

LIGHT CHAIN NOTATION!

1. Mutational Spectrum of Actinopterygii versus temperature and longevity (Time of maturation):
 - a. All nominally significant spearman rank correlations between frequencies of 4 transitions and temperature:

```
N = 128
• data: TemperMut$A_G and TemperMut$Temperature
S = 474663, p-value = 3.321e-05
alternative hypothesis: true rho is not equal to 0
sample estimates:
rho
-0.3581037
• data: TemperMut$T_C and TemperMut$Temperature
S = 256954, p-value = 0.002522
alternative hypothesis: true rho is not equal to 0
sample estimates:
rho
0.2648037
• data: allparameters$TCdivAG and allparameters$Temperature
S = 179782, p-value = 1.654e-07
alternative hypothesis: true rho is not equal to 0
sample estimates:
rho
0.447675
• other transitions give p-value >0,1
```

- b. PICs:

```
Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.961202 2.371449 -0.405 0.687
pic(data$Temperature, tree_pruned) -0.005479 0.091820 -0.060 0.953
pic(data$Tm, tree_pruned) 0.110200 0.127524 0.864 0.392
```

- c. Multiple models between temperature and fractions of T_C + A_G:

```
N=128
• lm(formula = Temperature ~ scale(T_C) + scale(A_G), data = allparameters)
(Intercept) 17.2395 0.6029 28.594 < 2e-16 ***
scale(T_C) 1.6769 0.6097 2.750 0.006835 **
scale(A_G) -2.4375 0.6097 -3.998 0.000109 ***
Residual standard error: 6.821 on 125 degrees of freedom
Multiple R-squared: 0.1753, Adjusted R-squared: 0.1621
F-statistic: 13.28 on 2 and 125 DF, p-value: 5.869e-06

N=65
• lm(formula = Temperature ~ scale(T_C) + scale(A_G), data = allparameters)
(Intercept) 15.9015 0.8532 18.638 < 2e-16 ***
scale(T_C) 2.9136 0.8660 3.364 0.00132 **
scale(A_G) -1.5153 0.8660 -1.750 0.08511 .
Residual standard error: 6.879 on 62 degrees of freedom
Multiple R-squared: 0.2053, Adjusted R-squared: 0.1796
F-statistic: 8.007 on 2 and 62 DF, p-value: 0.0008065
```

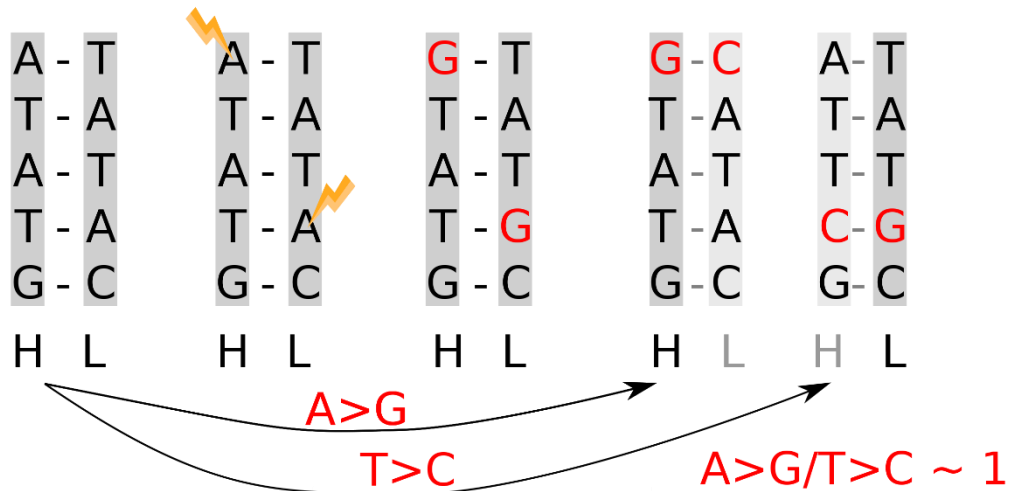
d. Model of asymmetrical chemical damage of mtDNA on heavy strand:

equivalent substitutions => (a)symmetry of mutagenesis

1) symmetrical mutagenesis:

the same probability of A>G on both heavy ('H') and light ('L') strands =>

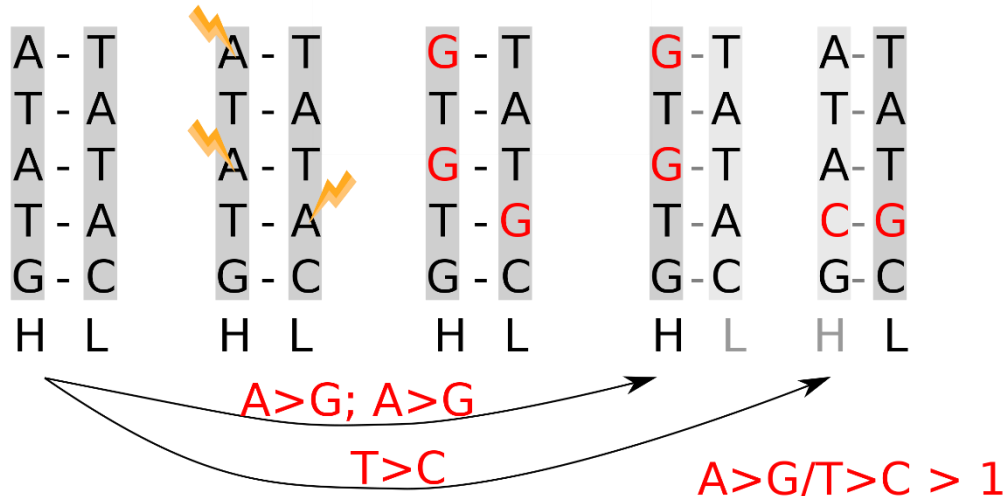
fractions of equivalent substitutions are similar



2) asymmetrical mutagenesis

A>G mainly occurs on heavy strand =>

fractions of equivalent substitutions are different



e. All multiple models between fractions of T_C and temperature + longevity:

N=65

• $\text{lm}(\text{formula} = T_C \sim \text{scale}(\text{Temperature}) * \text{scale}(T_m), \text{data} = \text{allparameters})$

(Intercept) 0.131507 0.008055 16.325 < 2e-16 ***
 scale(Temperature) 0.024866 0.008083 3.076 0.00313 **
 scale(Tm) -0.008903 0.008722 -1.021 0.31142
 scale(Temperature):scale(Tm) -0.000811 0.009005 -0.090 0.92854
 Residual standard error: 0.062 on 61 degrees of freedom
 Multiple R-squared: 0.1815, Adjusted R-squared: 0.1412
 F-statistic: 4.508 on 3 and 61 DF, p-value: 0.006387

• $\text{lm}(\text{formula} = T_C \sim \text{scale}(\text{Temperature}) + \text{scale}(T_m), \text{data} = \text{allparameters})$

(Intercept) 0.131723 0.007628 17.269 < 2e-16 ***
 scale(Temperature) 0.024931 0.007985 3.122 0.00273 **
 scale(Tm) -0.008600 0.007985 -1.077 0.28564
 Residual standard error: 0.0615 on 62 degrees of freedom
 Multiple R-squared: 0.1814, Adjusted R-squared: 0.1549

LIGHT CHAIN NOTATION!

```
F-statistic: 6.867 on 2 and 62 DF, p-value: 0.002023
• lm(formula = T_C ~ scale(Temperature), data = allparameters)
(Intercept)    0.131723  0.007637 17.247 < 2e-16 ***
scale(Temperature) 0.027259  0.007697  3.542 0.000755 ***
Residual standard error: 0.06158 on 63 degrees of freedom
Multiple R-squared:  0.166,    Adjusted R-squared:  0.1528
F-statistic: 12.54 on 1 and 63 DF, p-value: 0.0007547
• lm(formula = A_G ~ scale(Temperature) + scale(Tm), data = allparameters)
(Intercept)    0.068819  0.006021 11.430 < 2e-16 ***
scale(Temperature) -0.014254  0.006303 -2.261  0.0273 *
scale(Tm)        -0.007483  0.006303 -1.187  0.2397
Residual standard error: 0.04854 on 62 degrees of freedom
Multiple R-squared:  0.08108, Adjusted R-squared:  0.05144
F-statistic: 2.735 on 2 and 62 DF, p-value: 0.07271
• lm(formula = A_G ~ scale(Temperature), data = allparameters)
(Intercept)    0.068819  0.006041 11.393 < 2e-16 ***
scale(Temperature) -0.012228  0.006088 -2.009  0.0489 *
Residual standard error: 0.0487 on 63 degrees of freedom
Multiple R-squared:  0.06019, Adjusted R-squared:  0.04527
F-statistic: 4.035 on 1 and 63 DF, p-value: 0.04886
```

f. All multiple models between T_C : A_G and temperature + longevity:

```
N=123 (no NULL in A_G and T_C)
• lm(formula = log2(TCdivAG) ~ scale(Temperature), data = allparameters)
(Intercept)    1.2664  0.1194 10.607 < 2e-16 ***
scale(Temperature) 0.5674  0.1199  4.733 6.06e-06 ***
Residual standard error: 1.324 on 121 degrees of freedom
Multiple R-squared:  0.1562, Adjusted R-squared:  0.1492
F-statistic: 22.4 on 1 and 121 DF, p-value: 6.056e-06
• lm(formula = Temperature ~ scale(TCdivAG), data = allparameters)
(Intercept)    17.2793  0.6683 25.855 < 2e-16 ***
scale(TCdivAG)  1.2923  0.6711  1.926  0.0565 .
Residual standard error: 7.412 on 121 degrees of freedom
Multiple R-squared:  0.02974, Adjusted R-squared:  0.02172
F-statistic: 3.709 on 1 and 121 DF, p-value: 0.05648
N=62 (no NULL)
• lm(formula = Temperature ~ scale(TCdivAG), data = allparameters)
(Intercept)    16.0129  0.9507 16.844 < 2e-16 ***
scale(TCdivAG)  1.8008  0.9584  1.879  0.0651 .
Residual standard error: 7.486 on 60 degrees of freedom
Multiple R-squared:  0.05557, Adjusted R-squared:  0.03983
F-statistic: 3.53 on 1 and 60 DF, p-value: 0.06512
• lm(formula = log2(TCdivAG) ~ scale(Temperature) + scale(Tm),
  data = allparameters)
(Intercept)    1.11377  0.16982  6.559 1.51e-08 ***
scale(Temperature) 0.58133  0.17790  3.268  0.00181 **
scale(Tm)        0.03231  0.17790  0.182  0.85649
Residual standard error: 1.337 on 59 degrees of freedom
Multiple R-squared:  0.1597, Adjusted R-squared:  0.1313
F-statistic: 5.608 on 2 and 59 DF, p-value: 0.005891
```

g. All nominally significant spearman rank correlations between fractions of 4 transitions and longevity:

```
N=106
• data: MATUTmmut$G_C and MATUTmmut$Tm
S = 242544, p-value = 0.0222
alternative hypothesis: true rho is not equal to 0
sample estimates:
rho
-0.2219755
```

2. Whole genomes of Actinopterygii versus temperature and longevity (Time of maturation):

a. All nominally significant spearman rank correlations between fractions of 4 nucleotides and temperature:

```
• data: log2(SynNuc$Temperature) and SynNuc$FrA
S = 5335566, p-value = 0.03301
alternative hypothesis: true rho is not equal to 0
sample estimates:
rho
0.1172215
• data: log2(SynNuc$Temperature) and SynNuc$FrT
S = 6966996, p-value = 0.005369
alternative hypothesis: true rho is not equal to 0
sample estimates:
rho
```

LIGHT CHAIN NOTATION!

-0.1527014

- data: log2(SynNuc\$Temperature) and SynNuc\$FrG
S = 7546431, p-value = 4.711e-06
alternative hypothesis: true rho is not equal to 0
sample estimates:

rho

-0.2485698

- data: log2(SynNuc\$Temperature) and SynNuc\$FrC
S = 5248321, p-value = 0.01655
alternative hypothesis: true rho is not equal to 0
sample estimates:

rho

0.1316563

b. All multiple models between S_{AC}S_{TG} skew and temperature + longevity:

- lm(formula = TG_ACSkew ~ log2(Temperature + 2) + log2(Tm), data = SynNuc)
(Intercept) -0.140140 0.043625 -3.212 0.00167 **
log2(Temperature + 2) -0.056133 0.009553 -5.876 3.42e-08 ***
log2(Tm) -0.024618 0.006086 -4.045 8.99e-05 ***
Residual standard error: 0.08634 on 128 degrees of freedom
(4973 observations deleted due to missingness)
Multiple R-squared: 0.24, Adjusted R-squared: 0.2282
F-statistic: 20.22 on 2 and 128 DF, p-value: 2.346e-08
- lm(formula = TG_ACSkew ~ scale(Temperature + 2) + scale(Tm), data = SynNuc)
(Intercept) -0.421980 0.007940 -53.148 < 2e-16 ***
scale(Temperature + 2) -0.045806 0.007493 -6.113 1.10e-08 ***
scale(Tm) -0.026502 0.006590 -4.022 9.82e-05 ***
Residual standard error: 0.08541 on 128 degrees of freedom
(4973 observations deleted due to missingness)
Multiple R-squared: 0.2563, Adjusted R-squared: 0.2447
F-statistic: 22.06 on 2 and 128 DF, p-value: 5.876e-09

c. All multiple models between fraction of T and temperature + longevity:

- lm(formula = FrT ~ scale(Temperature) + scale(Tm), data = SynNuc)
(Intercept) 0.224467 0.004409 50.908 < 2e-16 ***
scale(Temperature) -0.015662 0.004161 -3.764 0.000254 ***
scale(Tm) -0.006686 0.003660 -1.827 0.070052 .
Residual standard error: 0.04743 on 128 degrees of freedom
(4973 observations deleted due to missingness)
Multiple R-squared: 0.1051, Adjusted R-squared: 0.09109
F-statistic: 7.514 on 2 and 128 DF, p-value: 0.0008213
- lm(formula = FrT ~ log2(Temperature + 2) + log2(Tm), data = SynNuc)
(Intercept) 0.309754 0.024281 12.757 < 2e-16 ***
log2(Temperature + 2) -0.017552 0.005317 -3.301 0.00125 **
log2(Tm) -0.005453 0.003387 -1.610 0.10989
Residual standard error: 0.04806 on 128 degrees of freedom
(4973 observations deleted due to missingness)
Multiple R-squared: 0.08145, Adjusted R-squared: 0.0671
F-statistic: 5.675 on 2 and 128 DF, p-value: 0.004351
- lm(formula = FrT ~ log2(Temperature + 2) * log2(Tm), data = SynNuc)
(Intercept) 0.422770 0.050387 8.390 8.02e-14 ***
log2(Temperature + 2) -0.043535 0.011464 -3.798 0.000225 ***
log2(Tm) -0.055592 0.019986 -2.782 0.006234 **
log2(Temperature + 2):log2(Tm) 0.011796 0.004637 2.544 0.012156 *
Residual standard error: 0.04706 on 127 degrees of freedom
(4973 observations deleted due to missingness)
Multiple R-squared: 0.126, Adjusted R-squared: 0.1053
F-statistic: 6.102 on 3 and 127 DF, p-value: 0.0006525

d. All multiple models between other fractions and temperature + longevity:

- lm(formula = FrG ~ log2(Temperature + 2) + log2(Tm), data = SynNuc)
(Intercept) 0.120175 0.013771 8.727 1.2e-14 ***
log2(Temperature + 2) -0.010514 0.003016 -3.487 0.000671 ***
log2(Tm) -0.006856 0.001921 -3.568 0.000506 ***
Residual standard error: 0.02726 on 128 degrees of freedom
(4973 observations deleted due to missingness)
Multiple R-squared: 0.1307, Adjusted R-squared: 0.1172
F-statistic: 9.626 on 2 and 128 DF, p-value: 0.0001275
- lm(formula = FrA ~ log2(Temperature + 2) + log2(Tm), data = SynNuc)
(Intercept) 0.249276 0.026709 9.333 4.08e-16 ***
log2(Temperature + 2) 0.023023 0.005849 3.936 0.000135 ***
log2(Tm) 0.014498 0.003726 3.891 0.000160 ***
Residual standard error: 0.05286 on 128 degrees of freedom
(4973 observations deleted due to missingness)
Multiple R-squared: 0.1562, Adjusted R-squared: 0.143
F-statistic: 11.85 on 2 and 128 DF, p-value: 1.904e-05

e. All multiple models between other nucleotide skews and temperature + longevity:

```

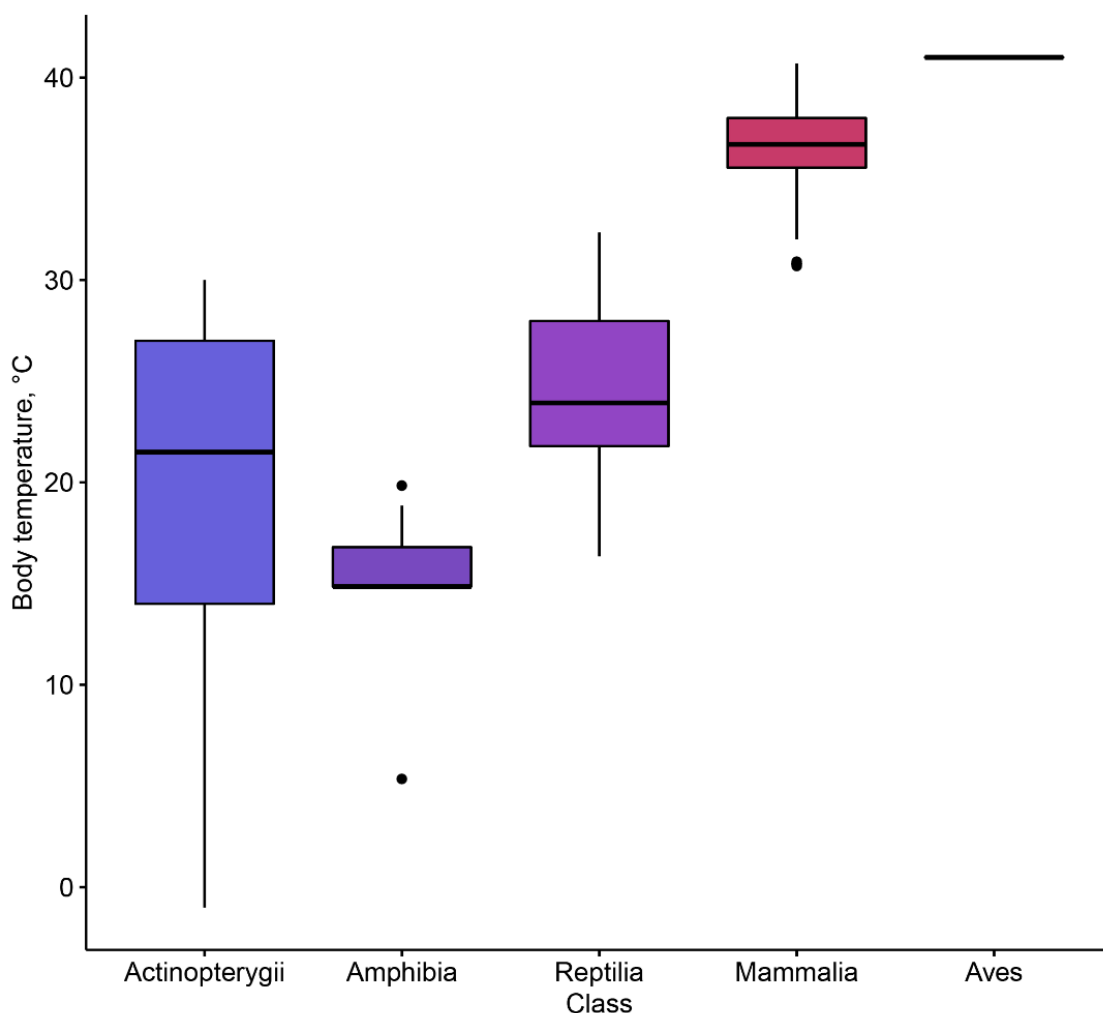
• lm(formula = GtoASkew ~ log2(Temperature + 2) + log2(Tm), data = SynNuc)
(Intercept)      -0.39217    0.06129  -6.399 2.70e-09 ***
log2(Temperature + 2) -0.05852    0.01342  -4.361 2.64e-05 ***
log2(Tm)          -0.03714    0.00855  -4.344 2.82e-05 ***
Residual standard error: 0.1213 on 128 degrees of freedom
(4973 observations deleted due to missingness)
Multiple R-squared:  0.1863, Adjusted R-squared:  0.1735
F-statistic: 14.65 on 2 and 128 DF,  p-value: 1.866e-06

• lm(formula = CtoTSkew ~ log2(Temperature + 2) + log2(Tm), data = SynNuc)
(Intercept)      -0.006336    0.082967  -0.076  0.9392
log2(Temperature + 2) 0.043809    0.018168    2.411  0.0173 *
log2(Tm)           0.011212    0.011575    0.969  0.3345
Residual standard error: 0.1642 on 128 degrees of freedom
(4973 observations deleted due to missingness)
Multiple R-squared:  0.04399, Adjusted R-squared:  0.02905
F-statistic: 2.945 on 2 and 128 DF,  p-value: 0.05618

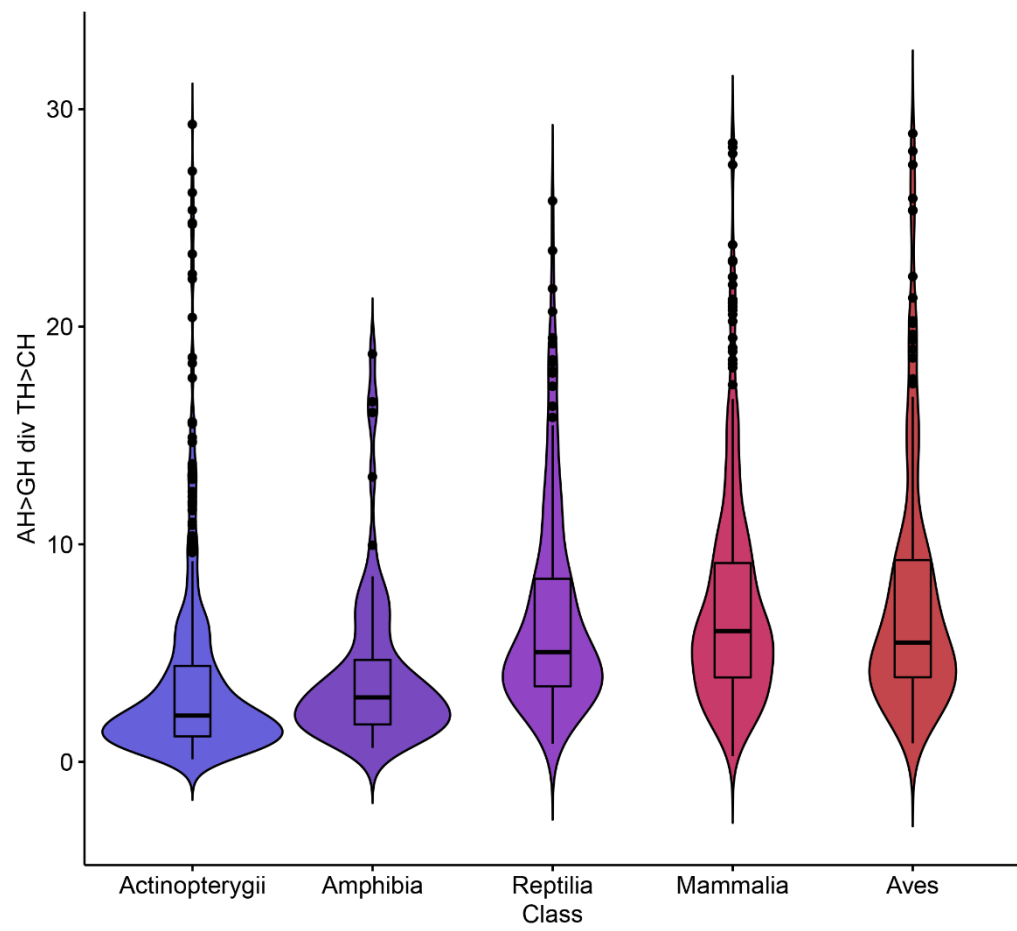
```

3. Whole genomes of Mammalis versus temperature and longevity (Generation length):

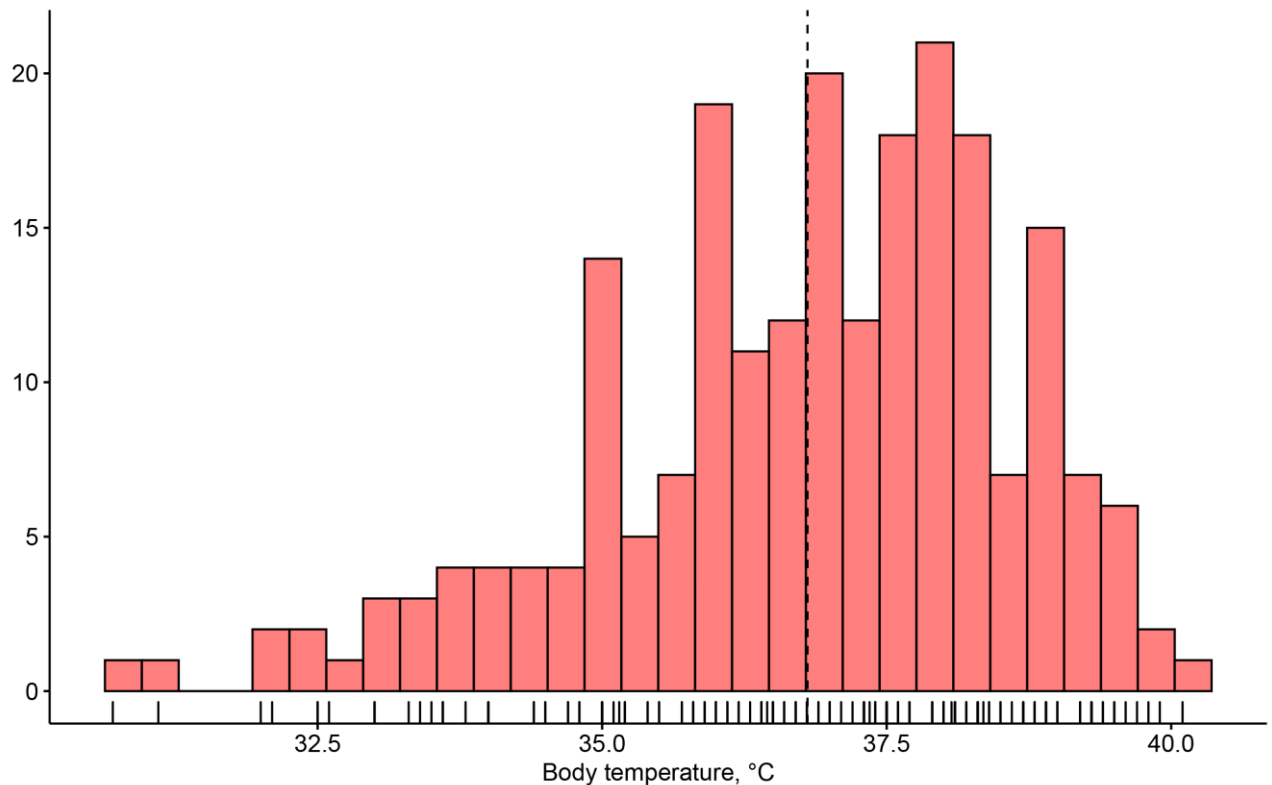
a. Average body temperature in Vertebrate classes (AnAge DB):



b. Average $A_H > G_H / T_H > C_H$ in Vertebrate classes:



c. A range of known mammalian body temperature:



d. Multiple model between $S_{AC}S_{TG}$ skew and temperature + longevity:

```

• lm(formula = TG_ACSkew ~ scale(Temper) + scale(GenerationLength_d), data =
  allparameters)
(Intercept)      -0.505937  0.006107 -82.839 < 2e-16 ***
scale(Temper)      -0.011729  0.006047 -1.940 0.053679 .
scale(GenerationLength_d) -0.028182  0.007514 -3.751 0.000225 ***
Residual standard error: 0.09029 on 221 degrees of freedom
(425 observations deleted due to missingness)
Multiple R-squared:  0.07463, Adjusted R-squared:  0.06626
F-statistic: 8.912 on 2 and 221 DF,  p-value: 0.0001896

```

e. Multiple model between $S_{AC}S_{TG}$ skew and longevity + all cold groups (incl. cold species t° mean <36.8):

```

• lm(formula = TG_ACSkew ~ log2(GenerationLength_d) + scale(allcolddummy), data =
  allparameters)
(Intercept)      -0.314532  0.030680 -10.252 < 2e-16 ***
log2(GenerationLength_d) -0.018255  0.002761 -6.611 8.00e-11 ***
scale(allcolddummy)    0.017912  0.003106  5.768 1.25e-08 ***
Residual standard error: 0.07848 on 646 degrees of freedom
Multiple R-squared:  0.1192, Adjusted R-squared:  0.1164
F-statistic: 43.69 on 2 and 646 DF,  p-value: < 2.2e-16

```

f. Multiple model between TC skew and all cold groups (incl. cold species t° mean <36.8):

```

• lm(formula = TtoCSkew ~ scale(Temper) + scale(GenerationLength_d), data =
  allparameters)
(Intercept)      -0.19540  0.01201 -16.264 < 2e-16 ***
scale(Temper)      -0.02751  0.01189 -2.313 0.0216 *
scale(GenerationLength_d) -0.09565  0.01478 -6.471 6.18e-10 ***
Residual standard error: 0.1776 on 221 degrees of freedom
(425 observations deleted due to missingness)
Multiple R-squared:  0.176, Adjusted R-squared:  0.1686
F-statistic: 23.61 on 2 and 221 DF,  p-value: 5.103e-10

```

g. Multiple model between fraction of T and all cold groups (incl. cold species t° mean <36.8):

LIGHT CHAIN NOTATION!

```
• lm(formula = FrT ~ log2(GenerationLength_d) + scale(allcolddummy), data =
  allparameters)
(Intercept)      0.326964  0.016474 19.848 < 2e-16 ***
log2(GenerationLength_d) -0.012105  0.001483 -8.164 1.70e-15 ***
scale(allcolddummy)      0.010043  0.001668  6.023 2.88e-09 ***
Residual standard error: 0.04214 on 646 degrees of freedom
Multiple R-squared:  0.1527,    Adjusted R-squared:  0.1501
F-statistic: 58.21 on 2 and 646 DF,  p-value: < 2.2e-16

• lm(formula = FrT ~ log2(GenerationLength_d), data = allparameters)
(Intercept)      0.338815  0.016796 20.173 <2e-16 ***
log2(GenerationLength_d) -0.013177  0.001512 -8.718 <2e-16 ***
Residual standard error: 0.04328 on 647 degrees of freedom
Multiple R-squared:  0.1051,    Adjusted R-squared:  0.1037
F-statistic: 76 on 1 and 647 DF,  p-value: < 2.2e-16

• lm(formula = FrT ~ scale(GenerationLength_d) + scale(allcolddummy), data =
  allparameters)
(Intercept)      0.193148  0.001694 114.050 < 2e-16 ***
scale(GenerationLength_d) -0.009939  0.001706 -5.825 9.03e-09 ***
scale(allcolddummy)      0.010528  0.001706  6.170 1.20e-09 ***
Residual standard error: 0.04314 on 646 degrees of freedom
Multiple R-squared:  0.1119,    Adjusted R-squared:  0.1092
F-statistic: 40.7 on 2 and 646 DF,  p-value: < 2.2e-16
```

h. Multiple model between fraction of T and temperature + longevity:

```
• lm(formula = FrT ~ scale(GenerationLength_d) + scale(Temper), data = allparameters)
(Intercept)      0.196165  0.003304 59.376 < 2e-16 ***
scale(GenerationLength_d) -0.021853  0.004065 -5.376 1.93e-07 ***
scale(Temper)      -0.006774  0.003271 -2.071 0.0395 *
Residual standard error: 0.04884 on 221 degrees of freedom
(425 observations deleted due to missingness)
Multiple R-squared:  0.1306, Adjusted R-squared:  0.1227
F-statistic: 16.59 on 2 and 221 DF,  p-value: 1.933e-07
```

i. Multiple model between fraction of T and cold species (t° mean <36.8):

```
• lm(formula = FrT ~ scale(GenerationLength_d) + scale(colddummy), data = allparameters)
(Intercept)      0.193148  0.001726 111.933 < 2e-16 ***
scale(GenerationLength_d) -0.010730  0.001731 -6.199 1.02e-09 ***
scale(colddummy)      0.006220  0.001731  3.594 0.000351 ***
Residual standard error: 0.04396 on 646 degrees of freedom
Multiple R-squared:  0.078, Adjusted R-squared:  0.07514
F-statistic: 27.32 on 2 and 646 DF,  p-value: 4.058e-12
```

j. Fraction of A versus longevity in mammals:

LIGHT CHAIN NOTATION!

