

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 for POMP models are in 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.

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.

Full-information and feature-based methods II

- However:
 - 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.

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

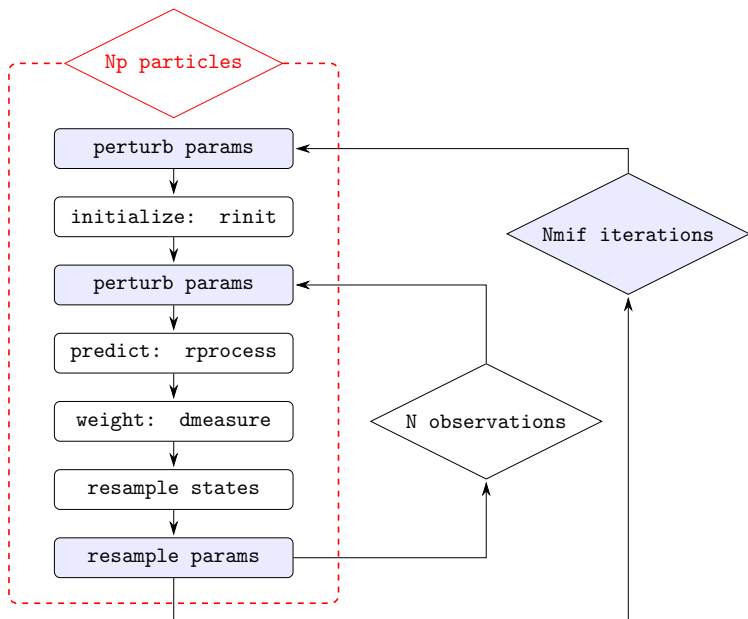
- Iterated filtering methods (Ionides *et al.*, 2006, 2015) are the only currently available, full-information, plug-and-play, frequentist methods for POMP models.
- Iterated filtering methods have been shown to solve likelihood-based inference problems for epidemiological situations which are computationally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

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.



IF2 algorithm pseudocode

filter inputs.

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 and corresponding mif2 arguments:

- number of iterations, $N_{\text{mif}} = M$
- number of particles, $N_p = J$
- initial parameter swarm, $\text{params} = \{\Theta_j^0, j = 1, \dots, J\}$
- random walk standard deviation for each parameter, rw.sd , squared to construct a diagonal variance matrix, V_n
- cooling fraction in 50 iterations, $\text{cooling.fraction.50} = a$

Output:

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

smaller perturbations are called "cooler" by analogy with physics, and optimization by "simulated annealing"

IF2 algorithm, pseudocode II

steps for filter

Procedure:

1 For m in 1: M 2 $\Theta_{0,j}^{F,m} \sim \text{Normal}(\Theta_j^{m-1}, V_0 a^{2m/50})$ for j in 1: J 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 $\Theta_{n,j}^{P,m} \sim \text{Normal}(\Theta_{n-1,j}^{F,m}, V_n a^{2m/50})$ for j in 1: J 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 8 Draw $k_{1:J}$ with $P[k_j = i] = w_{n,i}^m / \sum_{u=1}^J w_{n,u}^m$ 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

extension of
filter to
mif2
(maximization by filtering)
iterated← rinit
prediction:

r process

prediction
particlesfiltering:
d measurefilter particles
corresponding filter
parameter values.

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*.
- 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

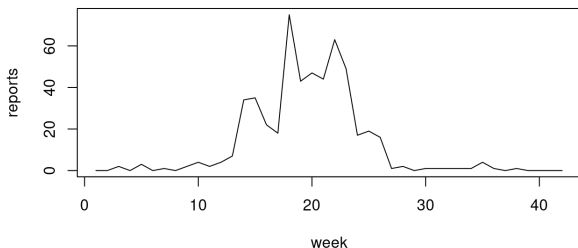
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Applying IF2 to the Consett measles outbreak

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, **pomp**, and the stochastic SIR model we constructed there.

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



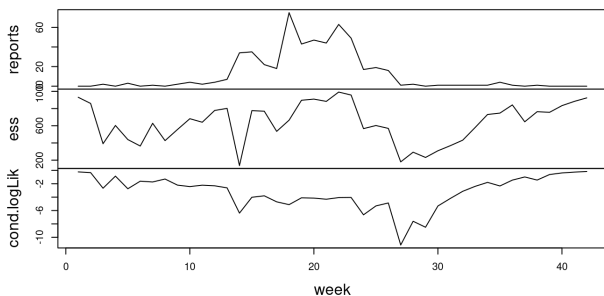
Testing the codes: filtering

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
```

```
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.

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
```

We proceed to estimate β , η , and ρ .

Parallel computing

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

```
library(foreach)
library(doFuture)
plan(multisession)
```

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,  
  .options.future=list(seed=TRUE)  
) %dofuture% {  
  measSIR |> pfilter(Np=5000)  
} -> pf  
  
pf |> logLik() |> logmeanexp(se=TRUE) -> L_pf  
L_pf
```

est	se
-284.606363	6.027021

In 5.33 seconds, using 10 cores, we obtain an unbiased likelihood estimate of -284.6 with a Monte Carlo standard error of 6.

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.

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.
- 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.
- 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.

A local search of the likelihood surface II

```

foreach(i=1:20,.combine=c,
  .options.future=list(seed=482947940)
) %dofuture% {
  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")
    )
} -> mifs_local

```

needed because
 pomp will have to
 compile the parameter
 transformations.

tells mif2 to operate on a log scale for Beta, which
 is in \mathbb{R}^+ , and logit scale for $[0,1]$ valued parameters.

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.

- This document describes the problem and the workaround.
- A Windows-safe version of the code for this document is available here.

for windows, don't compile within a parallel loop.

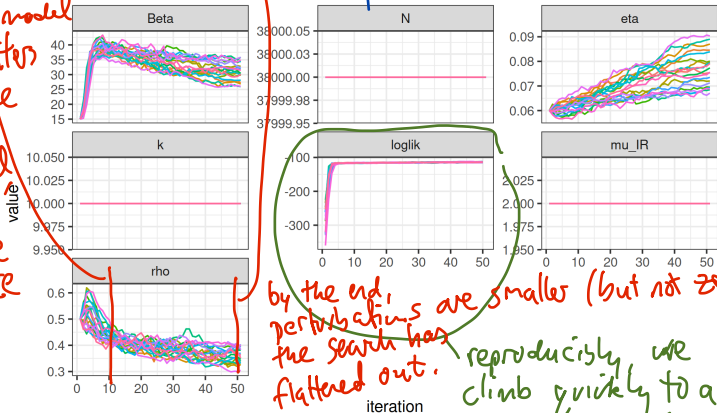
Iterated filtering diagnostics

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(~name,scales="free_y")
```

Iterated filtering diagnostics II

here we have a perturbed model which differs from the target model also incomplete convergence



spread here must be weakly identifiable not poor maximization - because of the loglik plot showing success.

by the end, perturbations are smaller (but not zero) and flattened out. reproducibly, we climb quickly to a neighborhood with similar loglik values - presumably, close to a local maximum.

it might be interesting to zoom into the loglik plot on a scale closer to the maximum.

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,
  .options.future=list(seed=900242057)
) %dofuture% {
  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
```

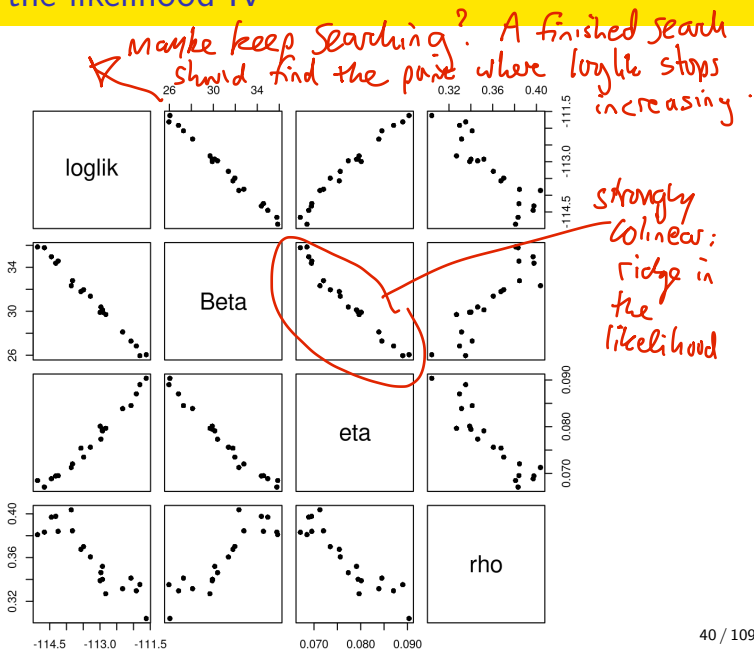
On 24 processors, this local investigation took 18 sec for the maximization and 7 sec for the likelihood evaluation.

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

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

A global search of the likelihood surface III

```

foreach(guess=iter(guesses,"row"), .combine=rbind,
  .options.future=list(seed=1270401374)
) %dofuture% {
  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

```

this mifd.pomp class object provides the algorithmic parameters for mif2, which we have already specified.

two searches

likelihood re-evaluation at the Candidate MLE.

this does one search with Nmif=50, inherited from mf1

this does a second stage of searching, re-starting from the value found in the first stage, and using Nmif=100,

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.

This multi-start, multi-stage search procedure has been found to be effective in practice.

A global search of the likelihood surface V

- 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 0.03.
- This took 6.5 minutes altogether using 250 processors.

the local search saved all the mifd-pomp objects. These can get big, especially as the model, data, and number of particles increases. Every pomp object has a copy of the data, at least. Pfilter & mif2 save everything needed for every diagnostic plot.

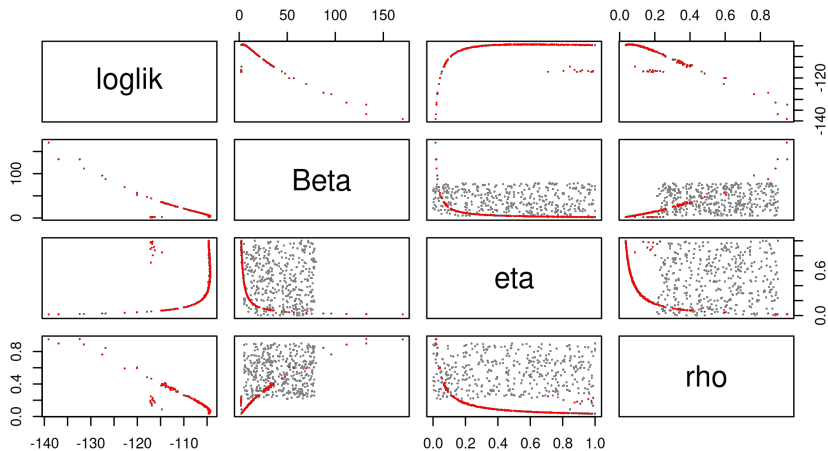
A global search of the likelihood surface VI

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



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.

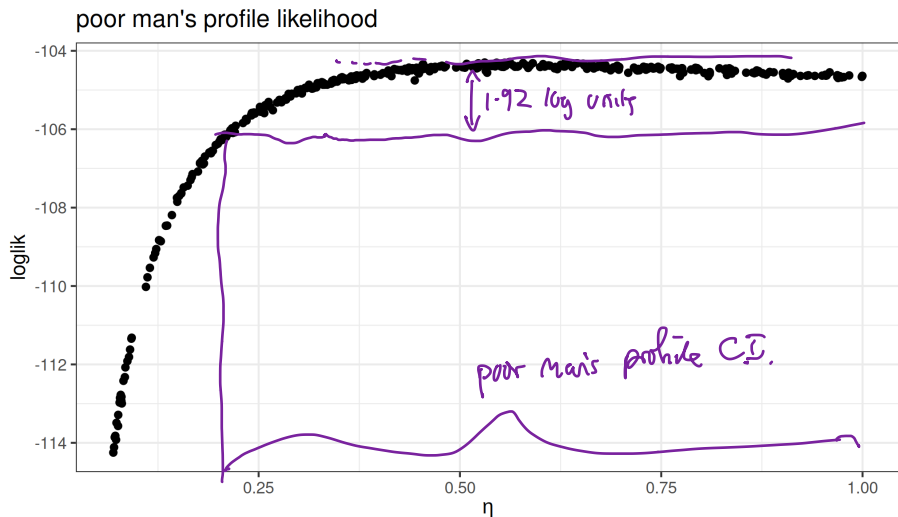
A global search of the likelihood surface IX

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"
  )
```

looking at the
log like in a
neighborhood of the
maximum, often
10 or 20 or 50 log
units from the max.

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 .

usually, practical computation involves using a smaller search box for the profile compared to the global search. The rationale is that the global search already looked for global features of interest.

Profile likelihood over η II

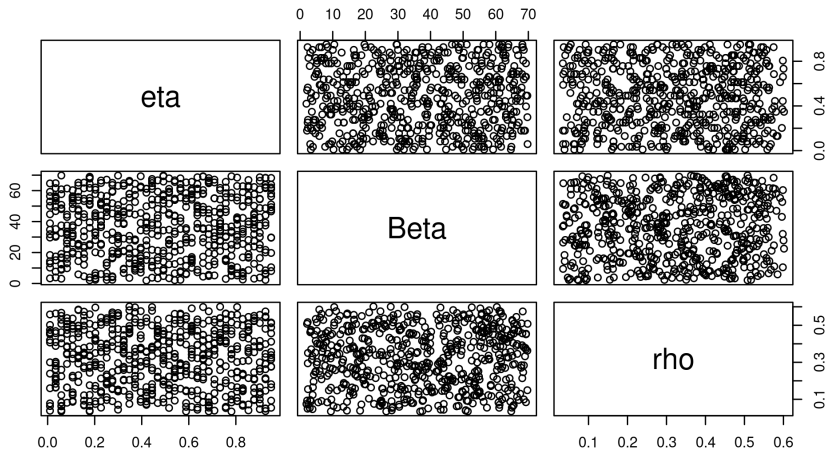
```
read_csv("measles_params.csv") |>
  filter(loglik>max(loglik)-20,loglik.se<2) |>
  sapply(range) -> box
```

```
box
```

	Beta	mu_IR	rho	k	eta	N
[1,]	1.824688	2	0.03405657	10	0.03628984	38000
[2,]	69.791919	2	0.60343428	10	0.99982180	38000
	loglik	loglik.se				
[1,]	-122.7423	0.01462075				
[2,]	-104.2847	0.56960880				

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)
```

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.
- 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,
  .options.future=list(seed=830007657)
) %dofuture% {
  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
```

Visualizing profile likelihood

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

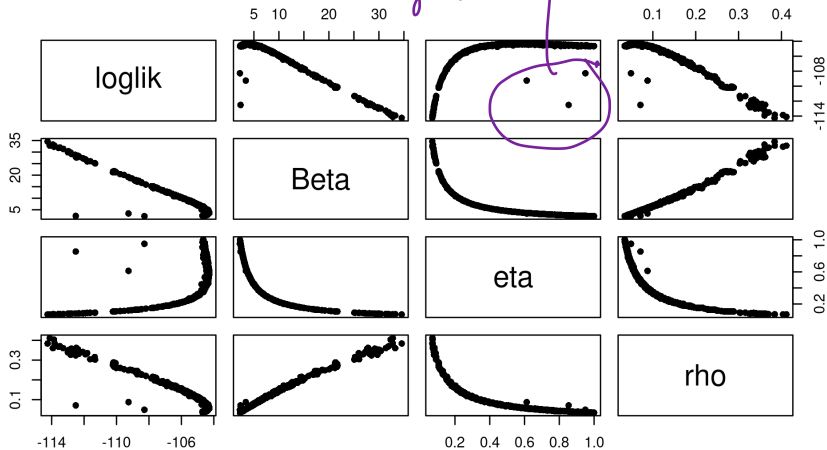
```
read_csv("measles_params.csv") |>
  bind_rows(results) |>
  filter(is.finite(loglik)) |>
  arrange(-loglik) |>
  write_csv("measles_params.csv")
```

```
read_csv("measles_params.csv") |>
  filter(loglik > max(loglik) - 10) -> all

pairs(~loglik + Beta + eta + rho, data = all, pch = 16)
```

Visualizing profile likelihood II

some searches fail to maximize...
 this is a Monte Carlo algorithm.

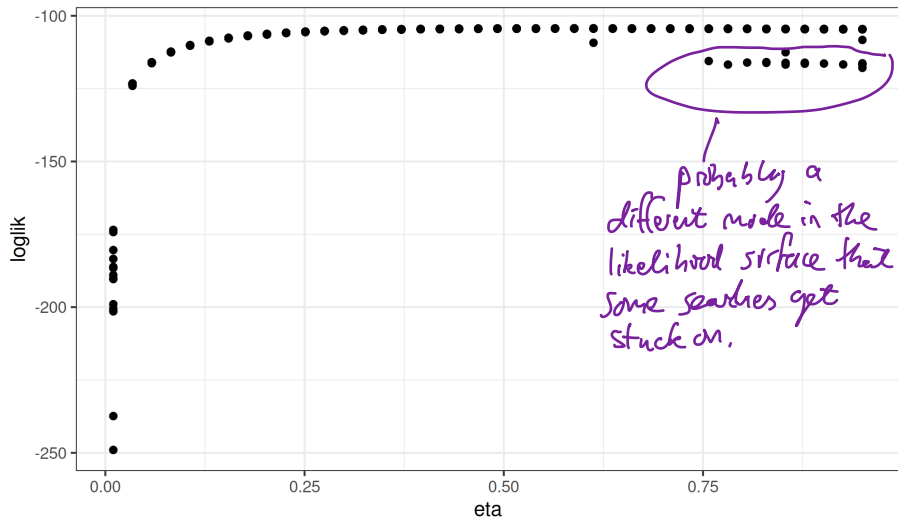


Visualizing profile likelihood III

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

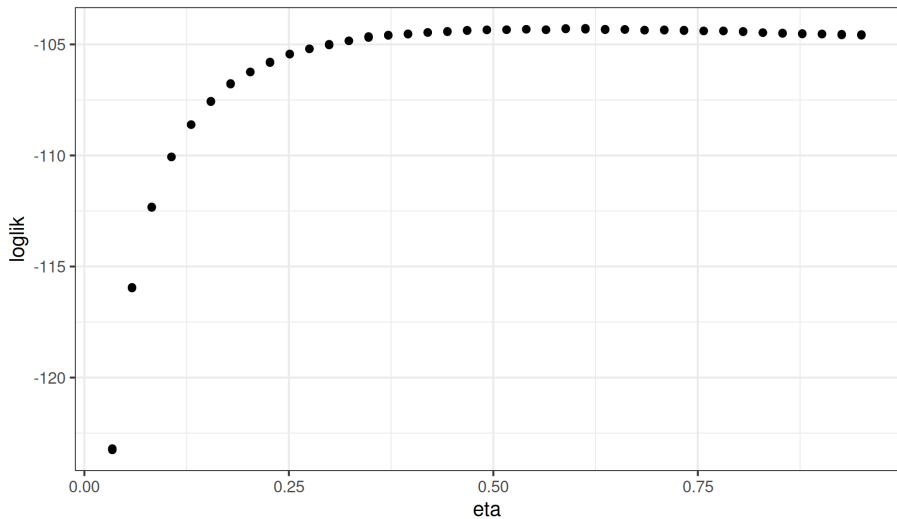


Visualizing profile likelihood V

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

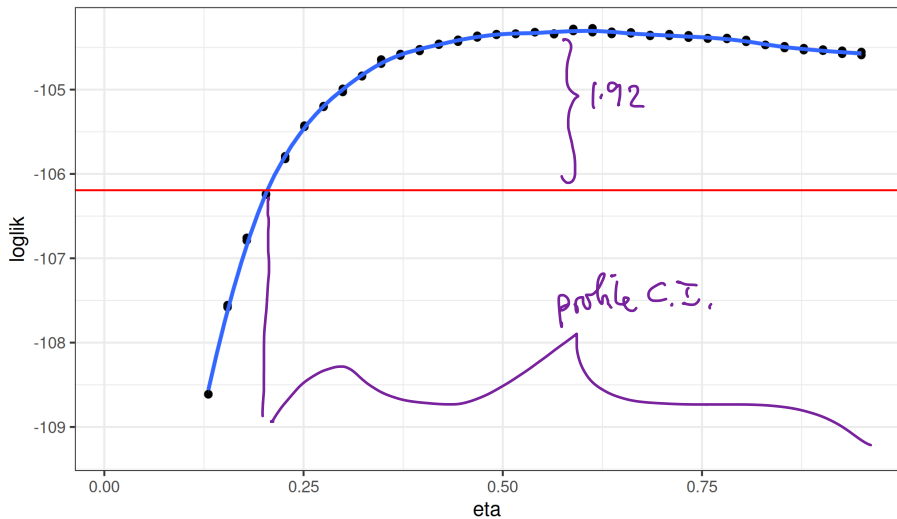
Focusing on just the top of the surface shows that, in fact, one is able to estimate η using these data. In the following plot, the cutoff for the 95% confidence interval (CI) is shown.

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



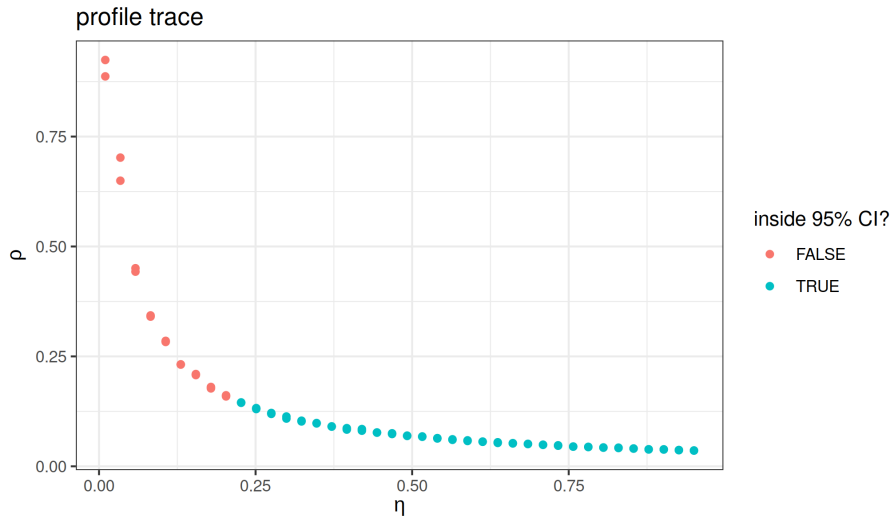
Visualizing profile likelihood X

- 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) |>
  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 4% 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
```

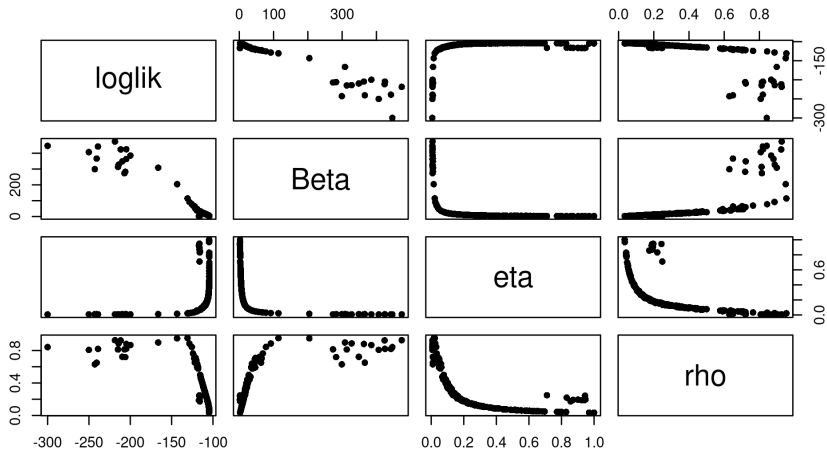
Profile over ρ II

```
foreach(guess=iter(guesses,"row"), .combine=rbind,  
  .options.future=list(seed=2105684752)  
) %dofuture% {  
  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

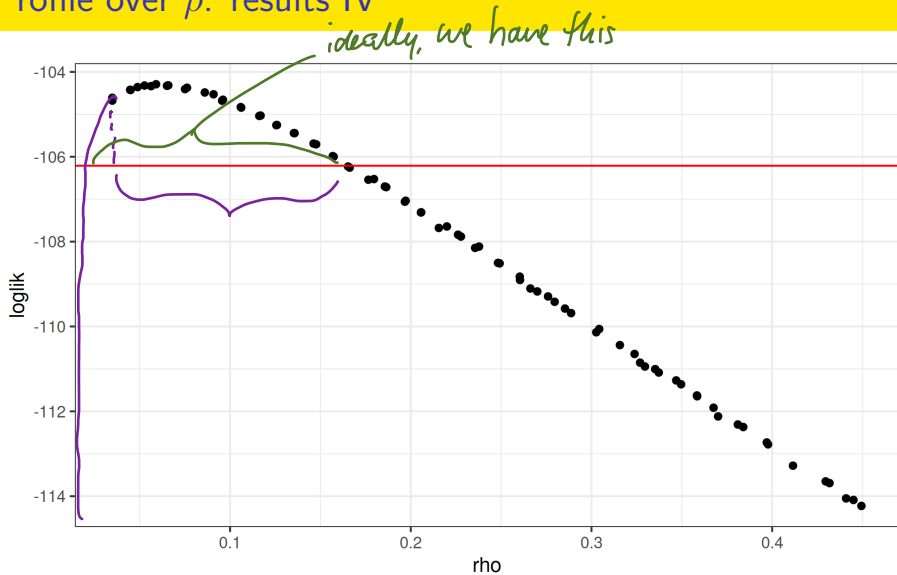
```
results |>
  filter(is.finite(loglik)) -> results

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

Profile over ρ : results II

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 3.4–16% range (95% CI).

Outline

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

Parameter estimates as model predictions

- 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.

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
```

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:

```
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
```

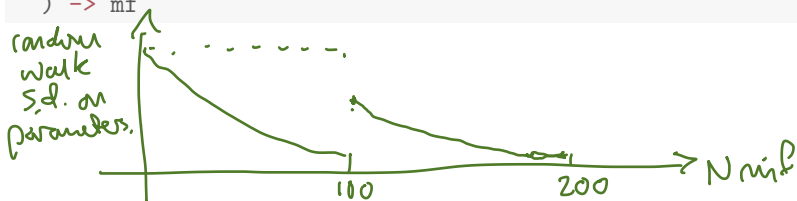
We use random perturbations of the same magnitude as before, taking care to transform the parameters we are estimating.

Another global search IV

heuristic... may or may not work.

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
```



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`.

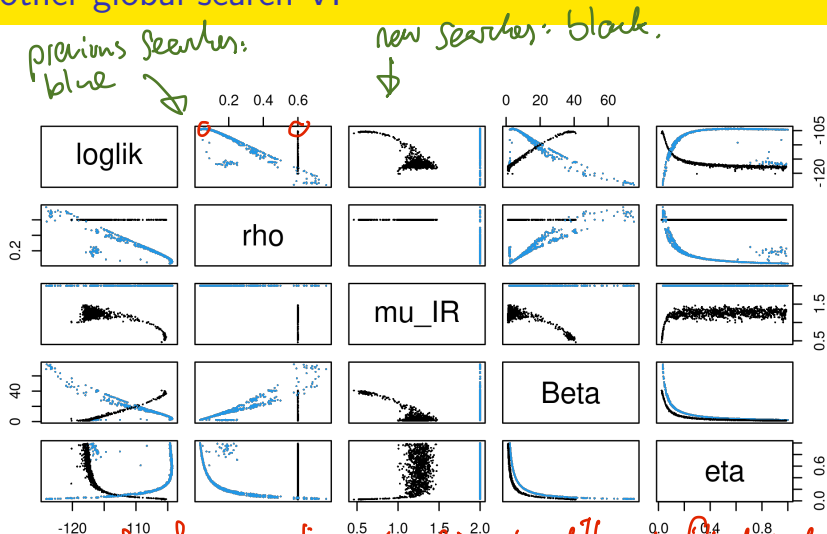
See the [R code for this lesson](#) to see exactly how this is done.

The computations above required 8.7 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

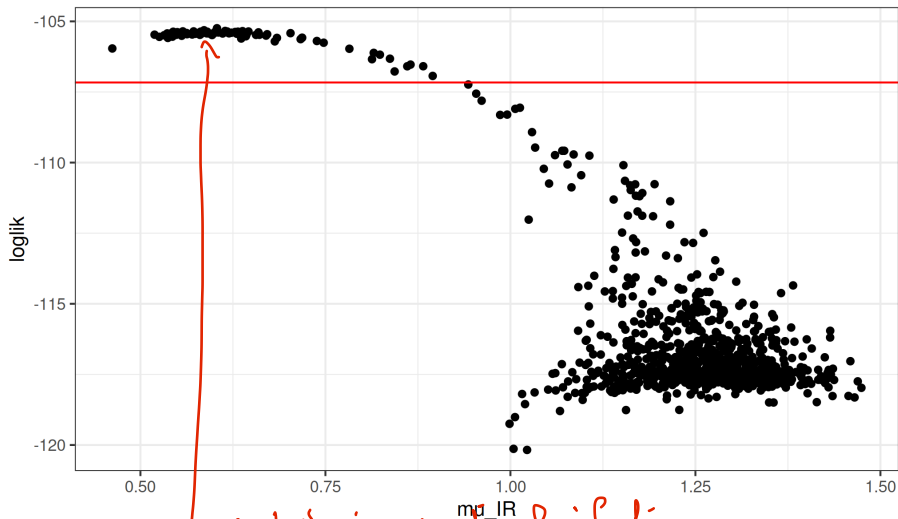


two sets of assumptions, leading to different fitted models but very similar maximized likelihood, differing by < 1 log unit.

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



$\approx 0.6 \text{ wk}^{-1}$, i.e. duration of infection
 $(0.6)^{-1} \text{ wk} \approx 1.67 \text{ wk}$

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
  ) |>
  sapply(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
```

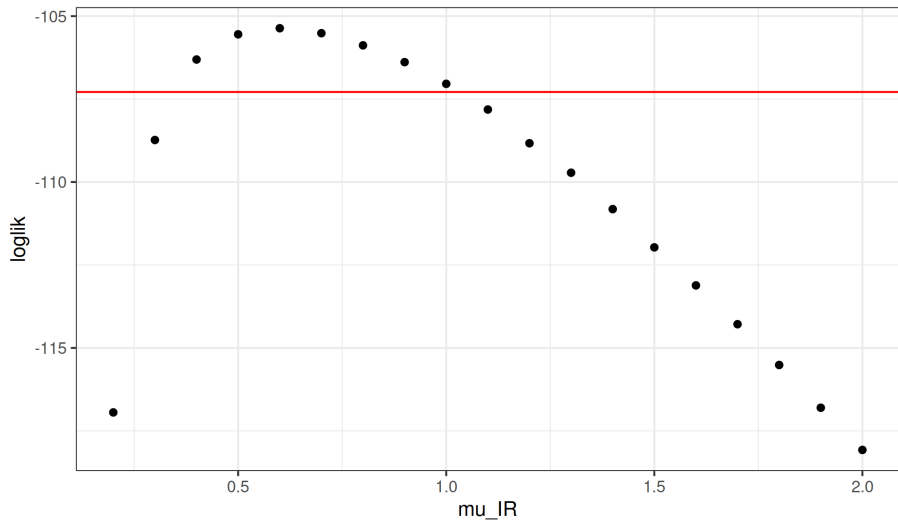
Profile over infectious period III

```
foreach(guess=iter(guesses,"row"), .combine=rbind,
  .options.future=list(seed=610408798)
) %dofuture% {
  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) |>
    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%.
- *What structural changes to the model might we make to improve its ability to explain the data?*

add a latent period...

Outline

- 1 Introduction
- 2 Classification of statistical methods for POMP models
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- 7 Exercises**

Exercise 4.1. Fitting the SEIR model

In this exercise, you will estimate the parameters and likelihood of the SEIR model you implemented in the earlier lessons by following the template above. Purely for the sake of simplicity, you may assume that the values of μ_{IR} and k are known. To do this efficiently, we will make use of a system of *run-levels*. At each run-level, we will select some number of particles (N_p), number of IF2 iterations (N_{mif}), and number of starting guesses, to achieve a particular result.

Exercise 4.1. Fitting the SEIR model II

- (A) First, conduct a local search and compute the likelihood at the end of each `mif2` run, as shown above. Use only as many parallel `mif2` computations as you have processors on your computer (or perhaps somewhat fewer). Track the time used and compute the amount of time used per cpu per IF2 iteration per 1000 particles. (Recall that one particle filter computation is roughly equal to a IF2 iteration in computational complexity if they both use the same number of particles.)

Exercise 4.1. Fitting the SEIR model III

- (B) At run-level 1, we want a quick calculation that verifies that the codes are working as expected. Using the expense estimates you generated in Step (A), choose a number of IF2 iterations so that you can do a very crude “global search” that will complete in two or three minutes. Do not reduce N_p drastically, as we don't want to degrade the performance of the individual IF2 computations. Run your global search with these settings. This serves to debug your global search code.
- (C) At run-level 2, we want a computation that gives us some results we can begin to interpret, but that is still as quick as possible. Choose N_{mif} and the number of random starts so that you can obtain the beginnings of a global search of the parameter space in one hour or less. Run your global search with these settings and plot the results.

Exercise 4.1. Fitting the SEIR model IV

- (D) Run-level 3 is intended for final or near-final results. You may want to tune your settings (`Nmif`, `Np`, `rw.sd`, `cooling.fraction.50`) at this point, based on what you found at run-level 2. Decide how much time in the next 18 hours is available to you for a computation. Choose the number of starting guesses so that you can obtain as thorough a global search as possible within this period. Run your global search and identify a maximum likelihood estimate.
- (E) How does the SEIR model compare with the SIR model? Discuss the overall quality of the fit as well as important differences in how the two models are explaining the data.

[Worked solution to the Exercise](#)

Exercise 4.2. Fitting all parameters of the SIR model

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. To accomplish this, use the same system of run-levels as in the previous Exercise.

How much is the fit improved? How has the model's explanation of the data changed?

[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.

(a) Does the code implement the model described?

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.

(b) What problems can arise due to the conflict between readability and reproducibility?

(b) What solutions are available?

[Worked solution to the Exercise](#)

Exercise 4.5. Beware errors in `rprocess`

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 you check 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 4.6: Choosing the algorithmic settings for IF2

Have a look at [our advice on tuning IF2](#). An exercise at the end of the linked document invites you to test this advice on the Consett measles example.

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References III

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License, acknowledgments, and links

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[R code for this lesson](#)