

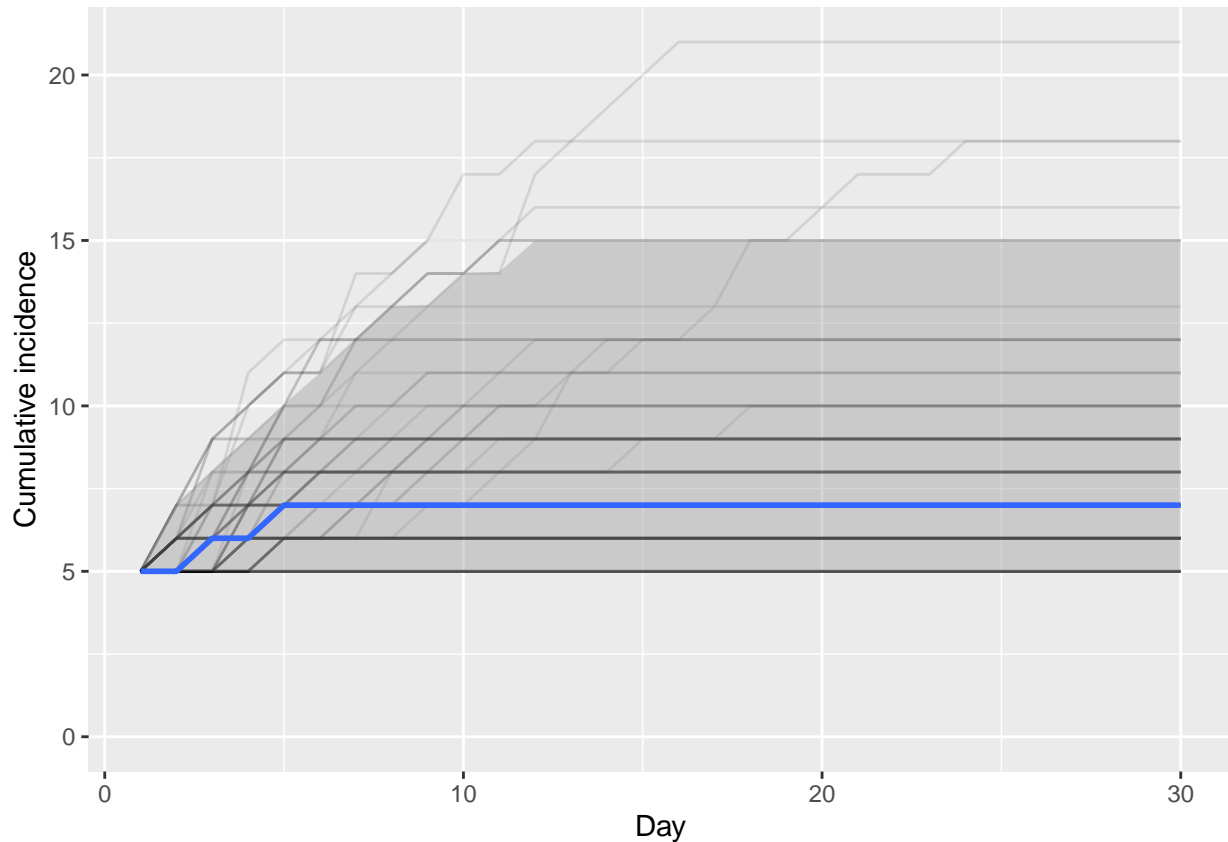
# idsim Package Demonstration

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```
cum_inc_final <- simulate_trajs(  
  n_simu = 100, n_days = 30,  
  ntot = 1000,  
  n0 = 5, n_days_inf = 5,  
  prob_infect = .1  
)  
cum_inc_final %>% head(3)  
  
## $simu_1  
## 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26  
## 5 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7  
## 27 28 29 30  
## 7 7 7 7  
##  
## $simu_2  
## 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26  
## 5 6 6 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7  
## 27 28 29 30  
## 7 7 7 7  
##  
## $simu_3  
## 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26  
## 5 5 5 6 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8  
## 27 28 29 30  
## 8 8 8 8  
  
result <- cum_inc_final %>%  
  bind_rows(.id = "simu") %>%  
  pivot_longer(cols = -simu, names_to = "day", values_to = "cum_incidence")  
  
result_sum <- result %>%  
  group_by(day) %>%  
  summarize(  
    median1 = median(cum_incidence),  
    upper = quantile(cum_incidence, .95),  
    lower = quantile(cum_incidence, .05)  
  )  
  
ggplot(  
  data = result,  
  aes(x = as.integer(day), y = cum_incidence, group = simu)  
) +  
  geom_line(alpha=.1) +
```

```
geom_smooth(
  data = result_sum,
  stat = "identity",
  aes(x = as.integer(day), y = median1, ymax = upper, ymin = lower, group = 1)) +
ylim(0, NA) +
labs(y = "Cumulative incidence", x = "Day")
```



We see here a sample of 100 different cumulative incidence trajectories, or “epidemic curves”, under the stochastic disease model described by the function `simu_cum_incidence`. The median and .05 and .95 lower quantiles of these 100 curves are also shown. We can see under the parameters chosen the epidemic dies out very quickly and very rarely leads to more than 15 infections and often leads to no further infections beyond the initial ones.

To see what might happen under different circumstances we can repeat the simulation with a great probability of infection and longer period of infectiousness.

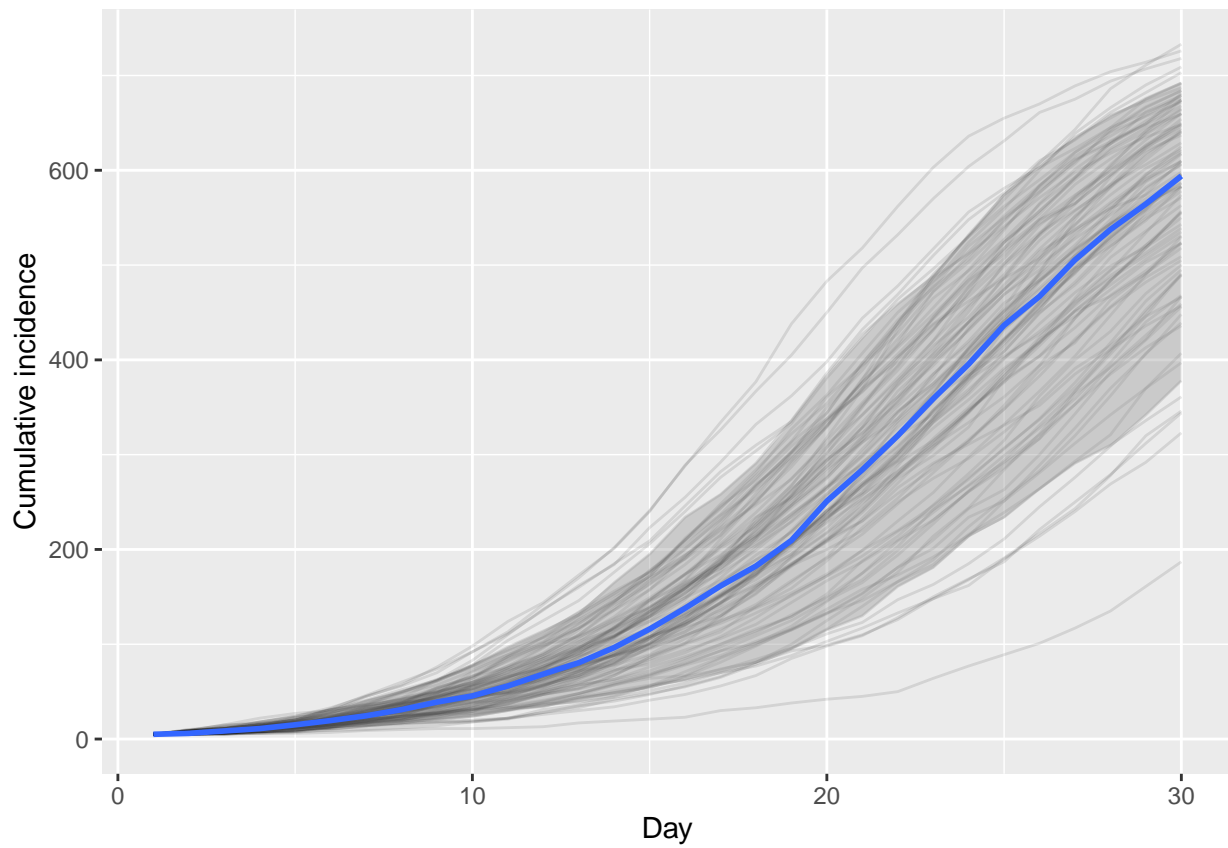
```
result2 <- simulate_trajs(
  n_simu = 100,
  n_days = 30,
  ntot = 1000,
  n0 = 5,
  n_days_inf = 7,
  prob_infect = .3
) %>%
  bind_rows(.id = "simu") %>%
  pivot_longer(cols = -simu,
    names_to = "day",
    values_to = "cum_incidence")
```

```

result_sum2 <- result2 %>%
  group_by(day) %>%
  summarize(
    median1 = median(cum_incidence),
    upper = quantile(cum_incidence, .95),
    lower = quantile(cum_incidence, .05)
  )

ggplot(data = result2,
       aes(x = as.integer(day), y = cum_incidence, group = simu)) +
  geom_line(alpha = .1) +
  geom_smooth(
    data = result_sum2,
    stat = "identity",
    aes(
      x = as.integer(day),
      y = median1,
      ymax = upper,
      ymin = lower,
      group = 1
    )
  ) +
  ylim(0, NA) +
  labs(y = "Cumulative incidence", x = "Day")

```



```
library(Rd2md)
Rd2markdown(rdf = "man/simulate_trajs.Rd",
            outfile = "simulate_trajs.md")
```

## Help file

### **simulate\_trajs**

Simulate infectious disease trajectories

### **Description**

Simulate infectious disease trajectories

### **Usage**

```
simulate_trajs(n_simu, ntot, n_days, n0, n_days_inf, prob_infect)
```

### **Arguments**

Argument	Description
<code>n_simu</code>	integer, number of simulated trajectories
<code>ntot</code>	integer, total number of individuals
<code>n_days</code>	integer, number of days in trajectory
<code>n0</code>	integer, number infected on day 1
<code>n_days_inf</code>	integer, for someone infected on day $t$ , we assume that they are infectious on day $(t, t+n\_days\_inf)$
<code>prob_infect</code>	numeric in $(0,1)$ , probability that a susceptible individual gets infected is $n\_infectious/ntot*prob\_infect$

### **Value**

list of simulated trajectories