In Silico Experimentation (cont'd)

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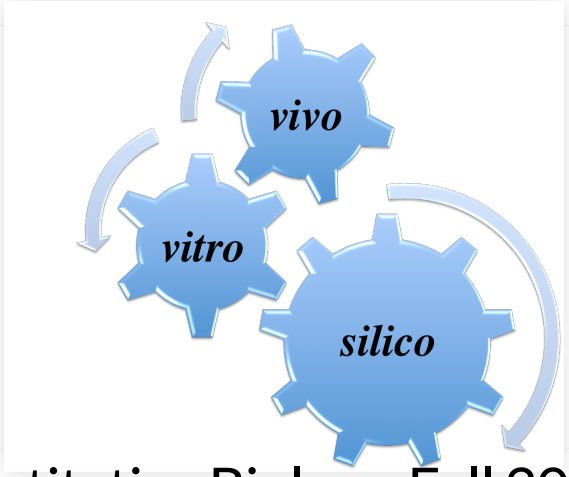

Introduction to Quantitative Biology, Fall 2016

Class announcements

- Reading Assignment (NO QUIZ): “Dynamics of Genes in Populations” (up until Random Genetic Drift)

Example: Simple Birth Rates

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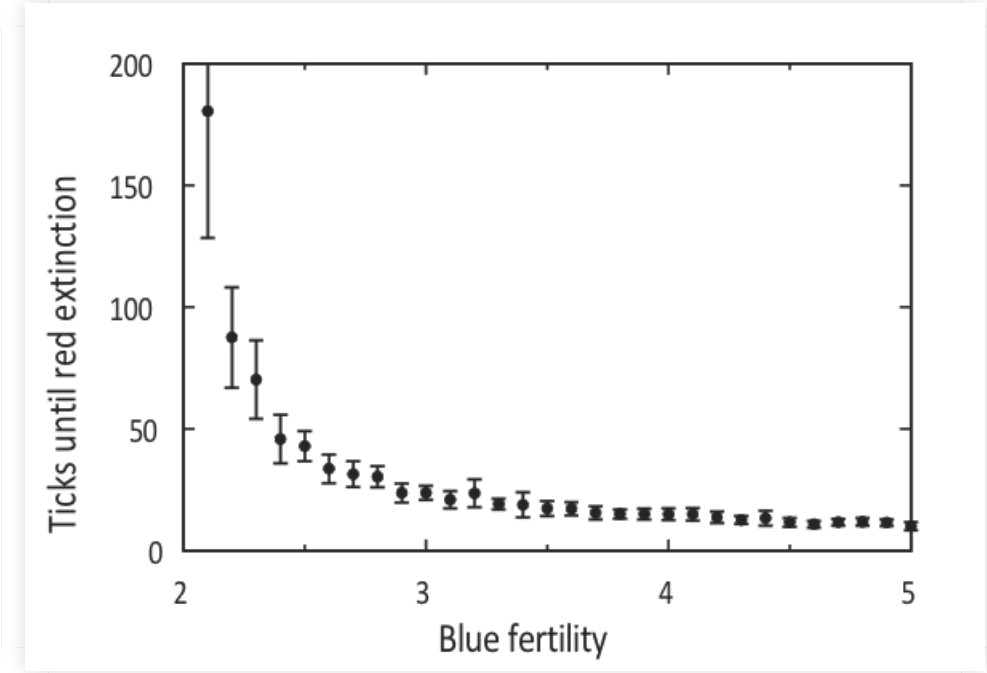
```
mydata <- read.csv("Simple Birth Rates
experiment-table.csv", header=TRUE, skip=6)
str(mydata)
```

```
'data.frame':   300 obs. of  6 variables:
 $ X.run.number.     : int  4 3 2 6 5 7 8 9 11
12 ...
 $ red.fertility     : int  2 2 2 2 2 2 2 2 2 2
...
 $ carrying.capacity: int  1000 1000 1000 1000
1000 1000 1000 1000 1000 1000 ...
 $ blue.fertility    : num  2.1 2.1 2.1 2.1 2.1
2.1 2.1 2.1 2.2 2.2 ...
 $ X.step.           : int  121 149 200 97 139
140 150 123 70 78 ...
 $ ticks             : int  121 149 200 97 139
140 150 123 70 78 ...
```

Example: Simple Birth Rates

We need to replicate this figure:



Example: Simple Birth Rates

First, we need the blue fertility values:

```
(bf.vals <- unique(mydata$blue.fertility))
```

```
 [1] 2.1 2.2 2.3 2.4 2.5 2.6 2.7 2.8 2.9 3.0
3.1 3.2 3.3 3.4 3.5 3.6 3.7
[18] 3.8 3.9 4.0 4.1 4.2 4.3 4.4 4.5 4.6 4.7
4.8 4.9 5.0
```

Example: Simple Birth Rates

Second, we need to compute the *average* ticks until red extinction.

```
N <- length(bf.vals) # How many bf.vals?
time.to.red.extinction <- rep(0,N) # Initialize
sdev <- rep(0,N)
for (i in 1:N) {
  # Subset the data
  tmp <- subset(mydata, mydata$blue.fertility
== bf.vals[i])

  # Compute average over subsetted data
  time.to.red.extinction[i] <- mean(tmp$ticks)

  # Compute standard deviation over subsetted
data
  sdev[i] <- sd(tmp$ticks)
}
```

Example: Simple Birth Rates

Let's plot!

```
plot(bf.vals, time.to.red.extinction, pch=19,
xlab="Blue fertility", ylab="Ticks until red
extinction")

arrows(bf.vals, time.to.red.extinction-sdev,
bf.vals, time.to.red.extinction+sdev,
length=0.05, angle=90, code=3)
```

Example: Simple Birth Rates