

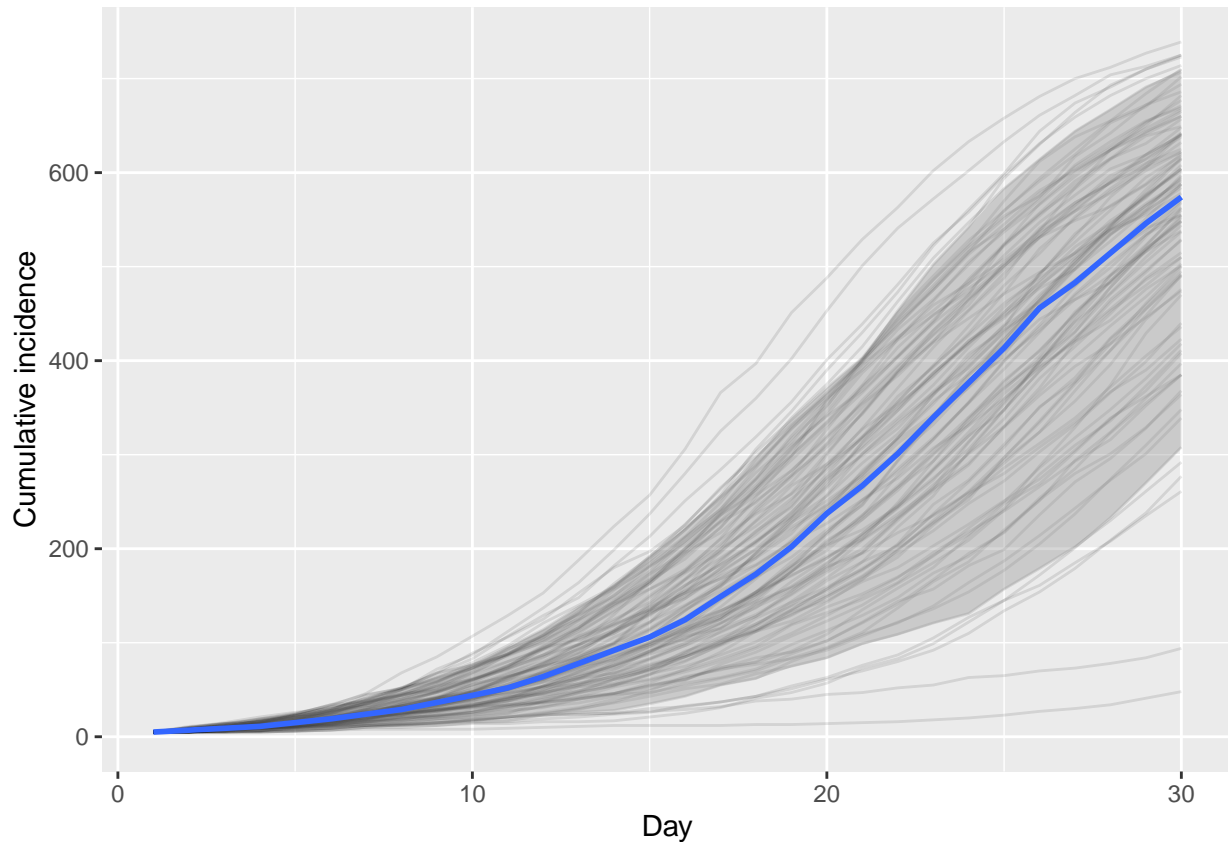
idsim Package Demonstration

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```
cum_inc_final <- simulate_trajs(  
  n_simu = 100, n_days = 30,  
  ntot = 1000,  
  n0 = 5, n_days_inf = 7,  
  prob_infect = .3  
)  
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  
##   5  7 10 13 15 20 29 35 42 45 51 61 77 86 98 115 131 154 182 205  
##  21 22 23 24 25 26 27 28 29 30  
## 236 265 293 332 369 405 452 483 522 562  
##  
## $simu_2  
##   1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20  
##   5  6 10 15 21 29 41 50 64 79 97 121 140 160 192 222 253 290 328 360  
##  21 22 23 24 25 26 27 28 29 30  
## 390 424 459 482 508 537 559 578 602 622  
##  
## $simu_3  
##   1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20  
##   5  6  9 13 15 19 24 28 39 48 63 77 97 121 150 176 211 255 298 358  
##  21 22 23 24 25 26 27 28 29 30  
## 400 453 502 542 594 630 664 693 710 723  
  
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 that at least under the parameters chosen for this simulation the distribution of cumulative incidence becomes fairly skewed by 30 days.

```
library(Rd2md)
Rd2markdown(rdfile = "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