For the data files associated with the manuscript “Selective predation can impact infection prevalence and host susceptibility” by S.O. Gutierrez, X.E. Bernal, and C.L. Searle.

Description of data files:  
“Population\_data\_Gutierrez\_etal”

“Susceptibility\_data\_Gutierrez\_etal”

“Length\_data\_Gutierrez\_etal”

For the file: “Population\_data\_Gutierrez\_etal.” These data are from the weekly sampling of the populations during the “population experiment” portion of the project.

Beaker = replicate number

Sample\_num = the week each sample was taken

Predation = the selective predation treatment where “Infected” = infected individuals were removed, “Uninfected” = uninfected individuals were removed, and “Random” = both infected and uninfected individuals were removed

\*Adult\_F = uninfected adult female

\*Ephi\_F = uninfected adult female carrying an ephippium (resting egg)

\*Juv\_F = uninfected juvenile female

\*Ad\_M = uninfected adult male

\*Juv\_M = uninfected juvenile male

\*Inf\_Ad\_F = infected adult female

\*Inf\_Ephi\_F = infected adult female carrying an ephippium (resting egg)

\*Inf\_Juv\_F = infected juvenile female

\*Inf\_Ad\_M = infected adult male

\*Inf\_Juv\_M = infected juvenile male

Total\_num = total number of individuals counted in the 100mL sample

Infected\_num = number infected

Prop\_inf = proportion infected

Prop\_juv = proportion juveniles

\*Values in columns with an asterisk are the number of individuals in each category found in the 100mL subsample of the population on a given sampling day.

For the file “Susceptibility\_data\_Gutierrez\_etal.” These data are the results of the infection trial in the “population susceptibility” portion of the project.

Beaker = replicate number of the original population

Predation = the selective predation treatment where “Infected” = infected individuals were removed, “Uninfected” = uninfected individuals were removed, and “Random” = both infected and uninfected individuals were removed

Num\_infected = the number of individuals identified as infected for each beaker at the end of the susceptibility trial

Num\_uninfected = the number of individuals identified as uninfected for each beaker at the end of the susceptibility trial

For the file “Length\_data\_Gutierrez\_etal.” These data are the measurements of length from the extra animals in the maternal lines from the “population experiment” portion of the projection.

Beaker = replicate number of the original population

Mat\_line = an indicator of the maternal line within each beaker (replicate). We started 20 maternal lines from each original beaker, but not all of them survived for us to measure.

Indiv\_num = an indicator of up to the three individuals measured for each maternal line within each beaker

Length\_mm = the length of each individual measured, in mm, from the middle of the eye to the base of the tail