Electronic Supplementary Material 1 (ESM1)

Models with species averages

Glucose model

```
 Iterations = 10001:5999901
 Thinning interval  = 100
 Sample size  = 59900

 DIC: -106.6529

 G-structure:  ~animal

       post.mean l-95% CI u-95% CI eff.samp
animal   0.03626 0.000596   0.1426    25802

              ~Method_Glu

           post.mean l-95% CI u-95% CI eff.samp
Method_Glu    0.8756 0.000616   0.9388    59900

 R-structure:  ~units

      post.mean  l-95% CI u-95% CI eff.samp
units   0.02191 0.0006759  0.07767    48120

 Location effects: logGlucose ~ Diet + Centered_logBM + Procedence

                           post.mean l-95% CI u-95% CI eff.samp  pMCMC
(Intercept)                  2.37100  0.82502  3.98545    59071 0.0103
*
DietTerrestrial_carnivore    0.02034 -1.05933  1.14510    59900 0.9732
DietAquatic_predator         0.01828 -1.37382  1.41625    59149 0.9776
DietHerbivore               -0.02100 -1.17104  1.13783    59900 0.9680
DietFrugivore_granivore     -0.04185 -1.39315  1.24717    59001 0.9539
Centered_logBM              -0.11365 -0.84646  0.64960    59130 0.7698
ProcedenceCaptive            0.03627 -1.29070  1.40114    59900 0.9589
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Glucose model with life history traits

```
Iterations = 10001:5999901
 Thinning interval  = 100
 Sample size  = 59900

 DIC: -74.58572

 G-structure:  ~animal

       post.mean  l-95% CI u-95% CI eff.samp
animal   0.05226 0.0006624   0.2157    29869

              ~Method_Glu

           post.mean  l-95% CI u-95% CI eff.samp
Method_Glu     1.268 0.0006281    1.323    59900

 R-structure:  ~units

      post.mean  l-95% CI u-95% CI eff.samp
units   0.02908 0.0007187   0.1087    51386
```

```
 Location effects: logGlucose ~ Diet + Centered_logBM + poly(ML, 2, ra
w = TRUE) + CM + DT + Procedence

                            post.mean l-95% CI u-95% CI eff.samp pMCMC
(Intercept)                  2.334820  0.399411 4.337178 59900 0.0257 *
DietTerrestrial_carnivore  -0.004026 -1.528592 1.541982 59900 0.9949
DietAquatic_predator       -0.010700 -1.596257 1.640390 60642 0.9921
DietHerbivore              -0.036708 -1.761151 1.630230 58817 0.9657
DietFrugivore_granivore    -0.030716 -7.794374 7.477946 59900 0.9931
Centered_logBM             -0.078237 -1.000564 0.890303 56515 0.8719
poly(ML, 2, raw = TRUE)1    0.176471 -3.238775 3.599515 60759 0.9254
poly(ML, 2, raw = TRUE)2  -0.393328 -14.806955 14.379736 59900 0.9541
CM                         -0.168559 -3.204873 2.815380 59967 0.9111
DT                         -0.040236 -4.049867 4.067674 59900 0.9832
ProcedenceCaptive           0.031314 -1.430862 1.537092 59900 0.9665
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Glycation model

```
Iterations = 10001:5999901
 Thinning interval  = 100
 Sample size  = 59900

 DIC: -106.7

 G-structure:  ~animal

       post.mean  l-95% CI u-95% CI eff.samp
animal   0.03487 0.0007631   0.1392    25819

               ~Method_Glu

            post.mean  l-95% CI u-95% CI eff.samp
Method_Glu    0.3444 0.0005727   0.3467    59900

 R-structure:  ~units

      post.mean  l-95% CI u-95% CI eff.samp
units   0.02111 0.0007395  0.07448    49146

 Location effects: logGlycation ~ Diet + Centered_logBM + Centered_log
Glucose

                           post.mean  l-95% CI  u-95% CI eff.samp pMCMC
(Intercept)                 1.255901  0.344806  2.134884    59900 0.012
*
DietTerrestrial_carnivore  0.052502 -1.044091  1.185074    59900 0.925
DietAquatic_predator       0.018310 -1.290381  1.300686    59900 0.982
DietHerbivore             -0.053868 -1.405728  1.257560    58559 0.937
DietFrugivore_granivore   -0.018507 -1.102124  1.105271    59900 0.974
Centered_logBM             0.008006 -0.696443  0.699297    61227 0.979
Centered_logGlucose        0.339051 -4.654194  5.325153    59900 0.893
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Glycation model with life history traits

```
Iterations = 10001:5999901
 Thinning interval  = 100
 Sample size  = 59900

 DIC: -75.40128

 G-structure:  ~animal
```

```
       post.mean  l-95% CI u-95% CI eff.samp
animal   0.04792 0.0005362   0.1982    32101

               ~Method_Glu

           post.mean  l-95% CI u-95% CI eff.samp
Method_Glu    0.2793 0.0005303   0.4877    59900

 R-structure:  ~units

      post.mean  l-95% CI u-95% CI eff.samp
units   0.02719 0.0007491   0.1021    52282

 Location effects: logGlycation ~ Diet + Centered_logBM + Centered_log
Glucose + ML + CM + DT

                         post.mean l-95% CI  u-95% CI eff.samp pMCMC
(Intercept)               1.227159 -0.058905  2.496171  59900 0.0595 .
DietTerrestrial_carnivore 0.077119 -1.379997  1.520340  59900 0.9173
DietAquatic_predator      0.008690 -1.495711  1.518194  59900 0.9930
DietHerbivore            -0.052138 -1.807832  1.645961  61691 0.9542
DietFrugivore_granivore  -0.078247 -2.194939  1.920607  59900 0.9352
Centered_logBM            0.016661 -0.841361  0.858227  59900 0.9681
Centered_logGlucose       0.179413 -6.579065  6.883513  59900 0.9562
ML                        0.002993 -3.083707  3.134078  60638 0.9977
CM                       -0.093355 -2.629818  2.406782  59900 0.9330
DT                       -0.130439 -4.199502  3.852793  59900 0.9494
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Glycation model with life history traits without glucose

```
Iterations = 10001:5999901
 Thinning interval  = 100
 Sample size  = 59900

 DIC: -75.51184

 G-structure:  ~animal

       post.mean  l-95% CI u-95% CI eff.samp
animal     0.045 0.0007373   0.1844    31737

 R-structure:  ~units

      post.mean  l-95% CI u-95% CI eff.samp
units   0.02685 0.0006839   0.1004    50556

 Location effects: logGlycation ~ Diet + Centered_logBM + ML + CM + DT

                         post.mean l-95% CI  u-95% CI eff.samp pMCMC
(Intercept)               1.217639  0.054541  2.310440 60601 0.0346 *
DietTerrestrial_carnivore 0.083666 -1.321588  1.489212 59900 0.9051
DietAquatic_predator      0.004772 -1.469288  1.512990 61482 0.9914
DietHerbivore            -0.059856 -1.696896  1.572570 59900 0.9431
DietFrugivore_granivore  -0.074390 -2.035350  1.894847 59900 0.9432
Centered_logBM            0.007357 -0.732469  0.739157 59900 0.9796
ML                        0.026304 -2.905055  3.003113 59900 0.9877
CM                       -0.108279 -2.658967  2.356612 59900 0.9308
DT                       -0.132416 -4.002316  3.945679 59900 0.9465
```

Models with individuals

Glucose model

```
Iterations = 10001:5999901
 Thinning interval  = 100
 Sample size  = 59900 

 DIC: -992.896 

 G-structure:  ~animal

       post.mean l-95% CI u-95% CI eff.samp
animal  0.008021 0.002293  0.01494    59597

               ~species

        post.mean l-95% CI u-95% CI eff.samp
species  0.002995 0.001171 0.005079    59900

 R-structure:  ~units

      post.mean l-95% CI u-95% CI eff.samp
units  0.003922 0.003325 0.004533    59900

 Location effects: logGlucose ~ Diet + Centered_logBM + Procedence 

                       post.mean l-95% CI  u-95% CI eff.samp pMCMC    
(Intercept)               2.358384 2.252259 2.459482 60833 < 2e-05 ***
DietTerrestrial_carnivore 0.037311 -0.038582 0.111453 59900 0.32174    
DietAquatic_predator      0.042473 -0.041770 0.127272 59900 0.31720    
DietHerbivore             0.002547 -0.101022 0.101821 59900 0.96551    
DietFrugivore_granivore  -0.053312 -0.132924 0.024621 59900 0.17843    
Centered_logBM          -0.066964 -0.105964 -0.028517 59148 0.00134 ** 
ProcedenceCaptive         0.057926 -0.007559 0.124586 59900 0.08344 .  
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Glucose model with life history traits

```
Iterations = 10001:5999901
 Thinning interval  = 100
 Sample size  = 59900 

 DIC: -822.3621 

 G-structure:  ~animal

       post.mean l-95% CI u-95% CI eff.samp
animal  0.008097 0.001737  0.01628    59900

               ~species

        post.mean l-95% CI u-95% CI eff.samp
species  0.003087 0.001147 0.005393    59900

 R-structure:  ~units

      post.mean l-95% CI u-95% CI eff.samp
units  0.004091 0.003425   0.0048    59900

 Location effects: logGlucose ~ Diet + Centered_logBM + poly(ML, 2, ra
w = TRUE) + CM + DT + Procedence 

                        post.mean l-95% CI u-95% CI eff.samp pMCMC
```

```
(Intercept)                2.38663  2.26809  2.50047  59900 < 2e-05 ***
DietTerrestrial_carnivore 0.02035 -0.05557  0.09867  59900 0.59205
DietAquatic_predator      0.03412 -0.04719  0.11187  59900 0.39309
DietHerbivore            -0.05276 -0.17692  0.07030  59900 0.39309
DietFrugivore_granivore  -0.05527 -0.23923  0.13503  59900 0.55790
Centered_logBM           -0.06103 -0.10638 -0.01516  59900 0.00908 **
poly(ML, 2, raw = TRUE)1  0.10739 -0.03536  0.25323  59900 0.14227
poly(ML, 2, raw = TRUE)2 -0.61582 -1.16638 -0.09541  59900 0.02611 *
CM                       -0.09497 -0.26479  0.06912  59900 0.25823
DT                        0.01082 -0.18470  0.21196  59900 0.91606
ProcedenceCaptive         0.03443 -0.03902  0.10580  59900 0.34648
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Glycation model

```
Iterations = 10001:5999901
 Thinning interval  = 100
 Sample size  = 59900 

 DIC: -933.1616 

 G-structure:  ~animal

       post.mean l-95% CI u-95% CI eff.samp
animal  0.007986 0.001979  0.01522    59900

               ~species

        post.mean l-95% CI u-95% CI eff.samp
species  0.004466  0.00202 0.007134    59900

 R-structure:  ~units

      post.mean l-95% CI u-95% CI eff.samp
units  0.004241   0.0036 0.004937    59900

 Location effects: logGlycation ~ Diet + Centered_logBM + Centered_log
Glucose 

                         post.mean  l-95% CI  u-95% CI eff.samp pMCMC    
(Intercept)               1.255213 1.161645 1.356336 59900 < 2e-05 ***
DietTerrestrial_carnivore 0.079586  0.000112 0.158918 59900 0.04938 *  
DietAquatic_predator      0.021792 -0.064410 0.111384 59900 0.62651    
DietHerbivore             0.005237 -0.104032 0.113390 59900 0.92511    
DietFrugivore_granivore  -0.010220 -0.090716 0.066216 59900 0.79736    
Centered_logBM            0.003794 -0.035404 0.041457 59900 0.84197    
Centered_logGlucose       0.150789  0.042859 0.258714 59900 0.00621 ** 
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Glycation model with life history traits

```
Iterations = 10001:5999901
 Thinning interval  = 100
 Sample size  = 59900 

 DIC: -757.4936 

 G-structure:  ~animal

       post.mean l-95% CI u-95% CI eff.samp
animal  0.009425 0.001817  0.01963    59900

               ~species

        post.mean l-95% CI u-95% CI eff.samp
```

```
species  0.005169 0.002237 0.008639    59900

 R-structure:  ~units

      post.mean l-95% CI u-95% CI eff.samp
units  0.004572 0.003795  0.00536    59900

 Location effects: logGlycation ~ Diet + Centered_logBM + Centered_log
Glucose + ML + CM + DT

                         post.mean l-95% CI u-95% CI eff.samp pMCMC    
(Intercept)               1.231839  1.111789 1.351048 59900 <2e-05 ***
DietTerrestrial_carnivore 0.100920  0.017273 0.187125 59900 0.0214 *  
DietAquatic_predator      0.026869 -0.062448 0.117517 59900 0.5491    
DietHerbivore            -0.018824 -0.160894 0.119239 59936 0.7812    
DietFrugivore_granivore   0.095183 -0.097946 0.291806 59900 0.3288    
Centered_logBM            0.003664 -0.043033 0.050278 58765 0.8760    
Centered_logGlucose       0.137154  0.011637 0.255134 59900 0.0273 *  
ML                        0.036577 -0.121966 0.195499 59043 0.6482    
CM                        0.150587 -0.030387 0.346258 59900 0.1139    
DT                        0.039982 -0.187558 0.265946 59303 0.7248    
```

Glycation model with life history traits without glucose

```
Iterations = 10001:5999901
 Thinning interval  = 100
 Sample size  = 59900 

 DIC: -756.3145 

 G-structure:  ~animal

       post.mean l-95% CI u-95% CI eff.samp
animal    0.0105 0.001971  0.02166    59900

               ~species

        post.mean l-95% CI u-95% CI eff.samp
species  0.005329 0.002197 0.008948    59900

 R-structure:  ~units

      post.mean l-95% CI u-95% CI eff.samp
units    0.0046 0.003839  0.00541    59186

 Location effects: logGlycation ~ Diet + Centered_logBM + ML + CM + DT 

                         post.mean l-95% CI u-95% CI eff.samp pMCMC    
(Intercept)               1.227931  1.106099 1.357043 59900 <2e-05 ***
DietTerrestrial_carnivore 0.106991  0.018900 0.192773 60415 0.0162 *  
DietAquatic_predator      0.031684 -0.058239 0.127370 59900 0.4962    
DietHerbivore            -0.028291 -0.171719 0.118113 59900 0.6928    
DietFrugivore_granivore   0.098888 -0.100352 0.297249 59900 0.3198    
Centered_logBM           -0.003569 -0.051527 0.044211 59900 0.8783    
ML                        0.048297 -0.113219 0.208916 58878 0.5488    
CM                        0.153343 -0.038424 0.347077 60758 0.1137    
DT                        0.042588 -0.190902 0.276599 59900 0.7191    
```

Age & Sex models

Glucose

```
 Iterations = 10001:5999901
 Thinning interval  = 100
 Sample size  = 59900 

 DIC: -635.2492 
```

```
 G-structure:  ~animal

       post.mean l-95% CI u-95% CI eff.samp
animal  0.008703 0.001214  0.01909    59900

               ~species

        post.mean  l-95% CI u-95% CI eff.samp
species  0.002923 0.0006328 0.005658    59900

 R-structure:  ~units

      post.mean l-95% CI u-95% CI eff.samp
units  0.003799 0.003072 0.004595    59900

 Location effects: logGlucose ~ Centered_logBM + poly(logit(Age_relati
ve, FALSE), 2, raw = TRUE) + Sex

                                                 post.mean  l-95% CI
u-95% CI
(Intercept)                                       2.391844  2.278127
2.506021
Centered_logBM                                   -0.052561 -0.097117
-0.006228
poly(logit(Age_relative, FALSE), 2, raw = TRUE)1  0.001298 -0.013674
0.016000
poly(logit(Age_relative, FALSE), 2, raw = TRUE)2 -0.001157 -0.004889
0.002654
SexM                                              0.005705 -0.012474
0.023691
                                                 eff.samp  pMCMC
(Intercept)                                         59186 <2e-05 ***
Centered_logBM                                      59101 0.0275 *
poly(logit(Age_relative, FALSE), 2, raw = TRUE)1    59900 0.8645
poly(logit(Age_relative, FALSE), 2, raw = TRUE)2    59900 0.5414
SexM                                                60869 0.5336
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Glycation

```
 Iterations = 10001:5999901
 Thinning interval  = 100
 Sample size  = 59900

 DIC: 1145.016

 G-structure:  ~animal

       post.mean l-95% CI u-95% CI eff.samp
animal      19.3    3.365    38.51    59900

               ~species

        post.mean l-95% CI u-95% CI eff.samp
species      5.82    1.536    10.92    59900

 R-structure:  ~units

      post.mean l-95% CI u-95% CI eff.samp
units     6.026    4.861    7.266    59742

 Location effects: Glycation ~ Centered_logBM + Centered_logGlucose +
poly(logit(Age_relative, FALSE), 2, raw = TRUE) + Sex

                                                 post.mean l-95% CI u-
95% CI eff.samp
```

```
(Intercept)                                        19.26559 14.02977 24
.55452    59900
Centered_logBM                                      1.12330 -0.88744  3
.12563    63546
Centered_logGlucose                                 9.74032  4.27174 15
.04954    59900
poly(logit(Age_relative, FALSE), 2, raw = TRUE)1  -0.07541 -0.66195  0
.53149    59900
poly(logit(Age_relative, FALSE), 2, raw = TRUE)2  -0.05413 -0.20650  0
.09595    60681
SexM                                                0.44836 -0.28507  1
.20100    59900
                                                    pMCMC
(Intercept)                                        < 2e-05 ***
Centered_logBM                                    0.269850
Centered_logGlucose                               0.000267 ***
poly(logit(Age_relative, FALSE), 2, raw = TRUE)1 0.806010
poly(logit(Age_relative, FALSE), 2, raw = TRUE)2 0.482771
SexM                                              0.233790
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Lysines model

```
Iterations = 10001:5999951
 Thinning interval  = 50
 Sample size  = 119800

 DIC: 111.8866

 G-structure:  ~animal

       post.mean l-95% CI u-95% CI eff.samp
animal     14.21   0.5989    45.07   111860

 R-structure:  ~units

      post.mean l-95% CI u-95% CI eff.samp
units     18.31    4.944    35.13   116731

 Location effects: Glycation ~ Lysines

            post.mean l-95% CI u-95% CI eff.samp pMCMC
(Intercept)   10.3914  -3.7127  24.9929   119800 0.144
Lysines        0.2462  -0.1438   0.6290   119800 0.196
```

Orders models

Glucose averages

```
 Iterations = 10001:5999901
 Thinning interval  = 100
 Sample size  = 59900

 DIC: -209.2166

 G-structure:  ~species

        post.mean  l-95% CI u-95% CI eff.samp
species  0.001705 0.0003464 0.003511    59900

              ~Method_Glu

            post.mean  l-95% CI u-95% CI eff.samp
Method_Glu  0.004672 0.0001915  0.01309    59900
```

```
 R-structure:  ~units

      post.mean l-95% CI u-95% CI eff.samp
units  0.003713 0.001608 0.005851    59900

 Location effects: logGlucose ~ order 

                         post.mean  l-95% CI  u-95% CI eff.samp pMCMC    
(Intercept)                2.442097  2.317939 2.562344 59900 <2e-05 ***
orderAnseriformes         -0.136101 -0.229771 -0.045736 59900 0.00367 ** 
orderApodiformes           0.104208 -0.063956  0.269026 59900 0.21910    
orderBucerotiformes        0.045225 -0.085697  0.177252 59900 0.49646    
orderCariamiformes         0.084108 -0.078716  0.255211 59900 0.31706    
orderCasuariiformes       -0.163069 -0.337731  0.011609 60636 0.06614 .  
orderCharadriiformes       0.005304 -0.095223  0.101372 59900 0.91780    
orderCiconiiformes        -0.039864 -0.150798  0.069105 59900 0.47349    
orderColumbiformes         0.062913 -0.047089  0.173563 59900 0.26331    
orderCoraciiformes         0.086470 -0.080365  0.253869 59900 0.30067    
orderGalliformes          -0.014638 -0.122414  0.088507 59900 0.78227    
orderGruiformes           -0.086754 -0.191388  0.019906 60809 0.10554    
orderMusophagiformes      -0.032880 -0.149817  0.083853 59900 0.57723    
orderPasseriformes         0.100976  0.004481  0.199953 59900 0.04374 *  
orderPelecaniformes       -0.078898 -0.182340  0.022862 59900 0.12725    
orderPhoenicopteriformes -0.196479 -0.328292 -0.059938 59900 0.00491 *
*  
orderProcellariiformes    -0.033725 -0.138918  0.071199 59900 0.52568    
orderPsittaciformes       -0.033701 -0.136006  0.070392 59900 0.51730    
orderRheiformes           -0.202339 -0.370220 -0.036105 59900 0.01930 *  
orderSphenisciformes      -0.131626 -0.249327 -0.012622 58358 0.02945 *  
orderStrigiformes          0.058533 -0.073821  0.193863 59900 0.38818    
orderSuliformes           -0.206606 -0.371552 -0.039227 60514 0.01603 *  
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Glycation averages

```
 Iterations = 10001:5999901
 Thinning interval  = 100
 Sample size  = 59900 

 DIC: 444.2672 

 G-structure:  ~species

        post.mean l-95% CI u-95% CI eff.samp
species     2.873   0.6036    5.908    59900

               ~Method_Glu

           post.mean l-95% CI u-95% CI eff.samp
Method_Glu     8.967   0.3913    25.25    59900

 R-structure:  ~units

      post.mean l-95% CI u-95% CI eff.samp
units     6.234    2.745    9.778    59900

 Location effects: Glycation ~ order 

                         post.mean l-95% CI u-95% CI eff.samp pMCMC    
(Intercept)                 23.8174  18.6864 29.0157 59085 0.000267 ***
orderAnseriformes           -9.0998 -12.8132 -5.3161 59900  < 2e-05 ***
orderApodiformes             1.6941  -5.1762  8.5942 59900 0.625309    
orderBucerotiformes         -3.8560  -9.1864  1.6821 59900 0.161536    
orderCariamiformes          -1.6412  -8.5153  5.1824 59900 0.638765    
orderCasuariiformes        -13.0636 -20.0693 -5.6892 59900 0.000401 ***
orderCharadriiformes        -3.4750  -7.4881  0.5848 59900 0.091386 .  
orderCiconiiformes          -2.3910  -6.9647  2.0819 60604 0.299299    
orderColumbiformes          -3.5363  -8.0847  1.0178 59900 0.127579    
```

```
orderCoraciiformes         0.7004  -5.8813  7.7817 59900 0.841002
orderGalliformes          -5.2965  -9.6262 -0.9362 59900 0.018030 *
orderGruiformes           -0.2166  -4.5451  4.1320 58975 0.917262
orderMusophagiformes      -1.3584  -6.2273  3.3938 58473 0.573823
orderPasseriformes        -4.5115  -8.4707 -0.4609 59900 0.028815 *
orderPelecaniformes       -4.9655  -9.1079 -0.7669 59900 0.020568 *
orderPhoenicopteriformes  -12.6524 -18.1743 -7.1537 59900  < 2e-05 ***
orderProcellariiformes    -3.5527  -7.7734  0.8770 59900 0.105275
orderPsittaciformes       -8.4290 -12.7042 -4.2682 59900 0.000134 ***
orderRheiformes            0.5901  -6.4606  7.2461 59900 0.868381
orderSphenisciformes      -6.4491 -11.4353 -1.7623 59900 0.009683 **
orderStrigiformes          1.7468  -3.7739  7.2189 59900 0.528013
orderSuliformes          -10.0020 -16.8119 -3.1082 59900 0.005376 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’
```

Glucose individuals

```
 Iterations = 10001:5999901
 Thinning interval  = 100
 Sample size  = 59900

 DIC: -989.3556

 G-structure:  ~species

        post.mean l-95% CI u-95% CI eff.samp
species   0.00332  0.00165 0.005173    59900

 R-structure:  ~units

      post.mean l-95% CI u-95% CI eff.samp
units  0.003992 0.003375 0.004628    59900

 Location effects: logGlucose ~ order

                         post.mean  l-95% CI  u-95% CI eff.samp pMCMC
(Intercept)                2.441807  2.363471 2.518260 59900 <2e-05 ***
orderAnseriformes        -0.134276 -0.218401 -0.046738 59900 0.003272 **
orderApodiformes           0.101579 -0.041054 0.236021 59600 0.144674
orderBucerotiformes        0.040000 -0.080951 0.157990 60680 0.507980
orderCariamiformes         0.080218 -0.066951 0.227669 59900 0.279399
orderCharadriiformes       0.009452 -0.083092 0.105417 59900 0.840534
orderCiconiiformes        -0.040935 -0.142712 0.060512 59900 0.416561
orderColumbiformes         0.065267 -0.066617 0.193642 59036 0.326811
orderCoraciiformes         0.082562 -0.078494 0.248061 61463 0.313222
orderGalliformes          -0.001747 -0.102287 0.099458 58770 0.978030
orderGruiformes           -0.089967 -0.189241 0.007686 59900 0.072287 .
orderMusophagiformes      -0.085619 -0.272281 0.096474 59900 0.365810
orderPasseriformes         0.086554 -0.003241 0.175723 59900 0.057763 .
orderPelecaniformes       -0.074397 -0.171168 0.018949 59900 0.121736
orderPhoenicopteriformes -0.291942 -0.439996 -0.144614 59900 0.000301
***
orderProcellariiformes    -0.039027 -0.134402 0.057526 60610 0.413523
orderPsittaciformes       -0.038279 -0.136047 0.057135 61190 0.431419
orderRheiformes          -0.206340 -0.349504 -0.061964 59900 0.006511 **
orderSphenisciformes      -0.136905 -0.243893 -0.031810 59900 0.012721 *
orderStrigiformes          0.034768 -0.119034 0.189827 59900 0.656528
orderSuliformes          -0.212732 -0.359269 -0.062097 61467 0.006344 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Glycation individuals

```
 Iterations = 10001:5999901
 Thinning interval  = 100
 Sample size  = 59900
```

```
 DIC: 2391.883 

 G-structure:  ~species

        post.mean l-95% CI u-95% CI eff.samp
species     8.851    5.417    12.71    59900

 R-structure:  ~units

      post.mean l-95% CI u-95% CI eff.samp
units     8.099    6.994    9.261    59900

 Location effects: Glycation ~ order 

                         post.mean l-95% CI u-95% CI eff.samp pMCMC
(Intercept)                23.3396  19.5523 27.2678 58787  < 2e-05 ***
orderAnseriformes          -9.4202 -13.6002 -5.1701 59146  < 2e-05 ***
orderApodiformes            1.5038  -5.4759  8.6581 59049 0.669516
orderBucerotiformes        -4.0335 -10.1095  1.8861 59082 0.185543
orderCariamiformes         -1.8113  -9.1594  5.6689 59900 0.629149
orderCasuariiformes       -11.9476 -20.6864 -2.7884 59900 0.009182 **
orderCharadriiformes       -2.4454  -7.0388  1.9826 59129 0.285576
orderCiconiiformes         -3.0298  -8.0497  2.0927 59187 0.237930
orderColumbiformes         -2.4171  -7.4663  2.7121 59900 0.347112
orderCoraciiformes          0.5462  -7.5072  8.6354 56042 0.894124
orderGalliformes           -5.4805 -10.3152 -0.5489 59900 0.029649 *
orderGruiformes            -0.8043  -5.8130  3.9945 61375 0.745643
orderMusophagiformes       -1.3513  -6.6584  3.7670 59900 0.604875
orderPasseriformes         -5.2095  -9.6273 -0.7066 58879 0.023306 *
orderPelecaniformes        -5.7022 -10.3614 -1.0444 58508 0.017596 *
orderPhoenicopteriformes  -12.8877 -18.7001 -7.0605 59900 6.68e-05 ***
orderProcellariiformes     -1.9987  -6.7284  2.7765 59146 0.406912
orderPsittaciformes        -8.4219 -12.9810 -3.6229 58856 0.000835 ***
orderRheiformes             0.4280  -6.8066  7.5473 59900 0.908414
orderSphenisciformes       -6.6127 -11.8293 -1.2290 59900 0.015559 *
orderStrigiformes           1.9480  -4.2668  8.1967 59900 0.533623
orderSuliformes           -10.1649 -17.7348 -2.8516 56705 0.007546 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

VIF models

Glucose averages

```
                   GVIF Df GVIF^(1/(2*Df))
Diet           1.713187  4        1.069610
Centered_logBM 1.494981  1        1.222694
Procedence     1.728314  1        1.314654
```

Glucose averages life history

```
                            GVIF Df GVIF^(1/(2*Df))
Diet                    3.923876  4        1.186354
Centered_logBM          1.991121  1        1.411071
poly(ML, 2, raw = TRUE) 1.822946  2        1.161966
CM                      2.657595  1        1.630213
DT                      1.392595  1        1.180083
Procedence              1.924601  1        1.387300
```

Glycation averages

```
                        GVIF Df GVIF^(1/(2*Df))
Diet                1.295990  4        1.032940
Centered_logBM      1.641464  1        1.281196
Centered_logGlucose 1.620827  1        1.273117
```

Glycation averages life-history

```
                        GVIF Df GVIF^(1/(2*Df))
Diet                3.151870  4        1.154306
Centered_logBM      1.971214  1        1.403999
Centered_logGlucose 2.188302  1        1.479291
ML                  1.380756  1        1.175056
CM                  2.098269  1        1.448540
DT                  1.295233  1        1.138083
```

Glycation averages life-history without glucose

```
                   GVIF Df GVIF^(1/(2*Df))
Diet           2.617272  4        1.127797
Centered_logBM 1.354690  1        1.163912
ML             1.314165  1        1.146370
CM             2.095152  1        1.447464
DT             1.276962  1        1.130027
```

Glucose individuals

```
                   GVIF Df GVIF^(1/(2*Df))
Diet           3.216096  4        1.157221
Centered_logBM 2.237036  1        1.495672
Procedence     2.252484  1        1.500828
```

Glucose individuals life-history

```
                             GVIF Df GVIF^(1/(2*Df))
Diet                    21.782694  4        1.469819
Centered_logBM           5.093717  1        2.256927
poly(ML, 2, raw = TRUE)  1.966756  2        1.184234
CM                       3.876582  1        1.968904
DT                       1.621283  1        1.273296
Procedence               3.362333  1        1.833666
```

Glycation individuals

```
                        GVIF Df GVIF^(1/(2*Df))
Diet                1.643911  4        1.064106
Centered_logBM      2.189558  1        1.479715
Centered_logGlucose 1.946567  1        1.395194
```

Glycation individuals life-history

```
                        GVIF Df GVIF^(1/(2*Df))
Diet                6.218989  4        1.256652
Centered_logBM      3.413201  1        1.847485
Centered_logGlucose 2.074540  1        1.440326
ML                  1.296298  1        1.138551
CM                  3.114929  1        1.764916
DT                  1.446495  1        1.202703
```

Glycation individuals life-history

```
                   GVIF Df GVIF^(1/(2*Df))
Diet           5.454035  4        1.236203
Centered_logBM 2.682914  1        1.637960
ML             1.291340  1        1.136371
CM             3.111995  1        1.764085
DT             1.433119  1        1.197129
```

Glucose age & sex

```
                                                  GVIF Df GVIF^(1/(2*Df))
Centered_logBM                                1.148783  1   1.071813
poly(logit(Age_relative, FALSE), 2, raw = TRUE) 1.146260  2   1.034715
Sex                                           1.008919  1   1.004450
```

Glycation age & sex

```
                                               GVIF Df GVIF^(1/(2*Df))
Centered_logBM                             1.949521  1        1.396252
Centered_logGlucose                        2.042604  1        1.429197
poly(logit(Age_relative, FALSE), 2, raw = TRUE) 1.200827  2        1.046815
Sex                                        1.029088  1        1.014440
```

Post-hoc comparisons for dietary categories

A=Omnivores; B=Terrestrial carnivores; C=Aquatic predators; D=Herbivores; E=Frugivores/Granivores

Glucose averages

```
> HPDinterval(AG_Dif_BC)
         lower    upper
var1 -1.414069 1.466687
attr(,"Probability")
[1] 0.95
> HPDinterval(AG_Dif_BD)
         lower    upper
var1 -1.222618 1.308603
attr(,"Probability")
[1] 0.95
> HPDinterval(AG_Dif_BE)
         lower    upper
var1 -1.393724 1.500328
attr(,"Probability")
[1] 0.95
> HPDinterval(AG_Dif_CD)
         lower    upper
var1 -1.551009 1.566369
attr(,"Probability")
[1] 0.95
> HPDinterval(AG_Dif_CE)
         lower    upper
var1 -1.717679 1.821919
attr(,"Probability")
[1] 0.95
> HPDinterval(AG_Dif_DE)
         lower    upper
var1 -1.446564 1.520309
attr(,"Probability")
[1] 0.95
```

Glucose averages life history

```
> HPDinterval(AGLH_Dif_BC)
        lower    upper
var1 -1.54855 1.531426
attr(,"Probability")
[1] 0.95
> HPDinterval(AGLH_Dif_BD)
         lower    upper
var1 -2.140114 2.182302
attr(,"Probability")
[1] 0.95
> HPDinterval(AGLH_Dif_BE)
         lower    upper
var1 -7.737039 7.508915
attr(,"Probability")
[1] 0.95
> HPDinterval(AGLH_Dif_CD)
         lower    upper
var1 -2.146583 2.220799
attr(,"Probability")
[1] 0.95
```

```
> HPDinterval(AGLH_Dif_CE)
         lower    upper
var1 -7.488458 7.862649
attr(,"Probability")
[1] 0.95
> HPDinterval(AGLH_Dif_DE)
         lower    upper
var1 -7.751623 7.691805
attr(,"Probability")
[1] 0.95
```

Glycation averages

```
> HPDinterval(AGly_Dif_BC)
       lower    upper
var1 -1.2729 1.341971
attr(,"Probability")
[1] 0.95
> HPDinterval(AGly_Dif_BD)
         lower   upper
var1 -1.305844 1.52542
attr(,"Probability")
[1] 0.95
> HPDinterval(AGly_Dif_BE)
         lower    upper
var1 -1.056829 1.224983
attr(,"Probability")
[1] 0.95
> HPDinterval(AGly_Dif_CD)
         lower    upper
var1 -1.433015 1.563042
attr(,"Probability")
[1] 0.95
> HPDinterval(AGly_Dif_CE)
         lower    upper
var1 -1.282198 1.396203
attr(,"Probability")
[1] 0.95
> HPDinterval(AGly_Dif_DE)
        lower    upper
var1 -1.40408 1.318576
attr(,"Probability")
[1] 0.95
```

Glycation averages life-history

```
> HPDinterval(AGlyLH_Dif_BC)
        lower    upper
var1 -1.36308 1.540043
attr(,"Probability")
[1] 0.95
> HPDinterval(AGlyLH_Dif_BD)
         lower    upper
var1 -2.008801 2.234876
attr(,"Probability")
[1] 0.95
> HPDinterval(AGlyLH_Dif_BE)
         lower    upper
var1 -1.774074 2.117975
attr(,"Probability")
[1] 0.95
> HPDinterval(AGlyLH_Dif_CD)
         lower    upper
var1 -2.048012 2.107497
attr(,"Probability")
[1] 0.95
> HPDinterval(AGlyLH_Dif_CE)
```

```
         lower   upper
var1 -2.005551 2.19016
attr(,"Probability")
[1] 0.95
> HPDinterval(AGlyLH_Dif_DE)
         lower    upper
var1 -2.183145 2.284387
attr(,"Probability")
[1] 0.95
```

Glycation averages life-history without glucose

```
> HPDinterval(AGlyLH_NG_Dif_BC)
         lower    upper
var1 -1.369687 1.504995
attr(,"Probability")
[1] 0.95
> HPDinterval(AGlyLH_NG_Dif_BD)
         lower    upper
var1 -1.810076 2.055283
attr(,"Probability")
[1] 0.95
> HPDinterval(AGlyLH_NG_Dif_BE)
         lower    upper
var1 -1.678796 2.054028
attr(,"Probability")
[1] 0.95
> HPDinterval(AGlyLH_NG_Dif_CD)
         lower    upper
var1 -1.917022 2.053911
attr(,"Probability")
[1] 0.95
> HPDinterval(AGlyLH_NG_Dif_CE)
         lower    upper
var1 -1.923162 2.114277
attr(,"Probability")
[1] 0.95
> HPDinterval(AGlyLH_NG_Dif_DE)
         lower    upper
var1 -2.117618 2.130004
attr(,"Probability")
[1] 0.95
```

Glucose individuals

```
> HPDinterval(IG_Dif_BC)
           lower      upper
var1 -0.07163346 0.05929215
attr(,"Probability")
[1] 0.95
> HPDinterval(IG_Dif_BD)
           lower     upper
var1 -0.08404549 0.1570657
attr(,"Probability")
[1] 0.95
> HPDinterval(IG_Dif_BE)
            lower     upper
var1 -0.006626182 0.1846572
attr(,"Probability")
[1] 0.95
> HPDinterval(IG_Dif_CD)
           lower     upper
var1 -0.08960038 0.1648752
attr(,"Probability")
[1] 0.95
> HPDinterval(IG_Dif_CE)
           lower     upper
var1 -0.01340042 0.2039278
```

```
attr(,"Probability")
[1] 0.95
> HPDinterval(IG_Dif_DE)
           lower    upper
var1 -0.06618755 0.176413
attr(,"Probability")
[1] 0.95
```

Glucose individuals life-history

```
> HPDinterval(IGLH_Dif_BC)
           lower      upper
var1 -0.08234745 0.05308559
attr(,"Probability")
[1] 0.95
> HPDinterval(IGLH_Dif_BD)
           lower     upper
var1 -0.06588702 0.2218879
attr(,"Probability")
[1] 0.95
> HPDinterval(IGLH_Dif_BE)
          lower     upper
var1 -0.1173287 0.2604363
attr(,"Probability")
[1] 0.95
> HPDinterval(IGLH_Dif_CD)
           lower     upper
var1 -0.05760069 0.2320285
attr(,"Probability")
[1] 0.95
> HPDinterval(IGLH_Dif_CE)
          lower    upper
var1 -0.1169439 0.282375
attr(,"Probability")
[1] 0.95
> HPDinterval(IGLH_Dif_DE)
          lower     upper
var1 -0.2299858 0.2335929
attr(,"Probability")
[1] 0.95
```

Glycation individuals

```
> HPDinterval(IGly_Dif_BC)
           lower     upper
var1 -0.01230547 0.1285872
attr(,"Probability")
[1] 0.95
> HPDinterval(IGly_Dif_BD)
           lower     upper
var1 -0.05044503 0.2006516
attr(,"Probability")
[1] 0.95
> HPDinterval(IGly_Dif_BE)
           lower     upper
var1 -0.01012096 0.1853377
attr(,"Probability")
[1] 0.95
> HPDinterval(IGly_Dif_CD)
          lower     upper
var1 -0.1140737 0.1468223
attr(,"Probability")
[1] 0.95
> HPDinterval(IGly_Dif_CE)
           lower     upper
var1 -0.07078775 0.1368791
attr(,"Probability")
[1] 0.95
```

```
> HPDinterval(IGly_Dif_DE)
          lower     upper
var1 -0.1086503 0.1426304
attr(,"Probability")
[1] 0.95
```

Glycation individuals life-history

```
> HPDinterval(IGlyLH_Dif_BC)
            lower     upper
var1 -0.001756023 0.1502896
attr(,"Probability")
[1] 0.95
> HPDinterval(IGlyLH_Dif_BD)
           lower     upper
var1 -0.03802143 0.2812876
attr(,"Probability")
[1] 0.95
> HPDinterval(IGlyLH_Dif_BE)
          lower     upper
var1 -0.1907319 0.2172327
attr(,"Probability")
[1] 0.95
> HPDinterval(IGlyLH_Dif_CD)
         lower     upper
var1 -0.117811 0.2090437
attr(,"Probability")
[1] 0.95
> HPDinterval(IGlyLH_Dif_CE)
          lower     upper
var1 -0.2768476 0.1317622
attr(,"Probability")
[1] 0.95
> HPDinterval(IGlyLH_Dif_DE)
         lower     upper
var1 -0.359544 0.1331044
attr(,"Probability")
[1] 0.95
```

Glycation individuals life-history without glucose

```
> HPDinterval(IGlyLH_NG_Dif_BC)
             lower     upper
var1 -0.0008724393 0.1537172
attr(,"Probability")
[1] 0.95
> HPDinterval(IGlyLH_NG_Dif_BD)
           lower     upper
var1 -0.03474923 0.2953013
attr(,"Probability")
[1] 0.95
> HPDinterval(IGlyLH_NG_Dif_BE)
          lower     upper
var1 -0.1988301 0.2156449
attr(,"Probability")
[1] 0.95
> HPDinterval(IGlyLH_NG_Dif_CD)
          lower     upper
var1 -0.1067734 0.2297418
attr(,"Probability")
[1] 0.95
> HPDinterval(IGlyLH_NG_Dif_CE)
          lower     upper
var1 -0.2779184 0.1386907
attr(,"Probability")
[1] 0.95
> HPDinterval(IGlyLH_NG_Dif_DE)
          lower     upper
```

```
var1 -0.3831259 0.1231232
attr(,"Probability")
[1] 0.95
```

Within species repeatability

Glucose

```
Linear mixed model fit by REML ['lmerMod']
Formula: logGlucose ~ (1 | species)
   Data: Bird.caracIndGlu

REML criterion at convergence: -875.1

Scaled residuals: 
    Min      1Q  Median      3Q     Max 
-3.7868 -0.5688 -0.0078  0.5683  2.8026 

Random effects:
 Groups   Name        Variance Std.Dev.
 species  (Intercept) 0.009768 0.09883 
 Residual             0.003869 0.06220 
Number of obs: 389, groups:  species, 75

Fixed effects:
            Estimate Std. Error t value
(Intercept)  2.39913    0.01214   197.7

Repeatability estimation using the lmm method

Repeatability for species
R  = 0.716
SE = 0.042
CI = [0.619, 0.785]
P  = 8.57e-80 [LRT]
     NA [Permutation]
```

Glycation

```
Linear mixed model fit by REML ['lmerMod']
Formula: Glycation ~ (1 | species)
   Data: Bird.caracIndGly

REML criterion at convergence: 2521.1

Scaled residuals: 
    Min      1Q  Median      3Q     Max 
-4.3646 -0.4484 -0.0123  0.4749  3.4483 

Random effects:
 Groups   Name        Variance Std.Dev.
 species  (Intercept) 18.898   4.347   
 Residual              7.994   2.827   
Number of obs: 471, groups:  species, 88

Fixed effects:
            Estimate Std. Error t value
(Intercept)  18.4571     0.4921   37.51


Repeatability estimation using the lmm method

Repeatability for species
R  = 0.703
SE = 0.042
CI = [0.603, 0.767]
P  = 3.53e-86 [LRT]
     NA [Permutation]
```

Variances explained by the tree

Glucose averages

```
0.3060753
            lower     upper
var1 9.658695e-07 0.8365601
attr(,"Probability")
[1] 0.95
```

Glucose averages life history

```
0.31353
            lower     upper
var1 1.769981e-06 0.8672609
attr(,"Probability")
[1] 0.95
```

Glycation averages

```
0.3324061
           lower     upper
var1 1.64774e-06 0.8480055
attr(,"Probability")
[1] 0.95
```

Glycation averages life-history

```
0.333346
            lower     upper
var1 2.934731e-06 0.8685776
attr(,"Probability")
[1] 0.95
```

Glycation averages life-history without glucose

```
0.5373031
          lower     upper
var1 0.07157126 0.9932748
attr(,"Probability")
[1] 0.95
```

Glucose individuals

```
0.5161435
         lower     upper
var1 0.2761292 0.7415861
attr(,"Probability")
[1] 0.95
```

Glucose individuals life-history

```
0.5025716
         lower     upper
var1 0.2420428 0.7546559
attr(,"Probability")
[1] 0.95
```

Glycation individuals

```
0.4590051
         lower    upper
```

```
var1 0.2151646 0.696498
attr(,"Probability")
[1] 0.95
```

Glycation individuals life-history

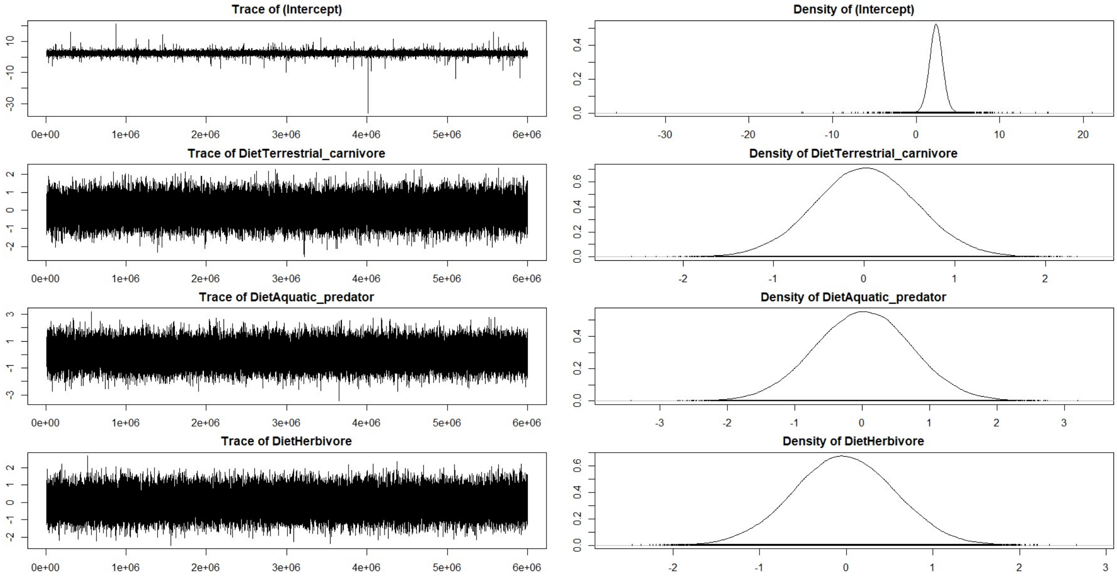
```
0.46431
         lower     upper
var1 0.1987901 0.7324513
attr(,"Probability")
[1] 0.95
```

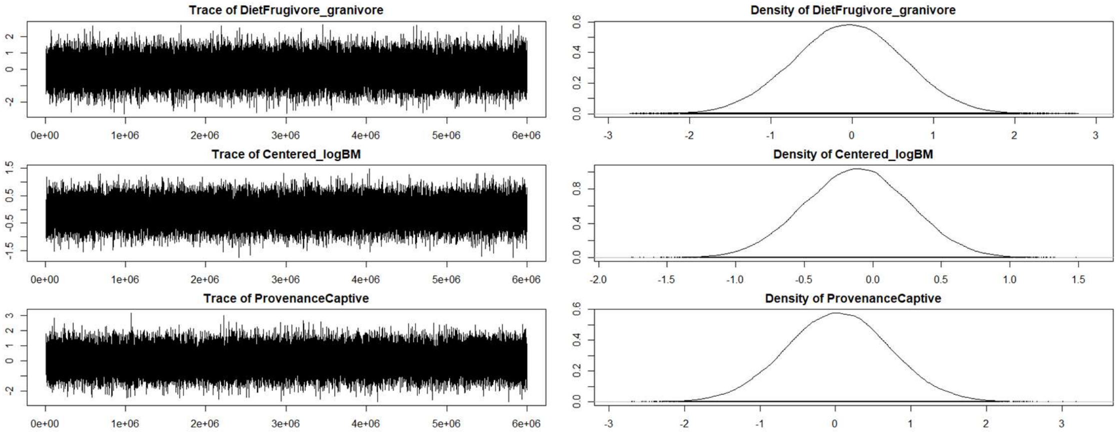
Glycation individuals life-history without glucose

```
0.485408
         lower     upper
var1 0.2080762 0.7528297
attr(,"Probability")
[1] 0.95
```

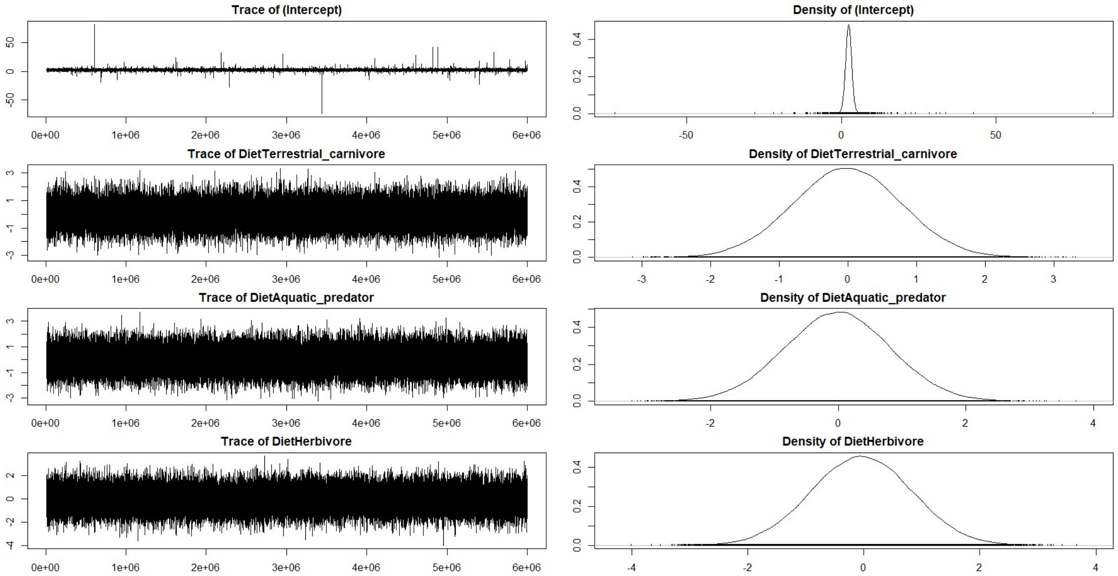
Traces and posterior distributions

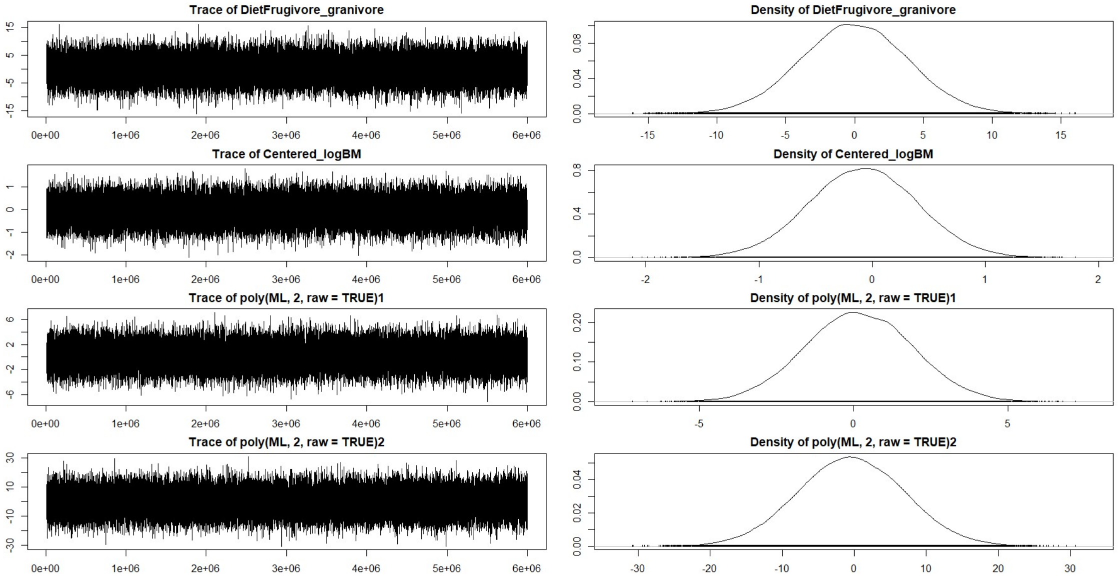
Glucose averages

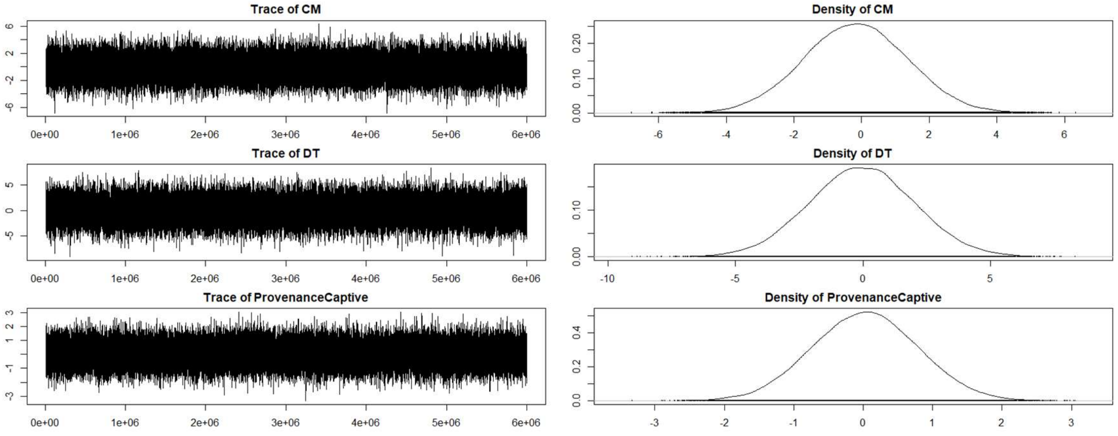




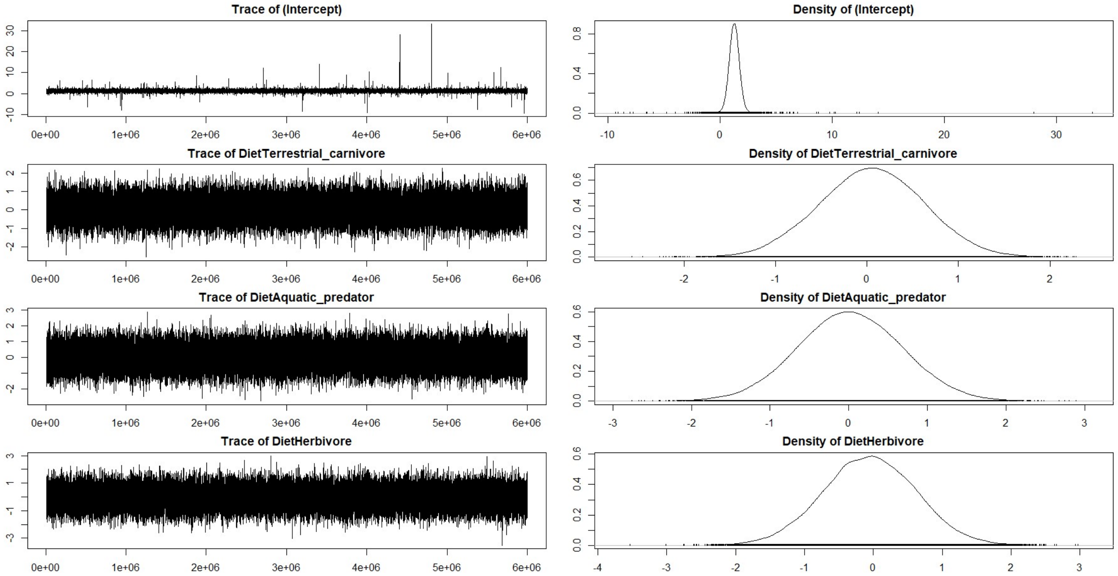
Glucose averages life history

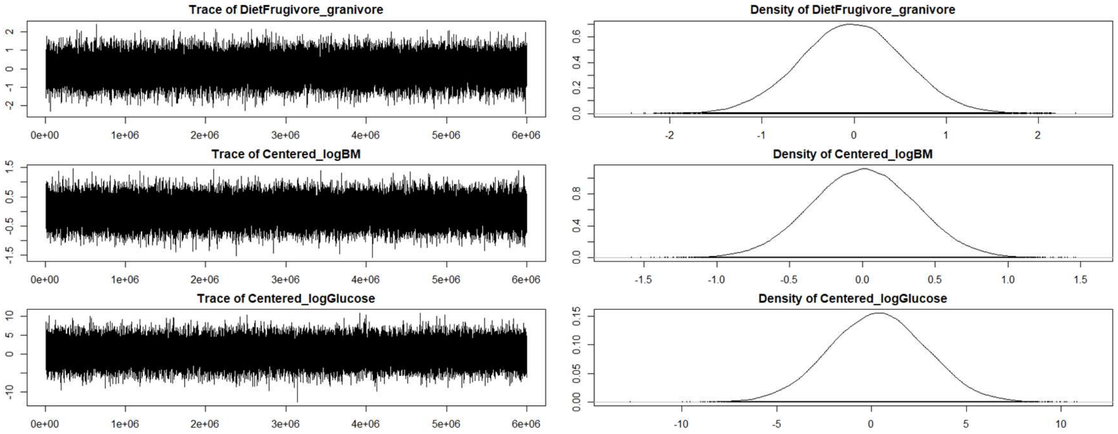




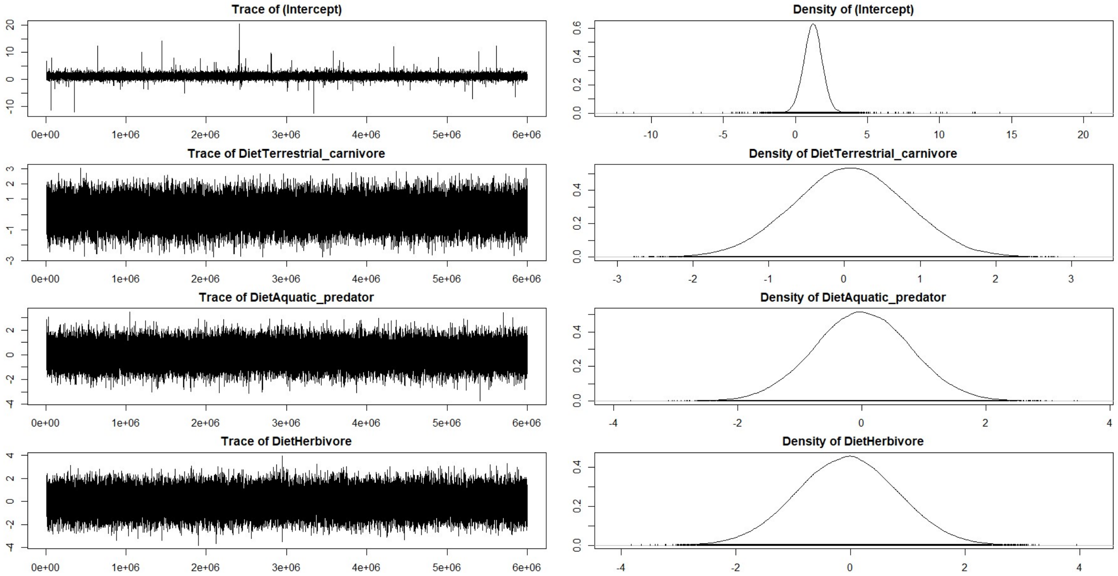


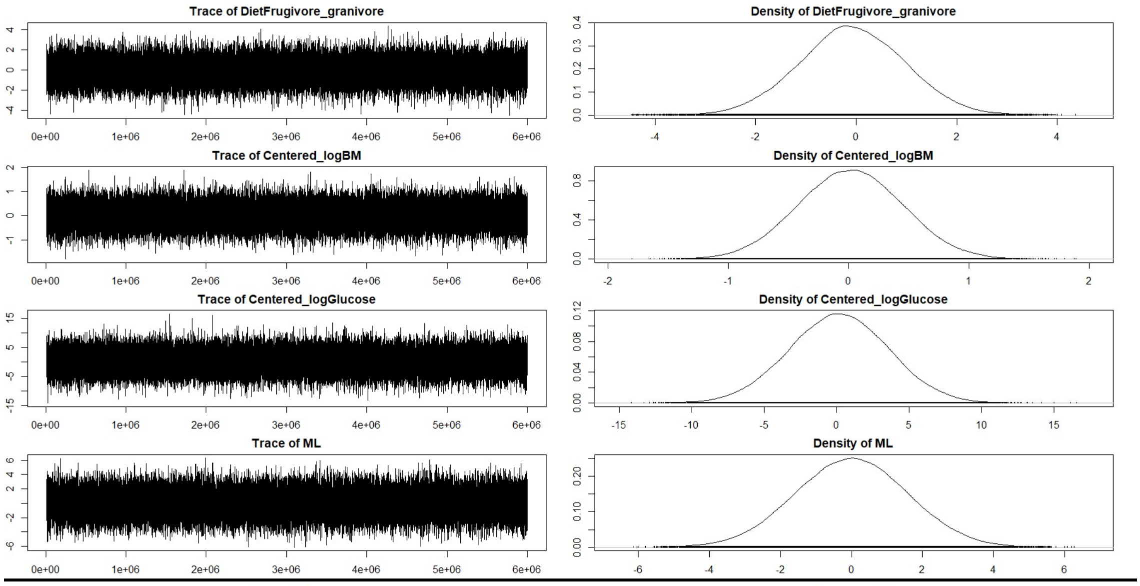
Glycation averages

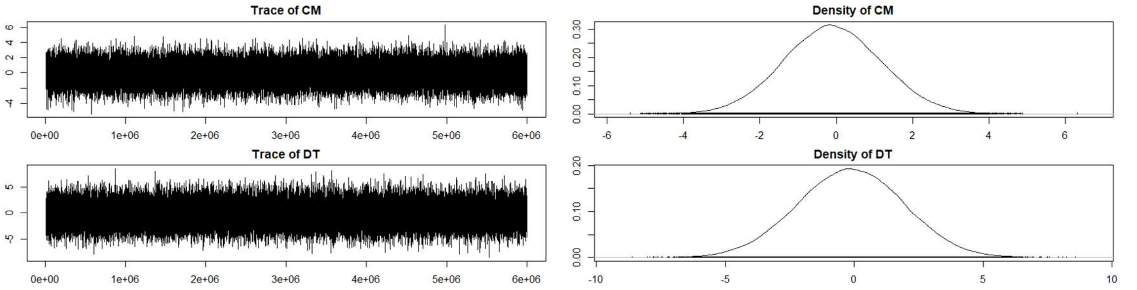




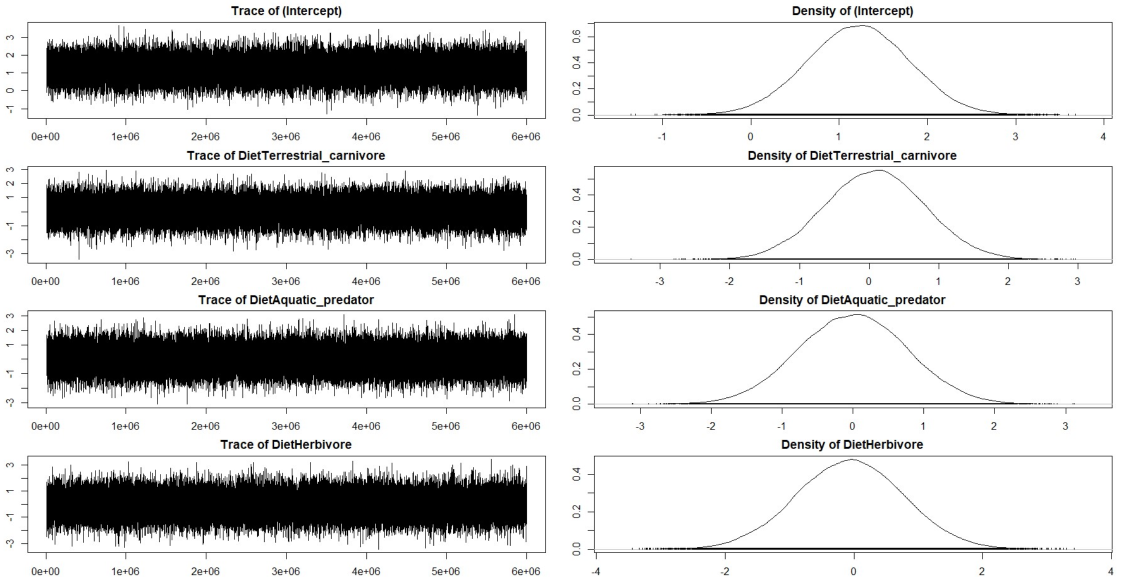
Glycation averages life-history

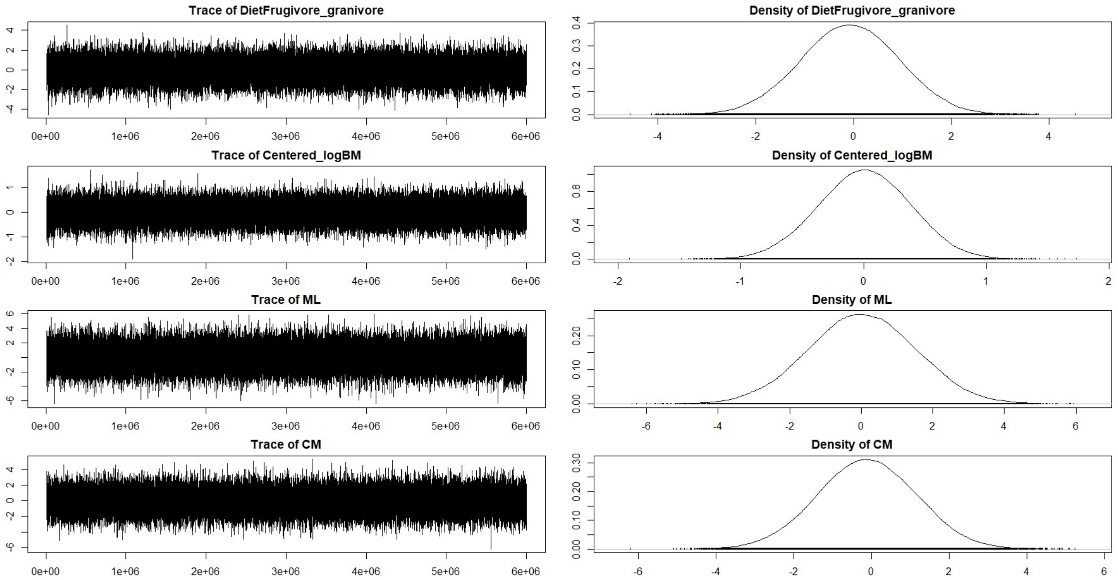


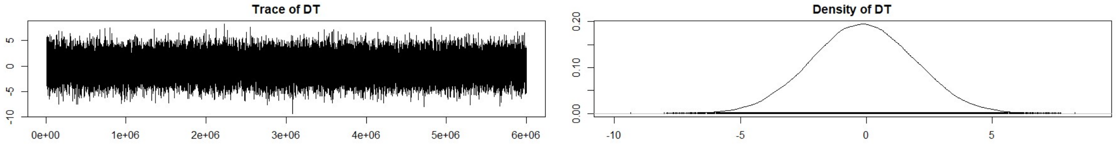




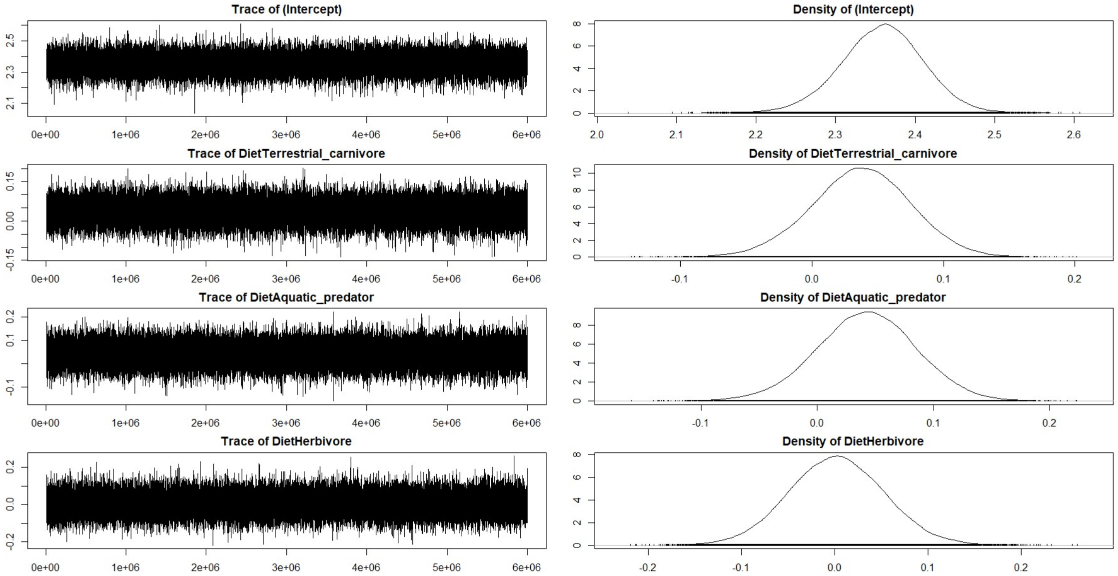
Glycation averages life-history without glucose

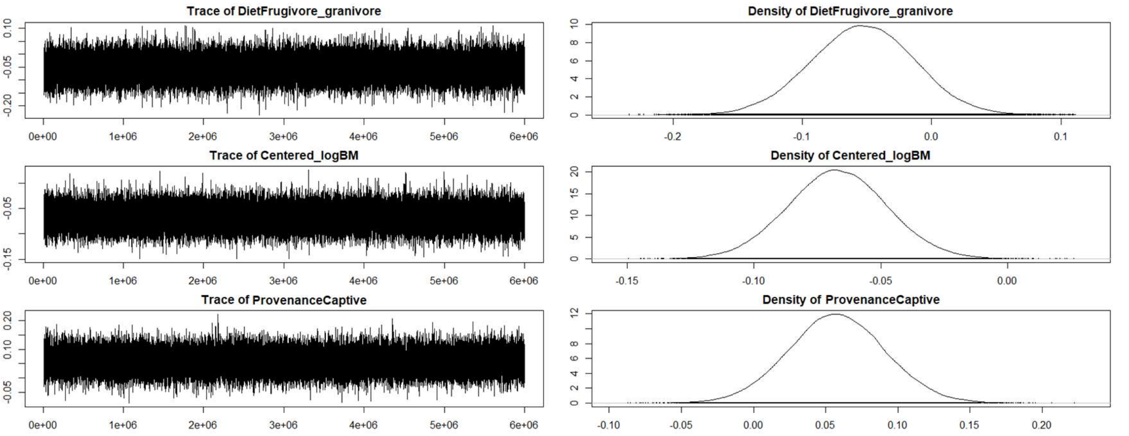




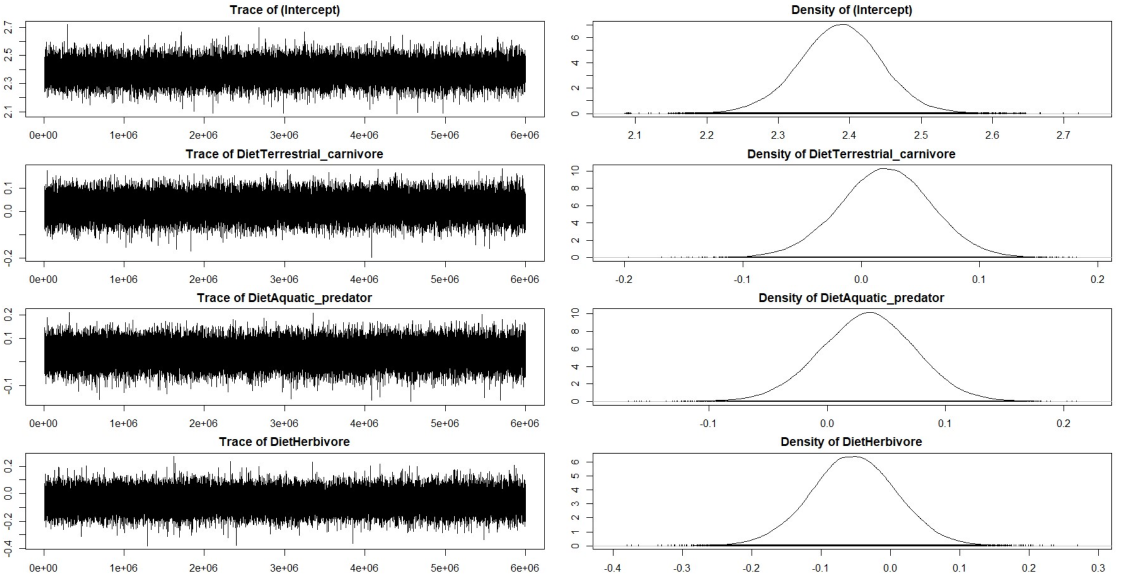


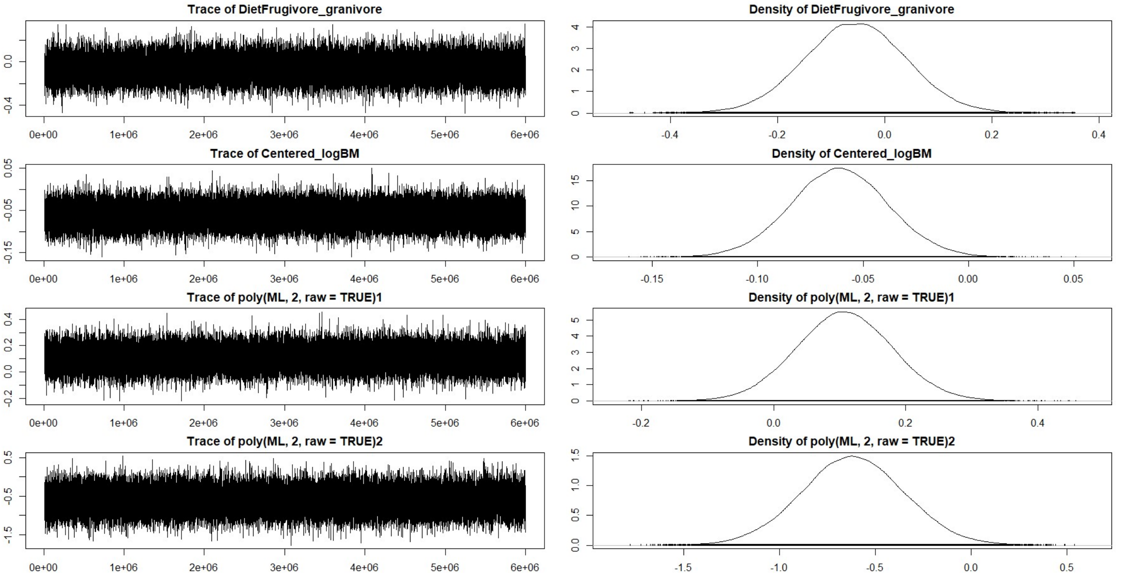
Glucose individuals

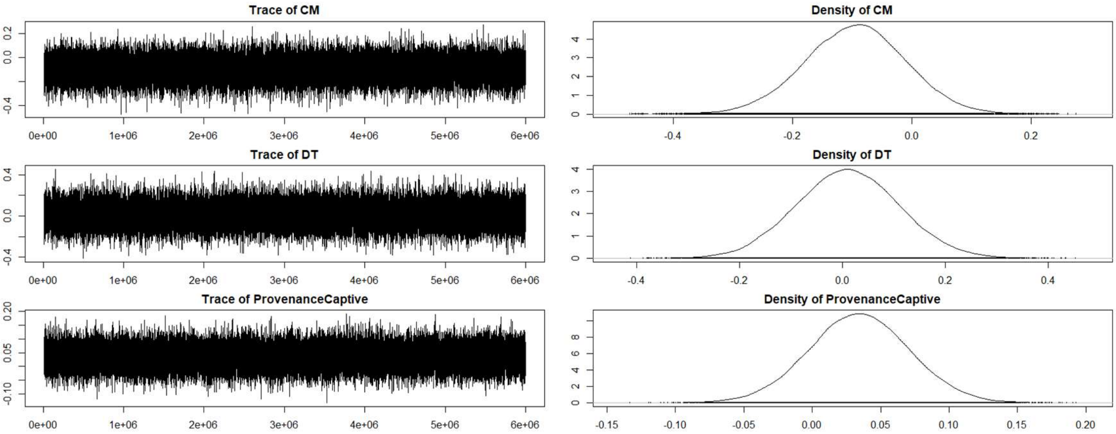




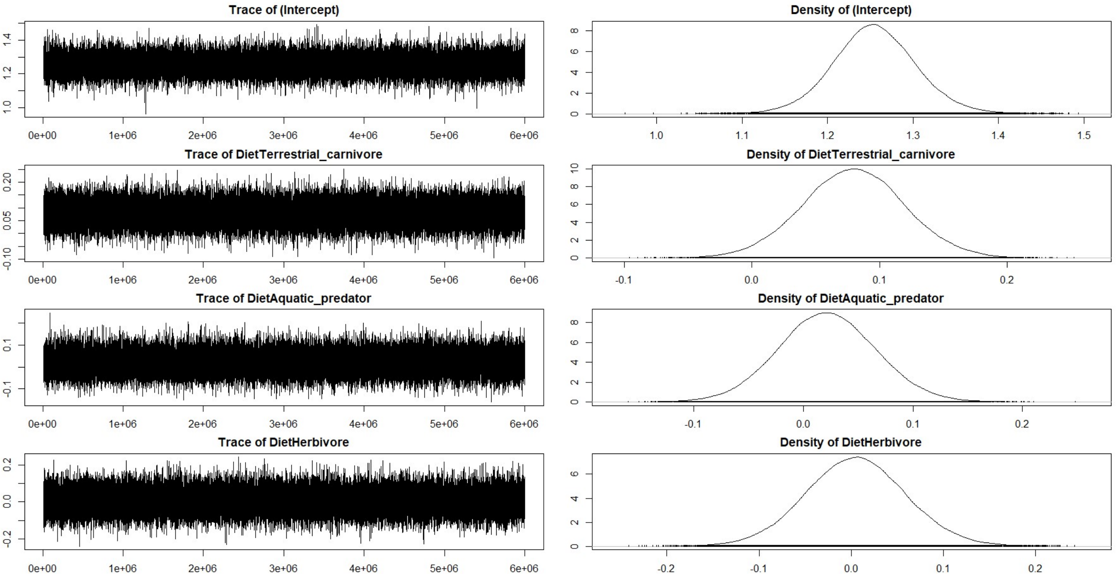
Glucose individuals life-history

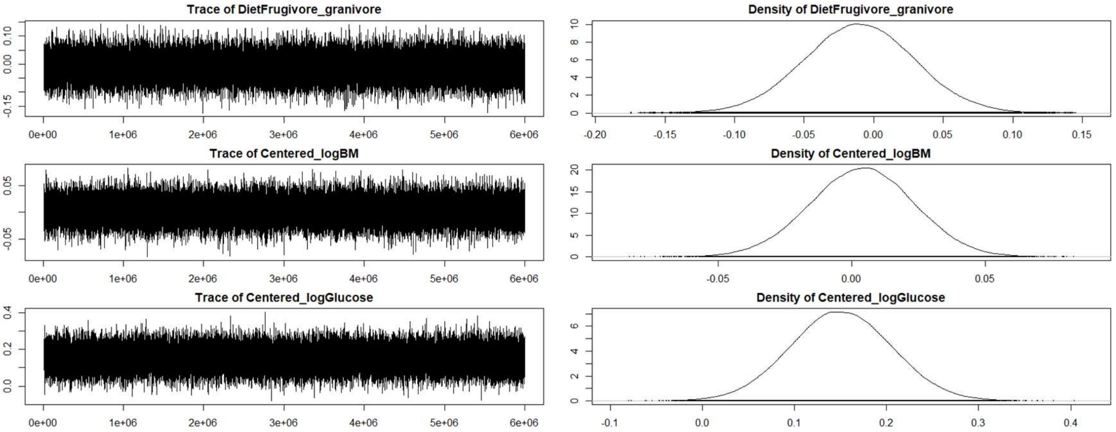




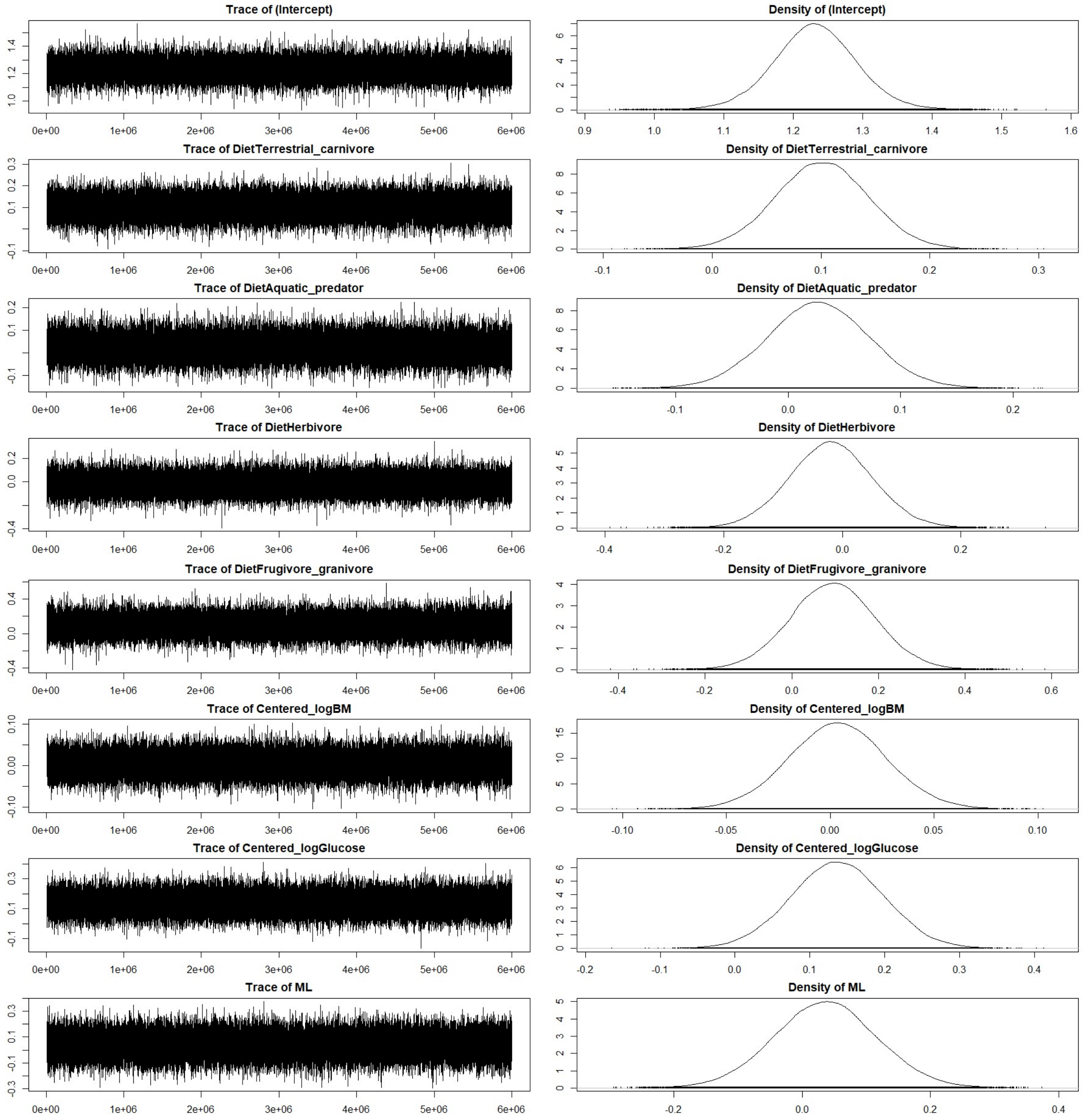


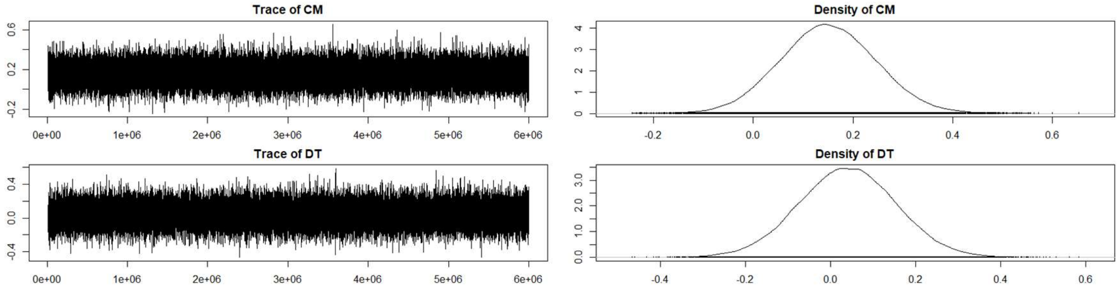
Glycation individuals





Glycation individuals life-history





Glycation individuals life-history without glucose

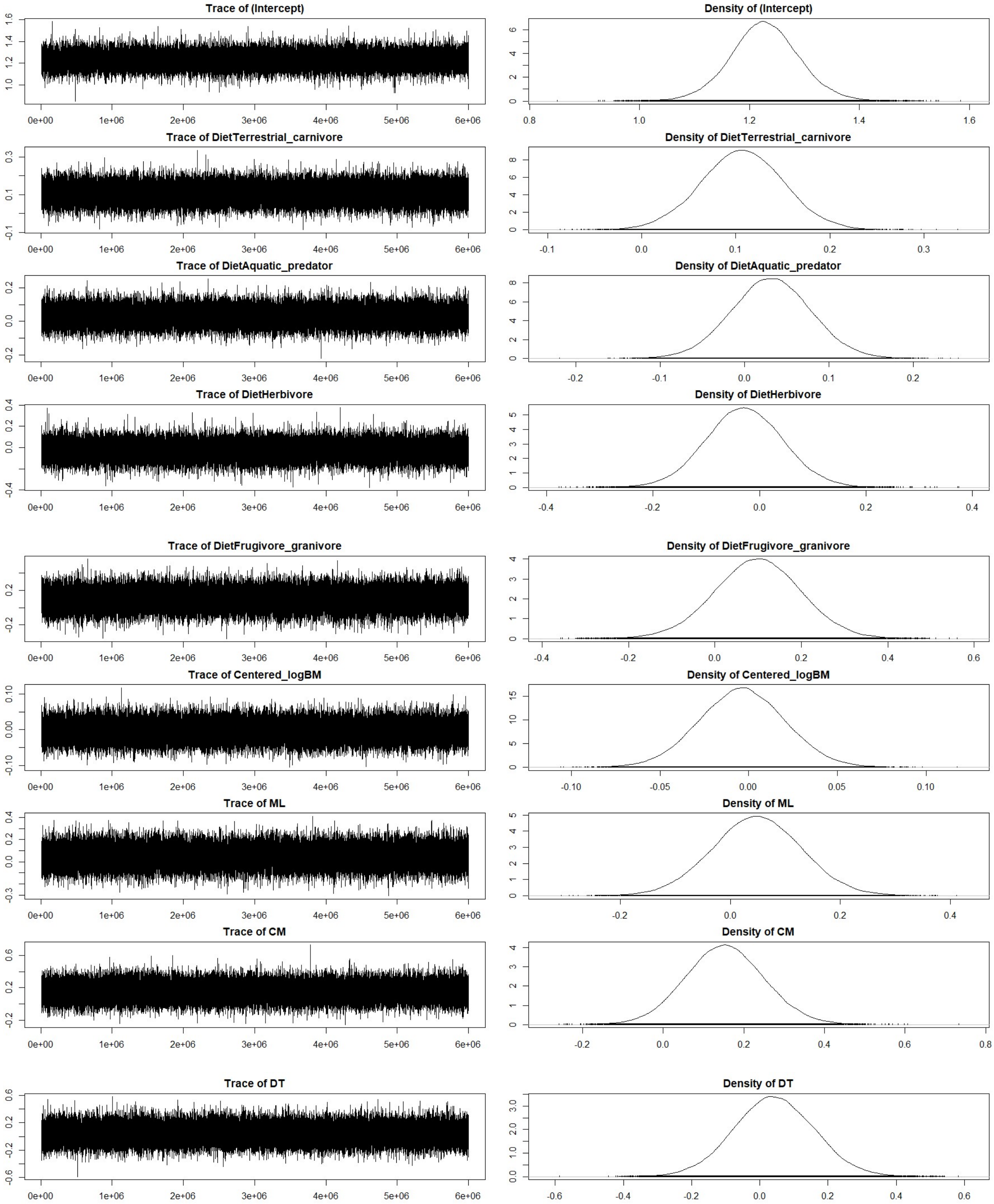

Trace of (Intercept)
Density of (Intercept)
Trace of DietTerrestrial_carnivore
Density of DietTerrestrial_carnivore
Trace of DietAquatic_predator
Density of DietAquatic_predator
Trace of DietHerbivore
Density of DietHerbivore
Trace of DietFrugivore_granivore
Density of DietFrugivore_granivore
Trace of Centered_logBM
Density of Centered_logBM
Trace of ML
Density of ML
Trace of CM
Density of CM
Trace of DT
Density of DT

Figure ESM1.1 Trace showing convergence of the models and posterior density plots of the parameters estimated.

Supplementary analyses of stress on glucose

Glucose repeatability

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['l
merModLmerTest']
Formula: Glucose ~ (1 | SpeciesBirdTree/Individual)
   Data: Tomasek2022

REML criterion at convergence: 44335.9
```

```
Scaled residuals: 
    Min      1Q  Median      3Q     Max 
-4.6683 -0.5772  0.0246  0.5585  4.0989 

Random effects:
 Groups                   Name        Variance Std.Dev.
 Individual:SpeciesBirdTree (Intercept) 5.188    2.278   
 SpeciesBirdTree          (Intercept) 2.222    1.490   
 Residual                             6.204    2.491   
Number of obs: 8862, groups:  Individual:SpeciesBirdTree, 1705; Specie
sBirdTree, 158

Fixed effects:
            Estimate Std. Error       df t value Pr(>|t|)    
(Intercept)  13.8677     0.1496 146.9083   92.67   <2e-16 ***


Repeatability estimation using the lmm method 

Repeatability for SpeciesBirdTree
R  = 0.163
SE = 0.024
CI = [0.117, 0.209]
P  = 0 [LRT]
     NA [Permutation]
```

For individuals within species:

```
> 5.188/(5.188+2.222+6.204)
[1] 0.3810783
```

Glucose repeatability (with stress effects)

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['l
merModLmerTest']
Formula: Glucose ~ Time + (1 | SpeciesBirdTree/Individual)
   Data: Tomasek2022

REML criterion at convergence: 40911.9

Scaled residuals: 
    Min      1Q  Median      3Q     Max 
-5.0618 -0.5405 -0.0221  0.5398  4.6158 

Random effects:
 Groups                   Name        Variance Std.Dev.
 Individual:SpeciesBirdTree (Intercept) 5.499    2.345   
 SpeciesBirdTree          (Intercept) 2.267    1.506   
 Residual                             3.864    1.966   
Number of obs: 8862, groups:  Individual:SpeciesBirdTree, 1705; Specie
sBirdTree, 158

Fixed effects:
             Estimate Std. Error        df t value Pr(>|t|)    
(Intercept) 1.211e+01  1.525e-01 1.573e+02   79.41   <2e-16 ***
TimeG15_    2.936e+00  5.458e-02 7.341e+03   53.79   <2e-16 ***
TimeG30_    2.905e+00  4.976e-02 7.271e+03   58.37   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Correlation of Fixed Effects:
         (Intr) TmG15_
TimeG15_ -0.140       
```

```
TimeG30_ -0.153  0.442


Levene's Test for Homogeneity of Variance (center = median)
        Df F value    Pr(>F)    
group    2  455.14 < 2.2e-16 ***
      8859                      


Kruskal-Wallis rank sum test

data:  Glucose by Time
Kruskal-Wallis chi-squared = 1347.7, df = 2, p-value < 2.2e-16


Repeatability estimation using the lmm method

Repeatability for SpeciesBirdTree
R  = 0.195
SE = 0.027
CI = [0.141, 0.248]
P  = 0 [LRT]
     NA [Permutation]
```

For individuals within species:

```
> 5.499/(5.499+2.267+3.864)
[1] 0.4728289
```

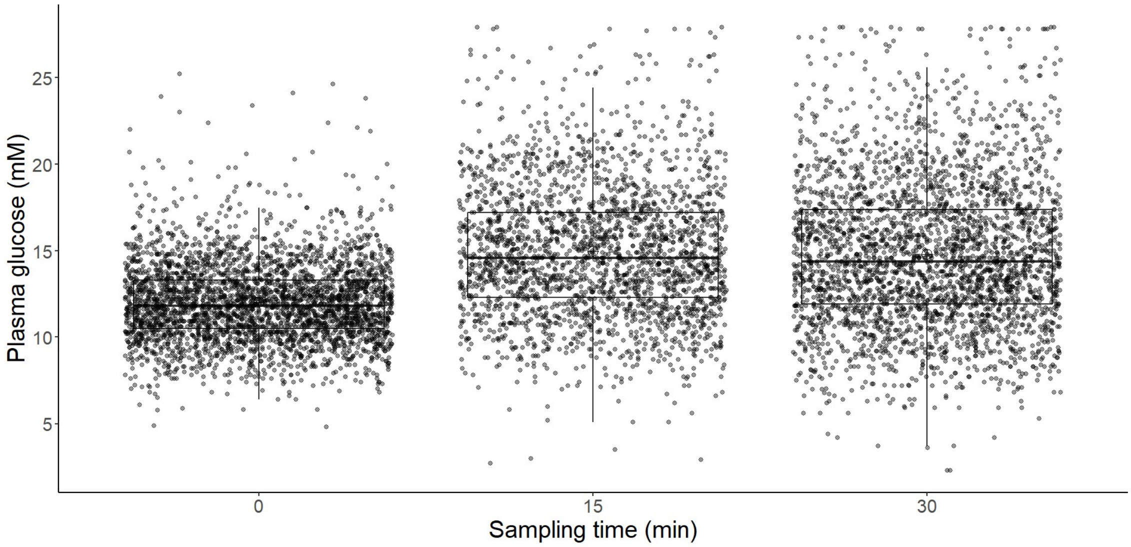


Figure ESM1.2 Glucose variation (in mM) with sampling time at 0, 15 and 30 min, showing clear heteroskedasticity. Data publicly available from Tomasek et al. 2022 (see ESM6).