Patrick’s check process of ZooMizer on Monday 11 January 2021

I too will work backwards from `a` on line 194 of fZooMizer\_run.R.

1. I used ZooMizer from the github branch <https://github.com/patricksykes/ZooMizer/tree/zoomssupdatecompare>
2. In this branch, we’re using cell 1 of the full environmental data (as in Ryan’s test)
3. I enter comparison.RMD and run all chunks
4. This fails on line 413 (which is fine because I want to know about up to line 412)
5. A\_iter[2,18] = 0.184373 but a[2,18] = 1.302383
6. A\_iter[2,18] = param$dt/param$dx \* gg[2,17] = 0.1 \* 1.84373 = 0.184373  
   a[2,18] = e\_growth[2, 17] \* dt / params@dw[18] = 3.372202e-08 \* 0.01 / 2.589254e-10 = 1.302384
7. e\_growth[2,17] = encounter[2,17]-params@metab[2,17] = 3.372202e-08 – 0.
8. encounter[2,17] = params@other\_params$temp\_eff[2,17] \* params@search\_vol[2,17] \* (phi\_prey\_species[2,17] + phi\_prey\_background[2,17]) =0.1350324 \* 3.358768e-05 \* (1.57591e-08+0.007435235). **Search volume agrees with ZooMSS**
9. phi\_prey\_background is roughly the equivalent of ingested\_phyto in ZooMSS. So I’ll focus on that.
10. The exact equivalent of ingested\_phyto would be params@other\_params$temp\_eff[2,17] \* params@search\_vol[2,17] \* phi\_prey\_background[2,17] = 3.372195e-08

phi\_prey\_background[2,17] = params@other\_params$assim\_phyto[2] \* params@species\_params$interaction\_resource[2]\* rowSums(sweep(params@pred\_kernel, 3, params@dw\_full \* params@w\_full \* n\_pp, "\*", check.margin = FALSE), dims = 2)[2,17]  
= 0.25 \* 1 \* 0.02974094 = 0.007435235

params@pred\_kernel[2,17,30] = 0.8478148  
params@dw\_full[30] = 6.503912e-13  
params@w\_full[30] = 2.511886e-12  
n\_pp[30] = 4.196033e+21

* n\_pp[30] = kappa\*params@w\_full[30]^(1-lambda) / params@dw\_full[30] = 0.001189637 \* 2.511886e-12 ^ (1 - 2.065569) / 6.503912e-13 = 2729071679 / 6.503912e-13 = 4.196046e+21

in ZooMSS, nPP[30] is 2729062754 – small rounding error in the 6th s.f. (for the same comparison as Ryan…ZooMizer has n\_pp[5] \* params@dw\_full[5] = 1.258739e+12 **equal to ZooMSS** nPP[5] = 1.258739e+12)

**Now try some different things…**

**Mizer method in ZooMSS**

I inserted this code at the end of the fZooMSS\_Setup.R code before return(model):

model$dw\_phyto <- (10^param$dx - 1) \* param$w\_phyto

model$phi\_prey\_background <- assim\_phyto \* phyto\_theta[,1] \* rowSums(sweep(model$phyto\_growthkernel2, 3, #model$dw\_phyto \* # should remove this to match zoomizer since N/NPP in ZooMSS is absolute, not normalised

model$param$w\_phyto \* model$nPP, "\*", check.margin = FALSE), dims = 2)

model$phyto\_encounter <- model$temp\_eff \* model$phi\_prey\_background #\* SearchVol #SearchVol already included in phyto\_growthkernel2

where:

phyto\_growthkernel2 = array(NA, dim = c(param$ngrps, param$ngrid, param$ngridPP)),  
  
model$phyto\_growthkernel2[i,,] <- matrix(SearchVol[i,], nrow = param$ngrid, ncol = param$ngridPP) \* sp\_phyto\_predkernel

model$phyto\_encounter[2,17] = 3.372195e-08 **Which agrees with the value from ZooMizer. This confirms that the two models are calculating the integrals differently, with the same inputs.**

However, ZooMSS gives model$ingested\_phyto[2,17] = 1.843728

This has to do with the log/absolute weights and is sorted out in the next step:

For ZooMSS: A\_iter[,idx\_iter] <- dt/dx \* (ingested\_phyto + cs)[,idx\_iter-1]  
A\_iter[2,18] = 0.01/0.1 \* (1.843728 + 2.319341e-0.9) = 0.184373

For ZooMizer: a[, idx] <- sweep(-r$e\_growth[, idx - 1, drop = FALSE] \* dt, 2, params@dw[idx], "/")

a[2,18] = -r$e\_growth[2, 17] \* 0.01 / params@dw[18] = 3.372202e-08 \* 0.01 / 2.589254e-10 = 1.302384

**Remove Simpson’s rule**

We can force ZooMSS to use rectangles by replacing sm\_phyto and sm\_dynam with dx. We can do this manually every time those terms appear, or an easier way is replacing line 121 of fZooMSS\_Setup with

sm\_phyto <- matrix(1, nrow = param$ngrid, ncol = param$ngridPP, byrow = TRUE) \* (param$dx)

and line 126 by

sm\_dynam <- matrix(1, nrow = param$ngrid, ncol = param$ngrid, byrow = TRUE) \* (param$dx)

Then A\_iter[2,18] = 0.184373 **so Simpson’s rule is working the same as using Riemann sums**

**Look into the log10 transformation…**

If we write out in full all the parts of the a and A\_iter matrices (for the phyto consumption part, substitute for for the dynamic part), we get…(for clarity I’ll use the usual names, not variable names). Note gg\_log\_t\_phyto = .

**ZooMSS:**

**ZooMizer:**

Noting that we should get

dw <- (10^param$dx - 1) \* param$w # This is a shortcut to w(i+1) – w(i) using the log-spacing of bins  
param$w \* log(10) / dw = 8.892851 **Not the factor of 7 I was expecting…have I missed something?**

In any case, shouldn’t a/A\_iter = 1?

Working it through a little further…