

Lesson 9:
Modeling stochasticity: Overdispersion in the Consett
measles data.
IN DEVELOPMENT

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Outline

- 1 Introduction
- 2 Adding overdispersion to the basic SIR model
- 3 Searching for the MLE
- 4 Adding a reservoir

Objectives

- We investigate the consequences of modeling overdispersion in the on the Consett measles outbreak dataset.
- More broadly, we consider the question of whether a model has sufficient stochasticity to explain the data.
- We extend the model used to demonstrate iterated filtering in Lesson 4.

Introduction

- This investigation provides a relatively simple example to better understand overdispersed Markov chain models that are essential for large populations such as the [city-level measles case study](#).
- We investigate whether fitting models with dynamic overdispersion (i.e., environmental stochasticity, also known as extra-demographic stochasticity) is helpful even for this relatively small population, for which demographic stochasticity is relatively large.
- We consider the respective roles of overdispersion in the measurement model and the dynamic model.
- We think about scientific interpretations of overdispersion if it is statistically evident.
- We demonstrate a way to implement overdispersion for POMP models using **pomp**.

Mean-variance relationships and overdispersion

- A good statistical model should describe both the mean (center) and variance (spread) of the data.
- In the language of forecasting, we want point predictions and uncertainty estimates.
- Appropriate modeling of uncertainty in the data is closely linked to appropriate assessment of uncertainty in parameter estimates (confidence intervals and hypothesis tests).
- Some basic models (especially for count data) constrain the variance as a function of the mean.
- A famous example arises in Poisson regression. The Poisson distribution has variance equal to its mean. What if the data have higher variance than its mean? This **overdispersion** is common. Checking and correcting for it are standard practice in generalized linear model regression analysis.

Mean-variance relationships and overdispersion II

- Overdispersion is also common in dynamic models. It can be natural to write down models building on Poisson or binomial increments, which therefore include specific mean-variance assumptions.
- These dynamic models may contain nonlinearities that complicate the mean-variance relationship, but the underlying issue remains.

Specification of a basic SIR model

- Our model is a variation on a basic SIR Markov chain
- State: $X(t) = (S(t), I(t), R(t))$; numbers of hosts in susceptible, infectious, and recovered classes.
- Assume: a single infection in week 0, i.e., that $I(0) = 1$.
- Each individual in S transitions to I at rate $\mu_{SI} = \beta I(t)/N$.
- Each individual in I transitions at rate μ_{IR} to R .
- $1/\mu_{IR}$ is the mean infectious period.

Adding overdispersion to the latent stochastic process

- We are going to extend the basic model to include stochastic variation by incorporating multiplicative noise,

$$\mu_{SI} = \beta \frac{I(t)}{N} d\Gamma/dt.$$

- Here, $\Gamma(t)$ is a gamma process with $\mathbb{E}[\Gamma(t)] = t$ and $\text{Var}[\Gamma(t)] = \sigma^2 t$.
- Thus, σ^2 is the **infinitesimal variance parameter** of the noise process, which we will call the **extrademographic process noise parameter**.
- We do not include overdispersion in the $I \rightarrow R$ transition, on the assumption this is a purely demographic process. This assumption could be checked.

Exercise 9.1. Why do we use multiplicative noise?

What difficulties arise if we use additive noise such as

$$\mu'_{SI} = \beta \frac{I(t)}{N} + dW/dt$$

Where dW/dt is some white noise process?

Gamma noise

- The gamma process has the property of being non-negative, which is the main reason it may be preferable to Gaussian noise.
- The gamma process is a pure jump process, constant between jumps. There are an infinite number of jumps in any finite time interval, but almost all of them are negligibly small. Thus, the derivative of the gamma process doesn't exist in the usual sense, but one can still give formal meaning to $d\Gamma/dt$. All this is similar to Gaussian noise, which can also be considered as the formal derivative of a non-differentiable process (Brownian motion).

Adding overdispersion to the measurement model

- Overdispersion in the measurement model may be appropriate for similar reasons. Measurement overdispersion might be considered together with, or in place of, dynamic overdispersion.
- Adding gamma noise to a Poisson measurement model leads to a negative binomial measurement model. The overdispersion parameter is ψ , with the variance for mean μ being $\mu + \mu^2/\psi$ and the Poisson model being recovered in the limit as $\psi \rightarrow \infty$.

Consett revisited

Recall the case report data on the 1948 measles outbreak in Consett, UK.

```
library(tidyverse)

courseurl <- "https://kingaa.github.io/sbied/"
datafile <- "mif/Measles_Consett_1948.csv"

read_csv(paste0(courseurl,datafile)) %>%
  select(week,reports=cases) %>%
  filter(week<=42) -> consett_data
```

Latent variables, observed variables and parameters

- We code the state variables (S , I and the accumulator variable H) as follows, noting that we do not need a representation of $R = N - S - I$.

```
consett_statenames <- c("S","I","H")
```

- Similarly, the parameters (β , η , μ_{IR} , ρ , N , σ , ψ) are:

```
consett_paramnames <- c("Beta","mu_IR","eta","rho",  
  "N","sigma","psi")
```

- The data variable name is taken from `consett_data`.

```
colnames(consett_data)
```

```
[1] "week"      "reports"
```

Latent variables, observed variables and parameters II

We now write the modified Csnippets.

```
consett_dmeas <- Csnippet("  
  lik = dnbinom_mu(reports, psi, rho*H, give_log);  
")  
  
consett_rmeas <- Csnippet("  
  reports = rnbinom_mu(psi, rho*H);  
")
```

Latent variables, observed variables and parameters III

```
consett_step <- Csnippet("  
  double dGamma = rgammawn(sigma,dt);  
  double dN_SI = rbinom(S,1-exp(-Beta*I/N*dGamma));  
  double dN_IR = rbinom(I,1-exp(-mu_IR*dt));  
  S -= dN_SI;  
  I += dN_SI - dN_IR;  
  H += dN_IR;  
  ")
```

```
consett_rinit <- Csnippet("  
  S = nearbyint(eta*N);  
  I = 1;  
  H = 0;  
  ")
```

Latent variables, observed variables and parameters IV

```
consett_data %>%  
  pomp(  
    times="week", t0=0,  
    rprocess=euler(consett_step, delta.t=1/7),  
    rinit=consett_rinit,  
    rmeasure=consett_rmeas,  
    dmeasure=consett_dmeas,  
    accumvars="H",  
    statenames=consett_statenames,  
    paramnames=consett_paramnames  
  ) -> consett
```


Testing the codes

To develop and debug code, it is useful to have testing codes that run quickly and fail if the codes are not working correctly.

As such a test, here we run some simulations and a particle filter.

We'll use the following parameters, derived from our earlier explorations, but adding in some small amount of overdispersion.

```
params <- c(Beta=20,mu_IR=2,rho=0.5,eta=0.1,N=38000,  
            sigma=0.1,psi=0.1)
```

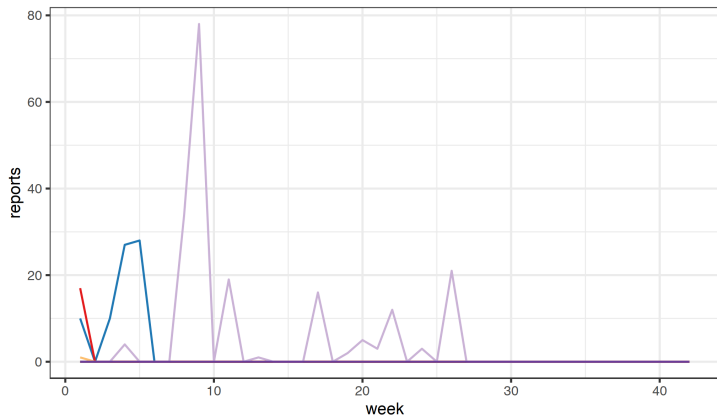
Testing the codes: simulation

Now to run and plot some simulations:

```
consett %>%  
  simulate(params=params,nsim=10,format="data.frame") -> y
```

```
y %>%  
  ggplot(aes(x=week,y=reports,group=.id,color=factor(.id)))+  
  geom_line()+  
  scale_color_brewer(type="qual",palette=3)+  
  guides(color=FALSE)
```

Testing the codes: simulation II



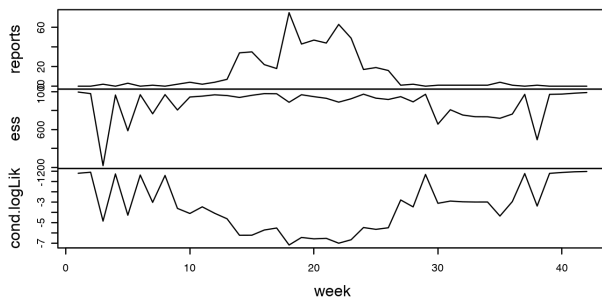
Testing the codes: filtering

Before engaging in iterated filtering, it is a good idea to check that the basic particle filter is working since we can't iterate something unless we can run it once! The simulations above check the `rprocess` and `rmeasure` codes; the particle filter depends on the `rprocess` and `dmeasure` codes and so is a check of the latter.

```
consette %>%  
  pfilter(Np=if(DEBUG) 100 else 1000, params=params) -> pf
```

```
plot(pf)
```

Testing the codes: filtering II



The above plot shows the data (`reports`), along with the *effective sample size* (ESS) of the particle filter (`ess`) and the log likelihood of each observation conditional on the preceding ones (`cond.logLik`). The ESS looks better than without overdispersion: the overdispersion helps to explain outliers.

Setting up the estimation problem

We follow the assumptions from the iterated filtering lesson, while adding overdispersion. We treat the population size, N , as known from the census. We also fix the infectious period in our model to 3.5 da, i.e., $\mu_{IR} = 2 \text{ wk}^{-1}$.

```
fixed_params <- c(N=38000, mu_IR=2)
```

We proceed to estimate β , η , ρ , σ and ψ .

Setup for parallel computing

```
library(doParallel)
registerDoParallel(detectCores())
library(doRNG)
registerDoRNG(582998)
```

Running a particle filter

We proceed to carry out replicated particle filters at an initial guess of $\beta = 20$, $\eta = 0.1$, and $\rho = 0.5$.

```
foreach(i=1:10,.combine=c) %dopar% {
  library(pomp)
  consette %>% pfilter(params=params,Np=10000)
} -> pf

pf %>% logLik() %>% logmeanexp(se=TRUE) -> L_pf
L_pf
```

```
                                se
-147.58396382      0.01533597
```

In 3.14 seconds, using 8 cores, we obtain an unbiased likelihood estimate of -147.6 with a Monte Carlo standard error of 0.015.

A local search of the likelihood surface

Let's carry out a local search using `mif2` around this point in parameter space.

- We need to choose the `rw.sd` and `cooling.fraction.50` algorithmic parameters.
- Since β , σ and ψ will be estimated on the log scale, and we expect that multiplicative perturbations of these parameters will have roughly similar effects on the likelihood, we'll use a perturbation size of 0.02, which we imagine will have a small but non-negligible effect.
- For simplicity, we'll use the same perturbation size on ρ and η .
- We fix `cooling.fraction.50`=0.5, so that after 50 `mif2` iterations, the perturbations are reduced to half their original magnitudes.

A local search of the likelihood surface II

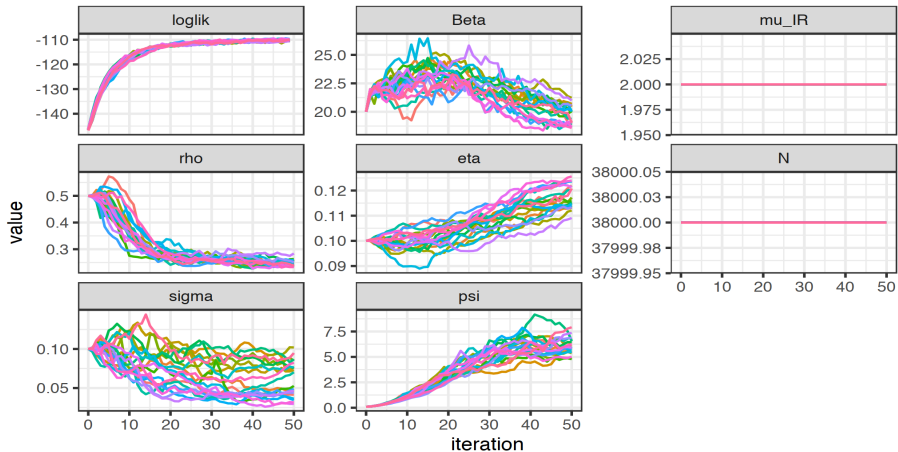
```
foreach(i=1:20,.combine=c) %dopar% {  
  library(pomp)  
  library(tidyverse)  
  consett %>%  
    mif2(  
      params=params,  
      Np=if(DEBUG) 50 else 2000, Nmif=if(DEBUG) 2 else 50,  
      partrans=parameter_trans(  
        log=c("Beta","sigma","psi"),  
        logit=c("rho","eta")  
      ),  
      paramnames=consett_paramnames,  
      cooling.fraction.50=0.5,  
      rw.sd=rw.sd(Beta=0.02, rho=0.02, sigma=0.02, psi=0.02, eta=iv)  
    )  
} -> mifs_local
```

Iterated filtering diagnostics

We obtain some diagnostic plots with the `plot` command applied to `mifs_local`. Here is a way to get a prettier version:

```
mifs_local %>%  
  traces() %>%  
  melt() %>%  
  ggplot(aes(x=iteration,y=value,group=L1,color=factor(L1)))+  
  geom_line()+  
  guides(color=FALSE)+  
  facet_wrap(~variable,scales="free_y")
```

Iterated filtering diagnostics II



Iterated filtering diagnostics III

- We see that the likelihood eventually increases as the iterations proceed, though there is considerable variability due to
 - (a) the poorness of our starting guess and
 - (b) the stochastic nature of this Monte Carlo algorithm.
- We see movement in the parameters, though considerable variability remains.

Estimating the likelihood

Although the filtering carried out by `mif2` in the final filtering iteration generates an approximation to the likelihood at the resulting point estimate, this is not good enough for reliable inference.

- Partly, this is because parameter perturbations are applied in the last filtering iteration, so that the likelihood reported by `mif2` is not identical to that of the model of interest.
- Partly, this is because `mif2` is usually carried out with fewer particles than are needed for a good likelihood evaluation.

Estimating the likelihood II

Therefore, we evaluate the likelihood, together with a standard error, using replicated particle filters at each point estimate.

```
foreach(mf=mifs_local,.combine=rbind) %dopar% {  
  library(pomp)  
  library(tidyverse)  
  evals <- replicate(if(DEBUG) 2 else 10,  
    logLik(pfilter(mf,Np=if(DEBUG) 50 else 20000)))  
  ll <- logmeanexp(evals,se=TRUE)  
  mf %>% coef() %>% bind_rows() %>%  
    bind_cols(loglik=ll[1],loglik.se=ll[2])  
} -> results
```

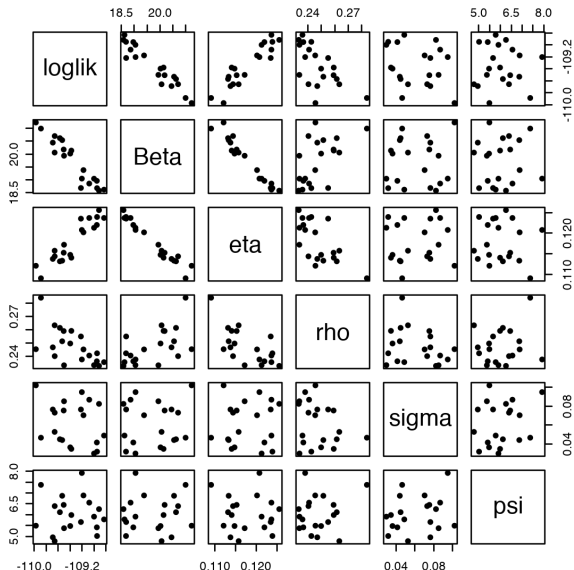
On 8 processors, this local investigation took 50 sec for the maximization and 71 sec for the likelihood evaluation.

Estimating the likelihood III

These repeated stochastic maximizations can also show us the geometry of the likelihood surface in a neighborhood of this point estimate:

```
pairs(~loglik+Beta+eta+rho+sigma+psi,data=results,pch=16)
```


Estimating the likelihood IV



Building up a picture of the likelihood surface

This plot shows a hint of a ridge in the likelihood surface (cf. the β - η panel). However, the sampling is as yet too sparse to give a clear picture. We add these newly explored points to our database,

```
read_csv("measles_params.csv") %>%  
  bind_rows(results) %>%  
  arrange(-loglik) %>%  
  write_csv("measles_params.csv")
```

and move on to a more thorough exploration of the likelihood surface.

A global search of the likelihood surface

For our measles model, a box containing reasonable parameter values might be $\beta \in (5, 80)$, $\rho \in (0.2, 0.9)$, $\eta \in (0, 0.4)$, $\sigma \in (0.01, 0.2)$, $\psi \in (1, 10)$.

We are now ready to carry out likelihood maximizations from diverse starting points.

```
set.seed(2062379496)

runifDesign(
  lower=c(Beta=5, rho=0.2, eta=0, sigma=0.01, psi=1),
  upper=c(Beta=80, rho=0.9, eta=0.4, sigma=0.2, psi=10),
  nseq=300
) -> guesses

mf1 <- mifs_local[[1]]
```

A global search of the likelihood surface II

```
registerDoRNG(1270401374)
foreach(guess=iter(guesses,"row"), .combine=rbind) %dopar% {
  library(pomp)
  library(tidyverse)
  mf1 %>%
    mif2(params=c(unlist(guess),fixed_params)) %>%
    mif2(Nmif=if(DEBUG) 2 else 100) -> mf
  replicate(
    if(DEBUG) 2 else 10,
    mf %>% pfilter(Np= if(DEBUG) 100 else 100000) %>% logLik()
  ) %>%
    logmeanexp(se=TRUE) -> ll
  mf %>% coef() %>% bind_rows() %>%
    bind_cols(loglik=ll[1],loglik.se=ll[2])
} -> results
```

A global search of the likelihood surface III

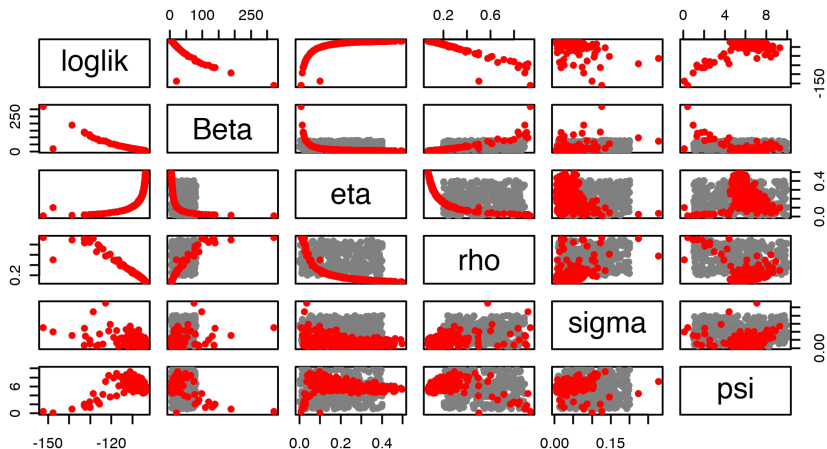
- The best result of this search had a likelihood of -103.7 with a standard error of 0.01.
- This took 107.1 minutes altogether using 8 processors.

A global search of the likelihood surface IV

Again, we attempt to visualize the global geometry of the likelihood surface using a scatterplot matrix. In particular, here we plot both the starting values (grey) and the IF2 estimates (red).

```
read_csv("measles_params.csv") %>%  
  filter(loglik>max(loglik)-50) %>%  
  bind_rows(guesses) %>%  
  mutate(type=if_else(is.na(loglik),"guess","result")) %>%  
  arrange(type) -> all  
  
pairs(~loglik+Beta+eta+rho+sigma+psi, data=all,  
      col=ifelse(all$type=="guess",grey(0.5),"red"),pch=16)
```

A global search of the likelihood surface V



A global search of the likelihood surface VI

- We see that the optimization searches head to a parameter subspace with high η and low ρ .
- According to this fit, there are many susceptibles and a large latent epidemic which depletes them.
- We do not think this was happening in reality.
- One curve cannot reliably fit many parameters!
- We have pushed up the likelihood bar - previous models under consideration had a log likelihood of around 120, so we have gained over 15 points of log likelihood.
- We would be happier to do this while maintaining a plausible model. That will require more work.

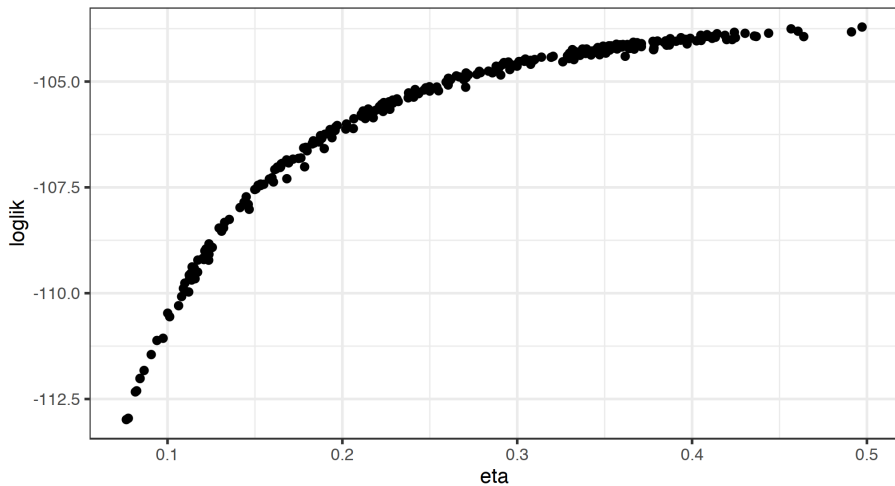
A global search of the likelihood surface VII

The projections of the estimates give us “poor man’s profiles”:

```
all %>%  
  filter(type=="result") %>%  
  filter(loglik>max(loglik)-10) %>%  
  ggplot(aes(x=eta,y=loglik))+  
  geom_point()+  
  labs(  
    x=expression("eta"),  
    title="poor man's profile likelihood"  
  )
```

A global search of the likelihood surface VIII

poor man's profile likelihood



Adding a reservoir

- Perhaps allowing for occasional cases to arrive from neighboring cities will help to explain the data?
- We add a “reservoir” term, ι , corresponding to a number of infected individuals visiting, on average, on any given day.
- Here, we fix this at $\iota = 0.05$, following results from He *et al.* (2010).
- We find the optimization still tends toward a regime with high η and low ρ , without increasing the maximized likelihood.
- With only one epidemic, it may be hard to get good information on the reporting rate.
- We could try other changes. These models have many parameters for the amount of data, but it would be nice to show that there exist models with both competitive likelihood and interpretable parameters.
- Further work is needed!

Adding a reservoir II

```
consett2_step <- Csnippet("  
  double dGamma = rgammawn(sigma,dt);  
  double dN_SI = rbinom(S,1-exp(-Beta*(I+iota)/N*dGamma));  
  double dN_IR = rbinom(I,1-exp(-mu_IR*dt));  
  S -= dN_SI;  
  I += dN_SI - dN_IR;  
  H += dN_IR;  
  ")
```

```
consett2_rinit <- Csnippet("  
  S = nearbyint(eta*N);  
  I = 0;  
  H = 0;  
  ")
```

Adding a reservoir III

```
consett2_paramnames <- c(consett_paramnames, "iota")
consett %>%
  pomp(
    rprocess=euler(consett2_step, delta.t=1/7),
    rinit=consett2_rinit,
    statenames=consett_statenames,
    paramnames=consett2_paramnames
  ) -> consett2
```

```
consett2_fixed_params <- c(N=38000, mu_IR=2, iota=0.05)
```

```
# DEBUG <- TRUE
```

```
set.seed(2062379496)
```

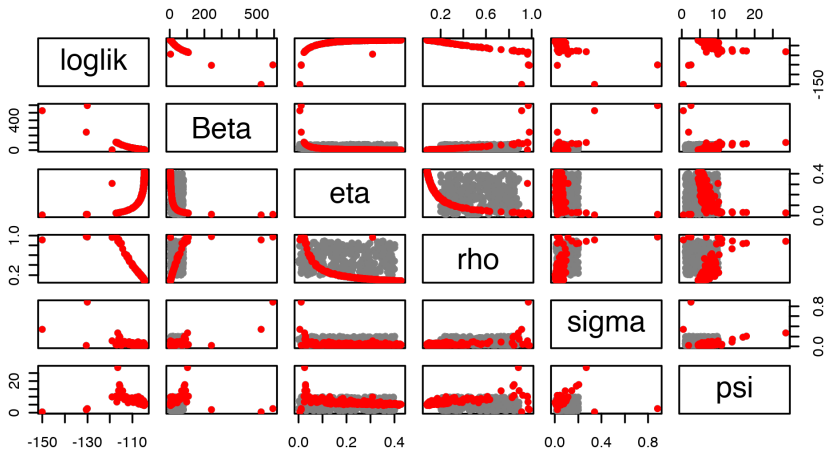
```
runifDesign(
  lower=c(Beta=5, rho=0.2, eta=0, sigma=0.01, psi=1),
  upper=c(Beta=80, rho=0.9, eta=0.4, sigma=0.2, psi=10),
  nseq=if(DEBUG) 20 else 300
) -> consett2_guesses
```

```
registerDoRNG(1270401374)
foreach(guess=iter(consett2_guesses, "row"),
  .combine=rbind) %dopar% {
  library(pomp)
  library(tidyverse)
  consett2 %>%
    mif2(
      params=c(unlist(guess), consett2_fixed_params),
      Np=if(DEBUG) 50 else 2000, Nmif=if(DEBUG) 2 else 50,
```

```

partrans=parameter_trans(
  log=c("Beta","sigma","psi"),
  logit=c("rho","eta")
),
paramnames=consett2_paramnames,
cooling.fraction.50=0.5,
rw.sd=rw.sd(Beta=0.02, rho=0.02,
  sigma=0.02, psi=0.02, eta=ivp(0.02))
) %>%
  mif2(Nmif=if(DEBUG) 2 else 100) -> mf
replicate(
  if(DEBUG) 2 else 10,
  mf %>% pfilter(Np= if(DEBUG) 100 else 10000) %>% logLik()
) %>%
  logmeanexp(se=TRUE) -> ll
mf %>% coef() %>% bind_rows() %>%
  bind_cols(loglik=ll[1],loglik.se=ll[2])
} -> consett2_results

```




Exercise 9.2. A profile over σ

- Is there evidence for the inclusion of overdispersion on the latent process?
- The scatterplots show little pattern for σ , which could be because the amount of information about σ is small in the context of this model (i.e., the profile has low curvature – it is close to flat).
- Construct a profile likelihood for σ to investigate whether this is the case.
- You'll have to work out a suitable range of σ for the profile. The above figure suggests that the interval used for σ in the profile for ρ may be too narrow.

References

He D, Ionides EL, King AA (2010). “Plug-and-play inference for disease dynamics: measles in large and small populations as a case study.” *Journal of the Royal Society, Interface*, **7**, 271–283.
[doi: 10.1098/rsif.2009.0151](https://doi.org/10.1098/rsif.2009.0151).

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[R codes for this lesson](#)