# Electronic supplementary materials for: Developmental temperature and repeatability of metabolic rate across temperatures

*Heterogenous Variance*

Model with homogenous variance was best supported by WAIC values. As such, we did not explicitly model residuals in all subsequent models

**Table S1** Comparisons of WAIC values for homogenous and hetergenous residuals

|  |  |  |  |
| --- | --- | --- | --- |
| Model | WAIC value | ELPD Diff | SE Diff |
| Homogenous residuals | -3.61 | 0 | 0 |
| Heterogenous residuals | -2.09 | -0.76 | 2.08 |

*The Influence of Developmental Temperature on the Thermal Reaction Norm of Metabolic Rate*

**Table S2** Model coefficients of full model testing whether developmental temperature affects the elevation and slope of the thermal reaction norm of metabolic rate. This model used a complete case dataset, n = 3818. The intercept is the cold developmental temperature. Mass and MR was log transformed and Age was z-transformed. Bolded estimates are significantly different from zero. COV represents covariance.

|  |  |  |  |
| --- | --- | --- | --- |
| Parameter | Estimate | Lower | Upper |
| *Fixed effects* |  |  |  |
| Intercept | **-6.294** | **-6.364** | **-6.22** |
| Treatment 29 | -0.001 | -0.062 | 0.058 |
| Temperature | **0.262** | **0.246** | **0.279** |
| Mass | **0.129** | **0.105** | **0.152** |
| Age | -0.035 | -0.078 | 0.008 |
| Treatment 29 Temperature | -0.016 | -0.039 | 0.006 |
| *Random Effects* |  |  |  |
| Lizard Identity |  |  |  |
| Intercept | **0.009** | **0.006** | **0.015** |
| Slope | **9.77e-5** | **1.12e-7** | **0.001** |
| COVIntercept – Slope | -0.00018 | -0.00128 | 0.000692 |
| Sampling Session |  |  |  |
| Intercept | **0.01** | **0.003** | **0.031** |
| Measurement Error |  |  |  |
| Intercept | **0.044** | **0.04** | **0.048** |
| Residual | **0.041** | **0.038** | **0.043** |

**Table S3** Model coefficients of main effects model testing developmental temperature affects the elevation of the thermal reaction norm of metabolic rate. This model used an imputed dataset of n = 6000. The intercept is the cold developmental temperature. Note that the imputation model also estimates an intercept and residual variance for mass as it was also missing data. MR were log transformed and mass, age and temperature was z-transformed. Bolded estimates are significantly different from zero. COV represents covariance.

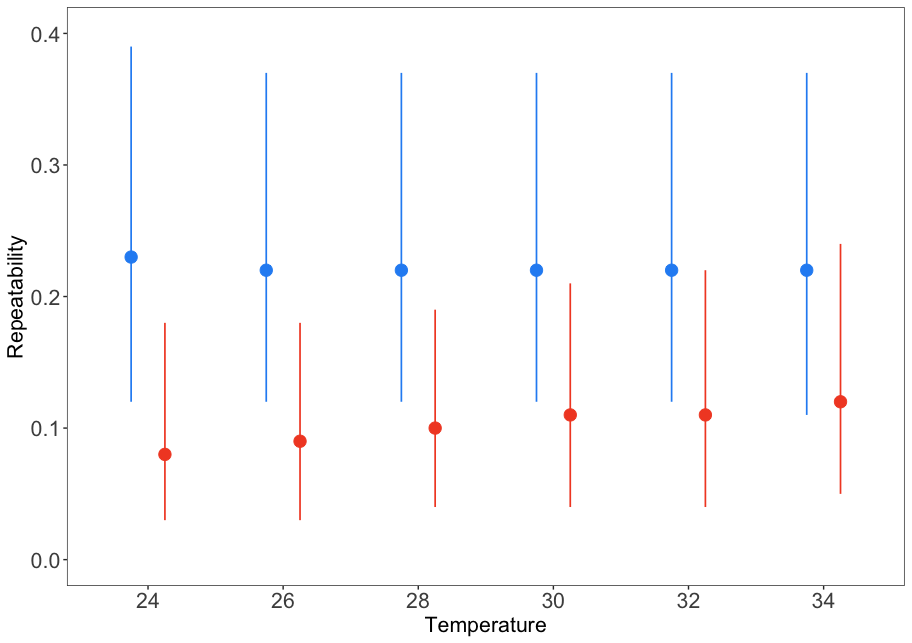
|  |  |  |  |
| --- | --- | --- | --- |
| Parameter | Estimate | Lower | Upper |
| *Fixed effects* |  |  |  |
| Intercept | **-6.292** | **-6.366** | **-6.219** |
| Treatment 29 | -0.003 | -0.062 | 0.055 |
| Temperature | **0.254** | **0.241** | **0.265** |
| Age | -0.034 | -0.077 | 0.009 |
| Mass | **0.128** | **0.104** | **0.152** |
| *Random Effects* |  |  |  |
| Lizard Identity |  |  |  |
| Intercept | **0.009** | **0.006** | **0.014** |
| Slope | **1.01e-4** | **6.34-8** | **0.00048** |
| COVIntercept – Slope | -0.00017 | -0.00122 | 0.000672 |
| Sampling Session |  |  |  |
| Intercept | **0.01** | **0.003** | **0.028** |
| Measurement Error |  |  |  |
| Intercept | **0.044** | **0.04** | **0.049** |
| Residuals | **0.041** | **0.038** | **0.044** |

**Table S4** Model coefficients of main effects model testing developmental temperature affects the elevation of the thermal reaction norm of metabolic rate. This model used a complete case dataset, n = 3818. The intercept is the cold developmental temperature. MR were log transformed and mass, age and temperature were z-transformed. Bolded estimates are significantly different from zero. COV represents covariance.

|  |  |  |  |
| --- | --- | --- | --- |
| Parameter | Estimate | Lower | Upper |
| *Fixed effects* |  |  |  |
| Intercept | **-6.293** | **-6.373** | **-6.218** |
| Treatment 29 | -0.003 | -0.064 | 0.057 |
| Temperature | **0.254** | **0.242** | **0.266** |
| Mass | **0.128** | **0.107** | **0.15** |
| Age | -0.034 | -0.078 | 0.008 |
| *Random Effects* |  |  |  |
| Lizard Identity |  |  |  |
| Intercept | **0.009** | **0.006** | **0.015** |
| Slope | **9.90e-5** | **1.24e-7** | **0.001** |
| COVIntercept – Slope | -0.000184 | -0.00131 | 0.000648 |
| Sampling Session |  |  |  |
| Intercept | **0.01** | **0.003** | **0.028** |
| Measurement Error |  |  |  |
| Intercept | **0.044** | **0.04** | **0.049** |
| Residuals | **0.041** | **0.038** | **0.043** |

We expected that treatment differences in thermal reaction norms would be greatest at the beginning of the study, as such we ran the full interaction model for just the first sampling session (nobservations= 600). Similar to the overall result, we found that developmental temperatures did not affect the intercept nor the slope of the thermal reaction norm (Estimate: Treatment 29 Temperature = 0, 95% CI [-0.02 -0.02]).

*The Influence of Developmental Temperature on the Repeatability of the Thermal Reaction Norm and Temperature Specific Repeatability of Metabolic Rate*



**Figure S1.** Adjusted repeatability for average metabolic rate for the ‘cold’ developmental temperature group (blue) and the ‘hot’ developmental temperature group (red). Estimates were calculated from a complete case analysis. There were no significant differences among treatment in repeatability estimates (see Table S5). Repeatability did not change with acute temperature. Error bars represent 95% credible intervals.

**Table S5** Temperature specific, adjusted repeatability estimates of log transformed metabolic rate for lizards from two developmental temperatures (nhot = 25, ncold = 26). These values were estimated from complete case dataset, nobs = 3818. Bolded values are significantly different from zero. There were no statistical differences among treatments at each acute temperature. T represents acute temperature, R represents repeatability, L and U represents the lower and upper 95% credible intervals, pd is the probability of direction

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Cold  nlizards = 26 | | | | Hot  nlizards = 25 | | | Treatment difference  (Hot - Cold) | | | |
| *T* (ºC) | *R* | L | U | *R* | L | U | Mean  difference | L | U | *pd* |
| 24 | **0.24** | **0.12** | **0.4** | **0.09** | **0.03** | **0.2** | -0.146 | -0.310 | 0.015 | 96.5% |
| 26 | **0.23** | **0.12** | **0.38** | **0.09** | **0.03** | **0.19** | -0.137 | -0.295 | 0.016 | 96.25% |
| 28 | **0.22** | **0.12** | **0.37** | **0.09** | **0.03** | **0.19** | -0.126 | -0.281 | 0.022 | 95.95% |
| 30 | **0.21** | **0.11** | **0.36** | **0.1** | **0.04** | **0.2** | -0.113 | -0.271 | 0.031 | 94.25% |
| 32 | **0.21** | **0.1** | **0.36** | **0.11** | **0.04** | **0.22** | -0.099 | -0.259 | 0.053 | 91% |
| 34 | **0.2** | **0.09** | **0.35** | **0.12** | **0.04** | **0.25** | -0.084 | -0.253 | 0.082 | 85.95% |



**Figure S2.** Violin plots of variance components for average metabolic rate for the ‘cold’ developmental temperature group (blue) and the ‘hot’ developmental temperature group (red) irrespective of acute temperature. *pd*Among ID = 98.35% , *pd*Residual = 100%.

**Table S6** Model coefficients of model whether body mass, temeperature and age predicts variation in metabolic rate. In this model, we fitted a ‘series’ as random intercept with temeperature as a random slope to estimate repeatability of the slope. See Statistical Analyses for details. This imputation model used a subset dataset of lizards in the cold developmental temperature only n = 26, nobs = 3000. MR were log transformed and mass, age and temperature were z-transformed. Bolded estimates are significantly different from zero. COV represents covariance.

|  |  |  |  |
| --- | --- | --- | --- |
| Parameter | Estimate | Lower | Upper |
| *Fixed effects* |  |  |  |
| Intercept | **-6.289** | **-6.342** | **-6.237** |
| Temperature | **0.261** | **0.244** | **0.278** |
| Age | -0.012 | -0.049 | 0.029 |
| Mass | **0.136** | **0.099** | **0.172** |
| *Random Effects* |  |  |  |
| Lizard Identity |  |  |  |
| Intercept | **0.015** | **0.007** | **0.028** |
| Slope | **0.00021** | **1.70e-7** | **0.001** |
| COVIntercept – Slope | -0.000579 | -0.00303 | 0.00084 |
| Series (Within individual) |  |  |  |
| Intercept | **0.015** | **0.01** | **0.022** |
| Slope | **0.0003** | **3.62e-7** | **0.002** |
| COVIntercept – Slope | -0.00043 | -0.00273 | 0.00136 |
| Measurement Error |  |  |  |
| Intercept | **0.037** | **0.03** | **0.043** |
| Residuals | **0.045** | **0.041** | **0.049** |

**Table S7** Model coefficients of model whether body mass, temeperature and age predicts variation in metabolic rate. In this model, we fitted a ‘series’ as random intercept with temeperature as a random slope to estimate repeatability of the slope. See Statistical Analyses for details. This imputation model used a subset dataset of lizards in the hot developmental temperature only n = 25, nobs = 3000. MR were log transformed and mass, age and temperature was z-transformed. Bolded estimates are significantly different from zero. COV represents covariance.

|  |  |  |  |
| --- | --- | --- | --- |
| Parameter | Estimate | Lower | Upper |
| *Fixed effects* |  |  |  |
| Intercept | **-6.299** | **-6.328** | **-6.268** |
| Temperature | **0.245** | **0.229** | **0.262** |
| Age | -0.003 | -0.038 | 0.03 |
| Mass | **0.124** | **0.093** | **0.155** |
| *Random Effects* |  |  |  |
| Lizard Identity |  |  |  |
| Intercept | **0.003** | **0** | **0.008** |
| Slope | **0.0003** | **8.50e-7** | **0.001** |
| COVIntercept – Slope | 0.000272 | -0.000577 | 0.00153 |
| Series (Within individual, among sessions) |  |  |  |
| Intercept | **0.001** | **0** | **0.002** |
| Slope | **0.00053** | **2.38e-6** | **0.002** |
| COVIntercept – Slope | -0.00134 | -0.00388 | 0.000432 |
| Measurement Error |  |  |  |
| Intercept | **0.035** | **0.03** | **0.041** |
| Residuals | **0.037** | **0.034** | **0.041** |

**Table S8** Model coefficients of model whether body mass, temeperature and age predicts variation in metabolic rate. In this model, we fitted a ‘series’ as random intercept with temeperature as a random slope to estimate repeatability of the slope. See Statistical Analyses for details. This model used a complete case dataset of lizards in the cold developmental temperature only n = 26, nobs = 1897. MR were log transformed and mass, age and temperature was z-transformed. Bolded estimates are significantly different from zero. COV represents covariance.

|  |  |  |  |
| --- | --- | --- | --- |
| Parameter | Estimate | Lower | Upper |
| *Fixed effects* |  |  |  |
| Intercept | **-6.291** | **-6.342** | **-6.241** |
| Temperature | **0.261** | **0.244** | **0.278** |
| Mass | **0.136** | **0.098** | **0.172** |
| Age | -0.011 | -0.05 | 0.028 |
| *Random Effects* |  |  |  |
| Lizard Identity |  |  |  |
| Intercept | **0.015** | **0.007** | **0.029** |
| Slope | **0.0002** | **3.93e-7** | **0.0009** |
| COVIntercept – Slope | -0.000575 | -0.00289 | 0.000882 |
| Series (Within individual) |  |  |  |
| Intercept | **0.015** | **0.01** | **0.022** |
| Slope | **0.0003** | **2.79e-7** | **0.00015** |
| COVIntercept – Slope | -0.000417 | -0.00283 | 0.00138 |
| Measurement Error |  |  |  |
| Intercept | **0.037** | **0.03** | **0.044** |
| Residual | **0.045** | **0.041** | **0.049** |

**Table S9** Model coefficients of model whether body mass, temeperature and age predicts variation in metabolic rate. In this model, we fitted a ‘series’ as random intercept with temeperature as a random slope to estimate repeatability of the slope. See Statistical Analyses for details. This model used a complete case dataset of lizards in the hot developmental temperature only n = 25, nobs = 1921. MR were log transformed and mass, age and temperature was z-transformed. Bolded estimates are significantly different from zero. COV represents covariance. Values with \* indicate very small values that are still greater than zero

|  |  |  |  |
| --- | --- | --- | --- |
| Parameter | Estimate | Lower | Upper |
| *Fixed effects* |  |  |  |
| Intercept | **-6.298** | **-6.329** | **-6.268** |
| Temperature | **0.246** | **0.229** | **0.263** |
| Mass | **0.124** | **0.095** | **0.155** |
| Age | -0.004 | -0.037 | 0.03 |
| *Random Effects* |  |  |  |
| Lizard Identity |  |  |  |
| Intercept | **0.003** | **2.5e-4** | **0.008** |
| Slope | **0.0003** | **4.3e-7** | **0.001** |
| COVIntercept – Slope | 0.000308 | -0.000551 | 0.00158 |
| Series (Within individual, among sessions) |  |  |  |
| Intercept | **0.013** | **0.008** | **0.019** |
| Slope | **0.0005** | **1.13e-6** | **0.002** |
| COVIntercept – Slope | -0.00134 | -0.00366 | 0.00037 |
| Measurement Error |  |  |  |
| Intercept | **0.035** | **0.03** | **0.042** |
| Residual | **0.037** | **0.034** | **0.041** |

**Table S10** Model coefficients of model whether body mass, temperature and age predict variation in metabolic rate. This imputation model used a subset dataset of lizards in the cold developmental temperature only n = 26, nobs = 3000*.* MR were log transformed and mass, age and temperature were z-transformed.Bolded estimates are significantly different from zero. COV represents covariance. Values with \* indicate very small values that are still greater than zero.

|  |  |  |  |
| --- | --- | --- | --- |
| Parameter | Estimate | Lower | Upper |
| *Fixed effects* |  |  |  |
| Intercept MR | **-6.29** | **-6.368** | **-6.211** |
| Temperature | **0.262** | **0.243** | **0.279** |
| Age | -0.025 | -0.093 | 0.036 |
| Mass | **0.117** | **0.081** | **0.153** |
| *Random Effects* |  |  |  |
| Lizard Identity |  |  |  |
| Intercept | **0.015** | **0.008** | **0.028** |
| Slope | **0.0002** | **2.1e-7** | **0.001** |
| COVIntercept – Slope | -0.000628 | -0.00292 | 0.000782 |
| Sampling Session |  |  |  |
| Intercept | **0.01** | **0.003** | **0.028** |
| Measurement Error |  |  |  |
| Intercept | **0.046** | **0.039** | **0.053** |
| Residual MR | **0.045** | **0.041** | **0.049** |

**Table S11** Model coefficients of model whether body mass, temperature and age predict variation in metabolic rate. This imputation model used a subset dataset of lizards in the hot developmental temperature only n = 25, n*o*bs = 3000*.* Note that the imputation model also estimates an intercept and residual variance for mass as it was also missing data. MR were log transformed and mass, age and temperature was z-transformed. Bolded estimates are significantly different from zero. Values with \* indicate very small values that are still greater than zero.

|  |  |  |  |
| --- | --- | --- | --- |
| Parameter | Estimate | Lower | Upper |
| *Fixed effects* |  |  |  |
| Intercept MR | **-6.296** | **-6.365** | **-6.228** |
| Temperature | **0.246** | **0.229** | **0.264** |
| Age | -0.025 | -0.072 | 0.022 |
| Mass | **0.132** | **0.104** | **0.164** |
| *Random Effects* |  |  |  |
| Lizard Identity |  |  |  |
| Intercept | **0.005** | **0.002** | **0.011** |
| Slope | **0.0002** | **6.01e-7** | **0.001** |
| COVIntercept – Slope | 0.000277 | -0.000651 | 0.00152 |
|  |  |  |  |
| Sampling Session |  |  |  |
| Intercept | **0.009** | **0.003** | **0.025** |
| Measurement Error |  |  |  |
| Intercept | **0.043** | **0.037** | **0.049** |
| Residuals | **0.037** | **0.034** | **0.041** |

**Table S12** Model coefficients of model testing whether body mass, temperature and age predict variation in metabolic rate. This model used a complete case dataset of lizards in the cold developmental temperature only n = 26, nobs = 1897. The intercept is the cold developmental temperature. MR were log transformed and mass, age and temperature were z-transformed. Bolded estimates are significantly different from zero. Values with \* indicate very small values that are still greater than zero

|  |  |  |  |
| --- | --- | --- | --- |
| Parameter | Estimate | Lower | Upper |
| *Fixed effects* |  |  |  |
| Intercept | **-6.293** | **-6.376** | **-6.214** |
| Temperature | **0.262** | **0.244** | **0.28** |
| Mass | **0.118** | **0.081** | **0.155** |
| Age | -0.027 | -0.094 | 0.037 |
| *Random Effects* |  |  |  |
| Lizard Identity |  |  |  |
| Intercept | **0.016** | **0.008** | **0.03** |
| Slope | **0.0002** | **3.68e-7** | **0.001** |
| COVIntercept – Slope | -0.000663 | -0.00306 | 0.000776 |
| Sampling Session |  |  |  |
| Intercept | **0.011** | **0.003** | **0.034** |
| Measurement Error |  |  |  |
| Intercept | **0.046** | **0.039** | **0.053** |
| Residual | **0.045** | **0.041** | **0.049** |

**Table S13** Model coefficients of model testing whether body mass, temperature and age predict variation in metabolic rate. This imputation model used a complete case dataset of lizards in the hot developmental temperature only n = 25, nobs = 1921. The intercept is the cold developmental temperature. MR were log transformed and mass, age and temperature were z-transformed. Bolded estimates are significantly different from zero. Values with \* indicate very small values that are still greater than zero

|  |  |  |  |
| --- | --- | --- | --- |
| Parameter | Estimate | Lower | Upper |
| *Fixed effects* |  |  |  |
| Intercept | **-6.293** | **-6.361** | **-6.222** |
| Temperature | **0.246** | **0.229** | **0.263** |
| Mass | **0.133** | **0.102** | **0.164** |
| Age | -0.025 | -0.07 | 0.018 |
| *Random Effects* |  |  |  |
| Lizard Identity |  |  |  |
| Intercept | **0.005** | **0.002** | **0.01** |
| Slope | **0.00027** | **2.62e-7** | **0.001** |
| COVIntercept – Slope | 0.000255 | -0.000688 | 0.00171 |
| Sampling Session |  |  |  |
| Intercept | **0.009** | **0.003** | **0.026** |
| Measurement Error |  |  |  |
| Intercept | **0.043** | **0.037** | **0.049** |
| Residuals | **0.037** | **0.034** | **0.041** |