Overall:

- No longer any complete plants listed as “error” when R-script is run

- I’ve now combined all other error issues into this file, a file with a summary of negative investment problems (very few), and a file “Error summary” which shows all my various cross checks, indicating which ones don’t work. I’ve tried to describe actual issues below.

- Remaining negative investment issues pasted into a single file. I’ve made notes as to what to do with each incidence. Some I am simply accepting, because there is no obvious fix. There are a few I am puzzled by, because with dynamic parts splitting they shouldn’t exist. And I can’t figure out the BAER problems – see below.

See BOLE for partial explanation.

- Lots of small problems with the implementation of “survival of the fittest”, mostly across stages where a large number of parts are shed – for instance between finished\_flower\_stigma and fruit\_just\_starting. Then for parts that legitimately jump from the bud stage straight to a young fruit stage, the fruiting part is assumed to be a derivation of a previously appeared flower/finished flower stigma, and the count of petals does not match up with “sum of fruiting parts”. For GRSP and GRBU I’ve solved most (all?) of them, by sometimes shifting the census where a part appears by 1. For HEPU I have not at this point, because I’d be changing the progressions of items too much. See below under “HEPU” for more.

Wondering if a solution to this problem could be to create a look-up table, indicating how many progression steps a given species\*part combination can “exist” before being counted as lost. Then parts that always progress could be coded as “1”, while others (like the BAER cones creating problems) can be coded as “8”.

COER, EPMI, GRSP, HATE, LEES, PELA, PILI

* ALL CORRECT

BAER

* cone\_green\_01 not correctly progressing to cone\_brown or cone\_brown\_DEF because 6 censuses between stages (BAER\_005, 803, 806, 902, 905, 907)  
  I would like you to be more specific with the problem. I can’t see with my math eyes what is it that makes the problem. I think it works correct…
* Minor issues with one cone – see error spreadsheet.  
  Possibly a coding issue. Cone aborted is on top of the map and hence will have priority over all others when choosing predecessors. The survival of the fittest do not act in the favour in this case.
* A handful of puzzling negative investment problems. In most cases the “To” part has an actual weight, so I assumed the problem was that the previous part had too high of a calculated weight. So I slightly reduced the dimensions of the “From” part to allow there to be a positive progression. But decreasing the dimensions didn’t change the investment numbers at all. (I reran all the bits of code that should recalculate individual weights and weights from dimensions.)

BOLE

* Finished\_flower has 2044 too many (see Error\_summary file). Checked repro spreadsheet and #2140 is correct for total number that “pass through”. I’m at a loss to explain this.
* Continued problem with negative investment going from “flower\_calyx” to “finished\_flower” although sums should work: flower\_calyx 🡪 finished\_flower + 4\*finished\_flower\_stigma (5.96 < 4.93 + 4\*.35)  
  Problem is connected to the way, we calculate carbon distribution in case of split.  
  The proportion of carbon going to “Finished flower” is only related on “Finished flower” and “Finished flower stigma weights”. If there is sufficiently big “flower\_calyx” negative investment is still possible.   
  Solution is either to change this particular rule of allocating carbon or check/change the weights of the plants.
* We need to add another bit to the plant map: Late\_flower\_petals ; I just finally weighed “late\_finished\_flower” separated from the petals (enormously decreasing its weight), but in the process determined that the flower petals increase in weight by ~30% in the flowers that have growing fruits in them. It would be a progression from “flower\_petals”  
  Could you please make first change in all the spread sheets before we follow with the changes in the code.
* Otherwise ALL CORRECT

GRBU

* Finished\_flower\_stigma has negative “lost” counts in many cases, causing me to stop looking in more detail. I am wondering if something has been mistyped in the plant map that skips some part of the pathway leading to or from “finished\_flower\_stigma”. I think part of this problem may be because until yesterday (Oct 22) afternoon, there were no weights for “finished\_flower\_stigma”, but these have now been added and the problems haven’t disappeared.  
  Fixed. Missing information in the “OrderedListOfParts.R” file has been now added.
* Infl\_bud\_small weighs more than infl\_stalk (Lizzy to fix; to begin with I’ll collect some new stalks and see if I collected different bits for just the stalk versus when I call it a “bud”)

HEPU

* With HEPU there are many individuals where Fin\_Dev calyx\_fruit does not add up to the sum of Fin\_Dev for (fruit\_young + fruit\_large\_immature + fruit\_mature). In most of these cases it is a “survival of the fittest” problem, where some of the previous censuses fruit\_young + fruit\_large\_immature have shed, and there are new fruit\_young + fruit\_large\_immature (+ calyx\_fruit) that have developed. However the exact development pattern means that the program assumes it is the previous ones developing further. The problem is that it knows the calyx\_fruit are new, so the number of calyx\_fruit exceeds the number of fruit\_young + fruit\_large\_immature, the latter of which are incorrect. I think a possible fix would be to use fruit\_young02, fruit\_large\_immature02, fruit\_large\_immature03 to clarify progression. Is this a big mess for you to implement on the plant map? If you can make the changes, I’d like to figure out exactly what added categories are needed first and then have you change things.  
  Lizzy prepare the list of necessary changes and I implement them later on.
* There is also a problem, shown on the excel error summary, that for HEPU\_001, HEPU\_002, HEPU\_003 and HEPU\_004, a number of the bits that are on the plant at the beginning of the experiment are not correctly being acknowledged as “errors”. I assume this means these individuals have too high a total investment number.

They were not being counted as errors. No backwards investment calculations was done at census 2 and hence no detection of the behaviour was made.

I have now modified the code and that kind of error is also stored and indicated in the results.   
The old action of the script could have affected the some of your calculations in Error\_summary.xlsx. I suggest those should be redone.

PEPU

* Remove “bud\_aborted” from plant map; never used
* Can’t check for negative investment problems until after I collect remaining parts
* But all parts sum up correctly

PHPH

* The number of flower petals does not equal the sum of (flower\_stigma + finished\_flower\_stigma + fruit\_just\_starting + fruit\_young + fruit\_large\_immature + fruit\_aborted + seed\_pod). It does equal if seed + seed\_aborted is substituted for seed pod. I think this is because the plant map is following backwards from the seed/aborted seed, rather than the seed pod. Since seed pods have variable seed number (0,1,2), but map assumes there are always 2, it makes the assumption that there are some fruit\_young and fruit\_large\_immature that have been "lost" when in reality they have turned into empty seed pods. However, if you consider "seed pod" the end of the developmental trajectory, then the numbers should add up. I'm guessing this is a change to the plant map.  
  To be continued….
* Otherwise ALL CORRECT

PUTU

* Quite a few “seed pods” are very lightweight, creating lots of negative investment issues. I’m tempted to leave this. Same issue for “fruit\_aborted”.
* Also quite a few negative investment issues with the lightest weight “bract\_flower\_or\_finished\_flower” and “flower\_calyx”, but these values are all high enough that they shouldn’t result in negative investment from the “big\_bud” stage. There is also an instance of this for PHPH. The individual based mechanism for dividing investment is now included, right?  
  There is no individual based mechanism. The mechanism is species specific.
* Still an error with too many “Finished\_flower\_stigma” ended up as a “Fin\_Dev” part. I’ve gone through many of the individuals and can’t find any mistakes in the repro spreadsheet but also can’t find any pattern that would explain the error. This may be the same sort of error as arises with PHPH. With both species, “seed pod” is the numerically accurate final development of the stigma 🡪 fruit progression, not “seed”

Mistakes are in:

(parts are 2x numbers in repro spreadsheet)

|  |  |  |  |
| --- | --- | --- | --- |
| Individual | petals | derived parts | diff |
| PUTU\_004 | 186 | 236 | -50 |
| PUTU\_005 | 136 | 168 | -32 |
| PUTU\_805 | 238 | 264 | -26 |
| PUTU\_003 | 106 | 116 | -10 |
| PUTU\_908 | 40 | 46 | -6 |
| PUTU\_902 | 296 | 300 | -4 |
| PUTU\_903 | 166 | 170 | -4 |
| PUTU\_403 | 94 | 96 | -2 |
| PUTU\_405 | 186 | 188 | -2 |
| PUTU\_804 | 30 | 32 | -2 |
| PUTU\_906 | 86 | 88 | -2 |