

Lifetime Event Update

Erin Feichtinger

May 3, 2016

I found a small problem while testing my functions just to make sure they are working correctly. I should have done this first but oh well. I used the orca whale data. Turns out that in the T^c matrix there should be a zero in entry 2,2. This is what Caswell has and when I replaced the value with zero, I got the same answer as Caswell for mean age at first reproduction of orca whales. My functions work correctly; I was missing one key step.

So, forget about what you saw yesterday. I think these are the correct numbers because they are on the scale of what I got when I fixed all parameters to see what number comes out. The pattern revealed yesterday, however, has not drastically changed (I don't think).

The range is almost the same for both phenotypes. The mean (of the mean) is higher for the slow phenotype and there is a higher variance. Does this make sense?

```
library(popbio)
library(ggplot2)

new.data <- read.csv("May3.csv", header=TRUE)
new.data[is.na(new.data)] <- 0

range(new.data$ages)
```

```
## [1] 0.000000 1.655673
```

```
range(new.data$agef)
```

```
## [1] 0.000000 1.655775
```

```
mean(new.data$ages)
```

```
## [1] 1.421
```

```
mean(new.data$agef)
```

```
## [1] 1.488955
```

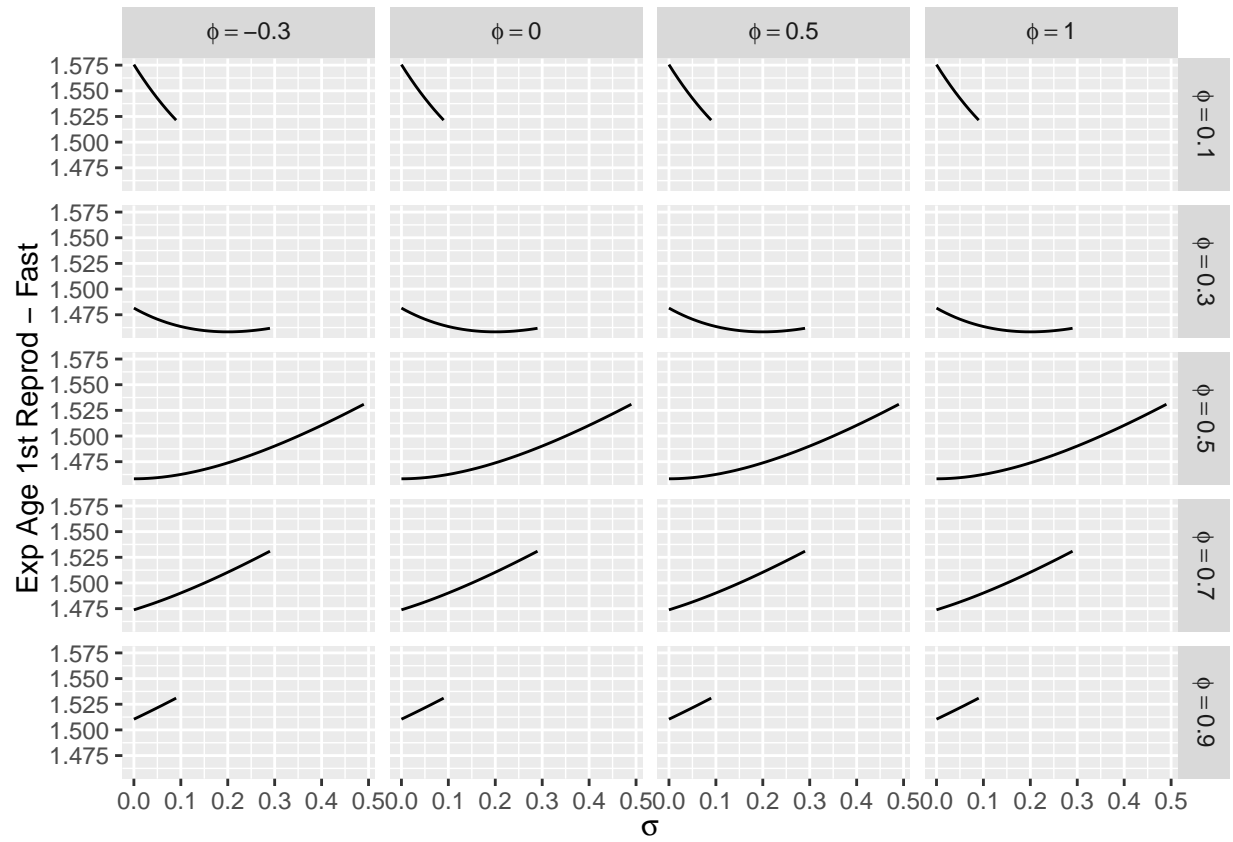
```
sd(new.data$ages)
```

```
## [1] 0.1329255
```

```
sd(new.data$agef)
```

```
## [1] 0.02797964
```

```
## Warning: The labeller API has been updated. Labellers taking `variable` and
## `value` arguments are now deprecated. See labellers documentation.
```



```
## Warning: The labeller API has been updated. Labellers taking `variable` and
## `value` arguments are now deprecated. See labellers documentation.
```

