Basic SIR fitting

April 2, 2017

1 Harbin

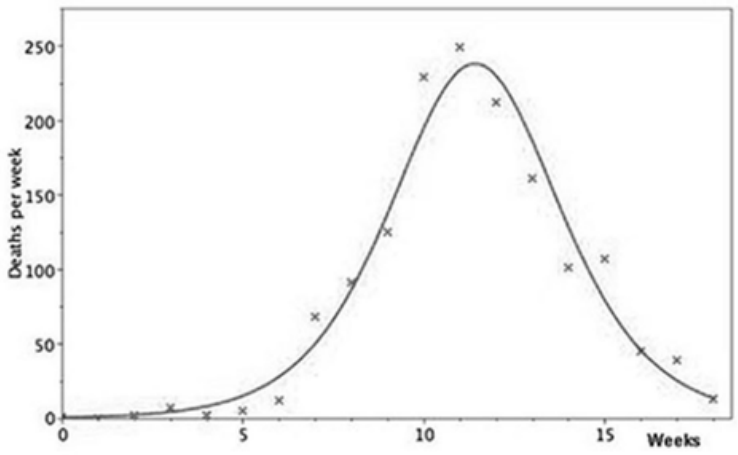


Figure 1: Unnumbered figure (p. 102) from Dietz (2009) showing the Harbin epidemic.

Figure 1 shows a Kermack-Mckendrick model fit to Harbin plague data. Based on the equations (1) and estimates ("$x_0 = 2985$, $\mathcal{R}_0 = 2.00$ and a mean infectious period of 11 days") that Dietz (2009) provides, we can compare how Kermack-Mckendrick model fit differs from SIR model fit based on maximum likelihood estimation.

$$\begin{aligned} \frac{dz}{dt} &= \frac{\gamma x_0}{2\mathcal{R}_0^2} c_1 \text{sech}^2(c_1 \gamma t - c_2), \\ c_1 &= \sqrt{(\mathcal{R}_0 - 1)^2 + \frac{2\mathcal{R}_0^2}{x_0}} \\ c_2 &= \tanh^{-1}\left(\frac{\mathcal{R}_0 - 1}{c_1}\right). \end{aligned} \tag{1}$$

We note that the original equation provided by Dietz (2009) contains a typo. $c_1\gamma t$ after sech^2 in the first equation should be corrected to $c_1\gamma t/2$ (Kermack and McKendrick, 1927).

First, load the pacakge:

```
library(fitsir)
```

Since `fitsir` package lazy loads all data, `data(harbin)` is unnecessary.

```
head(harbin)

##   week Deaths
## 1    2      2
## 2    3      7
## 3    4      2
## 4    5      6
## 5    6     12
## 6    7     68
```

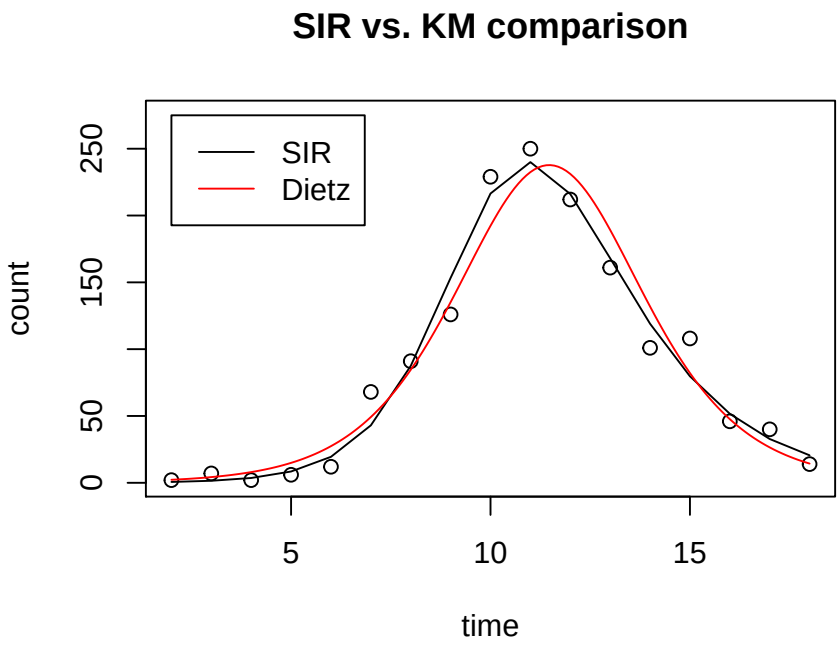
Then, we transform the parameters provided by Dietz (2009) into *unconstrained parameters* (`log.beta, log.gamma, log.N, logit.i`) so that they can be used as starting parameters for MLE. Although `fitsir` expects a dataframe with column names `times` and `count`, we can specify a time column and a count column with `tcol` and `icol` arguments.

```
dietz_harbin <- c(x0=2985,rzero=2,gamma=7/11)
dietz_lpars <- with(as.list(dietz_harbin),
      c(log.beta=log(rzero*gamma),
        log.gamma=log(gamma),
        log.N=log(x0),
        logit.i=qlogis(1e-3)))
(ff <- fitsir(harbin, start=dietz_lpars, type="death",
              tcol="week", icol="Deaths", method="BFGS"))

##
## Call:
## mle2(minuslogl = objfun, start = start, method = method, data = dataarg,
##     vecpar = TRUE, gr = gradfun, control = control)
##
## Coefficients:
##   log.beta  log.gamma      log.N    logit.i
##  0.4868478 -0.2708639  7.4966582 -8.1274230
##
## Log-likelihood: -68.27
```

In this case, BFGS method has been used because using sensitivity equations allows for more accurate computation of the Hessian matrix.

We can plot `fitsir` objects using `plot` function to see whether this fit is good or not (`plot(ff)`). Here, we plot SIR fit along with Dietz fit to compare how they differ:

```
plot(ff, main="SIR vs. KM comparison")
times <- with(as.list(harbin), seq(min(week), max(week), by = 0.1))
dpKM <- with(as.list(dietz_harbin),
        {
           c1 <- sqrt((rzero-1)^2+2*rzero^2/x0)
           c2 <- atanh((rzero-1)/c1)
           gamma*x0/(2*rzero^2)*c1*
               (1/cosh(c1*gamma*times/2-c2))^2
        })
lines(times,dpKM, col = 2)
legend(x=2, y=275, legend=c("SIR","Dietz"), col=c("black", "red"), lty = 1)
```



Apart from the differences in the estimated trajectories, we note that the Kermack-Mckendrick equation models the instantaneous change in the number of recovered individuals (dR/dt) whereas `fitsir` fits are based on the actual number of individuals that recovered during a given time interval ($R(\tau_{n+1}) - R(\tau_n)$).

We can also use the `summary` method provided by the `fitsir` package to see the summarized parameters:

```
summary(ff)

## Maximum likelihood estimation
##
## Call:
## mle2(minuslogl = objfun, start = start, method = method, data = dataarg,
##     vecpar = TRUE, gr = gradfun, control = control)
##
## Coefficients:
##                     R0          r     infper         i0         I0
## Estimate   2.1334e+00 8.6446e-01 1.3111e+00 2.9524e-04 5.3203e-01
## Std. Error 5.4710e-01 1.0344e-01 4.9281e-01 1.2155e-04 2.6501e-01
##                     S0       N
## Estimate   1.8015e+03 1802.01
## Std. Error 2.6259e+02  262.77
##
## -2 log L: 136.5431
```

MLE returns slightly higher $\mathcal{R}_0$ and longer infectious period but lower population size.

1.1 Overdispersion

In fact, this is not the best fit. By looking at the sum of Pearson residuals divided by the mean (given by `sigma`), we can see that the data is over dispersed

```
sigma(ff)

## [1] 4.056574
```

`fitsir` provides three ways of dealing with overdispersion (quasipossion, NB1, NB2) and in this case, using NB1 error function fits better (higher Log-likelihood) than using any of the provided error functions. First, to explore how these fits differ, we define a new data frame, namely `harbin2`, to avoid using `tcol` and `icol` arguments:

```
harbin2 <- setNames(harbin, c("times", "count"))
```

Then, we can fit:

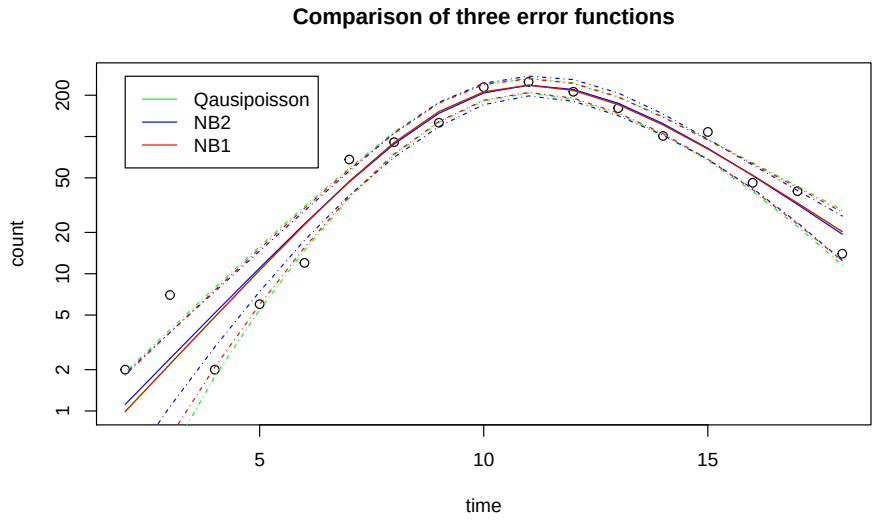
```
ff2 <- fitsir(harbin2, dist="quasipoisson", type="death", method="BFGS", start=dietz_lpars)
ff3 <- fitsir(harbin2, dist="nbinom", type="death", method="BFGS", start=dietz_lpars)
ff4 <- fitsir(harbin2, dist="nbinom1", type="death", method="BFGS", start=dietz_lpars)
```

If you run the code, you will notice that `nbinom` and `nbinom1` estimate 5 parameters rather than 4. The last parameter `log.dsp` is the log of dispersion

parameter. For NB2 (`nbinom`), `log.dsp` is log of the size parameter, whereas for NB1 (`nbinom1`), `log.dsp` is the log of τ, where $\mu = \tau \text{Var}$.

Again, we can plot these three fits to compare:

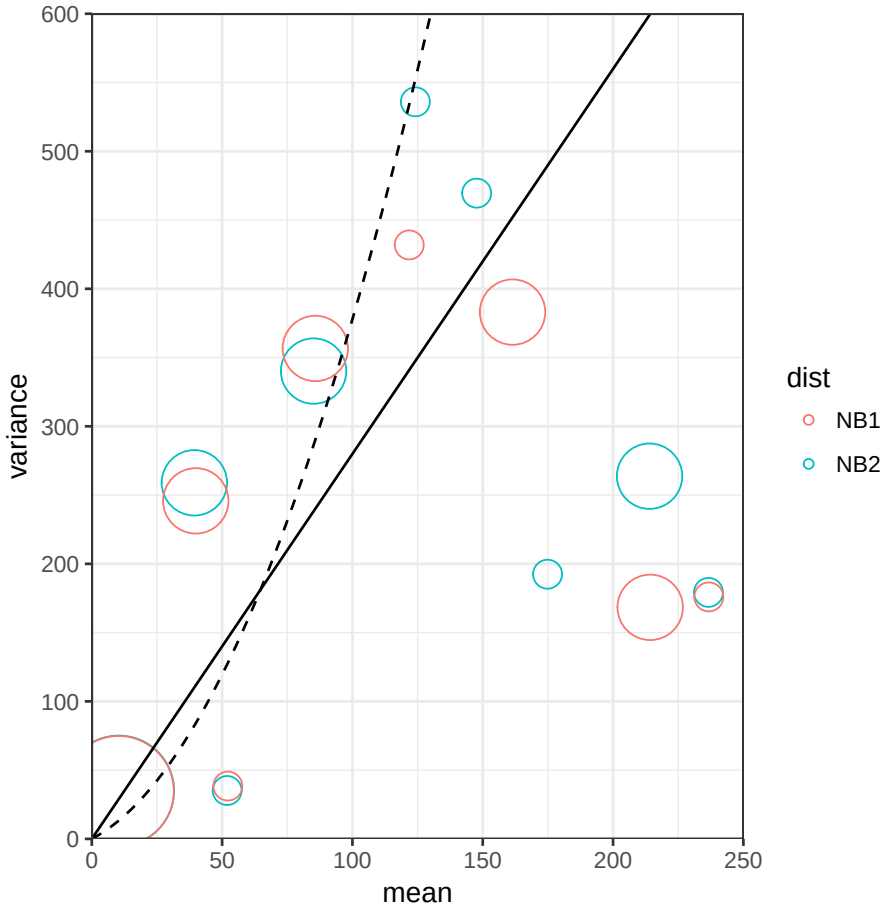
```
plot(ff2, level=0.95, col.traj="green", col.conf="green", log="y", main="Comparison of three
plot(ff3, level=0.95, add=TRUE, col.traj="blue", col.conf="blue")
plot(ff4, level=0.95, add=TRUE, col.traj="red", col.conf="red")
legend(x=2, y=275, legend=c("Qausipoisson","NB2", "NB1"), col=c("green", "blue", "red"), lty
```



All these three fits give us very similar expected trajectories as well as confidence intervals. However, if we compare their log-likelihoods, we find that NB1 gives us the best fit.

```
hfits <- list(QP=ff2, NB2=ff3, NB1=ff4)
lapply(hfits, logLik)

## $QP
## 'log Lik.' -71.73737 (df=4)
##
## $NB2
## 'log Lik.' -67.67009 (df=5)
##
## $NB1
## 'log Lik.' -64.63234 (df=5)
```

To understand why NB1 fits better than NB2, we can look at the mean variance relationship (we disregard quasipoisson due to its high log likelihood value).



Clearly, we can see that the quadratic mean-variance relationship is not appropriate in this case.

Summarizing the best fit, we underestimate $\mathcal{R}_0$ as well as the population size but the estimate of the infectious period is very close to that provided by Dietz.

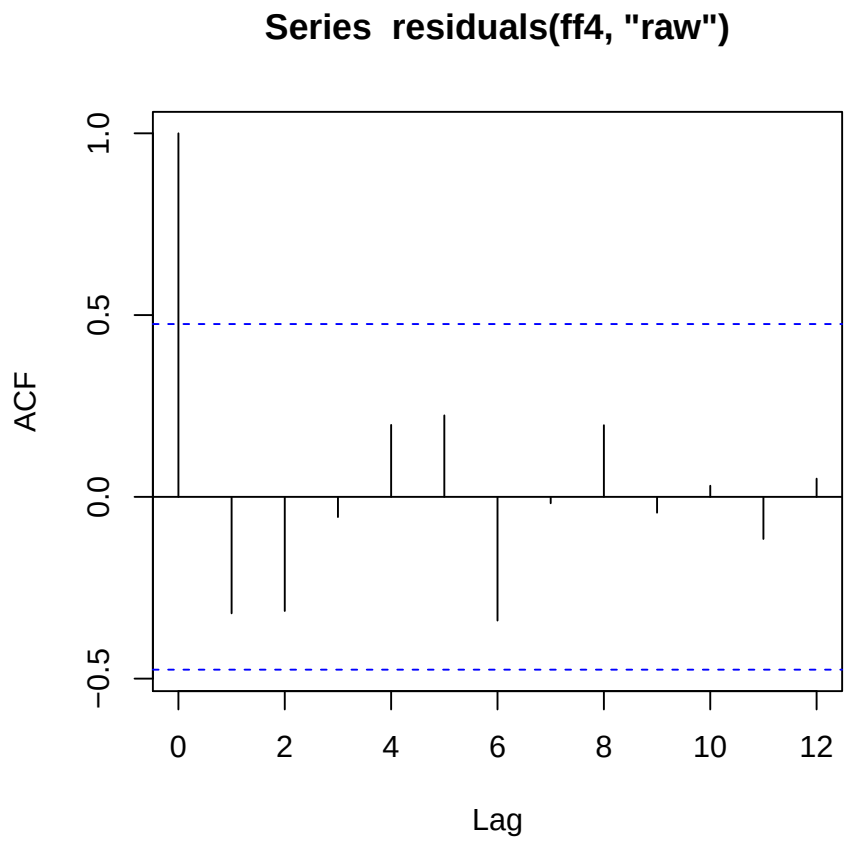
```
summary(ff4)

## Maximum likelihood estimation
##
## Call:
## mle2(minuslogl = objfun, start = start, method = method, data = dataarg,
##     vecpar = TRUE, gr = gradfun, control = control)
##
## Coefficients:
##                    R0          r     infper         i0         I0
## Estimate   1.8631e+00 7.9800e-01 1.0816e+00 3.5121e-04 7.0063e-01
```

```
## Std. Error 4.1027e-01 7.3291e-02 4.2898e-01 1.3291e-04 2.2956e-01
##                     S0       N
## Estimate   1.9942e+03 1994.89
## Std. Error 3.6759e+02  367.58
##
## -2 log L: 129.2647
```

1.2 Autocorrelation

We notice that all three models (quasipoisson, NB1, and NB2) provide extremely similar trajectories as well as confidence intervals. So we can test for auto correlation:

```
acf(residuals(ff4, "raw"))
```



This doesn't seem like they're autocorrelated...

2 1918 Philadelphia Flu

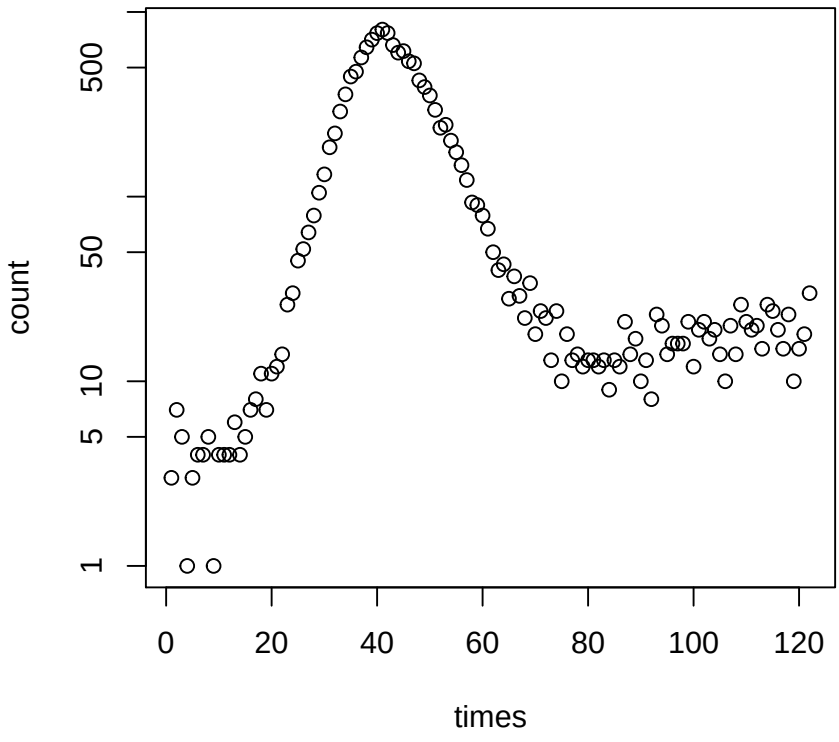
Another data set provided by the `fitsir` package is 1918 philadelphia flu data.

```
head(phila1918)
```

```
##         date pim
## 1 1918-09-01   3
## 2 1918-09-02   7
## 3 1918-09-03   5
## 4 1918-09-04   1
## 5 1918-09-05   3
## 6 1918-09-06   4
```

Notice that the first column is in the `Date` format. Since `fitsir` expects a time column to be a numeric vector, we can either add a new column or create a new data frame. Here, we create a new data frame to avoid using `tcol` and `icol` argument.

```
phila1918a <- with(phila1918, data.frame(times=seq_along(date), count=pim))
plot(phila1918a, log="y")
```

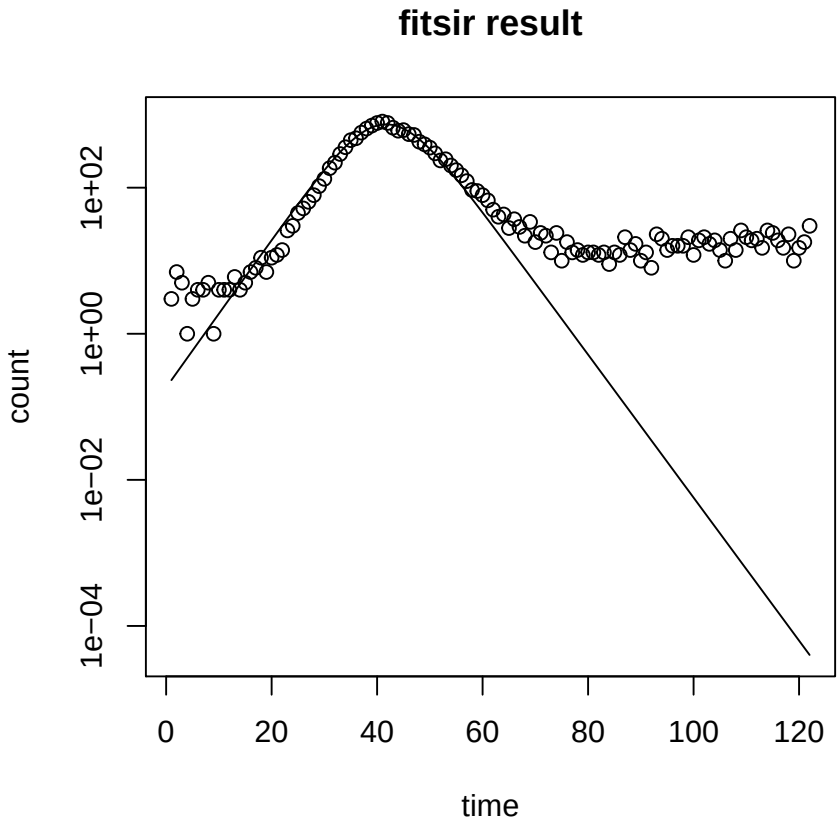


Notice that this data doesn't exactly follow the typical SIR trajectory. Due to its long tail, most models other than Gaussian fail. First, we can try to fit SIR model naively:

```
(pfit <- fitsir(phila1918a, type="death"))
```

```
##
## Call:
## mle2(minuslogl = objfun, start = start, method = method, data = dataarg,
##     vecpar = TRUE, gr = gradfun, control = control)
##
## Coefficients:
##   log.beta  log.gamma      log.N    logit.i
##   1.609535   1.561885  11.854347 -14.996334
##
## Log-likelihood: -559.23
```

```
plot(pfit, log="y")
```

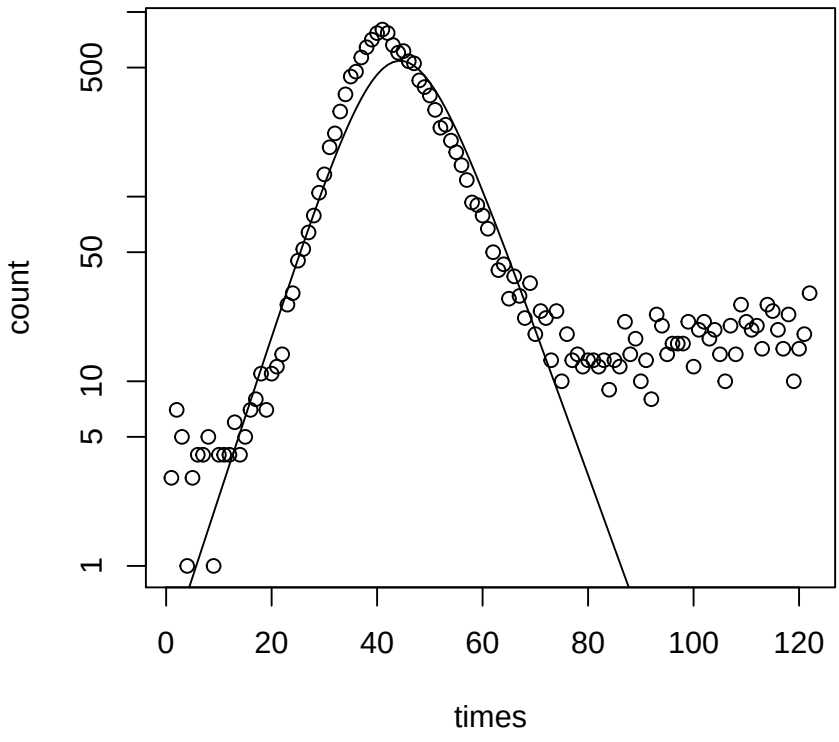


We get a decent fit. However, this is actually a local minima. To avoid falling in a local minima, we can either use a different starting point or try different method. Here, we present how using different starting values can yield different results.

2.1 Starting values

`fitsir` provides a function (`startfun`) that automatically finds a reasonable starting value:

```
(pstart <- startfun(phila1918a, type="death"))

##    log.beta   log.gamma       log.N     logit.i
##   0.4056541   0.2621422  10.7080677 -12.0158789

plot(phila1918a, log="y")
lines(SIR.detsim(phila1918a$times, trans.pars(pstart), type="death"))
```



Using this starting function, we can get a better fit:

```
(pfit2 <- fitsir(phila1918a, type="death", start=pstart))

##
## Call:
## mle2(minuslogl = objfun, start = start, method = method, data = dataarg,
##     vecpar = TRUE, gr = gradfun, control = control)
##
## Coefficients:
##    log.beta   log.gamma       log.N     logit.i
##   0.4193635   0.2440355  10.6548704 -12.8738550
##
## Log-likelihood: -549.81
```

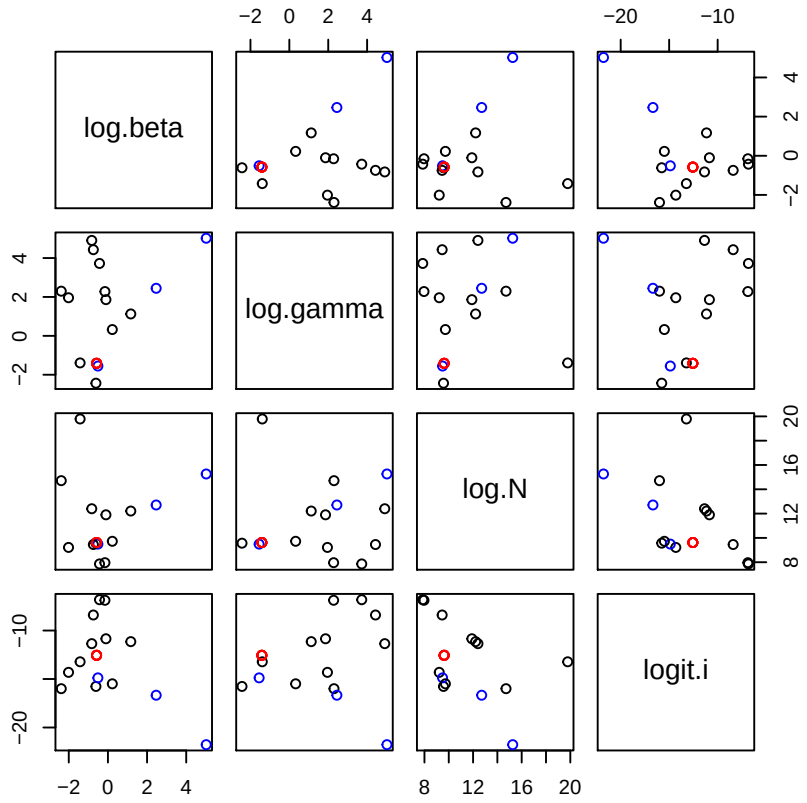
Yet, this is still not the best fit. We can further explore different starting values using Latin hypercube sampling.

```
set.seed(123)
lhsfun <- function(param, size=0.5, length.out=20) {
    seq((1-size)*param, (1+size)*param, length.out=length.out)
}

ltab <- sapply(pstart, lhsfun)
ltab <- apply(ltab,2, sample)
plist <- apply(ltab, 1, function(x) fitsir(phila1918a, type="death", start=x))
(pLik <- sapply(plist, logLik))
```

```
##  [1] -512.1786 -836.0653 -836.0653 -512.1786 -836.0654 -816.2729 -624.9263
##  [8] -836.0653 -562.4907 -836.0654 -553.9157 -512.1787 -512.1786 -836.0653
## [15] -561.2087 -512.1788 -705.8666 -836.0653 -512.1786 -836.0654
```

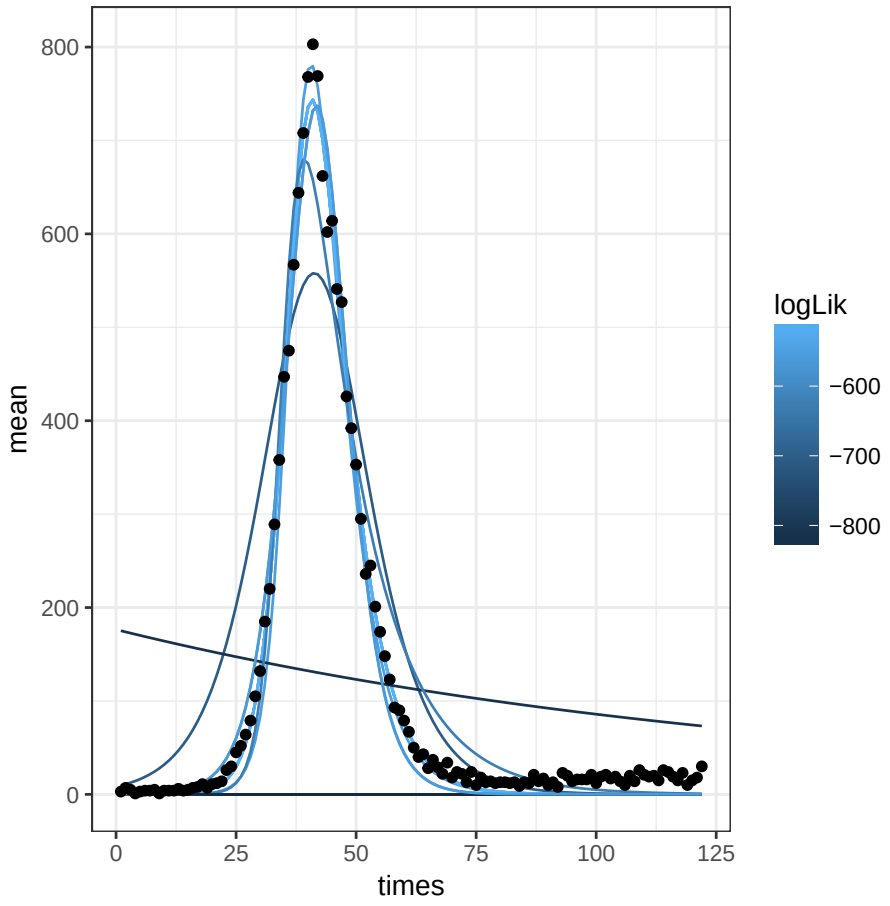
We can explore the parameter space

```
ppars <- as.data.frame(t(sapply(plist, coef)))
col <- c("black", "blue", "red")
ccol <- col[cut(pLik, breaks=c(-900, -600, -520, -500))]

plot(ppars, col=ccol)
```



We can see that the best fits (red points) converge to a single point. We get some fits that are not optimal but are close to the best fits (blue points). Then, there are fits that fail (black points).

```
ppred <- plist %>%
    lapply(predict) %>%
    bind_rows(.id="sim")

ppred$logLik <- rep(pLik, each=length(phila1918a$times))

ggplot(ppred) +
    geom_line(aes(times, mean, group=sim, col=logLik)) +
    geom_point(data=phila1918a, aes(times, count))
```



Looking at the best fit...

```
pbest <- plist[[which.max(pLik)]]
summary(pbest) ## Nelder-Mead being unstable

## Maximum likelihood estimation
##
## Call:
## mle2(minuslogl = objfun, start = start, method = method, data = dataarg,
##     vecpar = TRUE, gr = gradfun, control = control)
##
## Coefficients:
##                    R0          r     infper         i0         I0
## Estimate   2.3022e+00 3.1681e-01 4.1105e+00 3.5169e-06 5.2903e-02
## Std. Error         NA 5.1283e-04         NA 3.7652e-08 9.6588e-05
##                    S0        N
## Estimate   1.5043e+04 15042.72
```

```
## Std. Error 1.0010e+02   100.09
##
## -2 log L: 1024.357

pbest2 <- fitsir(phila1918a, type="death", start=coef(pbest), method="BFGS")
summary(pbest2)

## Maximum likelihood estimation
##
## Call:
## mle2(minuslogl = objfun, start = start, method = method, data = dataarg,
##     vecpar = TRUE, gr = gradfun, control = control)
##
## Coefficients:
##                    R0          r     infper         i0         I0
## Estimate   2.3022e+00 3.1681e-01 4.1104e+00 3.5169e-06 5.2903e-02
## Std. Error 1.3178e-01 8.6644e-03 3.1493e-01 7.4645e-07 1.2469e-02
##                    S0        N
## Estimate   1.5043e+04 15042.72
## Std. Error 4.0165e+02   401.66
##
## -2 log L: 1024.357
```

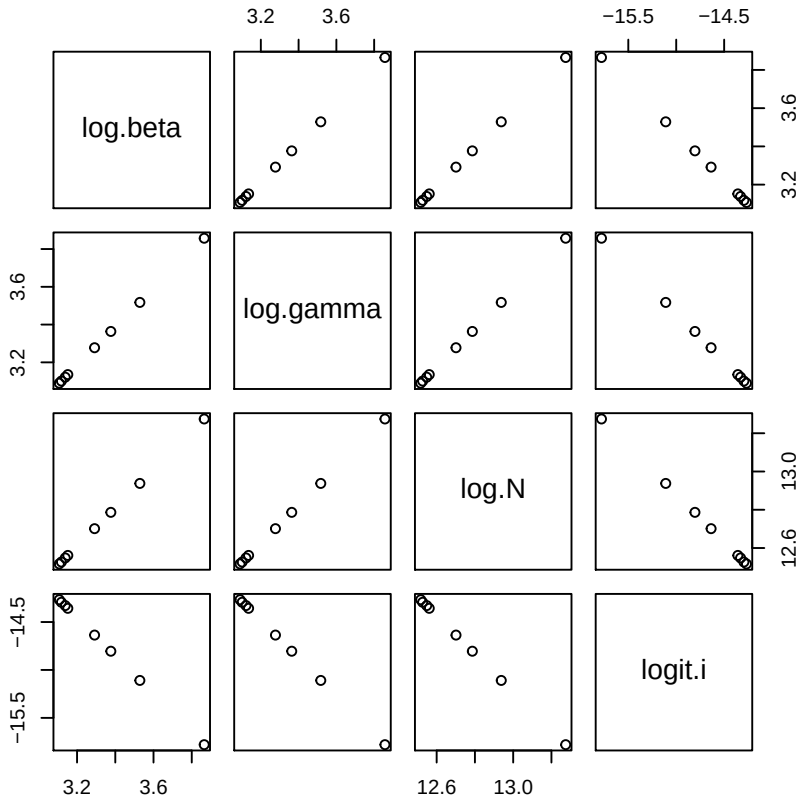
3 Bombay

In this section, we are going to be demonstrating some pathologies that might be associated with SIR fitting.

```
bombay2 <- setNames(bombay, c("times", "count"))
bb <- fitsir(bombay2, type="death", dist="nbinom", start=startfun(bombay2, type="death"))
```

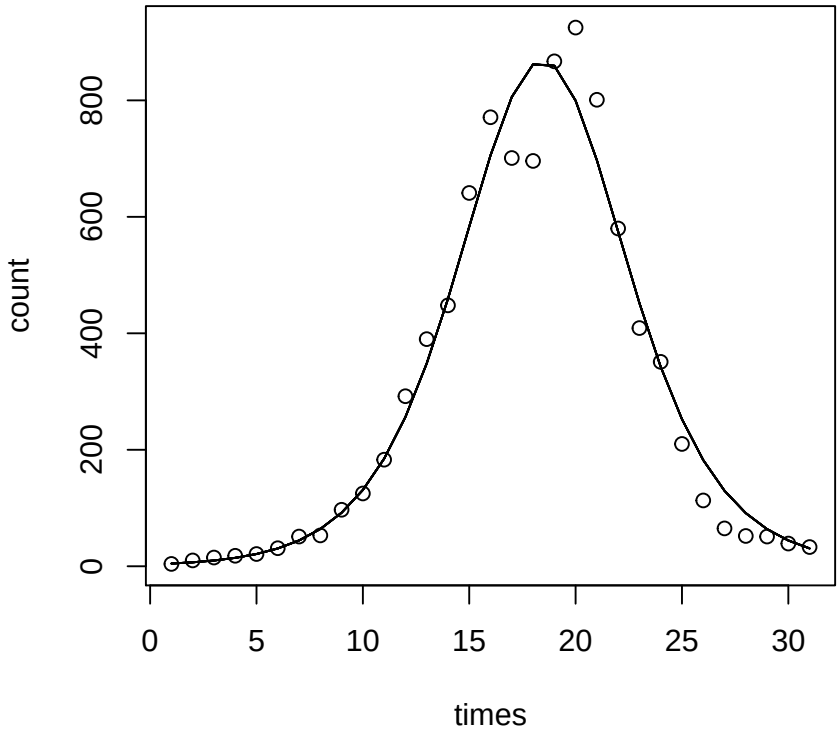
Multiple local minimas:

```
blist <- apply(ltab, 1, function(x) fitsir(bombay2, type="death", start=x, method="BFGS"))
bpars <- as.data.frame(t(sapply(blist, coef)))
bLik <- sapply(blist, logLik)
mle <- max(bLik)

goodfits <- which(1.001 * mle < bLik)

gpars <- bpars[goodfits,]

plot(gpars)
```



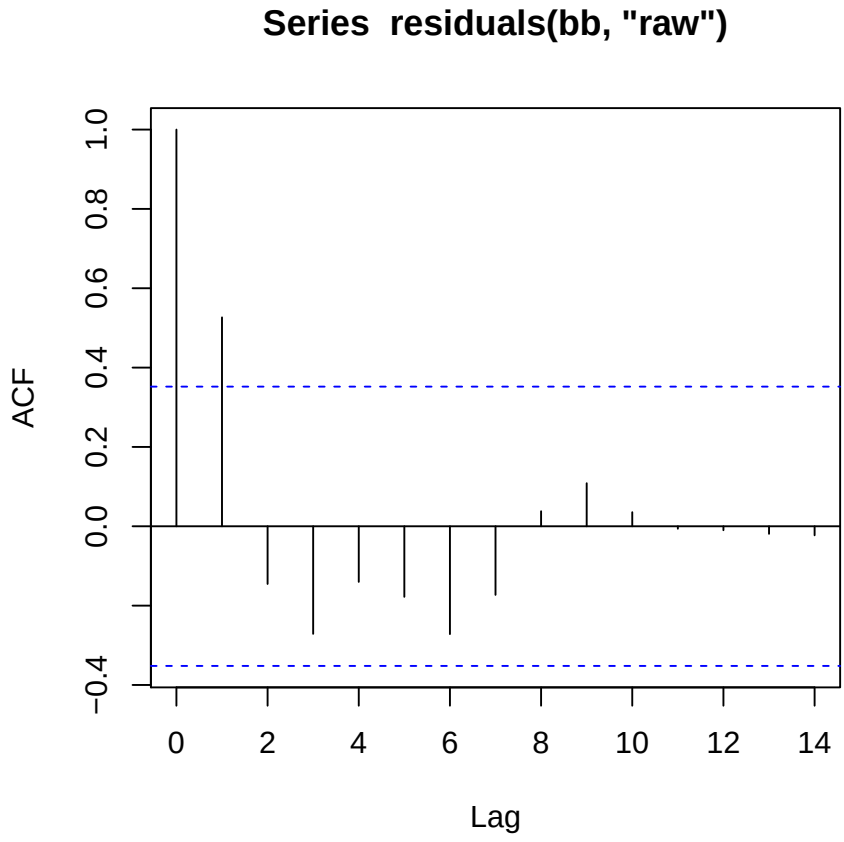
Difference is not noticeable:

```
plot(bombay2)
l <- lapply(blist[goodfits], function(x) plot(x, add=TRUE))
```



Autocorrelation:

```
acf(residuals(bb, "raw"))
```



References

Dietz, K. (2009, April). Epidemics: the fitting of the first dynamic models to data. *Journal of Contemporary Mathematical Analysis 44*(2), 97–104.

Kermack, W. O. and A. G. McKendrick (1927). A contribution to the mathematical theory of epidemics. In *Proceedings of the Royal Society of London A: mathematical, physical and engineering sciences*, Volume 115, pp. 700–721. The Royal Society.