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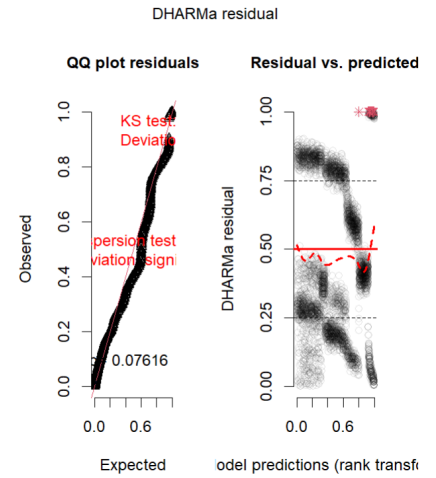
123 mod9 <- phylo_glmTMB(mean_death_burden ~ log(ratio)*hOrder + (1|binomial), # try adding t
124 data=mean_data,
125 phylo = bat_tree,
126 phylonm = "binomial",
127 control = glmTMBControl(),
128 family = nbinom1())
129 mod9_resid <- simulateResiduals(mod9, allow.new.levels=TRUE)
130 plot(mod9_resid) # better...
131 testDispersion(mod9_resid)
132
133 #Viruses hosted by bats have a significantly higher death burden then other species (may b
134 #Death burdens in humans changes based on how adapted to viruses bats are when they are th
135 #As the ratio of low (less susceptibility) to the death burden of bats decreases the
136
137 | (Top Level)
R Script

```

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R 4.2.2
P ratio and their interaction
+ data=mean_data,
+ phylo = bat_tree,
+ phylonm = "binomial",
+ control = glmTMBControl(),
+ family = nbinom1()
> mod9_resid <- simulateResiduals(mod9, allow.new.levels=TRUE)
Warning message:
In checkTerms(data.tmb1$terms, data.tmb0$terms) :
Predicting new random effect levels for terms: 1 | binomial
Disable this warning with 'allow.new.levels=TRUE'
> plot(mod9_resid) # better...
>

```



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177 # looks like we need the ratio, hOrder, and their interaction - what happens if we add the
178 #12 is best for CFR
179 mod12 <- phylo_glmTMB(mean_CFR_avg ~ log(ratio)*hOrder + log(ratio):order + (1|binomial),
180 data=mean_data,
181 phylo = bat_tree,
182 phylonm = "binomial",
183 control = glmTMBControl(),
184 family = gaussian())
185 mod12_resid <- simulateResiduals(mod12, allow.new.levels=TRUE)
186 plot(mod12_resid) # ...
187 testDispersion(mod12_resid)
188 summary(mod12)
189
190 # we can't actually properly compare mod7 and mod9 this way (for statistical reasons), but
191 anova(mod7, mod12)
192
193 | (Top Level)
R Script

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R 4.2.2
> mod12 <- phylo_glmTMB(mean_CFR_avg ~ log(ratio)*hOrder + log(ratio):order + (1|binomial),
+ data=mean_data,
+ phylo = bat_tree,
+ phylonm = "binomial",
+ control = glmTMBControl(),
+ family = gaussian())
> mod12_resid <- simulateResiduals(mod12, allow.new.levels=TRUE)
Warning message:
In checkTerms(data.tmb1$terms, data.tmb0$terms) :
Predicting new random effect levels for terms: 1 | binomial
Disable this warning with 'allow.new.levels=TRUE'
> plot(mod12_resid) # ...
>

```

