BIRTH-DEATH PROCESS

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INDEX

- BIRTH-DEATH PROCESS THEORY
- 2 STOCHASTIC SIMULATION ALGORITHM
- 3 STRUCTURE OF BIRTHDEATHPROCESS PACKAGE
- 4 References

BIRTH-DEATH PROCESS

- Simple model of population dynamics called a birth-death processes. Population fluctuations (birth and death rates, β_{birth} and β_{death}) depend only on the population size, n.
- Lets consider the following situation: protein synthesis. The rate at which the population increases depends only on the presence of the ingredients and is thus is fixed and a clearance rate (deaths) that is proportional to the total population, *n*.
- Two possible events: births (or synthesis) and deaths (or decays).

$$\beta_{birth} = (constant)$$

$$\beta_{death} = (k_0) * n$$

• β_{birth} and (k_0) are parameters of the model that would, in principle, be determined by experimental measurements. Both rates have units of [events/time].

BIRTH-DEATH PROCESS

• Deterministically, the population size *n* can be described by the ordinary differential equation:

$$\frac{dn(t)}{dt} = \beta - d \cdot n(t)$$

• Solving this differential equation we get:

$$n(t) = c \cdot e^{-d \cdot t} + \beta/d$$

Where $c = n(0) - \beta/d$.

SOLUTIONS

Simplest cases of pure birth process and pure death process.

- **pure birth process**, the governing equation is: $n(t) = b \cdot t + n(0)$. So any numerical solution that we obtain has to follow a linear pattern of β slope, for this case.
- pure death process, the governing equation is: $n(t) = e^{-d \cdot t} + n(0) 1$. In this case the decreasing exponential pattern has to be observed.

General equation, we obtain the asymptotic trend. With previous solution for the general problem: $n = \beta/d$. The concavity will depend on the sign of C.

INDEX

- BIRTH-DEATH PROCESS THEORY
- 2 STOCHASTIC SIMULATION ALGORITHM
- ③ STRUCTURE OF BIRTHDEATHPROCESS PACKAGE
- 4 REFERENCES

STOCHASTIC SIMULATION ALGORITHM

 Two possible events that might occur and these might each happen at different rates; birth and death.

$$\frac{\textit{trial}_{\textit{death}}}{\textit{trial}_{\textit{birth}} + \textit{trial}_{\textit{death}}} = \frac{\textit{d} \cdot \textit{N}}{\beta + \textit{d} \cdot \textit{N}}, \qquad \frac{\textit{trial}_{\textit{birth}}}{\textit{trial}_{\textit{death}} + \textit{trial}_{\textit{birth}}} = \frac{\beta}{\beta + \textit{d} \cdot \textit{N}}$$

- **Bernoulli Trial**. Event can either be a birth or a death, need to determine which event actually occured. Choose a random number between (0,1) and see if it is less than $\frac{d \cdot N}{\beta + d \cdot N}$ or bigger. In each case we add or subtract an individual to the population (Monte-Carlo simulation).
- For simplicity and to avoid divisions, we take a random number between $(0, d \cdot N + \beta)$. And we check that it is less than or greater than $d \cdot N$.

- Events in birth-death processes do not occur at regular time intervals. We can only say that the odds of an event occurring within any small time interval Δt is equal to $a_0 \Delta t$, where a_0 is the mean rate of event occurrences. A sequence of random wait times is an example of what is called a "Poisson Process."
- Wait-times between sequential events follow an exponential distribution where the probability of the next event occurring after a duration τ (give-or-take Δt) is given by:

$$P(\tau) = a_0 \cdot e^{-a_0 \cdot \tau}$$

• By superposition property we get that $\tau = -\frac{\log r}{\beta + d \cdot x}$. Where r is a random number between (0,1).

```
include("Utils.jl")

export gillespie

ex(tau::Number, mu::Number)::Number = - log(tau) / mu

include("Utils.jl")

export gillespie
```

```
function gillespie(β::Number, 6::Number, n::Number)::Tuple{Array{Float64,1},Array{Float64,1}}

t,n = 0, n;
population, times = Float64[];

while n > 0 & t < T

τ = random()

t = t + _ex(τ, β + 6 * n)

τ = random() * (β + 6 * n)

if τ < β

n = n + 1

else

n = n - 1

push!(times, t)
push!(times, t)
push!(population, n)

return times, population</pre>
```

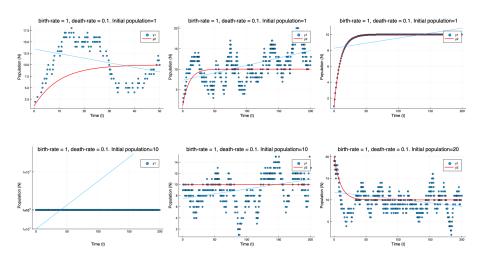
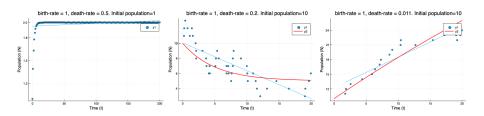
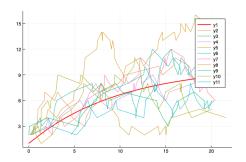


FIGURE: Some examples of simulation

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INDEX

- BIRTH-DEATH PROCESS THEORY
- 2 STOCHASTIC SIMULATION ALGORITHM
- 3 STRUCTURE OF BIRTHDEATHPROCESS PACKAGE
- 4 References



STRUCTURE OF BIRTHDEATHPROCESS PACKAGE

We have divided the package as follows:

- We have a file **Utils.jl** where we have the utility functions. Mainly we have the functionality to generate random numbers.
- **DefaultParameters.jl** where we have the structure to define the parameters β and d of the model.
- Gillespie.jl and RungeKutta.jl here we define the simulation algorithms.
- We have separated the visualization and the obtaining of statistics in independent files. Visualization.jl and Stats.jl.
- We expose the functions in the file BirthDeathProcess.jl.

Finally we have implemented tests and a documentation in html. These are located in the tests and doc folder.

GITHUB-CI WORKFLOW

We have also implemented a github-ci workflow (ci.yml).

- Compiles the package for different versions of julia and in mac, windows and ubuntu environments.
- Run the package tests. We have enabled a code coverage manager (codecov).
- Generate the documentation. Created with Documenter.jl
- Thanks to Julia's package manager, by having Manifest.toml,
 Project.toml, we can reproduce the environment with which this package has been developed and thus ensure reproducibility.

References I



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Stochastic simulation of chemical kinetics.

Annual review of physical chemistry, 58(1):35-55, 2007.



Nicolas Lanchier.

Stochastic modeling.

Springer, 2017.