

Lesson 4.

Iterated filtering: principles and practice

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Outline

- 1 Introduction
- 2 Classification of statistical methods for POMP models
- 3 Iterated filtering in theory
- 4 Iterated filtering in practice
- 5 Searching for the MLE
- 6 The investigation continues. . . .
- 7 Exercises

Introduction

- This tutorial covers likelihood estimation via the method of iterated filtering.
- It presupposes familiarity with building partially observed Markov process (POMP) objects in the R package **pomp** (King *et al.*, 2016).
- This tutorial follows on from the [topic of particle filtering](#) (also known as sequential Monte Carlo) via `pfilter` in **pomp**.

Objectives

- ① To review the available options for inference on POMP models, to put iterated filtering in context.
- ② To understand how iterated filtering algorithms carry out repeated particle filtering operations, with randomly perturbed parameter values, in order to maximize the likelihood.
- ③ To gain experience carrying out statistical investigations using iterated filtering in a relatively simple situation: fitting an SIR model to data from a measles outbreak.

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Classification of statistical methods for POMP models

- Many, many statistical methods have been proposed for inference on POMP models (He *et al.*, 2010; King *et al.*, 2016).
- The volume of research indicates both the importance and the difficulty of the problem.
- Let's start by considering three criteria to categorize inference methods:
 - the plug-and-play property
 - full-information or feature-based
 - frequentist or Bayesian

Plug-and-play (also called simulation-based) methods

- Inference methodology that calls `rprocess` but not `dprocess` is said to be *plug-and-play*. All popular modern Monte Carlo methods fall into this category.
- “Simulation-based” is equivalent to “plug-and-play”.
- Historically, simulation-based meant simulating forward from initial conditions to the end of the time series.
- However, particle filtering methods instead consider each observation interval sequentially. They carry out multiple, carefully selected, simulations over each interval.

Plug-and-play (also called simulation-based) methods II

- Plug-and-play methods can call `dmeasure`. A method that uses only `rprocess` and `rmeasure` is called “doubly plug-and-play”.
- Two *non-plug-and-play* methods—expectation-maximization (EM) and Markov chain Monte Carlo (MCMC)—have theoretical convergence problems for nonlinear POMP models. The failures of these two workhorses of statistical computation have prompted development of alternative methodologies.

EM和MCMC在非线性POMP模型上不一定收敛

Full-information and feature-based methods

- *Full-information* methods are defined to be those based on the likelihood function for the full data (i.e., likelihood-based frequentist inference and Bayesian inference).
- *Feature-based* methods either consider a summary statistic (a function of the data) or work with an alternative to the likelihood.
- Asymptotically, full-information methods are statistically efficient and feature-based methods are not.
- In some cases, loss of statistical efficiency might be an acceptable tradeoff for advantages in computational efficiency.

为了计算方便,可以牺牲一定准确率

Full-information and feature-based methods II

- However: 高维模型不好计算
 - Good low-dimensional summary statistics can be hard to find.
 - When using statistically inefficient methods, it can be hard to know how much information you are losing.
 - Intuition and scientific reasoning can be inadequate tools to derive informative low-dimensional summary statistics (Shrestha *et al.*, 2011; Ionides, 2011).

Bayesian and frequentist methods

- Recently, plug-and-play Bayesian methods have been discovered:
 - particle Markov chain Monte Carlo (PMCMC) (Andrieu *et al.*, 2010).
 - approximate Bayesian computation (ABC) (Toni *et al.*, 2009).
- Prior belief specification is both the strength and weakness of Bayesian methodology:
- The likelihood surface for nonlinear POMP models often contains nonlinear ridges and variations in curvature.

Bayesian and frequentist methods II

- These situations bring into question the appropriateness of independent priors derived from expert opinion on marginal distributions of parameters.
- They also are problematic for specification of “flat” or “uninformative” prior beliefs.
- Expert opinion can be treated as data for non-Bayesian analysis. However, our primary task is to identify the information in the data under investigation, so it can be helpful to use methods that do not force us to make our conclusions dependent on quantification of prior beliefs.

我们希望先验分布不会影响分析质量

POMP inference methodologies

	Frequentist	Bayesian
Plug-and-play		
Full-information	iterated filtering	particle MCMC
Feature-based	simulated moments synthetic likelihood (SL) nonlinear forecasting	ABC SL-based MCMC
Not plug-and-play		
Full-information	EM algorithm Kalman filter	MCMC
Feature-based	Yule-Walker ¹ extended Kalman filter ²	extended Kalman filter ²

¹Yule-Walker is a method of moments for ARMA, a linear Gaussian POMP.

²The Kalman filter gives the exact likelihood for a linear Gaussian POMP. The extended Kalman filter gives an approximation for nonlinear models that can be used for quasi-likelihood or quasi-Bayesian inference.

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Full-information, plug-and-play, frequentist methods

- Iterated filtering methods (Ionides *et al.*, 2006, 2015) are the only currently available, full-information, plug-and-play, frequentist methods for POMP models.
- Iterated filtering methods have been shown to solve likelihood-based inference problems for epidemiological situations which are computationally intractable for available Bayesian methodology (Ionides *et al.*, 2015).

贝叶斯方法不好解,但是用Iterated Filtering有效果

An iterated filtering algorithm (IF2)

We focus on the IF2 algorithm of Ionides *et al.* (2015). In this algorithm:

- Each iteration consists of a particle filter, carried out with the parameter vector, for each particle, doing a random walk.
- At the end of the time series, the collection of parameter vectors is recycled as starting parameters for the next iteration.
- The random-walk variance decreases at each iteration.

In theory, this procedure converges toward the region of parameter space maximizing the maximum likelihood. In practice, we can test this claim on examples.

1. 每次迭代获得参数向量
2. 将迭代获得的参数向量用于下次估计
3. 参数的方差会逐步减小

IF2 algorithm pseudocode

Input:

- simulators for $f_{X_0}(x_0; \theta)$ and $f_{X_n|X_{n-1}}(x_n|x_{n-1}; \theta)$;
- evaluator for $f_{Y_n|X_n}(y_n|x_n; \theta)$;
- data, $y_{1:N}^*$

Algorithmic parameters:

- number of iterations, M ;
 - number of particles, J ;
 - initial parameter swarm, $\{\Theta_j^0, j = 1, \dots, J\}$;
 - perturbation density, $h_n(\theta|\varphi; \sigma)$;
 - perturbation scale, $\sigma_{1:M}$
- perturbation, 对参数施加扰动误差
(通常用正态分布)
误差参数会逐渐减小

Output:

- final parameter swarm, $\{\Theta_j^M, j = 1, \dots, J\}$

IF2 algorithm pseudocode II

Procedure: 做M次时间序列长度为N的迭代

- 1 For m in $1:M$
- 2 $\Theta_{0,j}^{F,m} \sim h_0(\theta | \Theta_j^{m-1}; \sigma_m)$ for j in $1:J$ 使用上一次迭代的参数构造J个粒子的初始隐状态
- 3 $X_{0,j}^{F,m} \sim f_{X_0}(x_0; \Theta_{0,j}^{F,m})$ for j in $1:J$
- 4 For n in $1:N$
- 5 $\Theta_{n,j}^{P,m} \sim h_n(\theta | \Theta_{n-1,j}^{F,m}, \sigma_m)$ for j in $1:J$ 每次时间序列生成新的参数
- 6 $X_{n,j}^{P,m} \sim f_{X_n|X_{n-1}}(x_n | X_{n-1,j}^{F,m}; \Theta_{n,j}^{P,m})$ for j in $1:J$
- 7 $w_{n,j}^m = f_{Y_n|X_n}(y_n^* | X_{n,j}^{P,m}; \Theta_{n,j}^{P,m})$ for j in $1:J$ 执行常规的粒子滤波
- 8 Draw $k_{1:J}$ with $P[k_j = i] = w_{n,i}^m / \sum_{u=1}^J w_{n,u}^m$ 基于粒子滤波的权重,从参数中重采样
- 9 $\Theta_{n,j}^{F,m} = \Theta_{n,k_j}^{P,m}$ and $X_{n,j}^{F,m} = X_{n,k_j}^{P,m}$ for j in $1:J$
- 10 End For
- 11 Set $\Theta_j^m = \Theta_{N,j}^{F,m}$ for j in $1:J$
- 12 End For

IF2 algorithm pseudocode III

Remarks:

- The N loop (lines 4 through 10) is a basic particle filter applied to a model with stochastic perturbations to the parameters.
- The M loop repeats this particle filter with decreasing perturbations.
- The superscript F in $\Theta_{n,j}^{F,m}$ and $X_{n,j}^{F,m}$ denote solutions to the filtering problem, with the particles $j = 1, \dots, J$ providing a Monte Carlo representation of the conditional distribution at time n given data $y_{1:n}^*$ for filtering iteration m .
- The superscript P in $\Theta_{n,j}^{P,m}$ and $X_{n,j}^{P,m}$ denote solutions to the prediction problem, with the particles $j = 1, \dots, J$ providing a Monte Carlo representation of the conditional distribution at time n given data $y_{1:n-1}^*$ for filtering iteration m .
- The *weight* $w_{n,j}^m$ gives the likelihood of the data at time n for particle j in filtering iteration m .

Analogy with evolution by natural selection

- The parameters characterize the *genotype*. 用自然选择(遗传算法)来估计迭代过程
- The swarm of particles is a *population*.
- The likelihood, a measure of the compatibility between the parameters and the data, is the analogue of *fitness*.
- Each successive observation is a new *generation*.
- Since particles reproduce in each generation in proportion to their likelihood, the particle filter acts like *natural selection*.
- The artificial perturbations augment the “genetic” variance and therefore correspond to *mutation*.
- IF2 increases the *fitness* of the population of particles.
- However, because our scientific interest focuses on the model without the artificial perturbations, we decrease the intensity of the latter with successive iterations.

Outline

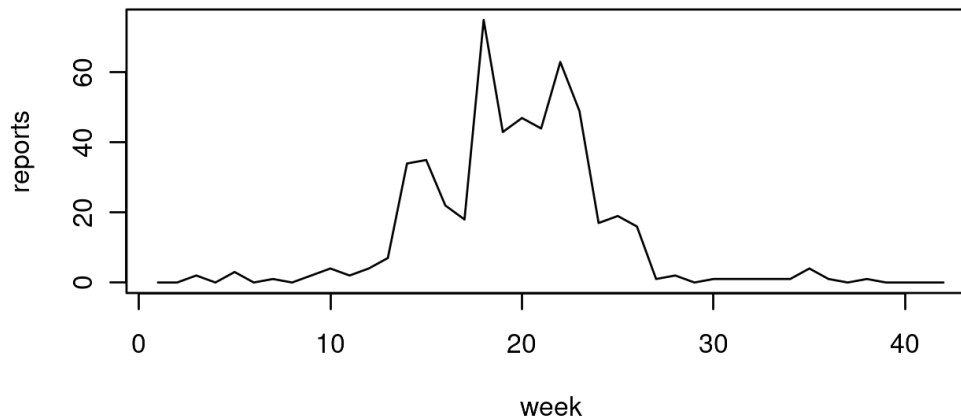
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Applying IF2 to the Consett measles outbreak

Let us apply IF2 to our analysis of the Consett measles outbreak we began to examine in Lessons 2 and 3.

The following loads the data and the stochastic SIR model we constructed there.

```
source("https://kingaa.github.io/sbied/pfilter/model.R")
```



Testing the codes: filtering

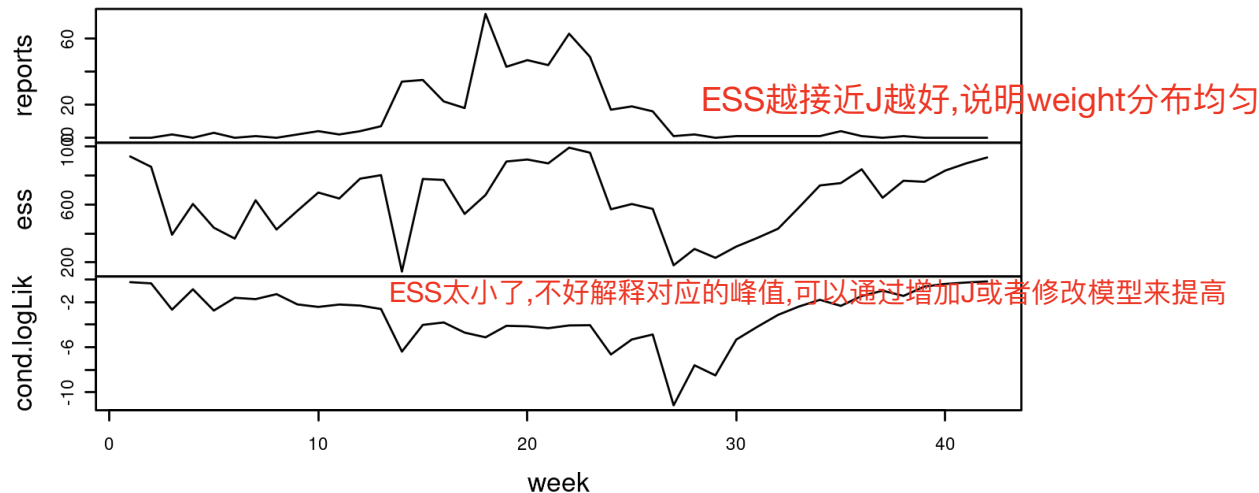
Before engaging in iterated filtering, it is a good idea to check that the basic particle filter is working since we can't iterate something unless we can run it once! The simulations above check the `rprocess` and `rmeasure` codes; the particle filter depends on the `rprocess` and `dmeasure` codes and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

```
measSIR %>%  
  pfilter(Np=1000) -> pf
```

先跑一次看看particle filter运行是否正常并绘图

```
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 is the equivalent number of independent particles. In this case, the ESS appears to be everywhere adequate.

如果weights分布很不均匀,Filter时可能只会从J个particle中抽取个别的,则ESS为抽取的particle数量

Setting up the estimation problem

Let's assume that the population size, N , is known accurately. We'll fix that parameter.

Let's revisit the assumption that the infectious period is 2 weeks, imagining that we have access to the results of household and clinical studies that have concluded that infected patients shed the virus for 3–4 da. We'll use these results to constrain the infectious period in our model to 3.5 da, i.e., $\mu_{IR} = 2 \text{ wk}^{-1}$. We also fix $k = 10$. Later, we can relax our assumptions.

```
fixed_params <- c(N=38000, mu_IR=2, k=10)
coef(measSIR, names(fixed_params)) <- fixed_params
```

固定了3个参数,估计剩下的3个,

但之后要检验所有参数效果

We proceed to estimate β , η , and ρ .

The key thing here is to do inference within a set of assumptions. We must remember to challenge the assumptions later.

Parallel computing

It will be helpful to parallelize most of the computations. [Lesson 3](#) discusses how to accomplish this using **foreach**.

```
library(foreach)
library(doParallel)
registerDoParallel()
```

```
library(doRNG)
registerDoRNG(625904618)
```

Running a particle filter

We proceed to carry out replicated particle filters at an initial guess of $\beta = 15$, $\eta = 0.06$, and $\rho = 0.5$.

```
foreach(i=1:10,.combine=c) %dopar% {
  library(pomp)
  measSIR %>% pfilter(Np=5000)
} -> pf

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

	se	
-278.66905	16.39569	likelihood是unbiased,但是log likelihood是bias

In 1.05 seconds, using 8 cores, we obtain an unbiased likelihood estimate of -278.7 with a Monte Carlo standard error of 16.

Building up a picture of the likelihood surface

- Given a model and a set of data, the likelihood surface is well defined, though it may be difficult to visualize.
- We can develop a progressively more complete picture of this surface by storing likelihood estimates whenever we compute them.
- It is a very good idea to set up a database within which to store the likelihood of every point for which we have an estimated likelihood.
- This will become larger and more complete as our parameter-space search goes on and will be a basis for a variety of explorations.

在迭代过程中,不仅仅找MLE点,而是利用迭代过程中的数据,建立整个likelihood surface

Building up a picture of the likelihood surface II

At this point, we've computed the likelihood at a single point. Let's store this point, together with the estimated likelihood and our estimate of the standard error on that likelihood, in a CSV file:

```
pf[[1]] %>% coef() %>% bind_rows() %>%  
  bind_cols(loglik=L_pf[1], loglik.se=L_pf[2]) %>%  
  write_csv("measles_params.csv")
```

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.
参数 random walk standard 的标准差 rw.sd 减小的速度
- Since β and μ_{IR} 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.
非负参数通常用 log 来估计
- For simplicity, we'll use the same perturbation size on ρ .
- We fix cooling.fraction.50=0.5, so that after 50 mif2 iterations, the perturbations are reduced to half their original magnitudes.

roughly 1% reduction per iteration, a good default value

A local search of the likelihood surface II

```
foreach(i=1:20,.combine=c) %dopar% {
  library(pomp)
  library(tidyverse)
  measSIR %>%
    mif2(
      Np=2000, Nmif=50,
      cooling.fraction.50=0.5,
      rw.sd=rw.sd(Beta=0.02, rho=0.02, eta=ivp(0.02)),
      partrans=parameter_trans(log="Beta",logit=c("rho","eta")),
      paramnames=c("Beta","rho","eta")
    ) 给C语言编译提供变量
} -> mifs_local
```

initial value parameter specified via `ivp()`, it only affects the latent states at $t=0$

范围是0-1的参数,通常在logit transformed后估计

$$\eta \rightarrow \frac{e^{\tilde{\eta}}}{1 + e^{\tilde{\eta}}}$$

$$\tilde{\eta} \approx \log \eta$$

Windows issues

Some Windows users have reported trouble with the above code. This appears to be due to certain Windows security features that make it impossible to compile codes inside a parallel block. We have found a workaround.

[Have a look at this document to learn about the workaround.](#)

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="none")+  
  facet_wrap(~variable, scales="free_y")
```

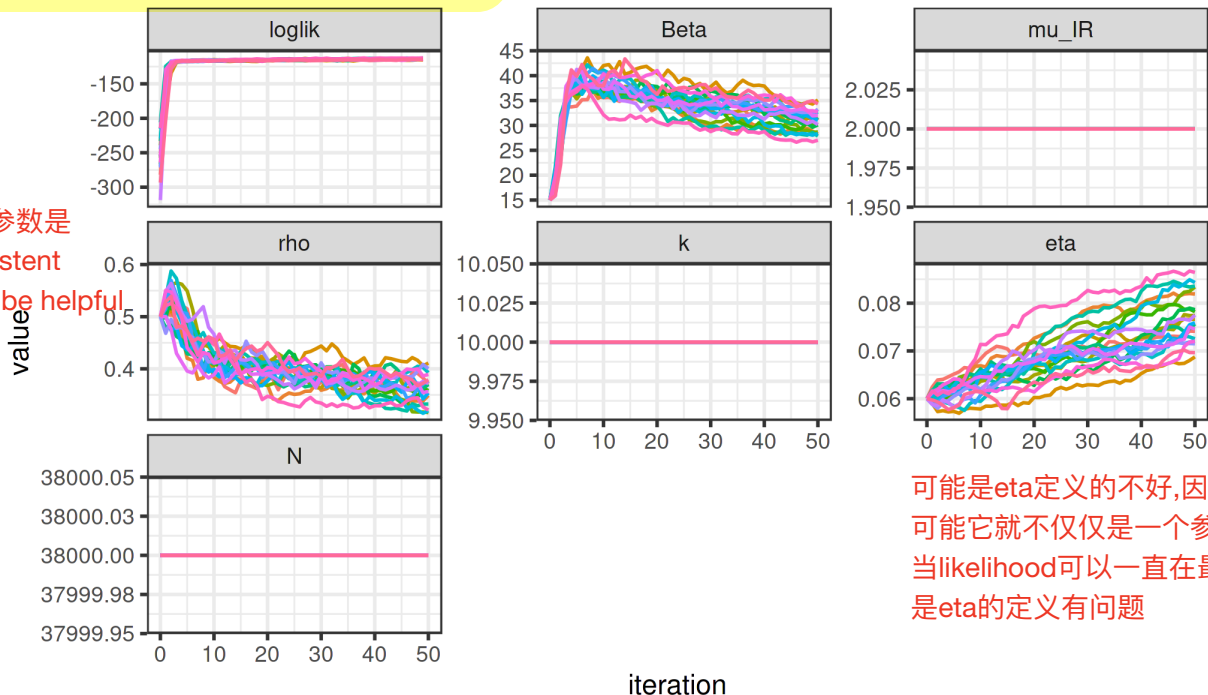
Iterated filtering diagnostics II

不需要大量searching就可以获得很高的likelihood

大扰动导致大Beta,小扰动反之

需要关注每个参数是
否表现的consistent

Large M may be helpful



可能是eta定义的不好,因为真实模型中
可能它就不仅仅是一个参数
当likelihood可以一直在最大,则大概率
是eta的定义有问题

Iterated filtering diagnostics III

- We see that the likelihood 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 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(10, logLik(pfilter(mf,Np=5000)))  
  ll <- logmeanexp(evals,se=TRUE)  
  mf %>% coef() %>% bind_rows() %>%  
    bind_cols(loglik=ll[1],loglik.se=ll[2])  
} -> results
```

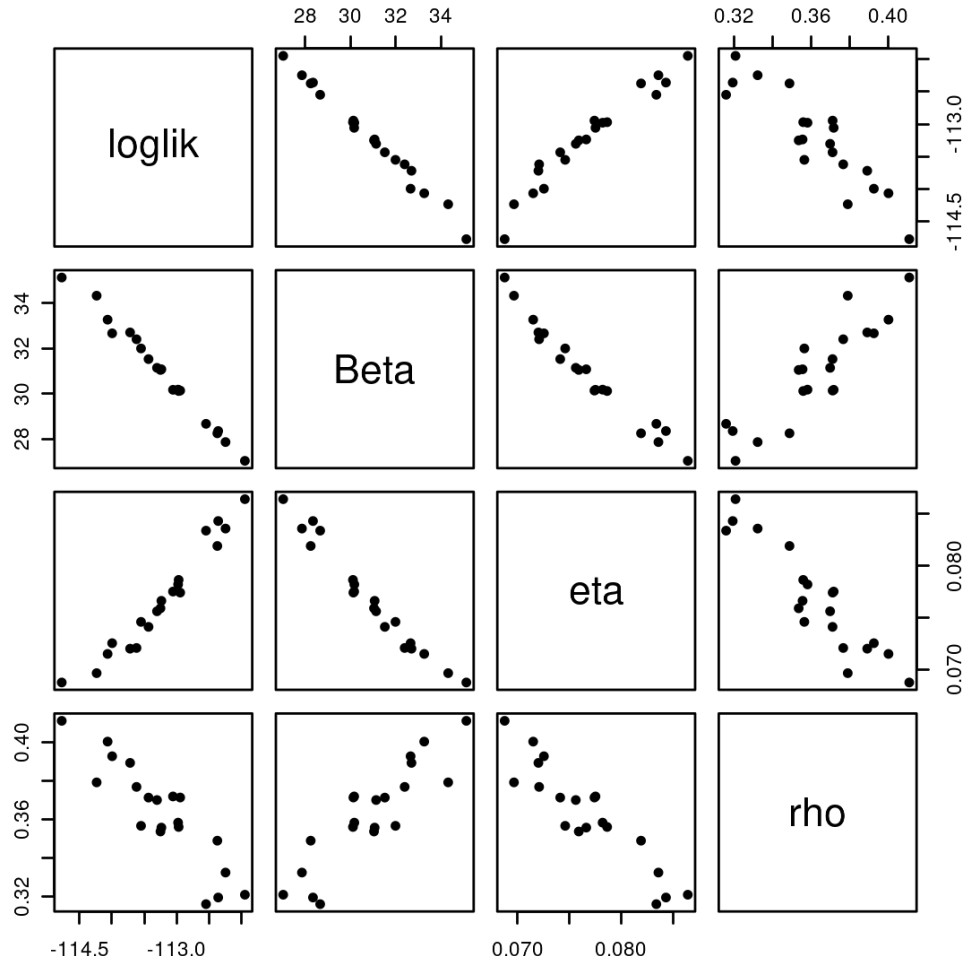
On 12 processors, this local investigation took 18 sec for the maximization and 8 sec for the likelihood evaluation.

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,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.

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A global search of the likelihood surface

- When carrying out parameter estimation for dynamic systems, we need to specify beginning values for both the dynamic system (in the state space) and the parameters (in the parameter space).
- To avoid confusion, we use the term “initial values” to refer to the state of the system at t_0 and “starting values” to refer to the point in parameter space at which a search is initialized.
- Practical parameter estimation involves trying many starting values for the parameters.
- One way to approach this is to choose a large box in parameter space that contains all remotely sensible parameter vectors.
- If an estimation method gives stable conclusions with starting values drawn randomly from this box, this gives some confidence that an adequate global search has been carried out.

A global search of the likelihood surface II

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

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

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

```
runif_design(  
  lower=c(Beta=5, rho=0.2, eta=0),  
  upper=c(Beta=80, rho=0.9, eta=1),  
  nseq=400  
) -> guesses
```

定一个一个参数范围,从中选取初始值进行参数搜索
runif_design是一个函数用来随机获得参数

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

不用重新定义模型

A global search of the likelihood surface III

```
foreach(guess=iter(guesses,"row"), .combine=rbind) %dopar% {  
  library(pomp)  
  library(tidyverse)  
  mf1 %>%  
    mif2(params=c(guess,fixed_params)) %>%  
    mif2(Nmif=100) -> mf  
  replicate(  
    10,  
    mf %>% pfilter(Np=5000) %>% logLik()  
  ) %>%  
    logmeanexp(se=TRUE) -> ll  
  mf %>% coef() %>% bind_rows() %>%  
    bind_cols(loglik=ll[1],loglik.se=ll[2])  
} -> results
```

mf1是一个保存了参数的pomp object
先进行了50次随机初始化
之后再进行100次search

A global search of the likelihood surface IV

- The above codes run one search from each of 400 starting values.
- Each search consists of an initial run of 50 IF2 iterations, followed by another 100 iterations.
- These codes exhibit a general **pomp** behavior:
 - Re-running a command on an object (i.e., `mif2` on `mf1`) created by the same command preserves the algorithmic arguments.
 - In particular, running `mif2` on the result of a `mif2` computation re-runs IF2 from the endpoint of the first run.
 - In the second computation, by default, all algorithmic parameters are preserved; here we overrode the default choice of `Nmif`.
- Following the `mif2` computations, the particle filter is used to evaluate the likelihood, as before.

A global search of the likelihood surface V

保存所有search过程占用空间太大了

- In contrast to the local-search codes above, here we return only the endpoint of the search, together with the likelihood estimate and its standard error in a named vector.
- The best result of this search had a likelihood of -104.3 with a standard error of 0.04.
- This took 2.1 minutes altogether using 250 processors.

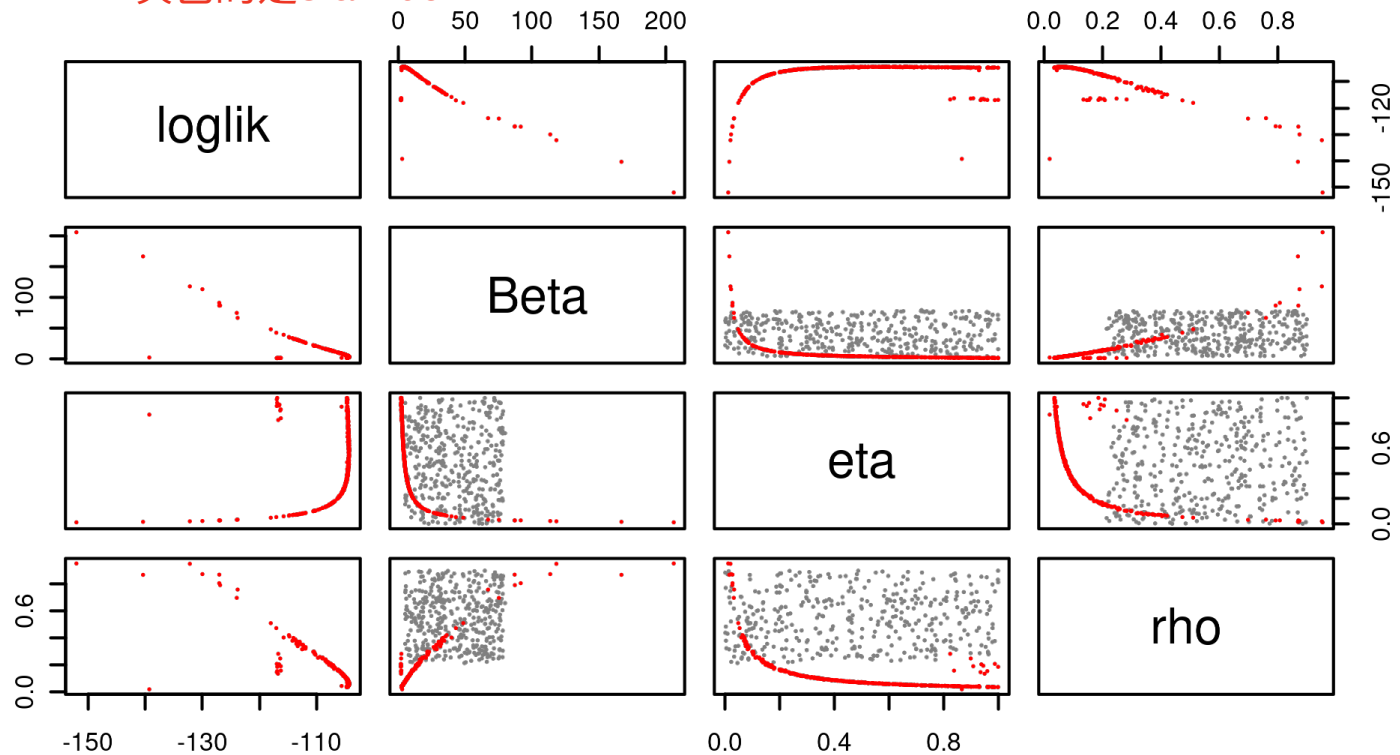
A global search of the likelihood surface VI

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, data=all, pch=16, cex=0.3,  
      col=ifelse(all$type=="guess",grey(0.5),"red"))
```

A global search of the likelihood surface VII

灰色的是start box



A global search of the likelihood surface VIII

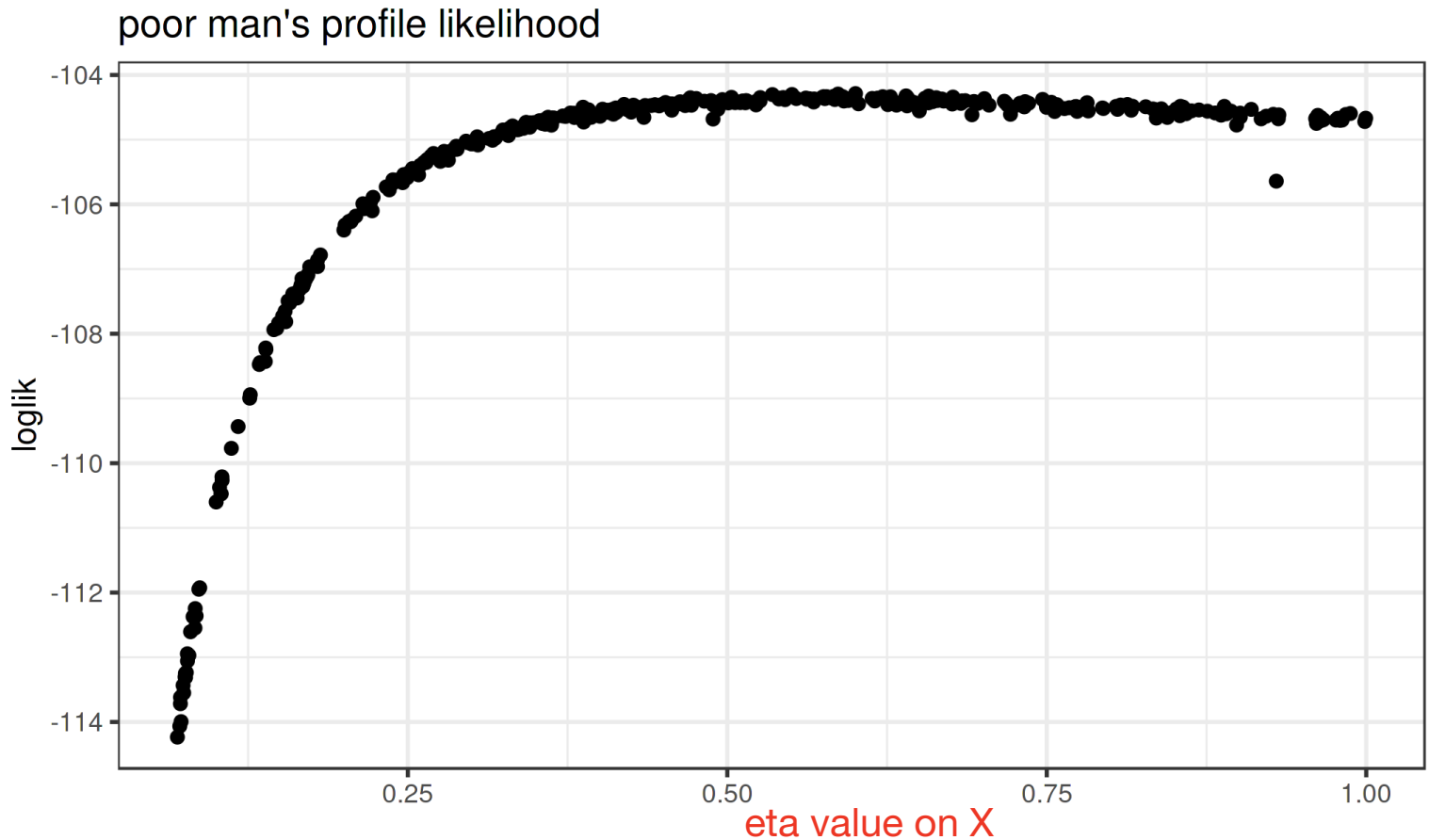
- We see that optimization attempts from diverse remote starting points converge on a particular region in parameter space.
- The estimates have comparable likelihoods, despite their considerable variability.
- This gives us some confidence in our maximization procedure.

A global search of the likelihood surface IX

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 X



Profile likelihood over η

- The curvature displayed in the upper envelope of the above plot suggests that there is indeed information in the data with respect to the susceptible fraction, η .
- To solidify this evidence, let's compute a profile likelihood over this parameter.
- Recall that this means determining, for each value of η , the best likelihood that the model can achieve.
- To do this, we'll first bound the uncertainty by putting a box around the highest-likelihood estimates we've found so far.
- Within this box, we'll choose some random starting points, for each of several values of η .

在likelihood较大的范围中重新开始搜索

Profile likelihood over η II

```
read_csv("measles_params.csv") %>%
  filter(loglik>max(loglik)-20,loglik.se<2) %>%
  sapply(range) -> box
box
```

	Beta	mu_IR	rho	k	eta	N
[1,]	1.782037	2	0.03431374	10	0.03272262	38000
[2,]	75.170745	2	0.75966698	10	0.99984295	38000

	loglik	loglik.se
[1,]	-123.9674	0.01543941
[2,]	-104.2873	0.23421034

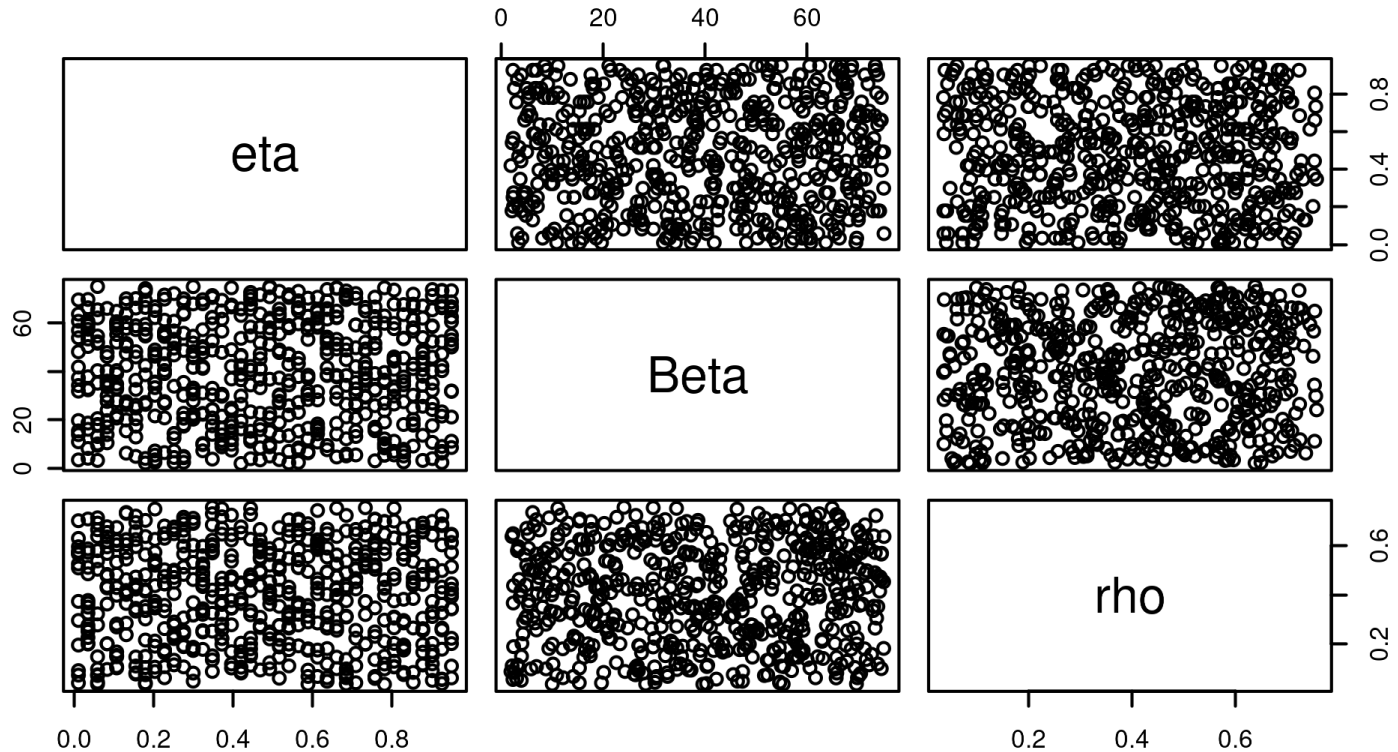
Profile likelihood over η III

```
freeze(seed=1196696958,  
  profile_design(  
    eta=seq(0.01,0.95,length=40),  
    lower=box[1,c("Beta","rho")],  
    upper=box[2,c("Beta","rho")],  
    nprof=15, type="runif"  
  )) -> guesses  
plot(guesses)
```

Sets up a matrix of parameter value to be used on starting points for calculating a profile

eta is profiled over: we specific eta on an equally spaced grid

Profile likelihood over η IV



Profile likelihood over η V

- Now, we'll start one independent sequence of iterated filtering operations from each of these points.
- We'll be careful to keep η fixed. 设置随机游走标准差为0即可
- This is accomplished by not giving this parameter a random perturbation in the `mif2` call.

Profile likelihood over η VI

```
foreach(guess=iter(guesses,"row"), .combine=rbind) %dopar% {  
  library(pomp)  
  library(tidyverse)  
  mf1 %>%  
    mif2(params=c(guess,fixed_params),  
          rw.sd=rw.sd(Beta=0.02,rho=0.02)) %>%  
    mif2(Nmif=100,cooling.fraction.50=0.3) -> mf  
  replicate(  
    10,  
    mf %>% pfilter(Np=5000) %>% logLik()) %>%  
    logmeanexp(se=TRUE) -> ll  
  mf %>% coef() %>% bind_rows() %>%  
    bind_cols(loglik=ll[1],loglik.se=ll[2])  
} -> results
```

这和global search几乎一样,除了eta的参数设置

Visualizing profile likelihood

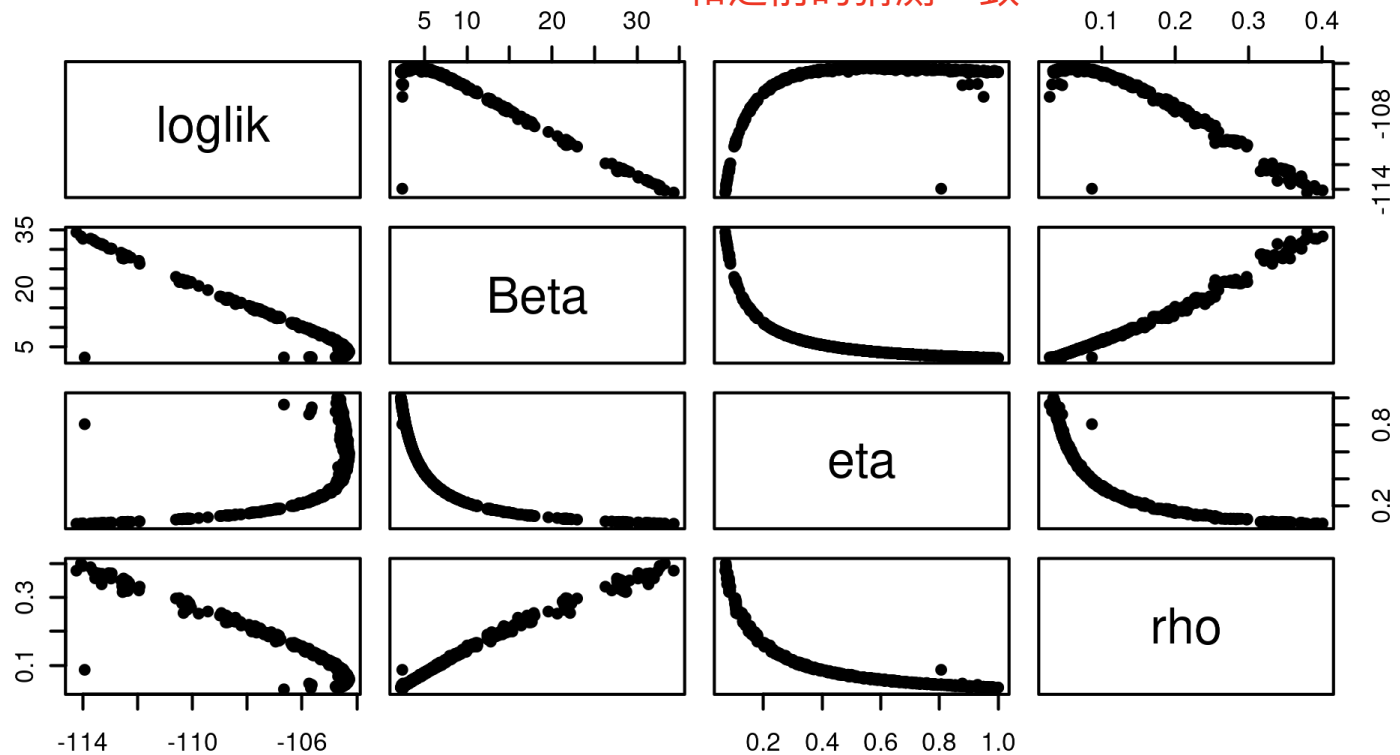
As always, we save the results in our global database and plot the results.

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

```
read_csv("measles_params.csv") %>%  
  filter(loglik>max(loglik)-10) -> all  
  
pairs(~loglik+Beta+eta+rho, data=all, pch=16)
```

Visualizing profile likelihood II

eta seems to be weakly identified
和之前的猜测一致

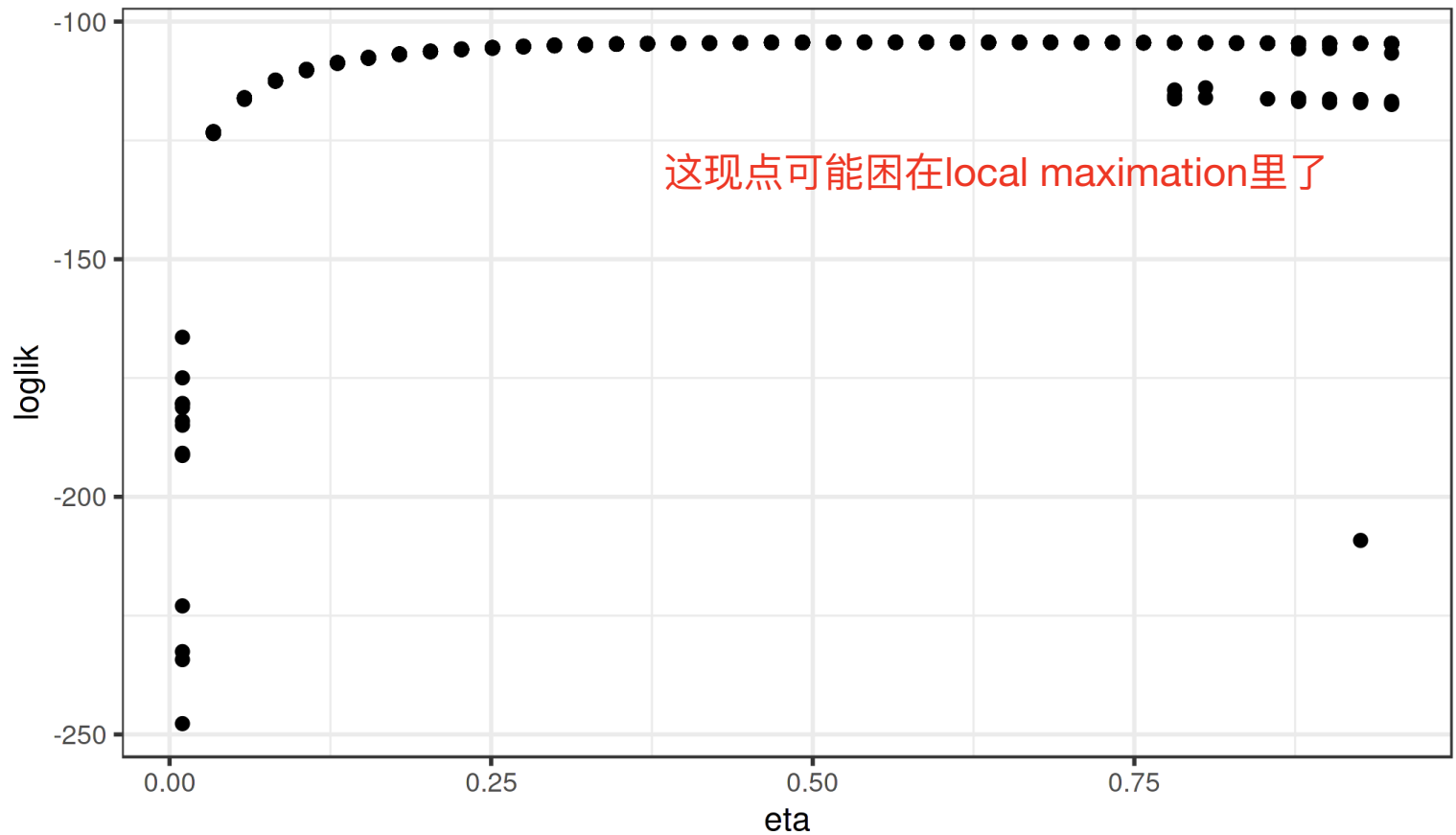


Visualizing profile likelihood III

Plotting just the results of the profile calculation reveals that, while some of the IF2 runs either become “stuck” on local minima or run out of opportunity to reach the heights of the likelihood surface, many of the runs converge on high likelihoods.

```
results %>%  
  ggplot(aes(x=eta,y=loglik))+  
  geom_point()
```

Visualizing profile likelihood IV

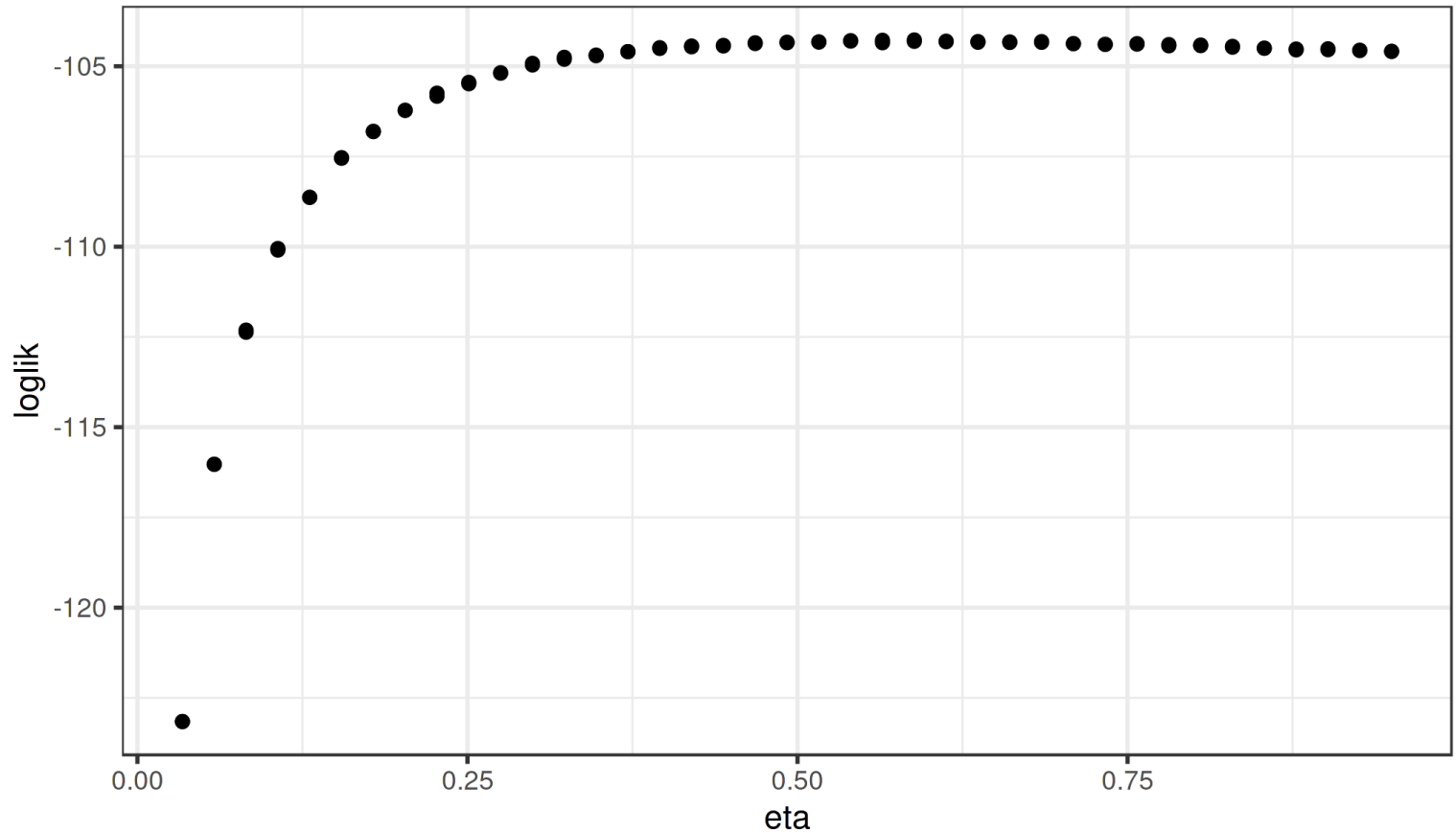


Visualizing profile likelihood V

A closer look shows what at first appears to be quite a flat surface over much of the explored range of η . Note that this appearance is due to the vertical scale, which is driven by the very low likelihoods associated with the smallest values of η .

```
results %>%  
  filter(is.finite(loglik)) %>%  
  group_by(round(eta,5)) %>%  
  filter(rank(-loglik)<3) %>%  
  ungroup() %>%  
  filter(loglik>max(loglik)-20) %>%  
  ggplot(aes(x=eta,y=loglik))+  
  geom_point()
```

Visualizing profile likelihood VI



Visualizing profile likelihood VII

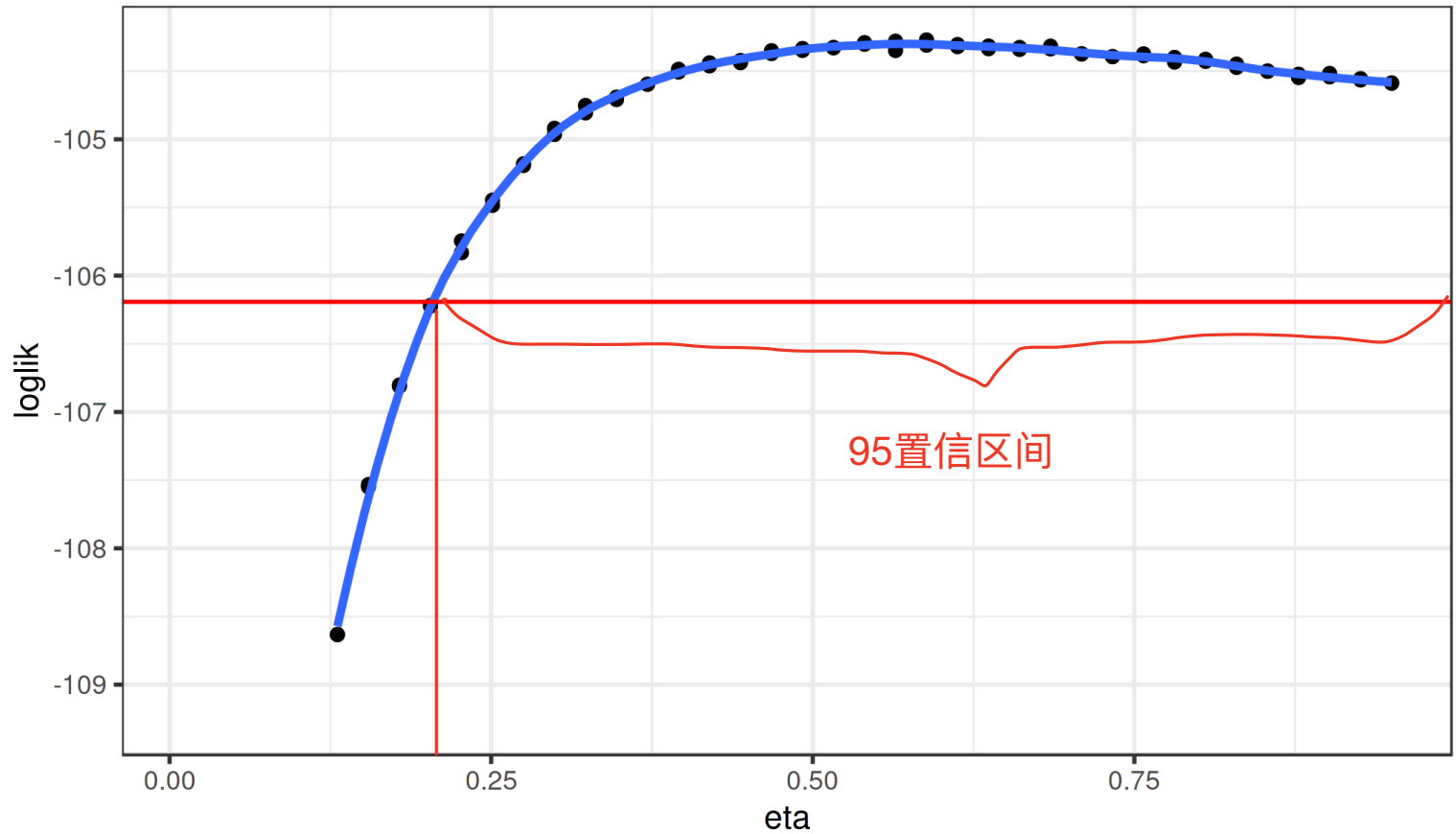
Focusing on just the top of the surface shows that, in fact, one is able to estimate η using these data. In the following plot, the cutoff for the 95% confidence interval (CI) is shown.

Visualizing profile likelihood VIII

```
maxloglik <- max(results$loglik, na.rm=TRUE)
ci.cutoff <- maxloglik - 0.5 * qchisq(df=1, p=0.95)

results %>%
  filter(is.finite(loglik)) %>%
  group_by(round(eta, 5)) %>%
  filter(rank(-loglik) < 3) %>%
  ungroup() %>%
  ggplot(aes(x=eta, y=loglik)) +
  geom_point() +
  geom_smooth(method="loess", span=0.25) +
  geom_hline(color="red", yintercept=ci.cutoff) +
  lims(y=maxloglik - c(5, 0))
```

Visualizing profile likelihood IX



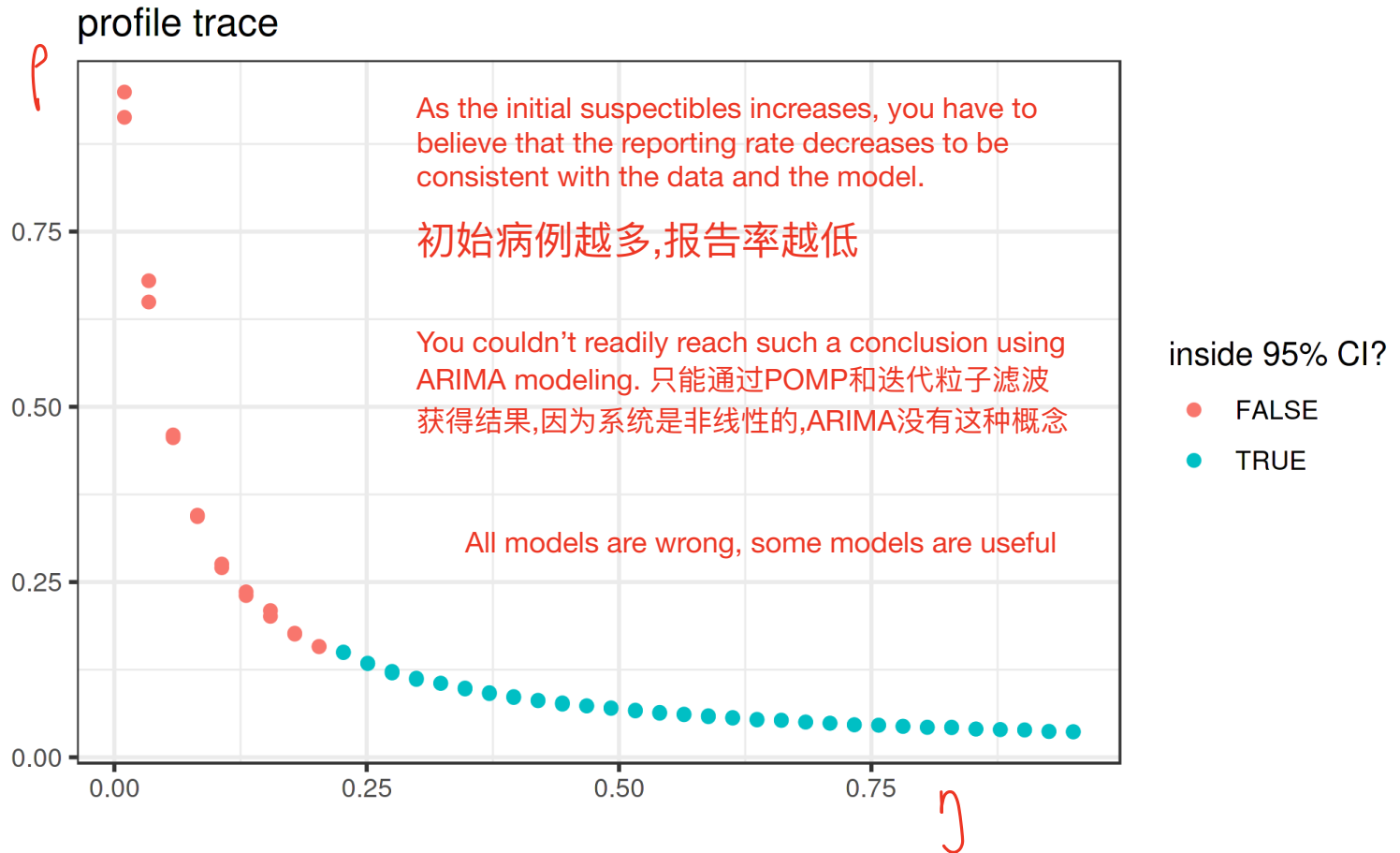
Visualizing profile likelihood X

- As one varies η across the profile, the model compensates by adjusting the other parameters.
- It can be very instructive to understand how the model does this.
- For example, how does the reporting efficiency, ρ , change as η is varied?
- We can plot ρ vs η across the profile.
- This is called a profile trace.

Visualizing profile likelihood XI

```
results %>%
  filter(is.finite(loglik)) %>%
  group_by(round(eta,5)) %>%
  filter(rank(-loglik)<3) %>%   We looked at just the most successful 2 maxi
                                action for each value of eta
  ungroup() %>%
  mutate(in_ci=loglik>max(loglik)-1.92) %>%
  ggplot(aes(x=eta,y=rho,color=in_ci))+
  geom_point()+
  labs(
    color="inside 95% CI?",
    x=expression(eta),
    y=expression(rho),
    title="profile trace"
  )
```

Visualizing profile likelihood XII



Profile over ρ

While the above profile trace is suggestive that the 95% CI for ρ must be between roughly 3% and 20%, to confirm this, we should construct a proper profile likelihood over ρ . We do so now.

This time, we will initialize the IF2 computations at points we have already established have high likelihoods.

```
read_csv("measles_params.csv") %>%  
  group_by(cut=round(rho,2)) %>%  
  filter(rank(-loglik)<=10) %>%  
  ungroup() %>%  
  arrange(-loglik) %>%  
  select(-cut,-loglik,-loglik.se) -> guesses
```

从之前的结果创建guesses
提高search效率,但可能陷入local minimum

Profile over ρ II

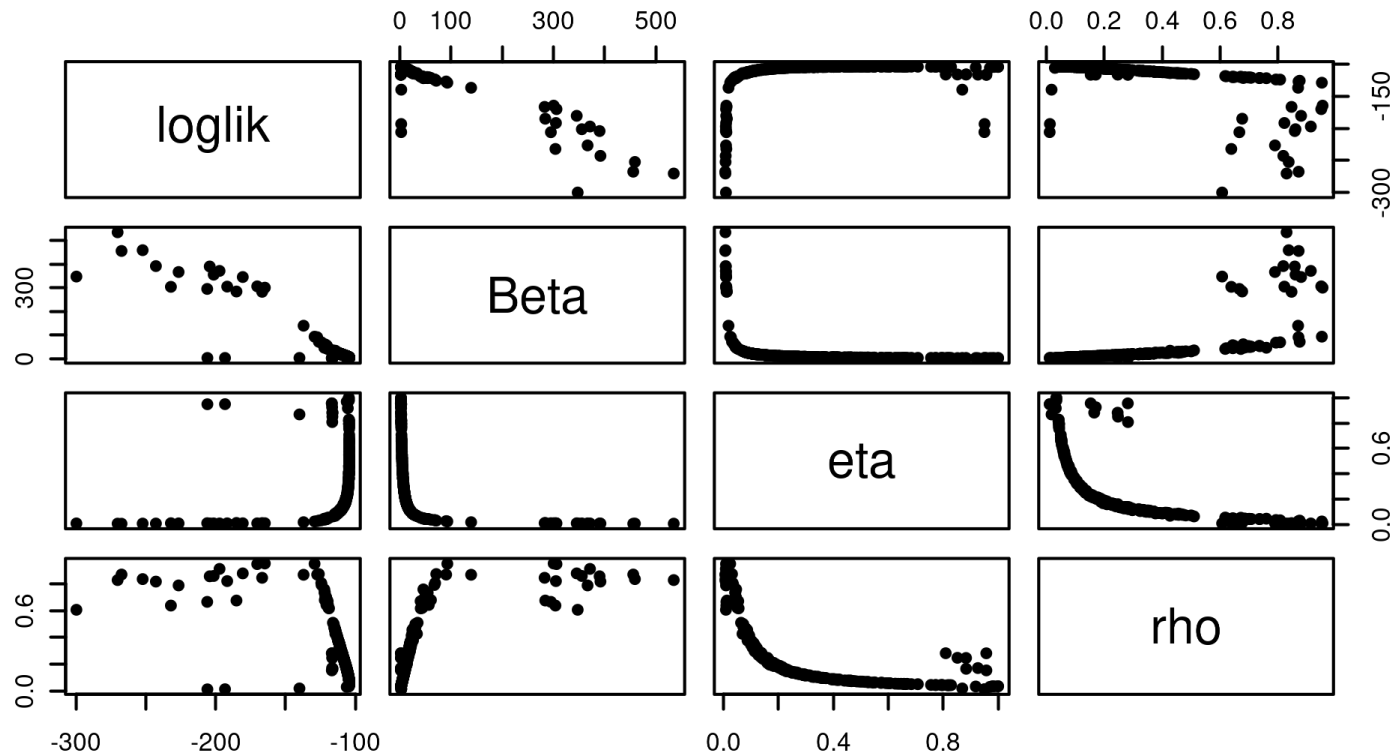
```
foreach(guess=iter(guesses,"row"), .combine=rbind) %dopar% {  
  library(pomp)  
  library(tidyverse)  
  mf1 %>%  
    mif2(params=guess,  
        rw.sd=rw.sd(Beta=0.02, eta=ivp(0.02))) %>%  
    mif2(Nmif=100, cooling.fraction.50=0.3) %>%  
    mif2() -> mf  
  replicate(  
    10,  
    mf %>% pfilter(Np=5000) %>% logLik()) %>%  
    logmeanexp(se=TRUE) -> ll  
  mf %>% coef() %>% bind_rows() %>%  
    bind_cols(loglik=ll[1], loglik.se=ll[2])  
} -> results
```

Profile over ρ : results

```
results %>%  
  filter(is.finite(loglik)) -> results  
  
pairs(~loglik+Beta+eta+rho,data=results,pch=16)
```


Profile over ρ : results II

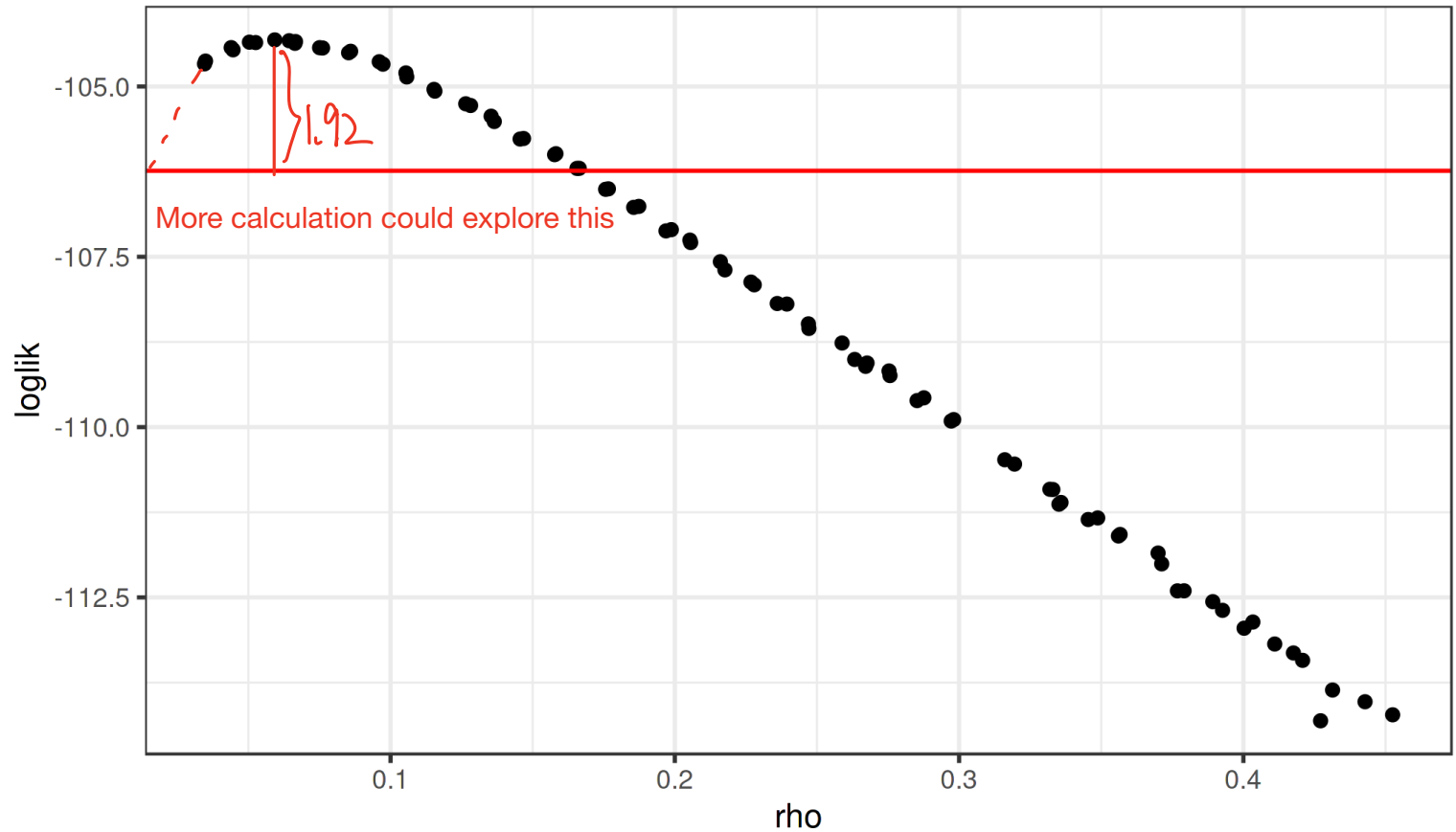
The best fits is in low reporting rate



Profile over ρ : results III

```
results %>%  
  filter(loglik>max(loglik)-10, loglik.se<1) %>%  
  group_by(round(rho,2)) %>%  
  filter(rank(-loglik)<3) %>%  
  ungroup() %>%  
  ggplot(aes(x=rho, y=loglik))+  
  geom_point()+  
  geom_hline(  
    color="red",  
    yintercept=max(results$loglik)-0.5*qchisq(df=1, p=0.95)  
  )
```

Profile over ρ : results IV



Profile over ρ : results V

```
results %>%  
  filter(loglik>max(loglik)-0.5*qchisq(df=1,p=0.95)) %>%  
  summarize(min=min(rho),max=max(rho)) -> rho_ci
```

The data appear to be consistent with reporting efficiencies in the 3–17% range (95% CI).

Outline

- 1 Introduction
- 2 Classification of statistical methods for POMP models
- 3 Iterated filtering in theory
- 4 Iterated filtering in practice
- 5 Searching for the MLE
- 6 The investigation continues. . . .**
- 7 Exercises

Parameter estimates as model predictions

参数估计是预测的一种

- The estimated parameters are one kind of model prediction.
- When we can estimate parameters using other data, we can test these predictions.
- In the case of a highly contagious, immunizing childhood infection such as measles, we can obtain an estimate of the reporting efficiency, ρ by simply regressing cumulative cases on cumulative births (Anderson and May, 1991) over many years.
- When we do this for Consett, we see that the reporting efficiency is roughly 60%.

Parameter estimates as model predictions II

- Since such a value makes the outbreak data quite unlikely, the prediction does not appear to be borne out.
- We can conclude that one or more of our model assumptions is inconsistent with the data.
- Let's revisit our assumption that the infectious period is known to be 0.5 wk.
- Indeed, it would not be surprising were we to find that the effective infectious period, at the population scale, were somewhat shorter than the *clinical* infectious period.

有效传染时间只有治疗时间的一半

Parameter estimates as model predictions III

- For example, confinement of patients should reduce contact rates, and might therefore curtail the effective infectious period.
- To investigate this, we'll relax our assumption about the value of μ_{IR} .

Another global search

We will estimate the model under the assumption that $\rho = 0.6$, but without making assumptions about the duration of the infectious period. As before, we'll construct a random design of starting parameters.

```
freeze(seed=55266255,  
  runif_design(  
    lower=c(Beta=5,mu_IR=0.2,eta=0),  
    upper=c(Beta=80,mu_IR=5,eta=0.99),  
    nseq=1000  
  )) %>%  
  mutate(  
    rho=0.6,  
    k=10,  
    N=38000  
  ) -> guesses
```

rho固定,对mu_IR进行估计

Another global search II

- For each of these starting points, we'll run a series of IF2 computations.
- Since we have gained some experience applying `mif2` to this model and these data, we have some expectation about how much computation is required.
- In the following, we'll use a lot more computational power than we have so far.

Another global search III

For each of the starting points, we'll first perform 100 IF2 iterations:

```
library(pomp)
library(tidyverse)
measSIR %>%
  mif2(params=guess, Np=2000, Nmif=100,
        cooling.fraction.50=0.5,
        partrans=parameter_trans(
          log=c("Beta", "mu_IR"),
          logit="eta"), paramnames=c("Beta", "mu_IR", "eta"),
        rw.sd=rw.sd(Beta=0.02, mu_IR=0.02, eta=ivp(0.02))) -> mf
```

We use random perturbations of the same magnitude as before, taking care to transform the parameters we are estimating.

Another global search IV

We adopt a simulated tempering approach (following a metallurgical analogy), in which we increase the size of the random perturbations some amount (i.e., “reheat”), and then continue cooling.

```
mf %>%  
  mif2(  
    Nmif=100, rw.sd=rw.sd(Beta=0.01, mu_IR=0.01, eta=ivp(0.01))  
  ) %>%  
  mif2(  
    Nmif=100,  
    rw.sd=rw.sd(Beta=0.005, mu_IR=0.005, eta=ivp(0.005))  
  ) -> mf
```

From previous slides, cooling function $.50=0.5$

end random walk standard deviation here is $0.01 * 0.5^2 = 0.0025$

here, we warm up to 0.005 and then cool to $0.005 * 0.5^2 = 0.00125$

Another global search V

We wrap the above in a `foreach` loop as before and take care to evaluate the likelihood at each end-point using `pfilter`.

See the [R code for this lesson](#) to see exactly how this is done.

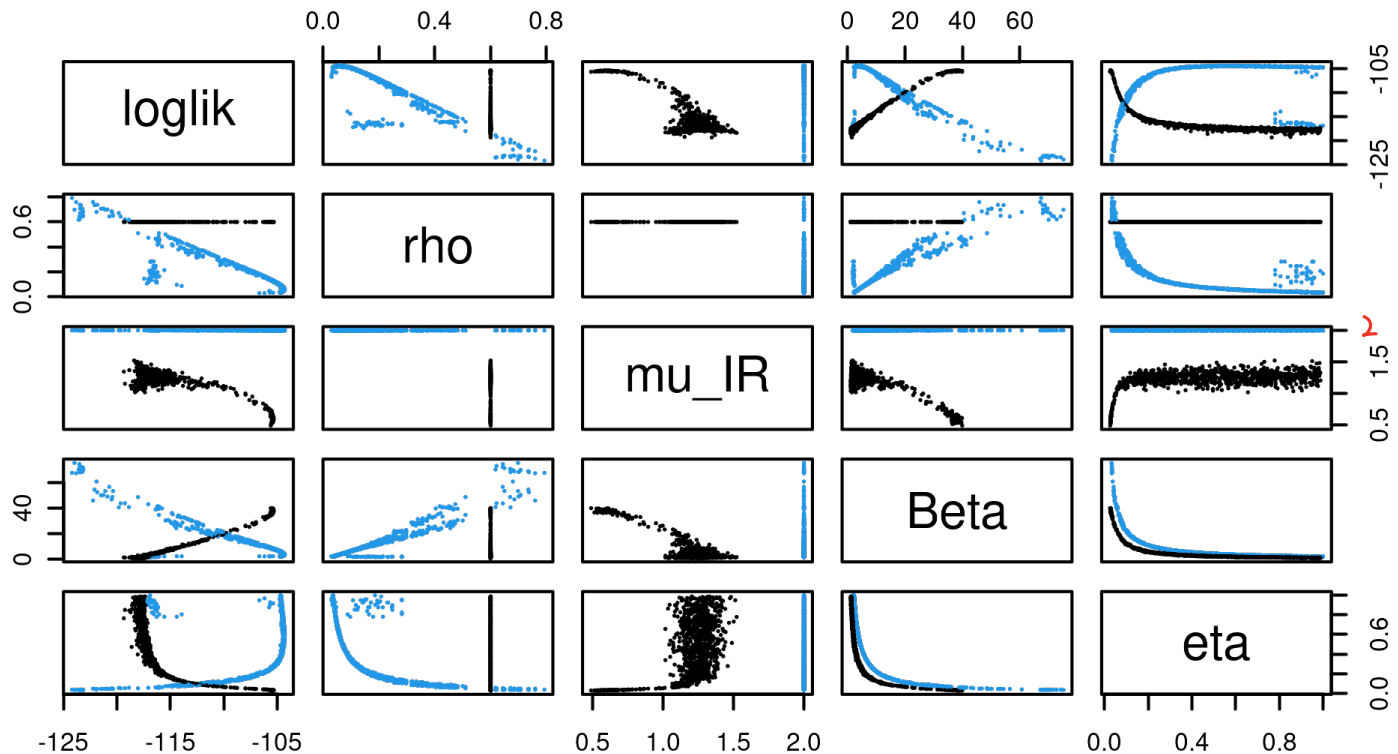
The computations above required 6.3 minutes on 250 processors.

```
read_csv("measles_params.csv") %>%  
  filter(loglik>max(loglik)-20) -> all  
  
pairs(~loglik+rho+mu_IR+Beta+eta,data=all,pch=16,cex=0.3,  
      col=if_else(round(all$rho,3)==0.6,1,4))
```

Another global search VI

蓝色的的是以前的结果,黑色的点是新计算结果

The different assumptions (fixing μ_{IR} or ρ) have various other consequences for what we infer



Do the data tell us which set of assumptions is better?

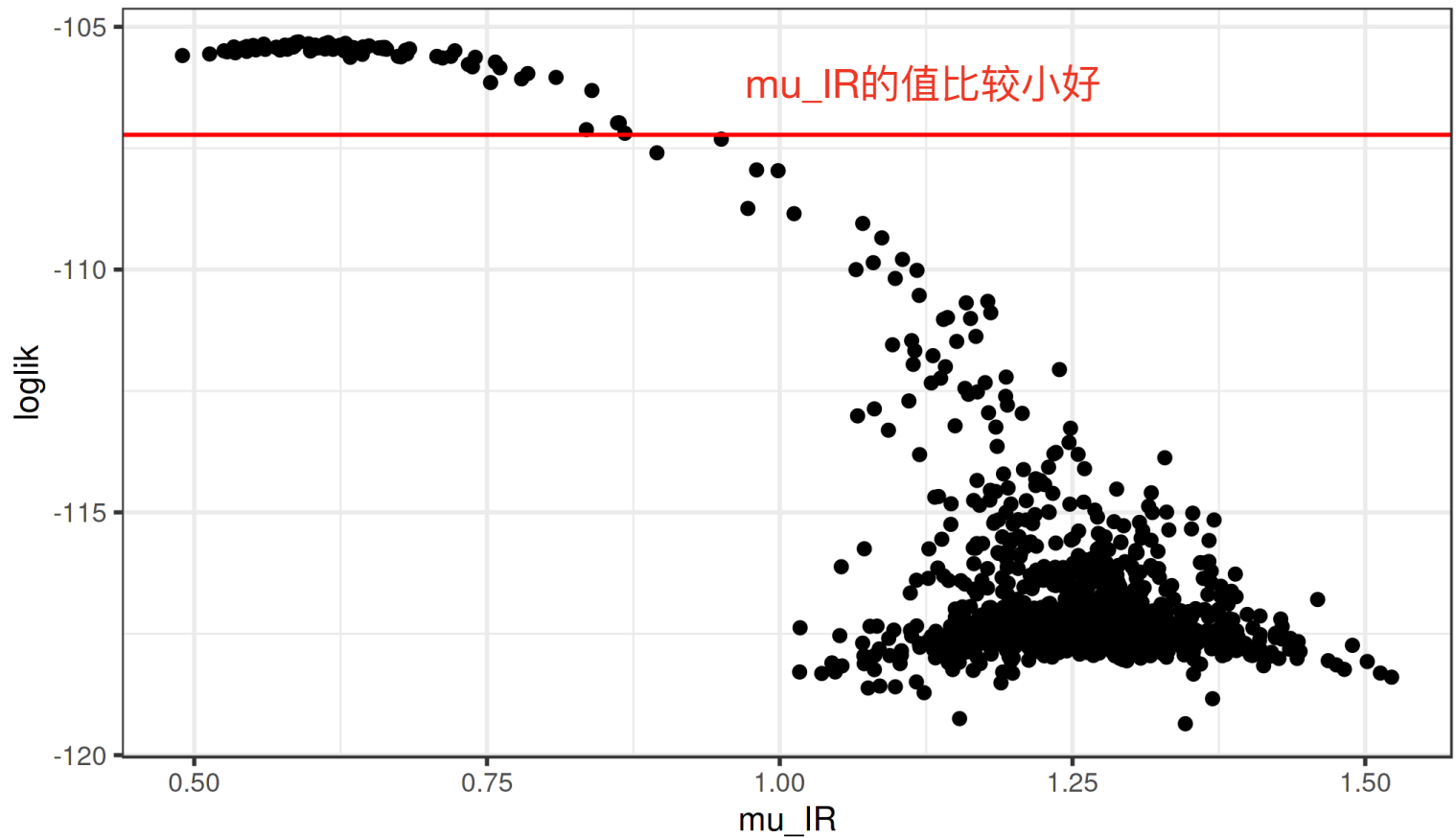
Hypotheses are not nested (we could embed them both in a bigger model) so we can't use LRT.

But we can still use AIC (The doc if same in our case, so we only consider log likelihood). The difference is very small, so there is no strong evidence so supremacy.

Another global search VII

```
results %>%  
  filter(loglik>max(loglik)-20,loglik.se<1) %>%  
  ggplot(aes(x=mu_IR,y=loglik))+  
  geom_point()+  
  geom_hline(  
    color="red",  
    yintercept=max(results$loglik)-0.5*qchisq(df=1,p=0.95)  
  )
```

Another global search VIII



Profile over infectious period

To make inferences about μ_{IR} , we can again compute a profile likelihood. As before, we bound the region we will search:

```
read_csv("measles_params.csv") %>%  
  filter(  
    loglik > max(loglik) - 20,  
    loglik.se < 2,  
    abs(rho - 0.6) < 0.01  
  ) %>%  
  apply(range) -> box
```

Profile over infectious period II

```
freeze(seed=610408798,  
  profile_design(  
    mu_IR=seq(0.2,2,by=0.1),  
    lower=box[1,c("Beta","eta")],  
    upper=box[2,c("Beta","eta")],  
    nprof=100, type="runif"  
  )) %>%  
  mutate(  
    N=38000,  
    rho=0.6,  
    k=10  
  ) -> guesses
```

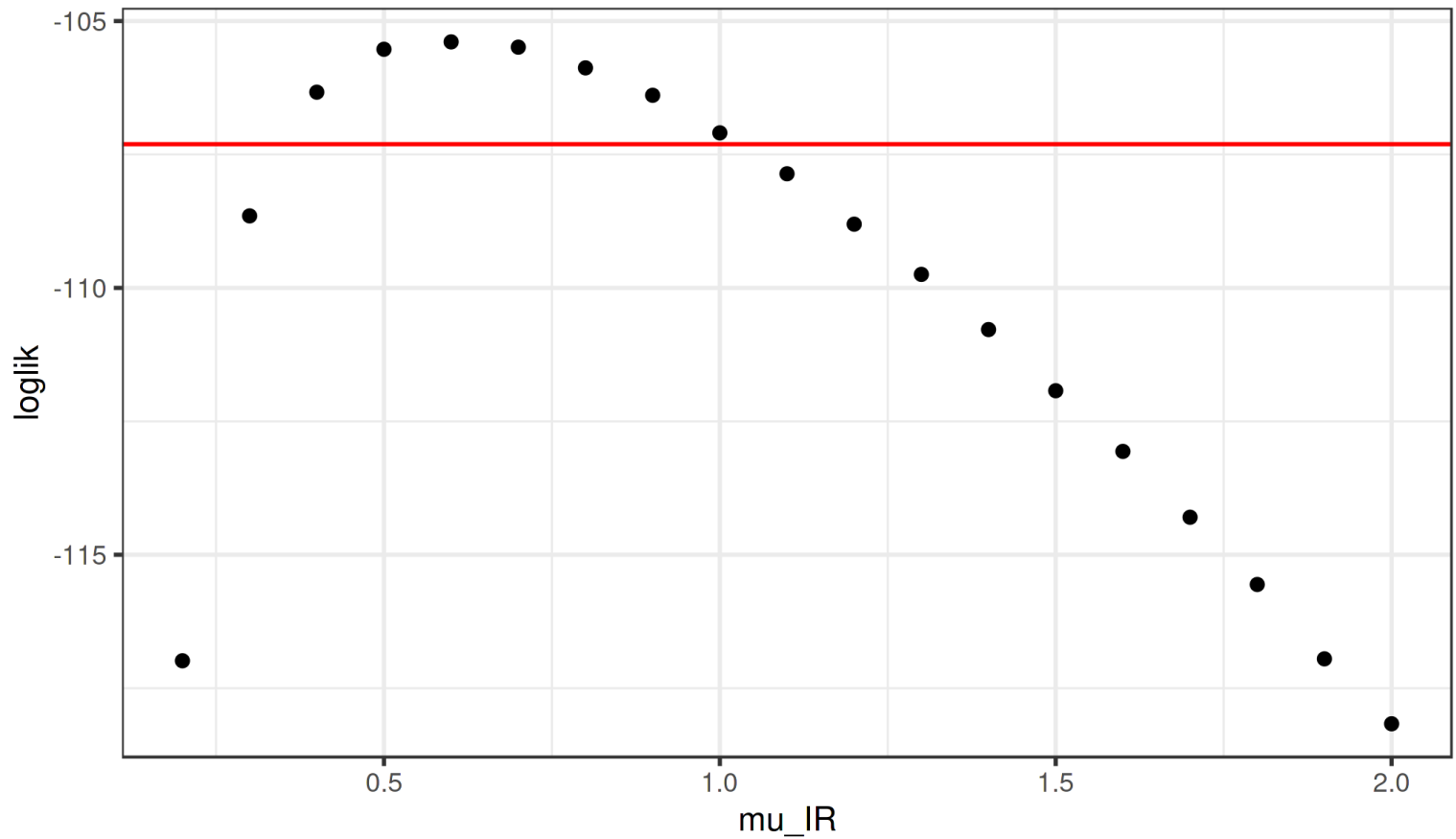
Profile over infectious period III

```
foreach(guess=iter(guesses,"row"), .combine=rbind) %dopar% {  
  library(pomp)  
  library(tidyverse)  
  measSIR %>%  
    mif2(params=guess, Np=2000, Nmif=100,  
        partrans=parameter_trans(log="Beta",logit="eta"),  
        paramnames=c("Beta","eta"), cooling.fraction.50=0.5,  
        rw.sd=rw.sd(Beta=0.02,eta=ivp(0.02))  
    ) %>% mif2(Nmif=100) %>% reheat  
    mif2(Nmif=100,rw.sd=rw.sd(Beta=0.01,eta=ivp(0.01))) %>%  
    mif2(Nmif=100,rw.sd=rw.sd(Beta=0.005,eta=ivp(0.005))) -> mf  
  replicate(10,mf %>% pfilter(Np=5000) %>% logLik()) %>%  
    logmeanexp(se=TRUE) -> ll  
  mf %>% coef() %>% bind_rows() %>%  
    bind_cols(loglik=ll[1],loglik.se=ll[2])  
} -> results
```

Infectious period profile

```
results %>%  
  group_by(round(mu_IR,2)) %>%  
  filter(rank(-loglik)<=1) %>%  
  ungroup() %>%  
  ggplot(aes(x=mu_IR,y=loglik))+  
  geom_point()+  
  geom_hline(  
    color="red",  
    yintercept=max(results$loglik)-0.5*qchisq(df=1,p=0.95)  
  )
```

Infectious period profile II



Infectious period profile III

- This suggests that $\rho = 0.6$ is consistent only with smaller values of μ_{IR} , and hence *longer* infectious periods than are possible if the duration of shedding is actually less than one week.
- Thus the model is incapable of reconciling both an infectious period of less than one week and a reporting rate of 60%.
当infectious小,report rate大于60的时候,模型不能很好拟合数据
- *What structural changes to the model might we make to improve its ability to explain the data?*

We need to improve the model
(add latent period)

We could fix both μ and ρ to biologically plausible values. If the data don't agree that both values can be simultaneously plausible for this model, this forces us into model misspecification.

We would have to be very careful of this if doing a Bayesian analysis. We might have inappropriate priors.

We may add a latent class (E) to fix this problem better

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Exercise 4.1. Fitting the SEIR model

Following the template above, estimate the parameters and likelihood of the SEIR model you implemented in the earlier lessons. Specifically:

- (a) First conduct a local search and then a global search using the multi-stage, multi-start method displayed above.
- (b) How does the maximized likelihood compare with what we obtained for the SIR model?
- (c) How do the parameter estimates differ?

You will need to tailor the intensity of your search to the computational resources at your disposal. In particular, choose the number of starts, number of particles employed, and the number of IF2 iterations to perform in view of the size and speed of your machine.

[Worked solution to the Exercise](#)

Exercise 4.2. Fitting all parameters

In all of the foregoing, we have assumed a fixed value of the dispersion parameter k , of the negative binomial measurement model. We've also fixed one or the other of μ_{IR} , η . Now attempt to estimate all the parameters simultaneously. How much is the fit improved?

Worked solution to the Exercise

Exercise 4.3. Construct a profile likelihood

How strong is the evidence about the contact rate, β , given this model and data? Use `mif2` to construct a profile likelihood. Due to time constraints, you may be able to compute only a preliminary version. It is also possible to profile over the basic reproduction number, $R_0 = \beta/\mu_{IR}$. Is this more or less well determined than β for this model and data?

Exercise 4.4. Checking the source code

Check the source code for the `measSIR` pomp object, using the `spy` command. Does the code implement the model described?

Exercise 4.4. Checking the source code II

For various reasons, it can be surprisingly hard to make sure that the written equations and the code are perfectly matched. Papers should be written to be readable, and therefore people rarely choose to clutter papers with numerical details which they hope and believe are scientifically irrelevant.

- (a) What problems can arise due to the conflict between readability and reproducibility?
- (b) What solutions are available?

Exercise 4.4. Checking the source code III

Suppose that there is an error in the coding of `rprocess` and suppose that plug-and-play statistical methodology is used to infer parameters. As a conscientious researcher, you carry out a simulation study to check the soundness of your inference methodology on this model. To do this, you use `simulate` to generate realizations from the fitted model and checking that your parameter inference procedure recovers the known parameters, up to some statistical error.

- (a) Will this procedure help to identify the error in `rprocess`?
- (b) If not, how might you debug `rprocess`?
- (c) What research practices help minimize the risk of errors in simulation code?

Worked solution to the Exercise

Exercise 4.5: Choosing the algorithmic settings for IF2

Have a look at [our advice on tuning IF2](#).

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References II

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References III

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- Produced with R version 4.1.1 and **pomp** version 4.0.11.0.
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[R code for this lesson](#)