

Suggested workflow for epidemiological modeling and inference

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Summary I

1. Data Preparation and Model Specification

- ▶ **Data Initialization:** Visualize the initial data to get a sense of the disease outbreak dynamics. (*Simulation P22*)
- ▶ **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. (*Simulation P36*)
 - ▶ Specify the measurement, process, and initialization functions along with model parameters. (*Simulation P38-40*)

2. Preliminary Analysis

- ▶ **Simulation and Visualization:** Simulate the SIR model to visualize potential outcomes and compare to data. (*Simulation P44*)
- ▶ **Likelihood Estimation:** Evaluate the likelihood and Effective Sample Size of the initial parameter estimates using particle filtering. (*likelihood P28-29*)

Summary II

3. Local Optimization

- ▶ **Iterated Filtering for Local Maximum:** Apply iterated filtering to find a local maximum near the initial guesses. (*Iterated filtering P27*)
- ▶ **Diagnostics and Visualization:** Diagnose the iterated filtering process and visualize parameter traces to assess convergence. (*Iterated filtering P30*)

4. Global Optimization

- ▶ **Set Up for Global Search:** Define a parameter space for global optimization. (*Iterated filtering P38*)
- ▶ **Global Search Execution:** Conduct global optimization using multiple starting points to ensure robustness of the findings. (*Iterated filtering P39*)
- ▶ **Result Compilation:** Compile and compare results from global searches, focusing on the best parameter estimates. (*Iterated filtering P42,45*)

Summary III

5. Profile Likelihood Estimation

- ▶ **Parameter Profiling:** For each parameter, perform profiling to map the likelihood landscape and establish confidence intervals. (*Iterated filtering P48,49,52*)
- ▶ **Visualization of Profile Likelihoods:** Visualize the profile likelihoods to understand parameter sensitivity and uncertainty. (*Iterated filtering P53, 57, 60*)

6. Final Model Evaluation

- ▶ **Model Predictions:** Use the best-fitting parameters to simulate the model outcomes and compare these against observed data. (*Iterated filtering P87*)
- ▶ **Visualization of Predictions:** Create visualizations to compare the model predictions with actual data, highlighting the prediction intervals. (*Iterated filtering P88*)

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.

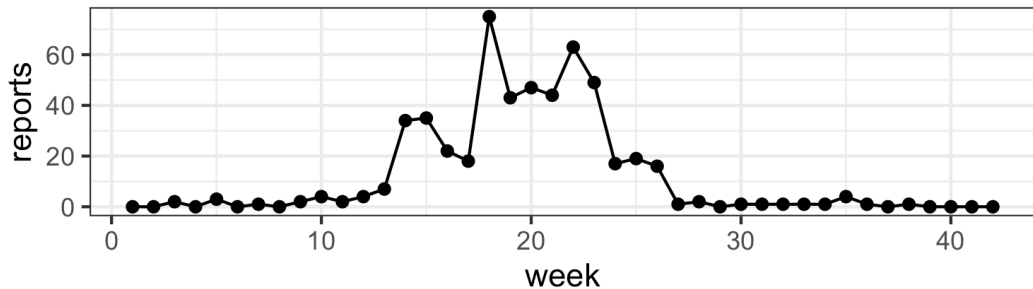
Measle example: Data initialization I

```
library(tidyverse)
read_csv("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

Measle example: Data initialization II

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



Measle example: stochastic SIR model in pomp I

```
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;"  
)
```

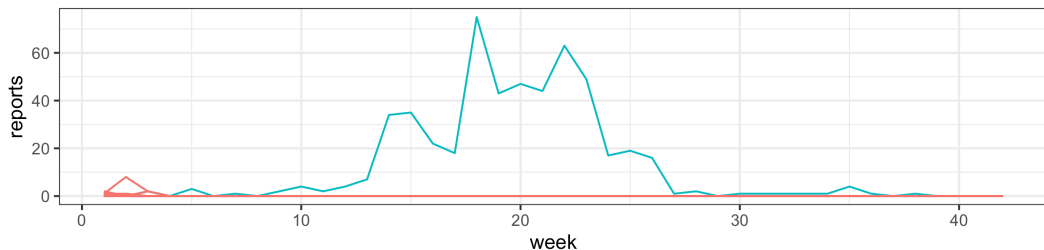
Measle example: stochastic SIR model in pomp II

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

meas |>
  pomp(
    times="week",t0=0,
    rprocess=euler(sir_stoch,delta.t=1/7),
    rinit=sir_init, rmeasure=rmeas,
    dmeasure=dmeas, accumvars="H",
    statenames=c("S","I","R","H"),
    paramnames=c("Beta","Gamma","Eta","Rho","k","N"),
    params=c(Beta=15,Gamma=2,Rho=0.5,k=10,Eta=0.06,N=38000)
  ) -> measSIR
```


Preliminary analysis: simulation and exploration

```
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")
```



Preliminary analysis: likelihood and ess I

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

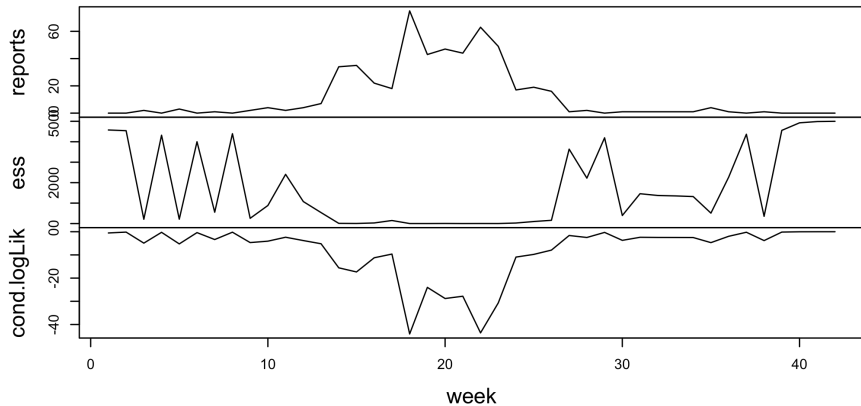
```
pf <- measSIR |> pfilter(Np=5000)  
min(pf@eff.sample.size)
```

```
[1] 1.103539
```

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

```
plot(pf)
```

Preliminary analysis: likelihood and ess II



Preliminary analysis: likelihood and ess III

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
-269.01842	19.98634

Preliminary analysis: likelihood and ess IV

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 I

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

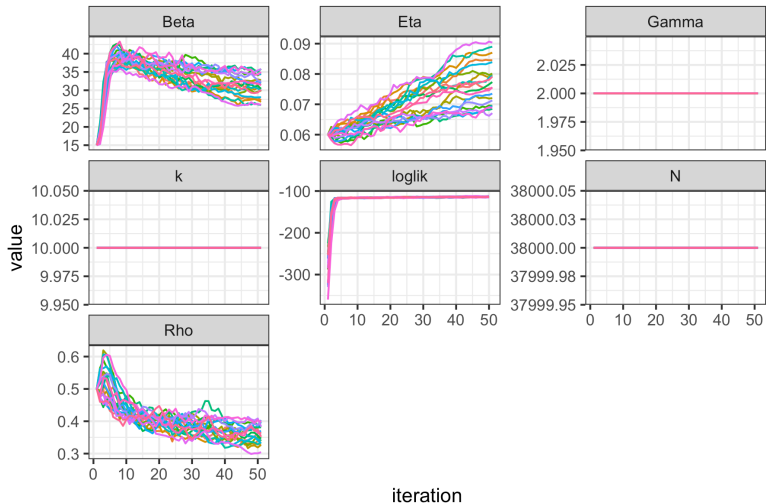
```
foreach(i=1:20,.combine=c,  
  .options.future=list(seed=482947940)) %dofuture% {  
  measSIR |>  
    mif2(  
      Np=2000, Nmif=50, cooling.fraction.50=0.5,  
      rw.sd=rw_sd(Beta=0.02, Rho=0.02, Eta=ivp(0.02)),  
      partrans=parameter_trans(  
        log="Beta",logit=c("Rho","Eta")  
      ),  
      paramnames=c("Beta","Rho","Eta")  
    )  
  } -> mifs_local
```

Local optimization II

► 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")
```

Local optimization III



Global optimization: setup I

1. Likelihood maximization 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

```
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
fixed_params <- c(N=38000, Gamma=2, k=10)
mf1 <- mifs_local[[1]]
```

Global optimization: global Search I

```
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
```

Global optimization: global Search II

Then get the best result

```
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

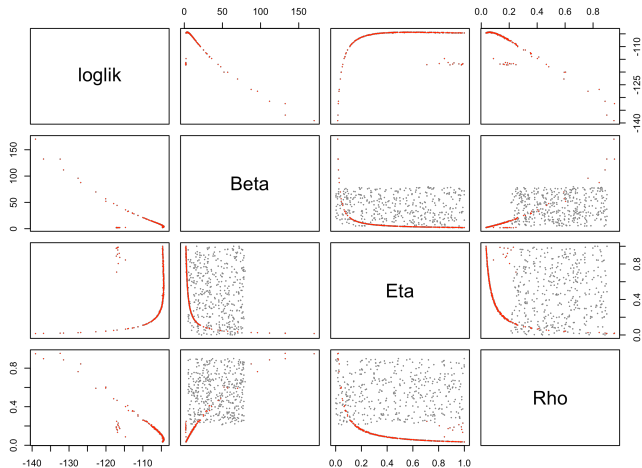
Global optimization: diagnostics and visualization I

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"))
```

Global optimization: diagnostics and visualization II

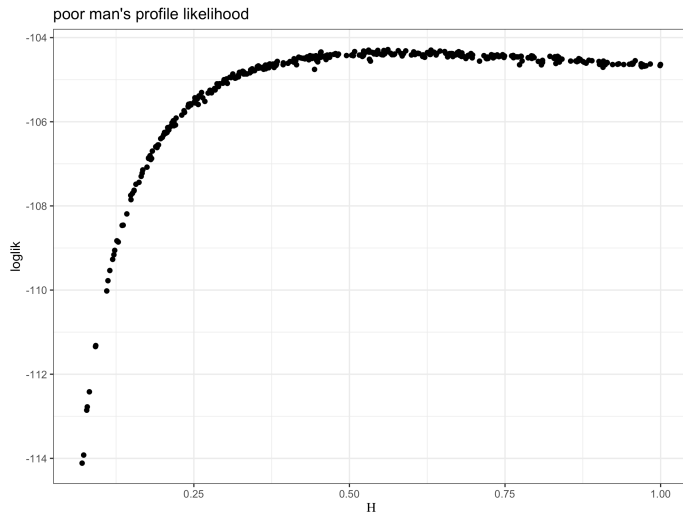


Global optimization: diagnostics and visualization III

The projections of the estimates give us 'poor mans 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"
  )
```

Global optimization: diagnostics and visualization IV



Profile: for the first parameter I

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

```
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

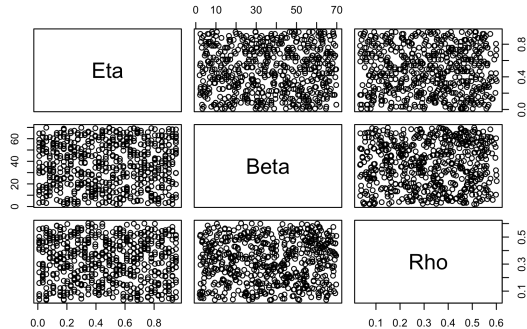
Profile: for the first parameter II

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

```
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
```

Profile: for the first parameter III

```
plot(guesses)
```



Profile: for the first parameter IV

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

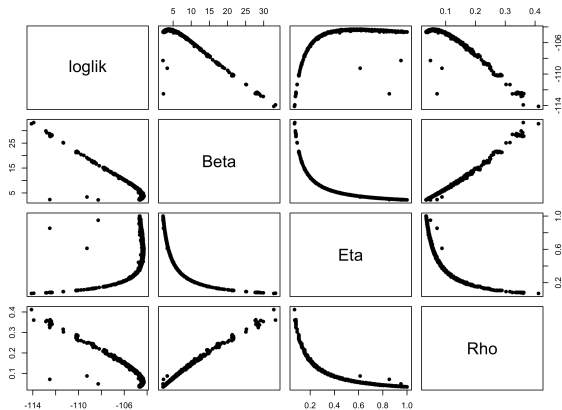
```
foreach(guess=iter(guesses,"row"), .combine=rbind,  
  .options.future=list(seed=830007657)  
) %dofuture% {  
  mf1 |>  
    mif2(params=c(guess,fixed_params),  
      rw.sd=rw_sd(Beta=0.02,Rho=0.02)) |>  
    mif2(Nmif=100,cooling.fraction.50=0.3) -> mf  
  replicate(10, mf |> pfilter(Np=5000) |> logLik()) |>  
    logmeanexp(se=TRUE) -> ll  
  mf |> coef() |> bind_rows() |>  
    bind_cols(loglik=ll[1],loglik.se=ll[2])  
} -> results
```

Profile visualization: for the first parameter I

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

pairs(~loglik+Beta+Eta+Rho,data=all,pch=16)
```

Profile visualization: for the first parameter Π

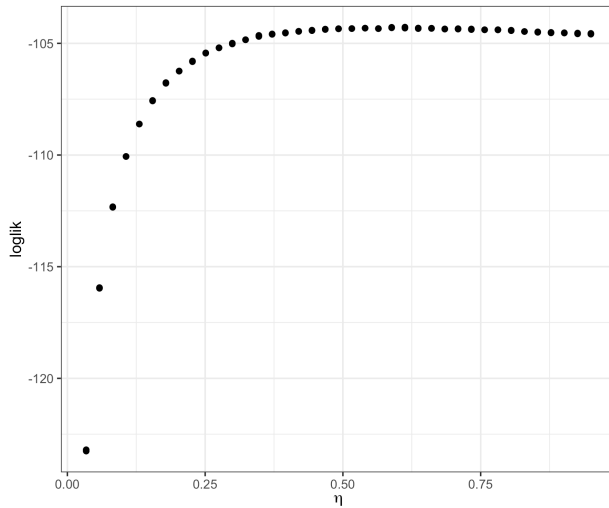


Profile visualization: for the first parameter III

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))
```

Profile visualization: for the first parameter IV



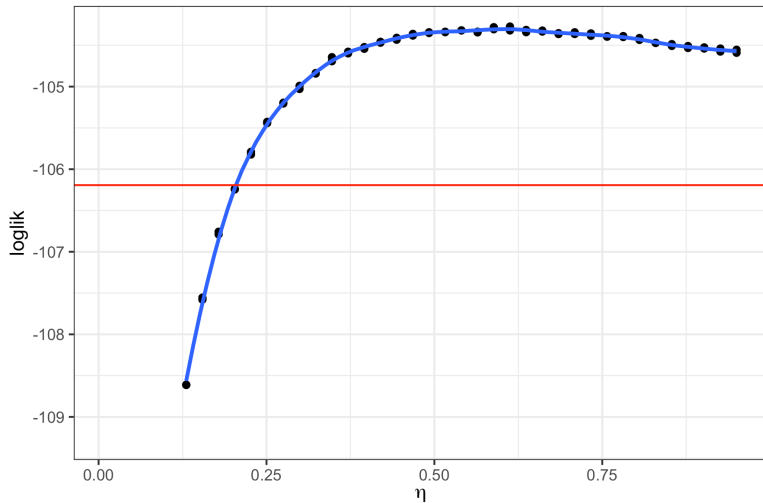
Profile visualization: for the first parameter V

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))
```


Profile visualization: for the first parameter η



Profile visualization: for the first parameter VII

```
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).

Profile: for the later parameters I

For the 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
```

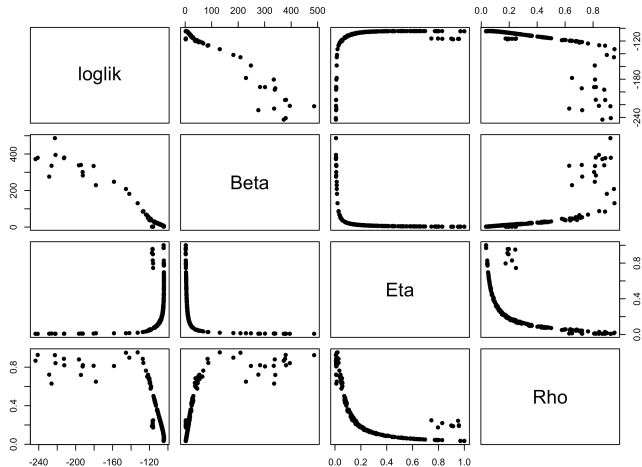
Profile: for the later parameters II

Then again, generate the profile likelihood

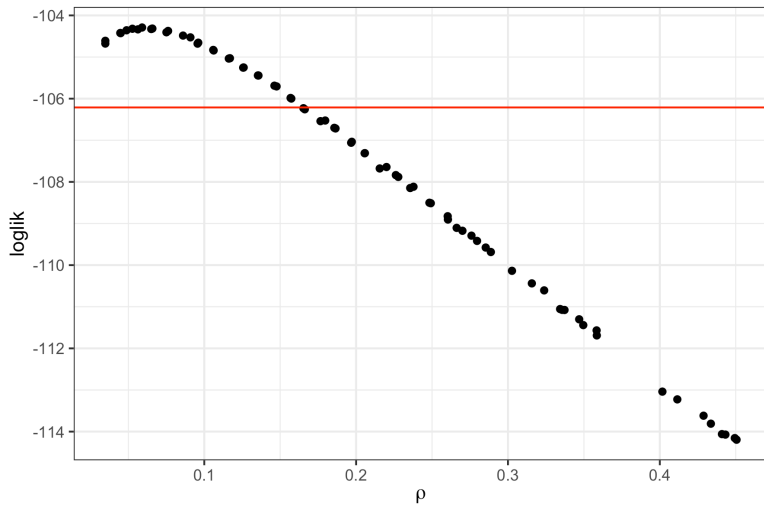
Profile: for the later parameters III

```
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 visualization: for the later parameters I



Profile visualization: for the later parameters II



Profile visualization: for the later parameters III

```
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).

Prediction 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.

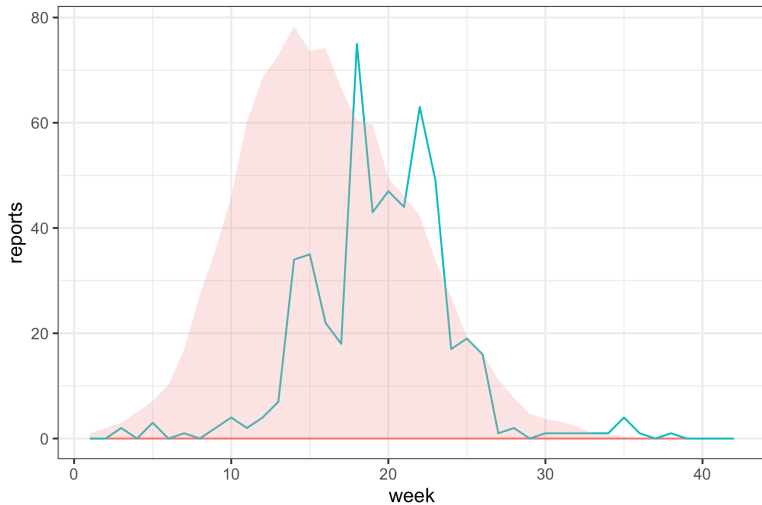
```
read_csv("measles_params.csv") |>
  filter(loglik == max(loglik)) |>
  select(-loglik, -loglik.se) -> best.params

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


Prediction 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")
```

Prediction III



License, acknowledgments, and links

- ▶ This lesson is prepared for the Simulation-based Inference for Epidemiological Dynamics module at the Summer Institute in Statistics and Modeling in Infectious Diseases, SIS MID.
- ▶ The materials build on previous versions of this course and related courses.
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- ▶ Produced with R version 4.4.0 and pomp version 5.9.
- ▶ Compiled on 2024-07-24.

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[R code for this lesson](#)