DEB Notes December 2023

Changing weights

Original weights:

Total length:

W{1} = [50 50 50 50

50 50 50 50 % 4 mg/L

50 50 50 50 % 2 mg/L

50 50 50 50

50 50 50 50 % 4 mg/L

50 50 50 50 % 3 mg/L

50 50 50 50

50 50 50 50

50 50 50 50 % 4 mg/L

50 50 50 50

50 50 50 50 % 4 mg/L

50 50 50 50 % 3 mg/L

36 36 36 36

30 30 30 30

36 36 36 36

11 11 11 11

189 189 189 189

391 391 391 391];

Egg buffer:

% weight factors (number of replicates per observation)

W{3} = [100 100 100 100

100 100 100 100

100 100 100 100

100 100 100 100

100 100 100 100];

Survival:

% % weight factors (number of tanks per observation)

W{4} = [1 1 1 1

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New weights

Total length:

* Number of datapoints based on sample size
  + 8 mg/L: 50+50+50+50+50+36+30+36+11+189+391 = 943
  + 4 mg/L: 50+50+50+50 = 200
  + 3 mg/L: 50+50 = 100
  + 2 mg/L: 50
* Number of datapoints based on values in matrix (I think this is the correct one to base it on – remove the weighting by sample size and then base it on the number of data points being used to fit the model)
  + 8 mg/L: 11
  + 4 mg/L: 4
  + 3 mg/L: 2
  + 2 mg/L: 1
* Weight to multiply it by the sample size and get same overall weight
  + 8 mg/L: 11\***4** = 44
  + 4 mg/L: 4\***11** = 44
  + 3 mg/L: 2\***22** = 44
  + 2 mg/L: 1\***44** = 44

Egg buffer:

* Number of datapoints based on sample size
  + 8 mg/L: 100
  + 4 mg/L: 100
  + 3 mg/L: 100
  + 2 mg/L: 100
* Number of datapoints based on values in matrix:
  + 8 mg/L: 2
  + 4 mg/L: 2
  + 3 mg/L: 2
  + 2 mg/L: 2
* Weight to use:
  + Keep them the same or maybe change so the data is weighted evenly with the other variables.
  + What would accomplish this? Have it add up to the same amount of total sample size (44)? Or should the weights just be on the same order of magnitude?

Survival:

* Number of datapoints based on sample size
  + 8 mg/L: 38+23+16+3 = 80
  + 4 mg/L: 10+10 = 20
  + 3 mg/L: 5+5 = 10
  + 2 mg/L: 5+5 = 10
* Number of datapoints based on values in matrix:
  + 8 mg/L: 80
  + 4 mg/L: 20
  + 3 mg/L: 10
  + 2 mg/L: 10
* Weight to use:
  + 8 mg/L: 80\*1=80
  + 4 mg/L: 20\*4=80
  + 3 mg/L: 10\*8=80
  + 2 mg/L: 10\*8=80

If I want all three variables to have similar weights I could just double the weights used for length and egg buffer mass so they add up to 88 instead of 44.

* I did this and it didn’t change the K estimated but I’ll just leave it like this.

New results table

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Parameter(s) affected by hypoxia | Estimated *Z* [95% CI) | AICc | ΔAICc | Akaike weight |
| *JaAm* | 3.019 [2.512-3.612] | 856.06 | 94.89 | 2.4e-21 |
| *yVA* | 1.818 [1.601-2.342] | 848.65 | 87.48 | 9.9e-20 |
| *JvM* | >1000 [7.978-1000] | 849.22 | 88.05 | 7.4e-20 |
| *μemb* | 0.9088 [0.6843-1.266] | 792.41 | 31.24 | 1.6e-7 |
| ***μlar*** | **0.3592 [0.2578-0.5068]** | **761.17** | 0 | **0.98** |
| *JaAm + JvM* | 3.105 [2.651-3.726] | 855.00 | 93.83 | 4.1e-21 |
| *yVA + JvM* | 1.985 [1.688-2.774] | 850.64 | 89.47 | 3.6e-20 |
| *JaAm + μemb* | 2.804 [1.605-3.287] | 823.24 | 62.07 | 3.2e-14 |
| *yVA + μemb* | 1.801 [1.570-2.167] | 808.12 | 46.95 | 6.2e-11 |
| *JvM + μemb* | 0.9463 [0.7125-1.325] | 796.55 | 35.38 | 2.0e-8 |
| *JaAm + μ­lar* | 2.930 [2.165-3.428] | 838.17 | 77 | 1.9e-17 |
| *yVA + μlar* | 1.767 [1.536-2.111] | 821.30 | 60.13 | 8.6e-14 |
| *JvM + μlar* | 0.3898 [0.2899-0.5443] | 768.89 | 7.72 | 0.021 |
| *μemb + μlar* | 1.252 [0.9706-1.668] | 773.91 | 12.74 | 0.0017 |
| *JaAm + μemb + μlar* | 2.819 [1.920-3.286] | 810.21 | 49.04 | 2.2e-11 |
| *yVA + μemb + μlar* | 1.827 [1.620-2.269] | 794.03 | 32.86 | 7.2e-8 |
| *JvM + μemb + μlar* | 1.286 [0.9959-1.721] | 777.59 | 16.42 | 2.7e-4 |
| *JaAm + JvM + μemb + μlar* | 2.913 [2.288, 3.387] | 809.96 | 48.79 | 2.5e-11 |
| *yVA + JvM + μemb + μlar* | 1.981 [1.700, 2.456] | 795.97 | 34.8 | 2.7e-8 |

Results table if you only include parameter combinations that result in all three variables being affected by hypoxia.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Parameter(s) affected by hypoxia | Estimated *Z* [95% CI) | AICc | ΔAICc | Akaike weight |
| *JaAm* | 3.019 [2.512-3.612] | 856.06 | 62.03 | 2.5e-14 |
| *yVA* | 1.818 [1.601-2.342] | 848.65 | 54.62 | 1.0e-12 |
| *JaAm + JvM* | 3.105 [2.651-3.726] | 855.00 | 60.97 | 4.2e-14 |
| *yVA + JvM* | 1.985 [1.688-2.774] | 850.64 | 56.61 | 3.7e-13 |
| *JaAm + μemb* | 2.804 [1.605-3.287] | 823.24 | 29.21 | 3.3e-7 |
| *yVA + μemb* | 1.801 [1.570-2.167] | 808.12 | 14.09 | 6.3e-4 |
| *JaAm + μ­lar* | 2.930 [2.165-3.428] | 838.17 | 44.14 | 1.9e-10 |
| *yVA + μlar* | 1.767 [1.536-2.111] | 821.30 | 27.27 | 8.7e-7 |
| *JaAm + μemb + μlar* | 2.819 [1.920-3.286] | 810.21 | 16.18 | 2.2e-4 |
| ***yVA + μemb + μlar*** | **1.827 [1.620-2.269]** | **794.03** | **0** | **0.72** |
| *JaAm + JvM + μemb + μlar* | 2.913 [2.288, 3.387] | 809.96 | 15.93 | 2.5e-4 |
| *yVA + JvM + μemb + μlar* | 1.981 [1.700, 2.456] | 795.97 | 1.94 | 0.27 |

The model with *yVA*, *μemb*, and *μlar* is 0.72/0.27=2.667 times as likely as the one that additionally has *JvM*.