

# Supplementary Online Material for Tamburello et al. - Energy and the scaling of animal space use

*Natascia Tamburello*

*Thursday, April 3, 2015*

This document is supplementary online material for Natascia Tamburello, Isabelle M. Cote, and Nicholas K. Dulvy. In press. Energy and the scaling of animal space use. The American Naturalist.

Load required packages and read in and subset the data by taxon and analysis groups of interest:

```
library("lme4")
```

```
## Loading required package: Matrix  
## Loading required package: Rcpp
```

```
library("lmerTest")
```

```
## Warning: package 'lmerTest' was built under R version 3.1.2
```

```
## KernSmooth 2.23 loaded  
## Copyright M. P. Wand 1997-2009  
##  
## Attaching package: 'lmerTest'  
##  
## The following object is masked from 'package:lme4':  
##  
##     lmer  
##  
## The following object is masked from 'package:stats':  
##  
##     step
```

```
library("MuMIn")
```

```
## Warning: package 'MuMIn' was built under R version 3.1.1
```

```
library("ggplot2")
```

```
## Warning: package 'ggplot2' was built under R version 3.1.2
```

```
library("scales")  
library("calibrate")
```

```
## Warning: package 'calibrate' was built under R version 3.1.2
```

```
## Loading required package: MASS
```

```
library("magicaxis")
```

```
## Warning: package 'magicaxis' was built under R version 3.1.2
```

```
## Loading required package: plotrix  
##  
## Attaching package: 'plotrix'  
##  
## The following object is masked from 'package:scales':  
##  
##      rescale  
##  
## Loading required package: sm  
## Package 'sm', version 2.2-5.4: type help(sm) for summary information  
##  
## Attaching package: 'sm'  
##  
## The following object is masked from 'package:MASS':  
##  
##      muscle
```

```
library("grid")
```

```
#download files from figshare (http://dx.doi.org/10.6084/m9.figshare.1365660) and assign as follows with the proper working directory on your machine
```

```
#main home range data set
```

```
data <- read.csv("C:/Research/Home Range Scaling/Tamburelloetal_HomeRangeDatabase.csv", header=T, sep=",")  
str(data)
```

```
## 'data.frame':   569 obs. of  24 variables:
## $ taxon          : Factor w/ 9 levels "birds","lake fishes",...: 2 6 6 6 6 5 5 5 5 ...
## $ common.name    : Factor w/ 569 levels "aardwolf","Abert's squirrel",...: 10 62 106 442 326 3
59 396 448 314 379 ...
## $ class          : Factor w/ 4 levels "actinopterygii",...: 1 1 1 1 1 1 1 1 1 ...
## $ order          : Factor w/ 51 levels "accipitriformes",...: 3 14 14 14 14 21 23 23 32 32 ...
## $ family         : Factor w/ 150 levels "acanthuridae",...: 9 22 43 43 43 55 60 60 1 1 ...
## $ genus          : Factor w/ 380 levels "abudeufduf","acanthurus",...: 20 220 46 83 303 130 280
280 2 228 ...
## $ species        : Factor w/ 517 levels "aberti","adspersus",...: 397 368 21 175 93 282 370 50
1 254 257 ...
## $ primarymethod  : Factor w/ 7 levels "\\","direct observation",...: 5 3 3 3 3 5 5 2 5 ...
## $ N              : Factor w/ 48 levels "1","10","104",...: 11 NA 16 22 12 38 15 15 NA 46 ...
## $ mean.mass.g    : num  887 562 34 4 4 ...
## $ log10.mass     : num  2.948 2.75 1.531 0.602 0.602 ...
## $ alt.mass.reference : Factor w/ 7 levels "Beck TDI, Brain CE. 1978. Weights of Colorado Sage Gro
use. The Condor 80(2), 241-243.",...: NA NA NA NA NA NA NA NA NA ...
## $ mean.hra.m2    : num  282750 282.1 116.1 125.5 87.1 ...
## $ log10.hra      : num  5.45 2.45 2.06 2.1 1.94 ...
## $ hra.reference   : Factor w/ 162 levels "Alberts AC. 1993. Relationship of Space Use to Popul
ation Density in an Herbivorous Lizard. Herpetologica 49(4), 469-479.",...: 92 92 92 92 92 92 134 134
103 85 ...
## $ realm          : Factor w/ 2 levels "aquatic","terrestrial": 1 1 1 1 1 1 1 1 1 ...
## $ thermoregulation : Factor w/ 2 levels "ectotherm","endotherm": 1 1 1 1 1 1 1 1 1 ...
## $ locomotion      : Factor w/ 4 levels "crawling","flying",...: 3 3 3 3 3 3 3 3 3 ...
## $ trophic.guild    : Factor w/ 2 levels "carnivore","herbivore": 1 1 1 1 1 1 1 1 2 2 ...
## $ dimension       : Factor w/ 2 levels "2D","3D": 2 1 1 1 1 1 1 1 1 ...
## $ preymass        : num  NA NA NA NA NA NA 1.39 NA NA NA ...
## $ log10.preymass   : num  NA NA NA NA NA ...
## $ PPMR            : num  NA NA NA NA NA NA 530 NA NA NA ...
## $ prey.size.reference: Factor w/ 26 levels "Brose U, et al. 2005b. Body sizes of consumers and th
eir resources. Ecology 86, 2545.",...: NA NA NA NA NA NA 1 NA NA NA ...
```

*#mock data set for prediction of carnivore-only mass models for Figure 3*

```
data.PM <-read.csv("C:/Research/Home Range Scaling/Tamburelloetal_Fig2_PreymassPredictionData.csv", h
eader=T, sep=",")
str(data.PM)
```

```
## 'data.frame':   36 obs. of  9 variables:
## $ group       : int  2 2 2 2 2 2 2 2 4 4 ...
## $ taxon       : Factor w/ 5 levels "birds","lake fish",...: 4 4 4 4 4 4 4 4 2 2 ...
## $ mass        : int  1 5 10 50 100 501 1000 3250 50 100 ...
## $ log10.mass   : num  0 0.7 1 1.7 2 2.7 3 3.51 1.7 2 ...
## $ log10.preymass: num  -1.02 -0.59 -0.39 0.04 0.23 0.67 0.85 1.17 0.04 0.23 ...
## $ locomotion   : Factor w/ 4 levels "crawling","flying",...: 3 3 3 3 3 3 3 3 3 3 ...
## $ dimension    : Factor w/ 2 levels "2D","3D": 1 1 1 1 1 1 1 1 2 2 ...
## $ class        : Factor w/ 4 levels "actinopterygii",...: 1 1 1 1 1 1 1 1 1 1 ...
## $ primarymethod : Factor w/ 1 level "telemetry": 1 1 1 1 1 1 1 1 1 1 ...
```

*#mock data set for prediction of global models for Figure A2*

```
data.FM <-read.csv("C:/Research/Home Range Scaling/Tamburelloetal_FigA2_MassPredictionDataAllModels.csv", header=T, sep=",")
```

*#Subsetting by order*

```
birds <-data[ which(data$class=='aves'),]
mammals <-data[ which(data$class=='mammalia'),]
reptiles <-data[ which(data$class=='reptilia'),]
fish <-data[ which(data$class=='actinopterygii'),]
```

*#Subsetting by analysis group*

```
carn.mammals <-data[ which(data$taxon=='mammals'& data$trophic.guild=='carnivore'),]
herb.mammals <-data[ which(data$taxon=='mammals'& data$trophic.guild=='herbivore'),]
```

```
carn.birds.2D <-data[ which(data$taxon=='birds'& data$trophic.guild=='carnivore'& data$dimension=='2D'),]
```

```
carn.birds.3D <-data[ which(data$taxon=='birds'& data$trophic.guild=='carnivore'& data$dimension=='3D'),]
```

```
herb.birds.2D <-data[ which(data$taxon=='birds'& data$trophic.guild=='herbivore'& data$dimension=='2D'),]
```

```
herb.birds.3D <-data[ which(data$taxon=='birds'& data$trophic.guild=='herbivore'& data$dimension=='3D'),]
```

```
carn.marfish <-data[ which(data$taxon=='marine fishes'& data$trophic.guild=='carnivore'),]
```

```
herb.marfish <-data[ which(data$taxon=='marine fishes'& data$trophic.guild=='herbivore'),]
```

```
carn.rivfish <-data[ which(data$taxon=='river fishes'),]
```

```
carn.lakefish <-data[ which(data$taxon=='lake fishes'),]
```

```
carn.snakes <-data[ which(data$taxon=='snakes'),]
```

```
carn.turtles <-data[ which(data$taxon=='turtles'),]
```

```
herb.turtles <-data[ which(data$taxon=='tortoises'),]
```

```
herb.lizards <-data[ which(data$taxon=='lizards'),]
```

Estimate parameters of home range allometry models for individual taxa as reported in Figure 1:

```
#Create a fake dataset to predict home range area at 1kg
taxonpredict <- data.frame(log10.mass = c(3), primarymethod = 'telemetry')

#Home range allometry models for bird taxa

#Carnivorous flying birds, because mix of tracking methods use mixed model
carn.birds.3D.mod = lmer(log10.hra ~ log10.mass + (1|primarymethod), data=carn.birds.3D)
summary(carn.birds.3D.mod)
```

```
## Linear mixed model fit by REML t-tests use Satterthwaite approximations
## to degrees of freedom [merModLmerTest]
## Formula: log10.hra ~ log10.mass + (1 | primarymethod)
## Data: carn.birds.3D
##
## REML criterion at convergence: 197
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.08252 -0.74883  0.06087  0.63243  2.63580
##
## Random effects:
##   Groups             Name             Variance Std.Dev.
##   primarymethod (Intercept) 0.3478      0.5897
##   Residual                  0.3472      0.5892
## Number of obs: 105, groups: primarymethod, 3
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)  2.79702    0.40538    2.08000    6.90  0.0183 *
## log10.mass   1.50145    0.07599  102.46000   19.76 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## log10.mass  -0.375
```

```
r.squaredGLMM(carn.birds.3D.mod)
```

```
##      R2m      R2c
## 0.6698751 0.8350729
```

```
10^(predict(carn.birds.3D.mod, newdata=taxonpredict)) #predict home range area 1kg (HRA1kg)
```

```
##          1
## 49421694
```

```
#Other birds tracked almost entirely using telemetry, use simple linear model
carn.birds.2D.mod = lm(log10.hra ~ log10.mass, data=carn.birds.2D)
summary(carn.birds.2D.mod)
```

```
##
## Call:
## lm(formula = log10.hra ~ log10.mass, data = carn.birds.2D)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.85236 -0.79633 -0.02016  0.22764  2.22043
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   2.6944     2.2035   1.223   0.256
## log10.mass    1.1364     0.8091   1.405   0.198
##
## Residual standard error: 1.002 on 8 degrees of freedom
## Multiple R-squared:  0.1978, Adjusted R-squared:  0.09754
## F-statistic: 1.973 on 1 and 8 DF,  p-value: 0.1978
```

```
10^(predict(carn.birds.2D.mod, newdata=taxonpredict)) #predict home range area 1kg (HRA1kg)
```

```
##          1
## 1268991
```

```
herb.birds.3D.mod = lm(log10.hra ~ log10.mass, data=herb.birds.3D)
summary(herb.birds.3D.mod)
```

```
##
## Call:
## lm(formula = log10.hra ~ log10.mass, data = herb.birds.3D)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.18849 -0.54586 -0.25179 -0.01388  2.37105
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   1.6271      1.6957   0.960   0.369
## log10.mass    1.7722      0.8066   2.197   0.064 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.135 on 7 degrees of freedom
## Multiple R-squared:  0.4082, Adjusted R-squared:  0.3236
## F-statistic: 4.827 on 1 and 7 DF,  p-value: 0.064
```

```
10^(predict(herb.birds.3D.mod, newdata=taxonpredict)) #predict home range area 1kg (HRA1kg)
```

```
##      1
## 8784892
```

```
herb.birds.2D.mod = lm(log10.hra ~ log10.mass, data=herb.birds.2D)
summary(herb.birds.2D.mod)
```

```
##
## Call:
## lm(formula = log10.hra ~ log10.mass, data = herb.birds.2D)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.5024 -0.8237 -0.1893  0.5123  2.1153
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   2.3119     1.2750   1.813   0.0929 .
## log10.mass    1.1323     0.3856   2.936   0.0116 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.074 on 13 degrees of freedom
## Multiple R-squared:  0.3987, Adjusted R-squared:  0.3525
## F-statistic: 8.621 on 1 and 13 DF,  p-value: 0.01158
```

```
10^(predict(herb.birds.2D.mod, newdata=taxonpredict)) #predict home range area 1kg (HRA1kg)
```

```
##      1
## 511463.6
```

```
#Mammals tracked almost entirely using telemetry, use simple linear model
carn.mammals.mod = lm(log10.hra ~ log10.mass , data=carn.mammals)
summary(carn.mammals.mod)
```



```
##
## Call:
## lm(formula = log10.hra ~ log10.mass, data = carn.mammals)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.94991 -0.53931  0.07877  0.65468  1.49646
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.66265     0.27608   6.022 5.31e-08 ***
## log10.mass   1.36405     0.08535  15.982 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8646 on 78 degrees of freedom
## Multiple R-squared:  0.7661, Adjusted R-squared:  0.7631
## F-statistic: 255.4 on 1 and 78 DF,  p-value: < 2.2e-16
```

```
10^(predict(carn.mammals.mod, newdata=taxonpredict)) #predict home range area 1kg (HRA1kg)
```

```
##      1
## 568576.6
```

```
herb.mammals.mod = lm(log10.hra ~ log10.mass, data=herb.mammals)
summary(herb.mammals.mod)
```

```
##
## Call:
## lm(formula = log10.hra ~ log10.mass, data = herb.mammals)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.89146 -0.55260 -0.03212  0.61269  2.79304
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.31996     0.17985   7.339 1.11e-11 ***
## log10.mass   1.08555     0.04969  21.845 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8308 on 156 degrees of freedom
## Multiple R-squared:  0.7536, Adjusted R-squared:  0.752
## F-statistic: 477.2 on 1 and 156 DF,  p-value: < 2.2e-16
```

```
10^(predict(herb.mammals.mod, newdata=taxonpredict)) #predict home range area 1kg (HRA1kg)
```

```
##      1
## 37721.82
```

```
##### All reptiles tracked almost entirely using telemetry, use simple linear model
carn.snakes.mod = lm(log10.hra ~ log10.mass, data=carn.snakes)
summary(carn.snakes.mod)
```

```
##
## Call:
## lm(formula = log10.hra ~ log10.mass, data = carn.snakes)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.38112 -0.48389  0.07222  0.51361  1.45851
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   1.9946     0.4056   4.918 1.62e-05 ***
## log10.mass    1.2222     0.1761   6.942 2.57e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.668 on 39 degrees of freedom
## Multiple R-squared:  0.5527, Adjusted R-squared:  0.5412
## F-statistic: 48.19 on 1 and 39 DF,  p-value: 2.573e-08
```

```
10^(predict(carn.snakes.mod, newdata=taxonpredict)) #predict home range area 1kg (HRA1kg)
```

```
##      1
## 458350.4
```

```
carn.turtles.mod = lm(log10.hra ~ log10.mass, data=carn.turtles)
summary(carn.turtles.mod)
```

```
##
## Call:
## lm(formula = log10.hra ~ log10.mass, data = carn.turtles)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.5854 -0.4126 -0.1223  0.2878  1.0270
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   2.6670      0.9439   2.826  0.0153 *
## log10.mass     0.7372      0.3371   2.187  0.0493 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5424 on 12 degrees of freedom
## Multiple R-squared:  0.2849, Adjusted R-squared:  0.2253
## F-statistic: 4.782 on 1 and 12 DF,  p-value: 0.0493
```

```
10^(predict(carn.turtles.mod, newdata=taxonpredict)) #predict home range area 1kg (HRA1kg)
```

```
##      1
## 75588.75
```

```
herb.turtles.mod = lm(log10.hra ~ log10.mass, data=herb.turtles)
summary(herb.turtles.mod)
```

```
##
## Call:
## lm(formula = log10.hra ~ log10.mass, data = herb.turtles)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.8956 -0.5292  0.1004  0.4694  0.7316
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   2.2661     1.0420   2.175  0.0547 .
## log10.mass    0.9289     0.3410   2.724  0.0214 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6263 on 10 degrees of freedom
## Multiple R-squared:  0.426, Adjusted R-squared:  0.3686
## F-statistic: 7.421 on 1 and 10 DF, p-value: 0.02141
```

```
10^(predict(herb.turtles.mod, newdata=taxonpredict)) #predict home range area 1kg (HRA1kg)
```

```
##      1
## 112924.6
```

```
herb.lizards.mod = lm(log10.hra ~ log10.mass, data=herb.lizards)
summary(herb.lizards.mod)
```

```
##
## Call:
## lm(formula = log10.hra ~ log10.mass, data = herb.lizards)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.85723 -0.36019 -0.01483  0.41726  0.68030
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.6683     0.5674   1.178 0.269066
## log10.mass    1.0723     0.1937   5.537 0.000363 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5414 on 9 degrees of freedom
## Multiple R-squared:  0.773, Adjusted R-squared:  0.7478
## F-statistic: 30.65 on 1 and 9 DF, p-value: 0.0003627
```

```
10^(predict(herb.lizards.mod, newdata=taxonpredict)) #predict home range area 1kg (HRA1kg)
```

```
##      1
## 7677.85
```

```
#almost all lake/river fish have same method, so omitted primarymethod and used lm instead
carn.rivfish.mod = lm(log10.hra ~ log10.mass, data=carn.rivfish)
summary(carn.rivfish.mod)
```

```
##
## Call:
## lm(formula = log10.hra ~ log10.mass, data = carn.rivfish)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.63690 -0.20955  0.02177  0.14605  0.99735
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   1.3279     0.2089   6.356 3.63e-05 ***
## log10.mass    0.6398     0.1150   5.564 0.000123 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4333 on 12 degrees of freedom
## Multiple R-squared:  0.7207, Adjusted R-squared:  0.6974
## F-statistic: 30.96 on 1 and 12 DF,  p-value: 0.0001229
```

```
10^(predict(carn.rivfish.mod, newdata=taxonpredict)) #predict home range area 1kg (HRA1kg)
```

```
##      1
## 1767.803
```

```
carn.lakefish.mod = lm(log10.hra ~ log10.mass, data=carn.lakefish)
summary(carn.lakefish.mod)
```

```
##
## Call:
## lm(formula = log10.hra ~ log10.mass, data = carn.lakefish)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.62251 -0.25583 -0.09229  0.09105  0.73648
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   1.8512     0.8842   2.094   0.0746 .
## log10.mass    0.9942     0.3551   2.800   0.0265 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4784 on 7 degrees of freedom
## Multiple R-squared:  0.5282, Adjusted R-squared:  0.4608
## F-statistic: 7.838 on 1 and 7 DF,  p-value: 0.02654
```

```
10^(predict(carn.lakefish.mod, newdata=taxonpredict)) #predict home range area 1kg (HRA1kg)
```

```
##      1
## 68180.39
```

```
#Marine fish tracked with a variety of methods, account for this as a random effect
carn.marfish.mod = lmer(log10.hra ~ log10.mass + (1|primarymethod), data=carn.marfish)
summary(carn.marfish.mod)
```



```
## Linear mixed model fit by REML t-tests use Satterthwaite approximations
##   to degrees of freedom [merModLmerTest]
## Formula: log10.hra ~ log10.mass + (1 | primarymethod)
##   Data: carn.marfish
##
## REML criterion at convergence: 200.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.8626 -0.6840  0.0735  0.6407  2.5128
##
## Random effects:
##   Groups             Name             Variance Std.Dev.
##   primarymethod (Intercept) 0.9290      0.9638
##   Residual                  0.9052      0.9514
## Number of obs: 70, groups: primarymethod, 3
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)   1.1020     0.6248   2.7600   1.764    0.184
## log10.mass     0.8215     0.1420  67.9900   5.784 2.02e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## log10.mass -0.411
```

```
r.squaredGLMM(carn.marfish.mod)
```

```
##           R2m           R2c
## 0.2880131 0.6486206
```

```
10^(predict(carn.marfish.mod, newdata=taxonpredict)) #predict home range area 1kg (HRA1kg)
```

```
##           1
## 42624.89
```

```
herb.marfish.mod = lmer(log10.hra ~ log10.mass + (1|primarymethod), data=herb.marfish)
summary(herb.marfish.mod)
```

```
## Linear mixed model fit by REML t-tests use Satterthwaite approximations
##   to degrees of freedom [merModLmerTest]
## Formula: log10.hra ~ log10.mass + (1 | primarymethod)
##   Data: herb.marfish
##
## REML criterion at convergence: 40.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.14624 -0.61207  0.03814  0.79727  1.12042
##
## Random effects:
##   Groups             Name             Variance Std.Dev.
##   primarymethod (Intercept) 2.1977      1.4825
##   Residual                  0.3265      0.5714
## Number of obs: 20, groups: primarymethod, 2
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept) -0.03399    1.13938   1.31300  -0.030    0.98
## log10.mass   1.20813    0.19114  17.31700   6.321 7.04e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## log10.mass -0.372
```

```
r.squaredGLMM(herb.marfish.mod)
```

```
##      R2m      R2c
## 0.2983579 0.9092397
```

```
10^(predict(herb.marfish.mod, newdata=taxonpredict)) #predict home range area 1kg (HRA1kg)
```

```
##      1
## 42104.61
```

Now we plot the individual taxon relationships. The output of this section forms the basis for Figure 2.

```
#####Creating Figure 2#####
#Set colours with transparency
#BW
```

```
colcarn = rgb(51,51,51,alpha=160, maxColorValue = 255)
colherb = rgb(166,166,166,alpha=160, maxColorValue = 255)
colpoly = rgb(166,166,166,alpha=70, maxColorValue = 255)
```

```
#Colours: mammals firebrick, reptiles olivedrab, fish steelblue, birds orchid4
```

```
colmamm = rgb(248,118,109, maxColorValue = 255)
colbird = rgb(199,124,255, maxColorValue = 255)
colrept = rgb(154,205,50, maxColorValue = 255)
colfish = rgb(0,191,196, maxColorValue = 255)
```

```
####Main plot with only line segments
```

```
plot(x=data$mean.mass.g, y=data$mean.hra.m2, type = "n", log = "xy", pch=1, col="white", axes=FALSE,
xlim=c(0.1,10000000), ylim=c(1, 10000000000), xlab = "Mean Species Body Mass (g)", ylab = "Mean Species Home Range Area (m2)")
magaxis(side=1:2, logpretty=TRUE)
```

```
#Carn Mammals
```

```
carn.mammals.range <- c(min(carn.mammals$log10.mass), max(carn.mammals$log10.mass))
carn.mammals.predict <- predict(carn.mammals.mod, newdata=data.frame(log10.mass=carn.mammals.range))
lines(x=10^(carn.mammals.range), y=10^(carn.mammals.predict), col = colmamm, lwd = 5)
text(min(10^carn.mammals.range),min(10^carn.mammals.predict),labels="CM", cex=0.5, col = "black")
```

```
#Herb Mammals
```

```
herb.mammals.range <- c(min(herb.mammals$log10.mass), max(herb.mammals$log10.mass))
herb.mammals.predict <- predict(herb.mammals.mod, newdata=data.frame(log10.mass=herb.mammals.range))
lines(x=10^(herb.mammals.range), y=10^(herb.mammals.predict), col = colmamm, lwd = 2)
text(min(10^herb.mammals.range),min(10^herb.mammals.predict),labels="HM", cex=0.5, col = "black")
```

```
#Carn Birds 3D
```

```
carn.birds.3D.range <- c(min(carn.birds.3D$log10.mass), max(carn.birds.3D$log10.mass))
newdata<-data.frame(log10.mass=carn.birds.3D.range)
carn.birds.3D.predict <- predict(carn.birds.3D.mod, newdata=newdata, re.form = NA)
lines(x=10^(carn.birds.3D.range), y=10^(carn.birds.3D.predict), col = colbird, lwd = 5)
text(min(10^carn.birds.3D.range),min(10^carn.birds.3D.predict),labels="CB3D", cex=0.5, col = "black")
```

```
#Carn Birds 2D
```

```
carn.birds.2D.range <- c(min(carn.birds.2D$log10.mass), max(carn.birds.2D$log10.mass))
newdata<-data.frame(log10.mass=carn.birds.2D.range)
carn.birds.2D.predict <- predict(carn.birds.2D.mod, newdata=newdata, re.form = NA)
lines(x=10^(carn.birds.2D.range), y=10^(carn.birds.2D.predict), col = colbird, lwd = 5)
text(min(10^carn.birds.2D.range),min(10^carn.birds.2D.predict),labels="CB2D", cex=0.5, col = "black")
```

```
#Herb Birds 2D
```

```
herb.birds.2D.range <- c(min(herb.birds.2D$log10.mass), max(herb.birds.2D$log10.mass))
newdata<-data.frame(log10.mass=herb.birds.2D.range)
herb.birds.2D.predict <- predict(herb.birds.2D.mod, newdata=newdata, re.form = NA)
lines(x=10^(herb.birds.2D.range), y=10^(herb.birds.2D.predict), col = colbird, lwd = 2)
```

```
text(min(10^herb.birds.2D.range),min(10^herb.birds.2D.predict),labels="HB2D", cex=0.5, col = "black")
```

#### *#Herb Birds 3D*

```
herb.birds.3D.range <- c(min(herb.birds.3D$log10.mass), max(herb.birds.3D$log10.mass))
newdata<-data.frame(log10.mass=herb.birds.3D.range)
herb.birds.3D.predict <- predict(herb.birds.3D.mod, newdata=newdata, re.form = NA)
lines(x=10^(herb.birds.3D.range), y=10^(herb.birds.3D.predict), col = colbird, lwd = 2)
text(min(10^herb.birds.3D.range),min(10^herb.birds.3D.predict),labels="HB3D", cex=0.5, col = "black")
```

#### *#Carn Snakes*

```
carn.snakes.range <- c(min(carn.snakes$log10.mass), max(carn.snakes$log10.mass))
carn.snakes.predict <- predict(carn.snakes.mod, newdata=data.frame(log10.mass=carn.snakes.range))
lines(x=10^(carn.snakes.range), y=10^(carn.snakes.predict), col = colrept, lwd = 5)
text(min(10^carn.snakes.range),min(10^carn.snakes.predict),labels="SN", cex=0.5, col = "black")
```

#### *#Carn Turtles*

```
carn.turtles.range <- c(min(carn.turtles$log10.mass), max(carn.turtles$log10.mass))
carn.turtles.predict <- predict(carn.turtles.mod, newdata=data.frame(log10.mass=carn.turtles.range))
lines(x=10^(carn.turtles.range), y=10^(carn.turtles.predict), col = colrept, lwd = 5)
text(min(10^carn.turtles.range),min(10^carn.turtles.predict),labels="TU", cex=0.5, col = "black")
```

#### *#Herb Turtles*

```
herb.turtles.range <- c(min(herb.turtles$log10.mass), max(herb.turtles$log10.mass))
herb.turtles.predict <- predict(herb.turtles.mod, newdata=data.frame(log10.mass=herb.turtles.range))
lines(x=10^(herb.turtles.range), y=10^(herb.turtles.predict), col = colrept, lwd = 2)
text(min(10^herb.turtles.range),min(10^herb.turtles.predict),labels="TOR", cex=0.5, col = "black")
```

#### *#Herb Lizards*

```
herb.lizards.range <- c(min(herb.lizards$log10.mass), max(herb.lizards$log10.mass))
herb.lizards.predict <- predict(herb.lizards.mod, newdata=data.frame(log10.mass=herb.lizards.range))
lines(x=10^(herb.lizards.range), y=10^(herb.lizards.predict), col = colrept, lwd = 2)
text(min(10^herb.lizards.range),min(10^herb.lizards.predict),labels="LIZ", cex=0.5, col = "black")
```

#### *#Carn Marine Fish*

```
carn.marfish.range <- c(min(carn.marfish$log10.mass), max(carn.marfish$log10.mass))
newdata<-data.frame(log10.mass=carn.marfish.range)
carn.marfish.predict <- predict(carn.marfish.mod, newdata=newdata, re.form = NA)
lines(x=10^(carn.marfish.range), y=10^(carn.marfish.predict), col = colfish, lwd = 5)
text(min(10^carn.marfish.range),min(10^carn.marfish.predict),labels="CMF", cex=0.5, col = "black")
```

#### *#Herb Marine Fish*

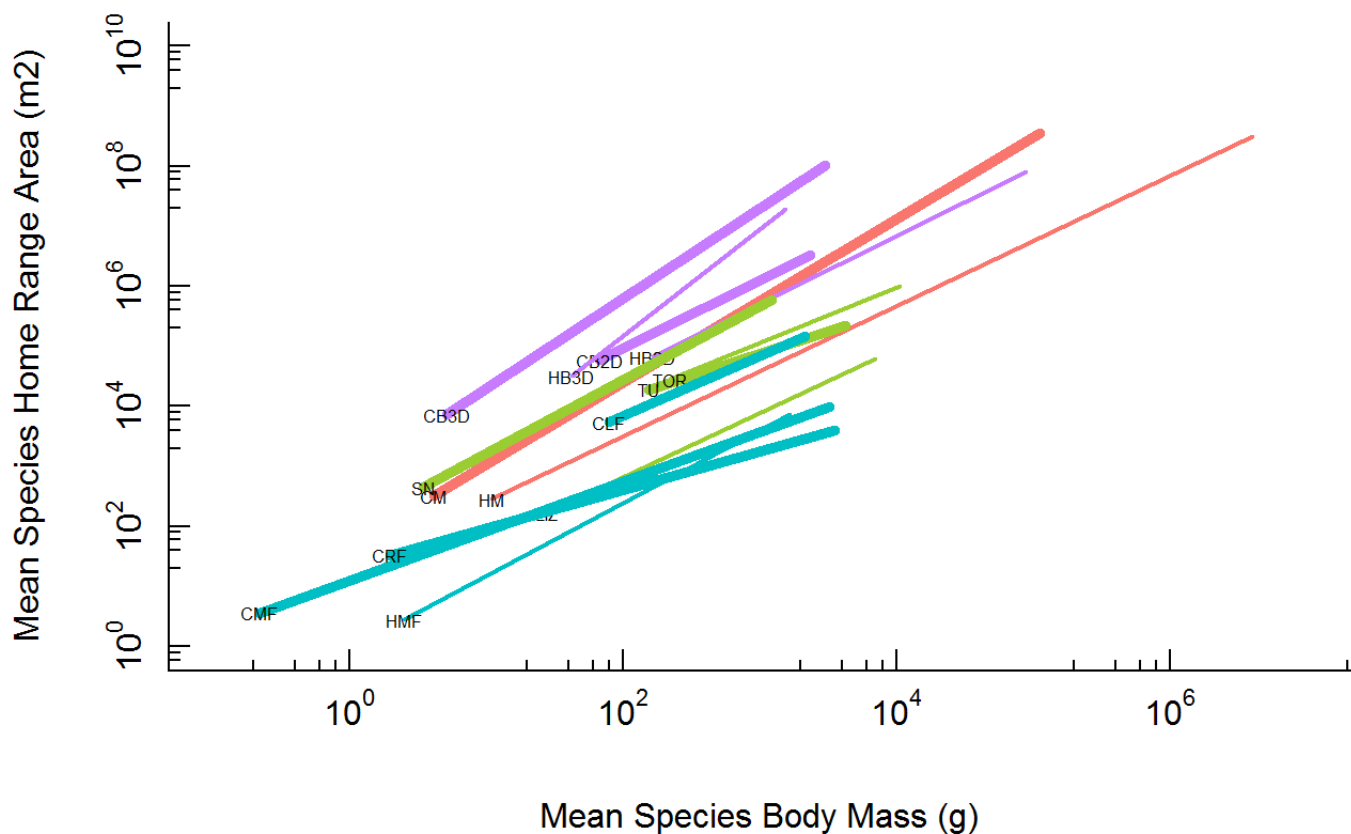
```
herb.marfish.range <- c(min(herb.marfish$log10.mass), max(herb.marfish$log10.mass))
newdata<-data.frame(log10.mass=herb.marfish.range)
herb.marfish.predict <- predict(herb.marfish.mod, newdata=newdata, re.form = NA)
lines(x=10^(herb.marfish.range), y=10^(herb.marfish.predict), col = colfish, lwd = 2)
text(min(10^herb.marfish.range),min(10^herb.marfish.predict),labels="HMF", cex=0.5, col = "black")
```

```
#Carn Lake Fish
```

```
carn.lakefish.range <- c(min(carn.lakefish$log10.mass), max(carn.lakefish$log10.mass))
carn.lakefish.predict <- predict(carn.lakefish.mod, newdata=data.frame(log10.mass=carn.lakefish.range))
lines(x=10^(carn.lakefish.range), y=10^(carn.lakefish.predict), col = colfish, lwd = 5)
text(min(10^carn.lakefish.range),min(10^carn.lakefish.predict),labels="CLF", cex=0.5, col = "black")
```

```
#Carn River Fish
```

```
carn.rivfish.range <- c(min(carn.rivfish$log10.mass), max(carn.rivfish$log10.mass))
carn.rivfish.predict <- predict(carn.rivfish.mod, newdata=data.frame(log10.mass=carn.rivfish.range))
lines(x=10^(carn.rivfish.range), y=10^(carn.rivfish.predict), col = colfish, lwd = 5)
text(min(10^carn.rivfish.range),min(10^carn.rivfish.predict),labels="CRF", cex=0.5, col = "black")
```



```
##### Subplots for figure 1
```

```
names(data)
```

## [1]	"taxon"	"common.name"	"class"
## [4]	"order"	"family"	"genus"
## [7]	"species"	"primarymethod"	"N"
## [10]	"mean.mass.g"	"log10.mass"	"alt.mass.reference"
## [13]	"mean.hra.m2"	"log10.hra"	"hra.reference"
## [16]	"realm"	"thermoregulation"	"locomotion"
## [19]	"trophic.guild"	"dimension"	"preymass"
## [22]	"log10.preymass"	"PPMR"	"prey.size.reference"

```
data.predict <- data[, c(1,3, 8, 11, 19, 20)]
```

```
#### Subset by analysis group
```

```
carn.mammals.p <-data.predict[ which(data.predict$taxon=='mammals'& data.predict$trophic.guild=='carnivore'),]
```

```
herb.mammals.p <-data.predict[ which(data.predict$taxon=='mammals'& data.predict$trophic.guild=='herbivore'),]
```

```
carn.birds.2D.p <-data.predict[ which(data.predict$taxon=='birds'& data.predict$trophic.guild=='carnivore'& data.predict$dimension=='2D'),]
```

```
carn.birds.3D.p <-data.predict[ which(data.predict$taxon=='birds'& data.predict$trophic.guild=='carnivore'& data.predict$dimension=='3D'),]
```

```
herb.birds.2D.p <-data.predict[ which(data.predict$taxon=='birds'& data.predict$trophic.guild=='herbivore'& data.predict$dimension=='2D'),]
```

```
herb.birds.3D.p <-data.predict[ which(data.predict$taxon=='birds'& data.predict$trophic.guild=='herbivore'& data.predict$dimension=='3D'),]
```

```
carn.marfish.p <-data.predict[ which(data.predict$taxon=='marine fishes'& data.predict$trophic.guild=='carnivore'),]
```

```
herb.marfish.p <-data.predict[ which(data.predict$taxon=='marine fishes'& data.predict$trophic.guild=='herbivore'),]
```

```
carn.rivfish.p <-data.predict[ which(data.predict$taxon=='river fishes'),]
```

```
carn.lakefish.p <-data.predict[ which(data.predict$taxon=='lake fishes'),]
```

```
carn.snakes.p <-data.predict[ which(data.predict$taxon=='snakes'),]
```

```
carn.turtles.p <-data.predict[ which(data.predict$taxon=='turtles'),]
```

```
herb.turtles.p <-data.predict[ which(data.predict$taxon=='tortoises'),]
```

```
herb.lizards.p <-data.predict[ which(data.predict$taxon=='lizards'),]
```

```
####For taxa modelled with lmer (marine fish, birds) use the methods below to obtain Figure 1 Subplots with 95% CI bands
```

```
#When using predict with lmer objects, we specify re.form = NA to only use the coefficients estimated in consideration of random effects, but not the random effects themselves, when predicting from new data for a more generalized prediction.
```

```
###Plot and 95% CIs for 3D Carnivorous Birds
```

```

carn.birds.3D.mod = lmer(log10.hra ~ log10.mass + (1|primarymethod), data=carn.birds.3D, REML = FALSE)
carn.birds.3D.p$log10.hra <- predict(carn.birds.3D.mod, newdata=carn.birds.3D.p, re.form = NA)
newdat <- carn.birds.3D.p

mm <- model.matrix(terms(carn.birds.3D.mod),newdat)
## or newdat$distance <- mm %>% fixef(fm1)
pvar1 <- diag(mm %>% tcrossprod(vcov(carn.birds.3D.mod),mm))
tvar1 <- pvar1 + VarCorr(carn.birds.3D.mod)$primarymethod[1] ## must be adapted for more complex models
newdat <- data.frame(
  newdat
  , plo = newdat$log10.hra-2*sqrt(pvar1)
  , phi = newdat$log10.hra+2*sqrt(pvar1)
  , tlo = newdat$log10.hra-2*sqrt(tvar1)
  , thi = newdat$log10.hra+2*sqrt(tvar1)
)
str(newdat)

```

```

## 'data.frame': 106 obs. of 11 variables:
## $ taxon : Factor w/ 9 levels "birds","lake fishes",...: 1 1 1 1 1 1 1 1 1 1 ...
## $ class : Factor w/ 4 levels "actinopterygii",...: 2 2 2 2 2 2 2 2 2 2 ...
## $ primarymethod: Factor w/ 7 levels "\\","direct observation",...: 6 6 6 6 5 6 6 6 6 6 ...
## $ log10.mass : num 3.48 2.93 3.23 3.31 2.99 ...
## $ trophic.guild: Factor w/ 2 levels "carnivore","herbivore": 1 1 1 1 1 1 1 1 1 1 ...
## $ dimension : Factor w/ 2 levels "2D","3D": 2 2 2 2 2 2 2 2 2 2 ...
## $ log10.hra : num 7.98 7.15 7.61 7.73 7.24 ...
## $ plo : num 7.36 6.55 7 7.12 6.65 ...
## $ phi : num 8.6 7.74 8.21 8.34 7.84 ...
## $ tlo : num 6.91 6.09 6.54 6.66 6.19 ...
## $ thi : num 9.05 8.2 8.67 8.79 8.3 ...

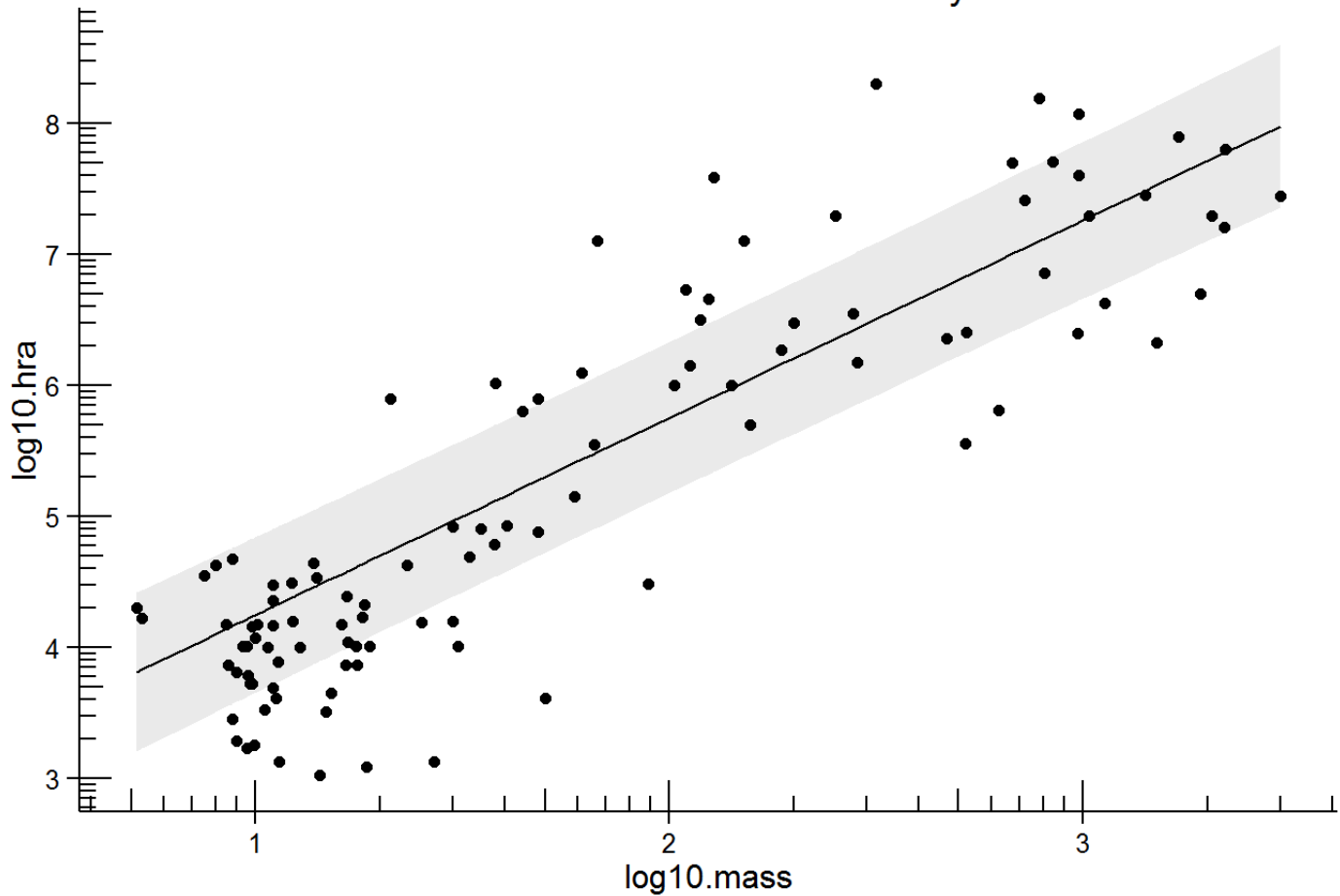
```

```

#fixef
g0 <- ggplot(newdat, aes(x=log10.mass, y=log10.hra))
g0 + annotation_logticks(short = unit(2,"mm"), mid = unit(3,"mm"), long = unit(4,"mm")) + theme_bw()
+ theme(panel.border = element_blank(), panel.grid.major = element_blank(),
panel.grid.minor = element_blank(), axis.line = element_line(colour = "black")) + geom_ribbon(aes(ymin = plo, ymax = phi, linetype = NA), alpha=0.1) + geom_line(aes(ymin = plo, ymax = phi)) + ggtitle("CI based on fixed-effects uncertainty ONLY") + geom_point(aes(x=carn.birds.3D$log10.mass, y = carn.birds.3D$log10.hra))

```

## CI based on fixed-effects uncertainty ONLY



###Plot and 95% CIs for 2D Carnivorous Birds

```
carn.birds.2D.mod = lmer(log10.hra ~ log10.mass + (1|primarymethod), data=carn.birds.2D, REML = FALSE)
```

```
carn.birds.2D.p$log10.hra <- predict(carn.birds.2D.mod, newdata=carn.birds.2D.p, re.form = NA)
```

```
newdat <- carn.birds.2D.p
```

```
mm <- model.matrix(terms(carn.birds.2D.mod),newdat)
```

```
pvar1 <- diag(mm %*% tcrossprod(vcov(carn.birds.2D.mod),mm))
```

```
tvar1 <- pvar1 + VarCorr(carn.birds.2D.mod)$primarymethod[1] ## must be adapted for more complex models
```

```
ts
```

```
tvar1 <-
```

```
newdat <- data.frame(
```

```
  newdat
```

```
  , plo = newdat$log10.hra-2*sqrt(pvar1)
```

```
  , phi = newdat$log10.hra+2*sqrt(pvar1)
```

```
  , tlo = newdat$log10.hra-2*sqrt(tvar1)
```

```
  , thi = newdat$log10.hra+2*sqrt(tvar1)
```

```
)
```

```
str(newdat)
```

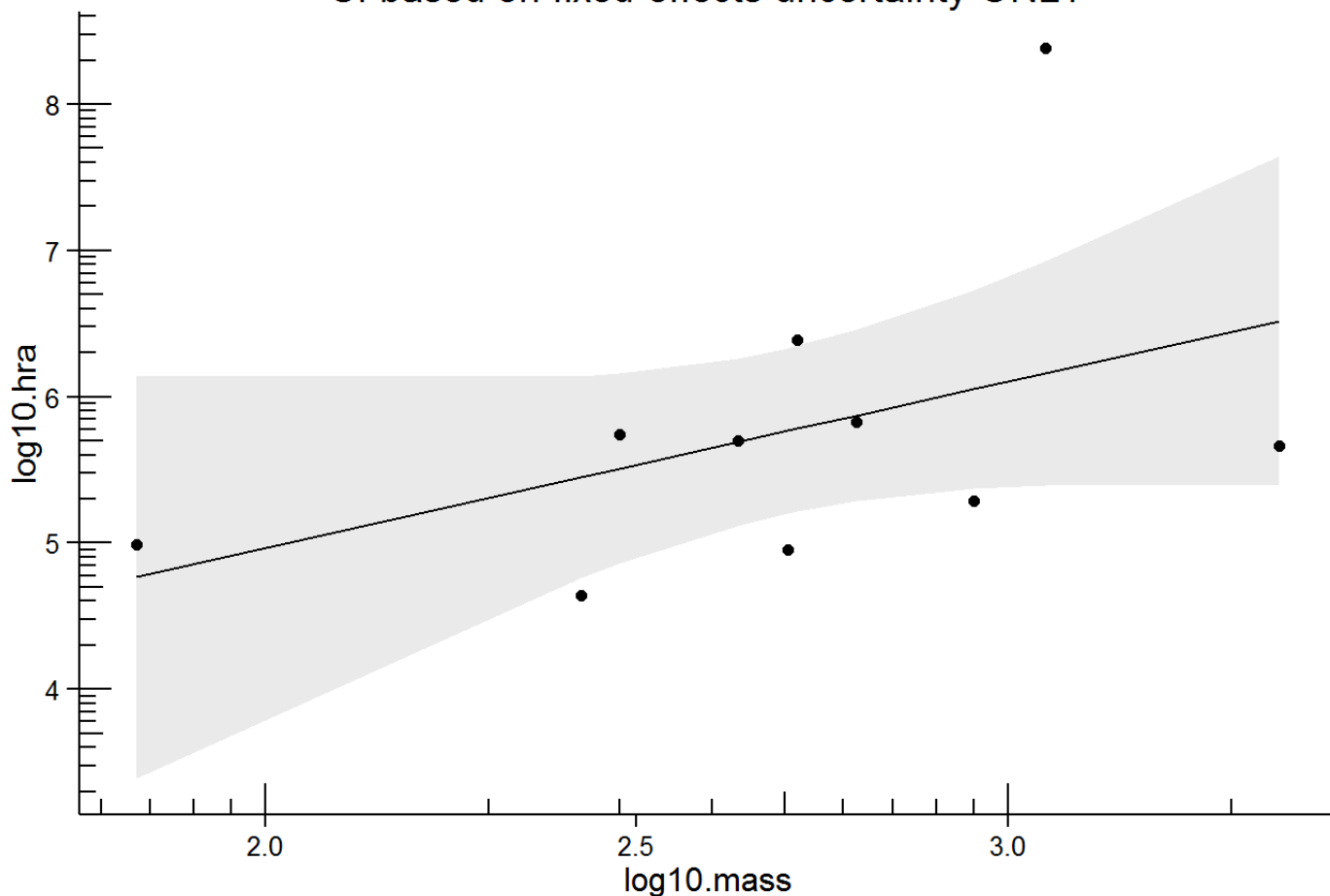


```
## 'data.frame':   10 obs. of  11 variables:
## $ taxon      : Factor w/ 9 levels "birds","lake fishes",...: 1 1 1 1 1 1 1 1 1 1
## $ class      : Factor w/ 4 levels "actinopterygii",...: 2 2 2 2 2 2 2 2 2 2
## $ primarymethod: Factor w/ 7 levels "\\","direct observation",...: 5 5 5 5 5 5 2 5 5 5
## $ log10.mass : num  3.37 2.72 2.48 2.64 3.05 ...
## $ trophic.guild: Factor w/ 2 levels "carnivore","herbivore": 1 1 1 1 1 1 1 1 1 1
## $ dimension  : Factor w/ 2 levels "2D","3D": 1 1 1 1 1 1 1 1 1 1
## $ log10.hra  : num  6.52 5.78 5.51 5.69 6.16 ...
## $ plo       : num  5.4 5.21 4.86 5.12 5.4 ...
## $ phi       : num  7.64 6.35 6.16 6.26 6.93 ...
## $ tlo       : num  5.4 5.21 4.86 5.12 5.4 ...
## $ thi       : num  7.64 6.35 6.16 6.26 6.93 ...
```

```
#fixef
```

```
g0 <- ggplot(newdat, aes(x=log10.mass, y=log10.hra))
g0 + annotation_logticks(short = unit(2,"mm"), mid = unit(3,"mm"), long = unit(4,"mm")) + theme_bw()
+ theme(panel.border = element_blank(), panel.grid.major = element_blank(),
panel.grid.minor = element_blank(), axis.line = element_line(colour = "black")) + geom_ribbon(aes(ymin
n = plo, ymax = phi, linetype = NA), alpha=0.1) + geom_line(aes(ymin = plo, ymax = phi)) + ggtitle("C
I based on fixed-effects uncertainty ONLY") + geom_point(aes(x=carn.birds.2D$log10.mass, y = carn.bir
ds.2D$log10.hra))
```

## CI based on fixed-effects uncertainty ONLY



### ###Plot and 95% CIs for 3D Herbivorous Birds

```
herb.birds.3D.mod = lmer(log10.hra ~ log10.mass + (1|primarymethod), data=herb.birds.3D, REML = FALSE)
herb.birds.3D.p$log10.hra <- predict(herb.birds.3D.mod, newdata=herb.birds.3D.p, re.form = NA)
newdat <- herb.birds.3D.p

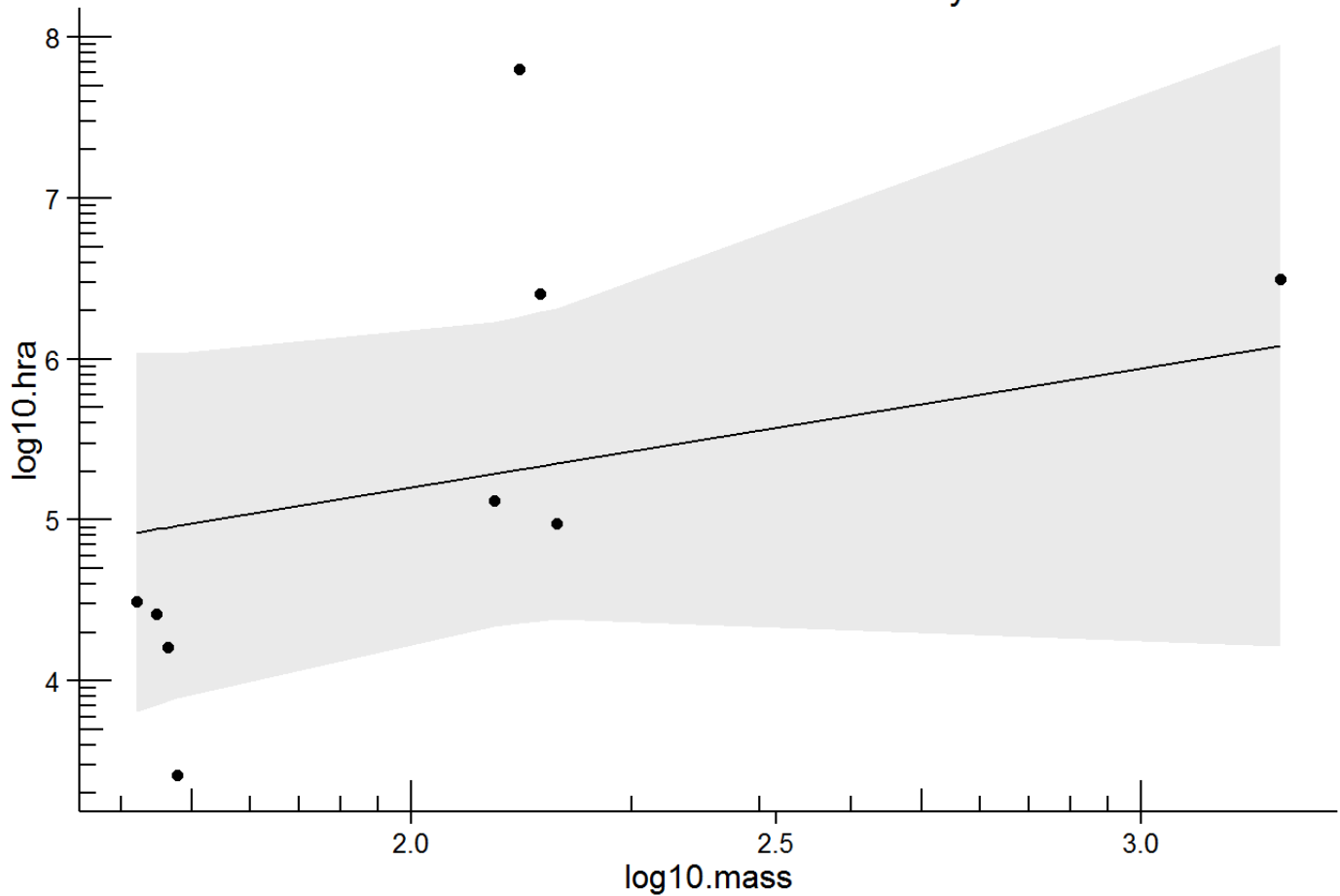
mm <- model.matrix(terms(herb.birds.3D.mod),newdat)
pvar1 <- diag(mm %*% tcrossprod(vcov(herb.birds.3D.mod),mm))
tvar1 <- pvar1 + VarCorr(herb.birds.3D.mod)$primarymethod[1] ## must be adapted for more complex models
tvar1 <-
  newdat <- data.frame(
    newdat
    , plo = newdat$log10.hra-2*sqrt(pvar1)
    , phi = newdat$log10.hra+2*sqrt(pvar1)
    , tlo = newdat$log10.hra-2*sqrt(tvar1)
    , thi = newdat$log10.hra+2*sqrt(tvar1)
  )
str(newdat)
```

```
## 'data.frame': 9 obs. of 11 variables:
## $ taxon : Factor w/ 9 levels "birds","lake fishes",...: 1 1 1 1 1 1 1 1 1
## $ class : Factor w/ 4 levels "actinopterygii",...: 2 2 2 2 2 2 2 2 2
## $ primarymethod: Factor w/ 7 levels "\\","direct observation",...: 2 6 6 2 3 2 2 6 5
## $ log10.mass : num 1.68 2.18 2.15 2.11 1.62 ...
## $ trophic.guild: Factor w/ 2 levels "carnivore","herbivore": 2 2 2 2 2 2 2 2 2
## $ dimension : Factor w/ 2 levels "2D","3D": 2 2 2 2 2 2 2 2 2
## $ log10.hra : num 4.96 5.33 5.31 5.29 4.92 ...
## $ plo : num 3.89 4.37 4.36 4.34 3.81 ...
## $ phi : num 6.04 6.29 6.26 6.23 6.04 ...
## $ tlo : num 3.13 3.56 3.54 3.52 3.06 ...
## $ thi : num 6.8 7.1 7.08 7.05 6.78 ...
```

### #fixef

```
g0 <- ggplot(newdat, aes(x=log10.mass, y=log10.hra))
g0 + annotation_logticks(short = unit(2,"mm"), mid = unit(3,"mm"), long = unit(4,"mm")) + theme_bw()
+ theme(panel.border = element_blank(), panel.grid.major = element_blank(),
panel.grid.minor = element_blank(), axis.line = element_line(colour = "black")) + geom_ribbon(aes(ymin = plo, ymax = phi, linetype = NA), alpha=0.1) + geom_line(aes(ymin = plo, ymax = phi)) + ggtitle("CI based on fixed-effects uncertainty ONLY") + geom_point(aes(x=herb.birds.3D$log10.mass, y = herb.birds.3D$log10.hra))
```

## CI based on fixed-effects uncertainty ONLY



###Plot and 95% CIs for 2D Herbivorous Birds

```
herb.birds.2D.mod = lmer(log10.hra ~ log10.mass + (1|primarymethod), data=herb.birds.2D, REML = FALSE)
```

```
herb.birds.2D.p$log10.hra <- predict(herb.birds.2D.mod, newdata=herb.birds.2D.p, re.form = NA)
```

```
newdat <- herb.birds.2D.p
```

```
mm <- model.matrix(terms(herb.birds.2D.mod),newdat)
```

```
pvar1 <- diag(mm %*% tcrossprod(vcov(herb.birds.2D.mod),mm))
```

```
tvar1 <- pvar1 + VarCorr(herb.birds.2D.mod)$primarymethod[1] ## must be adapted for more complex models
```

```
ls
```

```
tvar1 <-
```

```
newdat <- data.frame(
```

```
  newdat
```

```
  , plo = newdat$log10.hra-2*sqrt(pvar1)
```

```
  , phi = newdat$log10.hra+2*sqrt(pvar1)
```

```
  , tlo = newdat$log10.hra-2*sqrt(tvar1)
```

```
  , thi = newdat$log10.hra+2*sqrt(tvar1)
```

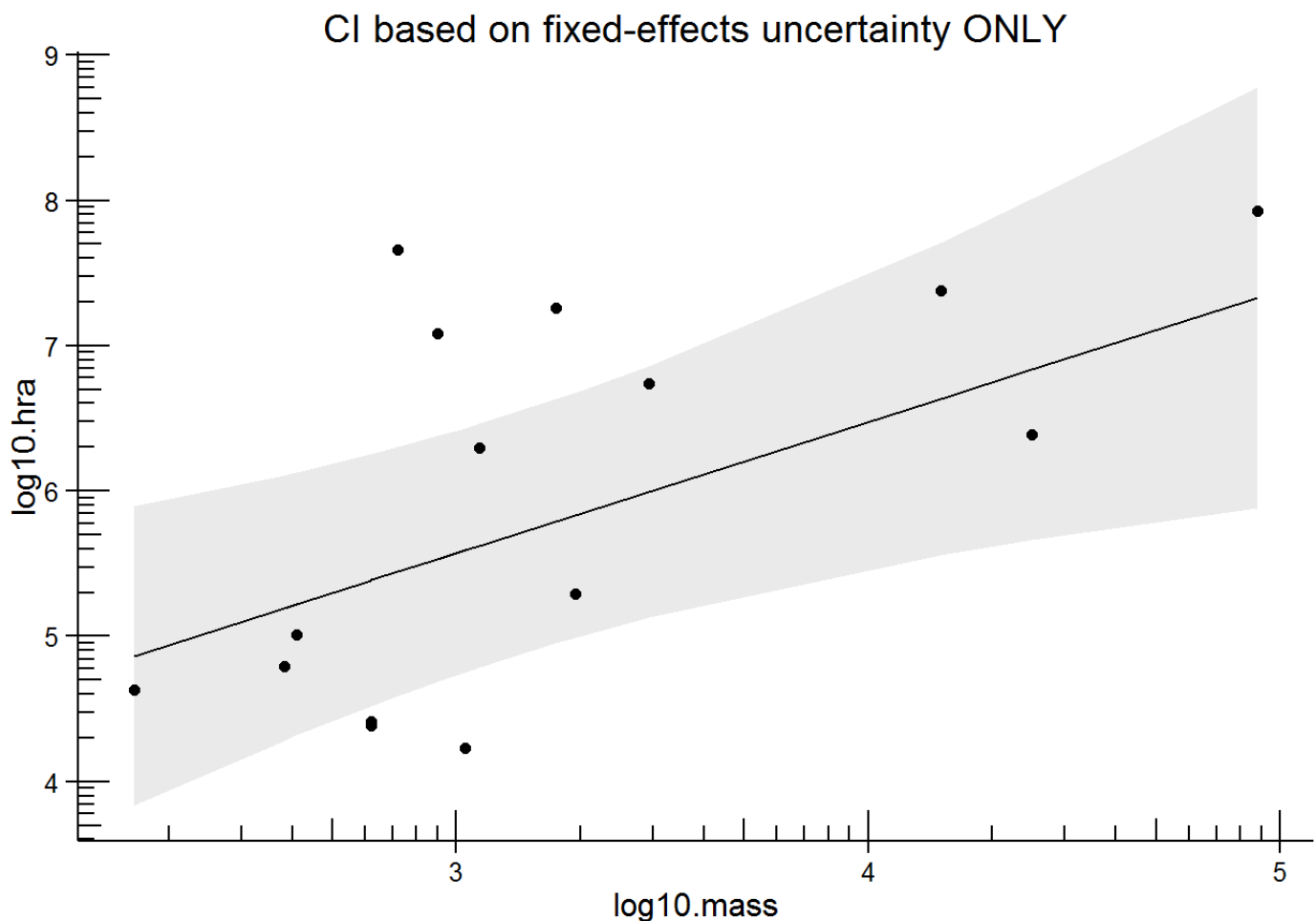
```
)
```

```
str(newdat)
```

```
## 'data.frame':   15 obs. of  11 variables:
## $ taxon      : Factor w/ 9 levels "birds","lake fishes",...: 1 1 1 1 1 1 1 1 1 ...
## $ class      : Factor w/ 4 levels "actinopterygii",...: 2 2 2 2 2 2 2 2 2 ...
## $ primarymethod: Factor w/ 7 levels "\\","direct observation",...: 5 6 5 2 2 6 6 6 5 ...
## $ log10.mass : num  2.86 2.61 3.24 3.02 2.79 ...
## $ trophic.guild: Factor w/ 2 levels "carnivore","herbivore": 2 2 2 2 2 2 2 2 2 ...
## $ dimension  : Factor w/ 2 levels "2D","3D": 1 1 1 1 1 1 1 1 1 ...
## $ log10.hra  : num  5.44 5.22 5.79 5.59 5.39 ...
## $ plo        : num  4.59 4.32 4.95 4.75 4.52 ...
## $ phi        : num  6.3 6.13 6.63 6.43 6.25 ...
## $ tlo        : num  3.96 3.71 4.32 4.12 3.9 ...
## $ thi        : num  6.93 6.73 7.26 7.06 6.87 ...
```

```
#fixef
```

```
g0 <- ggplot(newdat, aes(x=log10.mass, y=log10.hra))
g0 + annotation_logticks(short = unit(2,"mm"), mid = unit(3,"mm"), long = unit(4,"mm")) + theme_bw()
+ theme(panel.border = element_blank(), panel.grid.major = element_blank(),
panel.grid.minor = element_blank(), axis.line = element_line(colour = "black")) + geom_ribbon(aes(ymin = plo, ymax = phi, linetype = NA), alpha=0.1) + geom_line(aes(ymin = plo, ymax = phi)) + ggtitle("CI based on fixed-effects uncertainty ONLY") + geom_point(aes(x=herb.birds.2D$log10.mass, y = herb.birds.2D$log10.hra))
```



### ###Plot and 95% CIs for Carnivorous Marine Fish

```
carn.marfish.mod = lmer(log10.hra ~ log10.mass + (1|primarymethod), data=carn.marfish, REML = FALSE)
carn.marfish.p$log10.hra <- predict(carn.marfish.mod, newdata=carn.marfish.p, re.form = NA)
newdat <- carn.marfish.p

mm <- model.matrix(terms(carn.marfish.mod),newdat)
dim(mm)
```

```
## [1] 70  2
```

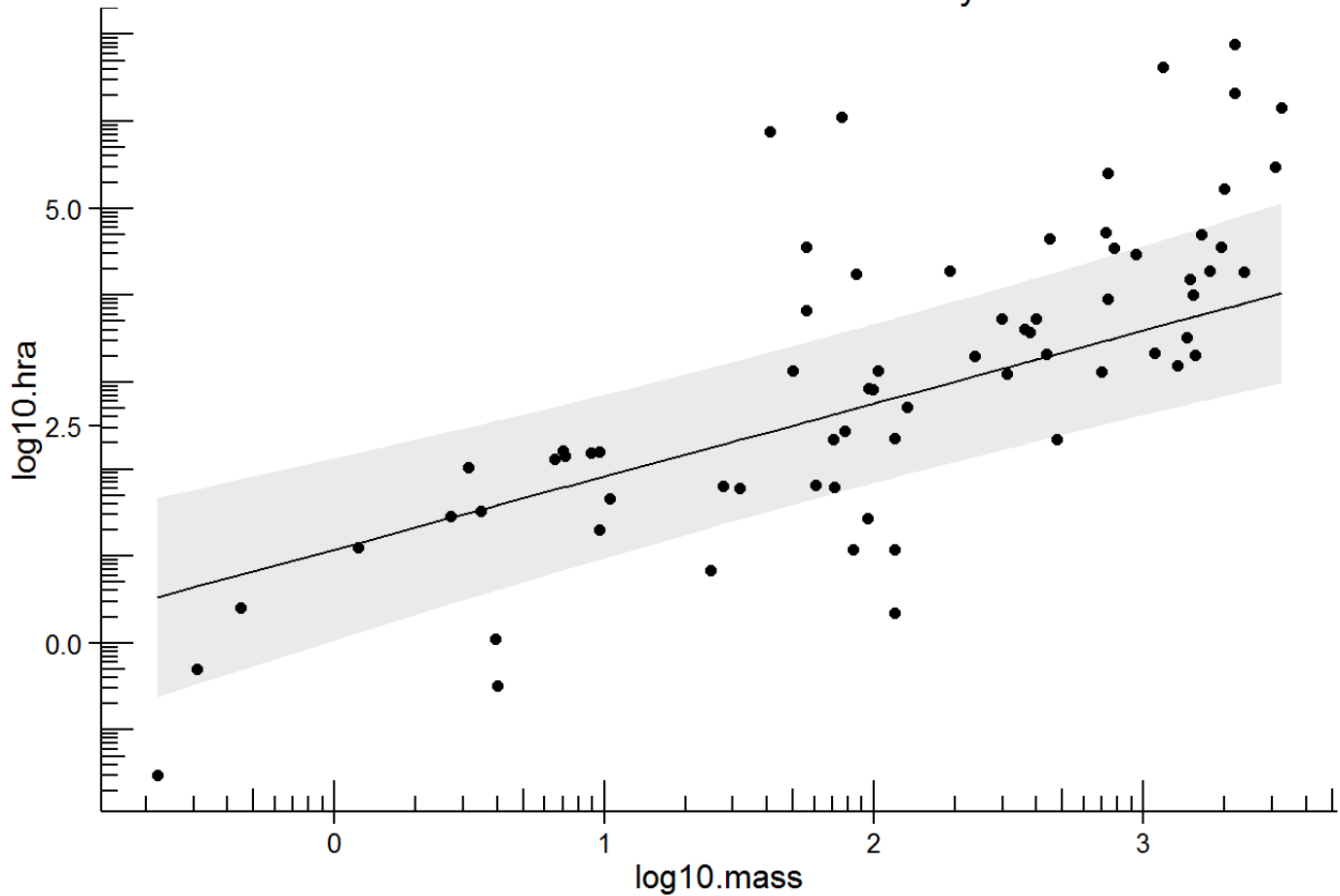
```
pvar1 <- diag(mm %*% tcrossprod(vcov(carn.marfish.mod),mm))
tvar1 <- pvar1 + VarCorr(carn.marfish.mod)$primarymethod[1] ## must be adapted for more complex models
tvar1 <-
  newdat <- data.frame(
    newdat
    , plo = newdat$log10.hra-2*sqrt(pvar1)
    , phi = newdat$log10.hra+2*sqrt(pvar1)
    , tlo = newdat$log10.hra-2*sqrt(tvar1)
    , thi = newdat$log10.hra+2*sqrt(tvar1)
  )
str(newdat)
```

```
## 'data.frame': 70 obs. of 11 variables:
## $ taxon : Factor w/ 9 levels "birds","lake fishes",...: 5 5 5 5 5 5 5 5 5 ...
## $ class : Factor w/ 4 levels "actinopterygii",...: 1 1 1 1 1 1 1 1 1 ...
## $ primarymethod: Factor w/ 7 levels "\\","direct observation",...: 5 5 5 2 2 2 2 2 5 2 ...
## $ log10.mass : num 2.87 2.65 2.86 1.44 1.5 ...
## $ trophic.guild: Factor w/ 2 levels "carnivore","herbivore": 1 1 1 1 1 1 1 1 1 ...
## $ dimension : Factor w/ 2 levels "2D","3D": 1 1 1 1 1 1 1 1 1 ...
## $ log10.hra : num 3.48 3.3 3.48 2.29 2.34 ...
## $ plo : num 2.52 2.36 2.52 1.37 1.42 ...
## $ phi : num 4.44 4.24 4.44 3.21 3.26 ...
## $ tlo : num 1.679 1.507 1.674 0.504 0.557 ...
## $ thi : num 5.29 5.1 5.28 4.07 4.12 ...
```

### #fixef

```
g0 <- ggplot(newdat, aes(x=log10.mass, y=log10.hra))
g0 + annotation_logticks(short = unit(2,"mm"), mid = unit(3,"mm"), long = unit(4,"mm")) + theme_bw()
+ theme(panel.border = element_blank(), panel.grid.major = element_blank(),
panel.grid.minor = element_blank(), axis.line = element_line(colour = "black")) + geom_ribbon(aes(ymin = plo, ymax = phi, linetype = NA), alpha=0.1) + geom_line(aes(ymin = plo, ymax = phi)) + ggtitle("CI based on fixed-effects uncertainty ONLY") + geom_point(aes(x=carn.marfish$log10.mass, y = carn.marfish$log10.hra))
```

### CI based on fixed-effects uncertainty ONLY



```
###Plot and 95% CIs for Herbivorous Marine Fish
```

```
herb.marfish.mod = lmer(log10.hra ~ log10.mass + (1|primarymethod), data=herb.marfish, REML = FALSE)
herb.marfish.p$log10.hra <- predict(herb.marfish.mod, newdata=herb.marfish.p, re.form = NA, type = "response")
newdat <- herb.marfish.p
```

```
mm <- model.matrix(terms(herb.marfish.mod),newdat)
dim(mm)
```

```
## [1] 20 2
```

```

pvar1 <- diag(mm %*% tcrossprod(vcov(herb.marfish.mod),mm))
tvar1 <- pvar1 + VarCorr(herb.marfish.mod)$primarymethod[1] ## must be adapted for more complex models
tvar1 <-
  newdat <- data.frame(
    newdat
    , plo = newdat$log10.hra-2*sqrt(pvar1)
    , phi = newdat$log10.hra+2*sqrt(pvar1)
    , tlo = newdat$log10.hra-2*sqrt(tvar1)
    , thi = newdat$log10.hra+2*sqrt(tvar1)
  )
str(newdat)

```

```

## 'data.frame':    20 obs. of  11 variables:
## $ taxon          : Factor w/ 9 levels "birds","lake fishes",...: 5 5 5 5 5 5 5 5 5 ...
## $ class          : Factor w/ 4 levels "actinopterygii",...: 1 1 1 1 1 1 1 1 1 ...
## $ primarymethod: Factor w/ 7 levels "\\","direct observation",...: 2 5 5 2 5 2 2 2 2 ...
## $ log10.mass     : num  2.038 2.888 2.181 0.792 3.036 ...
## $ trophic.guild: Factor w/ 2 levels "carnivore","herbivore": 2 2 2 2 2 2 2 2 2 ...
## $ dimension      : Factor w/ 2 levels "2D","3D": 1 1 1 1 1 1 1 1 1 ...
## $ log10.hra      : num  2.418 3.46 2.594 0.891 3.642 ...
## $ plo            : num  0.942 1.965 1.12 -0.674 2.137 ...
## $ phi            : num  3.89 4.95 4.07 2.46 5.15 ...
## $ tlo            : num  -0.1072 0.9236 0.0699 -1.6874 1.0996 ...
## $ thi            : num  4.94 6 5.12 3.47 6.18 ...

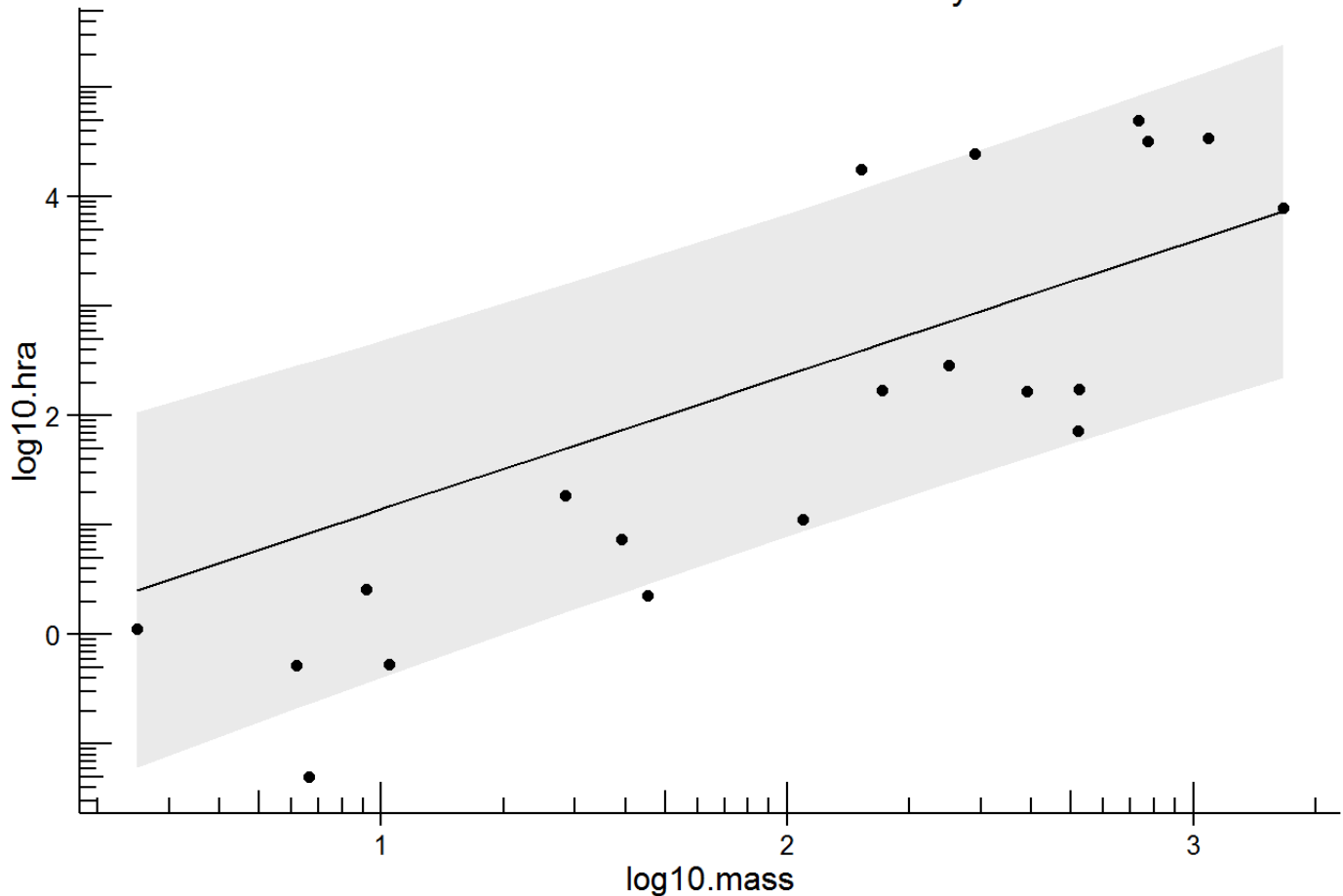
```

```

#fixef
g0 <- ggplot(newdat, aes(x=log10.mass, y=log10.hra))
g0 + annotation_logticks(short = unit(2,"mm"), mid = unit(3,"mm"), long = unit(4,"mm")) + theme_bw()
+ theme(panel.border = element_blank(), panel.grid.major = element_blank(),
panel.grid.minor = element_blank(), axis.line = element_line(colour = "black")) + geom_ribbon(aes(ymin
n = plo, ymax = phi, linetype = NA), alpha=0.1) + geom_line(aes(ymin = plo, ymax = phi)) + ggtitle("C
I based on fixed-effects uncertainty ONLY") + geom_point(aes(x=herb.marfish$log10.mass, y = herb.marf
ish$log10.hra))

```

## CI based on fixed-effects uncertainty ONLY

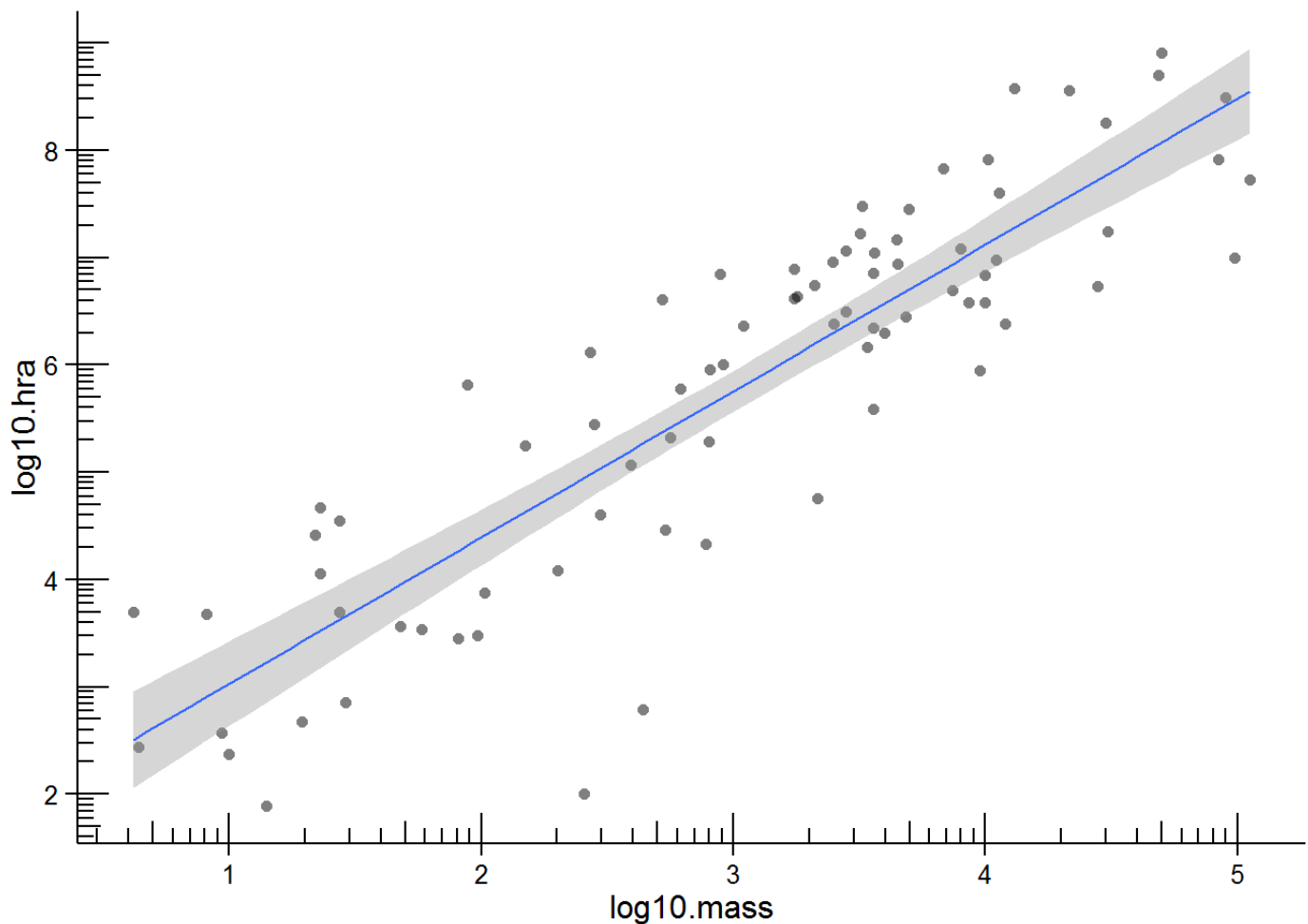


####For everything estimated with `lm` use `predict > se = TRUE` to obtain Figure 1 Subplots with 95% CI bands

*#Carn Mammals*

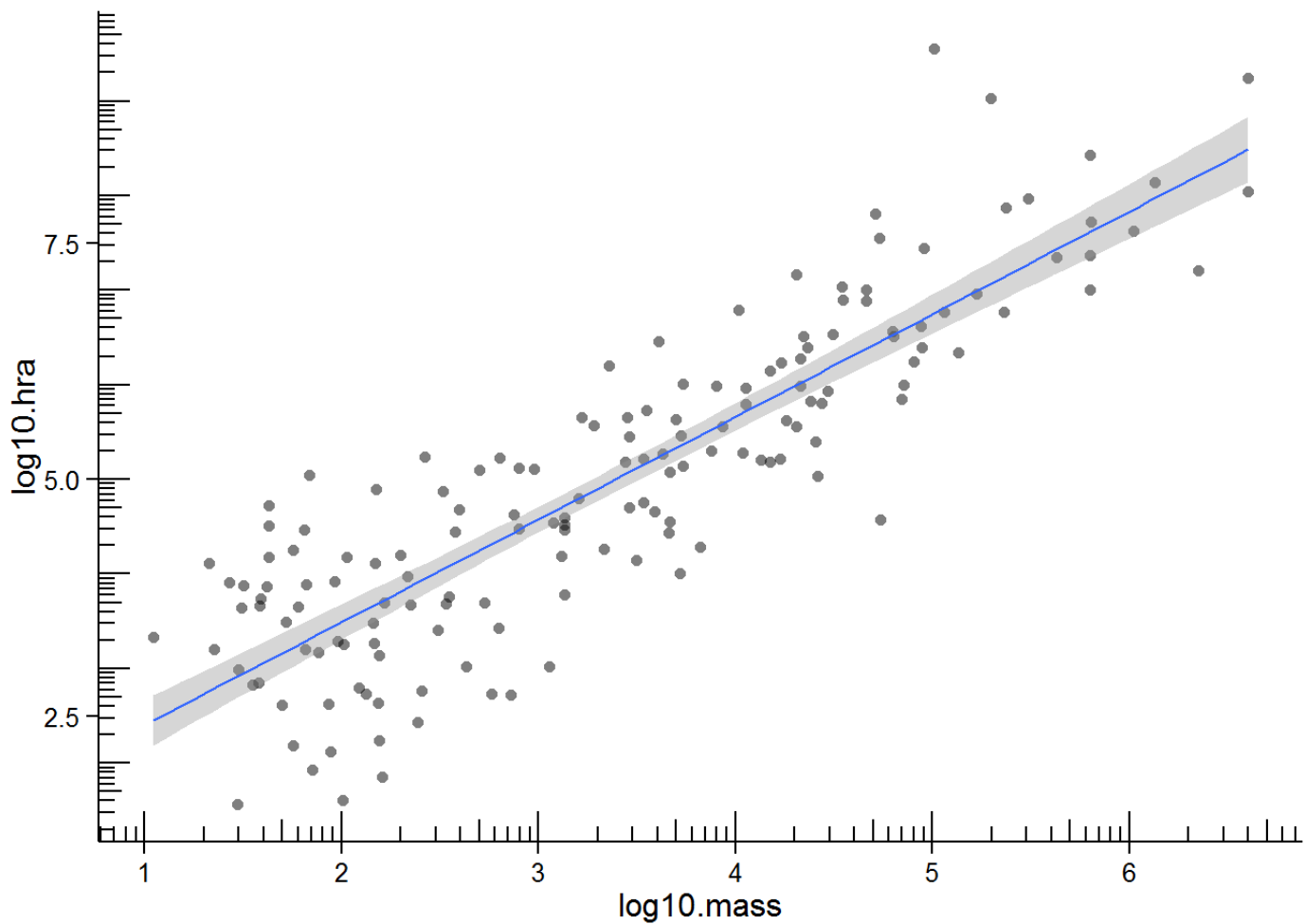
```
carn.mammals.mod = lm(log10.hra ~ log10.mass, data=carn.mammals)
pred1 <- predict(carn.mammals.mod, newdata = carn.mammals.p, se.fit = TRUE, type = "response")
g0 <- ggplot(carn.mammals, aes(x=log10.mass, y=log10.hra)) + geom_point(shape=16, alpha = 0.5) + scale_colour_hue(l=50) + # Use a slightly darker palette than normal
  geom_smooth(method=lm, # Add linear regression lines
             se=TRUE) # Decide if add shaded confidence region
g0 + annotation_logticks(short = unit(2,"mm"), mid = unit(3,"mm"), long = unit(4,"mm")) + theme_bw()
+ theme(panel.border = element_blank(), panel.grid.major = element_blank(),
panel.grid.minor = element_blank(), axis.line = element_line(colour = "black"))
```





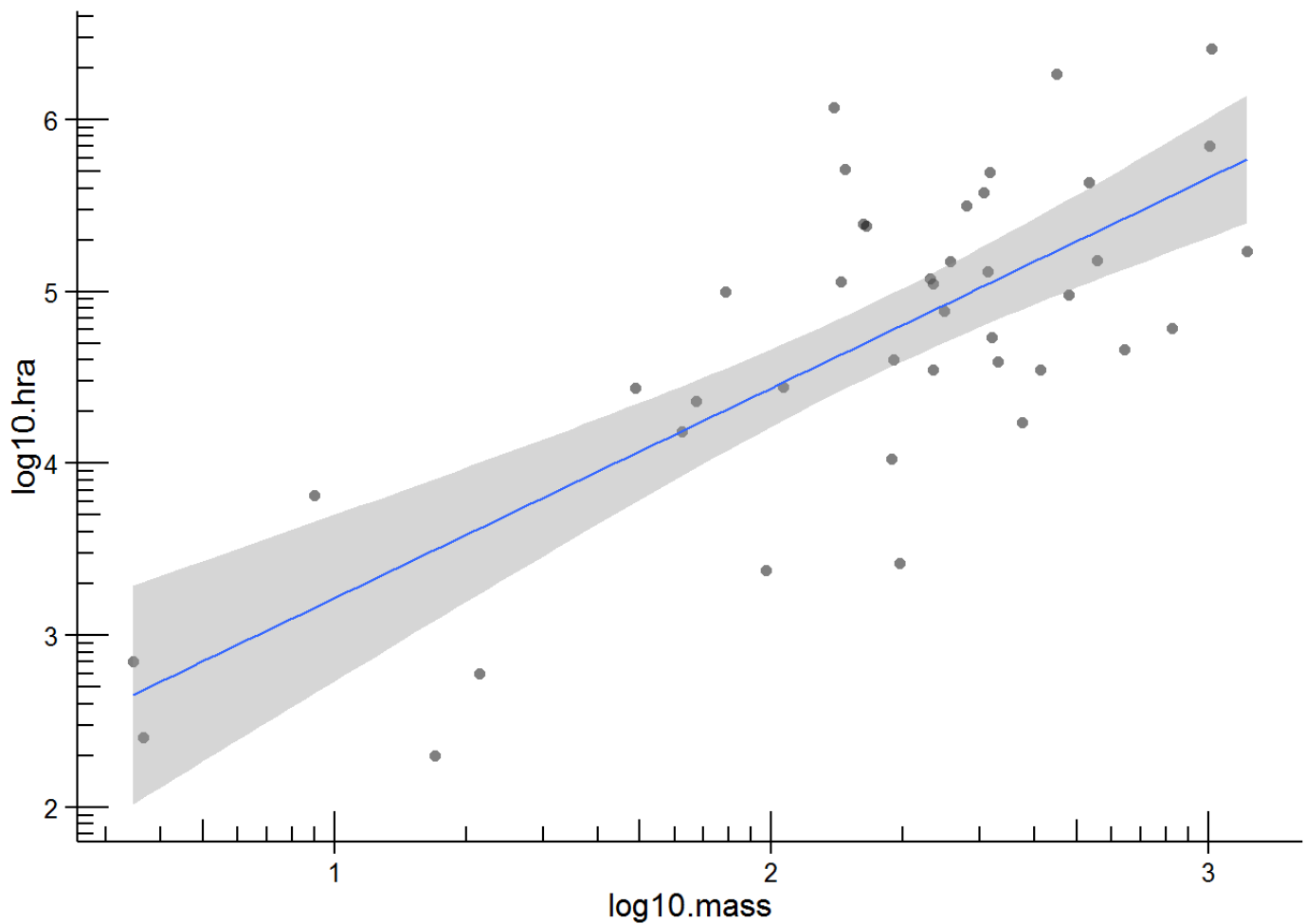
```
#Herb Mammals
```

```
herb.mammals.mod = lm(log10.hra ~ log10.mass, data=herb.mammals)
pred1 <- predict(herb.mammals.mod, newdata = herb.mammals.p, se.fit = TRUE, type = "response")
g0 <- ggplot(herb.mammals, aes(x=log10.mass, y=log10.hra)) + geom_point(shape=16, alpha = 0.5) + scale_colour_hue(l=50) + # Use a slightly darker palette than normal
  geom_smooth(method=lm, # Add linear regression lines
              se=TRUE) # Decide if add shaded confidence region
g0 + annotation_logticks(short = unit(2,"mm"), mid = unit(3,"mm"), long = unit(4,"mm")) + theme_bw()
+ theme(panel.border = element_blank(), panel.grid.major = element_blank(),
panel.grid.minor = element_blank(), axis.line = element_line(colour = "black"))
```



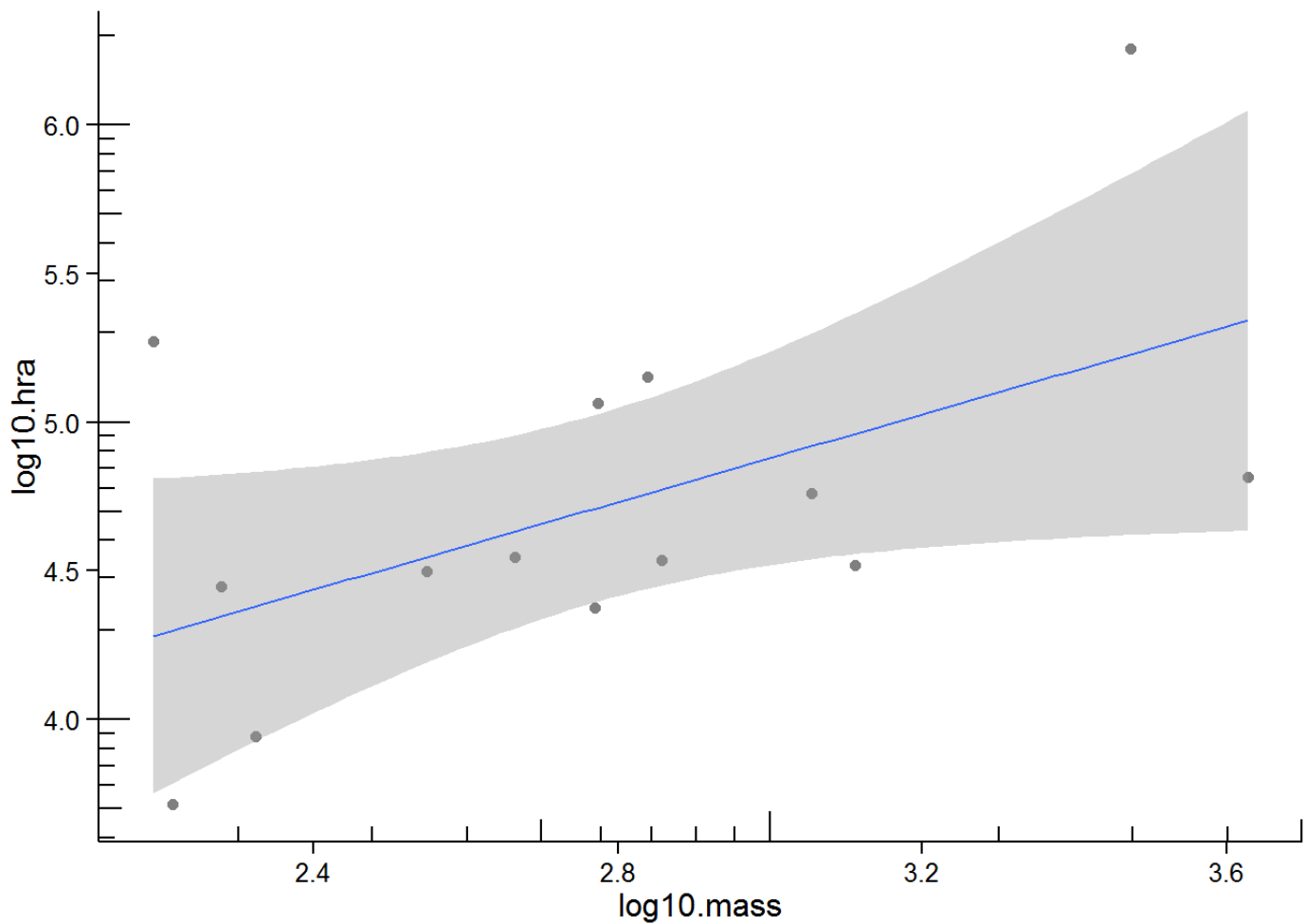
*#Carn Snakes*

```
carn.snakes.mod = lm(log10.hra ~ log10.mass, data=carn.snakes)
pred1 <- predict(carn.snakes.mod, newdata = carn.snakes.p, se.fit = TRUE, type = "response")
g0 <- ggplot(carn.snakes, aes(x=log10.mass, y=log10.hra)) + geom_point(shape=16, alpha = 0.5) + scale_colour_hue(l=50) + # Use a slightly darker palette than normal
  geom_smooth(method=lm, # Add linear regression lines
              se=TRUE) # Decide if add shaded confidence region
g0 + annotation_logticks(short = unit(2,"mm"), mid = unit(3,"mm"), long = unit(4,"mm")) + theme_bw()
+ theme(panel.border = element_blank(), panel.grid.major = element_blank(),
panel.grid.minor = element_blank(), axis.line = element_line(colour = "black"))
```



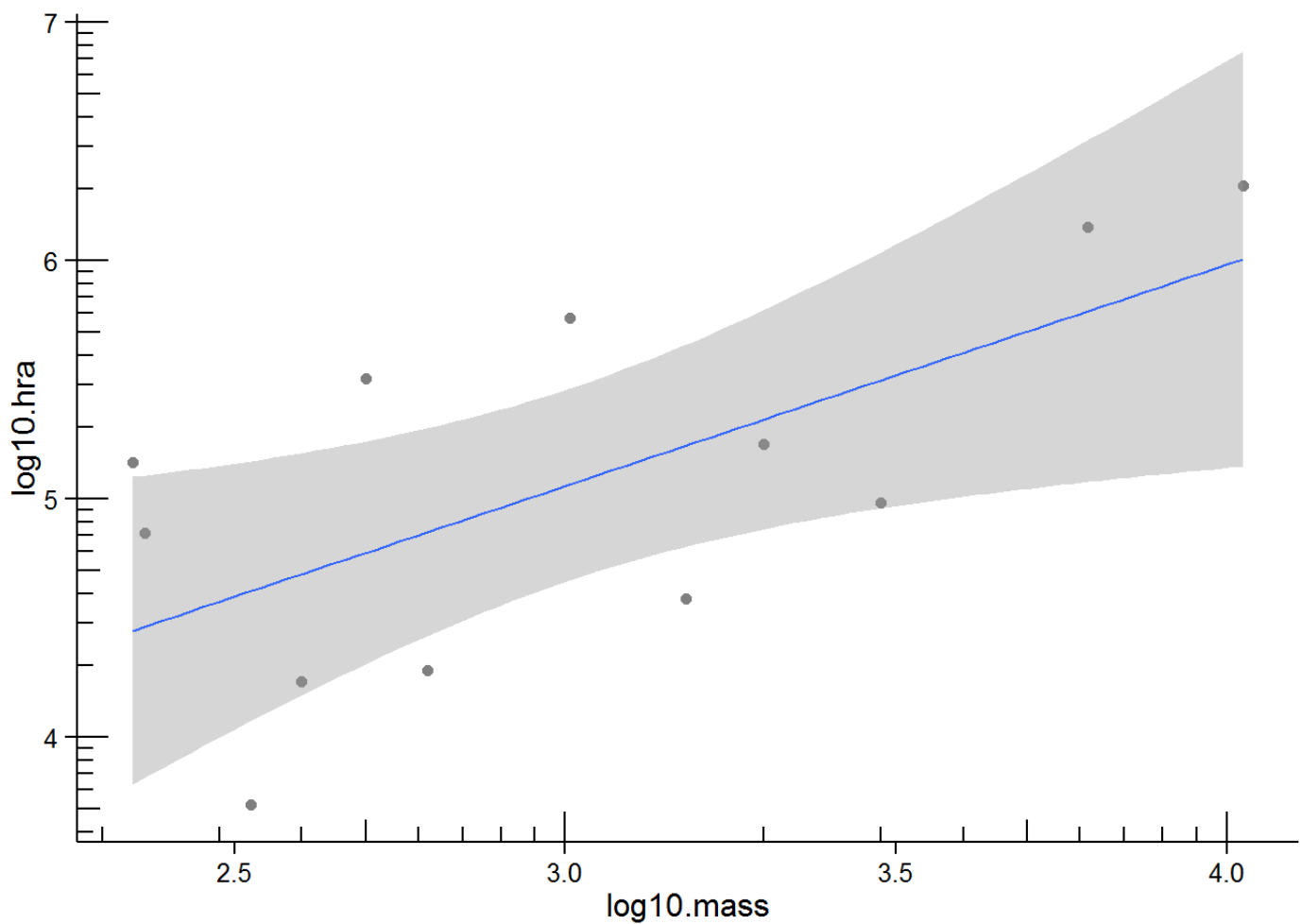
*#Carn Turtles*

```
carn.turtles.mod = lm(log10.hra ~ log10.mass, data=carn.turtles)
pred1 <- predict(carn.turtles.mod, newdata = carn.turtles.p, se.fit = TRUE, type = "response")
g0 <- ggplot(carn.turtles, aes(x=log10.mass, y=log10.hra)) + geom_point(shape=16, alpha = 0.5) + scale_colour_hue(l=50) + # Use a slightly darker palette than normal
  geom_smooth(method=lm, # Add linear regression lines
              se=TRUE) # Decide if add shaded confidence region
g0 + annotation_logticks(short = unit(2,"mm"), mid = unit(3,"mm"), long = unit(4,"mm")) + theme_bw()
+ theme(panel.border = element_blank(), panel.grid.major = element_blank(),
panel.grid.minor = element_blank(), axis.line = element_line(colour = "black"))
```



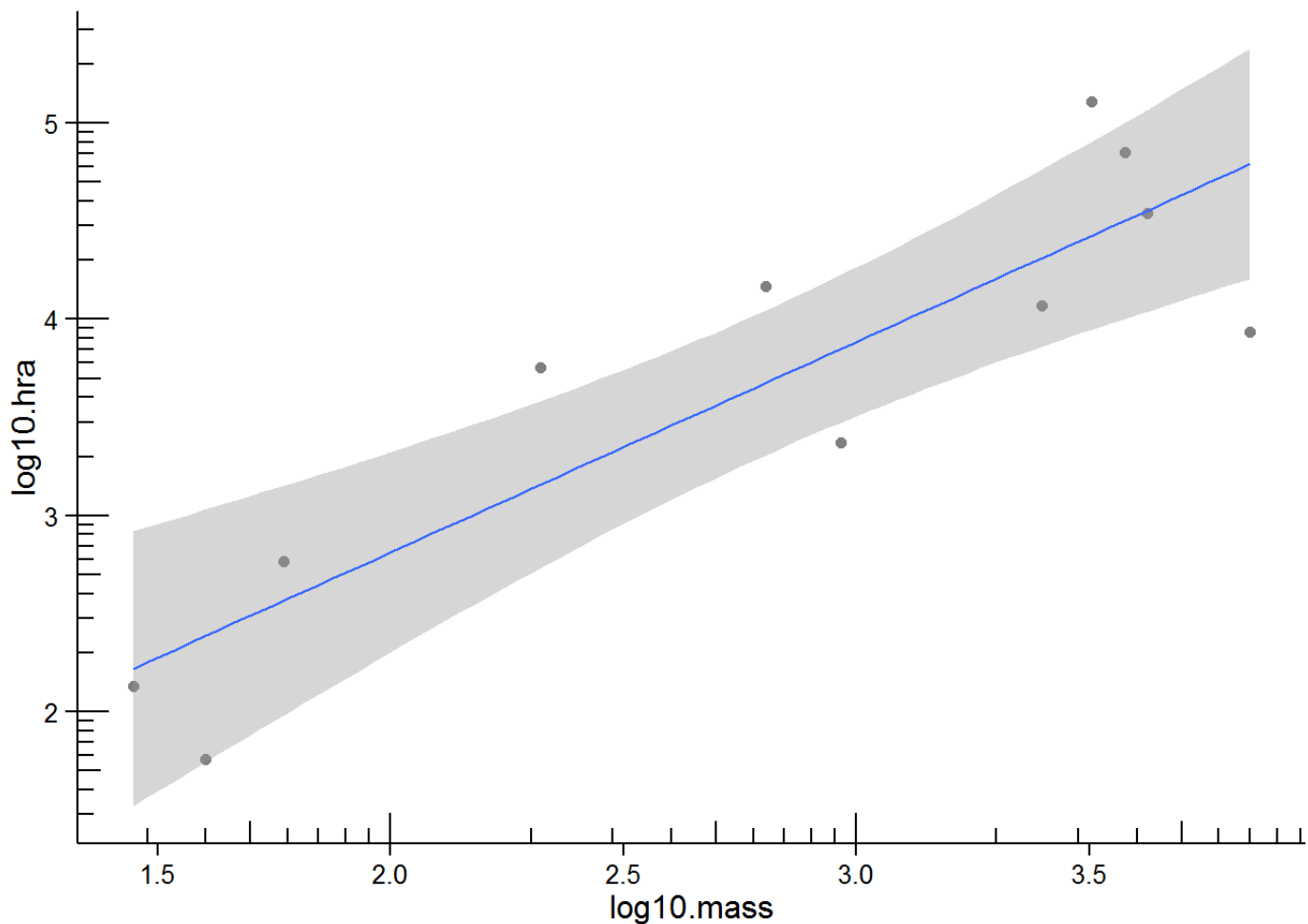
*#Herb Turtles*

```
herb.turtles.mod = lm(log10.hra ~ log10.mass, data=herb.turtles)
pred1 <- predict(herb.turtles.mod, newdata = herb.turtles.p, se.fit = TRUE, type = "response")
g0 <- ggplot(herb.turtles, aes(x=log10.mass, y=log10.hra)) + geom_point(shape=16, alpha = 0.5) + scale_colour_hue(l=50) + # Use a slightly darker palette than normal
  geom_smooth(method=lm, # Add linear regression lines
              se=TRUE) # Decide if add shaded confidence region
g0 + annotation_logticks(short = unit(2,"mm"), mid = unit(3,"mm"), long = unit(4,"mm")) + theme_bw()
+ theme(panel.border = element_blank(), panel.grid.major = element_blank(),
panel.grid.minor = element_blank(), axis.line = element_line(colour = "black"))
```

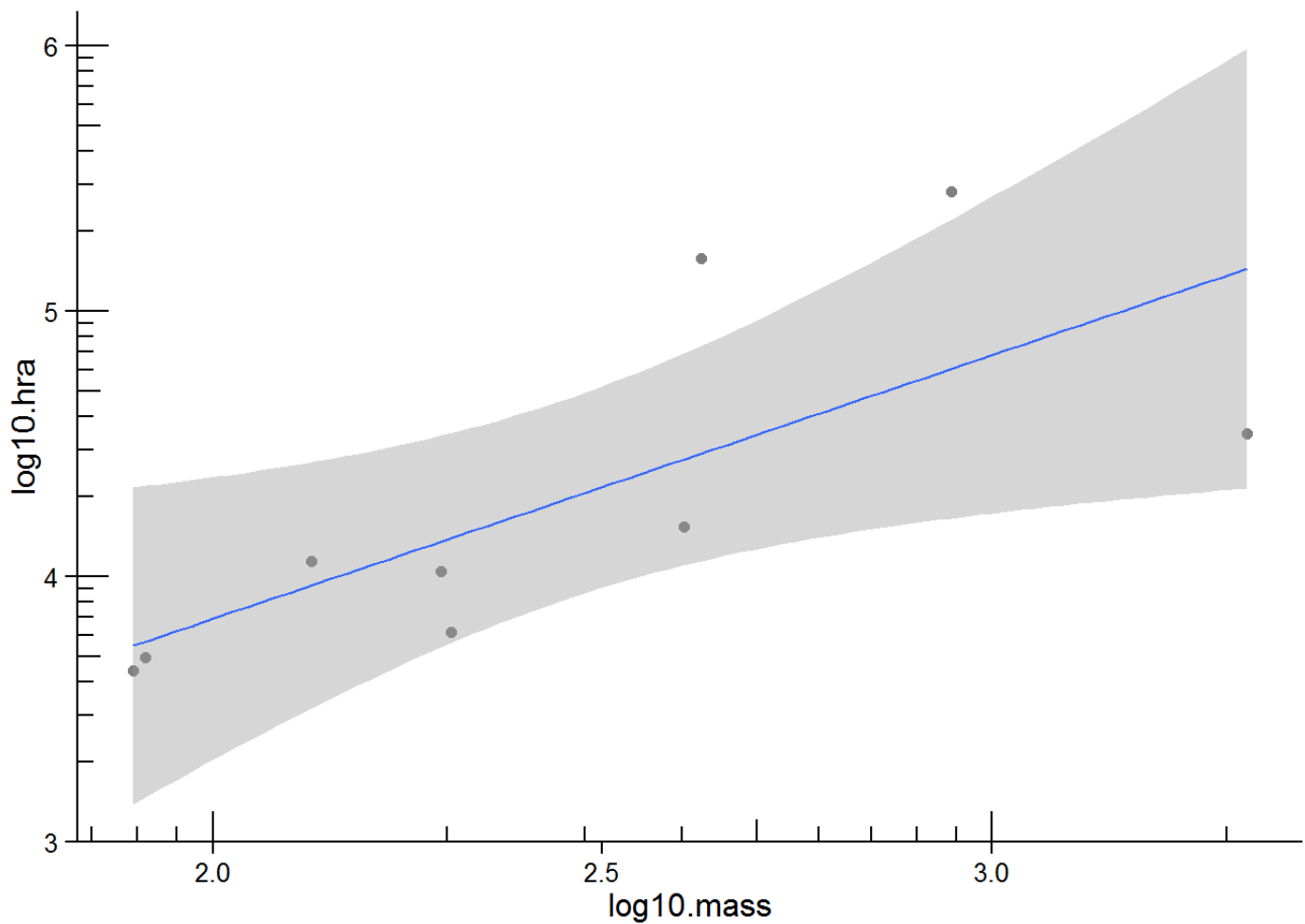


*#Herb Lizards*

```
herb.lizards.mod = lm(log10.hra ~ log10.mass, data=herb.lizards)
pred1 <- predict(herb.lizards.mod, newdata = herb.lizards.p, se.fit = TRUE, type = "response")
g0 <- ggplot(herb.lizards, aes(x=log10.mass, y=log10.hra)) + geom_point(shape=16, alpha = 0.5) + scale_colour_hue(l=50) + # Use a slightly darker palette than normal
  geom_smooth(method=lm, # Add linear regression lines
              se=TRUE) # Decide if add shaded confidence region
g0 + annotation_logticks(short = unit(2,"mm"), mid = unit(3,"mm"), long = unit(4,"mm")) + theme_bw()
+ theme(panel.border = element_blank(), panel.grid.major = element_blank(),
panel.grid.minor = element_blank(), axis.line = element_line(colour = "black"))
```

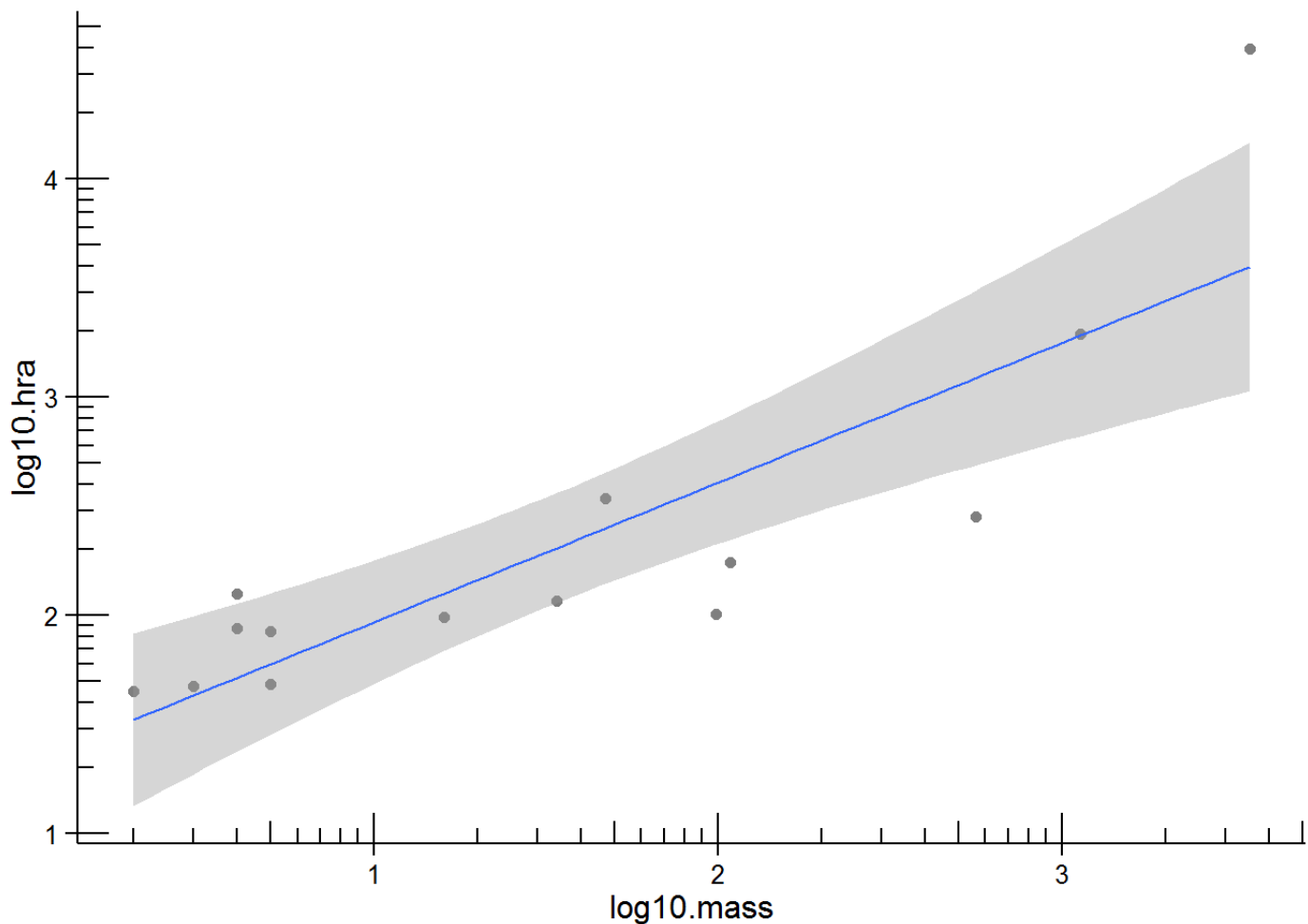


```
#Carn Lakefish
carn.lakefish.mod = lm(log10.hra ~ log10.mass, data=carn.lakefish)
pred1 <- predict(carn.lakefish.mod, newdata = carn.lakefish.p, se.fit = TRUE, type = "response")
g0 <- ggplot(carn.lakefish, aes(x=log10.mass, y=log10.hra)) + geom_point(shape=16, alpha = 0.5) + scale_colour_hue(l=50) + # Use a slightly darker palette than normal
  geom_smooth(method=lm, # Add linear regression lines
              se=TRUE) # Decide if add shaded confidence region
g0 + annotation_logticks(short = unit(2,"mm"), mid = unit(3,"mm"), long = unit(4,"mm")) + theme_bw()
+ theme(panel.border = element_blank(), panel.grid.major = element_blank(),
panel.grid.minor = element_blank(), axis.line = element_line(colour = "black"))
```



*#Carn River Fish*

```
carn.rivfish.mod = lm(log10.hra ~ log10.mass, data=carn.rivfish)
pred1 <- predict(carn.rivfish.mod, newdata = carn.rivfish.p, se.fit = TRUE, type = "response")
g0 <- ggplot(carn.rivfish, aes(x=log10.mass, y=log10.hra)) + geom_point(shape=16, alpha = 0.5) + scale_colour_hue(l=50) + # Use a slightly darker palette than normal
  geom_smooth(method=lm, # Add linear regression lines
              se=TRUE) # Decide if add shaded confidence region
g0 + annotation_logticks(short = unit(2,"mm"), mid = unit(3,"mm"), long = unit(4,"mm")) + theme_bw()
+ theme(panel.border = element_blank(), panel.grid.major = element_blank(),
panel.grid.minor = element_blank(), axis.line = element_line(colour = "black"))
```



Estimate parameters for global home range allometries including data from all taxa as reported in Table 2, accounting for systematic variation in Tracking Method and Phylogenetic class as random effects. We use `REML = FALSE` to allow comparisons of non-nested models via AICc and calculate the  $R^2_m$  and  $R^2_c$  values for mixed-effects models as per Nakagawa & Schielzeth 2012 using the `r.squaredGLMM` function in version 1.10.0 of the `MuMIn` package. We add a -1 to the model syntax for models with multi-level factors to force R to report the absolute parameter estimates for each factor as in Schielzeth 2010. For this approach to work in models with interaction terms (e.g. as for thermoregulation, dimension), we also omit mass as a stand-alone variable and include it only in interactions. Importantly, this change in syntax does NOT change the model results, only how the results are reported. The output of this section is the basis for Table 1.

```
#Baseline model where HRA is predicted by mass alone, used as the baseline AICc from which to calculate delta AICc values.
alltaxa.mass = lmer(log10.hra ~ log10.mass + (1|class) + (1|primarymethod), data=data, REML = FALSE)
summary(alltaxa.mass)
```



```
## Linear mixed model fit by maximum likelihood t-tests use Satterthwaite
## approximations to degrees of freedom [merModLmerTest]
## Formula: log10.hra ~ log10.mass + (1 | class) + (1 | primarymethod)
## Data: data
##
##      AIC      BIC   logLik deviance df.resid
## 1568.7   1590.4   -779.4   1558.7     563
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.54672 -0.67175  0.00355  0.66759  3.06284
##
## Random effects:
## Groups          Name          Variance Std.Dev.
## primarymethod (Intercept) 0.3029   0.5503
## class          (Intercept) 0.9209   0.9596
## Residual                0.8631   0.9290
## Number of obs: 568, groups: primarymethod, 7; class, 4
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)  1.87054    0.54804   6.10000   3.413   0.0138 *
## log10.mass   1.04847    0.03871 566.00000  27.083   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## log10.mass -0.154
```

```
AICc(alltaxa.mass)
```

```
## [1] 1568.815
```

```
r.squaredGLMM(alltaxa.mass)
```

```
##      R2m      R2c
## 0.4384276 0.7677465
```

```
#Model incorporating mass and an intercept effect of realm
alltaxa.realm = lmer(log10.hra ~ -1 + log10.mass + realm + (1|class) + (1|primarymethod), data=data,
REML = FALSE)
summary(alltaxa.realm)
```

```
## Linear mixed model fit by maximum likelihood t-tests use Satterthwaite
## approximations to degrees of freedom [merModLmerTest]
## Formula:
## log10.hra ~ -1 + log10.mass + realm + (1 | class) + (1 | primarymethod)
## Data: data
##
##      AIC      BIC   logLik deviance df.resid
## 1569.0   1595.1   -778.5   1557.0     562
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.55049 -0.66643  0.00623  0.66420  3.07322
##
## Random effects:
## Groups          Name          Variance Std.Dev.
## primarymethod (Intercept) 0.2928   0.5411
## class          (Intercept) 0.6000   0.7746
## Residual                        0.8631   0.9291
## Number of obs: 568, groups: primarymethod, 7; class, 4
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## log10.mass         1.0471     0.0387 566.5000  27.056 < 2e-16 ***
## realmaquatic        0.8963     0.8210   4.7000   1.092  0.32774
## realmterrestrial    2.1976     0.5203   6.3000   4.223  0.00492 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##           lg10.m rlmqtc
## realmaquatc -0.083
## relmtrrstrl -0.172  0.149
```

```
AICc(alltaxa.realm)
```

```
## [1] 1569.194
```

```
r.squaredGLMM(alltaxa.realm)
```

```
##      R2m      R2c
## 0.5580898 0.7827708
```

```
#Model incorporating mass and an intercept effect of thermoregulation
```

```
alltaxa.therm = lmer(log10.hra ~ -1 + log10.mass + thermoregulation + (1|class) + (1|primarymethod),  
data=data, REML = FALSE)  
summary(alltaxa.therm)
```

```
## Linear mixed model fit by maximum likelihood t-tests use Satterthwaite  
## approximations to degrees of freedom [merModLmerTest]  
## Formula: log10.hra ~ -1 + log10.mass + thermoregulation + (1 | class) +  
## (1 | primarymethod)  
## Data: data  
##  
##      AIC      BIC    logLik deviance df.resid  
## 1568.7 1594.8 -778.4 1556.7 562  
##  
## Scaled residuals:  
##      Min      1Q   Median      3Q      Max  
## -2.55339 -0.66215  0.00555  0.66604  3.05965  
##  
## Random effects:  
## Groups      Name      Variance Std.Dev.  
## primarymethod (Intercept) 0.2938  0.542  
## class        (Intercept) 0.5520  0.743  
## Residual                0.8631  0.929  
## Number of obs: 568, groups: primarymethod, 7; class, 4  
##  
## Fixed effects:  
##  
##              Estimate Std. Error      df t value Pr(>|t|)  
## log10.mass          1.04599    0.03871 566.00000 27.018 < 2e-16  
## thermoregulationectotherm 1.26632    0.58903  5.60000  2.150  0.07806  
## thermoregulationendotherm 2.48644    0.59560  5.90000  4.175  0.00612  
##  
## log10.mass          ***  
## thermoregulationectotherm .  
## thermoregulationendotherm **  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Correlation of Fixed Effects:  
##          lg10.m thrmrgltnct  
## thrmrgltnct -0.119  
## thrmrgltnnd -0.166  0.177
```

```
AICc(alltaxa.therm)
```

```
## [1] 1568.877
```

```
r.squaredGLMM(alltaxa.therm)
```

```
##           R2m           R2c  
## 0.5716630 0.7836588
```

```
#Model incorporating mass and both an intercept and slope effect of thermoregulation  
alltaxa.therm.int = lmer(log10.hra ~ -1 + log10.mass:thermoregulation + thermoregulation + (1|class)  
+ (1|primarymethod), data=data, REML = FALSE)  
summary(alltaxa.therm.int)
```

```

## Linear mixed model fit by maximum likelihood t-tests use Satterthwaite
## approximations to degrees of freedom [merModLmerTest]
## Formula:
## log10.hra ~ -1 + log10.mass:thermoregulation + thermoregulation +
## (1 | class) + (1 | primarymethod)
## Data: data
##
##      AIC      BIC   logLik deviance df.resid
##  1567.3   1597.7   -776.7   1553.3     561
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.61942 -0.65800  0.01214  0.65744  2.94742
##
## Random effects:
## Groups           Name             Variance Std.Dev.
## primarymethod (Intercept) 0.3197     0.5654
## class           (Intercept) 0.5817     0.7627
## Residual                        0.8570     0.9258
## Number of obs: 568, groups: primarymethod, 7; class, 4
##
## Fixed effects:
##
##              Estimate Std. Error      df
## thermoregulationectotherm      1.55961    0.62458    6.40000
## thermoregulationendotherm      2.39233    0.61387    6.00000
## log10.mass:thermoregulationectotherm  0.90071    0.08714  550.60000
## log10.mass:thermoregulationendotherm  1.07646    0.04195  563.20000
##
##              t value Pr(>|t|)
## thermoregulationectotherm      2.497  0.04418 *
## thermoregulationendotherm      3.897  0.00809 **
## log10.mass:thermoregulationectotherm  10.336 < 2e-16 ***
## log10.mass:thermoregulationendotherm  25.660 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##
##              thrmrgltnc thrmrgltnn lg10.mss:thrmrgltnc
## thrmrgltnc      0.152
## lg10.mss:thrmrgltnc -0.271      0.007
## lg10.mss:thrmrgltnn -0.005     -0.181      0.056

```

```
AICc(alltaxa.therm.int)
```

```
## [1] 1567.507
```

```
r.squaredGLMM(alltaxa.therm.int)
```

```
##          R2m          R2c
## 0.5656046 0.7882847
```

```
#Model incorporating mass and an intercept effect of dimension
```

```
alltaxa.dim = lmer(log10.hra ~ -1 + log10.mass + dimension + (1|class) + (1|primarymethod), data=dat  
a, REML = FALSE)  
summary(alltaxa.dim)
```

```
## Linear mixed model fit by maximum likelihood t-tests use Satterthwaite  
## approximations to degrees of freedom [merModLmerTest]  
## Formula: log10.hra ~ -1 + log10.mass + dimension + (1 | class) + (1 |  
## primarymethod)  
## Data: data  
##  
##      AIC      BIC    logLik deviance df.resid  
## 1530.9   1556.9   -759.4   1518.9     562  
##  
## Scaled residuals:  
##      Min      1Q  Median      3Q      Max  
## -2.6045 -0.6667 -0.0425  0.6562  3.1842  
##  
## Random effects:  
## Groups          Name          Variance Std.Dev.  
## primarymethod (Intercept) 0.3374   0.5809  
## class          (Intercept) 0.4666   0.6831  
## Residual                0.8067   0.8982  
## Number of obs: 568, groups: primarymethod, 7; class, 4  
##  
## Fixed effects:  
##              Estimate Std. Error      df t value Pr(>|t|)  
## log10.mass    1.0721    0.0376 566.3000  28.510 < 2e-16 ***  
## dimension2D   1.5903    0.4400  7.9000   3.615 0.007054 **  
## dimension3D   2.7336    0.4569  9.0000   5.983 0.000204 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Correlation of Fixed Effects:  
##              lg10.m dmns2D  
## dimension2D -0.193  
## dimension3D -0.148  0.924
```

```
AICc(alltaxa.dim)
```

```
## [1] 1531.021
```

```
r.squaredGLMM(alltaxa.dim)
```

```
##          R2m          R2c  
## 0.4840338 0.7415926
```

```
#Model incorporating mass and both an intercept and slope effect of dimension  
alltaxa.dim.int = lmer(log10.hra ~ -1 + log10.mass:dimension + dimension + (1|class) + (1|primarymeth  
od), data=data, REML = FALSE)  
summary(alltaxa.dim.int)
```

```
## Linear mixed model fit by maximum likelihood t-tests use Satterthwaite
## approximations to degrees of freedom [merModLmerTest]
## Formula:
## log10.hra ~ -1 + log10.mass:dimension + dimension + (1 | class) +
## (1 | primarymethod)
## Data: data
##
##      AIC      BIC   logLik deviance df.resid
##  1524.4   1554.8   -755.2   1510.4     561
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.6596 -0.6618 -0.0352  0.6346  3.2134
##
## Random effects:
## Groups          Name          Variance Std.Dev.
## primarymethod (Intercept) 0.3117   0.5583
## class          (Intercept) 0.5144   0.7172
## Residual                0.7946   0.8914
## Number of obs: 568, groups: primarymethod, 7; class, 4
##
## Fixed effects:
##
##              Estimate Std. Error      df t value Pr(>|t|)
## dimension2D          1.69361    0.44960    7.50000   3.767  0.00612 **
## dimension3D          2.14885    0.50474   11.80000   4.257  0.00116 **
## log10.mass:dimension2D  1.03366    0.03956  566.80000  26.126 < 2e-16 ***
## log10.mass:dimension3D  1.36878    0.10807  562.70000  12.666 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              dmns2D dmns3D l10.:2
## dimension3D  0.819
## lg10.mss:2D -0.204  0.004
## lg10.mss:3D  0.011 -0.413  0.014
```

```
AICc(alltaxa.dim.int)
```

```
## [1] 1524.61
```

```
r.squaredGLMM(alltaxa.dim.int)
```

```
##      R2m      R2c
## 0.4820572 0.7460576
```



```
#Model incorporating mass and an intercept effect of locomotion (i.e. walking, flying, etc.)
alltaxa.loc = lmer(log10.hra ~ -1 + log10.mass + locomotion + (1|class) + (1|primarymethod), data=dat
a, REML = FALSE)
summary(alltaxa.loc)
```

```
## Linear mixed model fit by maximum likelihood t-tests use Satterthwaite
## approximations to degrees of freedom [merModLmerTest]
## Formula: log10.hra ~ -1 + log10.mass + locomotion + (1 | class) + (1 |
## primarymethod)
## Data: data
##
##      AIC      BIC   logLik deviance df.resid
##  1511.1   1545.8   -747.5   1495.1     560
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.62677 -0.65369 -0.05421  0.64296  3.10914
##
## Random effects:
## Groups          Name          Variance Std.Dev.
## primarymethod (Intercept) 0.3635   0.6029
## class          (Intercept) 0.2251   0.4745
## Residual                0.7762   0.8810
## Number of obs: 568, groups: primarymethod, 7; class, 4
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## log10.mass      1.09766    0.03734 564.30000   29.397 < 2e-16 ***
## locomotioncrawling 2.31048    0.42755 11.20000    5.404 0.00020 ***
## locomotionflying  3.21433    0.42621 10.80000    7.542 1.3e-05 ***
## locomotionswimming 0.70775    0.55655  5.20000    1.272 0.25761
## locomotionwalking 1.61159    0.40189  9.00000    4.010 0.00307 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##           lg10.m lcmtnc lcmtnf lcmtns
## lcmtncrwlng -0.162
## lcmtnflyng -0.162  0.766
## lcmtnswmmng -0.122  0.312  0.302
## lcmtnwlkng -0.241  0.884  0.869  0.342
```

```
AICc(alltaxa.loc)
```

```
## [1] 1511.345
```

```
r.squaredGLMM(alltaxa.loc)
```

```
##          R2m          R2c
## 0.6025784 0.7739790
```

```
#Model incorporating mass and an intercept effect of trophic guild (i.e. carnivore, herbivore)
alltaxa.tg = lmer(log10.hra ~ -1 + log10.mass + trophic.guild + (1|class) + (1|primarymethod), data=d
ata, REML = FALSE)
summary(alltaxa.tg)
```

```
## Linear mixed model fit by maximum likelihood t-tests use Satterthwaite
## approximations to degrees of freedom [merModLmerTest]
## Formula: log10.hra ~ -1 + log10.mass + trophic.guild + (1 | class) + (1 |
## primarymethod)
## Data: data
##
##      AIC      BIC   logLik deviance df.resid
## 1438.4   1464.4   -713.2   1426.4     562
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.5799 -0.6645 -0.0323  0.7003  3.3575
##
## Random effects:
## Groups          Name          Variance Std.Dev.
## primarymethod (Intercept) 0.2248   0.4742
## class          (Intercept) 0.8061   0.8978
## Residual                0.6836   0.8268
## Number of obs: 568, groups: primarymethod, 7; class, 4
##
## Fixed effects:
##
##              Estimate Std. Error      df t value Pr(>|t|)
## log10.mass         1.13395    0.03515 565.60000  32.260  <2e-16 ***
## trophic.guildcarnivore 1.98722    0.50449  5.90000   3.939   0.0079 **
## trophic.guildherbivore 0.98590    0.50953  6.10000   1.935   0.1001
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          lg10.m trphc.gldc
## trphc.gldcr -0.142
## trphc.gldhr -0.173  0.987
```

```
AICc(alltaxa.tg)
```

```
## [1] 1438.53
```

```
r.squaredGLMM(alltaxa.tg)
```

```
##           R2m           R2c  
## 0.4917809 0.7973732
```

```
#Model incorporating mass and both an intercept and slope effect of trophic guild
```

```
alltaxa.tg.int = lmer(log10.hra ~ -1 + log10.mass:trophic.guild + trophic.guild + (1|class) + (1|primarymethod), data=data, REML = FALSE)  
summary(alltaxa.tg.int)
```

```

## Linear mixed model fit by maximum likelihood t-tests use Satterthwaite
## approximations to degrees of freedom [merModLmerTest]
## Formula: log10.hra ~ -1 + log10.mass:trophic.guild + trophic.guild + (1 |
## class) + (1 | primarymethod)
## Data: data
##
##      AIC      BIC   logLik deviance df.resid
##  1434.7   1465.1   -710.4   1420.7     561
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.5894 -0.6841 -0.0125  0.7239  3.4788
##
## Random effects:
## Groups          Name          Variance Std.Dev.
## primarymethod (Intercept) 0.2115    0.4599
## class          (Intercept) 0.8220    0.9067
## Residual                        0.6769    0.8227
## Number of obs: 568, groups: primarymethod, 7; class, 4
##
## Fixed effects:
##
##              Estimate Std. Error      df t value
## trophic.guildcarnivore      1.81118    0.51117    6.00000    3.543
## trophic.guildherbivore      1.22078    0.52055    6.50000    2.345
## log10.mass:trophic.guildcarnivore 1.21811    0.04964  564.70000   24.541
## log10.mass:trophic.guildherbivore 1.06739    0.04479  562.10000   23.831
##
##              Pr(>|t|)
## trophic.guildcarnivore      0.0121 *
## trophic.guildherbivore      0.0544 .
## log10.mass:trophic.guildcarnivore <2e-16 ***
## log10.mass:trophic.guildherbivore <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##
##              trphc.gldc trphc.gldh lg10.mss:trphc.gldc
## trphc.gldhr           0.932
## lg10.mss:trphc.gldc -0.199      0.017
## lg10.mss:trphc.gldh -0.020     -0.251      0.107

```

```
AICc(alltaxa.tg.int)
```

```
## [1] 1434.93
```

```
r.squaredGLMM(alltaxa.tg.int)
```

```
##          R2m          R2c
## 0.4977431 0.8012272
```

```
#Full model incorporating all retained invididual models with delta AICc < -2
alltaxa.full = lmer(log10.hra ~ log10.mass + trophic.guild + log10.mass:trophic.guild + dimension + 1
og10.mass:dimension + locomotion + (1|class) + (1|primarymethod), data=data, REML = FALSE)
summary(alltaxa.full)
```

```
## Linear mixed model fit by maximum likelihood t-tests use Satterthwaite
## approximations to degrees of freedom [merModLmerTest]
## Formula:
## log10.hra ~ log10.mass + trophic.guild + log10.mass:trophic.guild +
## dimension + log10.mass:dimension + locomotion + (1 | class) +
## (1 | primarymethod)
## Data: data
##
##          AIC          BIC    logLik deviance df.resid
## 1409.8    1461.9    -692.9   1385.8      556
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.5891 -0.6773  0.0148  0.6959  3.5011
##
## Random effects:
## Groups          Name          Variance Std.Dev.
## primarymethod (Intercept) 0.2229   0.4721
## class          (Intercept) 0.1836   0.4285
## Residual                0.6419   0.8012
## Number of obs: 568, groups: primarymethod, 7; class, 4
##
## Fixed effects:
##
##              Estimate Std. Error      df t value
## (Intercept)      2.17682    0.37942 12.00000    5.737
## log10.mass        1.17466    0.05611 566.10000   20.936
## trophic.guildherbivore -0.55681    0.20666 564.40000   -2.694
## dimension3D       -0.37350    0.37838 564.90000   -0.987
## locomotionflying     0.60208    0.38802 524.10000    1.552
## locomotionswimming  -1.50249    0.53123  4.00000   -2.828
## locomotionwalking   -0.19287    0.19198 533.30000   -1.005
## log10.mass:trophic.guildherbivore -0.11208    0.06715 564.30000   -1.669
## log10.mass:dimension3D  0.30891    0.11285 565.30000    2.737
##
##              Pr(>|t|)
## (Intercept)    9.35e-05 ***
## log10.mass      < 2e-16 ***
## trophic.guildherbivore 0.00726 **
## dimension3D     0.32402
```

```
## locomotionflying          0.12134
## locomotionswimming        0.04802 *
## locomotionwalking         0.31552
## log10.mass:trophic.guildherbivore 0.09564 .
## log10.mass:dimension3D     0.00639 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) lg10.m trphc. dmns3D lcmtnf lcmtns lcmtnw l10.:.
## log10.mass -0.275
## trphc.gldhr -0.176  0.658
## dimension3D -0.096  0.334  0.235
## locmtnflyng -0.223 -0.079 -0.045 -0.624
## lcmtnswmmng -0.441 -0.005 -0.034 -0.017  0.188
## locmtnwlkng -0.326 -0.167 -0.234 -0.074  0.463  0.282
## lg10.mss:t.  0.205 -0.764 -0.909 -0.258  0.058  0.020  0.134
## lg10.mss:3D  0.146 -0.483 -0.339 -0.708  0.174 -0.015  0.090  0.378
```

```
AICc(alltaxa.full)
```

```
## [1] 1410.362
```

```
r.squaredGLMM(alltaxa.full)
```

```
##          R2m          R2c
## 0.6798043 0.8039489
```

```
#Same full model relevelled to a baseline case of a swimming herbivorous fish
```

```
trophic.guild1 = relevel(data$trophic.guild, "herbivore")
locomotion1 = relevel(data$locomotion, "swimming")
dimension1 = relevel(data$dimension, "2D")

alltaxa.full1 = lmer(log10.hra ~ log10.mass + trophic.guild1 +
                     log10.mass:trophic.guild1 + dimension1 +
                     log10.mass:dimension1 + locomotion1 +
                     (1|class) + (1|primarymethod), data=data, REML = FALSE)
summary(alltaxa.full1)
```

```
## Linear mixed model fit by maximum likelihood t-tests use Satterthwaite
## approximations to degrees of freedom [merModLmerTest]
## Formula:
## log10.hra ~ log10.mass + trophic.guild1 + log10.mass:trophic.guild1 +
```

```

##      dimension1 + log10.mass:dimension1 + locomotion1 + (1 | class) +
##      (1 | primarymethod)
##      Data: data
##
##      AIC      BIC    logLik deviance df.resid
##  1409.8    1461.9   -692.9   1385.8     556
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.5891 -0.6773  0.0148  0.6959  3.5011
##
## Random effects:
##      Groups          Name          Variance Std.Dev.
##  primarymethod (Intercept) 0.2229    0.4721
##      class          (Intercept) 0.1836    0.4285
##      Residual                0.6419    0.8012
## Number of obs: 568, groups: primarymethod, 7; class, 4
##
## Fixed effects:
##
##              Estimate Std. Error      df t value
## (Intercept)      0.11752    0.50627   5.50000    0.232
## log10.mass        1.06258    0.04363  562.50000   24.353
## trophic.guild1carnivore 0.55681    0.20666  564.40000    2.694
## dimension13D      -0.37350    0.37838  564.90000   -0.987
## locomotion1crawling  1.50249    0.53123   4.00000    2.828
## locomotion1flying   2.10458    0.59613   6.20000    3.530
## locomotion1walking  1.30962    0.51150   3.40000    2.560
## log10.mass:trophic.guild1carnivore 0.11208    0.06715  564.30000    1.669
## log10.mass:dimension13D 0.30891    0.11285  565.30000    2.737
##
##              Pr(>|t|)
## (Intercept)      0.82478
## log10.mass        < 2e-16 ***
## trophic.guild1carnivore 0.00726 **
## dimension13D      0.32402
## locomotion1crawling 0.04802 *
## locomotion1flying  0.01178 *
## locomotion1walking 0.07268 .
## log10.mass:trophic.guild1carnivore 0.09564 .
## log10.mass:dimension13D 0.00639 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr) lg10.m trph.1 dmn13D lcmtn1c lcmtn1f lcmtn1w l10.:.
## log10.mass  -0.230
## trphc.gld1c -0.241  0.553
## dimensin13D  0.006  0.032 -0.235

```

```
## lcmtn1crwln -0.705 -0.023 -0.034 0.017
## lcmtn1flyng -0.621 -0.029 -0.001 -0.391 0.769
## lcmtn1wlkng -0.749 -0.028 0.053 -0.010 0.933 0.818
## lg10.mss:.1 0.197 -0.557 -0.909 0.258 0.020 -0.020 -0.030
## lg10.ms:13D -0.045 -0.040 0.339 -0.708 0.015 0.127 0.049 -0.378
```

```
AICc(alltaxa.full11)
```

```
## [1] 1410.362
```

```
r.squaredGLMM(alltaxa.full11)
```

```
##          R2m          R2c
## 0.6798043 0.8039489
```

Now we investigate the potential role of predator-prey mass ratio on home range scaling among the subset of carnivores for which PPMR data is available by comparing support for the full model with and without PPMR (omitting trophic.guild since all animals in this subset of data are carnivores). Next we determine prey mass-predator mass relationships for each class and predict HRA for the full model with and without PPMR. The output of this section is the basis for Figure 3:

```
# Determine prey mass predator mass relationships by taxonomic class
carndata.ppmr <-data[ which(data$log10.preymass!='NA'),]
str(carndata.ppmr)
```



```
## 'data.frame':    67 obs. of  24 variables:
## $ taxon          : Factor w/ 9 levels "birds","lake fishes",...: 5 5 5 5 5 2 5 5 5 ...
## $ common.name    : Factor w/ 569 levels "aardwolf","Abert's squirrel",...: 396 451 389 170 364
150 82 145 291 404 ...
## $ class          : Factor w/ 4 levels "actinopterygii",...: 1 1 1 1 1 1 1 1 1 ...
## $ order          : Factor w/ 51 levels "accipitriformes",...: 23 32 32 32 32 32 41 42 42 42
...
## $ family         : Factor w/ 150 levels "acanthuridae",...: 60 84 122 122 122 122 117 121 121
121 ...
## $ genus          : Factor w/ 380 levels "abudefduf","acanthurus",...: 280 199 61 125 125 279 3
07 317 317 317 ...
## $ species        : Factor w/ 517 levels "aberti","adspersus",...: 370 25 32 278 452 247 484 97
231 277 ...
## $ primarymethod   : Factor w/ 7 levels "\\","direct observation",...: 5 5 3 5 5 5 5 5 5 ...
## $ N              : Factor w/ 48 levels "1","10","104",...: 15 10 11 44 18 32 NA 33 26 38 ...
## $ mean.mass.g     : num  737 56 697 399 2362 ...
## $ log10.mass      : num  2.87 1.75 2.84 2.6 3.37 ...
## $ alt.mass.reference : Factor w/ 7 levels "Beck TDI, Brain CE. 1978. Weights of Colorado Sage Gro
use. The Condor 80(2), 241-243.",...: NA NA NA NA NA NA NA NA NA ...
## $ mean.hra.m2     : num  9056 6660 1300 5312 18305 ...
## $ log10.hra       : num  3.96 3.82 3.11 3.73 4.26 ...
## $ hra.reference    : Factor w/ 162 levels "Alberts AC. 1993. Relationship of Space Use to Popul
ation Density in an Herbivorous Lizard. Herpetologica 49(4), 469-479.",...: 134 52 141 77 12 162 92 14
9 94 149 ...
## $ realm           : Factor w/ 2 levels "aquatic","terrestrial": 1 1 1 1 1 1 1 1 1 1 ...
## $ thermoregulation : Factor w/ 2 levels "ectotherm","endotherm": 1 1 1 1 1 1 1 1 1 1 ...
## $ locomotion       : Factor w/ 4 levels "crawling","flying",...: 3 3 3 3 3 3 3 3 3 3 ...
## $ trophic.guild     : Factor w/ 2 levels "carnivore","herbivore": 1 1 1 1 1 1 1 1 1 1 ...
## $ dimension        : Factor w/ 2 levels "2D","3D": 1 1 1 1 1 1 2 1 1 1 ...
## $ preymass         : num  1.39 4.69 6.5 4.48 13.26 ...
## $ log10.preymass    : num  0.143 0.671 0.813 0.651 1.123 ...
## $ PPMR             : num  530 11.9 107.2 89 178.1 ...
## $ prey.size.reference: Factor w/ 26 levels "Brose U, et al. 2005b. Body sizes of consumers and th
eir resources. Ecology 86, 2545.",...: 1 19 4 14 20 24 9 17 8 17 ...
```

*#Comparing models with and without prey mass*

```
locomotion1 = relevel(carndata.ppmr$locomotion, "swimming")
dimension1 = relevel(carndata.ppmr$dimension, "2D")

carntaxa.full.int = lmer(log10.hra ~ log10.mass + dimension1 + log10.mass:dimension1 + locomotion1 +
(1|class) + (1|primarymethod), data=carndata.ppmr, REML = FALSE)
summary(carntaxa.full.int)
```

```
## Linear mixed model fit by maximum likelihood t-tests use Satterthwaite
## approximations to degrees of freedom [merModLmerTest]
## Formula: log10.hra ~ log10.mass + dimension1 + log10.mass:dimension1 +
## locomotion1 + (1 | class) + (1 | primarymethod)
## Data: carndata.ppmr
##
##      AIC      BIC    logLik deviance df.resid
##    142.3    164.2    -61.1    122.3      56
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.18748 -0.76505  0.02598  0.67674  2.48353
##
## Random effects:
##  Groups      Name      Variance Std.Dev.
##  class      (Intercept) 0.0000    0.0000
##  primarymethod (Intercept) 0.0381    0.1952
##  Residual                0.3536    0.5946
## Number of obs: 66, groups: class, 4; primarymethod, 4
##
## Fixed effects:
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)      1.2888     0.4762 43.8800   2.706 0.009656 **
## log10.mass        0.8140     0.1453 58.6900   5.602 5.93e-07 ***
## dimension13D      0.1003     1.0754 58.9300   0.093 0.925999
## locomotion1crawling 1.4589     0.2559 61.7700   5.702 3.56e-07 ***
## locomotion1flying  2.5840     0.6413 55.8200   4.029 0.000171 ***
## locomotion1walking 2.6807     0.3352 10.9600   7.997 6.72e-06 ***
## log10.mass:dimension13D 0.2198     0.3317 59.2200   0.663 0.510166
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr) lg10.m dmn13D lcmtn1c lcmtn1f lcmtn1w
## log10.mass -0.847
## dimensin13D -0.395  0.373
## lcmtn1crwln -0.446  0.169  0.207
## lcmtn1flyng -0.082  0.006 -0.451 -0.015
## lcmtn1wlkng -0.065 -0.365 -0.022  0.375  0.158
## lg10.ms:13D  0.381 -0.439 -0.812 -0.072 -0.082  0.147
```

```
AICc(carntaxa.full.int)
```

```
## [1] 146.2971
```

```
r.squaredGLMM(carntaxa.full.int)
```

```
##           R2m           R2c  
## 0.8339230 0.8500752
```

```
carntaxa.fullPM.int = lmer(log10.hra ~ log10.mass + log10.preymass + dimension1 + log10.mass:dimension1 + locomotion1 + (1|class) + (1|primarymethod), data=carndata.ppmr, REML = FALSE)  
summary(carntaxa.fullPM.int)
```

```

## Linear mixed model fit by maximum likelihood t-tests use Satterthwaite
## approximations to degrees of freedom [merModLmerTest]
## Formula:
## log10.hra ~ log10.mass + log10.preymass + dimension1 + log10.mass:dimension1 +
## locomotion1 + (1 | class) + (1 | primarymethod)
## Data: carndata.ppmr
##
##      AIC      BIC    logLik deviance df.resid
##    134.5    158.6    -56.2    112.5        55
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.9306 -0.6621 -0.1526  0.7606  2.4258
##
## Random effects:
## Groups           Name             Variance Std.Dev.
## class            (Intercept)  0.00000    0.0000
## primarymethod    (Intercept)  0.03893    0.1973
## Residual                    0.30304    0.5505
## Number of obs: 66, groups: class, 4; primarymethod, 4
##
## Fixed effects:
##
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)      2.58599      0.60010  62.72000   4.309 5.88e-05 ***
## log10.mass        0.20184      0.23141  58.76000   0.872  0.38665
## log10.preymass    0.50583      0.15555  59.03000   3.252  0.00190 **
## dimension13D      -0.02419      0.99639  58.89000  -0.024  0.98072
## locomotion1crawling  0.72604      0.32658  60.68000   2.223  0.02994 *
## locomotion1flying   1.82663      0.64341  60.44000   2.839  0.00616 **
## locomotion1walking   2.13369      0.35892  19.99000   5.945 8.20e-06 ***
## log10.mass:dimension13D 0.31635      0.30864  59.16000   1.025  0.30955
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr) lg10.m lg10.p dmn13D lcmtn1c lcmtn1f lcmtn1w
## log10.mass  -0.908
## lg10.prymss  0.671 -0.814
## dimensin13D -0.317  0.249 -0.040
## lcmtn1crwln -0.698  0.631 -0.688  0.177
## lcmtn1flyng -0.312  0.305 -0.371 -0.400  0.244
## lcmtn1wlkng -0.367  0.199 -0.469  0.001  0.557  0.317
## lg10.ms:13D  0.346 -0.334  0.099 -0.811 -0.120 -0.113  0.078

```

```
AICc(carntaxa.fullPM.int)
```

```
## [1] 139.387
```

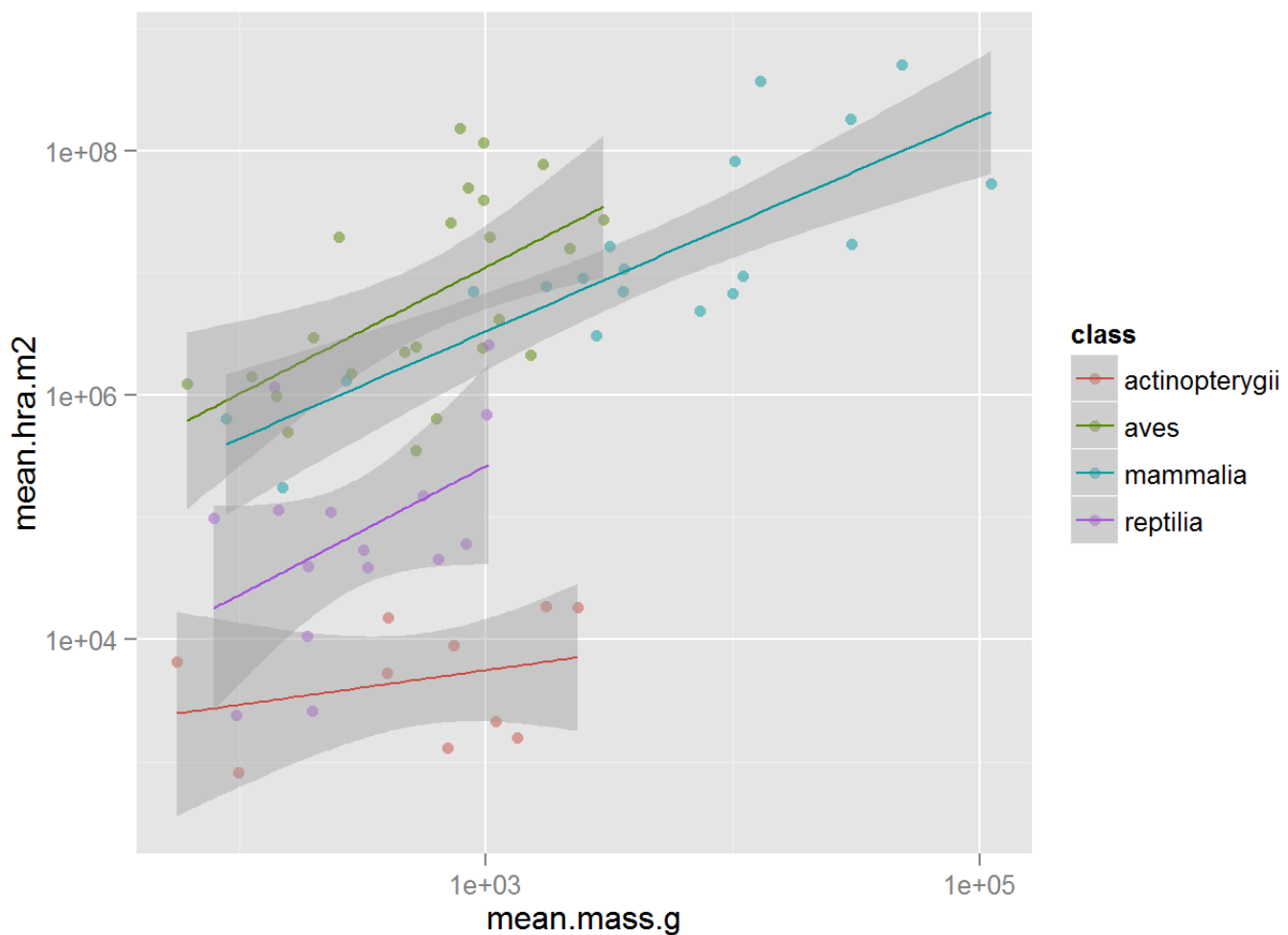
```
r.squaredGLMM(carntaxa.fullPM.int)
```

```
##          R2m          R2c  
## 0.8571056 0.8733713
```

```
#delta AICc here  
AICc(carntaxa.fullPM.int)-AICc(carntaxa.full.int)
```

```
## [1] -6.91015
```

```
#Plot of prey mass vs. predator mass by taxonomic class in the real data set  
ggplot(carndata.ppmr, aes(y=mean.hra.m2, x=mean.mass.g, color = class)) + scale_x_log10() + scale_y_log10() +  
  geom_point(shape=16, alpha = 0.5) +  
  scale_colour_hue(l=50) + # Use a slightly darker palette than normal  
  geom_smooth(method=lm, # Add linear regression lines  
              se=TRUE) # Decide if add shaded confidence region
```



*#Subset the data and model these prey size-predator size relationships to be able to predict prey masses for hypothetical data*

```
carn.birds <- carndata.ppmr[ which(carndata.ppmr$class=='aves'),]
```

```
carn.mammals <- carndata.ppmr[ which(carndata.ppmr$class=='mammalia'),]
```

```
carn.reptiles <- carndata.ppmr[ which(carndata.ppmr$class=='reptilia'),]
```

```
carn.fish <- carndata.ppmr[ which(carndata.ppmr$class=='actinopterygii'),]
```

*#For each taxon we create a linear model of prey-predator masses, and make a mock log10.mass dataset bounded by the limits of the real data for that taxon to predict prey masses for feeding back into the global carnivore-only model.*

*#BIRDS*

```
carn.birds.predprey <- lm(log10.preymass ~ log10.mass, data=carn.birds)
summary(carn.birds.predprey)
```

```
##
## Call:
## lm(formula = log10.preymass ~ log10.mass, data = carn.birds)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.47525 -0.26399  0.01235  0.26370  0.46144
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -0.9027      0.3834  -2.354   0.0284 *
## log10.mass    1.0494      0.1379   7.609 1.82e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2825 on 21 degrees of freedom
## Multiple R-squared:  0.7338, Adjusted R-squared:  0.7211
## F-statistic: 57.89 on 1 and 21 DF,  p-value: 1.823e-07
```

```
carn.birds.PM <- data.frame(log10.mass=c(0.7,1,1.7,2,2.7,3,3.7), log10.preymass = c(NA,NA,NA,NA,NA,NA,NA,NA))
carn.birds.PM$log10.preymass <- predict(carn.birds.predprey, newdata=carn.birds.PM)
```

*#MAMMALS*

```
carn.mammals.predprey <- lm(log10.preymass ~ log10.mass, data=carn.mammals)
summary(carn.mammals.predprey)
```

```
##
## Call:
## lm(formula = log10.preymass ~ log10.mass, data = carn.mammals)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.7818 -0.4892  0.1100  0.3224  0.8242
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -1.9512     0.5539  -3.523  0.00261 **
## log10.mass    1.3432     0.1490   9.014 6.93e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5255 on 17 degrees of freedom
## Multiple R-squared:  0.827, Adjusted R-squared:  0.8168
## F-statistic: 81.25 on 1 and 17 DF, p-value: 6.932e-08
```

```
carn.mammals.PM <- data.frame(log10.mass=c(0.7,1,1.7,2,2.7,3,3.7,4,4.7,5.05), log10.preymass = c(NA,NA,NA,NA,NA,NA,NA,NA,NA,NA))
```

```
carn.mammals.PM$log10.preymass <- predict(carn.mammals.predprey, newdata=carn.mammals.PM)
```

```
#REPTILES
```

```
carn.reptiles.predprey <- lm(log10.preymass ~ log10.mass, data=carn.reptiles)
summary(carn.reptiles.predprey)
```

```
##
## Call:
## lm(formula = log10.preymass ~ log10.mass, data = carn.reptiles)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.7612 -0.3441 -0.1044  0.3156  0.9900
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -0.9686     0.9846  -0.984  0.3432
## log10.mass    1.1325     0.3962   2.859  0.0134 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5384 on 13 degrees of freedom
## Multiple R-squared:  0.386, Adjusted R-squared:  0.3388
## F-statistic: 8.173 on 1 and 13 DF, p-value: 0.01343
```

```

carn.reptiles.PM <- data.frame(log10.mass=c(0.7,1,1.7,2,2.7,3.08), log10.preymass = c(NA,NA,NA,NA,NA,NA))
carn.reptiles.PM$log10.preymass <- predict(carn.reptiles.predprey, newdata=carn.reptiles.PM)

#FISH
carn.fish.predprey <- lm(log10.preymass ~ log10.mass, data=carn.fish)
summary(carn.fish.predprey)

```

```

##
## Call:
## lm(formula = log10.preymass ~ log10.mass, data = carn.fish)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.62736 -0.24660 -0.00256  0.05541  0.68448
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -1.0242     0.7625  -1.343   0.2161
## log10.mass    0.6258     0.2733   2.290   0.0513 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4318 on 8 degrees of freedom
## Multiple R-squared:  0.3959, Adjusted R-squared:  0.3204
## F-statistic: 5.242 on 1 and 8 DF,  p-value: 0.0513

```

```

carn.fish.PM <- data.frame(log10.mass=c(0,0.7,1,1.7,2,2.7,3,3.32,3.51), log10.preymass = c(NA,NA,NA,NA,NA,NA,NA,NA,NA))
carn.fish.PM$log10.preymass <- predict(carn.fish.predprey, newdata=carn.fish.PM)

#Now predict home range area over a hypothetical data set using the full carnivore model with or without the predicted prey masses for mammals and fishes

#Read in mock data with predicted prey masses from the prey size-predator size relationships
#For CI predictions on the lmer model outputs, it is important that our mock data include all other variables in the model and includes all taxa used to parameterize the original model
str(data.PM)

```



```
## 'data.frame':   36 obs. of  9 variables:
## $ group       : int  2 2 2 2 2 2 2 2 4 4 ...
## $ taxon       : Factor w/ 5 levels "birds","lake fish",...: 4 4 4 4 4 4 4 4 2 2 ...
## $ mass        : int  1 5 10 50 100 501 1000 3250 50 100 ...
## $ log10.mass  : num  0 0.7 1 1.7 2 2.7 3 3.51 1.7 2 ...
## $ log10.preymass: num  -1.02 -0.59 -0.39 0.04 0.23 0.67 0.85 1.17 0.04 0.23 ...
## $ locomotion  : Factor w/ 4 levels "crawling","flying",...: 3 3 3 3 3 3 3 3 3 3 ...
## $ dimension   : Factor w/ 2 levels "2D","3D": 1 1 1 1 1 1 1 2 2 ...
## $ class       : Factor w/ 4 levels "actinopterygii",...: 1 1 1 1 1 1 1 1 1 1 ...
## $ primarymethod : Factor w/ 1 level "telemetry": 1 1 1 1 1 1 1 1 1 1 ...
```

*#Now we plot our predictions and corresponding confidence intervals for lmer objects for carnivore models with and without prey mass*

*#Home range area predictions on mock data from full model WITHOUT prey mass*

```
carntaxa.full.int = lmer(log10.hra ~ log10.mass + dimension + log10.mass:dimension + locomotion +
(1|class) + (1|primarymethod), data=carndata.ppmr, REML = FALSE)
```

```
data.PM$log10.hra <- predict(carntaxa.full.int, newdata=data.PM)
str(data.PM)
```

```
## 'data.frame':   36 obs. of  10 variables:
## $ group       : int  2 2 2 2 2 2 2 2 4 4 ...
## $ taxon       : Factor w/ 5 levels "birds","lake fish",...: 4 4 4 4 4 4 4 4 2 2 ...
## $ mass        : int  1 5 10 50 100 501 1000 3250 50 100 ...
## $ log10.mass  : num  0 0.7 1 1.7 2 2.7 3 3.51 1.7 2 ...
## $ log10.preymass: num  -1.02 -0.59 -0.39 0.04 0.23 0.67 0.85 1.17 0.04 0.23 ...
## $ locomotion  : Factor w/ 4 levels "crawling","flying",...: 3 3 3 3 3 3 3 3 3 3 ...
## $ dimension   : Factor w/ 2 levels "2D","3D": 1 1 1 1 1 1 1 2 2 ...
## $ class       : Factor w/ 4 levels "actinopterygii",...: 1 1 1 1 1 1 1 1 1 1 ...
## $ primarymethod : Factor w/ 1 level "telemetry": 1 1 1 1 1 1 1 1 1 1 ...
## $ log10.hra    : num  1.39 1.96 2.21 2.78 3.02 ...
```

```
newdat<-data.PM
```

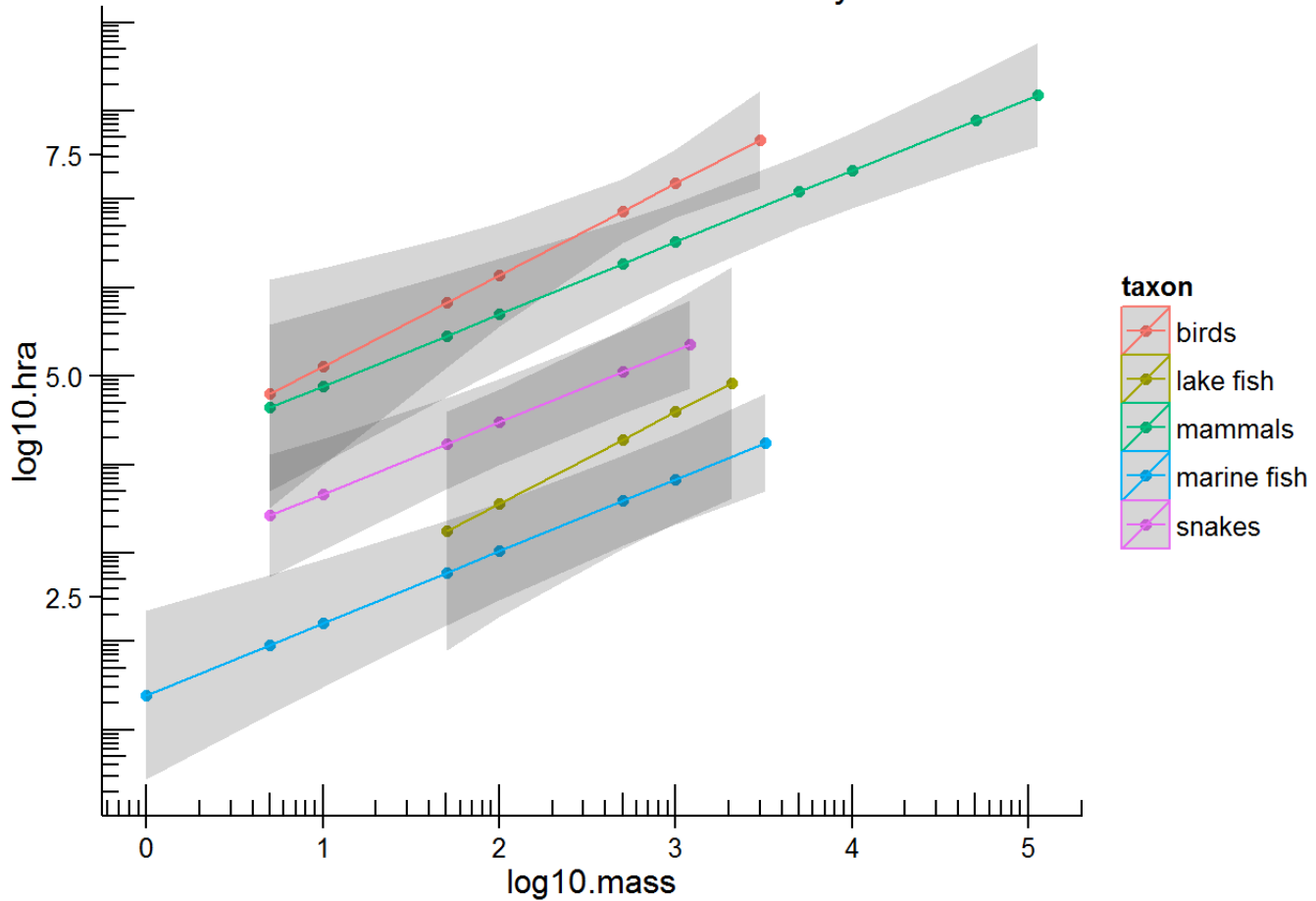
```
#Plotting predictions of lmer models with confidence intervals from glmm.wikidot.com/faq
```

```
mm <- model.matrix(terms(carntaxa.full.int),newdat)
pvar1 <- diag(mm %%% tcrossprod(vcov(carntaxa.full.int),mm))
tvar1 <- pvar1 + VarCorr(carntaxa.full.int)$class[1]+ VarCorr(carntaxa.full.int)$primarymethod[1] ##
must be adapted for more complex models
tvar1 <-
  newdat <- data.frame(
    newdat
    , plo = newdat$log10.hra-2*sqrt(pvar1)
    , phi = newdat$log10.hra+2*sqrt(pvar1)
    , tlo = newdat$log10.hra-2*sqrt(tvar1)
    , thi = newdat$log10.hra+2*sqrt(tvar1)
  )
str(newdat)
```

```
## 'data.frame':   36 obs. of  14 variables:
## $ group        : int  2 2 2 2 2 2 2 2 4 4 ...
## $ taxon        : Factor w/ 5 levels "birds","lake fish",...: 4 4 4 4 4 4 4 4 2 2 ...
## $ mass         : int  1 5 10 50 100 501 1000 3250 50 100 ...
## $ log10.mass   : num  0 0.7 1 1.7 2 2.7 3 3.51 1.7 2 ...
## $ log10.preymass: num  -1.02 -0.59 -0.39 0.04 0.23 0.67 0.85 1.17 0.04 0.23 ...
## $ locomotion   : Factor w/ 4 levels "crawling","flying",...: 3 3 3 3 3 3 3 3 3 3 ...
## $ dimension    : Factor w/ 2 levels "2D","3D": 1 1 1 1 1 1 1 1 2 2 ...
## $ class        : Factor w/ 4 levels "actinopterygii",...: 1 1 1 1 1 1 1 1 1 1 ...
## $ primarymethod: Factor w/ 1 level "telemetry": 1 1 1 1 1 1 1 1 1 1 ...
## $ log10.hra    : num  1.39 1.96 2.21 2.78 3.02 ...
## $ plo          : num  0.439 1.174 1.483 2.181 2.466 ...
## $ phi          : num  2.34 2.75 2.93 3.37 3.57 ...
## $ tlo          : num  0.362 1.083 1.384 2.064 2.342 ...
## $ thi          : num  2.42 2.84 3.03 3.49 3.7 ...
```

```
g0 <- ggplot(newdat, aes(x=log10.mass, y=log10.hra, colour=taxon))
g0 + annotation_logticks(short = unit(2,"mm"), mid = unit(3,"mm"), long = unit(4,"mm")) + theme_bw()
+ theme(panel.border = element_blank(), panel.grid.major = element_blank(),
panel.grid.minor = element_blank(), axis.line = element_line(colour = "black")) + geom_point() + geom_
ribbon(aes(ymin = plo, ymax = phi, linetype = NA), alpha=0.2) + geom_line(aes(ymin = plo, ymax = phi))
+ ggtitle("CI based on fixed-effects uncertainty ONLY")
```

## CI based on fixed-effects uncertainty ONLY



```
#Reload data for round 2, to get home range area predictions on full model WITH prey mass
rm(newdat)
data.PM <- read.csv("C:/Research/Home Range Scaling/Tamburelloetal_Fig2_PreymassPredictionData.csv", header=T, sep=",")
str(data.PM)
```

```
## 'data.frame':   36 obs. of  9 variables:
## $ group       : int  2 2 2 2 2 2 2 2 4 4 ...
## $ taxon       : Factor w/ 5 levels "birds","lake fish",...: 4 4 4 4 4 4 4 4 2 2 ...
## $ mass        : int  1 5 10 50 100 501 1000 3250 50 100 ...
## $ log10.mass   : num  0 0.7 1 1.7 2 2.7 3 3.51 1.7 2 ...
## $ log10.preymass: num  -1.02 -0.59 -0.39 0.04 0.23 0.67 0.85 1.17 0.04 0.23 ...
## $ locomotion   : Factor w/ 4 levels "crawling","flying",...: 3 3 3 3 3 3 3 3 3 3 ...
## $ dimension    : Factor w/ 2 levels "2D","3D": 1 1 1 1 1 1 1 1 2 2 ...
## $ class        : Factor w/ 4 levels "actinopterygii",...: 1 1 1 1 1 1 1 1 1 1 ...
## $ primarymethod: Factor w/ 1 level "telemetry": 1 1 1 1 1 1 1 1 1 1 ...
```

```
carntaxa.fullPM.int = lmer(log10.hra ~ log10.mass + dimension +
                           log10.mass:dimension + locomotion +
                           log10.preymass +
                           (1|class) + (1|primarymethod), data=carndata.ppmr, REML = FALSE)

data.PM$log10.hra <- predict(carntaxa.fullPM.int, newdata=data.PM)
str(data.PM)
```

```
## 'data.frame':   36 obs. of  10 variables:
## $ group       : int  2 2 2 2 2 2 2 2 4 4 ...
## $ taxon       : Factor w/ 5 levels "birds","lake fish",...: 4 4 4 4 4 4 4 4 2 2 ...
## $ mass        : int  1 5 10 50 100 501 1000 3250 50 100 ...
## $ log10.mass   : num  0 0.7 1 1.7 2 2.7 3 3.51 1.7 2 ...
## $ log10.preymass: num  -1.02 -0.59 -0.39 0.04 0.23 0.67 0.85 1.17 0.04 0.23 ...
## $ locomotion   : Factor w/ 4 levels "crawling","flying",...: 3 3 3 3 3 3 3 3 3 3 ...
## $ dimension    : Factor w/ 2 levels "2D","3D": 1 1 1 1 1 1 1 1 2 2 ...
## $ class        : Factor w/ 4 levels "actinopterygii",...: 1 1 1 1 1 1 1 1 1 1 ...
## $ primarymethod : Factor w/ 1 level "telemetry": 1 1 1 1 1 1 1 1 1 1 ...
## $ log10.hra    : num  2.2 2.55 2.72 3.07 3.23 ...
```

```
newdat<-data.PM
```

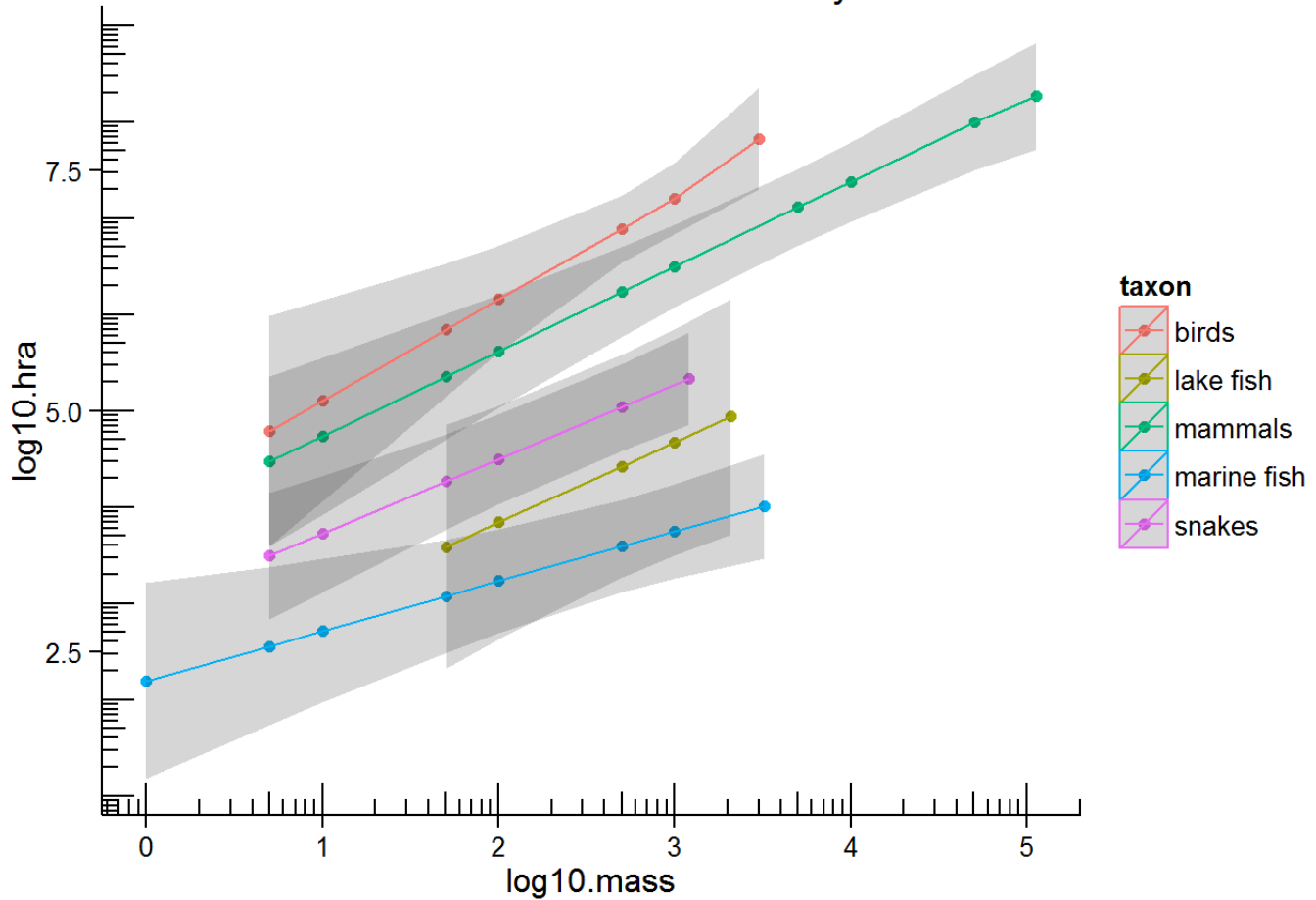
*#Plotting predictions of lmer models with confidence intervals from [glmm.wikidot.com/faq](http://glmm.wikidot.com/faq)*

```
mm <- model.matrix(terms(carntaxa.fullPM.int),newdat)
## or newdat$distance <- mm %%% fixef(fm1)
pvar1 <- diag(mm %%% tcrossprod(vcov(carntaxa.fullPM.int),mm))
tvar1 <- pvar1 + VarCorr(carntaxa.fullPM.int)$class[1]+ VarCorr(carntaxa.fullPM.int)$primarymethod[1]
## must be adapted for more complex models
tvar1 <-
  newdat <- data.frame(
    newdat
    , plo = newdat$log10.hra-2*sqrt(pvar1)
    , phi = newdat$log10.hra+2*sqrt(pvar1)
    , tlo = newdat$log10.hra-2*sqrt(tvar1)
    , thi = newdat$log10.hra+2*sqrt(tvar1)
  )
str(newdat)
```

```
## 'data.frame':   36 obs. of  14 variables:
## $ group       : int  2 2 2 2 2 2 2 2 4 4 ...
## $ taxon       : Factor w/ 5 levels "birds","lake fish",...: 4 4 4 4 4 4 4 4 2 2 ...
## $ mass        : int  1 5 10 50 100 501 1000 3250 50 100 ...
## $ log10.mass  : num  0 0.7 1 1.7 2 2.7 3 3.51 1.7 2 ...
## $ log10.preymass: num  -1.02 -0.59 -0.39 0.04 0.23 0.67 0.85 1.17 0.04 0.23 ...
## $ locomotion  : Factor w/ 4 levels "crawling","flying",...: 3 3 3 3 3 3 3 3 3 3 ...
## $ dimension   : Factor w/ 2 levels "2D","3D": 1 1 1 1 1 1 1 1 2 2 ...
## $ class       : Factor w/ 4 levels "actinopterygii",...: 1 1 1 1 1 1 1 1 1 1 ...
## $ primarymethod : Factor w/ 1 level "telemetry": 1 1 1 1 1 1 1 1 1 1 ...
## $ log10.hra    : num  2.2 2.55 2.72 3.07 3.23 ...
## $ plo         : num  1.18 1.73 1.97 2.48 2.69 ...
## $ phi         : num  3.21 3.37 3.46 3.66 3.77 ...
## $ tlo         : num  1.11 1.64 1.87 2.36 2.56 ...
## $ thi         : num  3.28 3.46 3.56 3.78 3.9 ...
```

```
g0 <- ggplot(newdat, aes(x=log10.mass, y=log10.hra, colour=taxon))
g0 + annotation_logticks(short = unit(2,"mm"), mid = unit(3,"mm"), long = unit(4,"mm")) + theme_bw()
+ theme(panel.border = element_blank(), panel.grid.major = element_blank(),
panel.grid.minor = element_blank(), axis.line = element_line(colour = "black")) + geom_point() + geom_
m_ribbon(aes(ymin = plo, ymax = phi, linetype = NA), alpha=0.2) + geom_line(aes(ymin = plo, ymax = ph
i)) + ggtitle("CI based on fixed-effects uncertainty ONLY")
```

## CI based on fixed-effects uncertainty ONLY



Creating online Figure A1.

```
##### Plots and 95% CI bands for Figure A1
```

```
#####PLOT BY BIOME
```

```
names(data)
```

```
## [1] "taxon"          "common.name"    "class"
## [4] "order"          "family"         "genus"
## [7] "species"        "primarymethod"  "N"
## [10] "mean.mass.g"    "log10.mass"     "alt.mass.reference"
## [13] "mean.hra.m2"    "log10.hra"      "hra.reference"
## [16] "realm"          "thermoregulation" "locomotion"
## [19] "trophic.guild"  "dimension"      "preymass"
## [22] "log10.preymass" "PPMR"           "prey.size.reference"
```

```
data.predict.bio <- data[, c(3, 8, 11, 16)]
names(data.predict.bio)
```

```
## [1] "class"          "primarymethod"  "log10.mass"     "realm"
```

```

alltaxa.bio = lmer(log10.hra ~ -1 + log10.mass + realm + (1|class) + (1|primarymethod), data=data, RE
ML = FALSE)
data.predict.bio$log10.hra <- predict(alltaxa.bio, newdata=data.predict.bio, re.form=NA)

newdat <- data.predict.bio

mm <- model.matrix(terms(alltaxa.bio),newdat)
## or newdat$distance <- mm %%% fixef(fm1)
pvar1 <- diag(mm %%% tcrossprod(vcov(alltaxa.bio),mm))
tvar1 <- pvar1 + VarCorr(alltaxa.bio)$class[1] + VarCorr(alltaxa.bio)$primarymethod[1] ## must be ada
pted for more complex models
tvar1 <-
  newdat <- data.frame(
    newdat
    , plo = newdat$log10.hra-2*sqrt(pvar1)
    , phi = newdat$log10.hra+2*sqrt(pvar1)
    , tlo = newdat$log10.hra-2*sqrt(tvar1)
    , thi = newdat$log10.hra+2*sqrt(tvar1)
  )
str(newdat)

```

```

## 'data.frame':   569 obs. of  9 variables:
## $ class          : Factor w/ 4 levels "actinopterygii",...: 1 1 1 1 1 1 1 1 1 1 ...
## $ primarymethod: Factor w/ 7 levels "\\","direct observation",...: 5 3 3 3 3 5 5 5 2 5 ...
## $ log10.mass     : num  2.948 2.75 1.531 0.602 0.602 ...
## $ realm          : Factor w/ 2 levels "aquatic","terrestrial": 1 1 1 1 1 1 1 1 1 1 ...
## $ log10.hra      : num  3.98 3.78 2.5 1.53 1.53 ...
## $ plo            : num  2.344 2.138 0.864 -0.112 -0.112 ...
## $ phi            : num  5.62 5.41 4.14 3.17 3.17 ...
## $ tlo            : num  1.48184 1.27483 0.00025 -0.97453 -0.97453 ...
## $ thi            : num  6.48 6.28 5 4.03 4.03 ...

```

```

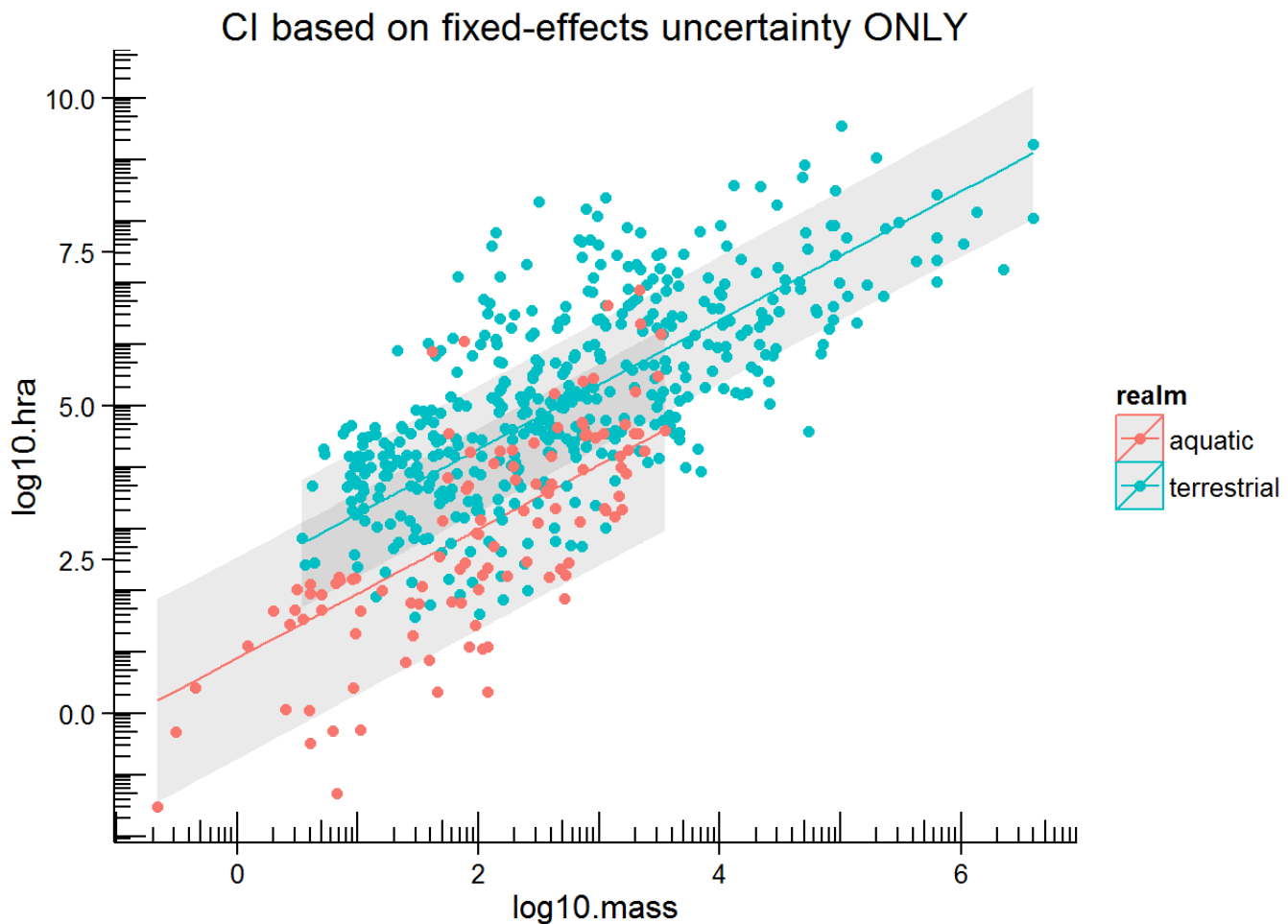
#Subset data for plotting
data.terr <-data[ which(data$realm=='terrestrial'),]
data.aq <-data[ which(data$realm=='aquatic'),]

#fixef
g0 <- ggplot(newdat, aes(x=log10.mass, y=log10.hra, color = realm))

g1 <- g0 + annotation_logticks(short = unit(2,"mm"), mid = unit(3,"mm"), long = unit(4,"mm")) + theme_
e_bw() + theme(panel.border = element_blank(), panel.grid.major = element_blank(),
panel.grid.minor = element_blank(), axis.line = element_line(colour = "black")) + geom_ribbon(aes(ymin
n = plo, ymax = phi, linetype = NA), alpha=0.1) + geom_line(aes(ymin = plo, ymax = phi)) + ggtitle("C
I based on fixed-effects uncertainty ONLY")

g1 + geom_point(data=data.terr, aes(x=log10.mass, y=log10.hra)) + geom_point(data=data.aq, aes(x=log1
0.mass, y=log10.hra))

```



```

#####PLOT BY THERMOREGULATION
names(data)

```



## [1] "taxon"	"common.name"	"class"
## [4] "order"	"family"	"genus"
## [7] "species"	"primarymethod"	"N"
## [10] "mean.mass.g"	"log10.mass"	"alt.mass.reference"
## [13] "mean.hra.m2"	"log10.hra"	"hra.reference"
## [16] "realm"	"thermoregulation"	"locomotion"
## [19] "trophic.guild"	"dimension"	"preymass"
## [22] "log10.preymass"	"PPMR"	"prey.size.reference"

```
data.predict.therm <- data[, c(3, 8, 11, 17)]
```

```
alltaxa.therm = lmer(log10.hra ~ -1 + log10.mass + thermoregulation + (1|class) + (1|primarymethod),
data=data, REML = FALSE)
```

```
data.predict.therm$log10.hra <- predict(alltaxa.therm, newdata=data.predict.therm, re.form=NA)
```

```
newdat <- data.predict.therm
```

```
mm <- model.matrix(terms(alltaxa.therm),newdat)
```

```
## or newdat$distance <- mm %%% fixef(fm1)
```

```
pvar1 <- diag(mm %%% tcrossprod(vcov(alltaxa.therm),mm))
```

```
tvar1 <- pvar1 + VarCorr(alltaxa.therm)$class[1] + VarCorr(alltaxa.therm)$primarymethod[1] ## must be
adapted for more complex models
```

```
tvar1 <-
```

```
  newdat <- data.frame(
```

```
    newdat
```

```
    , plo = newdat$log10.hra-2*sqrt(pvar1)
```

```
    , phi = newdat$log10.hra+2*sqrt(pvar1)
```

```
    , tlo = newdat$log10.hra-2*sqrt(tvar1)
```

```
    , thi = newdat$log10.hra+2*sqrt(tvar1)
```

```
  )
```

```
str(newdat)
```

```
## 'data.frame': 569 obs. of 9 variables:
```

```
## $ class : Factor w/ 4 levels "actinopterygii",...: 1 1 1 1 1 1 1 1 1 ...
```

```
## $ primarymethod : Factor w/ 7 levels "\\","direct observation",...: 5 3 3 3 3 5 5 2 5 ...
```

```
## $ log10.mass : num 2.948 2.75 1.531 0.602 0.602 ...
```

```
## $ thermoregulation: Factor w/ 2 levels "ectotherm","endotherm": 1 1 1 1 1 1 1 1 1 ...
```

```
## $ log10.hra : num 4.35 4.14 2.87 1.9 1.9 ...
```

```
## $ plo : num 3.177 2.971 1.698 0.723 0.723 ...
```

```
## $ phi : num 5.52 5.31 4.04 3.07 3.07 ...
```

```
## $ tlo : num 2.168 1.962 0.688 -0.286 -0.286 ...
```

```
## $ thi : num 6.53 6.32 5.05 4.08 4.08 ...
```

```

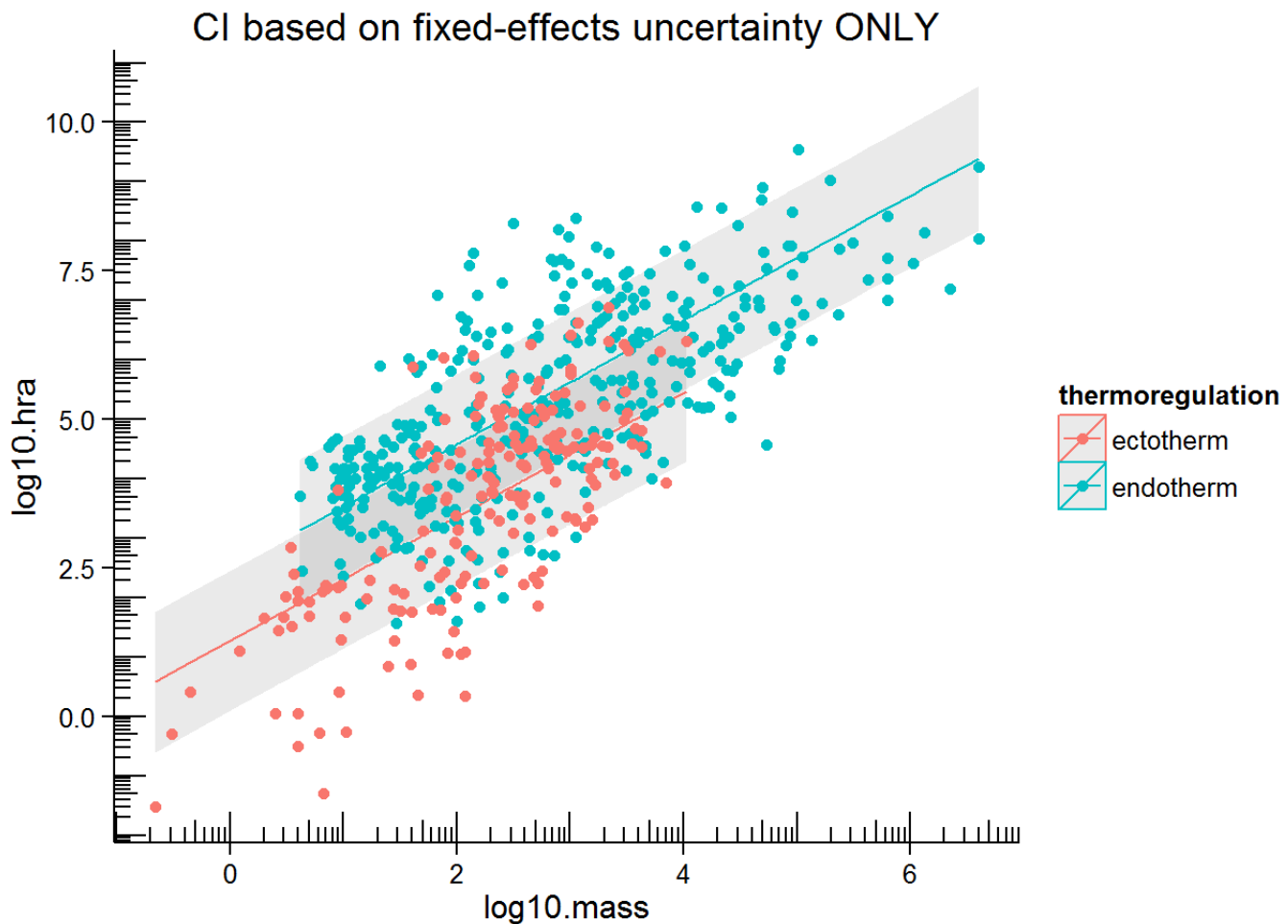
#Subset data for plotting
data.endo <-data[ which(data$thermoregulation=='endotherm'),]
data.ecto <-data[ which(data$thermoregulation=='ectotherm'),]

#fixef
g0 <- ggplot(newdat, aes(x=log10.mass, y=log10.hra, color = thermoregulation))

g1 <- g0 + annotation_logticks(short = unit(2,"mm"), mid = unit(3,"mm"), long = unit(4,"mm")) + them
e_bw() + theme(panel.border = element_blank(), panel.grid.major = element_blank(),
panel.grid.minor = element_blank(), axis.line = element_line(colour = "black")) + geom_ribbon(aes(ymin
n = plo, ymax = phi, linetype = NA), alpha=0.1) + geom_line(aes(ymin = plo, ymax = phi)) + ggtitle("C
I based on fixed-effects uncertainty ONLY")

g1 + geom_point(data=data.endo, aes(x=log10.mass, y=log10.hra)) + geom_point(data=data.ecto, aes(x=lo
g10.mass, y=log10.hra))

```



```

#####PLOT BY LOCOMOTION
names(data)

```

## [1] "taxon"	"common.name"	"class"
## [4] "order"	"family"	"genus"
## [7] "species"	"primarymethod"	"N"
## [10] "mean.mass.g"	"log10.mass"	"alt.mass.reference"
## [13] "mean.hra.m2"	"log10.hra"	"hra.reference"
## [16] "realm"	"thermoregulation"	"locomotion"
## [19] "trophic.guild"	"dimension"	"preymass"
## [22] "log10.preymass"	"PPMR"	"prey.size.reference"

```
data.predict.loc <- data[, c(3, 8, 11, 18)]
```

```
alltaxa.loc = lmer(log10.hra ~ log10.mass + locomotion + 0 + (1|class) + (1|primarymethod), data=data, REML = FALSE)
```

```
data.predict.loc$log10.hra <- predict(alltaxa.loc, newdata=data.predict.loc, re.form=NA)
```

```
newdat <- data.predict.loc
```

```
mm <- model.matrix(terms(alltaxa.loc),newdat)
```

```
## or newdat$distance <- mm %%% fixef(fm1)
```

```
pvar1 <- diag(mm %%% tcrossprod(vcov(alltaxa.loc),mm))
```

```
tvar1 <- pvar1 + VarCorr(alltaxa.loc)$class[1] + VarCorr(alltaxa.loc)$primarymethod[1] ## must be adapted for more complex models
```

```
tvar1 <-
```

```
  newdat <- data.frame(
```

```
    newdat
```

```
    , plo = newdat$log10.hra-2*sqrt(pvar1)
```

```
    , phi = newdat$log10.hra+2*sqrt(pvar1)
```

```
    , tlo = newdat$log10.hra-2*sqrt(tvar1)
```

```
    , thi = newdat$log10.hra+2*sqrt(tvar1)
```

```
  )
```

```
str(newdat)
```

```
## 'data.frame': 569 obs. of 9 variables:
```

```
## $ class : Factor w/ 4 levels "actinopterygii",...: 1 1 1 1 1 1 1 1 1 1 ...
```

```
## $ primarymethod: Factor w/ 7 levels "\\","direct observation",...: 5 3 3 3 3 5 5 5 2 5 ...
```

```
## $ log10.mass : num 2.948 2.75 1.531 0.602 0.602 ...
```

```
## $ locomotion : Factor w/ 4 levels "crawling","flying",...: 3 3 3 3 3 3 3 3 3 3 ...
```

```
## $ log10.hra : num 3.94 3.73 2.39 1.37 1.37 ...
```

```
## $ plo : num 2.84 2.62 1.28 0.26 0.26 ...
```

```
## $ phi : num 5.05 4.83 3.49 2.48 2.48 ...
```

```
## $ tlo : num 2.051 1.834 0.498 -0.524 -0.524 ...
```

```
## $ thi : num 5.84 5.62 4.28 3.26 3.26 ...
```

```

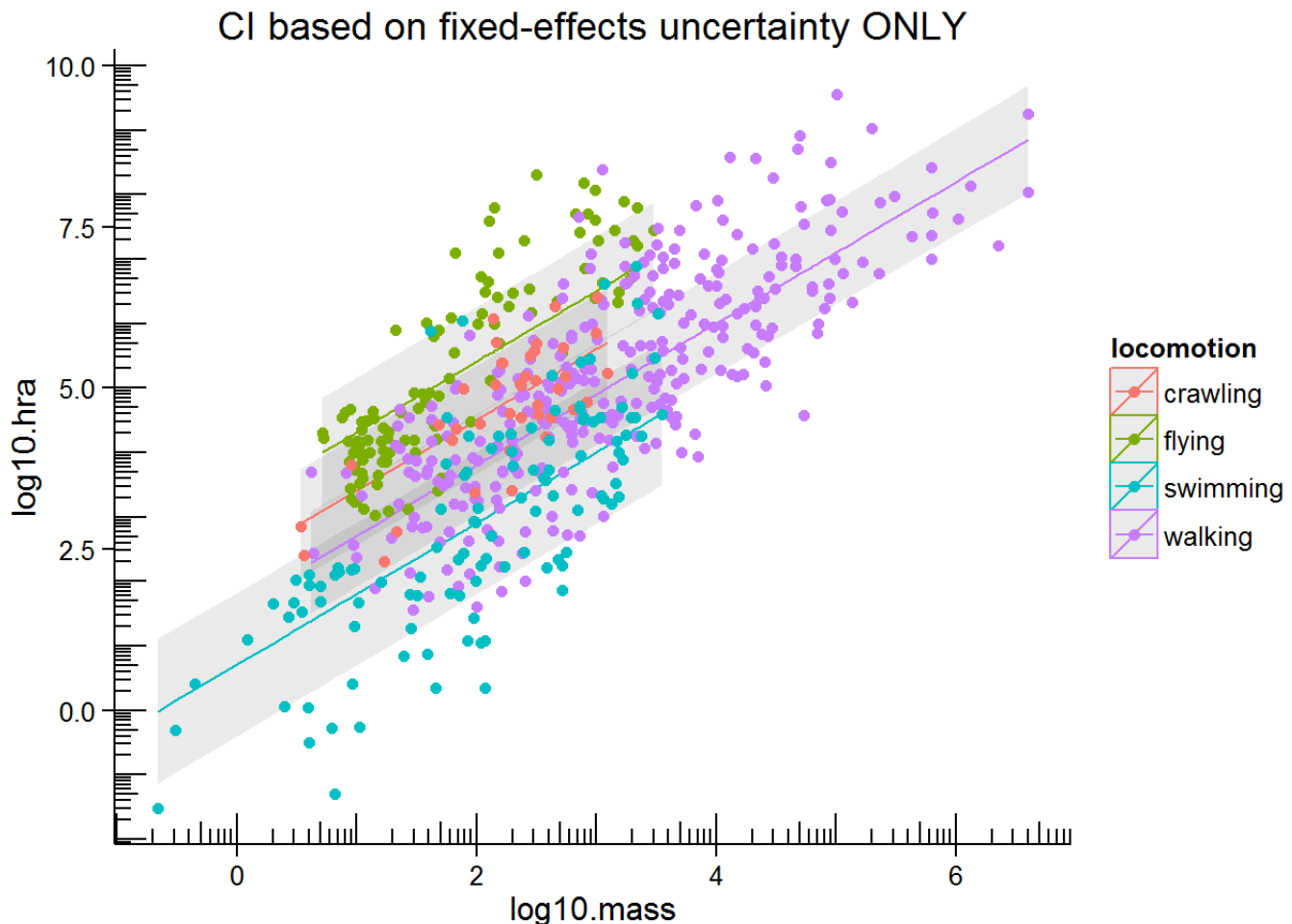
#Subset data for plotting
data.fly <-data[ which(data$locomotion=='flying'),]
data.walk <-data[ which(data$locomotion=='walking'),]
data.crawl <-data[ which(data$locomotion=='crawling'),]
data.swim <-data[ which(data$locomotion=='swimming'),]

#fixef
g0 <- ggplot(newdat, aes(x=log10.mass, y=log10.hra, color = locomotion))

g1 <- g0 + annotation_logticks(short = unit(2,"mm"), mid = unit(3,"mm"), long = unit(4,"mm")) + them
e_bw() + theme(panel.border = element_blank(), panel.grid.major = element_blank(),
panel.grid.minor = element_blank(), axis.line = element_line(colour = "black")) + geom_ribbon(aes(ymin
n = plo, ymax = phi, linetype = NA), alpha=0.1) + geom_line(aes(ymin = plo, ymax = phi)) + ggtitle("C
I based on fixed-effects uncertainty ONLY")

g1 + geom_point(data=data.fly, aes(x=log10.mass, y=log10.hra)) + geom_point(data=data.walk, aes(x=log
10.mass, y=log10.hra)) + geom_point(data=data.crawl, aes(x=log10.mass, y=log10.hra)) + geom_point(dat
a=data.swim, aes(x=log10.mass, y=log10.hra))

```



```

#####PLOT BY DIMENSION
names(data)

```

## [1] "taxon"	"common.name"	"class"
## [4] "order"	"family"	"genus"
## [7] "species"	"primarymethod"	"N"
## [10] "mean.mass.g"	"log10.mass"	"alt.mass.reference"
## [13] "mean.hra.m2"	"log10.hra"	"hra.reference"
## [16] "realm"	"thermoregulation"	"locomotion"
## [19] "trophic.guild"	"dimension"	"preymass"
## [22] "log10.preymass"	"PPMR"	"prey.size.reference"

```
data.predict.dim <- data[, c(3, 8, 11, 20)]
alltaxa.dim.int = lmer(log10.hra ~ dimension + log10.mass:dimension + (1|class) + (1|primarymethod),
data=data, REML = FALSE)

data.predict.dim$log10.hra <- predict(alltaxa.dim.int, newdata=data.predict.dim, re.form=NA)
newdat <- data.predict.dim

mm <- model.matrix(terms(alltaxa.dim.int),newdat)
## or newdat$distance <- mm %%% fixef(fm1)
pvar1 <- diag(mm %%% tcrossprod(vcov(alltaxa.dim.int),mm))
tvar1 <- pvar1 + VarCorr(alltaxa.dim.int)$class[1] + VarCorr(alltaxa.dim.int)$primarymethod[1] ## must be adapted for more complex models
tvar1 <-
  newdat <- data.frame(
    newdat
    , plo = newdat$log10.hra-2*sqrt(pvar1)
    , phi = newdat$log10.hra+2*sqrt(pvar1)
    , tlo = newdat$log10.hra-2*sqrt(tvar1)
    , thi = newdat$log10.hra+2*sqrt(tvar1)
  )
str(newdat)
```

```
## 'data.frame':   569 obs. of  9 variables:
## $ class       : Factor w/ 4 levels "actinopterygii",...: 1 1 1 1 1 1 1 1 1 1 ...
## $ primarymethod: Factor w/ 7 levels "\\","direct observation",...: 5 3 3 3 3 5 5 5 2 5 ...
## $ log10.mass   : num  2.948 2.75 1.531 0.602 0.602 ...
## $ dimension    : Factor w/ 2 levels "2D","3D": 2 1 1 1 1 1 1 1 1 1 ...
## $ log10.hra    : num  6.18 4.54 3.28 2.32 2.32 ...
## $ plo          : num  5.24 3.66 2.39 1.43 1.43 ...
## $ phi          : num  7.13 5.42 4.16 3.21 3.21 ...
## $ tlo          : num  4.135 2.516 1.256 0.292 0.292 ...
## $ thi          : num  8.23 6.56 5.3 4.34 4.34 ...
```

```

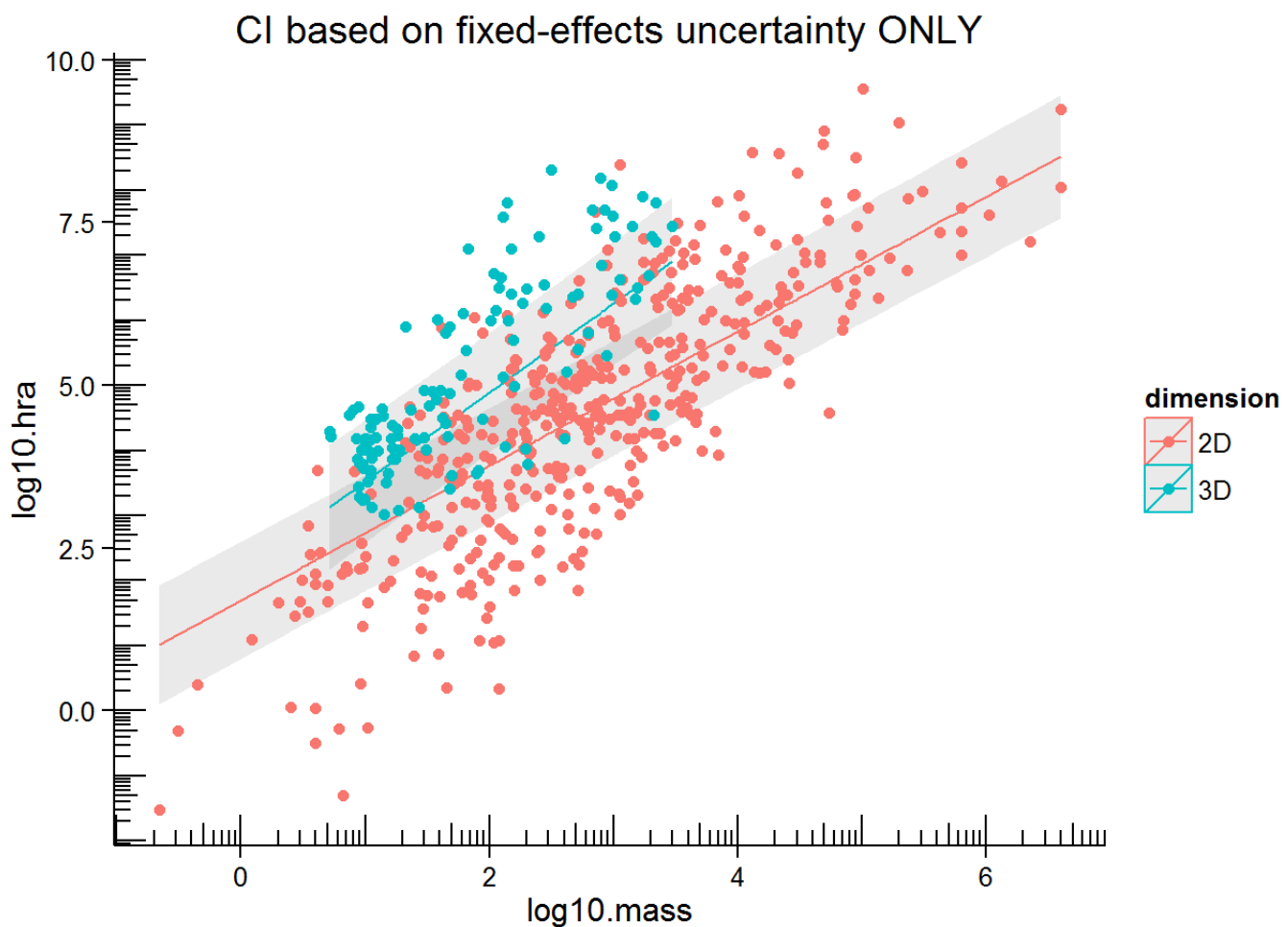
#Subset data for plotting
data.2D <- data[ which(data$dimension=='2D'),]
data.3D <- data[ which(data$dimension=='3D'),]

#fixef
g0 <- ggplot(newdat, aes(x=log10.mass, y=log10.hra, color = dimension))

g1 <- g0 + annotation_logticks(short = unit(2,"mm"), mid = unit(3,"mm"), long = unit(4,"mm")) + theme_
e_bw() + theme(panel.border = element_blank(), panel.grid.major = element_blank(),
panel.grid.minor = element_blank(), axis.line = element_line(colour = "black")) + geom_ribbon(aes(ymin
n = plo, ymax = phi, linetype = NA), alpha=0.1) + geom_line(aes(ymin = plo, ymax = phi)) + ggtitle("C
I based on fixed-effects uncertainty ONLY")

g1 + geom_point(data=data.2D, aes(x=log10.mass, y=log10.hra)) + geom_point(data=data.3D, aes(x=log1
0.mass, y=log10.hra))

```



```

#####PLOT BY TROPHIC GUILD
names(data)

```

## [1] "taxon"	"common.name"	"class"
## [4] "order"	"family"	"genus"
## [7] "species"	"primarymethod"	"N"
## [10] "mean.mass.g"	"log10.mass"	"alt.mass.reference"
## [13] "mean.hra.m2"	"log10.hra"	"hra.reference"
## [16] "realm"	"thermoregulation"	"locomotion"
## [19] "trophic.guild"	"dimension"	"preymass"
## [22] "log10.preymass"	"PPMR"	"prey.size.reference"

```
data.predict.tg <- data[, c(3, 8, 11, 19)]
alltaxa.tg.int = lmer(log10.hra ~ trophic.guild + log10.mass:trophic.guild + (1|class) + (1|primarymethod), data=data, REML = FALSE)

data.predict.tg$log10.hra <- predict(alltaxa.tg.int, newdata=data.predict.tg, re.form=NA)
newdat <- data.predict.tg

mm <- model.matrix(terms(alltaxa.tg.int),newdat)
## or newdat$distance <- mm %%% fixef(fm1)
pvar1 <- diag(mm %%% tcrossprod(vcov(alltaxa.tg.int),mm))
tvar1 <- pvar1 + VarCorr(alltaxa.tg.int)$class[1] + VarCorr(alltaxa.tg.int)$primarymethod[1] ## must be adapted for more complex models
tvar1 <-
  newdat <- data.frame(
    newdat
    , plo = newdat$log10.hra-2*sqrt(pvar1)
    , phi = newdat$log10.hra+2*sqrt(pvar1)
    , tlo = newdat$log10.hra-2*sqrt(tvar1)
    , thi = newdat$log10.hra+2*sqrt(tvar1)
  )
str(newdat)
```

```
## 'data.frame': 569 obs. of 9 variables:
## $ class : Factor w/ 4 levels "actinopterygii",...: 1 1 1 1 1 1 1 1 1 1 ...
## $ primarymethod: Factor w/ 7 levels "\\","direct observation",...: 5 3 3 3 3 5 5 5 2 5 ...
## $ log10.mass : num 2.948 2.75 1.531 0.602 0.602 ...
## $ trophic.guild: Factor w/ 2 levels "carnivore","herbivore": 1 1 1 1 1 1 1 1 2 2 ...
## $ log10.hra : num 5.4 5.16 3.68 2.54 2.54 ...
## $ plo : num 4.4 4.16 2.67 1.53 1.53 ...
## $ phi : num 6.41 6.16 4.68 3.56 3.56 ...
## $ tlo : num 3.134 2.893 1.409 0.273 0.273 ...
## $ thi : num 7.67 7.43 5.94 4.82 4.82 ...
```

```

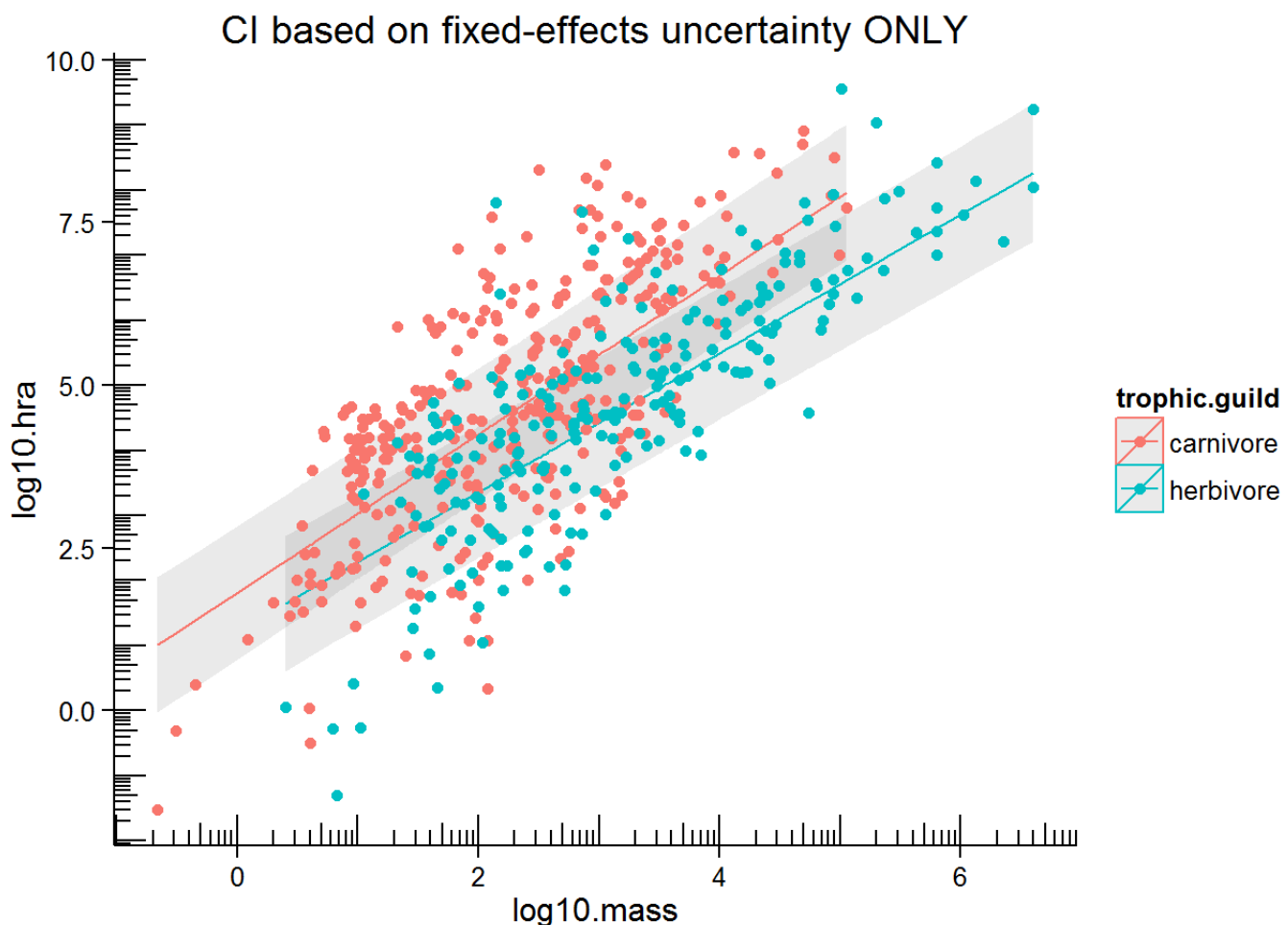
#Subset data for plotting
data.carnivore <-data[ which(data$trophic.guild=='carnivore'),]
data.herbivore <-data[ which(data$trophic.guild=='herbivore'),]

#fixef
g0 <- ggplot(newdat, aes(x=log10.mass, y=log10.hra, color = trophic.guild))

g1 <- g0 + annotation_logticks(short = unit(2,"mm"), mid = unit(3,"mm"), long = unit(4,"mm")) + them
e_bw() + theme(panel.border = element_blank(), panel.grid.major = element_blank(),
panel.grid.minor = element_blank(), axis.line = element_line(colour = "black")) + geom_ribbon(aes(ymin
n = plo, ymax = phi, linetype = NA), alpha=0.1) + geom_line(aes(ymin = plo, ymax = phi)) + ggtitle("C
I based on fixed-effects uncertainty ONLY")

g1 + geom_point(data=data.carnivore, aes(x=log10.mass, y=log10.hra)) + geom_point(data=data.herbivor
e, aes(x=log10.mass, y=log10.hra))

```



Creating the online Figure A2.

```

### Make predictions using the full model against a mock dataset.
data.FM <-read.csv("C:/Research/Home Range Scaling/Tamburelloetal_FigA2_MassPredictionDataAllModels.c
sv", header=T, sep=",")
str(data.FM)

```



```
## 'data.frame':   66 obs. of  8 variables:
## $ group      : int  1 1 1 1 1 1 1 1 2 2 ...
## $ mass       : int  2 5 10 50 100 501 1000 1667 1 5 ...
## $ log10.mass : num  0 0.7 1 1.7 2 2.7 3 3.7 0 0.7 ...
## $ locomotion : Factor w/ 4 levels "crawling","flying",...: 3 3 3 3 3 3 3 3 3 3 ...
## $ dimension  : Factor w/ 2 levels "2D","3D": 1 1 1 1 1 1 1 1 1 1 ...
## $ trophic.guild: Factor w/ 2 levels "carnivore","herbivore": 2 2 2 2 2 2 2 2 1 1 ...
## $ class      : Factor w/ 4 levels "actinopterygii",...: 1 1 1 1 1 1 1 1 1 1 ...
## $ primarymethod: Factor w/ 1 level "telemetry": 1 1 1 1 1 1 1 1 1 1 ...
```

```
trophic.guild1 = relevel(data.FM$trophic.guild, "herbivore")
locomotion1 = relevel(data.FM$locomotion, "swimming")
dimension1 = relevel(data.FM$dimension, "2D")
data.FM$log10.hra
```

```
## NULL
```

```
#### Feed groups into full HRA model
```

```
alltaxa.full = lmer(log10.hra ~ log10.mass + log10.mass:dimension + log10.mass:trophic.guild + trophic.guild + locomotion + dimension + (1|class) + (1|primarymethod), data=data, REML = FALSE)
summary(alltaxa.full)
```

```
## Linear mixed model fit by maximum likelihood t-tests use Satterthwaite
## approximations to degrees of freedom [merModLmerTest]
## Formula:
## log10.hra ~ log10.mass + log10.mass:dimension + log10.mass:trophic.guild +
## trophic.guild + locomotion + dimension + (1 | class) + (1 |
## primarymethod)
## Data: data
##
##      AIC      BIC   logLik deviance df.resid
## 1409.8   1461.9   -692.9   1385.8     556
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.5891 -0.6773  0.0148  0.6959  3.5011
##
## Random effects:
## Groups      Name      Variance Std.Dev.
## primarymethod (Intercept) 0.2229   0.4721
## class        (Intercept) 0.1836   0.4285
## Residual                0.6419   0.8012
## Number of obs: 568, groups: primarymethod, 7; class, 4
##
```

```
## Fixed effects:
##
##              Estimate Std. Error      df t value
## (Intercept)      2.17682    0.37942  12.00000    5.737
## log10.mass        1.17466    0.05611  566.10000   20.936
## trophic.guildherbivore -0.55681    0.20666  564.40000   -2.694
## locomotionflying      0.60208    0.38802  524.10000    1.552
## locomotionswimming   -1.50249    0.53123    4.00000   -2.828
## locomotionwalking    -0.19287    0.19198  533.30000   -1.005
## dimension3D         -0.37350    0.37838  564.90000   -0.987
## log10.mass:dimension3D  0.30891    0.11285  565.30000    2.737
## log10.mass:trophic.guildherbivore -0.11208    0.06715  564.30000   -1.669
##
##              Pr(>|t|)
## (Intercept)      9.35e-05 ***
## log10.mass        < 2e-16 ***
## trophic.guildherbivore 0.00726 **
## locomotionflying      0.12134
## locomotionswimming    0.04802 *
## locomotionwalking      0.31552
## dimension3D          0.32402
## log10.mass:dimension3D 0.00639 **
## log10.mass:trophic.guildherbivore 0.09564 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) lg10.m trphc. lcmtnf lcmtns lcmtnw dmns3D l10.:3
## log10.mass   -0.275
## trphc.gldhr  -0.176  0.658
## lcmtnflyng   -0.223 -0.079 -0.045
## lcmtnswmmng  -0.441 -0.005 -0.034  0.188
## lcmtnwlkng   -0.326 -0.167 -0.234  0.463  0.282
## dimension3D  -0.096  0.334  0.235 -0.624 -0.017 -0.074
## lg10.mss:3D   0.146 -0.483 -0.339  0.174 -0.015  0.090 -0.708
## lg10.mss:t.   0.205 -0.764 -0.909  0.058  0.020  0.134 -0.258  0.378
```

```
r.squaredGLMM(alltaxa.full)
```

```
##          R2m          R2c
## 0.6798043 0.8039489
```

```
#PREDICTIONS for HRA for all combo groups
data.FM$log10.hra <- predict(alltaxa.full, newdata=data.FM)
data.FM$group <- as.factor(data.FM$group)
newdat<- data.FM
str(data.FM)
```

```
## 'data.frame':    66 obs. of  9 variables:
## $ group          : Factor w/ 9 levels "1","2","3","4",...: 1 1 1 1 1 1 1 1 2 2 ...
## $ mass           : int  2 5 10 50 100 501 1000 1667 1 5 ...
## $ log10.mass     : num  0 0.7 1 1.7 2 2.7 3 3.7 0 0.7 ...
## $ locomotion     : Factor w/ 4 levels "crawling","flying",...: 3 3 3 3 3 3 3 3 3 3 ...
## $ dimension      : Factor w/ 2 levels "2D","3D": 1 1 1 1 1 1 1 1 1 1 ...
## $ trophic.guild: Factor w/ 2 levels "carnivore","herbivore": 2 2 2 2 2 2 2 2 1 1 ...
## $ class          : Factor w/ 4 levels "actinopterygii",...: 1 1 1 1 1 1 1 1 1 1 ...
## $ primarymethod: Factor w/ 1 level "telemetry": 1 1 1 1 1 1 1 1 1 1 ...
## $ log10.hra      : num  0.624 1.368 1.687 2.431 2.749 ...
```

##### *Plotting with Confidence intervals from [glmm.wikidot.com/faq](http://glmm.wikidot.com/faq)*

```
mm <- model.matrix(terms(alltaxa.full),newdat)
pvar1 <- diag(mm %*% tcrossprod(vcov(alltaxa.full),mm))
tvar1 <- pvar1 + VarCorr(alltaxa.full)$class[1]+ VarCorr(alltaxa.full)$primarymethod[1] ## must be adapted for more complex models
tvar1 <-
  newdat <- data.frame(
    newdat
    , plo = newdat$log10.hra-2*sqrt(pvar1)
    , phi = newdat$log10.hra+2*sqrt(pvar1)
    , tlo = newdat$log10.hra-2*sqrt(tvar1)
    , thi = newdat$log10.hra+2*sqrt(tvar1)
  )
str(newdat)
```

```
## 'data.frame':    66 obs. of  13 variables:
## $ group          : Factor w/ 9 levels "1","2","3","4",...: 1 1 1 1 1 1 1 1 2 2 ...
## $ mass           : int  2 5 10 50 100 501 1000 1667 1 5 ...
## $ log10.mass     : num  0 0.7 1 1.7 2 2.7 3 3.7 0 0.7 ...
## $ locomotion     : Factor w/ 4 levels "crawling","flying",...: 3 3 3 3 3 3 3 3 3 3 ...
## $ dimension      : Factor w/ 2 levels "2D","3D": 1 1 1 1 1 1 1 1 1 1 ...
## $ trophic.guild: Factor w/ 2 levels "carnivore","herbivore": 2 2 2 2 2 2 2 2 1 1 ...
## $ class          : Factor w/ 4 levels "actinopterygii",...: 1 1 1 1 1 1 1 1 1 1 ...
## $ primarymethod: Factor w/ 1 level "telemetry": 1 1 1 1 1 1 1 1 1 1 ...
## $ log10.hra      : num  0.624 1.368 1.687 2.431 2.749 ...
## $ plo           : num  -0.388 0.368 0.691 1.442 1.762 ...
## $ phi           : num  1.64 2.37 2.68 3.42 3.74 ...
## $ tlo           : num  -1.004 -0.2526 0.0687 0.8169 1.1368 ...
## $ thi           : num  2.25 2.99 3.3 4.04 4.36 ...
```

```
#plot confidence
```

```
#subset newdat by taxa
```

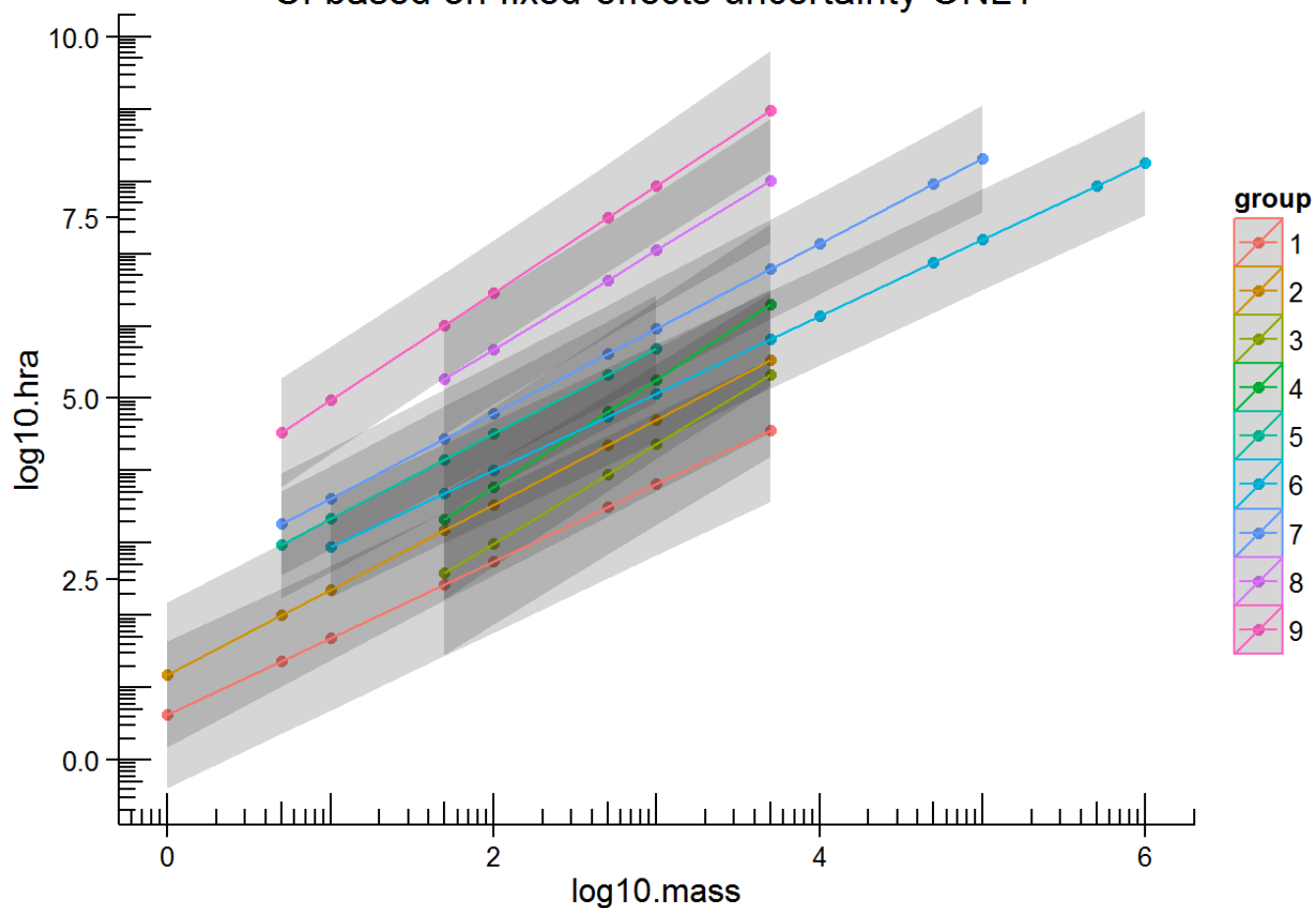
```
newdat.fish <- newdat[ which(newdat$class=='actinopterygii'),]  
newdat.mammals <- newdat[ which(newdat$class=='mammalia'),]  
newdat.reptiles <- newdat[ which(newdat$class=='reptilia'),]  
newdat.birds <-newdat[ which(newdat$class=='aves'),]
```

```
grp1 <-data.FM[ which(data.FM$group=='1'),]  
grp2 <-data.FM[ which(data.FM$group=='2'),]  
grp3 <-data.FM[ which(data.FM$group=='3'),]  
grp4 <-data.FM[ which(data.FM$group=='4'),]  
grp5 <-data.FM[ which(data.FM$group=='5'),]  
grp6 <-data.FM[ which(data.FM$group=='6'),]  
grp7 <-data.FM[ which(data.FM$group=='7'),]  
grp8 <-data.FM[ which(data.FM$group=='8'),]  
grp9 <-data.FM[ which(data.FM$group=='9'),]
```

```
#### Plot with 95% CI for ALL GROUPS
```

```
g0 <- ggplot(newdat, aes(x=log10.mass, y=log10.hra, color=group))  
g0 + annotation_logticks(short = unit(2,"mm"), mid = unit(3,"mm"), long = unit(4,"mm")) + theme_bw()  
+ theme(panel.border = element_blank(), panel.grid.major = element_blank(),  
panel.grid.minor = element_blank(), axis.line = element_line(colour = "black")) + geom_point() + geom_ribbon(aes(ymin = plo, ymax = phi, linetype = NA), alpha=0.2) + geom_line(aes(ymin = plo, ymax = phi)) + ggtitle("CI based on fixed-effects uncertainty ONLY")
```

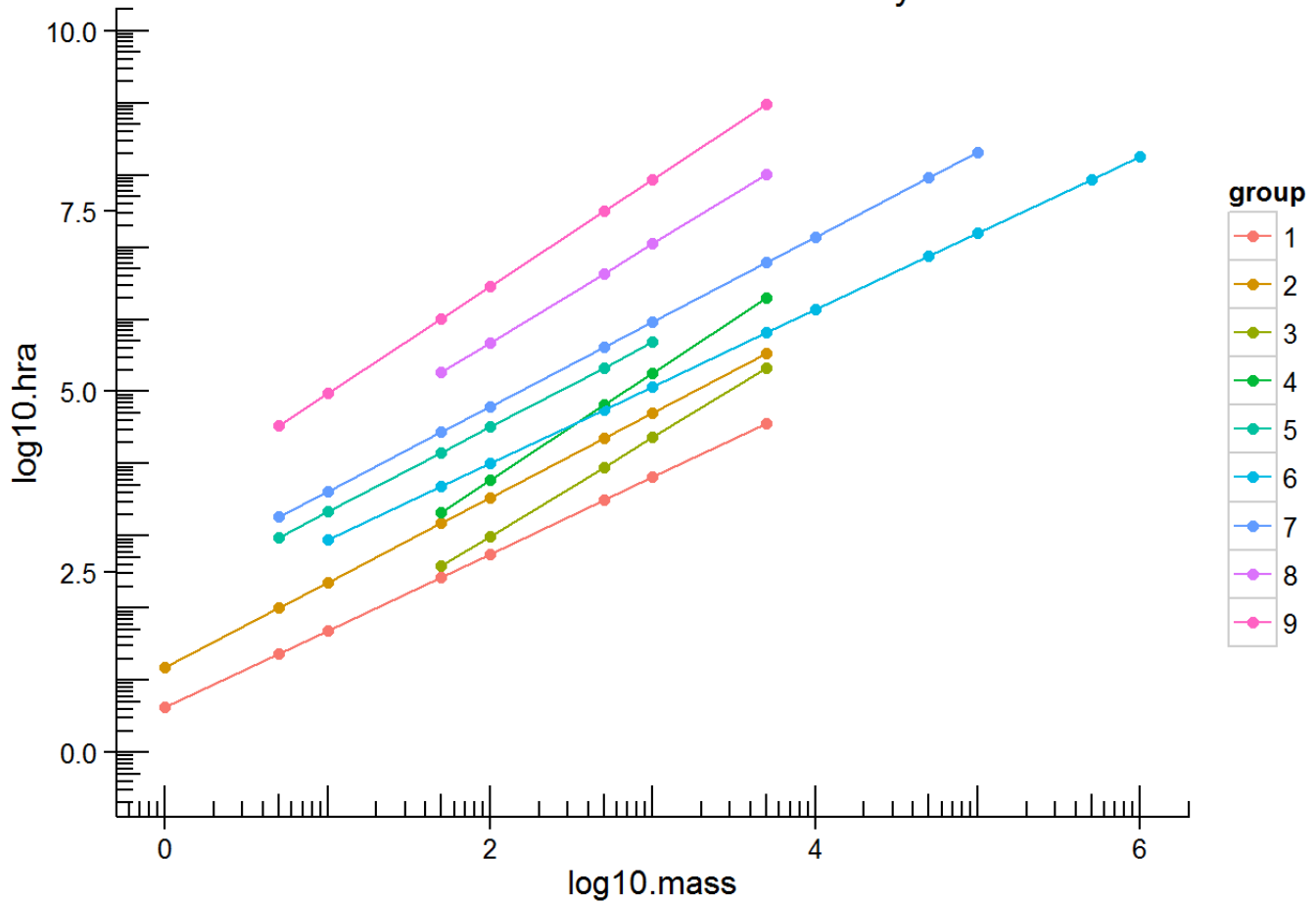
# CI based on fixed-effects uncertainty ONLY



#No 95% CI ribbon

```
g0 <- ggplot(newdat, aes(x=log10.mass, y=log10.hra, color=group))
g0 + annotation_logticks(short = unit(2,"mm"), mid = unit(3,"mm"), long = unit(4,"mm")) + theme_bw()
+ theme(panel.border = element_blank(), panel.grid.major = element_blank(),
panel.grid.minor = element_blank(), axis.line = element_line(colour = "black")) + geom_point() + geo
m_line(aes(ymin = plo, ymax = phi)) + ggtitle("CI based on fixed-effects uncertainty ONLY")
```

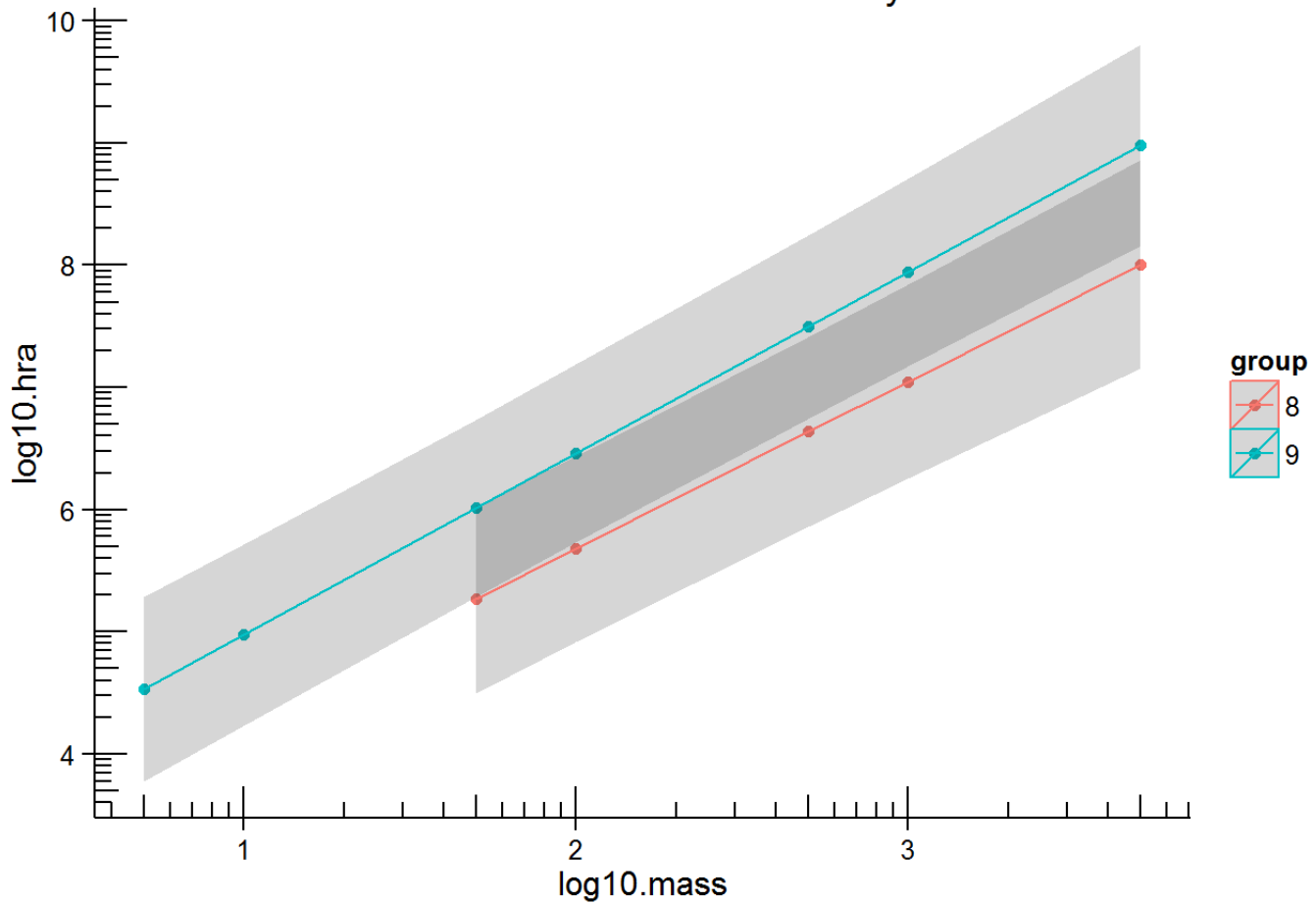
# CI based on fixed-effects uncertainty ONLY



#####JUST BIRDS

```
g0 <- ggplot(newdat.birds, aes(x=log10.mass, y=log10.hra, color=group))
g0 + annotation_logticks(short = unit(2,"mm"), mid = unit(3,"mm"), long = unit(4,"mm")) + theme_bw()
+ theme(panel.border = element_blank(), panel.grid.major = element_blank(),
panel.grid.minor = element_blank(), axis.line = element_line(colour = "black")) + geom_point() + geom_
m_ribbon(aes(ymin = plo, ymax = phi, linetype = NA), alpha=0.2) + geom_line(aes(ymin = plo, ymax = phi)) + ggtitle("CI based on fixed-effects uncertainty ONLY")
```

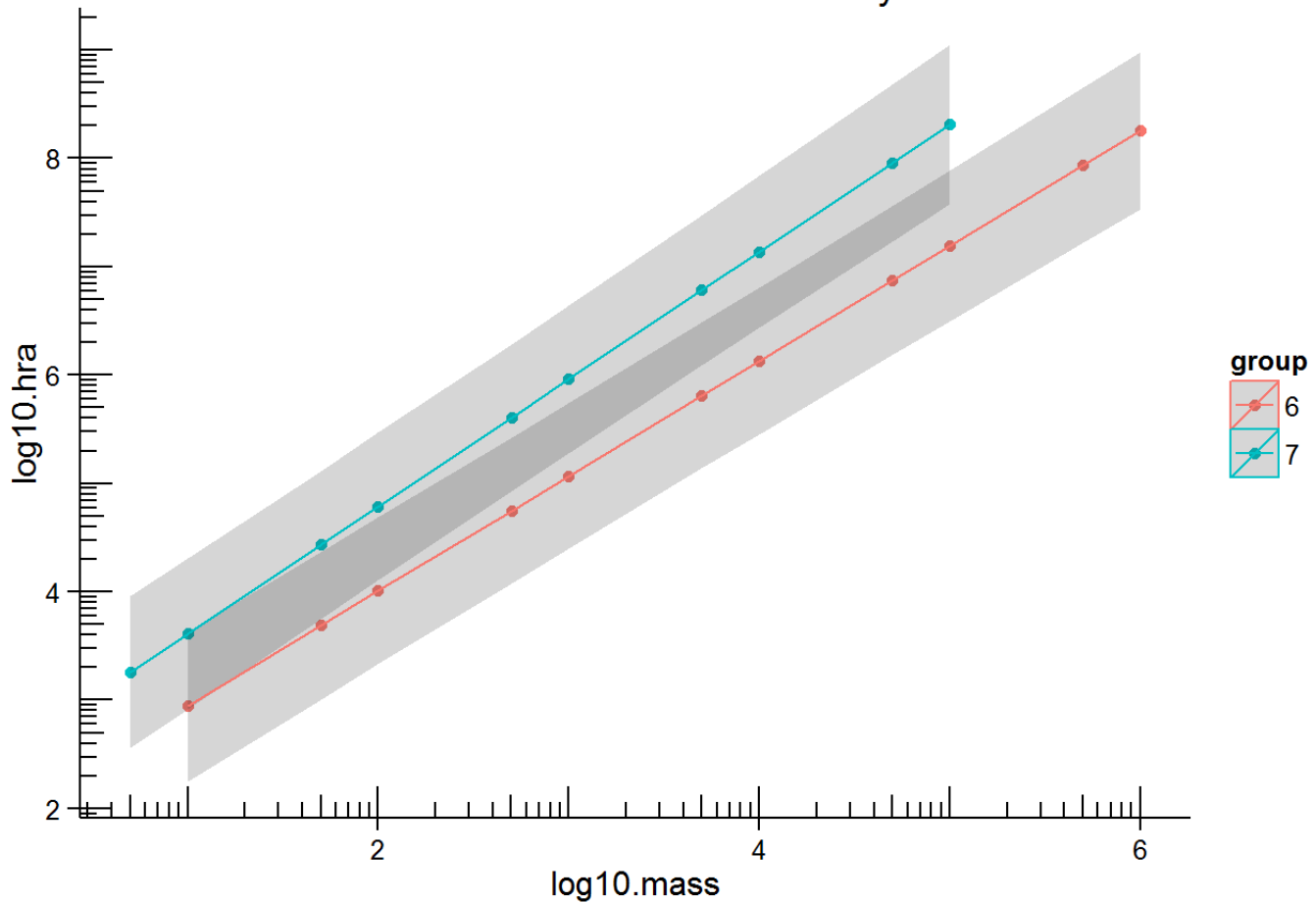
## CI based on fixed-effects uncertainty ONLY



#####JUST MAMMALS

```
g0 <- ggplot(newdat.mammals, aes(x=log10.mass, y=log10.hra, color=group))
g0 + annotation_logticks(short = unit(2,"mm"), mid = unit(3,"mm"), long = unit(4,"mm")) + theme_bw()
+ theme(panel.border = element_blank(), panel.grid.major = element_blank(),
panel.grid.minor = element_blank(), axis.line = element_line(colour = "black")) + geom_point() + geom_
m_ribbon(aes(ymin = plo, ymax = phi, linetype = NA), alpha=0.2) + geom_line(aes(ymin = plo, ymax = phi)) + ggtitle("CI based on fixed-effects uncertainty ONLY")
```

# CI based on fixed-effects uncertainty ONLY

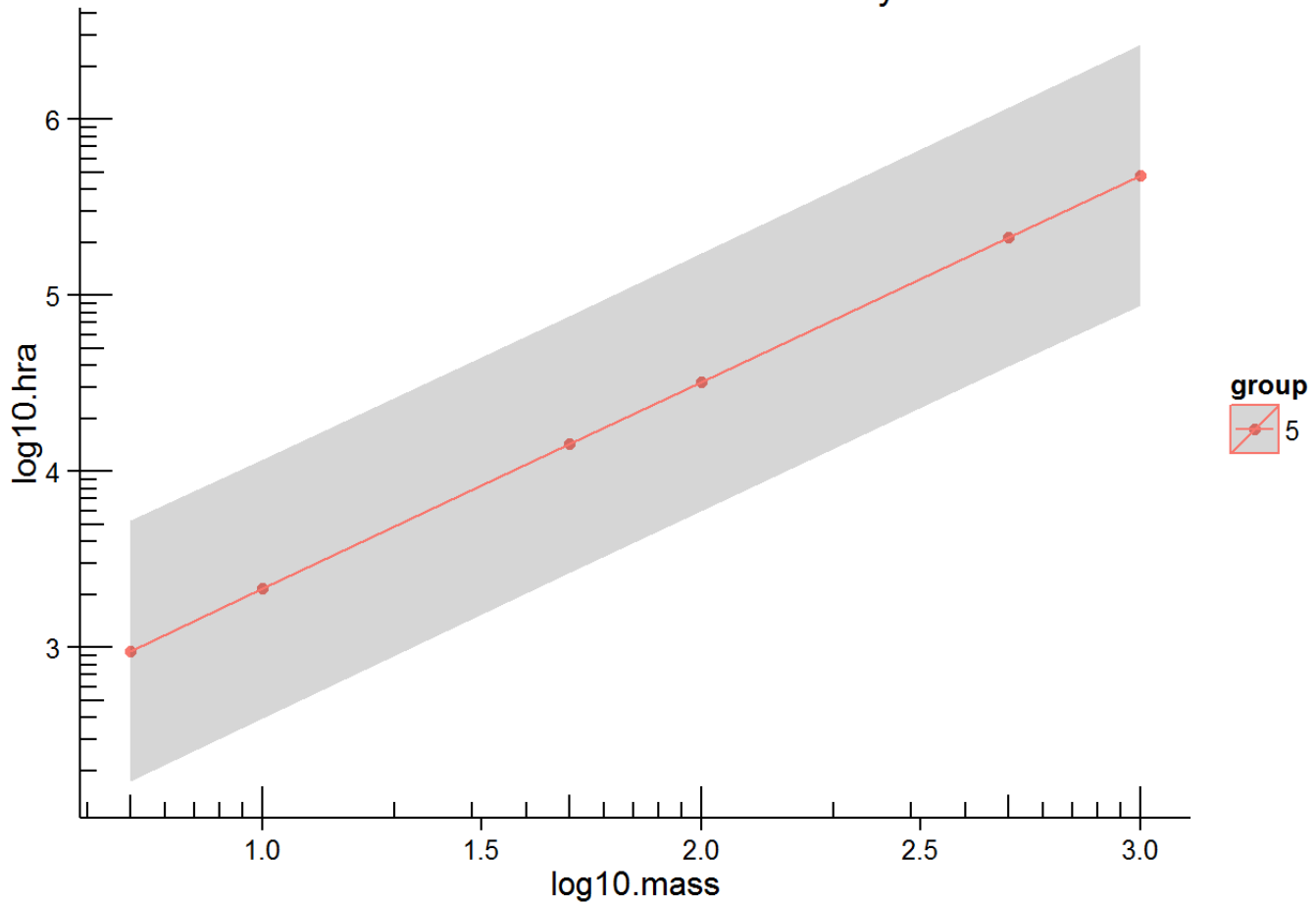


#####JUST REPTILES

```
g0 <- ggplot(newdat.reptiles, aes(x=log10.mass, y=log10.hra, color=group))
g0 + annotation_logticks(short = unit(2,"mm"), mid = unit(3,"mm"), long = unit(4,"mm")) + theme_bw()
+ theme(panel.border = element_blank(), panel.grid.major = element_blank(),
panel.grid.minor = element_blank(), axis.line = element_line(colour = "black")) + geom_point() + geo
m_ribbon(aes(ymin = plo, ymax = phi, linetype = NA), alpha=0.2) + geom_line(aes(ymin = plo, ymax = ph
i)) + ggtitle("CI based on fixed-effects uncertainty ONLY")
```



## CI based on fixed-effects uncertainty ONLY



#####JUST FISH

```
g0 <- ggplot(newdat.fish, aes(x=log10.mass, y=log10.hra, color=group))
g0 + annotation_logticks(short = unit(2,"mm"), mid = unit(3,"mm"), long = unit(4,"mm")) + theme_bw()
+ theme(panel.border = element_blank(), panel.grid.major = element_blank(),
panel.grid.minor = element_blank(), axis.line = element_line(colour = "black")) + geom_point() + geom_
m_ribbon(aes(ymin = plo, ymax = phi, linetype = NA), alpha=0.2) + geom_line(aes(ymin = plo, ymax = phi)) + ggtitle("CI based on fixed-effects uncertainty ONLY")
```

CI based on fixed-effects uncertainty ONLY

