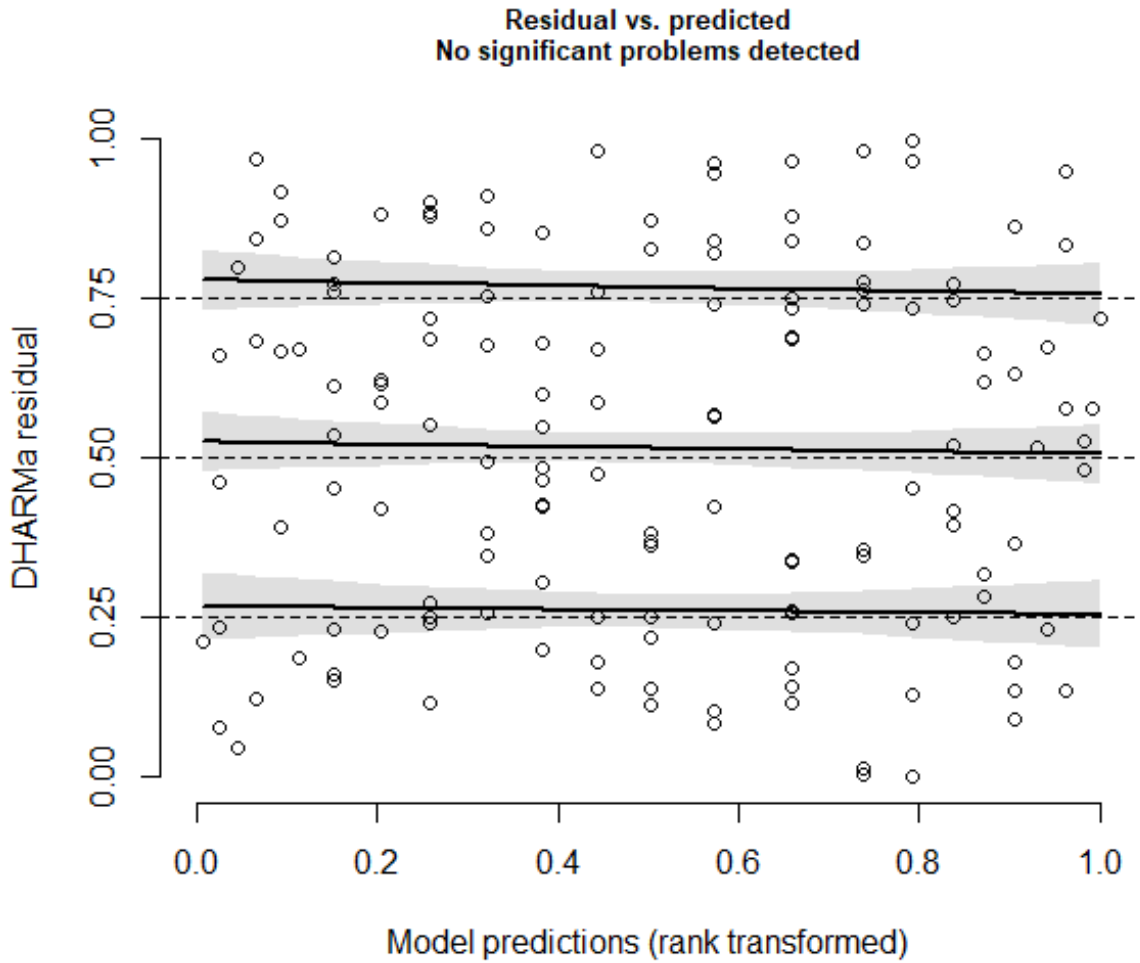
Since we have binomial data (dead or alive), we'll use a binomial GLM using the `glmmTMB` package

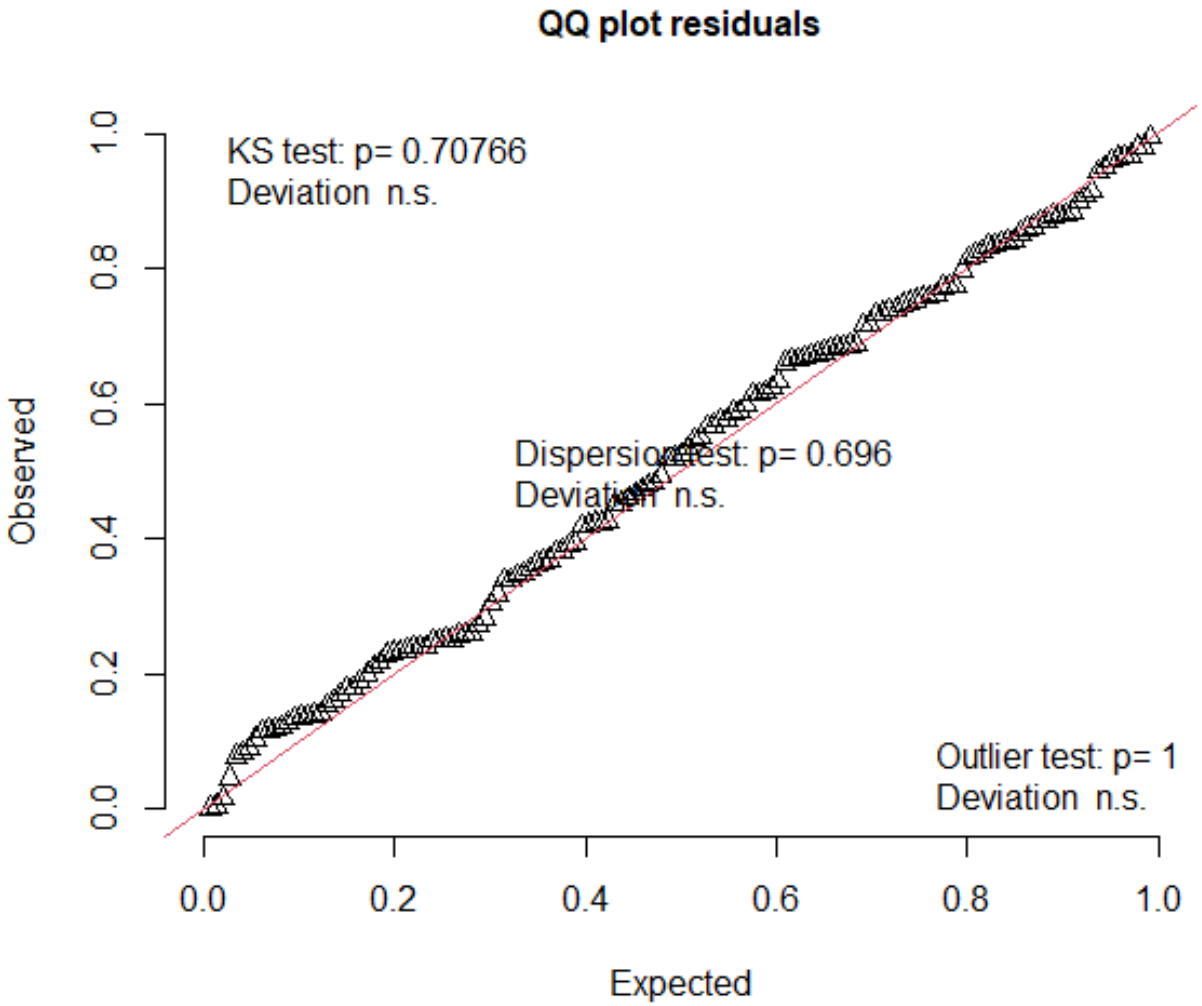
```
sparrow.glm = glmmTMB::glmmTMB(survival ~ tarsus,
family = binomial(link = "logit"),
data = sparrow.data)
```

Check the model diagnostics using the `DHARMa` package

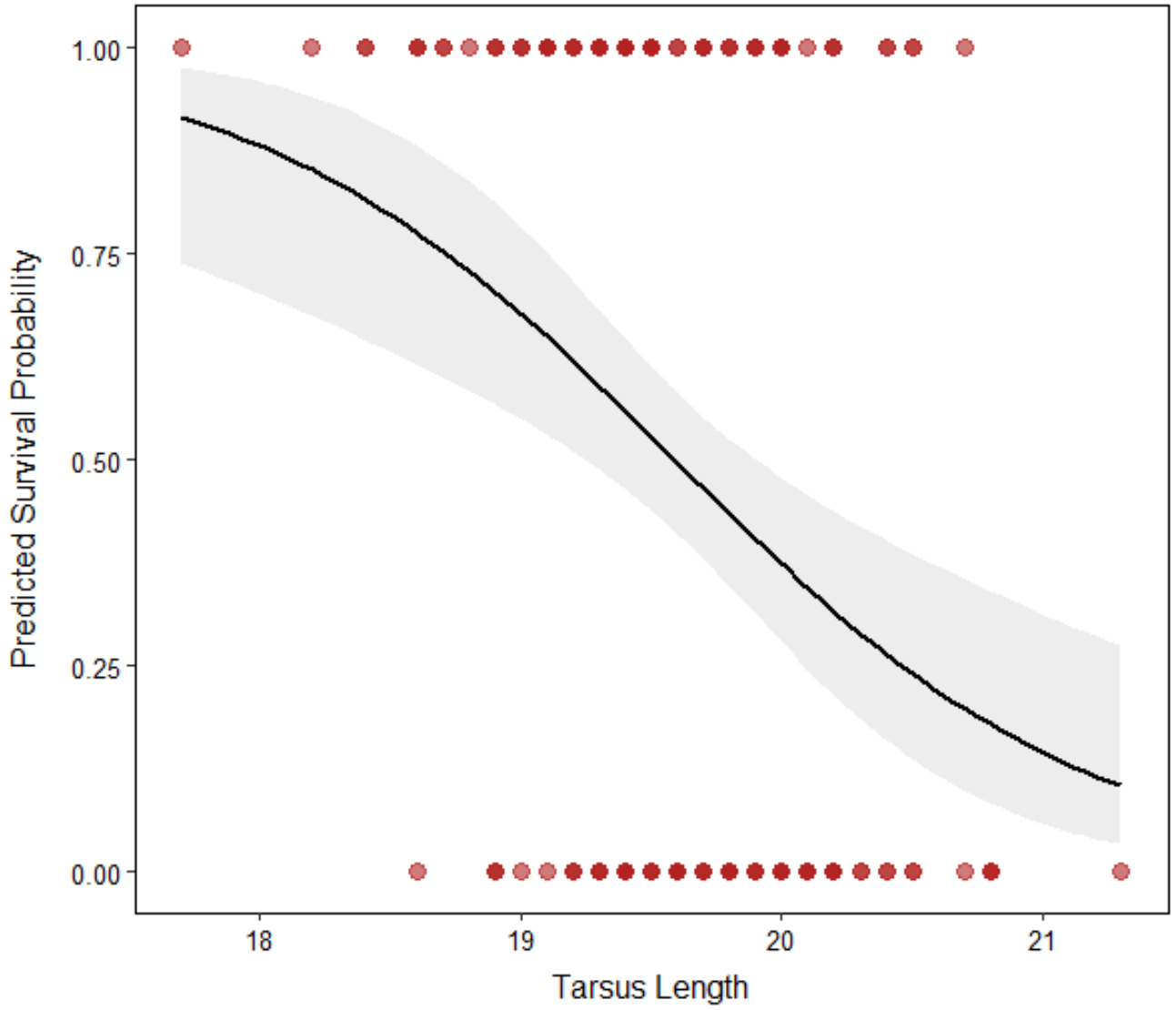
```
DHARMa::plotResiduals(sparrow.glm)
DHARMa::plotQQunif(sparrow.glm)
```

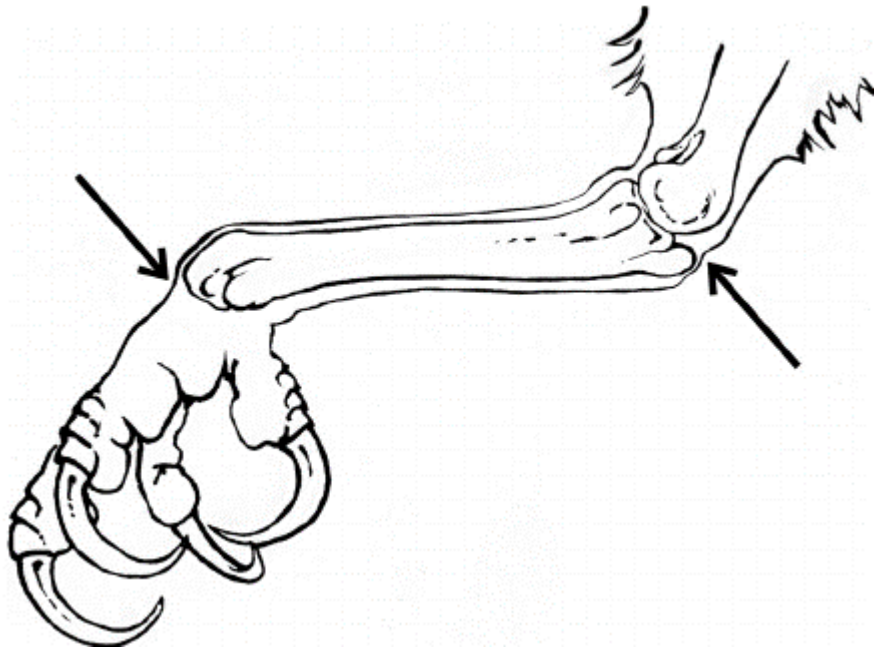
Looks like a good model





Plot our binomial GLM:





Check for significance using a Wald Chi-square test:

```
> car::Anova(sparrow.glm, test = "Chisq", type = "II")

Analysis of Deviance Table (Type II Wald chisquare tests)

Response: survival
        Chisq Df Pr(>Chisq)
tarsus 13.391  1  0.0002529 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1>
```

Tarsus length has a significant effect on survival
(χ^2 = 13.4, d.f. = 1, p < 0.001)

Let's look at the beta coefficients:

```
>summary(sparrow.glm)

 Family: binomial  ( logit )
Formula:          survival ~ tarsus
Data: sparrow.data

     AIC      BIC   logLik deviance df.resid
   189.0    195.0    -92.5    185.0      143


Conditional model:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  24.6361 β0   6.7454   3.652 0.000260 ***
tarsus       -1.2578 β1   0.3437  -3.659 0.000253 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Since this was a logistic regression, we need to get the exponentiated value for the β_1 coefficient (log odds):

exp(-1.2578) = 0.28 (this is now the odds ratio. Note the - sign)
For every mm ↑ in tarsus length, the odds of survival ↓ by a factor of 0.28
As a percentage: (0.28 – 1) x 100 = -72% (i.e. a 72% decrease in the odds of survival)

95% confidence interval:
Lower = exp(-1.97) = 0.14
Upper = exp(-0.58) = 0.56

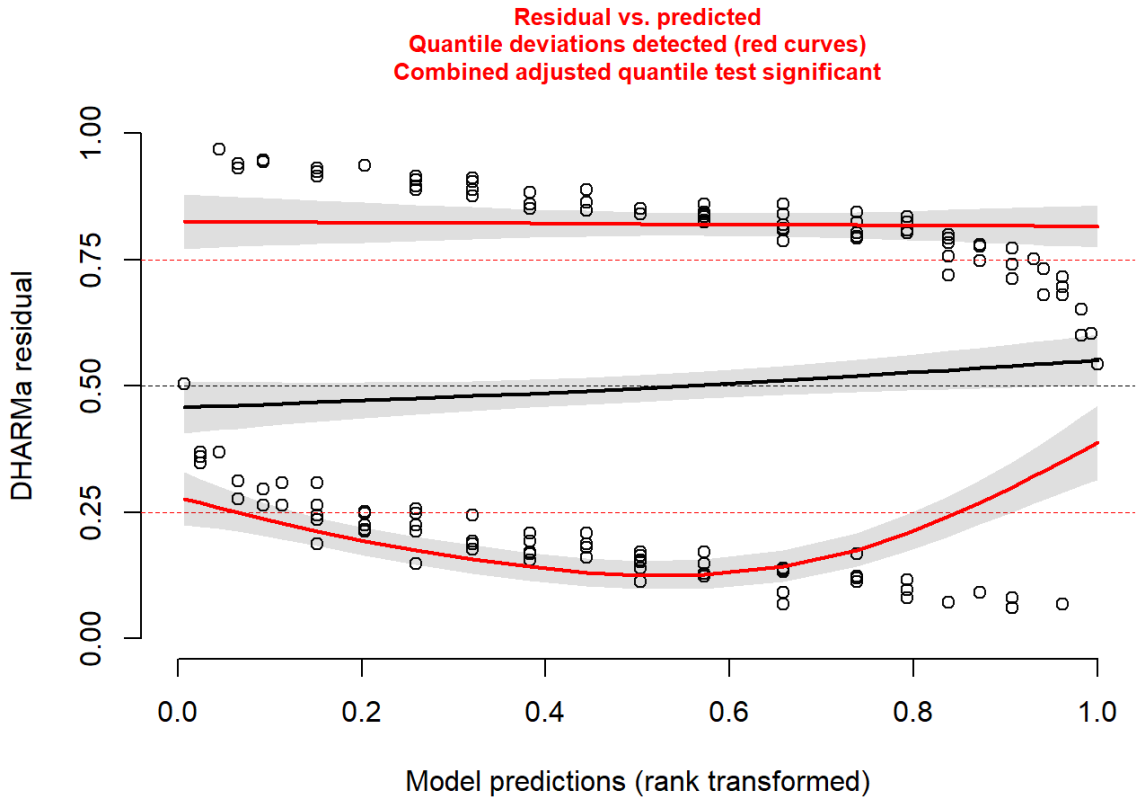
Characteristic	exp(Beta)	95% CI[1]	p-value
tarsus	0.28	0.14, 0.56	<0.001

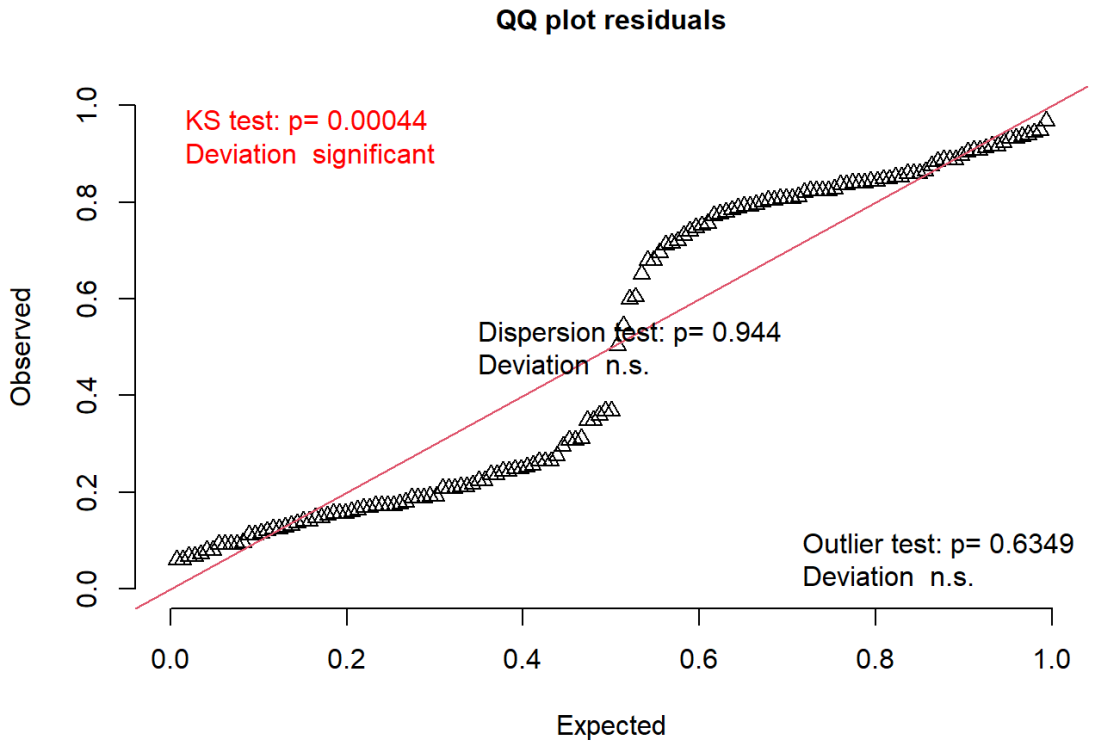
[1] CI = Confidence Interval

95 out of 100 times, we will get an odds ratio between 0.14 and 0.56

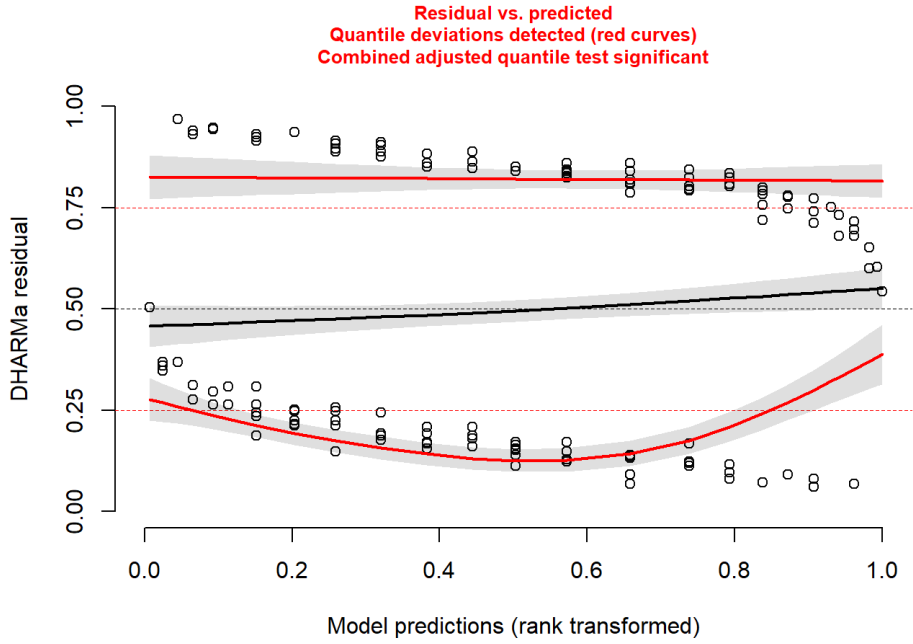
What would happen if we tried running a standard LM, rather than a binomial GLM?

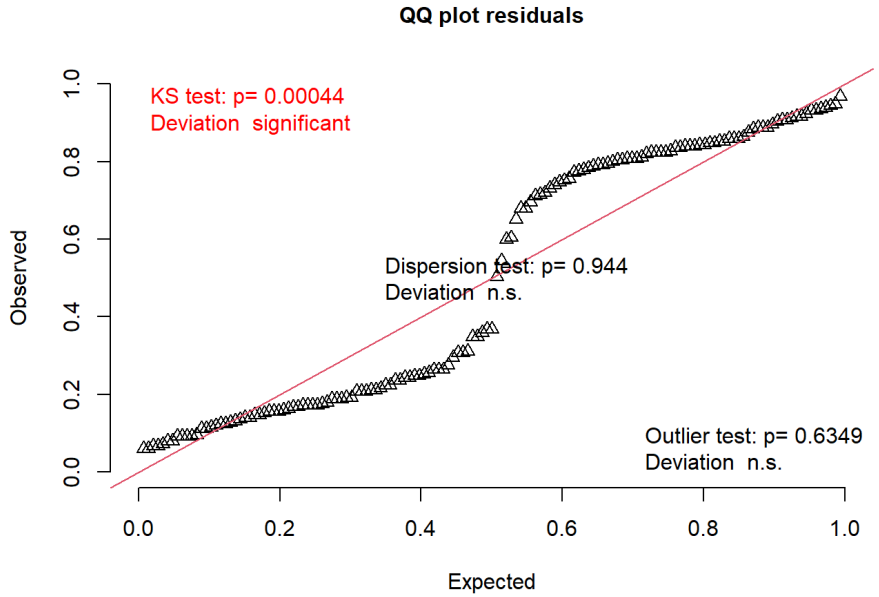
```
sparrow.lm = lm(survival ~ tarsus, data = sparrow.data)
DHARMa::plotResiduals(sparrow.lm)
```





LINEAR MODEL





BINOMIAL GLM