Notes from meeting with Roger 6/20/24

Treatment of eggs and embryos in std deb vs debkiss

* He discussed with Kooijman in context of Louise’s paper
* We don’t want to get into std vs debkiss debate

Hatching/birth issue

* None of the processes of the model are described with sufficient precision to allow within day fitting/resolution
* Could also have transition at some point when yolk is above zero….but don’t want to try that
* It limits the generality of the approach – can’t be applied as is to other species

Pushing back against idea that wee shouldhave just run it and see what happens

* Roger’s point about how this suggests a purpose for more suborganisml measurements
* Is the large body of info published in or synthesized somewhere else I have written? If not, its valuable to keep it in
* Sabrina Russo – overview of deb models for plants – similar large body of background to get a a list of stylized facts – pushed back at reviewer by saying readers all have interest and knowledge of deb theory not all biological systems – this is modeling strongly driven by underlying biology – should still trim it but also push back
* Separate general info on fish larvae and hypoxia from things that relate to silversides and related species
* Some of it can go in SI, in terms of synthesis citing original studies. Condense by citing text book but have separate list of references in supplement.

“Best practice to estimate all params simultanesouly”

* Something they talked about in Louise’s work – they had to separate it out because if try to do simultaneously you were overparameterizing.
* We can defend delta\_M thing
* It’s a matter of debate whether its best practice to fit simultansouly. Does AmP even do it? They deal wth overparameterization by assuming some params are governed by size scaling relationships – addt’l model assumptions involved. Here we are not making addt’l assumptions. Look back at what did to get delta\_M but if nec can defend. Just because can’t do it in BYOM not a good reason. Point that it has minimal impact is a strong one.
  + I think it is also used to convert dWV back to total length in the estimation so it is pretty important.

Roger could put together something to address debkiss vs std deb thing

Lit on separating out parameters

* Fed radioactive food, may be stable isotope papers that trace these things – C/N for food vs body tissue, can get at assimilation efficiency
* Make this a lower priority

Roger can turn it around in a few days

A graph with blue dots

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