

# Mean age of first reproduction

*Erin Feichtinger*

*Friday, April 29, 2016*

## Lifetime event

From Bruce's comments on the manuscript regarding the residences times of individuals in each stage from the fundamental matrix comes this...

### Estimating the expected age of first reproduction

I followed Caswell in Chapter 5 by first decomposing the life cycle and understanding it as a Markov chain. To estimate mean age at reproduction, it involves a new transition matrix based on the addition of another absorbing state. In this case, both death and reproduce-before-dying are absorbing states. The estimation involves several steps with matrix operations. After several frustrating hours, I finally figured out which model parameters go where in the new matrices (T' and M', see Caswell pg) for both a single type and a two phenotype model.

I wrote functions for each step in the process. I used the orca whale data to test the functions and I get the same answer as Caswell in each step and the estimate for the mean age of first reproduction for orcas. Then, I arbitrarily chose values for each parameter in the growth model (single type) to see what number I get. Then, I repeated the process for the two type model.

I think I have the correct elements in the T' and M' matrices. I'm confused on one detail, however.

$$t_{i,j}$$

is an element of T (original transition matrix) and it is the probability that an individual in stage j at time t is alive and in stage i and time t + 1. As I understand it, this would be sg.

```
##           [,1]      [,2]
## [1,]  1.462585  3.333333
```

The expected age of first reproduction in this example is 1.46. However, this is with no variation in growth and one phenotype only. I added the steps to find expected age of first reproduction to the simulation (2 types with sigma as a standard deviation). The average age at first reproduction is higher, 2. something for both phenotypes. Not sure why, not sure it matters...?

Anyway, I was successful in adding the additional steps to the simulation and collecting the output of interest, the mean age of first reproduction for each phenotype. I checked the set up of T' and M' several times so I'm fairly confident that I placed the elements in the correct place within the matrices.

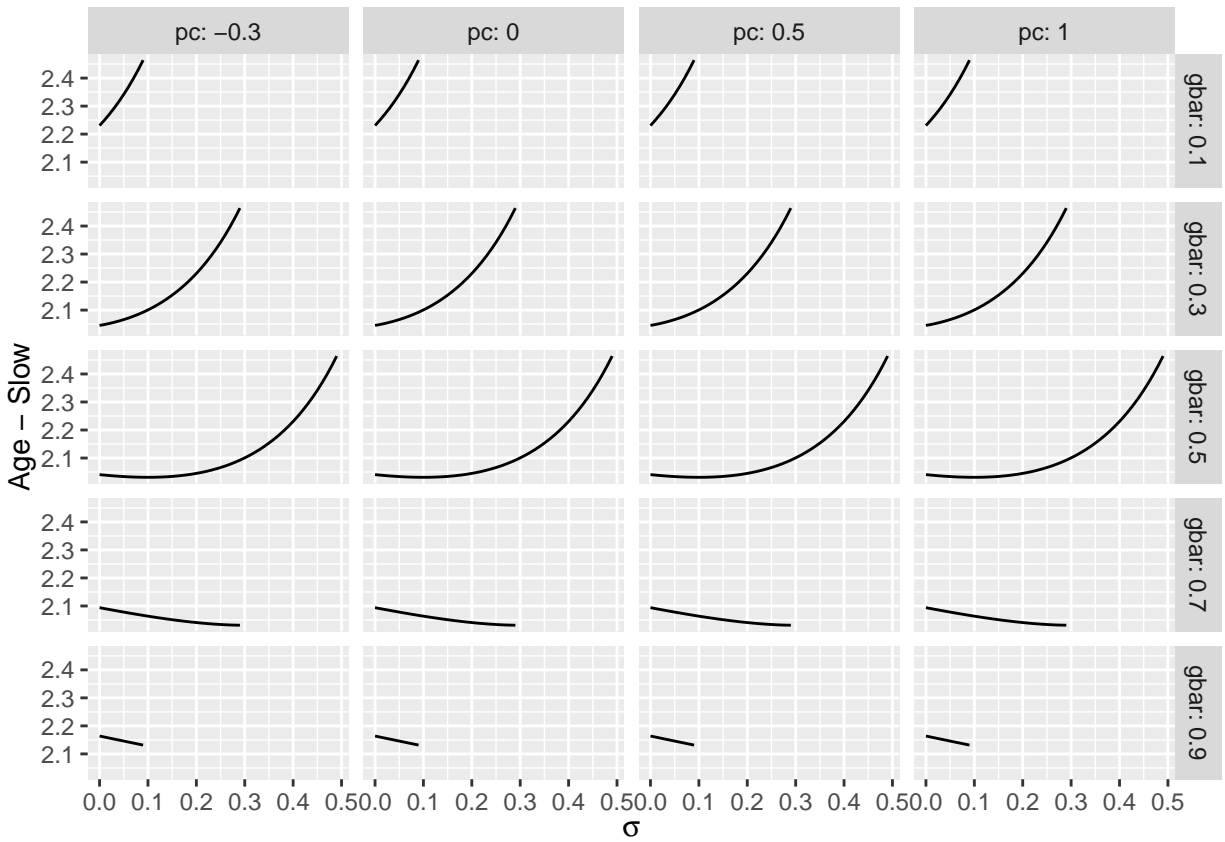
I only ran the program with one value of juvenile survival so I could save time and make sure the program worked. It takes about 15 minutes to go through the simulation with one value of S. Each additional value adds 15-20 minutes. 4 values of S takes about an hour. Now that I know it works, I can re-run the program with more values of S (although none of the other results depended very strongly on S).

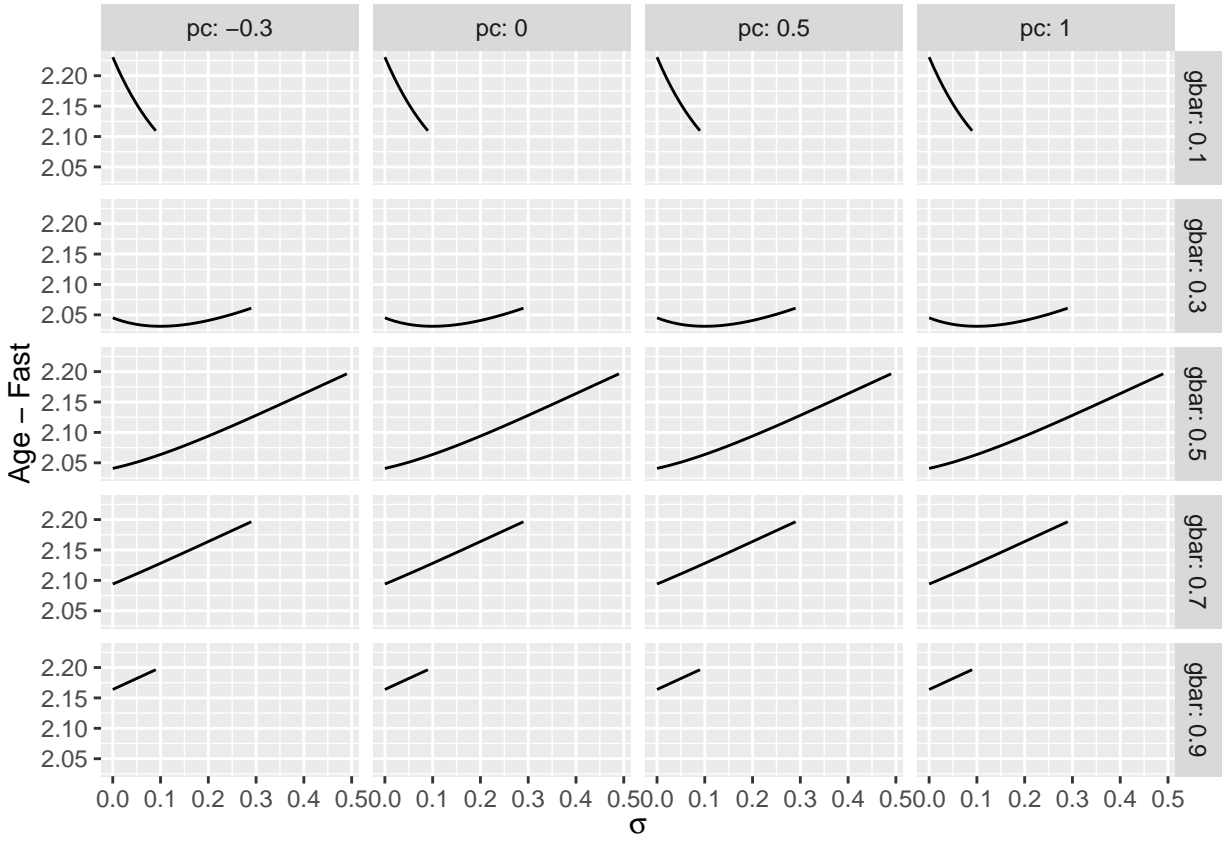
I used S = 0.6 for the test run. The expected age at first reproduction is around 2 for both phenotypes with the expected age lower for the fast phenotype although the magnitude of difference is small. Another thing to note is that the expectation is the same when sigma = 0 (which should happen I would think!) Thus, the range of values for both phenotypes is the same.

- Range 2.031250 to 2.463782
- Mean of the expected age
  - slow = 2.130505, SD = 0.115
  - fast = 2.107819, SD = 0.057

I think this makes sense but a discussion is needed.

By making simple plots of sigma and the expected age, my first thoughts on the interpretation is that as sigma increases, the age at first reproduction increases for the slow phenotype. However, for the fast phenotype, as sigma increases the mean age decreases. Additionally, there is less variation in this quantity for the fast phenotype than the slow.





Results don't appear to be dependent on  $\phi$ , looks like  $g$  and  $\sigma$  are key here. I don't know what to think of this.