sir_model_compare

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```
suppressPackageStartupMessages(library(EpiModel))
```

```
## Warning: package 'EpiModel' was built under R version 4.1.2

## Warning: package 'deSolve' was built under R version 4.1.2

## Warning: package 'networkDynamic' was built under R version 4.1.2

## Warning: package 'network' was built under R version 4.1.2

## Warning: package 'tergm' was built under R version 4.1.2

## Warning: package 'ergm' was built under R version 4.1.2

## Warning: package 'statnet.common' was built under R version 4.1.2
```

```
suppressPackageStartupMessages(library(knitr))
suppressPackageStartupMessages(library(dplyr))
suppressPackageStartupMessages(library(ggplot2))
set.seed(97)
```

Stochastic Model n = 100, p =.05, infectious period = 1 day (model1)

Below is a stochastic SIR flu simulation using the R package EpiModel. The model is first validated by replicating a published, peer-review model.

In the paper, Green Simulation of Pandemic Disease Propagation (Wilson,et al., 2019), a stochastic SIR model with the parameters n = 100, p = .05, and an infectious period lasting exactly one day yeilds the following distribution of pandemic lengths after 1,000,000 replications.

See figure 8 https://www.mdpi.com/2073-8994/11/4/580/htm

The model below seeks to replicate the paper's result.

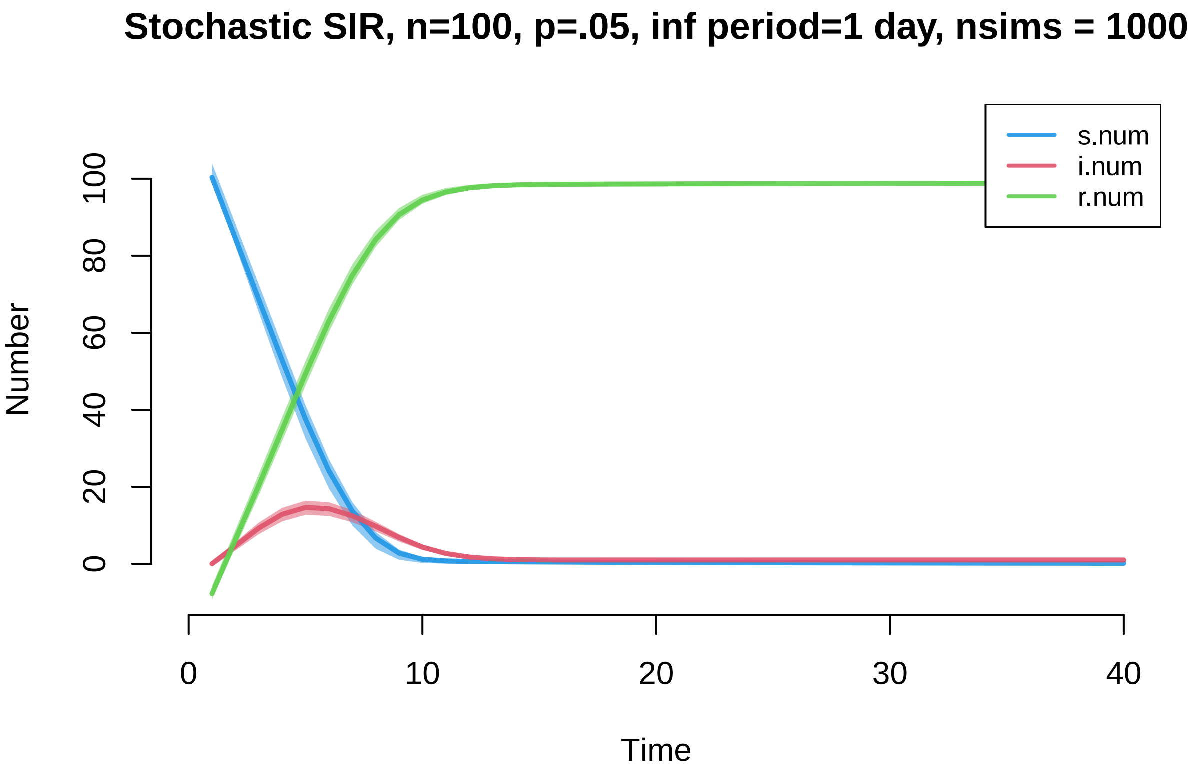
-inf.prob is the probability of infection for each interaction with infected agent -act.rate is set to n-1 to ensure each agent interacts in every simulation -rec.rate is a vector assigning the probability of recovery for each day in the length of infection -s.num is number of susceptible sgents set to n-1 -i.num is the number of initially infected agents -r.num is the number of initially recovered/immune agents -n.steps is the amount of days in the simulation -nsteps is the number of days in eacj simulation -nsims is the number of simulations

Model:

```
param1 <- param.icm(inf.prob = .05, act.rate = 99, rec.rate = c(0,1))
init1 <- init.icm(s.num = 99, i.num = 1, r.num = 0)
control1 <- control.icm(type = "SIR", nsteps = 40, nsims = 1000)
model1 <- icm(param1, init1, control1)
```

Time-series plot S, I, and R

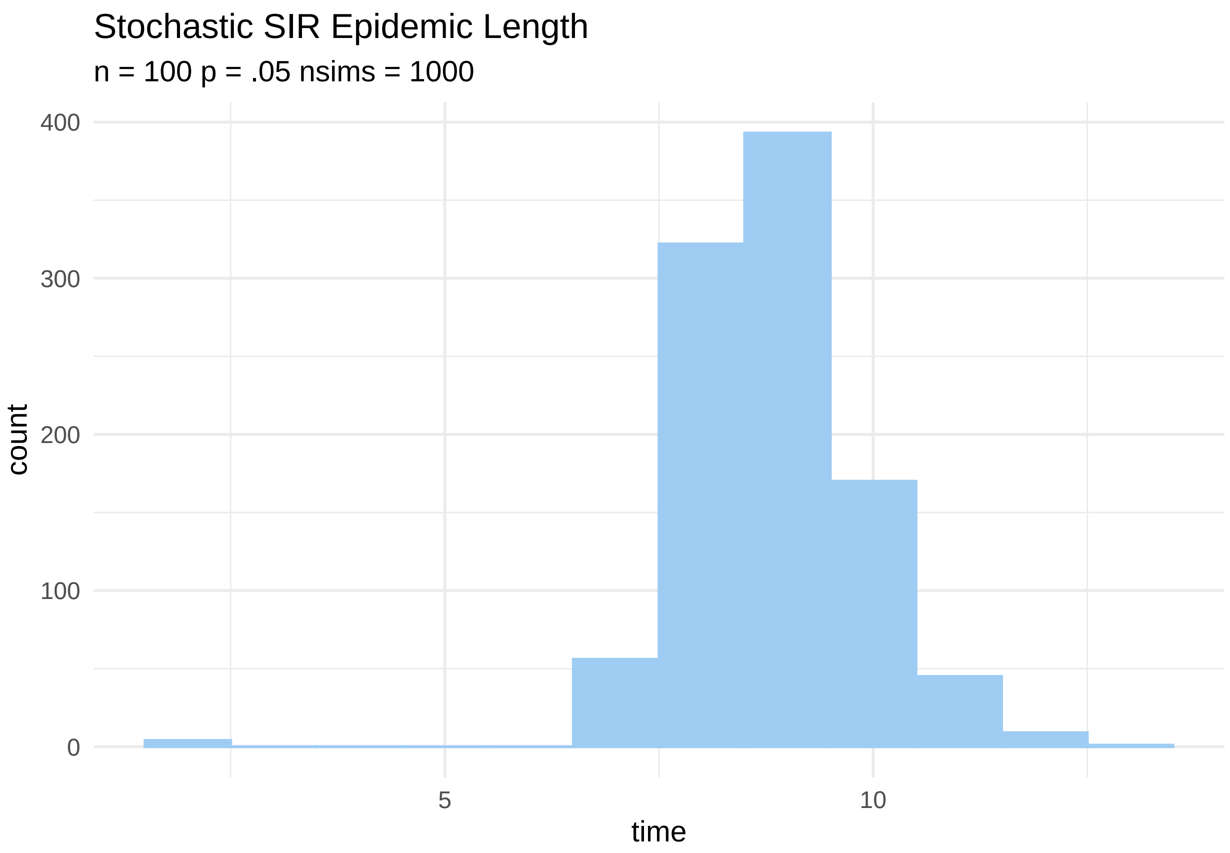
```
plot(model1, main = paste("Stochastic SIR, n=100, p=.05, inf period=1 day, nsims = 1000"))
```



Plot epidemic length:

```
# df of epidemic end date for each simulation based on si.flow = 0
df_end <- as.data.frame(model1) %>%
  filter(si.flow == 0) %>%
  group_by(sim) %>%
  summarise(time = min(time[time != min(time)]))
# Second occurrence of si.flow = 0. The first is in the initial state.

ggplot(df_end, aes(x = time)) +
  geom_histogram(binwidth=1, color = "#9eccf2", fill= "#9eccf2")+
  labs(title = "Stochastic SIR Epidemic Length",
       subtitle = "n = 100 p = .05 nsims = 1000")+
  theme_minimal()
```



Stochastic SIR Model n = 21, p =.02, infectious period = 3 days (model2)

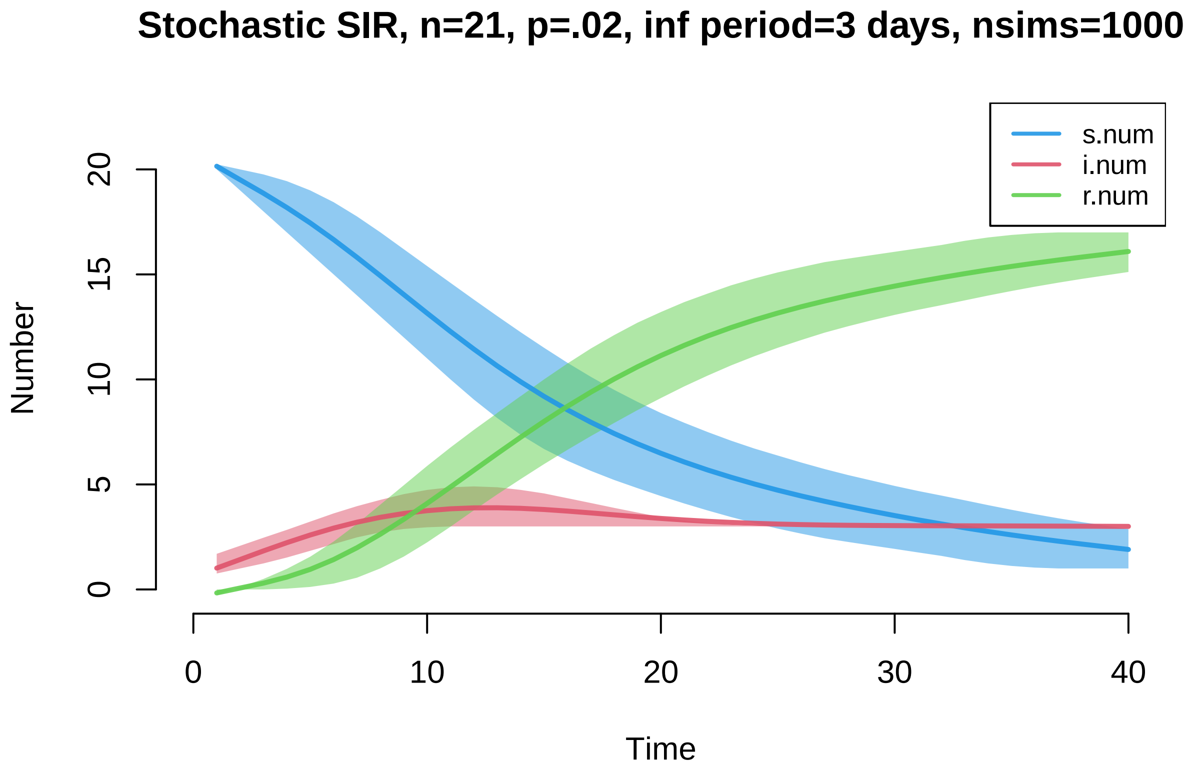
Below is the same stochastic model with parameters from the project prompt.

Model:

```
param2 <- param.icm(inf.prob = .02, act.rate = 20, rec.rate = c(0,0,0,1))
init2 <- init.icm(s.num = 20, i.num = 1, r.num = 0)
control2 <- control.icm(type = "SIR", nsteps = 40, nsims = 1000)
model2 <- icm(param2, init2, control2)
```

Time-series plot S, I, and R

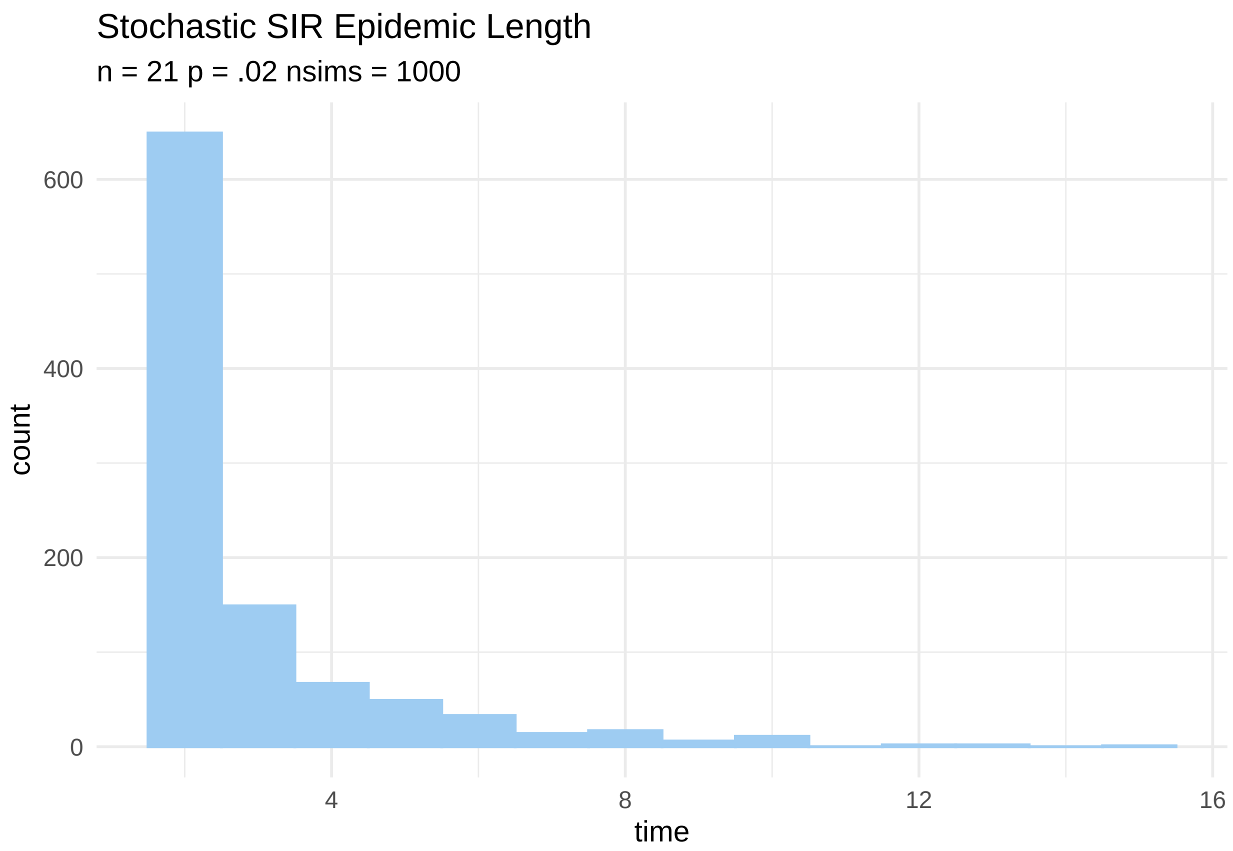
```
plot(model2, main = "Stochastic SIR, n=21, p=.02, inf period=3 days, nsims=1000")
```



Plotting Pandemic Length:

```
# df of epidemic end date for each simulation based on si.flow = 0
df_end <- as.data.frame(model2) %>%
  filter(si.flow == 0) %>%
  group_by(sim) %>%
  summarise(time = min(time[time != min(time)]))
# Second occurrence of si.flow = 0. The first is in the initial state.

ggplot(df_end, aes(x = time)) +
  geom_histogram(binwidth=1, color = "#9eccf2", fill= "#9eccf2")+
  labs(title = "Stochastic SIR Epidemic Length",
       subtitle = "n = 21 p = .02 nsims = 1000")+
  theme_minimal()
```



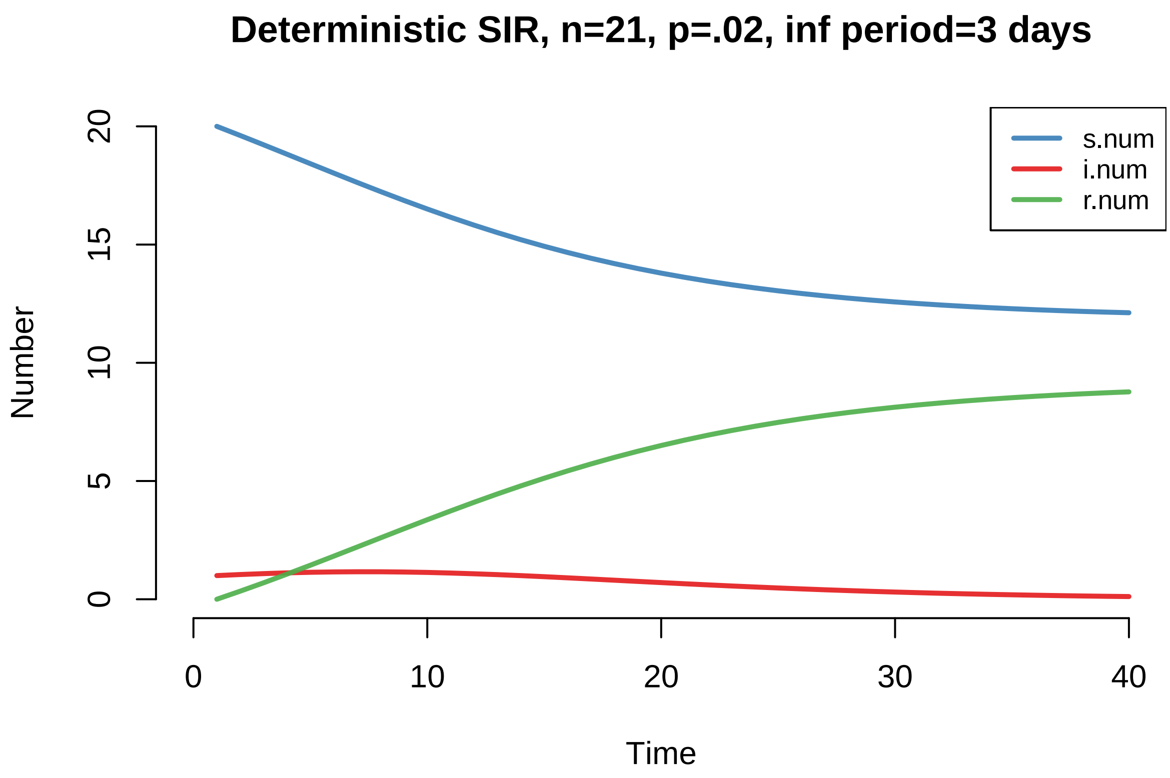
Deterministic SIR Model n = 21, p =.02, infectious period = 3 days (model3)

Below is the same model parameters from the project prompt in a deterministic model that uses dsolve()

```
param3 <- param.dcm(inf.prob = .02, act.rate = 20, rec.rate = 1/3)
#rec.rate must be reciprocal of duration for deterministic models
init3 <- init.dcm(s.num = 20, i.num = 1, r.num = 0)
control3 <- control.dcm(type = "SIR", nsteps = 40, dt = 1)
model3 <- dcm(param3, init3, control3)
```

Time-series plot S, I, and R

```
plot(model3, main = "Deterministic SIR, n=21, p=.02, inf period=3 days")
```


Deterministic SIR, n=21, p=.02, inf period=3 days
s.num
i.num
r.num
Number
0
5
10
15
20
0
10
20
30
40
Time