## Analyses Methods

* Hamiltonian Monte Carlo from rstan using rethinking package.
* Model setup:
  + 10,000 iterations with 1000 for warmup.
  + 4 chains.
* Priors – same for all models:
  + a ~ dnorm(0.25, 1)
  + b ~ dnorm(0, 1)
    - b ~ dnorm(0, 10) for comparison with RMR
  + sigma ~ dunif(0, 1)
* Convergence checked through number of effective samples, Rhat, and traceplots.

## Species

* Convergence achieved.
* Means (from Bayesian analysis):
  + K. anderssoni = 0.2459 (sd 0.0227)
  + E. antarctica = 0.2318 (sd = 0.0222)
  + G. braueri = 0.2252 (sd = 0.0223)
  + E. carlsbergi = 0.1958 (sd = 0.0226)
  + P. bolini = 0.1875 (sd 0.0222)
  + G. nicholsi = 0.1526 (sd 0.0222)



Fig – Density plot of 10,000 estimates of M per individual, grouped by species.

* Appear to be three groups:
  + High = K. anderssoni, E. Antarctica and G. braueri
  + Mid = E. carlbergi and P. bolini
  + Low = G. nicholsi



Fig – Cluster analysis with three groups, based on 10,000 M value estimates per individual, grouped by species. Arrow = increasing M.

* Results:
  + G. nicholsi – plots predominately in cluster a
  + P. bolini and E. carlsbergi – plots across clusters but mostly a and b
  + E. Antarctica, G. braueri and K. anderssoni – across clusters but mostly b and c
* A lot of overlap (caused by spread of M for individuals?) but broadly supports the three groupings.

## Comparison with Mass-Specific RMR

* Equation from Belcher et al. 2019.
* Ln(RMR) = –1.315 (±0.468) – 0.2665 (±0.0516) × Ln(RMR) + 0.0848 (±0.0108) × Temperature
  + Temperature from otolith measures.



Fig – M values with Ln(Mass-Specific Respiration) (ul O2 mg WM-1 h-1).

* Would expect positive relationship between respiration and M, if FMR was a simple multiplication of RMR.
* Plots opposite to what we expect – apparent negative relationship.
  + G. nicholsi has highest respiration (because of high temp?) but lowest M values.
  + K. anderssoni has highest M values, but lowest respiration (because of low temp?)
* Bayesian model did not converge (with species as random factor).

## Ln Weight

### Full Model



Fig – M and SD with log10Weight.

* Species as a random factor.
* Flat relationship with weight.
  + b = 0.0044 (SD 0.0133).
  + Could be positive or negative.
* Species tend to group together.
* Unconvinced of proper chain mixing, from traceplots.

|  |  |  |
| --- | --- | --- |
|  | Mean | SD |
| a | 0.2028 | 0.0257 |
| b | 0.0019 | 0.0058 |
| a\_var(ELN) | 0.0270 | 0.0244 |
| a\_var(ELC) | -0.0139 | 0.0251 |
| a\_var(GYR) | 0.0178 | 0.0248 |
| a\_var(GYN) | -0.0573 | 0.0266 |
| a\_var(KRA) | 0.0426 | 0.0262 |
| a\_var(PRM) | -0.0159 | 0.0256 |
| sigma | 0.0040 | 0.0024 |
| sigma\_species | 0.0525 | 0.0294 |

### Within Species

* P. bolini the only species where scaling exponent is consistently inferred as either positive or negative (b = 0.0257 SD 0.0118)
  + Opposite direction to expected – mass specific metabolic rate should decrease with increasing mass.



Fig – M and SD with lnWeight for P. bolini.

## Temperature

### Full Model



Fig – M with temperature, with SD bars.

* Appears to be a negative relationship between M and temperature.
  + Maybe due to pseudoreplication (i.e. replication within species).
* Model with species as a random factor.
* Model did not converge – no relationship.

|  |  |  |
| --- | --- | --- |
|  | Mean | SD |
| a | 0.2091 | 0.0196 |
| b | -0.0018 | 0.0019 |
| a\_var(ELN) | 0.0227 | 0.0200 |
| a\_var(ELC) | -0.0106 | 0.0205 |
| a\_var(GYR) | 0.0137 | 0.0199 |
| a\_var(GYN) | -0.0527 | 0.0204 |
| a\_var(KRA) | 0.0375 | 0.0205 |
| a\_var(PRM) | -0.0207 | 0.0194 |
| sigma | 0.0031 | 0.0023 |
| sigma\_species | 0.0454 | 0.0233 |

### Within Species

* No species had scaling exponent which was consistently inferred as positive or negative.