Structured Models with Variability in 2 Examples: (i) Dynamics of *Mycobacterium marinum* Infections, and (ii) Invasive Species Population Dynamics

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Overview

- Mathematics as a means to address real problems
- Fields of mathematics arose out of applications
- Used to gain insights in applications
- Relationship between mathematics and physics well known, fruitful
- More recently, life sciences as a source of problems and new approaches in applied mathematics
Integrating mathematics and science/engineering

The Iterative Modeling Process

(i) Empirical Observations (experiments and data collection)

(ii) Formalization of properties, relationships and mechanisms which result in a biological or physical model

(iii) Abstraction or Mathematization resulting in a mathematical model

(iv) Formalization of Uncertainty/Variability in model and data resulting in a statistical model

(v) Model Analysis

(vi) Interpretation and Comparison (with the real system)

(vii) Changes in understanding of mechanisms, etc., in the real system.

Formation Stage: (i), (ii), (iii), (iv)
Solution Stage: (v)
Interpretation Stage: (vi), (vii)
Key Questions

From application/scientific standpoint:

- Model:
  - Hypothesis testing tool
- Analysis:
  - Insight to underlying mechanism
  - identify key components
- Calibrated model:
  - Predictive capability
  - improved experimental design

From mathematical/statistical standpoint:

- Develop framework of mathematical model
- Long-term/Qualitative analysis
- Numerical approximations
- Computational Issues
1. *Mycobacterium marinum* Infections

2. Invasive Species: *Pomacea maculata*

3. Graduate Studies at UL Lafayette
Joint work with:

- Dr. Azmy Ackleh, Dr. Mark Delcambre, Lihong Zhao, Department of Mathematics, UL Lafayette
- Dr. Don Ennis & students, Department of Biology, UL Lafayette
Mycobacterium marinum Infections

- Human TB is still leading infectious disease (just not in Europe or US)
  - \( \approx 9 \) million Mtb cases become acute TB,
  - \( \approx 2 \) million deaths annually,

- Studying *Mycobacterium marinum* (Mm) has some advantages to studying human TB:
  - One of most closely genetically related species to human TB
  - Life cycle/progression faster/obvious ethical advantages
  - Low risk to researchers - human infection common but not serious
  - Can eliminate some sources of variability

- Mm infections parallel human TB burden
  - Scale: wild and aquaculture fisheries (human food sources), pet aquarium, research stock

- Chronic (asymptomatic) infection extremely common

- Chronic serves as pool for more susceptible subpopulations

- Plausible transmission mechanisms only recently established (by Don Ennis and others)
Variability in Infection Progression and Outcome

Mycobacterium marinum Infections

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Structured Models with Variability

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**Proposed transmission network**

- **Mycobacterium marinum Infections**
- **Human Activities**
  - Uninfected
  - Ingestion
  - Infected
  - Ingestion
  - Shed
  - “1” Ingestion
  - “2” Shed
  - “3” Ingestion
  - Biofilms (Unactivated?)
  - Intermediate Carriers
  - Activated Bacteria
  - Activated Planktonic Mycobacteria
  - Activated Planktonic Bacteria

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Mathematical Model

Key components

- **Structured by infection**
- Physiological differences (metabolic, immunological: susceptibility, progression, etc.)
  - Groups $i = 1, ..., m$
  - $S^i(t)$: number of susceptible fish of physiological type $i$ at time $t$
  - $I^i(t, x)$: density of infected fish of type $i$, at time $t$ and bacterial load $x$
  - $Y(t) = \sum_{i=1}^{m} S^i(t) + \int_{x_{\text{min}}}^{x_{\text{max}}} I^i(t, x)dx$

- Species involved in propagation of infection
  - $B_u(t)$: unactivated bacteria at time $t$
  - $B_a(t)$: activated bacteria at time $t$
  - $B_d(t)$: bacteria residing in fish carcasses at time $t$
  - $L(t)$: mosquito larvae carrying bacteria at time $t$
Susceptible fish:

\[
\frac{dS^i}{dt} = F^i(Y) - \mu^i S^i - \nu_1 \delta B_a S^i - \nu_2 c_1^i B_d S^i - \nu_3 \eta c_2^i L S^i,
\]

- \(F^i(Y) = \sum_{j=1}^{m} r_{ij} b^i(Y) Y^j\): birth of susceptible fish, from groups \(j\)
- \(\mu^i S^i\): natural death rate
- \(\nu_1 \delta B_a S^i\): infection through direct uptake of Mm (perhaps fecal grazing)
- \(\nu_2 c_1^i B_d S^i\): infection via consumption of infected carcasses
- \(\nu_3 \eta c_2^i L S^i\): infection via consumption of carrier mosquito larvae
Infection-structured Model

Infected fish:

\[
\frac{\partial I^i}{\partial t} + \frac{\partial (g^i I^i)}{\partial x} + \tilde{\mu}^i I^i = 0,
\]

- \(\tilde{\mu}^i I^i = \exp(b \frac{x - x_{\text{min}}}{x_{\text{max}} - x_{\text{min}}})\mu\): modified death rate of infected fish
- \(g^i(x, B_a, B_d, L) = \beta^i(x) + \sigma_1 \delta B_a + \sigma_2 e^{-\alpha^1 x} c_1^i B_d + \sigma_3 \eta e^{-\alpha^2 x} c_2^i L\): progression of infection
- \(g^i I^i \big|_{x_{\text{min}}} = \nu_1 \delta B_a S^i + \nu_2 c_1^i B_d S^i + \nu_3 \eta c_2^i L S^i\): new infections
### Infection-structured Model

**Activated Bacteria:**

\[
\frac{dB_a}{dt} = I(t; \rho) - \delta B_a Y - \gamma B_a - \kappa B_a
\]

- \(\rho^i(x) = \check{\rho}^i \frac{x - x_{\text{min}}}{x_{\text{max}} - x_{\text{min}}}:\) (per capita) rate of shed from infected fish
- \(I(t; \rho) = \sum_{i=1}^{m} \int_{x_{\text{min}}}^{x_{\text{max}}} \rho(x)I^i \, dx:\) total shedding rate of bacteria from infected fish
- \(\delta B_a Y: \) loss of bacteria through uptake by fish pop’n
- \(\gamma B_a: \) inactivation of bacteria
- \(\kappa B_a: \) removal by ‘fecal grazing’, by other animals
Infection-structured Model

Unactivated Bacteria:

\[
\frac{dB_u}{dt} = H(t, B_u) + \gamma B_a - c_L L^* B_u - \tilde{\delta} B_u Y - \kappa B_u
\]

- \( H(t, B_u) \): Effect of human interaction on biofilms
- \( c_L L^* B_u \): consumption of biofilms by mosquitos (total mosquito population, \( L^* \), assumed constant)
- \( \tilde{\delta} B_u Y \): uptake via fish
- \( \kappa B_u \): removal by fecal grazing by other animals
Mycobacterium marinum Infections

Infection-structured Model

Bacteria from dead fish:

\[
\frac{dB_d}{dt} = I(t; x\tilde{\mu}) - B_d (S(t; c_2) + I(t; e^{-\alpha^2x}c_2)) - \zeta B_d.
\]

- \(I(t; x\tilde{\mu})\): source of bacteria through the death of fish
- \(B_d (S(t; c_2) + I(t; e^{-\alpha^2x}c_2))\): consumption of bacteria (carcasses) by fish
- \(\zeta B_d\): consumption of bacteria (carcasses) by other fish species, not explicitly included
Carrier mosquito larvae:

\[ \frac{dL}{dt} = \epsilon c_L (L^* - L) B_u - \mu_L L - L \left( S(t; c_2) + I(t; e^{-\alpha_2 \times c_2}) \right) \]

- \( \epsilon c_L (L^* - L) B_u \): larvae that become effective carriers upon consuming bacteria
- \( \mu_L L \): maturation rate out of larval stage
- \( L \left( S(t; c_2) + I(t; e^{-\alpha_2 \times c_2}) \right) \): consumption of carrier larvae by all fish
Model is necessarily complex → qualitative analysis intractable
Study approximate solutions numerically
Develop finite difference scheme
- Convergence of scheme (to a unique solution)
- Preservation of positivity of solutions (nontrivial for large mortality terms)
- Computational cost, accuracy, stability concerns
- Developed 1st order scheme for bacterial load-structured model
- Established results for a 1st- and 2nd-order scheme in a size-structured model
Model verification

- Model should reproduce observed behavior
  - measure of confidence
- Physiological groups required to reproduce initial experiments by Don Ennis’ lab
  - Fish fed carrier mosquito larvae
  - Time courses of dead fish (and subsequent bacterial loads counted)
  - Bacterial load counts of all fish at final time
- Justified inclusion of more than one physiological group
Figure: Time course of dead fish as compared with trends seen in the experimental setting (with $m = 6$).
Figure: The final distribution of infected fish densities in the slowest ($i = 1$), medium ($i = 3$), and fastest ($i = 5$) progressing classes. Note: density approaches zero prior to $\log(x_{\text{max}})$.
More reasonable for \( \frac{dx}{dt} = \beta^i(x) \) to be very different (not simply exponential)

Current work: allow \( \beta \) to sample from a family of progression rate functions \( \mathcal{B} \) according to some probability distribution \( P \).

Neglect several physiological groups

Need to establish validity of numerical approximations for \( \mathcal{B} \) finite and infinite-dimensional (family of functions approximated by finite (parameterized, e.g., splines) family)

Goal is to use in inverse problem \( \rightarrow \) convergence of parameter estimates \( \theta_n \) as the number of observations \( n \rightarrow \infty \)?

Computational considerations: over-parameterization, or principle of parsimony
Other future work

Intra-host studies
- Integrate current and future experiments (efforts led by Don Ennis) to develop and refine forms for intra-host progression rates $\beta(x)$

Population-level studies
- Use progress in understanding of biology & mathematical framework → simulation studies
  - What are effects of up-/down-regulation of components of food network?
  - Are certain components more critical to infection transmission than others?
  - Are there observable effects of un-observable quantities?
  - Can we infer some key rates that we cannot directly measure?
  - Design experiments via information theoretic approaches
  - Is model sufficient as is? Or, is expansion to a more naturally occurring setting feasible?
Other applications

- Applications often involve similar/identical mathematical formulation.
- Individual growth rates often highly variable
- Population dynamics governed by birth, death (predation, competition/crowding) often dependent on size
- Size-structured population models (Sinko-Streifer ‘67 - age-/size-structured)
- Another current project → *Pomacea maculata* invasive species
1. *Mycobacterium marinum* Infections

2. Invasive Species: *Pomacea maculata*

3. Graduate Studies at UL Lafayette
Invasive Species: *Pomacea maculata*

Joint work with:

- Lihong Zhao, Department of Mathematics at UL Lafayette
- Jacoby Carter, USGS National Wetlands Research Center
- *Pomacea maculata*, is recently renamed from the island applesnail, *Pomacea insularum*.
- Native to the Amazon basin.
Invasive Species: *Pomacea maculata*

**Background (con’t)**

- Feeds on aquatic, submerged plants.
- Introduced into United States through pet trade.
- Documented in Alabama, Florida, Georgia, Hawaii, Louisiana, and Texas.
- Once established, they are very difficult to remove.
- Overgrazing can greatly alter natural balance of local ecosystem.  
  [Carlsson et al. 2004]
- Major pest in rice fields in the Phillippines, China, Laos.
Rapid and profuse reproduction.
Unknown predator community.
Potential of population explosion.
Potentially a vector for snail borne diseases.
Little has been quantified re: life cycle
  - Eggs in clutches [Colin et al. 2013]
  - Clutches contain $\geq 1000$ eggs [Colin et al. 2013]
  - Non-native range, even more [Colin et al. 2013]
  - Eggs begin hatching out, presumably in layers, around 21 days.
  - From our preliminary work, approximately 200 days to maximum size.

Growth dynamics, size distribution, sex differences previously not quantified.
Growth Experiments

- Measurements taken roughly weekly, for 13 weeks.
- Snails were individually marked
  - Opaque florescent alpha numeric tags: originally attached to outside of the shell, later glued to operculum instead.
  - PIT tags: originally injected, later glued to the shell instead.
  - Marking procedures in development: most individuals < 13 weeks
- Recorded: weight, length of operculum, sex (if possible), identification, date.
- Egg masses removed from tank (no birth).
- Fed leafy plants, vegetables from grocery store.
- All snails used in this study were raised from eggs collected from the field (closed population).
Invasive Species: *Pomacea maculata*

Sex Ratio and Weight Differences

- Number of snails sexed: 99 female and 44 male
- Sex ratio is NOT 1:1.
  - 1:1 sex ratio common assumption
- More dynamics observed in weight than operculum size
- The maximal weight observed: 105.1g for female and 77.2g for male

**Table:** Basic Statistics for Weight

<table>
<thead>
<tr>
<th></th>
<th>Female</th>
<th>Male</th>
</tr>
</thead>
<tbody>
<tr>
<td>Top</td>
<td>Mean</td>
<td>Standard Deviation</td>
</tr>
<tr>
<td>50 %</td>
<td>68.61397</td>
<td>14.1872</td>
</tr>
<tr>
<td>10 %</td>
<td>89.64636</td>
<td>5.6071</td>
</tr>
<tr>
<td>50 %</td>
<td>62.79249</td>
<td>6.287704</td>
</tr>
<tr>
<td>10 %</td>
<td>72.27843</td>
<td>2.542464</td>
</tr>
</tbody>
</table>
The weight distribution for females and males are different.
Females and males may have different growth dynamics.
Individual Variation

- Large degree of variation in individual growth rates.
- However, some trends were observed:
  - hypothesize that growth rates differ depending on size (development),
  - consistent with ecological theory: energy shift in initial growth to sexual reproduction.
- Calculated growth rates in weight *ranges*

\[ g(x) = \begin{cases} 
  g_1, & \text{if } x_{\text{min}} \leq x \leq x_1 \\
  g_2, & \text{if } x_1 < x \leq x_{\text{max}}
\end{cases} \]
Growth rates from direct calculation not statistically supported.

**Table:** Basic Statistics for Growth Rates–Female (99 Total)

<table>
<thead>
<tr>
<th>Stages</th>
<th>≤ 23g</th>
<th>23.1 – 40g</th>
<th>40.1 – 53g</th>
<th>53.1 – 71g</th>
<th>&gt; 71g</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean</td>
<td>0.3531553</td>
<td>0.2316956</td>
<td>0.2332250</td>
<td>0.0626806</td>
<td>0.0935414</td>
</tr>
<tr>
<td>std.</td>
<td>0.1199893</td>
<td>0.1525451</td>
<td>0.2550575</td>
<td>0.6382982</td>
<td>0.1362457</td>
</tr>
<tr>
<td>N</td>
<td>38</td>
<td>45</td>
<td>40</td>
<td>36</td>
<td>29</td>
</tr>
</tbody>
</table>

**Table:** Basic Statistics for Growth Rates–Male (44 Total)

<table>
<thead>
<tr>
<th>Stages</th>
<th>≤ 24g</th>
<th>24.1 – 40g</th>
<th>40.1 – 55g</th>
<th>&gt; 55g</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean</td>
<td>0.302</td>
<td>0.1255556</td>
<td>0.2083333</td>
<td>0.05481481</td>
</tr>
<tr>
<td>std.</td>
<td>0.1031504</td>
<td>0.1399206</td>
<td>0.2375723</td>
<td>0.137795</td>
</tr>
<tr>
<td>N</td>
<td>10</td>
<td>9</td>
<td>24</td>
<td>27</td>
</tr>
</tbody>
</table>
Initial Conclusions

- Noticeable differences in female and male populations
- Growth appears to change throughout snail’s lifespan
- Individual data too incomplete to yield reasonable estimates to characterize growth dynamics
- Population-level approach may be better (records complete unless snail was missed on observation date)
Invasive Species: *Pomacea maculata*

**Female Population Growth Model**

Since birth/death/predation/growth rates depend on size, we propose a size-structured model governing the dynamics of the female snail population density $p(t, x)$:

$$
\frac{\partial p(t, x)}{\partial t} + \frac{\partial (g(x)p(t, x))}{\partial x} = -\mu p(t, x),
$$

$$
p(0, x) = p_0(x).
$$

for $t > 0$, and $x_{\text{min}} \leq x \leq x_{\text{max}}$, where $x_{\text{min}}$ and $x_{\text{max}}$ represent the minimum and maximum weight achievable by an applesnail.

- $g(x)$: growth rate
- $\mu$: death (and predation) rate:
- BC: birth rate $(g(x)p(t, x))|_{x_{\text{min}}} = \int_{x_{\text{min}}}^{x_{\text{max}}} \beta_F(t, x)p(t, x)dx$
- $\beta_F(t, x)$: rate at which females give birth to female snails (zero for lab)
Male Population Growth Model

Male population dynamics model is given by

\[
\frac{\partial q(t, x)}{\partial t} + \frac{\partial (h(x)q(t, x))}{\partial x} = -\mu q(t, x),
\]

\[q(0, x) = q_0(x).\]

- growth rate: \(h(x)\)
- BC: birth rate \((h(x)q(t, x))\) at \(x_{\min}\)
  \[= \int_{x_{\min}}^{x_{\max}} \beta_M(t, x)p(t, x)dx\]
- Uncoupled from females due to (current) rates being independent of population density, and zero birth rate in lab.
We then discretize the model using the following explicit finite difference approximation:

\[
\frac{p(x_j, t_{k+1}) - p(x_j, t_k)}{\Delta t} + \frac{(g(x_j)p(x_j, t_k) - g(x_{j-1})p(x_{j-1}, t_k))}{\Delta x} + \mu(x_j)p(x_j, t_k) = 0
\]

\[
(g(x)p(t, x))|_{x_{\text{min}}} = B = 0, \quad p(0, x) = IC
\]

\[
t_k = t_0 + k\Delta t, \quad k = 0, \ldots, K
\]

\[
x_j = x_{\text{min}} + j\Delta x, \quad j = 0, \ldots, J, \quad x_0 = x_{\text{min}}, \quad x_J = x_{\text{max}}
\]

The convergence of this 1st order scheme has been shown for this and even more general schemes.
Model Comparison (RSS-based) Statistic

- Appropriate number of ‘stages’ in the growth functions?
- Model comparison statistic $\Rightarrow$ inclusion of which end points gives statistically sig. improvement?

Define the restricted parameter space to be

$$\Theta_H = \{\theta \in \Theta \mid H\theta = c\}$$

where

- $H$: an $r \times n_p$ matrix
- $n_p$: number of parameters in $\Theta$
- $r$: degrees of freedom
- $c$: a known constant
For example, consider female snails:

- $H_a$: General case $m = 9$, $\{x_i\}_{i=1}^8 = \{17, 23, 40, 47, 53, 60, 71, 85\}$
- $H_0$: Restricted case $m = 7$, a special case of the general case with $g_4 = g_5$, $g_6 = g_7$
- $\hat{\theta} = (\hat{g}_1, \ldots, \hat{g}_9)$, $\Theta \in \mathbb{R}^9$, $n_p = 9$
- 2 more degrees of freedom in the general case than the restricted case, i.e., $r = 2$
- $\Theta_H = \{\theta \in \Theta | H\theta = c\}$

where

$$H = \begin{pmatrix} 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 \end{pmatrix}$$

$$c = \begin{pmatrix} 0 \\ 0 \end{pmatrix}$$
Observe that

\[ J_K(Y, \hat{\theta}_H^K) \geq J_K(Y, \hat{\theta}_K^K) \]

We define the statistic by

\[ U_K(Y) = \frac{T_K(Y)}{J_K(Y, \theta_K)} = \frac{K \cdot (J_K(Y, \hat{\theta}_H^K) - J_K(Y, \hat{\theta}_K^K))}{J_K(Y, \theta_K)} \]

with corresponding realizations \( \hat{U}_K = U_K(y) \).

If \( H_0 \) is true, \( U_K \overset{D}{\to} U(r) \) as \( K \to \infty \) where \( U \sim \chi^2(r) \), a \( \chi^2 \) distribution with \( r \) degrees of freedom.
### Table: RSS Statistic: 1-stage vs multi-stages—Female

<table>
<thead>
<tr>
<th>$H_0$: m</th>
<th>$H_a$: m; ${x_i}$</th>
<th>U</th>
<th>Df</th>
<th>Confidence</th>
<th>Rej.</th>
<th>$H_0$</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>2; ${23}$</td>
<td>0.618175916</td>
<td>1</td>
<td></td>
<td>56%</td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>2; ${40}$</td>
<td>5.865695809</td>
<td>1</td>
<td></td>
<td>98%</td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>3; ${23, 40}$</td>
<td>5.979250924</td>
<td>2</td>
<td></td>
<td>94%</td>
<td></td>
</tr>
</tbody>
</table>

- Multi-stage growth functions have statistically significant improvements than single-stage growth function.
- ⇒ Single-stage growth function is not suitable for female.
Growth functions with $m > 3$ stages don't provide any statistically significant improvements

$\Rightarrow$ More than 3 stages are not necessary.

Including 40 as an end point does provide statistically significant improvements

$\Rightarrow$ 40 should be included as an end point.
Thus, the 2-stage growth function

\[ g(x) = \begin{cases} 
0.286278628, & x \in [x_{\text{min}}, 40] \\
0.0912533, & x \in (40, x_{\text{max}}^F] 
\end{cases} \]

is the best for females, and the 2-stage growth function

\[ h(x) = \begin{cases} 
0.230553432, & x \in [x_{\text{min}}, 24] \\
0.103575229, & x \in (24, x_{\text{max}}^M] 
\end{cases} \]

is the best for males.
Results from Data

Table: Piecewise Constant Function

<table>
<thead>
<tr>
<th></th>
<th>$\theta$</th>
<th>$\hat{\theta}$</th>
<th>$SE(\hat{\theta})$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Female</td>
<td>$g_1$</td>
<td>0.286278628</td>
<td>0.020640053</td>
</tr>
<tr>
<td></td>
<td>$g_2$</td>
<td>0.0912533</td>
<td>0.033049222</td>
</tr>
<tr>
<td>Male</td>
<td>$h_1$</td>
<td>0.230553432</td>
<td>0.024843199</td>
</tr>
<tr>
<td></td>
<td>$h_2$</td>
<td>0.103575229</td>
<td>0.01161497</td>
</tr>
</tbody>
</table>
Invasive Species: *Pomacea maculata*

**Piecewise Constant Growth Function – Female**

- **$g(x)$ Female**
  - Weight (g) vs. Growth Rate
  - **x(t) Female**
    - Weight (Unit: g) vs. Time (day)
    - $x(t)$ and 95% CI

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Structured Models with Variability  
March 8, 2016
Invasive Species: *Pomacea maculata*

**Piecewise Constant Growth Function – Male**

- **h(x) Male**
  - Growth Rate
  - Weight (g)
  - Weight (Unit: g)

- **x(t) Male**
  - Time (day)
  - Weight (Unit: g)
  - 95% CI

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Structured Models with Variability

March 8, 2016
Further analysis and data

- Other growth models tried; piecewise constant the ‘best’ with given data set
- Concurrently, large number (1287) snails hatched out in 1 week in overcrowded tank
- Weighed and measured length; in triplicate for 675;
- Better characterize variability in population
Invasive Species: *Pomacea maculata*

Large sample size

Variability in growth rate strongly suggested!
Invasive Species: *Pomacea maculata*

Large sample size

Assume Snails Hatched out in Layers in Week 1

Even if we roughly scale for possible differences in birth (largest snails hatched out 1st day, etc.), appears to be substantial variability in growth rate.
Invasive Species: *Pomacea maculata*

**Current/Future work**

Mathematically:
- Mathematical framework and results from Mm infection project useful here.
- New knowledge of variability in growth rates effects on previous population results?
- Sample size, number of time points, and at which life stages required to characterize growth rate/function?

Experimentally:
- Currently measuring distribution of the hatch out process (i.e., birth rate)
- Currently measuring small snail weights (hatchling to around 8 g), and survivability
Mathematical framework and results necessary to address questions in Mm infection dynamics and applesnail population dynamics.

Future integration of mathematical and biological experiments to understand intra-host Mm dynamics likely useful.

Parameter estimation and model comparison statistic used to infer information on applesnail when direct measurement failed.
1. *Mycobacterium marinum* Infections

2. Invasive Species: *Pomacea maculata*

3. Graduate Studies at UL Lafayette
Graduate studies in mathematics at UL Lafayette

- Research Areas
  - Algebra (3)
  - Analysis (2)
  - Applied Mathematics (10)
  - Topology (3)
  - Statistics (4)

- Stipends:
  - Master’s: $\geq 15k$
  - Ph.D.: $\geq 17k$
  - possible summer teaching

- Application information
  - Directly to Graduate School (gradschool.louisiana.edu)
  - Master’s not required for admission to Ph.D.
  - Contact Dr. Arturo Magidin: magidin@louisiana.edu

- Recent graduates:
  - $\approx 80\%$ work in field
  - Median time to completion: 5 1/2 yrs
Applications information

- graduate school
- Master’s not required for admission to Ph.D.
- Contact Dr. Arturo Magidin: magidin@louisiana.edu

Recent graduates:

- $\approx 80\%$ work in field
- Median time to completion: 5 1/2 yrs
Thank you!