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#### AUTHOR INFORMATION:

Julie S. Miller  
University of California, Los Angeles  
612 Charles E. Young Dr. South  
Los Angeles, CA 90095  
[julie.serena@gmail.com](mailto:julie.serena@gmail.com)

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#### SHARING INFORMATION:

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#### DATA & FILE OVERVIEW

##### File list:

2-Choice-Rdata.csv  
2-Choice Expt.R  
Microcosm.xls  
Microcosms.R  
Brood Schedule TP Combined.csv  
BroodPhenology\_Randomization\_and\_Model.R  
Permutation Results.csv  
Demographics - Total.csv  
Host Density Foitzik MyData Combined.csv  
Demographics\_XYcoord.csv  
SpatialStats.R  
Encounter Rate Calculations.R  
FieldDemographics\_Calculations.xlsx

##### Relationships between files:

- (1) **Two-Choice Test:** 2-Choice-Rdata.csv is used in 2-Choice Expt.R
- (2) **Microcosm:** Values from the "summary" tab of the Microcosm.csv are used in Microcosms.R
- (3) **Brood Phenology:** Brood Schedule TP Combined.csv is used in BroodPhenology\_Randomization\_and\_Model.R. The output from some of this code is Permutation Results.csv.

(4) Field Data:

(i) **Host Density:** Host Density Foitzik MyData Combined.csv is used in Encounter Rate Calculations.R.

(ii) **Spatial Statistics:** Demographics\_XYcoord.csv and Demographics - Total.csv are used in Spatial Stats.R.

DATA-SPECIFIC INFORMATION

2-Choice-Rdata.csv

Number of rows: 19

Definition of variables:

1. **RaidDate:** Date of raid trial
2. **PID:** *T. americanus* colony identity
3. **1stFind\_Nest:** Size of the nest that was found first (small or large)
4. **1stRaid:** Size of the nest that was raided first (small or large)
5. **RaidSumm:** A summary of the raiding outcomes. Were both nests raided, or only the small or large?
6. **BothFound:** Were both nests found? (1=Yes, 0 = No)
7. **BothFoundB4:** Were both nests found before any raids occurred? (1=Yes, 0 = No)
8. **RaidStart:** Time from the start of trial when the raid initiated (in seconds)
9. **1stExit:** Time from the start of the trial when the first *T. americanus* scout exited its nest (in seconds)
10. **SearchTime\_1stFind:** Time *T. americanus* colony spent searching before its first host nest was discovered. Measured as the time from "1stExit" until the first host nest was discovered (in seconds).
11. **Latency:** Time from discovery until first raid initiation (in seconds)
12. **Pw:** Number of *T. americanus* workers in the colony, not including the queen.

Brood Schedule TP Combined.csv

Number of rows: 604

Definition of variables:

1. **Sp:** Species of colony measured (T=*T. longispinosus*, P = *T. americanus*)
2. **ID:** Unique colony identification number
3. **Xfer:** Date at which colony was removed from Ziploc bag and processed for counts and measurement
4. **Q:** Number of queens in the colony
5. **Tw:** Number of *T. longispinosus* workers in the colony (applies to both T and P colonies)
6. **TPupq:** Number of *T. longispinosus* queen pupae in the colony
7. **TPupm:** Number of *T. longispinosus* male pupae in the colony
8. **TPupw:** Number of *T. longispinosus* worker pupae in the colony
9. **L:** Number of larvae in the colony
10. **UnID:** Number of unidentifiable brood in the colony
11. **TotB:** Total number of brood in the colony
12. **Wpupae:** Number of *T. longispinosus* worker pupae in the colony

13. **Date:** Date colony was collected
14. **LID:** Specific location colony was collected (AVT; BALDHILL; BB; BEAR; BFC; BLP; BLRO; BM-202; BM-202N; BR; BRIDGE; CAMP1;CC;CORNELL-INTXN; CP; ELM; FCVN; FOF; GY; HALE; HB; HH; KRd; LB; LID; LS; LT; McW; MP; MR; OH; PH & B; PALMER; PHR; PP; RENW; RT; SAMPSON; SLM; TWLM; VCT; WARREN WOODS; WLK; WLM; WOOD RD).
15. **Loc:** Region colony was collected.
16. **Year:** Year of collection.
17. **Day:** Day of the year colony was collected (out of 365).
18. **Julian:** Year and day of year combined
19. **PamW:** Number of *T. americanus* workers in colony
20. **PamPupw:** Number of *T. americanus* worker pupae in colony
21. **PamPupq:** Number of *T. americanus* queen pupae in colony
22. **PamPupm:** Number of *T. americanus* male pupae in colony

Demographics - Total.csv

Number of rows: 93

Definition of variables:

1. **PlotID:** Identity of plot (A, B, C, D, E, F, BM1, BM2, BR)
2. **NestID:** Unique colony identity
3. **Species:** Species identity (Pam = *T. americanus*; Tlong = *T. longispinosus*)
4. **Distance:** Distance of nest from *T. americanus* nest in center of plot
5. **Angle:** Angle of nest from North (0-360 degrees)
6. **TlongQ:** Number of queens in *T. longispinosus* nest
7. **Tw:** Number of workers in *T. longispinosus* nest
8. **Twpupae:** Number of worker pupae in *T. longispinosus* nest
9. **Tlarv:** Number of larvae in *T. longispinosus* nest
10. **BroodTot:** Total number of larvae and worker pupae in *T. longispinosus* nest
11. **PamQ:** Number of queens in *T. americanus* nest
12. **PamW:** Number of *T. americanus* workers in *T. americanus* nest
13. **PpupW:** Number of *T. americanus* worker pupae in *T. americanus* nest
14. **PpupQ:** Number of *T. americanus* queen pupae in *T. americanus* nest
15. **PpupM:** Number of *T. americanus* male pupae in *T. americanus* nest
16. **P Twpup:** Number of *T. longispinosus* worker pupae in *T. americanus* nest
17. **Plarv:** Number of larvae in *T. americanus* nest
18. **PTw:** Number of *T. longispinosus* workers in *T. americanus* nest
19. **PW:Tpup:** Ratio of number of *T. longispinosus* worker pupae to number of *T. americanus* workers

Demographics XYcoord.csv

Number of rows: 93

1. **x:** X-coordinate of nest location
2. **y:** Y-coordinate of nest location
3. **PlotID:** Identity of plot (A, B, C, D, E, F, BM1, BM2, BR)

4. **NestID:** Identity of nest at plot
5. **Species:** Species identity of colony (Pam = *T. americanus*; Tlong = *T. longispinosus*)
6. **DatabaseID:** Unique colony ID

Host Density Foitzik MyData Combined.csv

Number of rows: 20

1. **DataSource:** Source of data. My data = the radial plots surveyed in this study. Foitzik = data from plot surveys taken from several different publications, listed in the manuscript text.
2. **Plot:** Identity of the plot.
3. **hostspm2:** Hosts per square meter; Number of *T. longispinosus* nests divided by the size of the area surveyed (in m<sup>2</sup>).
4. **hostpsm:** Hosts per slave-maker; Number of *T. longispinosus* nests per *T. americanus* nests.

#### SUMMARY OF ANALYSIS FILES

(1) Two-Choice Test:

`2-Choice Expt.R` includes code for the chi-square test, logistic regression and latency to raid.

(2) Microcosm:

`Microcosms.R` contains code for the chi-square tests.

(3) Brood Phenology:

`BroodPhenology_Randomization_and_Model.R` includes code for polynomial fitting for proportion of brood that are pupae over time for both host and parasite and the randomization test. It also includes a multiple regression and associated model selection of how proportion of brood that are pupae is affected by day of year and species identity.

(4) Field Data:

`Encounter Rate Calculations.R` calculates the mean and standard error encounter rates.

`Spatial Stats.R` script calculates Clark Evan's index and Levene's test using my plot data, and includes code for creating figures of each plot using x-y coordinates.

`FieldDemographics_Calculations.xlsx` spreadsheet contains the data for and the calculations of means and variance of host nest contents in each study plot.