How much does evolution delay doom?

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Collaborators







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References

- Gomulkiewicz, Krone, & Remien. 2017. Evolutionary Applications 10:471-484.
- Bull, Krone, & Remien. 2019. PeerJ 7:e7921 http://doi.org/10.7717/peerj.7921

Rescue vs Doom

 $X_{t+1} = (1+r)X_t + \text{noise}$



Can the Doomed be Rescued by Evolution?





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Research



The probability of evolutionary rescue: towards a quantitative comparison between theory and evolution experiments

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"Measuring the probability of rescue is not that straightforward. First, one must choose the time period over which populations can be said to be either doomed or rescued." (2013)

Time to Doom

 $X_{t+1} = (1+r)X_t + noise$



Questions

- 1. What is the distribution of time to extinction for evolving populations?
- 2. How does this distribution depend on genetic diversity and abundances?
- 3. How does adaptive evolution affect the longevity of populations headed to extinction?

Adaptive Evolution & Time to Extinction

Evolution, 49(1), 1995, pp. 201-207

WHEN DOES EVOLUTION BY NATURAL SELECTION PREVENT EXTINCTION?

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Basic Model of Demography & Evolution

- ► *G* clones
- $X_i(t) \ge 0$ is **density** of clone *i* at time t (i = 1, ..., G)
- Each X_i an independent continuous branching diffusion
- Genotype *i* characterized by intrinsic growth rate *r_i* & reproductive variance *v_i*
- Genotype dynamics described by stochastic differential equation and initial condition

$$dX_i = r_i X_i dt + \sqrt{v_i X_i} dW_i$$

 $X_i(0) = x_i$

Genetically Uniform Populations

- Population monomorphic for genotype with growth & variance parameters g = (r, v)
- Dynamics: $dX = rXdt + \sqrt{vX}dW$
- Initial density X(0) = x
- P(extinct at time t) = $[f(t;g)]^x$
- Genotypic Risk Function:

$$\ln f(t;g) = \begin{cases} -2r/[v(1-e^{-rt})] & \text{if } r \neq 0\\ -2/(vt) & \text{if } r = 0. \end{cases}$$



r

Extinction Time Percentiles: No Evolution



r

Extinction Time Percentiles: No Evolution



Genotypic Risk Functions, f(t;g)

















Genotypic Risks over Time



t

Polymorphic Populations

- Genotypes: $g_i = (r_i, v_i)$
- Initial densities: $X_i(0) = x_i$
- Genotypic risk functions:

$$\ln f(t; g_i) = \begin{cases} -2r_i / [v_i (1 - e^{-r_i t})] & \text{if } r_i \neq 0 \\ -2 / (v_i t) & \text{if } r_i = 0. \end{cases}$$

• P(extinct at time t) = $\prod_{i=1}^{G} [f(t; g_i)]^{x_i}$

Three Types of Change

Polymorphic analysis key result: abundance, genetic diversity, vital rates have distinct effects

- 1. Genetic Diversity
 - change diversity without changing *total* abundance or individual vital rates
 - e.g., mutation
- 2. Vital Rates
 - changes in environment that enhance or impair survival & reproduction

3. Abundance

- supplementation
- removal



k

Three types of rescue can avert extinction in a changing environment

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Edited by James H. Brown, University of New Mexico, Albuquerque, NM, and approved July 7, 2015 (received for review March 8, 2015)



1. Change Genetic Diversity

- Genetically uniform "ancestral" population
 - density x
 - growth parameters r and v
- Substitution/Mutation
 - replace x^{*} individuals with mutant genotype
- Hufbauer et al. *Tribolium* experiments
 - ancestral r < 0
 - "mutant" r* > 0
 - small populations: x^{*} = 1
 - large populations: $x^* = 3$

Impact of Novel Mutation



2. Impact of Abrupt Environment Change



3. Impacts of Abundance Change

- Supplementation: add density y_i of genotype with growth parameters r_i and v_i, i = 1,..., G
 - Hufbauer et al.:
 - *r** > 0
 - y* = 1 (small populations)
 - y* = 3 (large populations)
 - Conservation/management goal: ensure Pr(extinction) no more than ϕ at time τ
- *Removal*: remove density z_i of genotype with growth parameters
 r_i and v_i, i = 1,..., G
 - disease management goal: ensure Pr(eradicate) at least ϕ at time τ

Deliberate Supplementation or Removal

- Change densities and/or frequencies of genotypes to achieve management goals
 - Conservation: P(extinct before time τ) $\leq \phi$
 - Pest/Pathogen: P(extinct before time τ) $\geq \phi$
- "management gap": $S(\phi, \tau, \mathbf{x}) = \log \phi \sum_{i=1}^{G} x_i \log f(\tau; g_i)$
- Additions (y_1, y_2, \ldots, y_G) satisfy

$$\sum_{i=1}^{G} y_i \log f(\tau; g_i) = S(\phi, \tau, \mathbf{x}) < 0$$

• Removals (z_1, z_2, \ldots, z_G) satisfy

$$\sum_{i=1}^{G} z_i |\log f(\tau; g_i)| = S(\phi, \tau, \mathbf{x}) > 0$$

Spatially-structured Gene Drives & Parasite "Doom"



- Engineered gene drive eradication effective in well-mixed systems
- Real world has spatial structure
- More opportunities for resistance, but cause for concern?
- Yes, perhaps more than expected
- Model and analysis details: Steve Krone's Thursday presentation

Summary of General Findings

- Process-based theoretical framework for predicting time to extinction of evolving populations
 - useful for basic and applied biology (human health, agriculture, conservation)
- Genetic abundances and diversity both affect persistence
 - impacts are distinct but cannot be cleanly separated
- Genotypic risk functions define "maladaptive" landscape
- Prediction: Impact of adaptive evolution on time to extinction is small
 - larger in demographically benign than in harsh conditions
- Spatial structure can undermine parasite eradication by gene drive cargo
 - use models to explore strategies that mitigate gene drive failure

Merci

- Steve Krone
- Chris Remien
- Jim Bull
- Department of Biology, University of Idaho
- Department of Mathematics, University of Idaho

