Workflow part

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Workflow Summary I

1. **Data Preparation and Model Specification**
   - **Data Initialization**: Visualize the initial data to get a sense of the disease outbreak dynamics.
   - **Model Definition**: Implement the defined SIR model in `pomp`
     - Set up a stochastic SIR (Susceptible, Infected, Recovered) model using custom C snippets for state transitions and measurements.
     - Specify the measurement, process, and initialization functions along with model parameters.
2. **Preliminary Analysis**
   - **Simulation and Visualization**: Simulate the SIR model to visualize potential outcomes and compare to data.
   - **Likelihood Estimation**: Evaluate the likelihood and Effective Sample Size of the initial parameter estimates using particle filtering.
3. **Local Optimization**

Workflow Summary II

  - **Iterated Filtering for Local Maximum**: Apply iterated filtering to find a local maximum near the initial guesses.
  - **Diagnostics and Visualization**: Diagnose the iterated filtering process and visualize parameter traces to assess convergence.

4. **Global Optimization**
   - **Set Up for Global Search**: Define a parameter space for global optimization.
   - **Global Search Execution**: Conduct global optimization using multiple starting points to ensure robustness of the findings.
   - **Result Compilation**: Compile and compare results from global searches, focusing on the best parameter estimates.
5. **Profile Likelihood Estimation**
   - **Parameter Profiling**: For each parameter, perform profiling to map the likelihood landscape and establish confidence intervals.
   - **Visualization of Profile Likelihoods**: Visualize the profile likelihoods to understand parameter sensitivity and uncertainty.

Workflow Summary III

6. **Final Model Evaluation**
   - **Model Predictions**: Use the best-fitting parameters to simulate the model outcomes and compare these against observed data.
   - **Visualization of Predictions**: Create visualizations to compare the model predictions with actual data, highlighting the prediction intervals.
7. **Documentation and Storage**
   - **Record-Keeping**: All intermediate and final results should be stored in CSV files for further analysis or reproducibility of the study.

Example: measles I

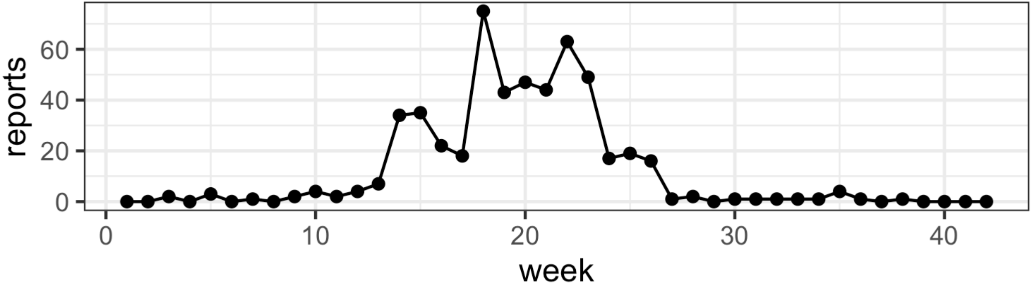
Data initialization I

```
library(tidyverse)
read_csv("https://kingaa.github.io/sbied/pfilter/Measles_Consett_1948.csv")
  select(week,reports=cases) |>
  filter(week<=42) -> meas
meas |> as.data.frame() |> head(n=3)
```

```
 week reports
    1       0
    2       0
    3       2
```

Data initialization II

```
meas |>
  ggplot(aes(x=week,y=reports)) +
  geom_line() +
  geom_point()
```



Model Definition I

Set up a stochastic SIR model

Model Definition II

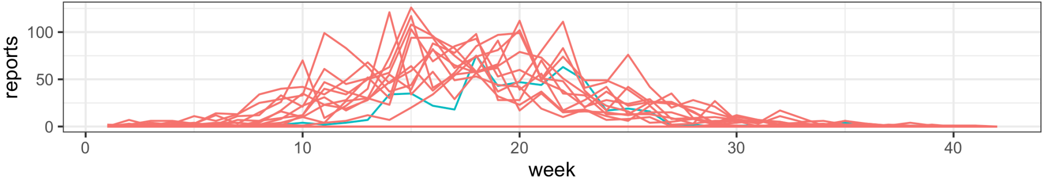
```
sir_stoch <- Csnippet("
  double dN_SI = rbinom(S,1-exp(-Beta*I/N*dt));
  double dN_IR = rbinom(I,1-exp(-Gamma*dt));
  S -= dN_SI; I += dN_SI - dN_IR;
  R += dN_IR; H += dN_IR;"
)
sir_init <- Csnippet("
  S = nearbyint(Eta*N);
  I = 1;
  R = nearbyint((1-Eta)*N);
  H = 0;"
)
```

```
dmeas <- Csnippet("
  lik = dnbinom_mu(reports,k,Rho*H,give_log);"
```

Preliminary Analysis I

Simulation with the initial guess

```
measSIR |>
  simulate(nsim=20,format="data.frame",include.data=TRUE) |>
  ggplot(aes(x=week,y=reports,group=.id,color=.id=="data")) +
  geom_line() + guides(color="none")
```



Check likelihood and ess

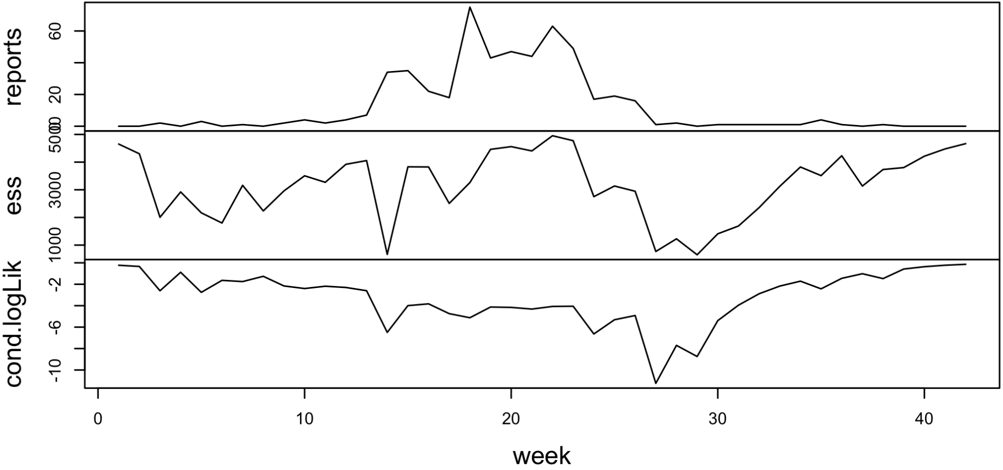
Evaluate the likelihood and Effective Sample Size (ESS) of the initial parameter estimates using particle filtering

```r
pf <- measSIR |> pfilter(Np=5000)
min(pf@eff.sample.size)
```

```
[1] 650.2484
```

ESS refers to the number of particles that effectively contribute to the approximation of the posterior distribution.

```
plot(pf)
```


reports
60
20
0
ess
5000
3000
1000
cond.logLik
-2
-6
-10
0
10
20
30
40
week

Use repeated particle filtering to refine estimates

```
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
-130.376686    3.313859
```

Then we get likelihood at a single point. Store this point, together with the estimated likelihood and SE:

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

Local Optimization (IF2)

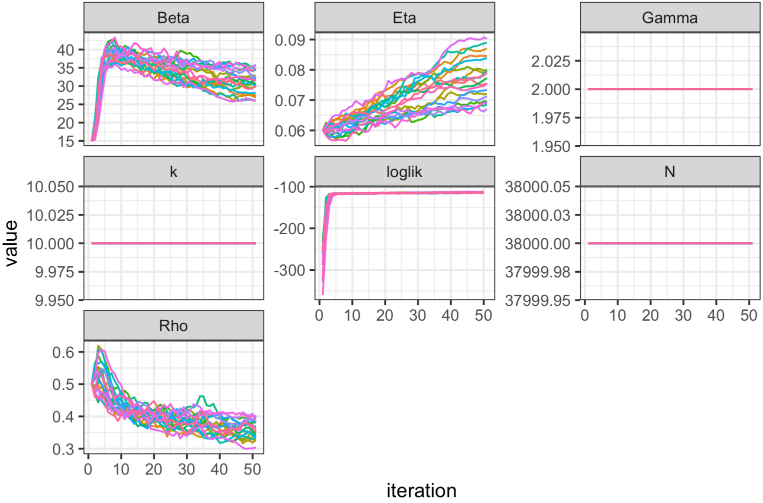
Apply iterated filtering to find a local maximum near the initial guesses

```
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
```

Diagnostics and Visualization

```
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") -> plot
```

```
plot
```


Beta
Eta
Gamma
k
loglik
N
Rho
40
35
30
25
20
15
0.09
0.08
0.07
0.06
2.025
2.000
1.975
1.950
10.050
10.025
10.000
9.975
9.950
-100
-200
-300
38000.05
38000.03
38000.00
37999.98
37999.95
0.6
0.5
0.4
0.3
0
10
20
30
40
50
value
iteration

Global Optimization

Set Up for Global Search

1. likelihood maximizations from diverse starting points.
2. A large box in parameter space.
3. expect to see stable conclusions with starting values drawn randomly from this box

```r
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]]
```

Global Search

```r
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
```

Then get the best result

```r
results |> filter(loglik==max(loglik))
```

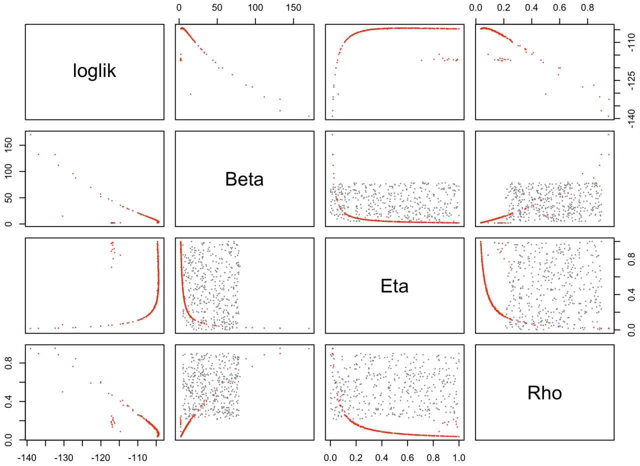
```
# A tibble: 1 x 8
   Beta    Rho   Eta     N Gamma     k loglik loglik.se
  <dbl>  <dbl> <dbl> <dbl> <dbl> <dbl>  <dbl>     <dbl>
1  3.96 0.0602 0.562 38000     2    10  -104.    0.0273
```

Diagnostics and Visualization

Again, we attempt to visualize the global geometry of the likelihood surface using a scatterplot matrix. Then plot contains 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
```

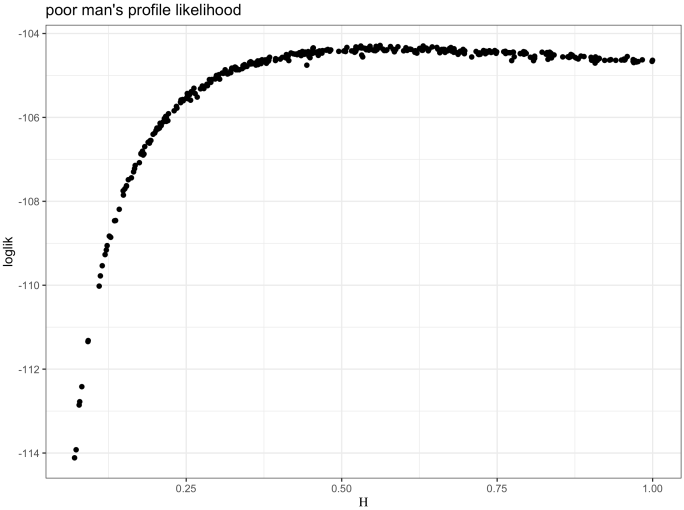
```
pairs(~loglik+Beta+Eta+Rho, data=all, pch=16, cex=0.3,
  col=ifelse(all$type=="guess",grey(0.5),"red"))
```



The projections of the estimates give us ‘poor mans profiles’ ’:

```r
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"
  ) -> plot
```

plot


poor man's profile likelihood
-104
-106
-108
-110
-112
-114
loglik
0.25
0.50
0.75
1.00
H

Profile Likelihood Estimation

For the first parameter

first bound the uncertainty by putting a box around the highest-likelihood

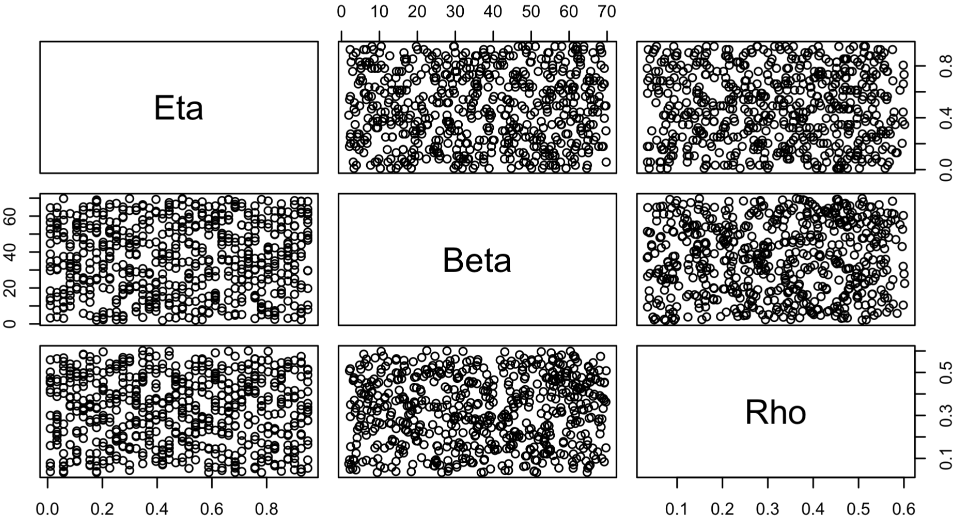
```r
read_csv("measles_params.csv") |>
  filter(loglik>max(loglik)-20,loglik.se<2) |>
  sapply(range) -> box
box
```

```
          Beta Gamma        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
```

Within this box, we'll choose some random starting points

```r
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
```

```r
plot(guesses)
```

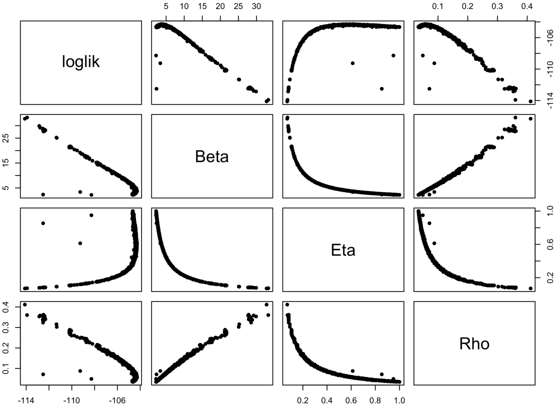


Now, we’ll start one independent sequence of iterated filtering operations from each of these points.

```r
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

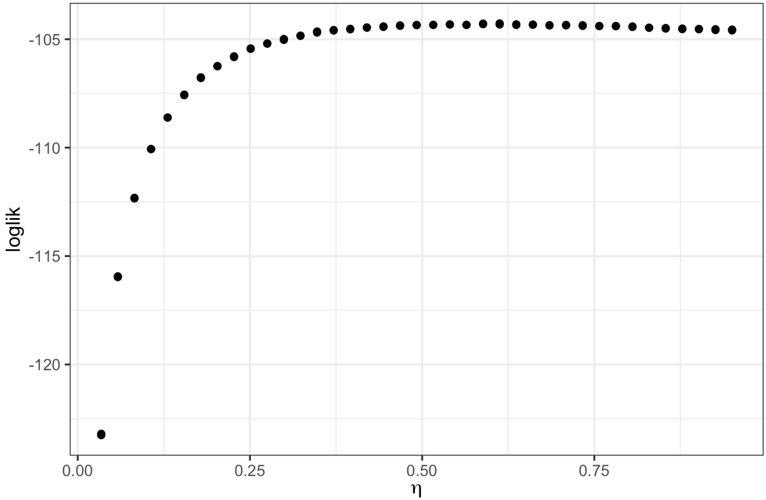
```
read_csv("measles_params.csv") |> filter(loglik>max(loglik)-10) -> all
pairs(~loglik+Beta+Eta+Rho,data=all,pch=16)
```



Focusing on the top of the surface

```
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() + xlab(expression(eta)) -> plot
```

```
plot
```

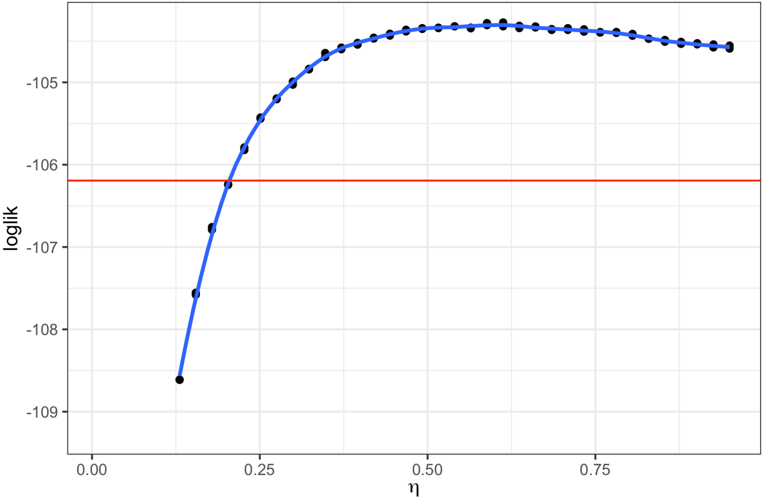


estimate η with 95% CI using these data

```
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() + xlab(expression(eta)) +
  geom_smooth(method="loess",span=0.25)+
  geom_hline(color="red",yintercept=ci.cutoff)+
  lims(y=maxloglik-c(5,0)) -> plot
```

```
plot
```



```r
results |>
  filter(is.finite(loglik)) |>
  filter(loglik>max(loglik)-0.5*qchisq(df=1,p=0.95)) |>
  summarize(min=min(Eta),max=max(Eta)) -> Eta_ci
```

Then we know η is in the 0.23–0.95% range (95% CI).

For the later parameters

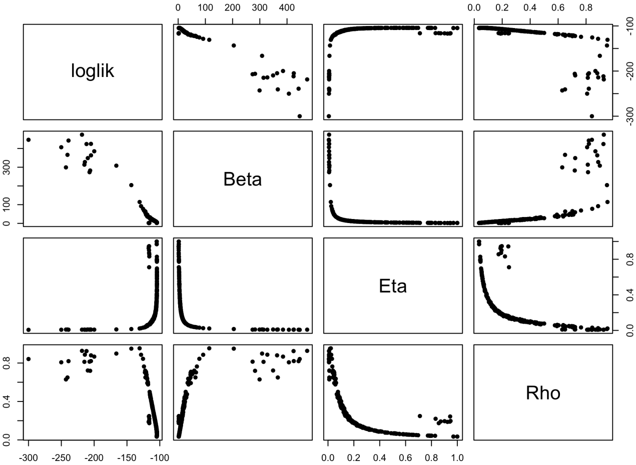
for next parameter, we can initialize the IF2 computations at points we have already established have high likelihoods.

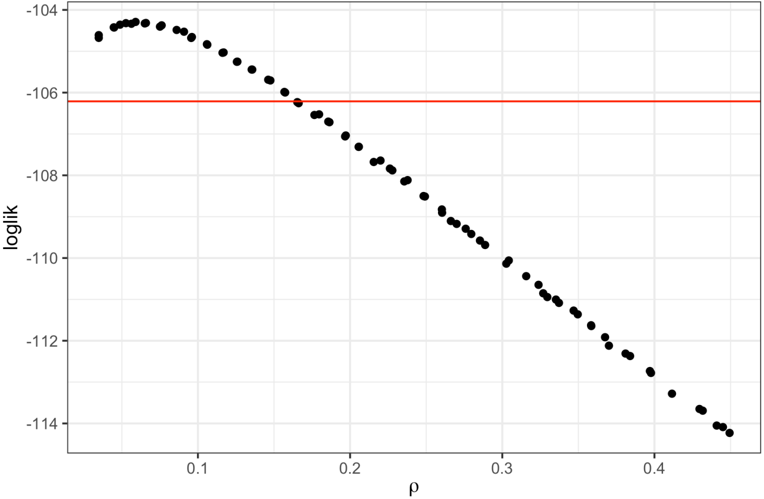
```
read_csv("measles_params.csv") |>
  group_by(cut=round(Rho,2)) |>
  filter(rank(-loglik)<=10) |>
  ungroup() |>
  arrange(-loglik) |>
  select(-cut,-loglik,-loglik.se) -> guesses
```

then again, generate the profile likelihood

```
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
```

Visualizing profile likelihood




-104
-106
-108
-110
-112
-114
loglik
0.1
0.2
0.3
0.4
ρ

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

Then we know reporting efficiencies ρ is in the 3.4–16% range (95% CI).

The investigation continues....

Check predictions I

After all these analyses, we would like to visualize how exactly the model with the MLEs matches the data. We can do it by plotting the simulations with 95% the prediction interval.

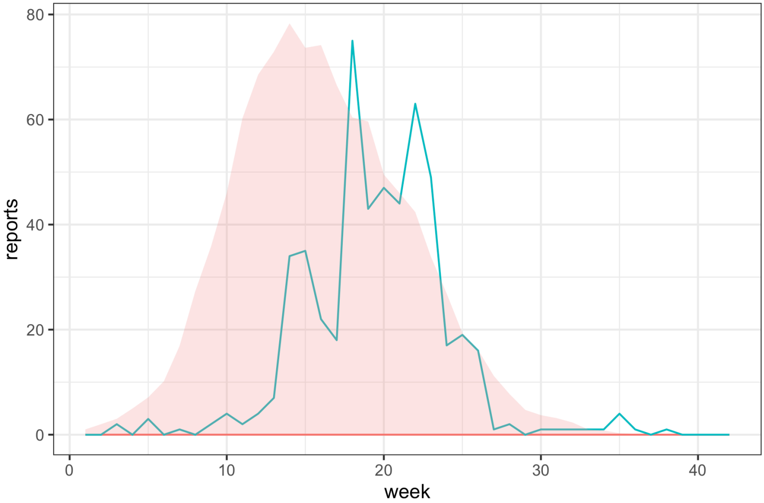
```r
read_csv("measles_params.csv") |>
  filter(loglik == max(loglik)) |>
  select(-loglik, -loglik.se) -> best.params

measSIR |>
  simulate(
    params=unlist(best.params),
    nsim=1000, format="data.frame", include.data=TRUE
  ) -> sims
```

Check predictions II

```
sims |>
  mutate(data=.id=="data") |>
  group_by(week,data) |>
  reframe(
    p=c(0.025,0.5,0.975),
    value=wquant(reports,probs=p),
    name=c("lo","med","up")
  ) |>
  select(-p) |> pivot_wider() |> ungroup() |>
  ggplot(aes(x=week,y=med,color=data,fill=data,ymin=lo,ymax=up))+
  geom_line()+ geom_ribbon(alpha=0.2,color=NA) +
  labs(y="reports")+
  theme_bw() + guides(color="none",fill="none")
```

Check predictions III


reports
week