Comparing the results of R funcitons to Csnippets

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This document is focused on comparing the simulation results from a simple SI model setup in R functions to the same model implemented in Csnippets. It can be helpful to modify this file to sort out a new model when you are switching to csnippets, and then copy and paste the step, rinit, rmeasure, and dmeasure fucntions back into your main file once you get it working.

Load in data - from github, your computer, etc.

```r
library(readr) #this library is used to help load the csv file.
simuldata <-read_csv("https://raw.githubusercontent.com/kmontovan/pomp/refs/heads/main/SimulatedPompitia
```

```
## Rows: 150 Columns: 2
## -- Column specification ----------------------------------------------------------
## Delimiter: ","
## dbl (2): day, NewCases
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

R functions

```r
#Setup Model Step function
R_step <- function(S, I, NewI, Beta, gamma, delta.t, ...){
  infections <- rbinom(n=1,size=S, prob=1-exp(-Beta*I*delta.t))
  recover <- rbinom(n=1,size=I, prob=1-exp(-gamma*delta.t))
  S <- S - infections + recover
  I <- I+ infections - recover
  NewI <- NewI + infections
  c(S=S, I=I, NewI=NewI)}

R_rinit <- function(N, phi, ...){
  c(S = round((1-phi)*N),
    I= round(phi*N), NewI=0)}

R_rmeas <- function(NewI, rho,k,...){
  c(NewCases=rnbinom(n=1,size=k,
                     mu=rho*NewI))}

R_dmeas <- function(log,NewCases, NewI, rho, k, ...){
```

```
  dnbinom(x=NewCases, size=k, mu=rho*NewI, log=log)
}
```

Csnippets

```r
C_step <- Csnippet("
  double infections = rbinom(S,1-exp(-Beta*I*dt));
  double recoveries = rbinom(I,1-exp(-gamma*dt));
  S += -infections + recoveries;
  I += infections - recoveries;
  NewI += infections;
")

C_rinit <- Csnippet("
  S = nearbyint((1-phi)*N);
  I = nearbyint(phi*N);
  NewI = 0;
")

C_rinit <- Csnippet("
  S = N-4;
  I = 4;
  NewI = 0;
")

C_rmeas <- Csnippet("
  NewCases = rnbinom_mu(k,rho*NewI);
  ")

C_dmeas <- Csnippet("
    lik = dnbinom_mu(NewCases,k,rho*NewI, give_log);
  ")
```

Setup Pomp structure with the R function compoenents

```r
SI_ModelR <- pomp(
  data = simuldata,
    times="day",
    t0=0,
    statenames=c("S","I","NewI"),
    accumvars="NewI",
    paramnames=c("Beta","gamma","rho","k","N","phi"),
    params= c(N=1000, #population size
              phi = 0.004, #fraction of population infected at time 0
              Beta=.0024, # rate of spread of illness - per day
              gamma=.1, #recovery rate
              rho=.8, #fraction of new infections that are recorded
              k=5 ), #changes the variability of reporting accuracy
    rinit=R_rinit,
    rprocess=euler(R_step,delta.t= 1/4),
```

```
    rmeasure=R_rmeas,
    dmeasure=R_dmeas
)
```

Setup Pomp structure with the R function compoenents

```
SI_ModelC <- pomp(
  data = simuldata,
    times="day",
    t0=0,
    statenames=c("S","I","NewI"),
    accumvars="NewI",
    paramnames=c("Beta","gamma","rho","k","N","phi"),
    params= c(N=1000, #population size
              phi = 0.004, #fraction of population infected at time 0
              Beta=.0024, # rate of spread of illness - per day
              gamma=.1, #recovery rate
              rho=.8, #fraction of new infections that are recorded
              k=5 ), #changes the variability of reporting accuracy
    rinit=C_rinit,
    rprocess=euler(C_step,delta.t= 1/4),
    rmeasure=R_rmeas,
    dmeasure=C_dmeas
)
```

Compare

Simulate the results and plot them on the same graph for the R functions and Csnippet versions of the model
to make sure they are doing roughly the same thing. If there is an error somewhere, they might be doing
drastically different things, so this is just a quick check.

```
simsR <- SI_ModelR |>
  simulate(
    nsim=25,
    format="data.frame",
    include.data=FALSE
)

simsC <- SI_ModelC |>
  simulate(
    nsim=25,
    format="data.frame",
    include.data=FALSE
)


ggplot()+
  geom_line(data=simsR, aes(x=day,y=NewCases,group=.id),color="blue",alpha=.5)+
  geom_line(data=simsC, aes(x=day,y=NewCases,group=.id),color="gray",alpha=.5)+
```

```
guides(color="none")+
theme_bw()
```