GAM Assumption Checks

Journal: Ecology

Title: Temperature niche and body-size conditions phenological responses of moths to urbanization in subtropical environments

Authors: Michael W. Belitz, Asia Sawyer, Lillian K. Hendrick, Robert P. Guralnick

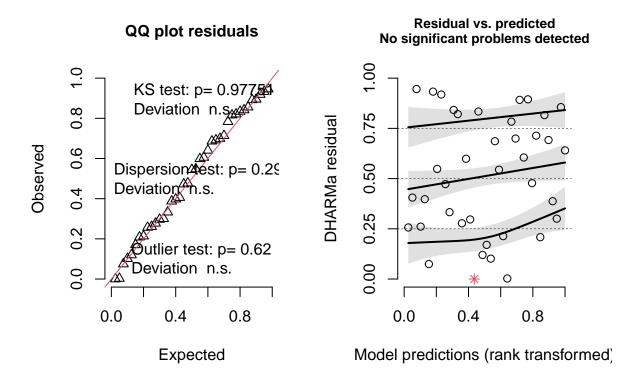
In this document, we show DHARMa residual checks of models fit with both negative binomial distributions and Poisson distributions. The negative binomial distribution fit our pooled community data well, while the Poisson distribution performed less well. We also tested examined the residuals of models fit with the negative binomial distribution and the Poisson distribution for our species-specific models. Those results also indicate that the negative binomial distribution fits our data better, although those results are not plotted below.

Pooled Macro-moth checks

First negative binomial distributions

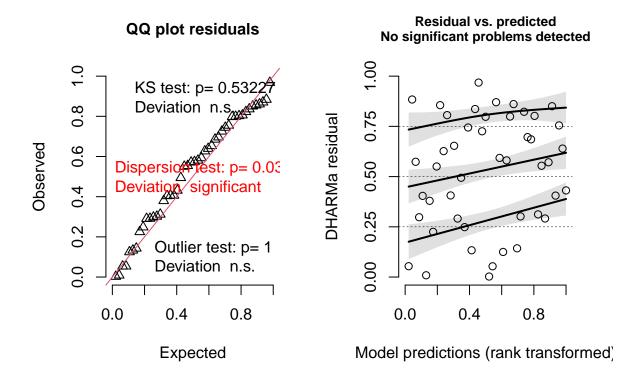
We first show the residual checks for models fit using the negative binomial distribution to our pooled macro-moth data.

Site: AUCA



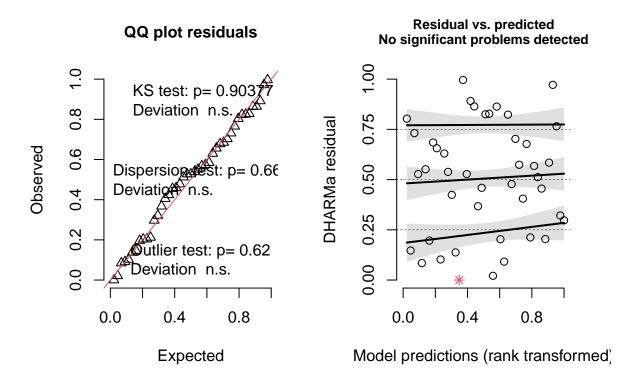
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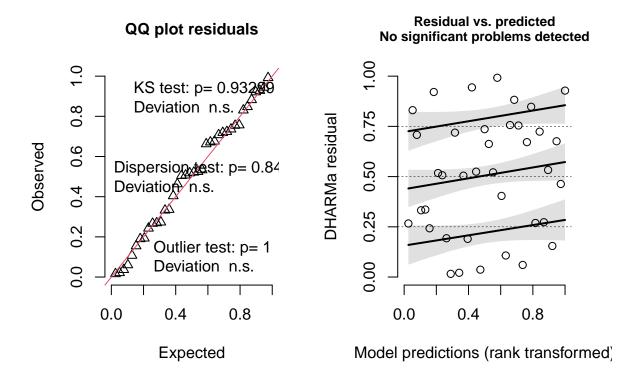
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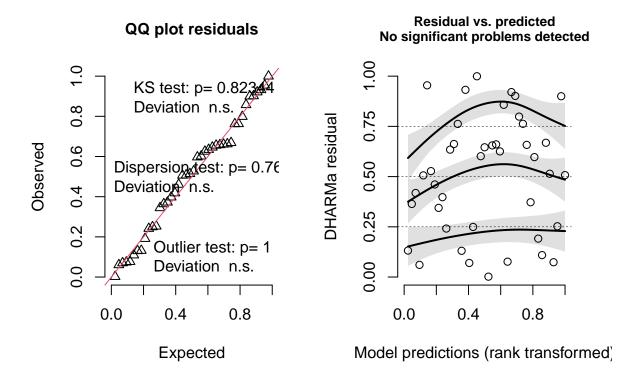
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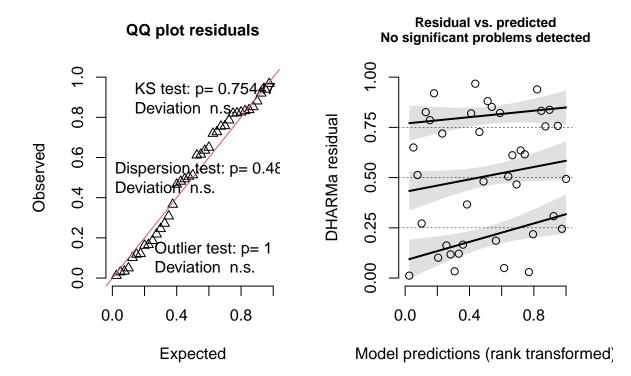
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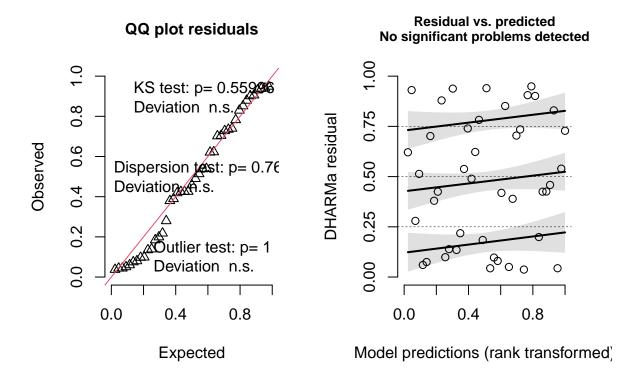
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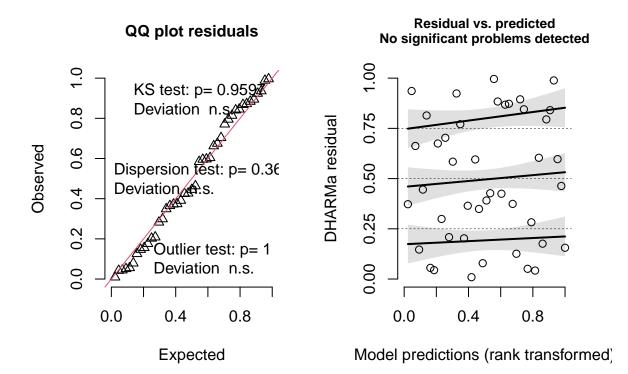
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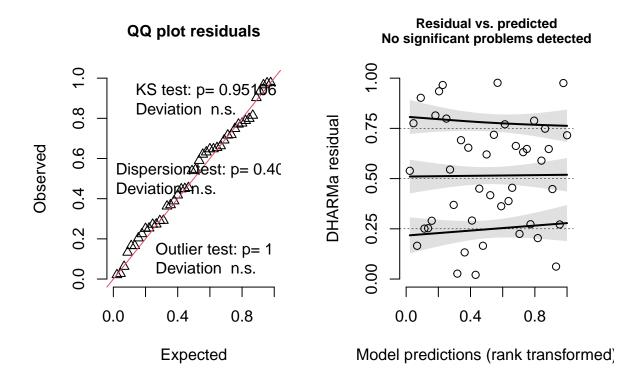
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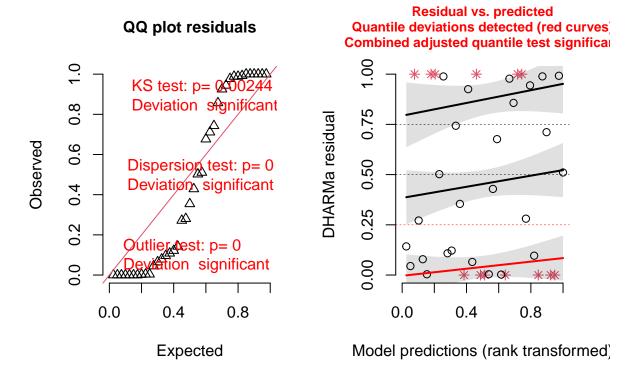
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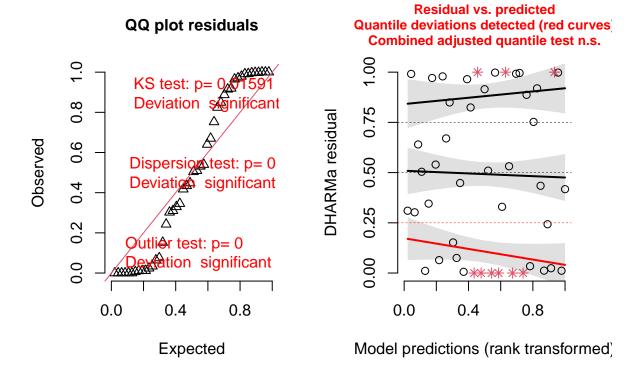
Poisson distribution

We now show the residual checks for models fit to our pooled macro-moth data using the Poisson distribution. Site: AUCA



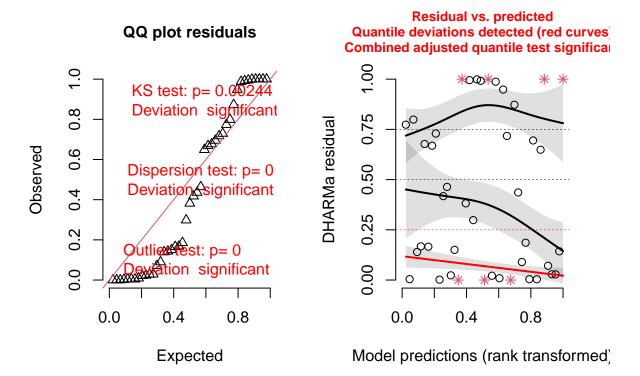
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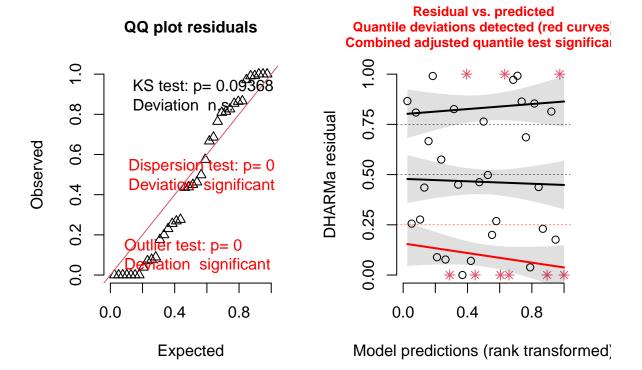
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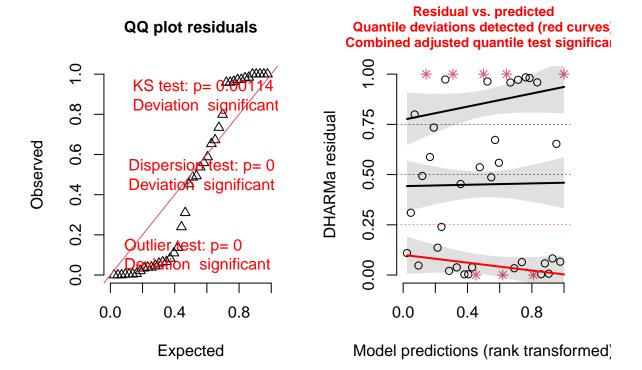
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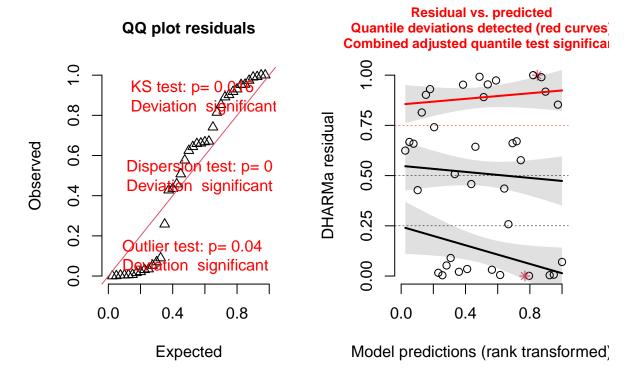
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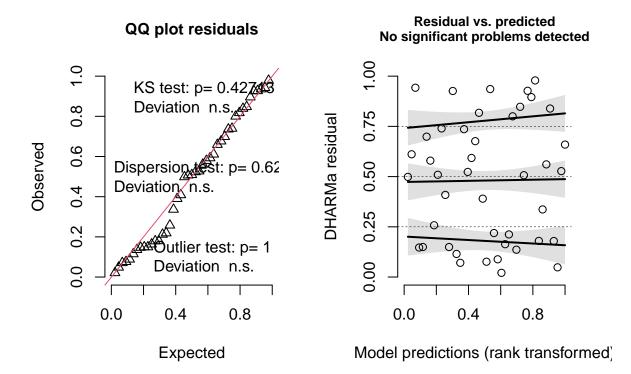
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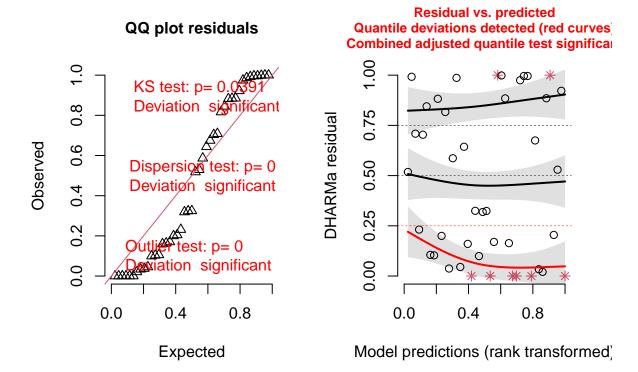
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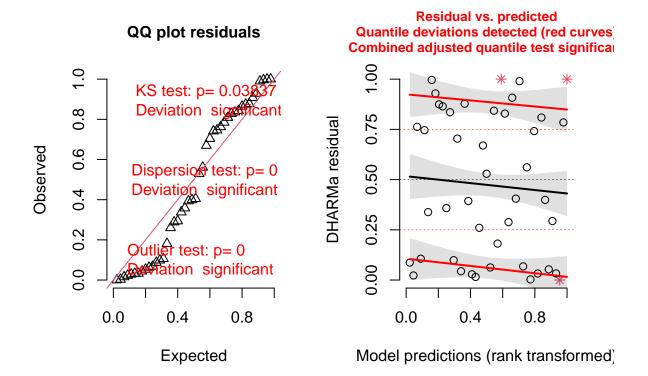
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Site: Joma



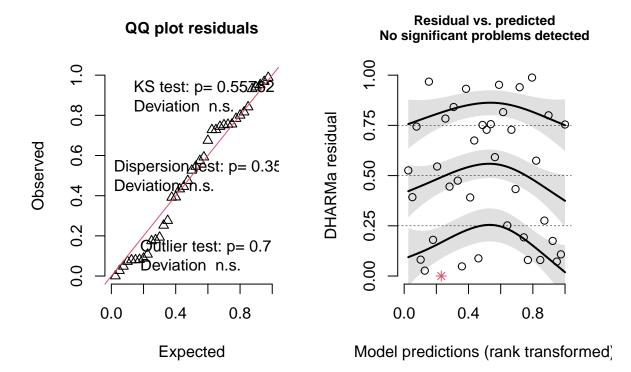
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Pooled micro-moth checks

Negative binomial distributions

We now show the residual checks for models fit using the negative binomial distribution to our pooled micro-moth data.

Site: AUCA

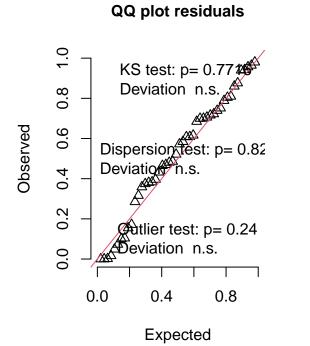


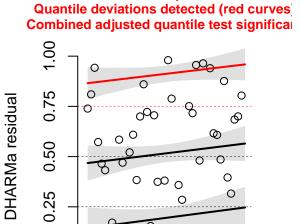
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0.00

0.0





Residual vs. predicted

Model predictions (rank transformed)

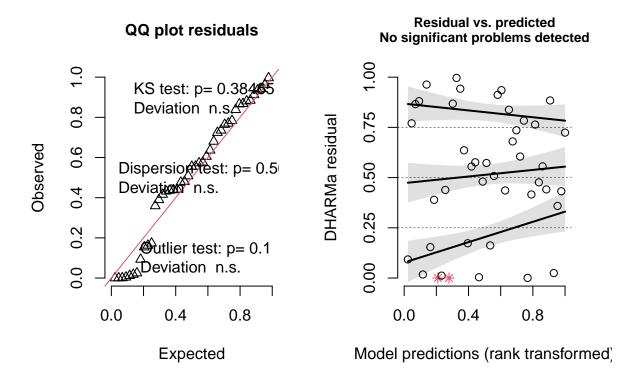
0.4

8.0

0

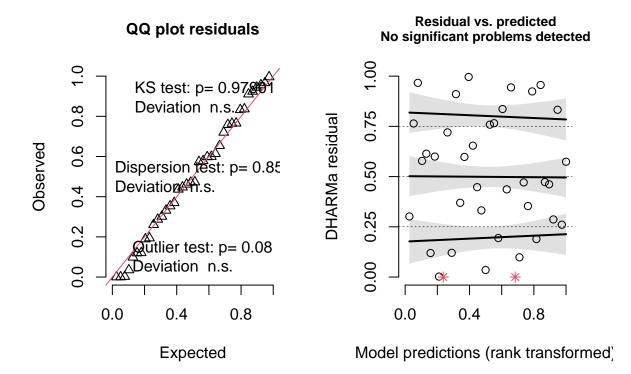
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Site: Demi



NULL

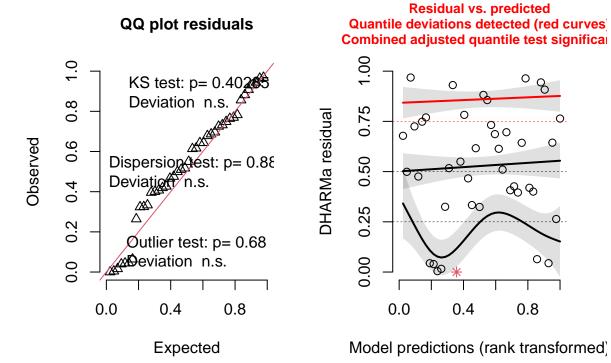
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0

8

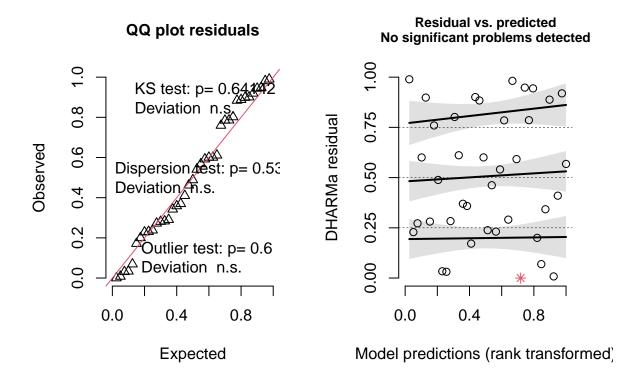
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8.0



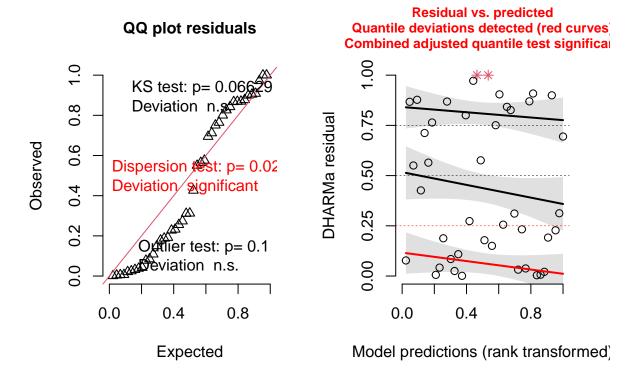
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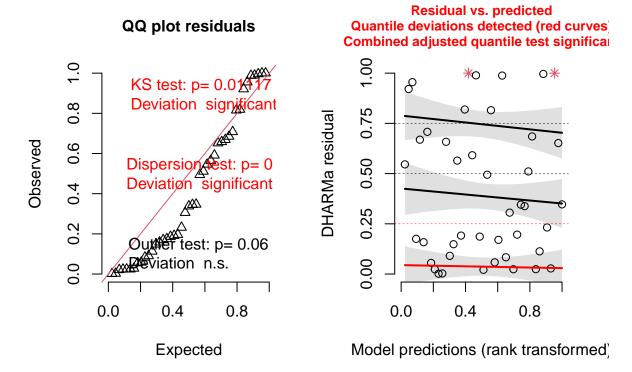
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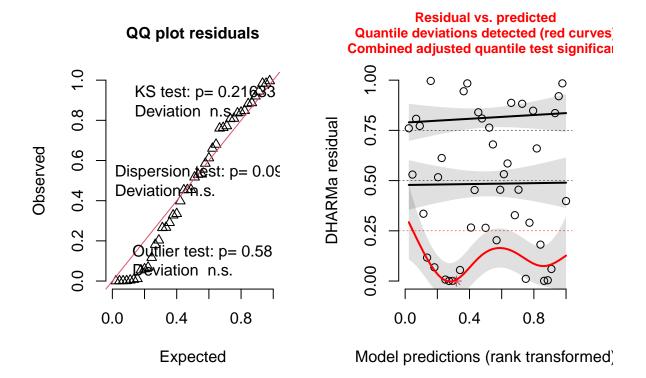
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Site: Joma

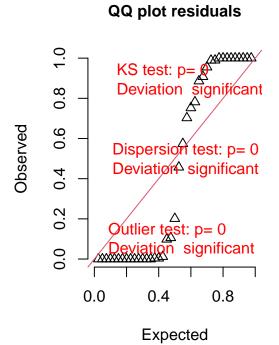


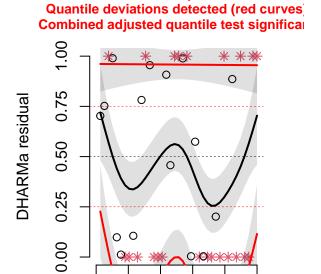
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Now fit using poisson

And finally, we show the residual checks for models fit using the Poisson distribution to our pooled micromoth data.

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Residual vs. predicted

Model predictions (rank transformed)

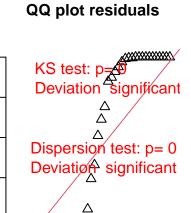
0.4

0.0

8.0

NULL

Site: PRCR



Outlier test: p= 0

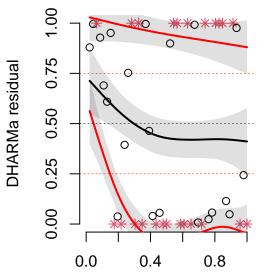
0.4

Expected

significant

8.0

Residual vs. predicted
Quantile deviations detected (red curves)
Combined adjusted quantile test significal



Model predictions (rank transformed)

NULL

0.8

9.0

0.4

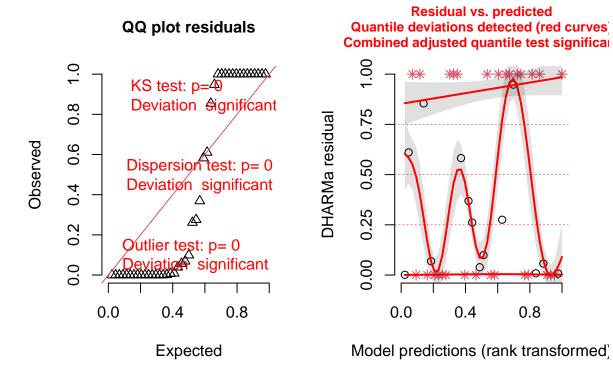
0.2

0.0

0.0

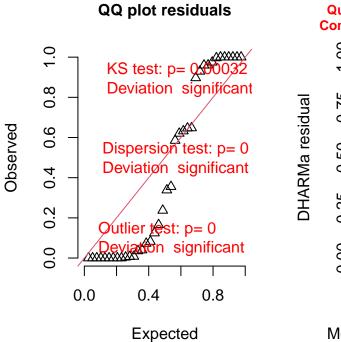
Observed

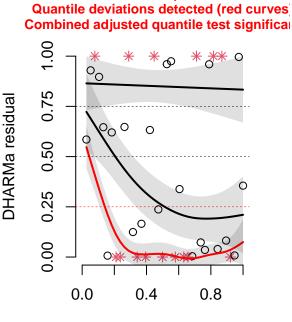
Site: Rist



NULL

Site: Demi



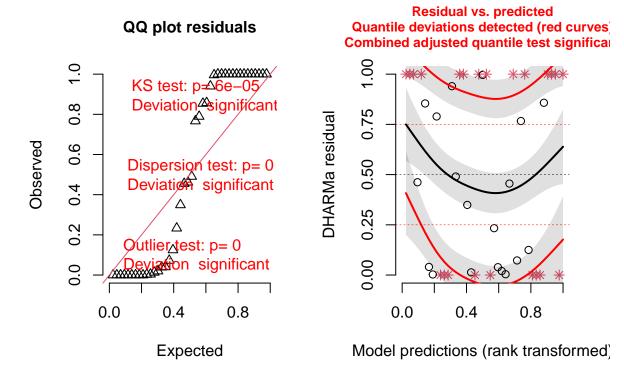


Residual vs. predicted

Model predictions (rank transformed)

NULL

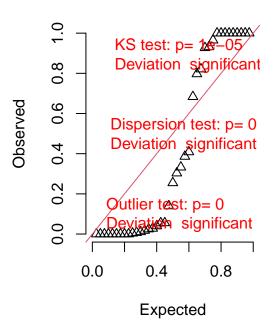
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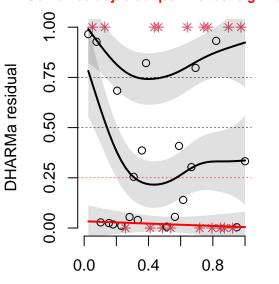
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Site: Biva

QQ plot residuals



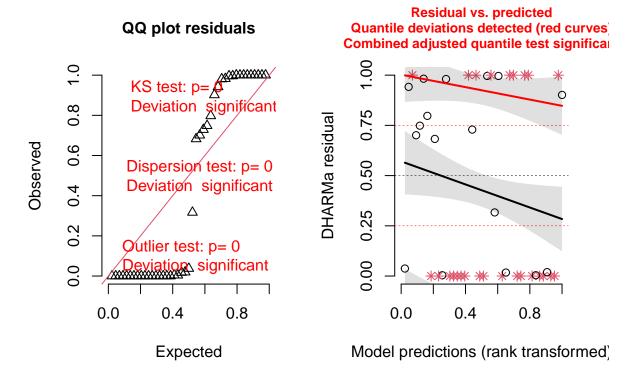
Residual vs. predicted
Quantile deviations detected (red curves)
Combined adjusted quantile test significant



Model predictions (rank transformed)

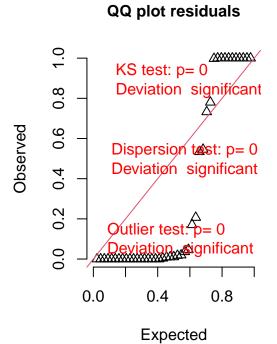
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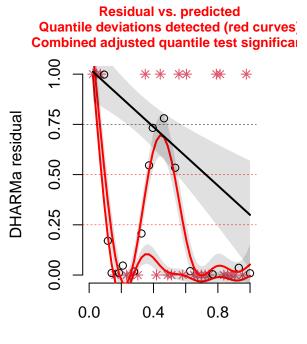
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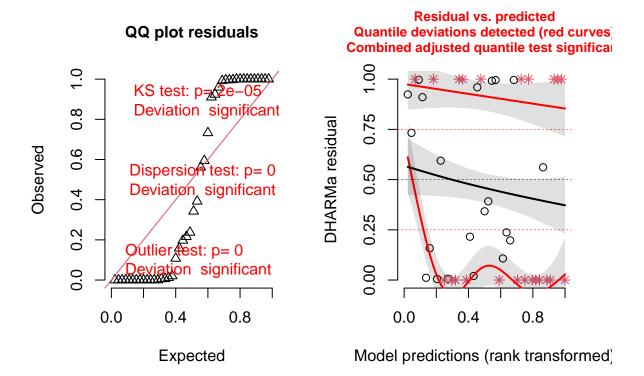




Model predictions (rank transformed)

NULL

Site: Joma



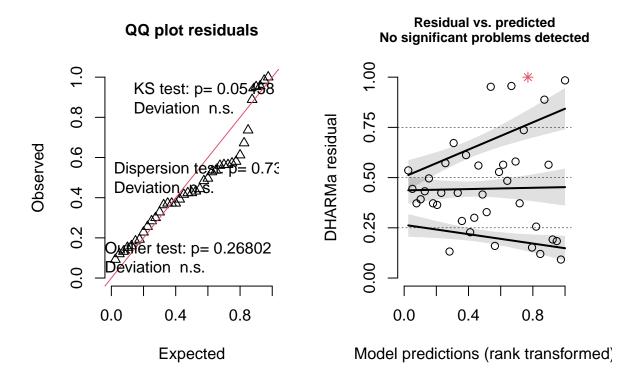
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Frass model residual checks

Fit with gaussian distribution

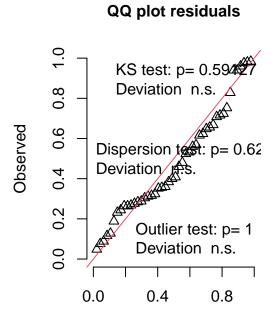
We end with checks on our models fit to the frass data.

Site: AUCA

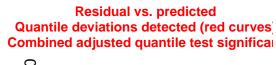


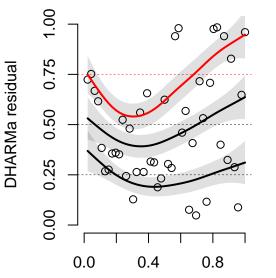
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Expected

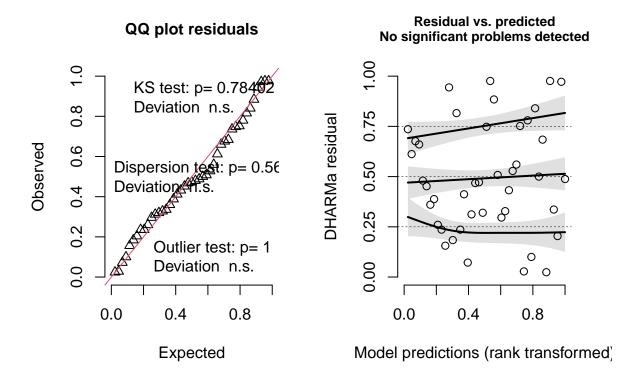




Model predictions (rank transformed)

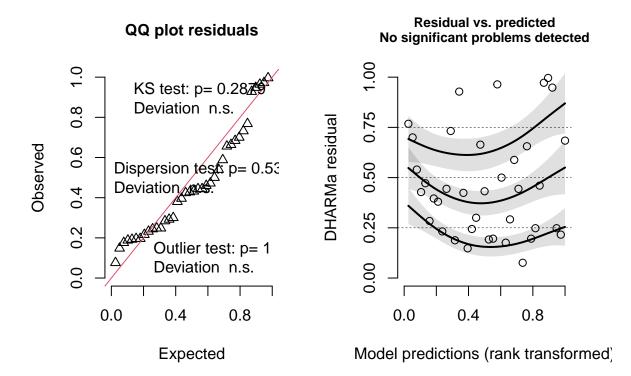
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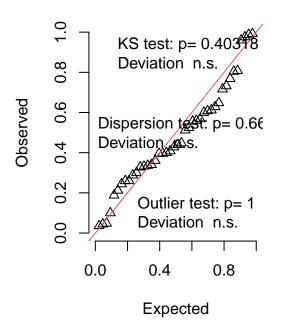
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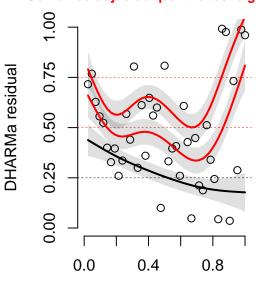
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Site: Bowa





Residual vs. predicted
Quantile deviations detected (red curves)
Combined adjusted quantile test significant

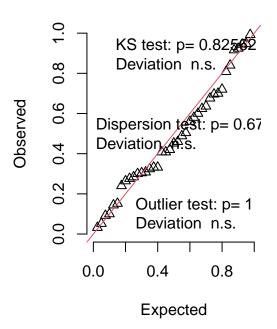


Model predictions (rank transformed)

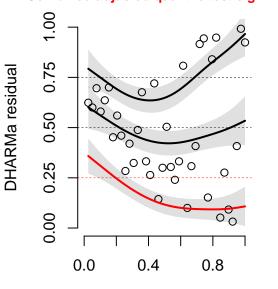
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Site: Biva

QQ plot residuals



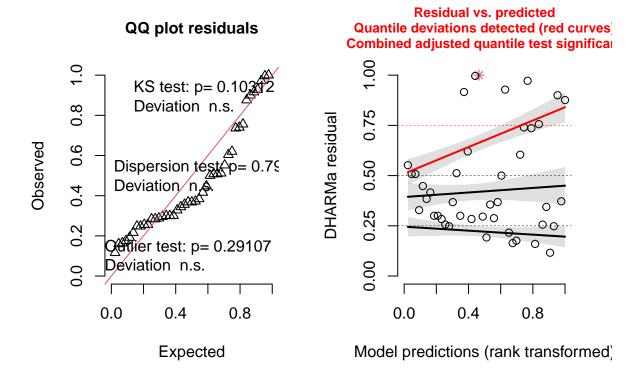
Residual vs. predicted
Quantile deviations detected (red curves)
Combined adjusted quantile test significant



Model predictions (rank transformed)

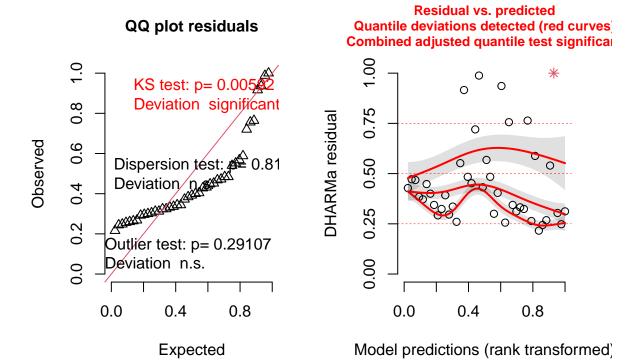
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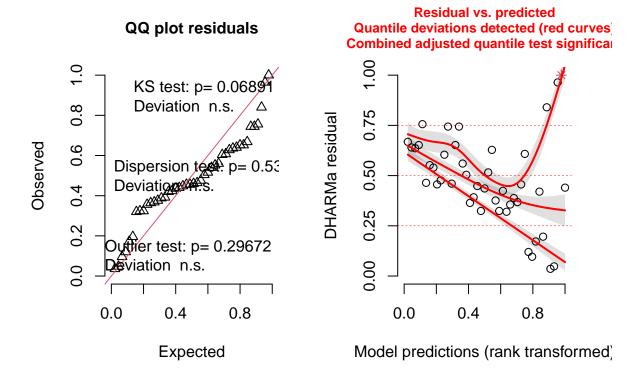
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