

discrete/binomial pomp analysis

2025-05-22

$$f_{proc} = \text{discrete}, f_{meas} = \text{binomial}$$

We will first present the one-unit (London case) discrete + binomial scenario, and then show how to match it to the WWR model.

Preparation for the pomp

```
## ----packages,incluxde=F,echo=F,cache=F-----
library("pomp")
library("spatPomp")
library("ggplot2")
library("tidyverse")
library("knitr")
library("doRNG")
library("doParallel")

set.seed(12345)

measles_cases <- read.csv("case1.csv")
measles_covar <- read.csv("covar2.csv")

measles_cases<- measles_cases[measles_cases$city == "LONDON", ]
measles_covar <- measles_covar[measles_covar$city == "LONDON", ]

measles_cases <- measles_cases[,-1]
measles_covar <- measles_covar[,-1]

colnames(measles_cases) <- c("time", "cases1")
colnames(measles_covar) <- c("time",
                             "lag_birthrte1", "pop1")

basic_params <- c(
  alpha      = 1,
  iota       = 0,
  betabar    = 10,
  c          = 0.1,
  a          = 0.3,
  rho        = 0.1,
  gamma      = 0.1,
  delta      = 0.02/(26*4), # Here is a time scale transform.
```

```

sigma_xi = 2,
qmean    = 0.7,
qvar     = 0.2,
g        = 0,
S_0      = 0.015,
E_0      = 0.0002,
I_0      = 0.0002
)

```

f_{proc} = discrete

```

rproc <- Csnippet("
double t_mod = fmod(t, 364.0);
double br1;
double beta1, seas1;
double foi1;
double xi1;
double betafinal1;
static double betafinal1_prev = 0.0;

int trans_S1[2], trans_E1[2], trans_I1[2];
double prob_S1[2], prob_E1[2], prob_I1[2];

if ((t_mod >= 6 && t_mod < 99) ||
    (t_mod >= 115 && t_mod < 198) ||
    (t_mod >= 252 && t_mod < 299) ||
    (t_mod >= 308 && t_mod < 355)) {
    seas1 = 1.0 + a * 2 * (1 - 0.759);
} else {
    seas1 = 1.0 - 2 * a * 0.759;
}

beta1 = betabar * seas1;

if (fabs(t_mod - 248.5) < 0.5) {
    br1 = c * lag_birthrate1;
} else {
    br1 = (1.0 - c) * lag_birthrate1 / 103.0;
}

double I_ratio1 = I1 / pop1;

foi1 = pow((I1 + iota) / pop1, alpha);

stepCount += 1.0;

if (fabs(fmod(stepCount, 4.0)) < 1e-8) {
    xi_current = rgamma(sigma_xi, 1 / sigma_xi);
    betafinal1 = beta1 * I_ratio1 * xi_current;
} else {
    betafinal1 = betafinal1_prev;
}

```

```

    betafinal1_prev = betafinal1;

    int SD1 = rbinom(S1, delta);
    int ED1 = rbinom(E1, delta);
    int ID1 = rbinom(I1, delta);
    int RD1 = rbinom(R1, delta);

    S1 -= SD1;
    E1 -= ED1;
    I1 -= ID1;
    R1 -= RD1;

    prob_S1[0] = exp(-dt * betafinal1);
    prob_S1[1] = 1 - exp(-dt * betafinal1);

    prob_E1[0] = exp(-dt * rho);
    prob_E1[1] = 1 - exp(-dt * rho);

    prob_I1[0] = exp(-dt * gamma);
    prob_I1[1] = 1 - exp(-dt * gamma);

    rmultinom(S1, prob_S1, 2, trans_S1);
    rmultinom(E1, prob_E1, 2, trans_E1);
    rmultinom(I1, prob_I1, 2, trans_I1);

    S1 = trans_S1[0] + rpois(br1);
    E1 = trans_E1[0] + trans_S1[1];
    I1 = trans_I1[0] + trans_E1[1];
    R1 += trans_I1[1];
    C1 += trans_I1[1];

    q1 = -1;
    while (q1 < 0 || q1 > 1) {
        q1 = rnorm(qmean, qvar);
    }
");

```

$f_{meas} = \text{binomial}$

```

# --- 5.1 dmeasure ---
dmeas <- Csnippet("
    lik = dbinom(cases1, C1, q1, 1);
");

# --- 5.2 rmeasure ---
rmeas <- Csnippet("
    cases1 = rbinom(C1,q1);
");

```

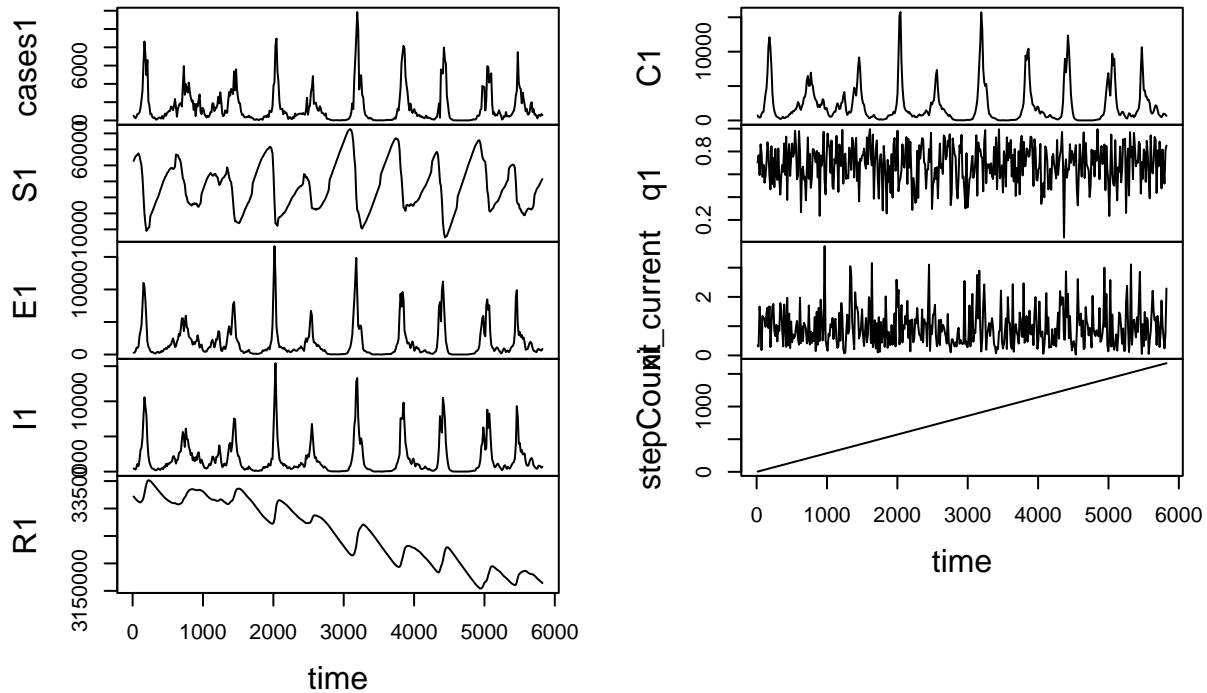
Build the rinit

```
rinit <- Csnippet("  
  double probs1[4];  
  probs1[0] = S_0;  
  probs1[1] = E_0;  
  probs1[2] = I_0;  
  probs1[3] = 1.0 - probs1[0] - probs1[1] - probs1[2];  
  
  int counts1[4];  
  rmultinom(pop1, probs1, 4, counts1);  
  
  S1 = counts1[0];  
  E1 = counts1[1];  
  I1 = counts1[2];  
  R1 = counts1[3];  
  C1 = 0;  
  xi_current = 1;  
  stepCount = 0;  
")
```

Construct the POMP

```
basic_log_names <- c("rho", "gamma", "sigma_xi", "betabar", "g", "iota", "delta")  
basic_logit_names <- c("a", "alpha", "c", "qmean", "S_0", "E_0", "I_0", "qvar")  
log_names <- basic_log_names  
logit_names <- basic_logit_names  
measles_partrans <- parameter_trans(  
  log = log_names,  
  logit = logit_names  
)  
  
one_city_pomp <- pomp(  
  data = measles_cases,  
  times = "time",  
  t0 = 0,  
  rprocess = discrete_time(rproc, delta.t = 3.5),  
  rinit = rinit,  
  dmeasure = dmeas,  
  rmeasure = rmeas,  
  statenames = c("S1", "E1", "I1", "R1", "C1", "q1", "xi_current", "stepCount"),  
  paramnames = c("alpha", "iota", "betabar", "c", "a", "rho", "gamma",  
    "delta", "sigma_xi", "g", "qmean", "qvar",  
    "S_0", "E_0", "I_0"),  
  covar = covariate_table(measles_covar, times = "time"),  
  covarnames = c("lag_birthrate1", "pop1"),  
  accumvars = c("C1")  
)  
  
coef(one_city_pomp) <- basic_params  
  
sim <- simulate(one_city_pomp, params = basic_params)
```

```
plot(sim)
```



Make the simulation

```
# Number of simulations
n_simulations <- 1000

# Placeholder to store the results
results <- data.frame(
  mean = numeric(n_simulations),
  median = numeric(n_simulations),
  variance = numeric(n_simulations)
)

# Loop through the simulations
for (i in 1:n_simulations) {

  # Simulate the system
  sim <- simulate(one_city_pomp, params = basic_params)
  sim_data <- as.data.frame(sim)
  simlondon <- sim_data$cases1

  # Calculate the mean, median, and variance of the simulation data
  results$mean[i] <- mean(simlondon, na.rm = TRUE)
  results$median[i] <- median(simlondon, na.rm = TRUE)
  results$variance[i] <- var(simlondon, na.rm = TRUE)
}
```

Python code for simulation

```
import os
os.environ["PYTHONHASHSEED"] = "12345"

import random
import numpy as np
import pandas as pd
import tensorflow as tf
import tensorflow_probability as tfp
import matplotlib.pyplot as plt
from scipy.optimize import minimize

import sys
sys.path.append('Scripts/')
from measles_simulator_KH import *

SEED = 12345
random.seed(SEED)
np.random.seed(SEED)
tf.random.set_seed(SEED)

UKbirths_array = np.load("Data/UKbirths_array.npy")
UKpop_array = np.load("Data/UKpop_array.npy")
measles_distance_matrix_array = np.load("Data/measles_distance_matrix_array.npy")
UKmeasles_array = np.load("Data/UKmeasles_array.npy")
modelA_array = np.load("Data/Parameter/final_parameters_lookahead_A.npy")

UKbirths = tf.convert_to_tensor(UKbirths_array, dtype = tf.float32)
UKpop = tf.convert_to_tensor(UKpop_array, dtype = tf.float32)
measles_distance_matrix = tf.convert_to_tensor(measles_distance_matrix_array,
dtype = tf.float32)
UKmeasles = tf.convert_to_tensor(UKmeasles_array, dtype = tf.float32)

df = pd.read_csv("Data/londonbirth.csv")
data_array = df.values
UKbirths = tf.convert_to_tensor(data_array, dtype=tf.float32)

df1 = pd.read_csv("Data/londonpop.csv")
data_array1 = df1.values
UKpop = tf.convert_to_tensor(data_array1, dtype=tf.float32)

term = tf.convert_to_tensor([6, 99, 115, 198, 252, 299, 308, 355, 366],
dtype = tf.float32)
school = tf.convert_to_tensor([0, 1, 0, 1, 0, 1, 0, 1, 0], dtype =
tf.float32)

n_cities = tf.constant(40, dtype = tf.int64)

initial_pop = UKpop[:,0]

T = UKmeasles.shape[1]
intermediate_steps = 4
h = tf.constant(14/tf.cast(intermediate_steps, dtype = tf.float32), dtype =
```

```

tf.float32)
is_school_term_array, is_start_school_year_array, times_total, times_obs =
school_term_and_school_year(T, intermediate_steps, term, school)

is_school_term_array = tf.convert_to_tensor(is_school_term_array, dtype =
tf.float32)
is_start_school_year_array = tf.convert_to_tensor(is_start_school_year_array,
dtype = tf.float32)

pi_0_1 = 0.02545
pi_0_2 = 0.00422
pi_0_3 = 0.000061
pi_0 = tf.convert_to_tensor([[pi_0_1, pi_0_2, pi_0_3, 1 - pi_0_1 - pi_0_2 -
pi_0_3]], dtype = tf.float32)*tf.ones((n_cities, 4), dtype = tf.float32)

initial_pop = UKpop[:,0]

beta_bar = tf.convert_to_tensor( [[6.32]], dtype =
tf.float32)*tf.ones((n_cities, 1), dtype = tf.float32)
rho = tf.convert_to_tensor([[0.142]], dtype =
tf.float32)*tf.ones((n_cities, 1), dtype = tf.float32)
gamma = tf.convert_to_tensor([[0.0473]], dtype =
tf.float32)*tf.ones((n_cities, 1), dtype = tf.float32)

g = tf.convert_to_tensor([[0]], dtype = tf.float32)*tf.ones((n_cities, 1),
dtype = tf.float32)
p = tf.constant(0.759, dtype = tf.float32)
a = tf.constant(0.1476, dtype = tf.float32)
c = tf.constant(0.219, dtype = tf.float32)

Xi = tfp.distributions.Gamma(concentration = 0.318, rate = 0.318)
Q = tfp.distributions.TruncatedNormal( 0.7, 0.306, 0, 1)

delta_year = tf.convert_to_tensor([[1/50]], dtype =
tf.float32)*tf.ones((n_cities, 4), dtype = tf.float32)

T_small = tf.constant(415, dtype = tf.float32)

# Initialize result lists
means = np.zeros((40, 25))
variances = np.zeros((40, 25))
medians = np.zeros((40, 25))

# Perform 1000 simulations
for i in range(25):
    X_t, Y_t, Xi_t, Q_t = run(T_small, intermediate_steps, UKbirths, UKpop,
    g, measles_distance_matrix,
                                initial_pop, pi_0, beta_bar, p, a, is_school_term_array,
                                is_start_school_year_array, h, rho, gamma, Xi, Q, c, n_cities, delta_year)

    max_time = 415

```

```

# Calculate the log values for each city Y_t_log
for city in range(40):
    Y_t_log = Y_t[1:(max_time + 1), city, 0]
    # Calculate mean, variance, median
    means[city, i] = np.mean(Y_t_log)
    variances[city, i] = np.var(Y_t_log)
    medians[city, i] = np.median(Y_t_log)

# Initialize an empty list to store the results for each city
all_results = []

for city_index in range(40):
    # Create a DataFrame for the current city
    results_df_city = pd.DataFrame({
        'Simulation': np.arange(25),
        'Mean': means[city_index, :],
        'Variance': variances[city_index, :],
        'Median': medians[city_index, :]
    })

    # Add city column
    results_df_city['City'] = city_index

    # Add the current city's results to the total list
    all_results.append(results_df_city)

# Combine results from all cities
combined_results_df = pd.concat(all_results, ignore_index=True)

# Save to a new CSV file
combined_results_df.to_csv("/Users/mac/Desktop/PAL_measles/combined_simulation_results_for_1000_times.csv")

combined_simulation_results_for_1000_times <-
  read.csv("combined_simulation_results_for_1000_times.csv")

t.test(results$mean, combined_simulation_results_for_1000_times$Mean)

##
## Welch Two Sample t-test
##
## data: results$mean and combined_simulation_results_for_1000_times$Mean
## t = 0.24729, df = 1984.4, p-value = 0.8047
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -8.482432 10.930195
## sample estimates:
## mean of x mean of y
## 1416.620 1415.396

t.test(results$median, combined_simulation_results_for_1000_times$Median)

##
## Welch Two Sample t-test
##

```



```

## data: results$median and combined_simulation_results_for_1000_times$Median
## t = 0.22122, df = 1996.4, p-value = 0.8249
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -13.56325 17.01225
## sample estimates:
## mean of x mean of y
## 783.0875 781.3630

t.test(results$variance,combined_simulation_results_for_1000_times$Variance)

##
## Welch Two Sample t-test
##
## data: results$variance and combined_simulation_results_for_1000_times$Variance
## t = -0.29231, df = 1997.7, p-value = 0.7701
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -81435.56 60308.73
## sample estimates:
## mean of x mean of y
## 2999552 3010115

data <- data.frame(
  value = c(results$median, combined_simulation_results_for_1000_times$Median),
  group = rep(c("POMP", "WWR"),
              c(length(results$median), length(combined_simulation_results_for_1000_times$Median)))
)

p_median <- ggplot(
  data.frame(
    value = c(results$median, combined_simulation_results_for_1000_times$Median),
    group = rep(c("POMP", "WWR"),
                c(length(results$median),
                  length(combined_simulation_results_for_1000_times$Median)))
  ),
  aes(x = value, fill = group)
) +
  geom_density(alpha = 0.5) +
  labs(title = "Median Density", x = "Value", y = "Density") +
  theme_minimal() +
  scale_fill_manual(values = c("blue", "red"))

p_mean <- ggplot(
  data.frame(
    value = c(results$mean, combined_simulation_results_for_1000_times$Mean),
    group = rep(c("POMP", "WWR"),
                c(length(results$mean),
                  length(combined_simulation_results_for_1000_times$Mean)))
  ),
  aes(x = value, fill = group)
) +
  geom_density(alpha = 0.5) +
  labs(title = "Mean Density", x = "Value", y = "Density") +
  theme_minimal() +

```

```

scale_fill_manual(values = c("blue", "red"))

p_variance <- ggplot(
  data.frame(
    value = c(results$variance, combined_simulation_results_for_1000_times$Variance),
    group = rep(c("POMP", "WWR"),
                c(length(results$variance),
                  length(combined_simulation_results_for_1000_times$Variance)))
  ),
  aes(x = value, fill = group)
) +
  geom_density(alpha = 0.5) +
  labs(title = "Variance Density", x = "Value", y = "Density") +
  theme_minimal() +
  scale_fill_manual(values = c("blue", "red"))

```

```
library(cowplot)
```

```

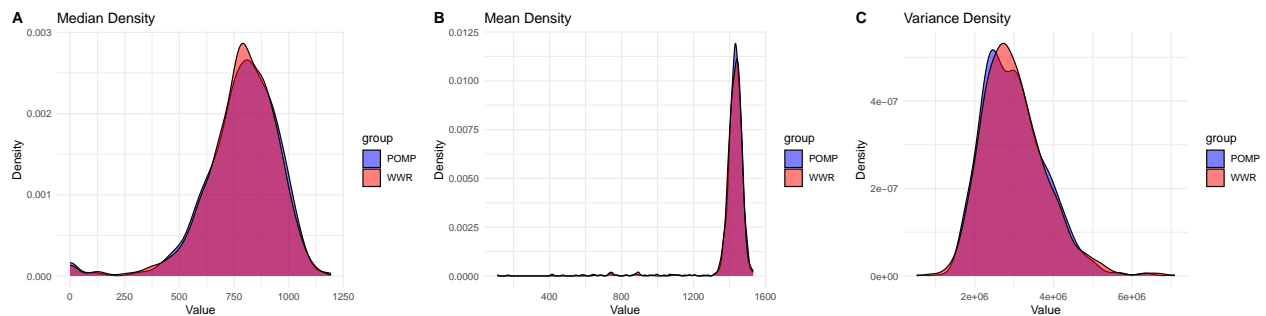
##
## Attaching package: 'cowplot'
## The following object is masked from 'package:lubridate':
##
## stamp

```

```

plot_grid(
  p_median, p_mean, p_variance,
  labels = c("A", "B", "C"),
  ncol = 3,
  align = "h"
)

```



$f_{proc} = \text{discrete}, f_{meas} = \text{gaussian}$

```

basic_params <- c(
  alpha = 1,
  iota = 0,
  betabar = 7.32,
  c = 0.219,
  a = 0.1476,
  rho = 0.142,
  gamma = 0.0473,

```

```

delta      = 0.02/(26*4), # timescale transform
sigma_xi   = 0.318,
gaussianrho = 0.7,
psi        = 0.306,
g          = 0,
S_0        = 0.02545,
E_0        = 0.00422,
I_0        = 0.000061
)

```

```

rproc <- Csnippet("
double t_mod = fmod(t, 364.0);
double br1;
double beta1, seas1;
double foi1;
double x1;
double betafinal1;
static double betafinal1_prev = 0.0;

int trans_S1[2], trans_E1[2], trans_I1[2];
double prob_S1[2], prob_E1[2], prob_I1[2];

if ((t_mod >= 6 && t_mod < 99) ||
    (t_mod >= 115 && t_mod < 198) ||
    (t_mod >= 252 && t_mod < 299) ||
    (t_mod >= 308 && t_mod < 355)) {
    seas1 = 1.0 + a * 2 * (1 - 0.759);
} else {
    seas1 = 1.0 - 2 * a * 0.759;
}

beta1 = betabar * seas1;

if (fabs(t_mod - 248.5) < 0.5) {
    br1 = c * lag_birthrate1;
} else {
    br1 = (1.0 - c) * lag_birthrate1 / 103.0;
}

double I_ratio1 = I1 / pop1;

foi1 = pow((I1 + iota) / pop1, alpha);

stepCount += 1.0;

if (fabs(fmod(stepCount, 4.0)) < 1e-8) {
    xi_current = rgamma(sigma_xi, 1 / sigma_xi);
    betafinal1 = beta1 * I_ratio1 * xi_current;
} else {
    betafinal1 = betafinal1_prev;
}

betafinal1_prev = betafinal1;

```

```

int SD1 = rbinom(S1, delta);
int ED1 = rbinom(E1, delta);
int ID1 = rbinom(I1, delta);
int RD1 = rbinom(R1, delta);

S1 -= SD1;
E1 -= ED1;
I1 -= ID1;
R1 -= RD1;

prob_S1[0] = exp(-dt * betafinal1);
prob_S1[1] = 1 - exp(-dt * betafinal1);

prob_E1[0] = exp(-dt * rho);
prob_E1[1] = 1 - exp(-dt * rho);

prob_I1[0] = exp(-dt * gamma);
prob_I1[1] = 1 - exp(-dt * gamma);

rmultinom(S1, prob_S1, 2, trans_S1);
rmultinom(E1, prob_E1, 2, trans_E1);
rmultinom(I1, prob_I1, 2, trans_I1);

S1 = trans_S1[0] + rpois(br1);
E1 = trans_E1[0] + trans_S1[1];
I1 = trans_I1[0] + trans_E1[1];
R1 += trans_I1[1];
C1 += trans_I1[1];
");

## ----dmeasure-----
dmeas <- Csnippet("
double m = gaussianrho*C1;
double v = m*(1.0-gaussianrho+psi*psi*m);
double tol = 0.0;
if (cases1 > 0.0) {
    lik = pnorm(cases1+0.5,m,sqrt(v)+tol,1,0)
        - pnorm(cases1-0.5,m,sqrt(v)+tol,1,0) + tol;
} else {
    lik = pnorm(cases1+0.5,m,sqrt(v)+tol,1,0) + tol;
}
if (give_log) lik = log(lik);
");

## ----rmeasure-----
rmeas <- Csnippet("
double m = gaussianrho*C1;
double v = m*(1.0-gaussianrho+psi*psi*m);
double tol = 0.0;
cases1 = rnorm(m,sqrt(v)+tol);

```

```

    if (cases1 > 0.0) {
      cases1 = nearbyint(cases1);
    } else {
      cases1 = 0.0;
    }
  })

rinit <- Csnippet("
  double probs1[4];
  probs1[0] = S_0;
  probs1[1] = E_0;
  probs1[2] = I_0;
  probs1[3] = 1.0 - probs1[0] - probs1[1] - probs1[2];

  int counts1[4];
  rmultinom(pop1, probs1, 4, counts1);

  S1 = counts1[0];
  E1 = counts1[1];
  I1 = counts1[2];
  R1 = counts1[3];
  C1 = 0;
  xi_current = 1;
  stepCount = 0;
");

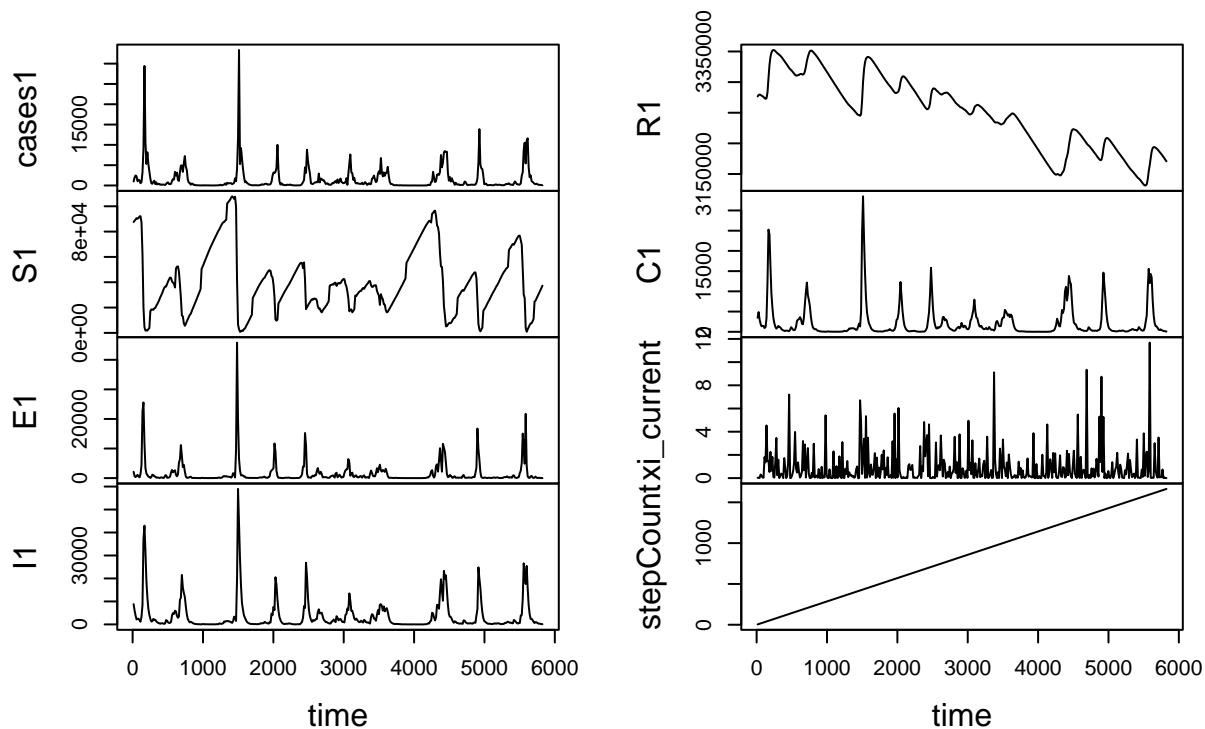
basic_log_names <- c("rho", "gamma", "sigma_xi", "betabar", "g", "iota", "delta")
basic_logit_names <- c("a", "alpha", "c", "gaussianrho", "S_0", "E_0", "I_0", "psi")
log_names <- basic_log_names
logit_names <- basic_logit_names
measles_partrans <- parameter_trans(
  log = log_names,
  logit = logit_names
)

one_city_pomp <- pomp(
  data = measles_cases,
  times = "time",
  t0 = 0,
  rprocess = discrete_time(rproc, delta.t = 3.5),
  rinit = rinit,
  dmeasure = dmeas,
  rmeasure = rmeas,
  statenames = c("S1", "E1", "I1", "R1", "C1", "xi_current", "stepCount"),
  paramnames = c("alpha", "iota", "betabar", "c", "a", "rho", "gamma",
    "delta", "sigma_xi", "g", "gaussianrho", "psi",
    "S_0", "E_0", "I_0"),
  covar = covariate_table(measles_covar, times = "time"),
  covarnames = c("lag_birthrate1", "pop1"),
  accumvars = c("C1")
)

coef(one_city_pomp) <- basic_params

```

```
sim <- simulate(one_city_pomp, params = basic_params, seed = 154234)
plot(sim)
```



Compute the loglik

```
tmp <- pfilter(sim, Np = 10000)
tmp@loglik
```

```
## [1] -Inf
```

```
tmp@cond.logLik
```

```
## [1] -9.494812 -10.787597 -12.623799 -12.869915 -14.154716 -13.166800
## [7] -11.890800 -11.898447 -9.724651 -14.525150 -Inf -Inf
## [13] -Inf -Inf -Inf -Inf -Inf -Inf
## [19] -15.574410 -6.203311 -7.839913 -8.636693 -8.524084 -6.560429
## [25] -7.990728 -6.046247 -6.200163 -5.509151 -6.782622 -5.313677
## [31] -5.461666 -5.526466 -5.001368 -9.374375 -8.340343 -6.653450
## [37] -10.211281 -10.172066 -10.683442 -8.429386 -10.086998 -10.381961
## [43] -8.003158 -9.678449 -8.957706 -9.927371 -9.131922 -7.986091
## [49] -10.933448 -9.764193 -8.283301 -10.676415 -9.373010 -8.283960
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