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

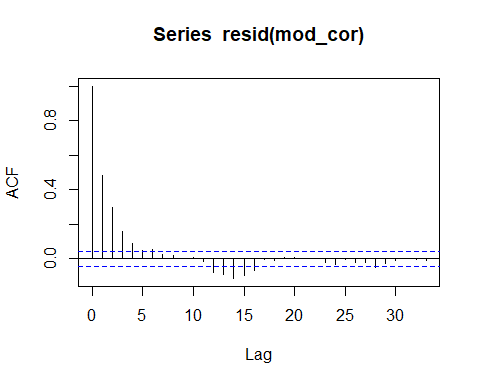
library(MASS) ## To check the distribution of the data and run glm.nb

## 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\_both <- 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)  
#summary(mod\_BVD\_sp\_cor2)  
#confint(mod\_BVD\_sp\_cor2)  
acf(resid(mod\_cor))



knitr::kable(em, digits=2)

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Species | Category | emmean | SE | df | lower.CL | upper.CL |
| BCHU | Normothermic | 33.03 | 1.83 | 28 | 29.29 | 36.77 |
| BLUH | Normothermic | 31.81 | 0.68 | 28 | 30.42 | 33.19 |
| RIHU | Normothermic | 30.93 | 0.52 | 28 | 29.85 | 32.00 |
| BCHU | Shallow Torpor | 30.40 | 1.91 | 28 | 26.48 | 34.32 |
| BLUH | Shallow Torpor | 29.03 | 0.78 | 28 | 27.44 | 30.62 |
| RIHU | Shallow Torpor | 27.48 | 0.51 | 28 | 26.44 | 28.53 |
| BCHU | Transition | 21.56 | 1.85 | 28 | 17.77 | 25.36 |
| BLUH | Transition | 22.07 | 1.00 | 28 | 20.02 | 24.13 |
| RIHU | Transition | 22.71 | 0.66 | 28 | 21.37 | 24.06 |
| BCHU | Deep Torpor | 15.10 | 1.82 | 28 | 11.37 | 18.84 |
| BLUH | Deep Torpor | 15.46 | 1.02 | 28 | 13.38 | 17.54 |
| RIHU | Deep Torpor | 15.67 | 0.59 | 28 | 14.46 | 16.89 |

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

|  |  |  |  |
| --- | --- | --- | --- |
|  | lower | est. | upper |
| (Intercept) | 34.39 | 46.51 | 58.62 |
| Amb\_Temp | 0.02 | 0.05 | 0.08 |
| CategoryShallow Torpor | -4.90 | -3.19 | -1.48 |
| CategoryTransition | -18.67 | -16.91 | -15.15 |
| CategoryDeep Torpor | -28.14 | -26.60 | -25.05 |
| SpeciesBLUH | -6.21 | -1.23 | 3.76 |
| SpeciesRIHU | -6.65 | -2.10 | 2.45 |
| Cap\_mass | -0.61 | 0.29 | 1.19 |
| Year | -1.65 | -0.92 | -0.19 |
| Amb\_Temp:CategoryShallow Torpor | -0.01 | 0.05 | 0.10 |
| Amb\_Temp:CategoryTransition | 0.36 | 0.46 | 0.55 |
| Amb\_Temp:CategoryDeep Torpor | 0.61 | 0.73 | 0.84 |
| CategoryShallow Torpor:SpeciesBLUH | -1.90 | -0.15 | 1.61 |
| CategoryTransition:SpeciesBLUH | -0.23 | 1.74 | 3.70 |
| CategoryDeep Torpor:SpeciesBLUH | -0.23 | 1.58 | 3.39 |
| CategoryShallow Torpor:SpeciesRIHU | -2.60 | -0.81 | 0.98 |
| CategoryTransition:SpeciesRIHU | 1.53 | 3.25 | 4.98 |
| CategoryDeep Torpor:SpeciesRIHU | 1.18 | 2.67 | 4.17 |

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

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Value | Std.Error | DF | t-value | p-value |
| (Intercept) | 46.51 | 6.18 | 2012 | 7.53 | 7.754187e-14 |
| Amb\_Temp | 0.05 | 0.01 | 2012 | 3.58 | 3.527205e-04 |
| CategoryShallow Torpor | -3.19 | 0.85 | 53 | -3.74 | 4.470935e-04 |
| CategoryTransition | -16.91 | 0.88 | 53 | -19.31 | 1.207151e-25 |
| CategoryDeep Torpor | -26.60 | 0.77 | 53 | -34.53 | 0.000000e+00 |
| SpeciesBLUH | -1.23 | 2.44 | 28 | -0.50 | 6.187366e-01 |
| SpeciesRIHU | -2.10 | 2.22 | 28 | -0.95 | 3.519506e-01 |
| Cap\_mass | 0.29 | 0.44 | 28 | 0.67 | 5.104162e-01 |
| Year | -0.92 | 0.36 | 28 | -2.59 | 1.493106e-02 |
| Amb\_Temp:CategoryShallow Torpor | 0.05 | 0.03 | 2012 | 1.67 | 9.417691e-02 |
| Amb\_Temp:CategoryTransition | 0.46 | 0.05 | 2012 | 9.13 | 1.654906e-19 |
| Amb\_Temp:CategoryDeep Torpor | 0.73 | 0.06 | 2012 | 12.69 | 2.000000e-35 |
| CategoryShallow Torpor:SpeciesBLUH | -0.15 | 0.87 | 53 | -0.17 | 8.686112e-01 |
| CategoryTransition:SpeciesBLUH | 1.74 | 0.98 | 53 | 1.78 | 8.160316e-02 |
| CategoryDeep Torpor:SpeciesBLUH | 1.58 | 0.90 | 53 | 1.75 | 8.573507e-02 |
| CategoryShallow Torpor:SpeciesRIHU | -0.81 | 0.89 | 53 | -0.91 | 3.674662e-01 |
| CategoryTransition:SpeciesRIHU | 3.25 | 0.86 | 53 | 3.78 | 3.981113e-04 |
| CategoryDeep Torpor:SpeciesRIHU | 2.67 | 0.74 | 53 | 3.59 | 7.180289e-04 |

## Models for proportion of night spent in each category ##  
m.prop\_dur\_both$variable <- factor(m.prop\_dur\_both$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\_both, family=poisson())  
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 | 3.51 | 0.07 | Inf | 3.39 | 3.64 |
| Shallow Torpor | BCHU | 1.55 | 0.17 | Inf | 1.21 | 1.89 |
| Transition | BCHU | 2.52 | 0.11 | Inf | 2.31 | 2.73 |
| Deep Torpor | BCHU | 3.90 | 0.05 | Inf | 3.79 | 4.00 |
| 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 | 3.76 | 0.04 | Inf | 3.67 | 3.85 |
| Shallow Torpor | RIHU | 3.48 | 0.05 | Inf | 3.38 | 3.58 |
| Transition | RIHU | 2.06 | 0.10 | Inf | 1.86 | 2.26 |
| Deep Torpor | RIHU | 2.82 | 0.07 | Inf | 2.69 | 2.96 |

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

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| variable | Species | emmean | SE | df | asymp.LCL | asymp.UCL |
| Normothermic | BCHU | 3.51 | 0.47 | Inf | 2.59 | 4.43 |
| Shallow Torpor | BCHU | 1.55 | 0.50 | Inf | 0.58 | 2.52 |
| Transition | BCHU | 2.52 | 0.48 | Inf | 1.59 | 3.45 |
| Deep Torpor | BCHU | 3.90 | 0.47 | Inf | 2.98 | 4.81 |
| Normothermic | BLUH | 4.20 | 0.33 | Inf | 3.56 | 4.85 |
| Shallow Torpor | BLUH | 3.24 | 0.33 | Inf | 2.58 | 3.89 |
| Transition | BLUH | 1.17 | 0.36 | Inf | 0.46 | 1.87 |
| Deep Torpor | BLUH | 1.46 | 0.35 | Inf | 0.76 | 2.15 |
| Normothermic | RIHU | 3.76 | 0.36 | Inf | 3.06 | 4.46 |
| Shallow Torpor | RIHU | 3.48 | 0.36 | Inf | 2.78 | 4.18 |
| Transition | RIHU | 2.06 | 0.37 | Inf | 1.33 | 2.78 |
| Deep Torpor | RIHU | 2.82 | 0.36 | Inf | 2.11 | 3.53 |

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

## variableNormothermic variableShallow Torpor   
## 3.5136754 1.5505974   
## variableTransition variableDeep Torpor   
## 2.5199980 3.8976343   
## SpeciesBLUH SpeciesRIHU   
## 0.6899506 0.2475248   
## variableShallow Torpor:SpeciesBLUH variableTransition:SpeciesBLUH   
## 0.9953254 -2.0423434   
## variableDeep Torpor:SpeciesBLUH variableShallow Torpor:SpeciesRIHU   
## -3.1322976 1.6831179   
## variableTransition:SpeciesRIHU variableDeep Torpor:SpeciesRIHU   
## -0.7091346 -1.3217980