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| 1. MutSpec of Actinipterigii versus temperature and longevity (Time of maturation) | 1. **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**  1. **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   1. **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**  1. **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  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   1. **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 | VertebratePolymorphisms.MutSpecComparisons.Ecology.Actinopterygii.MutSpectrum.R  VertebratePolymorphisms.MutSpecComparisons.Ecology.Actinopterygii.FishBaseData.R | [Fig1A](https://github.com/polarsong/mtDNA_mutspectrum/blob/TemperatureVSVertabrates/Body/4Figures/VertebratePolymorphisms.MutSpecComparisons.Analyses.Ecology.Actinopterygii.FishBaseData.FIGURE1A.pdf)  [Fig1B](https://github.com/polarsong/mtDNA_mutspectrum/blob/TemperatureVSVertabrates/Body/4Figures/VertebratePolymorphisms.MutSpecComparisons.Analyses.Ecology.Actinopterygii.FishBaseData.FIGURE1B.pdf)  [Fig1C](https://github.com/polarsong/mtDNA_mutspectrum/blob/TemperatureVSVertabrates/Body/4Figures/VertebratePolymorphisms.MutSpecComparisons.Analyses.Ecology.Actinopterygii.FishBaseData.FIGURE1C.pdf) |
| 1. Whole genomes of Actinipterigii versus temperature and longevity (Time of maturation) | 1. **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**   1. **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) 0.422770 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  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   1. **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 | WholeGenomeAnalyses.EcologyAndMutSpecChordata.Actinopterygii.FishBaseData.R | [Fig2A](https://github.com/polarsong/mtDNA_mutspectrum/blob/TemperatureVSVertabrates/Body/4Figures/WholeGenomeAnalyses.NucContent.Analyses.Ecology.Actinopterygii.FishBaseData.FIGURE2A.pdf) |
| 1. Whole genomes of Mammalia versus temperature and longevity (Generation length) | 1. **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   1. **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   1. **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   1. **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   1. **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 | WholeGenomeAnalyses.EcologyAndMutSpecChordata.Mammals.KuptsovData.R | [Fig3](https://github.com/polarsong/mtDNA_mutspectrum/blob/TemperatureVSVertabrates/Body/4Figures/WholeGenomeAnalyses.EcologyAndMutSpecChordata.Mammals.KuptsovData.FIGURE3.pdf) |