ShallowTables

Anusha Shankar

5/5/2021

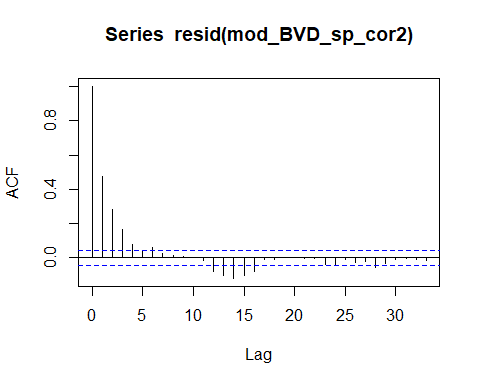
library(here)

## 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  
library(emmeans)

## Warning: package 'emmeans' was built under R version 4.0.4

#getwd()  
here <- here::here  
therm\_all <- read.csv(here("..", "..", "Data", "All\_data.csv"))  
#head(therm\_all)  
  
therm\_all$Category <- factor(therm\_all$Category, levels=c("Normothermic", "Shallow Torpor", "Transition", "Deep Torpor"))  
therm\_all$Species <- as.factor(therm\_all$Species)  
  
mod\_BVD\_sp\_cor2 <- nlme::lme(data=therm\_all, fixed=Surf\_Temp ~   
 Amb\_Temp +   
 Category +   
 Amb\_Temp:Category +   
 Species +   
 Cap\_mass +  
 Species:Category,   
 random= ~1|Indiv\_numeric/Category,   
 correlation=corAR1(form=~1|Indiv\_numeric/Category))  
em2 <- emmeans(mod\_BVD\_sp\_cor2, ~Species:Category)  
#em2  
#summary(mod\_BVD\_sp\_cor2)  
#confint(mod\_BVD\_sp\_cor2)  
acf(resid(mod\_BVD\_sp\_cor2))



knitr::kable(em2, digits=2)

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Species | Category | emmean | SE | df | lower.CL | upper.CL |
| BCHU | Normothermic | 32.13 | 1.92 | 29 | 28.20 | 36.07 |
| BLHU | Normothermic | 31.91 | 0.72 | 29 | 30.43 | 33.39 |
| MAHU | Normothermic | 31.04 | 0.55 | 29 | 29.92 | 32.16 |
| BCHU | Shallow Torpor | 29.60 | 2.01 | 29 | 25.50 | 33.71 |
| BLHU | Shallow Torpor | 29.18 | 0.81 | 29 | 27.51 | 30.84 |
| MAHU | Shallow Torpor | 27.54 | 0.54 | 29 | 26.44 | 28.64 |
| BCHU | Transition | 20.72 | 1.95 | 29 | 16.72 | 24.71 |
| BLHU | Transition | 22.17 | 1.02 | 29 | 20.08 | 24.27 |
| MAHU | Transition | 22.94 | 0.67 | 29 | 21.57 | 24.31 |
| BCHU | Deep Torpor | 14.30 | 1.93 | 29 | 10.36 | 18.24 |
| BLHU | Deep Torpor | 15.64 | 1.04 | 29 | 13.52 | 17.76 |
| MAHU | Deep Torpor | 15.76 | 0.61 | 29 | 14.51 | 17.01 |

knitr::kable(summary(mod\_BVD\_sp\_cor2)$tTable, digits=2)

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Value | Std.Error | DF | t-value | p-value |
| (Intercept) | 30.89 | 1.47 | 2012 | 21.06 | 0.00 |
| Amb\_Temp | 0.05 | 0.01 | 2012 | 3.53 | 0.00 |
| CategoryShallow Torpor | -3.07 | 0.83 | 53 | -3.70 | 0.00 |
| CategoryTransition | -16.86 | 0.85 | 53 | -19.73 | 0.00 |
| CategoryDeep Torpor | -26.76 | 0.74 | 53 | -35.91 | 0.00 |
| SpeciesBLHU | -0.23 | 2.58 | 29 | -0.09 | 0.93 |
| SpeciesMAHU | -1.09 | 2.34 | 29 | -0.47 | 0.64 |
| Cap\_mass | 0.09 | 0.46 | 29 | 0.20 | 0.84 |
| Amb\_Temp:CategoryShallow Torpor | 0.05 | 0.03 | 2012 | 1.64 | 0.10 |
| Amb\_Temp:CategoryTransition | 0.46 | 0.05 | 2012 | 9.28 | 0.00 |
| Amb\_Temp:CategoryDeep Torpor | 0.75 | 0.06 | 2012 | 13.38 | 0.00 |
| CategoryShallow Torpor:SpeciesBLHU | -0.20 | 0.84 | 53 | -0.24 | 0.81 |
| CategoryTransition:SpeciesBLHU | 1.69 | 0.95 | 53 | 1.77 | 0.08 |
| CategoryDeep Torpor:SpeciesBLHU | 1.56 | 0.88 | 53 | 1.78 | 0.08 |
| CategoryShallow Torpor:SpeciesMAHU | -0.98 | 0.86 | 53 | -1.14 | 0.26 |
| CategoryTransition:SpeciesMAHU | 3.32 | 0.83 | 53 | 4.00 | 0.00 |
| CategoryDeep Torpor:SpeciesMAHU | 2.54 | 0.71 | 53 | 3.57 | 0.00 |