

Predator-Prey Population Dynamics

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November 13, 2018



Predator-Prey model (Lotka-Volterra system)

Stochastic model as continuous-time Markov chain

A simple Predator-Prey model

- Populations of X prey molecules and Y predator molecules
- Three possible reactions (events)
 - 1) Prey reproduction: $X \rightarrow 2X$

2) Prey consumption to generate predator: $X+Y \rightarrow 2Y$

- 3) Predator death:
- \blacktriangleright Each prey reproduces at rate lpha

 \Rightarrow Population of X preys $\Rightarrow \alpha X =$ rate of first reaction

- Prey individual consumed by predator individual on chance encounter
 ⇒ β = Rate of encounters between prey and predator individuals
 ⇒ X preys and Y predators ⇒ βXY = rate of second reaction
- \blacktriangleright Each predator dies off at rate γ

 \Rightarrow Population of Y predators $\Rightarrow \gamma Y =$ rate of third reaction

 $Y \rightarrow \emptyset$





- Study population dynamics $\Rightarrow X(t)$ and Y(t) as functions of time t
- ► Conventional approach: model via system of differential eqs. ⇒ Lotka-Volterra (LV) system of differential equations
- Change in prey (dX(t)/dt) = Prey generation Prey consumption
 ⇒ Prey is generated when it reproduces (rate αX(t))
 ⇒ Prey consumed by predators (rate βX(t)Y(t))

$$\frac{dX(t)}{dt} = \alpha X(t) - \beta X(t) Y(t)$$

• Predator change (dY(t)/dt) = Predator generation - consumption

 \Rightarrow Predator is generated when it consumes prey (rate $\beta X(t)Y(t)$)

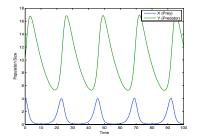
 \Rightarrow Predator consumed when it dies off (rate $\gamma Y(t)$)

$$\frac{dY(t)}{dt} = \beta X(t)Y(t) - \gamma Y(t)$$

Solution of the Lotka-Volterra equations



▶ LV equations are non-linear but can be solved numerically

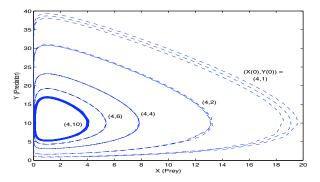


- Prey reproduction rate $\alpha = 1$
- \blacktriangleright Predator death rate $\gamma=0.1$
- Predator consumption of prey $\beta = 0.1$
- Initial state X(0) = 4, Y(0) = 10
- Boom and bust cycles
- Start with prey reproduction > consumption \Rightarrow prey X(t) increases
- Predator production picks up (proportional to X(t)Y(t))
- ▶ Predator production > death \Rightarrow predator Y(t) increases
- Eventually prey reproduction < consumption \Rightarrow prey X(t) decreases
- Predator production slows down (proportional to X(t)Y(t))
- Predator production < death \Rightarrow predator Y(t) decreases
- Prey reproduction > consumption (start over)

State-space diagram



- State-space diagram \Rightarrow plot Y(t) versus X(t)
 - \Rightarrow Constrained to single orbit given by initial state (X(0), Y(0))

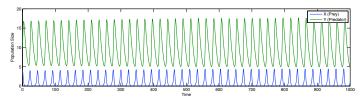


Buildup: Prey increases fast, predator increases slowly (move right and slightly up)Boom: Predator increases fast depleting prey (move up and left)Bust: When prey is depleted predator collapses (move down almost straight)

Two observations





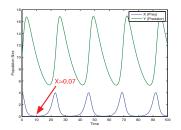


• X(t), Y(t) modeled as continuous but actually discrete. Is this a problem?

 If X(t), Y(t) large can interpret as concentrations (molecules/volume)

 \Rightarrow Often accurate (millions of molecules)

- If X(t), Y(t) small does not make sense
 ⇒ We had 7/100 prey at some point!
- There is an extinction event we are missing





- Deterministic model is useful \Rightarrow Boom and bust cycles
 - \Rightarrow Important property that the model predicts and explains
- But it does not capture some aspects of the system
 - ⇒ Non-discrete population sizes (unrealistic fractional molecules)
 - \Rightarrow No random variation (unrealistic regularity)
- ► Possibly missing important phenomena ⇒ Extinction
- ► Shortcomings most pronounced when number of molecules is small ⇒ Biochemistry at cellular level (1 ~ 5 molecules typical)
- Address these shortcomings through a stochastic model



Predator-Prey model (Lotka-Volterra system)

Stochastic model as continuous-time Markov chain



- Three possible reactions (events) occurring at rates c_1 , c_2 and c_3
 - 1) Prey reproduction: $X \xrightarrow{c_1} 2X$ 2) Prey consumption to generate predator: $X+Y \xrightarrow{c_2} 2Y$
 - 3) Predator death: $Y \stackrel{c_3}{\to} \emptyset$
- Denote as X(t), Y(t) the number of molecules by time t
- ► Can model X(t), Y(t) as continuous time Markov chains (CTMCs)?
- ► Large population size argument not applicable

 \Rightarrow Interest in systems with small number of molecules/individuals



- ► Consider system with 1 prey molecule x and 1 predator molecule y
- ► Let $T_2(1,1)$ be the time until x reacts with y ⇒ Time until x, y meet, and x and y move randomly around ⇒ Reasonable to model $T_2(1,1)$ as memoryless
 - $P(T_2(1,1) > s + t | T_2(1,1) > s) = P(T_2(1,1) > t)$
- $T_2(1,1)$ is exponential with parameter (rate) c_2



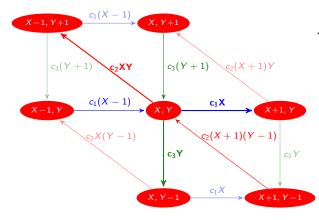
- ► Suppose now there are X preys and Y predators ⇒ There are XY possible predator-prey reactions
- Let $T_2(X, Y)$ be the time until the first of these reactions occurs
- Min. of exponential RVs is exponential with summed parameters $\Rightarrow T_2(X, Y)$ is exponential with parameter c_2XY
- Likewise, time until first reaction of type 1 is $T_1(X) \sim \exp(c_1 X)$
- Time until first reaction of type 3 is $T_3(Y) \sim \exp(c_3 Y)$

CTMC model



If reaction times are exponential can model as CTMC

 \Rightarrow CTMC state (X, Y) with nr. of prey and predator molecules



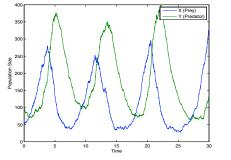
Transition rates

- $(X, Y) \rightarrow (X + 1, Y)$: Reaction $1 = c_1 X$
- $(X, Y) \rightarrow (X-1, Y+1)$: Reaction $2 = c_2 X Y$
- $(X, Y) \rightarrow (X, Y 1)$: Reaction $3 = c_3 Y$
- State-dependent rates

Simulation of CTMC model

Use CTMC model to simulate predator-prey dynamics

• Initial conditions are X(0) = 50 preys and Y(0) = 100 predators



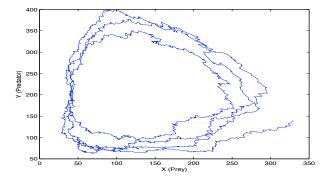
- Prey reproduction rate c₁ = 1 reactions/second
- Rate of predator consumption of prey c₂ = 0.005 reactions/second
- Predator death rate c₃ = 0.6 reactions/second

Boom and bust cycles still the dominant feature of the system
 But random fluctuations are apparent





▶ Plot Y(t) versus X(t) for the CTMC \Rightarrow state-space representation

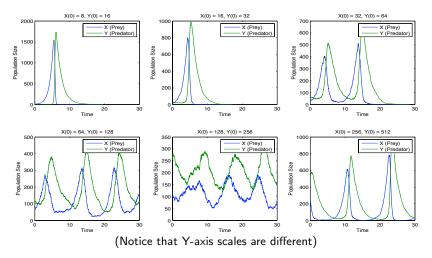


No single fixed orbit as before

 \Rightarrow Randomly perturbed version of deterministic orbit



Chance of extinction captured by CTMC model (top plots)





- Deterministic vs. stochastic (random) modeling
- Deterministic modeling is simpler

 \Rightarrow Captures dominant features (boom and bust cycles)

- CTMC-based stochastic simulation more complex
 - \Rightarrow Less regularity (all runs are different, state orbit not fixed)
 - \Rightarrow Captures effects missed by deterministic solution (extinction)
- ► Gillespie's algorithm. Optional reading in class website
 - \Rightarrow CTMC model for every system of reactions is cumbersome
 - \Rightarrow Impossible for hundreds of types and reactions
 - \Rightarrow Q: Simulation for generic system of chemical reactions?