## D13C - Initial Analysis

### Species Differences

#### Boxplot

* Most negative d13C (highest MR):
  + E. Antarctica
  + G. braueri
  + K. andersoni
* Least negative d13C (lowest MR):
  + E. carlsbergi
  + G. nicholsi
  + P. bolini

#### Kruskal-Wallis Test

* Significant difference between species.
  + Chi-squared = 82.414
  + Df = 5
  + p-value = 2.61 x 10^-16

#### Dunn Test (from dunn.test package)

* Bonferroni correction

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | E. antarctica | E. carlsbergi | G. braueri | G. nicholsi | P. bolini | K. anderssoni |
| E. Antarctica |  | <0.01 | N/S | <0.01 | <0.01 | N/S |
| E. carlsbergi | <0.01 |  | <0.01 | N/S | N/S | <0.01 |
| G. braueri | N/S | <0.01 |  | <0.01 | <0.01 | N/S |
| G. nicholsi | <0.01 | N/S | <0.01 |  | N/S | <0.01 |
| P. bolini | <0.01 | N/S | <0.01 | N/S |  | <0.05 |
| K. anderssoni | N/S | <0.01 | N/S | <0.01 | <0.05 |  |

* Supports three groups as seen in boxplot

### Log10\_Weight vs. d13C

#### Plot

* Decrease in d13C with weight with E. carlsbergi and G. nicholsi as outliers.
  + Decrease in mass specific metabolic rate with weight (expected).

#### Spearman’s Rank Test

* No significant correlation between d13C and log10\_Weight.
  + Rho = -0.0292
  + P = 0.7637

### D18O vs. d13C

#### Plot

* Decrease in d13C with increase in d18O. H
  + Higher metabolic rate at lower temperatures (counter-intuative).

#### Spearman’s Rank Test

* Significant negative correlation.
  + Rho = -0.6721
  + P = 1.695 x 10^-15

### D13C with Depth

* Nothing interesting on the metabolic side.
* E. carlsbergi and G. braueri mostly caught shallow (>250m).

## D13C – Sherwood & Rose & My Data Comparison

### Species Comparisons

* E. Antarctica – same value as *Chaetodon ulietensis* (Pacific double-saddle butterflyfish, Chaetodontidae).
* G. braueri – same value as *Oncorhynchus nerka* (sockeye salmon, Salmonidae).
* K. andersoni – same value as *Maena maena* (now *Spicara maena,* blotched picarel, Centracanthidae).
* E. carlsbergi – same values as *Clupea pallasii* (Pacific herring, Clupeidae).
* G. nicholsi – same values as *Beryx splendens* (splendid alfonsino, Berycidae) and *Osmerus mordax* (rainbow smelt, Osmeridae).
* P. bolini – between *Centrolophus niger* (rudderfish, Centrolophidae) and *Merluccius merluccius* (European hake, Gadidae).
* Possible action?: run data against known RMR and compare.

### K\_caud vs. d13C

#### Spearman’s Rank Analysis

* Significant negative correlation between K\_caud and d13C.
  + Rho = -0.66
  + P = 1.79 x 10^-11

#### Bayesian Analysis (without n as a random factor)

* All species, except G. nicholsi, plot outside 95% HDPI, but within range of other species.
  + Lower d13C than expected given K\_caud.
  + High metabolic rate for activity level.
  + C. maderensis is also below the line.

### D18O vs. d13C

#### Spearman’s Rank Analysis

* Significant positive relationship between d18O and d13C.
  + Rho = 0.52
  + P = 8.26 x 10^-7
  + Increasing MR with increasing temperature.

#### Bayesian Analysis (without n as a random factor)

* Higher d18O than Sherwood & Rose fishes.
  + At lower temperatures.
* G. nicholsi and E. carlsbergi plot within 95% HDPI.
* K. anderssoni, E. Antarctica and G. braueri (and P. bolini, just) all plotting below the line.
  + Lower d13C than expected given d18O.
  + High metabolic rate for temperature.
  + But C. maderensis plots outside HDPI as well.
  + Not metabolic cold adaptation, or it would affect all of them?
* Possible action?: look into metabolic cold adaptation.
* Note: cannot do against weights as they are max. weights and missing for many species.

## M-Values – Initial Analysis

* 0.14 – 0.30
  + SD of estimates with 10,000 replicates: 0.02-0.04

### Species Differences

#### Boxplot

* Higher M
  + K. anderssoni (mean\_M = 0.25 sd\_M = 0.02)
  + E. Antarctica (mean\_M = 0.24 sd\_M = 0.03)
  + G. braueri (mean\_M = 0.24 sd\_M = 0.02)
* Lower M
  + E. carlsbergi (mean\_M = 0.20 sd\_M = 0.01)
  + P. bolini (mean\_M = 0.19 sd\_M = 0.03)
  + G. nicholsi (mean\_M = 0.15 sd\_M = 0.02)

#### Kruskal-Wallis Test

* Repeated 1000 times
* Significant difference between species.
  + Chi-squared = 48.95 (95% HDI 37.92 – 61.35)
  + Df = 5
  + P = 2.26x10^-8 (95% HDI 1.32 x 10^-13 – 1.80 x 10^-07)

With multiple repeats

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | E. antarctica | E. carlsbergi | G. braueri | G. nicholsi | P. bolini | K. anderssoni |
| E. Antarctica |  | 0.04  (0.00 to 1) | 1  (1 to 1) | 7.26e-6  (1.85e-3 to 3.08e-4) | 0.01  (2.64e-4 to 0.49) | 1  (1 to 1) |
| E. carlsbergi |  |  | 0.07  (0.01 to 1) | 0.01  (0.02 to 1) | 1  (1 to 1) | 3.06e-3  (1.74e-6 to 1.85e-1) |
| G. braueri |  |  |  | 9.40e-6  (4.93e-8 to 6.87e-4) | 0.03  (4.42e-5 to 0.80) | 1  (0.58 to 1) |
| G. nicholsi |  |  |  |  | 0.16  (0.05 to 1) | 2.87e-7  (1.03e-10 to 8.04e-6) |
| P. bolini |  |  |  |  |  | 7.35e-4  (1.80e-7 to 3.74e-2) |
| K. anderssoni |  |  |  |  |  |  |

### Log10\_Weight vs. M

#### Plot

* No discernible relationship, apart from GYN (with largest weight) having lowest M.

#### Spearman’s Rank Test

* 1000 repeats
* Significant negative correlation between M and log10\_Weight.
  + Rho = -0.22 (95% HDI -0.31 to -0.12)
  + P = 0.01 (95% HDI 5.65e-5 to 0.16)

### Temperature vs. Species

* Temperature range from -3.43C to 3.88C (sd 1.19 to 1.36).
* Seems low – may be due to parameters being derived from cod data.

#### Plot

* E. carlsbergi (2.76 mean) and G. nicholsi (2.31 mean) found at highest temps.
* G. braueri at lowest temps (mean -1.65).

#### K-W Test

* 1000 repeats
* Significant difference between species.
  + Chi = 52.17 (95% HDI 42.08 to 63.07)
  + P = 9.81e-10 (95% HDI 1.37e-13 to 3.02e-8)

## Model Comparison – Myctophids Only

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Model** | **Model Type** | **a** | **b** | **R-Squared** | **p-Value** | **AIC** |
| **M ~ Temperature** | LM | 0.22 (0.22 to 0.23) | -0.01 (-0.01 to -0.00) | 0.08 (0.03 to 0.19) | 3.21e-4  (1.06e-8 to 3.44 e-2) | -362 (-389 to -339) |
| **M ~ Temperature + (1|Species)** | LMM | 0.21 (0.21 to 0.22) | 0.00 (-0.00 to 0.00) | 0.48 (0.38 to 0.60) | 0.20 (6.39e-4 to 0.94) | -375 (-403 to -347) |
| **M ~ log10(Weight)** | LM | 0.23 (0.22 to 0.24) | -0.02 (-0.03 to 0.01) | 0.05 (0.01 to 0.11) | 6.35e-3 (3.45e-5 to 0.18) | -359 (-378 to -333) |
| **M ~ log10(Weight) + (1|Species)** | LMM | 0.21 (0.20 to 0.23) | 0.00 (-0.01 to 0.00) | 0.50 (0.39 to 0.60) | 0.69 (0.06 to 0.99) | -375 (-402 to -345) |
| **M ~ Temperature \* log10(Weight)** | LM | 0.23 (0.22 to 0.24) | **T**  0.00 (-0.01 to 0.00) | 0.17 (0.09 to 0.26) | **T**  0.05 (2.91e-6 to 0.91) | -368 (-395 to -341) |
| **W**  -0.01 (-0.03 to 0.00) | **W**  0.03 (5.29e-5 to 0.60) |
| **T\*W**  0.00 (-0.01 to 0.00) | **T\*W**  0.09 (0.00 to 0.93) |
| **M ~ Temperature \* log10(Weight) +(1|Species)** | LMM | 0.22 (0.20 to 0.23) | **T**  0.00 (-0.01 to 0.00) | 0.50 (0.37 to 0.64) | **T**  0.10 (0.00 to 0.93) | -358 (-382 to -330) |
| **W**  0.00 (-0.02 to 0.01) |
| **W**  0.16 (0.05 to 0.98) |
| **T\*W**  0.00 (0.00 to 0.01) | **T\*W**  0.36 (0.07 to 1) |

## Bayesian Models

* Iter = 10000
* Warmup = 1000
* Chains = 4
* Adapt\_delta = 0.99

### Log10 Weight

#### Whole Model

* With species as a random factor.
* Does not converge.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Parameter | Value | SD | N\_eff | Rhat |
| A | 0.20 | 0.03 | 307 | 1.01 |
| B | 0.00 | 0.01 | 355 | 1.00 |
| sigma | 0.00 | 0.00 | 75 | 1.07 |
| Sigma\_species | 0.05 | 0.03 | 613 | 1.01 |

#### By Species

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Species | Converge? | a | | | | b | | | | Sigma | | | |
| Mean | SD | N\_eff | Rhat | Mean | SD | N\_eff | R\_hat | Mean | SD | N\_eff | R\_hat |
| ELN | Yes | 0.22 | 0.02 | 6481 | 1 | 0.02 | 0.03 | 6284 | 1 | 0.01 | 0.01 | 1238 | 1 |
| ELC | No | 0.28 | 0.12 | 182 | 1.02 | -0.10 | 0.16 | 204 | 1.02 | 0.01 | 0.01 | 15 | 1.11 |
| GYR | Yes | 0.27 | 0.04 | 756 | 1 | -0.05 | 0.04 | 708 | 1 | 0.01 | 0.01 | 800 | 1 |
| GYN | No | 0.15 | 0.10 | 20 | 1.25 | 0.00 | 0.07 | 20 | 1.25 | 0.01 | 0.00 | 10 | 1.12 |
| KRA | No | 0.25 | 0.01 | 7 | 1.20 | -0.02 | 0.03 | 447 | 1.01 | 0.01 | 0.01 | 8 | 1.14 |
| PRM | Yes? | 0.18 | 0.01 | 5498 | 1 | 0.06 | 0.01 | 4527 | 1 | 0.01 | 0.01 | 857 | 1.01 |

### Temperature

#### Whole Model

* With species as a random factor.
* Does not converge.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Parameter | Value | SD | N\_eff | Rhat |
| A | 0.21 | 0.03 | 316 | 1.03 |
| B | 0.00 | 0.00 | 750 | 1.01 |
| sigma | 0.00 | 0.00 | 0.01 | 1.02 |
| Sigma\_species | 0.05 | 0.03 | 644 | 1.01 |

#### By Species

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Species | Converge? | a | | | | b | | | | Sigma | | | |
| Mean | SD | N\_eff | Rhat | Mean | SD | N\_eff | R\_hat | Mean | SD | N\_eff | R\_hat |
| ELN | Yes | 0.23 | 0.01 | 8307 | 1 | 0.00 | 0.01 | 4813 | 1 | 0.01 | 0.01 | 1495 | 1 |
| ELC | No | 0.18 | 0.02 | 325 | 1.01 | 0.00 | 0.01 | 196 | 1.02 | 0.01 | 0.01 | 74 | 1.05 |
| GYR | No | 0.23 | 0.01 | 2044 | 1.01 | 0.00 | 0.01 | 3486 | 1 | 0.01 | 0.01 | 494 | 1.02 |
| GYN | Yes | 0.15 | 0.01 | 3535 | 1 | 0.00 | 0.01 | 3614 | 1 | 0.01 | 0.01 | 1003 | 1 |
| KRA | Yes | 0.25 | 0.01 | 2677 | 1 | 0.00 | 0.01 | 2429 | 1 | 0.01 | 0.01 | 851 | 1 |
| PRM | Yes  But chains look weird | 0.20 | 0.01 | 3785 | 1 | -0.01 | 0.01 | 2030 | 1 | 0.01 | 0.01 | 663 | 1 |

### Species

* Convergence looks ok?

Mean StdDev lower 0.89 upper 0.89 n\_eff Rhat

a 0.2063 0.0218 0.1732 0.2375 889 1.0031

a\_Var[1] 0.0255 0.0222 -0.0091 0.0568 929 1.0033

a\_Var[2] -0.0105 0.0226 -0.0452 0.0215 1052 1.0026

a\_Var[3] 0.0189 0.0223 -0.0132 0.0527 935 1.0031

a\_Var[4] -0.0537 0.0222 -0.0869 -0.0215 896 1.0028

a\_Var[5] 0.0396 0.0227 0.0061 0.0733 873 1.0021

a\_Var[6] -0.0188 0.0222 -0.0498 0.0159 909 1.0037

sigma\_Species 0.0486 0.0245 0.0202 0.0756 2398 1.0007

sigma 0.0038 0.0024 0.0002 0.0070 256 1.0148

* Means:
  + ELN = 0.2318
  + ELC = 0.1958
  + GYR = 0.2252
  + GYN = 0.1526
  + KRA = 0.2459
  + PRM = 0.1875

### Group

* Did not converge

Mean StdDev lower 0.89 upper 0.89 n\_eff Rhat

a 0.2010 0.2307 -0.2719 0.4927 14 1.1505

a\_Var[1] 0.0327 0.2310 -0.2609 0.5056 13 1.1521

a\_Var[2] -0.0269 0.2301 -0.3192 0.4417 14 1.1457

sigma\_Group 0.2852 0.2496 0.0153 0.6726 62 1.0874

sigma 0.0064 0.0045 0.0005 0.0126 3 1.6387

## Supplementary Analyses

### Crushed vs. Milled

* No difference within PRM

Df Sum Sq Mean Sq F value Pr(>F)

Otolith 1 0.001403 0.0014033 1.629 0.218

Residuals 18 0.015508 0.0008615

* Significant for whole data set (with species as a random factor).

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: M ~ Otolith + (1 | sciname)

Data: myct

REML criterion at convergence: -480

Scaled residuals:

Min 1Q Median 3Q Max

-1.93278 -0.66784 -0.09104 0.60911 2.85008

Random effects:

Groups Name Variance Std.Dev.

sciname (Intercept) 0.0010002 0.03163

Residual 0.0005074 0.02253

Number of obs: 108, groups: sciname, 6

Fixed effects:

Estimate Std. Error df t value Pr(>|t|)

(Intercept) 0.23803 0.01803 12.62251 13.200 9.31e-09 \*\*\*

OtolithY -0.03112 0.01519 74.28266 -2.049 0.044 \*

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

Correlation of Fixed Effects:

(Intr)

OtolithY -0.687

### Station

* Only significant for one

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: M ~ Station + (1 | sciname)

Data: myct

REML criterion at convergence: -400.4

Scaled residuals:

Min 1Q Median 3Q Max

-2.8725 -0.6056 0.0000 0.4922 2.5553

Random effects:

Groups Name Variance Std.Dev.

sciname (Intercept) 0.0004377 0.02092

Residual 0.0002419 0.01555

Number of obs: 108, groups: sciname, 6

Fixed effects:

Estimate Std. Error df t value Pr(>|t|)

(Intercept) 0.2235289 0.0236359 2.7214367 9.457 0.00370 \*\*

StationJR15004/65/2 0.0182709 0.0311587 4.5634432 0.586 0.58541

StationJR15004/66/1 -0.0008586 0.0155547 76.9645693 -0.055 0.95612

StationJR15004/72/1 -0.0101265 0.0280963 3.0331702 -0.360 0.74217

StationJR15004/73/1 0.0110633 0.0155547 76.9645693 0.711 0.47908

StationJR15004/91/1 -0.0157818 0.0291528 3.5111516 -0.541 0.62076

StationJR15004/96/1 -0.0072958 0.0124715 76.9645693 -0.585 0.56026

StationJR15004/96/2 -0.0743022 0.0320403 2.2986468 -2.319 0.12968

StationJR16003/112/2 -0.0165928 0.0275345 2.8086955 -0.603 0.59192

StationJR16003/113/1 -0.0059250 0.0274543 2.7857248 -0.216 0.84396

StationJR16003/113/2 -0.0054790 0.0311587 4.5634432 -0.176 0.86795

StationJR16003/129/1 0.0254767 0.0273666 2.7430134 0.931 0.42634

StationJR16003/129/2 0.0262259 0.0272239 2.6881560 0.963 0.41382

StationJR16003/146/1 0.0209251 0.0280169 3.0063303 0.747 0.50924

StationJR16003/146/2 0.0638992 0.0288352 3.3799673 2.216 0.10340

StationJR16003/147/1 0.0163227 0.0280169 3.0063303 0.583 0.60098

StationJR16003/39/1 0.0144358 0.0311587 4.5634432 0.463 0.66440

StationJR16003/39/2 -0.0256132 0.0311587 4.5634432 -0.822 0.45186

StationJR177/161/2 -0.0671749 0.0334262 2.7214367 -2.010 0.14733

StationJR177/165/2 -0.0728682 0.0351893 3.3378119 -2.071 0.12089

StationJR177/199/2 -0.0055151 0.0291528 3.5111516 -0.189 0.86037

StationJR177/205/1 -0.0351696 0.0311587 4.5634432 -1.129 0.31483

StationJR177/301/1 -0.0402017 0.0280860 3.0296744 -1.431 0.24687

StationJR177/305/1 0.0104865 0.0311494 4.5594784 0.337 0.75131

StationJR177/305/2 0.0376067 0.0124715 76.9645693 3.015 0.00348 \*\*

StationJR177/328/1 0.0006599 0.0278574 2.9429977 0.024 0.98262

StationJR177/334/2 -0.0217537 0.0351893 3.3378119 -0.618 0.57610

StationJR177/357/1 -0.0223008 0.0318035 2.2315275 -0.701 0.54912

* StationJR38/185/1 -0.0539458 0.0351893 3.3378119 -1.533 0.21373