Jump process using DiffEqBiological

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Introduction

This implementation defines the model as a combination of two jump processes, infection and recovery, simulated using the Doob-Gillespie algorithm.

Libraries

```
using DiffEqBiological
using Random
using DataFrames
using StatsPlots
using BenchmarkTools
```

Transitions

```
sir_model = @reaction_network sir_rn begin
  0.5/1000, s + i --> 2i
  0.25, i --> r
end
(::Main.WeaveSandBox48.sir_rn) (generic function with 2 methods)
```

Time domain

```
tmax = 40.0
tspan = (0.0,tmax);

For plotting, we can also define a separate time series.

δt = 0.1
t = 0:δt:tmax;
```

Initial conditions

```
u0 = [990,10,0]; # S,I,R
```

Random number seed

We set a random number seed for reproducibility.

```
Random.seed!(1234);
```

Running the model

Running this model involves:

- Setting up the problem as a DiscreteProblem;
- Adding the jumps and setting the algorithm using JumpProblem; and
- Running the model, specifying SSAStepper

Post-processing

In order to get output comparable across implementations, we output the model at a fixed set of times.

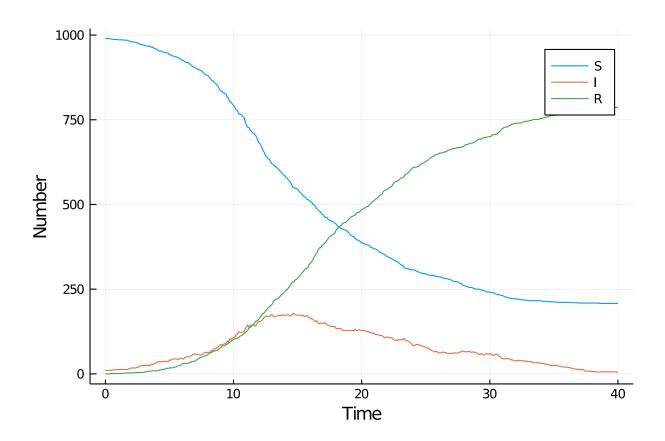
```
out_jump = sol_jump(t);
```

We can convert to a dataframe for convenience.

```
df_jump = DataFrame(out_jump')
df_jump[!,:t] = out_jump.t;
```

Plotting

We can now plot the results.



Benchmarking

```
@benchmark solve(prob_jump,FunctionMap())
```

Error: UndefVarError: FunctionMap not defined

Appendix

Computer Information

```
Julia Version 1.4.0
Commit b8e9a9ecc6 (2020-03-21 16:36 UTC)
Platform Info:
    OS: Windows (x86_64-w64-mingw32)
    CPU: Intel(R) Core(TM) i7-8550U CPU @ 1.80GHz
    WORD_SIZE: 64
    LIBM: libopenlibm
    LLVM: libLLVM-8.0.1 (ORCJIT, skylake)
Environment:
    JULIA_NUM_THREADS = 4
```

Package Information

Status `~\.julia\environments\v1.4\Project.toml`

```
[46ada45e-f475-11e8-01d0-f70cc89e6671] Agents 3.0.0
[b19378d9-d87a-599a-927f-45f220a2c452] ArrayFire 1.0.6
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[37e2e46d-f89d-539d-b4ee-838fcccc9c8e] LinearAlgebra
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```