1. MutSpec of Actinipterigii versus temperature and longevity (Time of maturation)

LIGHT CHAIN NOTATION!

A. all nominally significant spearman rank correlations between fractions of 4 transitions and temp:

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. multiple model between temp 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

C. 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

- **other transitions give p-value >0,1**

D. all multiple models between fractions of T_C and temp + longevity:

N=65

- lm(formula = T_C ~ scale(Temperature) * scale(Tm), data = 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

VertebratePolymorphisms.MutSpecComparisons.Ecology.Actinopterygii.MutSpectrum.R
VertebratePolymorphisms.MutSpecComparisons.Ecology.Actinopterygii.FishBaseData.R

Fig1A
Fig1B
Fig1C

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

- lm(formula = T_C ~ scale(Temperature) + scale(Tm), data = 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
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

E. all multiple models between TCdivAG and temp + 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

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

A. whole genome analysis vs temperature ALL genes

- 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
-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. Fraction of nucleotides versus Temp and 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

- 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

WholeGenomeAnalyses.EcologyAndMutSpecChordata.ActinopterygiiFishBaseData.R

Fig2A

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

C. Skews vs temp and maturation

- 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
all:
lm(formula = TtoCSkew ~ log2(Temperature + 2) + log2(Tm), data = SynNuc)

Residuals:
Min 1Q Median 3Q Max
-0.32465 -0.09402 -0.03624 0.06334 0.60995

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(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

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

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

Call:
lm(formula = TG_ACSkew ~ log2(Temperature + 2) + log2(Tm), data = SynNuc)

Residuals:
Min 1Q Median 3Q Max
-0.250963 -0.050503 -0.002484 0.044010 0.278793

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(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 ***

```
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

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

Call:
lm(formula = TG_ACSkew ~ scale(Temperature + 2) + scale(Tm),
    data = SynNuc)

Residuals:
      Min        1Q    Median        3Q       Max
-0.251003 -0.054465  0.001959  0.044391  0.252806

Coefficients:
                    Estimate Std. Error t value Pr(>|t|)
(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 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

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
```

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

A. multiple model between fraction of T and temperature + generation length

- 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

B. multiple model between fraction of T and cold species (mean temp 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

C. multiple model between fraction of T and all cold groups (incl. cold species <36.8)

- 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

D. multiple model between AC_TG skew and all cold groups (incl. cold species <36.8)

- lm(formula = TG_ACSkew ~ scale(Temper) + scale(GenerationLength_d),
data = allparameters)

Residuals:
Min 1Q Median 3Q Max
-0.214389 -0.063779 0.000369 0.065939 0.218460

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(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 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.09029 on 221 degrees of freedom
(425 observations deleted due to missingness)

WholeGenomeAnalyses.EcologyAndMutSpecChordata.Mammals.KuptsovData.R

Fig3

Multiple R-squared: 0.07463, Adjusted R-squared: 0.06626
F-statistic: 8.912 on 2 and 221 DF, p-value: 0.0001896

- lm(formula = TG_ACSkew ~ log2(GenerationLength_d) + scale(allcolddummy), data = allparameters)

Residuals:
Min 1Q Median 3Q Max
-0.219527 -0.059518 -0.006372 0.055587 0.217413

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(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 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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

E. multiple model between fraction of T and Xenantra

- lm(formula = FrT ~ scale(GenerationLength_d) + scale(Xen), data = allparameters)

(Intercept) 0.193148 0.001662 116.218 < 2e-16 ***
scale(GenerationLength_d) -0.011780 0.001665 -7.075 3.90e-12 ***
scale(Xen) -0.013354 0.001665 -8.020 4.97e-15 ***
Residual standard error: 0.04234 on 646 degrees of freedom
Multiple R-squared: 0.1447, Adjusted R-squared: 0.1421
F-statistic: 54.66 on 2 and 646 DF, p-value: < 2.2e-16

- lm(formula = FrT ~ scale(GenerationLength_d) + scale(Xen) + scale(allcolddummy), data = allparameters)

(Intercept) 0.193148 0.001593 121.211 < 2e-16 ***
scale(GenerationLength_d) -0.010427 0.001606 -6.491 1.70e-10 ***
scale(Xen) -0.014793 0.001608 -9.202 < 2e-16 ***
scale(allcolddummy) 0.012282 0.001617 7.596 1.07e-13 ***
Residual standard error: 0.04059 on 645 degrees of freedom
Multiple R-squared: 0.215, Adjusted R-squared: 0.2113
F-statistic: 58.87 on 3 and 645 DF, p-value: < 2.2e-16

F. multiple model between fraction of G and Xenantra

- lm(formula = FrG ~ scale(GenerationLength_d), data = allparameters)

(Intercept) 0.0486843 0.0007496 64.947 <2e-16 ***
scale(GenerationLength_d) 0.0008111 0.0007502 1.081 0.28
Residual standard error: 0.0191 on 647 degrees of freedom
Multiple R-squared: 0.001803, Adjusted R-squared: 0.0002607
F-statistic: 1.169 on 1 and 647 DF, p-value: 0.28

- lm(formula = FrG ~ scale(GenerationLength_d) + scale(Hib.unconfirmedHib), data = allparameters)

(Intercept) 0.0486843 0.0007491 64.993 <2e-16 ***
scale(GenerationLength_d) 0.0008504 0.0007502 1.134 0.257
scale(Hib.unconfirmedHib) 0.0010408 0.0007502 1.387 0.166
Residual standard error: 0.01908 on 646 degrees of freedom
Multiple R-squared: 0.004769, Adjusted R-squared: 0.001688
F-statistic: 1.548 on 2 and 646 DF, p-value: 0.2135

- lm(formula = FrG ~ scale(allcolddummy), data = allparameters)

(Intercept) 0.0486843 0.0007480 65.086 <2e-16 ***
scale(allcolddummy) -0.0014891 0.0007486 -1.989 0.0471 *
Residual standard error: 0.01906 on 647 degrees of freedom
Multiple R-squared: 0.006079, Adjusted R-squared: 0.004543

F-statistic: 3.957 on 1 and 647 DF, p-value: 0.0471

- lm(formula = FrG ~ scale(GenerationLength_d) * scale(allcolddummy), data = allparameters)

(Intercept) 0.0491286 0.0007429 66.135 < 2e-16 ***
scale(GenerationLength_d) 0.0011614 0.0007504 1.548 0.122
scale(allcolddummy) -0.0007401 0.0007563 -0.979 0.328
scale(GenerationLength_d):scale(allcolddummy) 0.0038472 0.0008318 4.625 4.52e-06 ***
Residual standard error: 0.01877 on 645 degrees of freedom
Multiple R-squared: 0.03908, Adjusted R-squared: 0.03461
F-statistic: 8.744 on 3 and 645 DF, p-value: 1.084e-05

G. mulltiple model between TC skew and all cold groups (incl. cold species <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