ShallowTables

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library(here)

## Warning: package 'here' was built under R version 4.0.5

## here() starts at C:/Users/nushi/OneDrive - Cornell University/Shallow\_Torpor/Code/TorporShallowDeep

library(nlme) ## for gls model to compare them with lmer, account for autocorrelation

## Warning: package 'nlme' was built under R version 4.0.5

library(emmeans)

## Warning: package 'emmeans' was built under R version 4.0.5

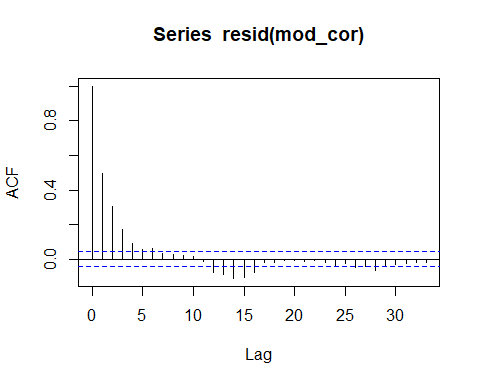
library(MASS) ## To check the distribution of the data and run glm.nb

## Warning: package 'MASS' was built under R version 4.0.5

#getwd()  
here <- here::here  
therm\_all <- read.csv(here("..", "..", "Data", "All\_data.csv"))  
m.prop\_dur <- read.csv(here("..", "..", "Data", "Prop\_Duration\_Categories.csv"))  
head(therm\_all)

## X Indiv\_ID Date Time Hour Amb\_Temp Surf\_Temp Year pasted Category  
## 1 1 BCHU01 610 103 1 11.86208 14.46594 17 BCHU01\_061017 Deep Torpor  
## 2 2 BCHU01 610 118 1 11.66303 13.95339 17 BCHU01\_061017 Deep Torpor  
## 3 3 BCHU01 610 120 1 11.17115 13.80842 17 BCHU01\_061017 Deep Torpor  
## 4 4 BCHU01 610 124 1 11.72952 13.98437 17 BCHU01\_061017 Deep Torpor  
## 5 5 BCHU01 610 126 1 12.13652 15.57582 17 BCHU01\_061017 Deep Torpor  
## 6 6 BCHU01 610 136 1 14.33345 17.17813 17 BCHU01\_061017 Deep Torpor  
## Cap\_mass Indiv\_numeric Species Species\_numeric  
## 1 3.02 1 BCHU 1  
## 2 3.02 1 BCHU 1  
## 3 3.02 1 BCHU 1  
## 4 3.02 1 BCHU 1  
## 5 3.02 1 BCHU 1  
## 6 3.02 1 BCHU 1

therm\_all$Category <- factor(therm\_all$Category, levels=c("Normothermic", "Shallow Torpor", "Transition", "Deep Torpor"))  
#therm\_all$Species <- as.factor(therm\_all$Species)  
  
mod\_cor <- nlme::lme(data=therm\_all, fixed=Surf\_Temp ~   
 Amb\_Temp +   
 Category +   
 Amb\_Temp:Category +   
 Species +   
 Cap\_mass +  
 Year +  
 Species:Category,   
 random= ~1|Indiv\_numeric/Category,   
 correlation=corAR1(form=~1|Indiv\_numeric/Category))  
em <- emmeans(mod\_cor, ~Species:Category)  
acf(resid(mod\_cor))



knitr::kable(em, digits=2)

| Species | Category | emmean | SE | df | lower.CL | upper.CL |
| --- | --- | --- | --- | --- | --- | --- |
| BCHU | Normothermic | 33.05 | 1.83 | 29 | 29.31 | 36.78 |
| BLUH | Normothermic | 31.80 | 0.67 | 29 | 30.43 | 33.16 |
| RIHU | Normothermic | 31.03 | 0.51 | 29 | 29.98 | 32.08 |
| BCHU | Shallow Torpor | 30.41 | 1.92 | 29 | 26.48 | 34.34 |
| BLUH | Shallow Torpor | 28.97 | 0.78 | 29 | 27.38 | 30.57 |
| RIHU | Shallow Torpor | 27.64 | 0.50 | 29 | 26.62 | 28.66 |
| BCHU | Transition | 21.54 | 1.85 | 29 | 17.75 | 25.33 |
| BLUH | Transition | 22.22 | 1.02 | 29 | 20.13 | 24.30 |
| RIHU | Transition | 22.47 | 0.63 | 29 | 21.18 | 23.77 |
| BCHU | Deep Torpor | 15.08 | 1.82 | 29 | 11.35 | 18.80 |
| BLUH | Deep Torpor | 15.41 | 1.03 | 29 | 13.29 | 17.53 |
| RIHU | Deep Torpor | 15.40 | 0.57 | 29 | 14.22 | 16.57 |

knitr::kable(intervals(mod\_cor)$fixed, digits=2)

|  | lower | est. | upper |
| --- | --- | --- | --- |
| (Intercept) | 34.79 | 46.53 | 58.28 |
| Amb\_Temp | 0.03 | 0.06 | 0.09 |
| CategoryShallow Torpor | -4.85 | -3.06 | -1.26 |
| CategoryTransition | -19.12 | -17.31 | -15.51 |
| CategoryDeep Torpor | -28.05 | -26.43 | -24.81 |
| SpeciesBLUH | -6.20 | -1.25 | 3.70 |
| SpeciesRIHU | -6.53 | -2.02 | 2.50 |
| Cap\_mass | -0.59 | 0.30 | 1.19 |
| Year | -1.63 | -0.93 | -0.22 |
| Amb\_Temp:CategoryShallow Torpor | -0.02 | 0.04 | 0.09 |
| Amb\_Temp:CategoryTransition | 0.39 | 0.49 | 0.59 |
| Amb\_Temp:CategoryDeep Torpor | 0.60 | 0.71 | 0.83 |
| CategoryShallow Torpor:SpeciesBLUH | -2.06 | -0.18 | 1.69 |
| CategoryTransition:SpeciesBLUH | -0.16 | 1.92 | 4.00 |
| CategoryDeep Torpor:SpeciesBLUH | -0.35 | 1.58 | 3.52 |
| CategoryShallow Torpor:SpeciesRIHU | -2.65 | -0.75 | 1.15 |
| CategoryTransition:SpeciesRIHU | 1.16 | 2.95 | 4.74 |
| CategoryDeep Torpor:SpeciesRIHU | 0.77 | 2.34 | 3.91 |

knitr::kable(summary(mod\_cor)$tTable, digits = c(2,2,0,2,35))

|  | Value | Std.Error | DF | t-value | p-value |
| --- | --- | --- | --- | --- | --- |
| (Intercept) | 46.53 | 5.99 | 2062 | 7.77 | 1.230534e-14 |
| Amb\_Temp | 0.06 | 0.01 | 2062 | 4.10 | 4.238913e-05 |
| CategoryShallow Torpor | -3.06 | 0.90 | 56 | -3.41 | 1.211003e-03 |
| CategoryTransition | -17.31 | 0.90 | 56 | -19.19 | 2.711200e-26 |
| CategoryDeep Torpor | -26.43 | 0.81 | 56 | -32.66 | 0.000000e+00 |
| SpeciesBLUH | -1.25 | 2.42 | 29 | -0.52 | 6.098429e-01 |
| SpeciesRIHU | -2.02 | 2.21 | 29 | -0.91 | 3.684170e-01 |
| Cap\_mass | 0.30 | 0.43 | 29 | 0.69 | 4.976488e-01 |
| Year | -0.93 | 0.34 | 29 | -2.70 | 1.151341e-02 |
| Amb\_Temp:CategoryShallow Torpor | 0.04 | 0.03 | 2062 | 1.27 | 2.033778e-01 |
| Amb\_Temp:CategoryTransition | 0.49 | 0.05 | 2062 | 9.91 | 1.169062e-22 |
| Amb\_Temp:CategoryDeep Torpor | 0.71 | 0.06 | 2062 | 12.27 | 1.960000e-33 |
| CategoryShallow Torpor:SpeciesBLUH | -0.18 | 0.94 | 56 | -0.19 | 8.466820e-01 |
| CategoryTransition:SpeciesBLUH | 1.92 | 1.04 | 56 | 1.85 | 6.905843e-02 |
| CategoryDeep Torpor:SpeciesBLUH | 1.58 | 0.97 | 56 | 1.64 | 1.066377e-01 |
| CategoryShallow Torpor:SpeciesRIHU | -0.75 | 0.95 | 56 | -0.79 | 4.321857e-01 |
| CategoryTransition:SpeciesRIHU | 2.95 | 0.89 | 56 | 3.30 | 1.701234e-03 |
| CategoryDeep Torpor:SpeciesRIHU | 2.34 | 0.78 | 56 | 2.99 | 4.187740e-03 |

## Models for proportion of night spent in each category ##  
m.prop\_dur$variable <- factor(m.prop\_dur$variable, levels=c("Normothermic", "Shallow Torpor", "Transition", "Deep Torpor"))  
  
## This model has residual deviance >> degrees of freedom  
mod\_glm\_freq\_sp <- glm(freq~variable\*Species-1, data=m.prop\_dur, family=poisson())  
mod\_glm\_freq\_sp

##   
## Call: glm(formula = freq ~ variable \* Species - 1, family = poisson(),   
## data = m.prop\_dur)  
##   
## Coefficients:  
## variableNormothermic variableShallow Torpor   
## 3.64880 1.55060   
## variableTransition variableDeep Torpor   
## 2.44854 3.80983   
## SpeciesBLUH SpeciesRIHU   
## 0.55482 0.02653   
## variableShallow Torpor:SpeciesBLUH variableTransition:SpeciesBLUH   
## 1.13045 -1.83576   
## variableDeep Torpor:SpeciesBLUH variableShallow Torpor:SpeciesRIHU   
## -2.90937 1.85189   
## variableTransition:SpeciesRIHU variableDeep Torpor:SpeciesRIHU   
## 0.11904 -1.04001   
##   
## Degrees of Freedom: 136 Total (i.e. Null); 124 Residual  
## Null Deviance: 19670   
## Residual Deviance: 2252 AIC: 2770

knitr::kable(summary(mod\_glm\_freq\_sp)$tTable, digits=2)

|| || || ||

knitr::kable(emmeans(mod\_glm\_freq\_sp,specs=~variable\*Species), digits=2)

| variable | Species | emmean | SE | df | asymp.LCL | asymp.UCL |
| --- | --- | --- | --- | --- | --- | --- |
| Normothermic | BCHU | 3.65 | 0.06 | Inf | 3.53 | 3.77 |
| Shallow Torpor | BCHU | 1.55 | 0.17 | Inf | 1.21 | 1.89 |
| Transition | BCHU | 2.45 | 0.11 | Inf | 2.23 | 2.67 |
| Deep Torpor | BCHU | 3.81 | 0.06 | Inf | 3.70 | 3.92 |
| Normothermic | BLUH | 4.20 | 0.03 | Inf | 4.14 | 4.27 |
| Shallow Torpor | BLUH | 3.24 | 0.05 | Inf | 3.13 | 3.34 |
| Transition | BLUH | 1.17 | 0.15 | Inf | 0.88 | 1.46 |
| Deep Torpor | BLUH | 1.46 | 0.13 | Inf | 1.20 | 1.71 |
| Normothermic | RIHU | 3.68 | 0.04 | Inf | 3.59 | 3.76 |
| Shallow Torpor | RIHU | 3.43 | 0.05 | Inf | 3.33 | 3.53 |
| Transition | RIHU | 2.59 | 0.08 | Inf | 2.45 | 2.74 |
| Deep Torpor | RIHU | 2.80 | 0.07 | Inf | 2.66 | 2.93 |

# coef(mod\_glm\_freq\_sp)  
  
## Because residual variance >> degrees of freedom, trying a quasipoisson  
## But the dispersion parameter is still 12.5, which is much greater than 1, meaning it's overdispersed  
#mod\_glm\_freq\_sp\_quasi <- glm(freq~variable\*Species-1, data=m.prop\_dur\_both, family=quasipoisson())  
# summary(mod\_glm\_freq\_sp\_quasi)  
  
## Running a negative binomial model, definitely the best. No overdispserion now, much lower residual variance.  
mod\_glm\_freq\_sp\_nb <- glm.nb(freq~variable\*Species-1, data=m.prop\_dur)  
mod\_glm\_freq\_sp\_nb

##   
## Call: glm.nb(formula = freq ~ variable \* Species - 1, data = m.prop\_dur,   
## init.theta = 0.6245829332, link = log)  
##   
## Coefficients:  
## variableNormothermic variableShallow Torpor   
## 3.64880 1.55060   
## variableTransition variableDeep Torpor   
## 2.44854 3.80983   
## SpeciesBLUH SpeciesRIHU   
## 0.55482 0.02653   
## variableShallow Torpor:SpeciesBLUH variableTransition:SpeciesBLUH   
## 1.13045 -1.83576   
## variableDeep Torpor:SpeciesBLUH variableShallow Torpor:SpeciesRIHU   
## -2.90937 1.85189   
## variableTransition:SpeciesRIHU variableDeep Torpor:SpeciesRIHU   
## 0.11904 -1.04001   
##   
## Degrees of Freedom: 136 Total (i.e. Null); 124 Residual  
## Null Deviance: 2888   
## Residual Deviance: 161.5 AIC: 1066

knitr::kable(emmeans(mod\_glm\_freq\_sp\_nb,specs=~variable\*Species), digits=2)

| variable | Species | emmean | SE | df | asymp.LCL | asymp.UCL |
| --- | --- | --- | --- | --- | --- | --- |
| Normothermic | BCHU | 3.65 | 0.48 | Inf | 2.70 | 4.59 |
| Shallow Torpor | BCHU | 1.55 | 0.51 | Inf | 0.55 | 2.55 |
| Transition | BCHU | 2.45 | 0.49 | Inf | 1.49 | 3.41 |
| Deep Torpor | BCHU | 3.81 | 0.48 | Inf | 2.87 | 4.75 |
| Normothermic | BLUH | 4.20 | 0.34 | Inf | 3.54 | 4.87 |
| Shallow Torpor | BLUH | 3.24 | 0.34 | Inf | 2.56 | 3.91 |
| Transition | BLUH | 1.17 | 0.37 | Inf | 0.44 | 1.89 |
| Deep Torpor | BLUH | 1.46 | 0.36 | Inf | 0.75 | 2.16 |
| Normothermic | RIHU | 3.68 | 0.35 | Inf | 2.98 | 4.37 |
| Shallow Torpor | RIHU | 3.43 | 0.35 | Inf | 2.73 | 4.12 |
| Transition | RIHU | 2.59 | 0.36 | Inf | 1.89 | 3.30 |
| Deep Torpor | RIHU | 2.80 | 0.36 | Inf | 2.10 | 3.50 |

coef(mod\_glm\_freq\_sp\_nb)

## variableNormothermic variableShallow Torpor   
## 3.64880123 1.55059741   
## variableTransition variableDeep Torpor   
## 2.44853901 3.80983206   
## SpeciesBLUH SpeciesRIHU   
## 0.55482472 0.02652526   
## variableShallow Torpor:SpeciesBLUH variableTransition:SpeciesBLUH   
## 1.13045127 -1.83575857   
## variableDeep Torpor:SpeciesBLUH variableShallow Torpor:SpeciesRIHU   
## -2.90936955 1.85188940   
## variableTransition:SpeciesRIHU variableDeep Torpor:SpeciesRIHU   
## 0.11904168 -1.04001451