Basic SIR fitting

March 22, 2017

1 Harbin

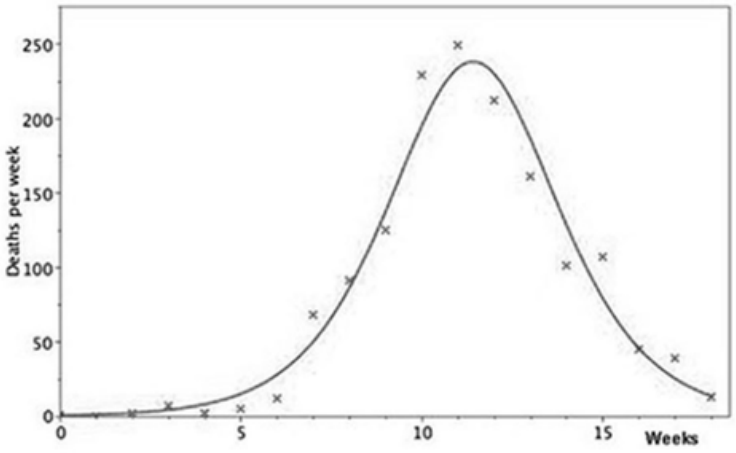


Figure 1: Unnumbered figure (p. 102) from Dietz (2009) showing the Harbin epidemic.

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.

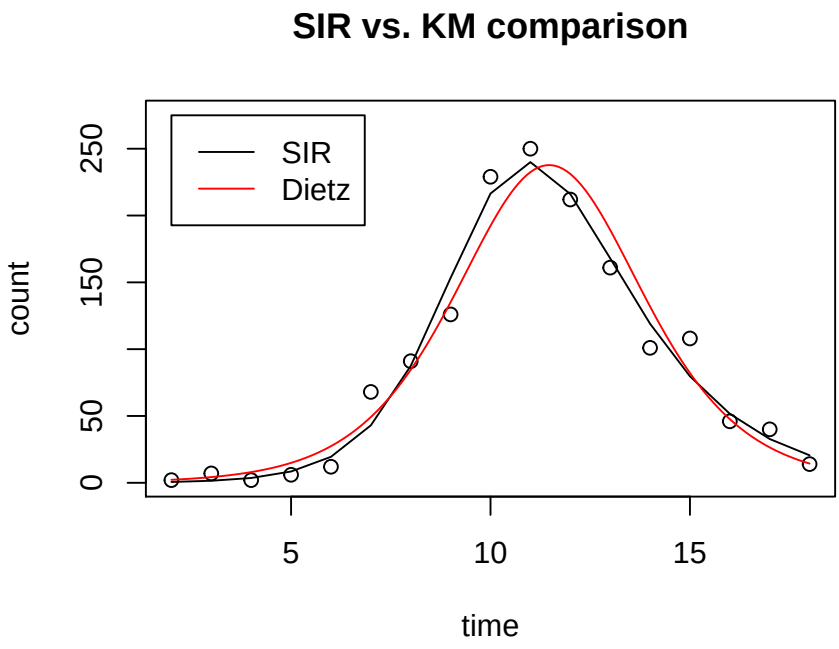
```
dietz_harbin <- c(x0=2985,rzero=2,gamma=7/11)
dietz_lpars <- with(as.list(dietz_harbin),
      c(log.beta=log(rzero*gamma),
        log.gamma=log(gamma),
        log.N=log(x0),
        logit.i=qlogis(1e-3)))
(ff <- fitsir(harbin, start=dietz_lpars, type="death",
              tcol="week", icol="Deaths",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

In fact, this is not the best fit. By looking at the Pearson residual, we can see that the data is over dispersed

```
pp <- predict(ff)
(pr <- sum((harbin$Deaths-pp$mean)^2/pp$mean)/(nrow(harbin)-1))

## [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"))
```

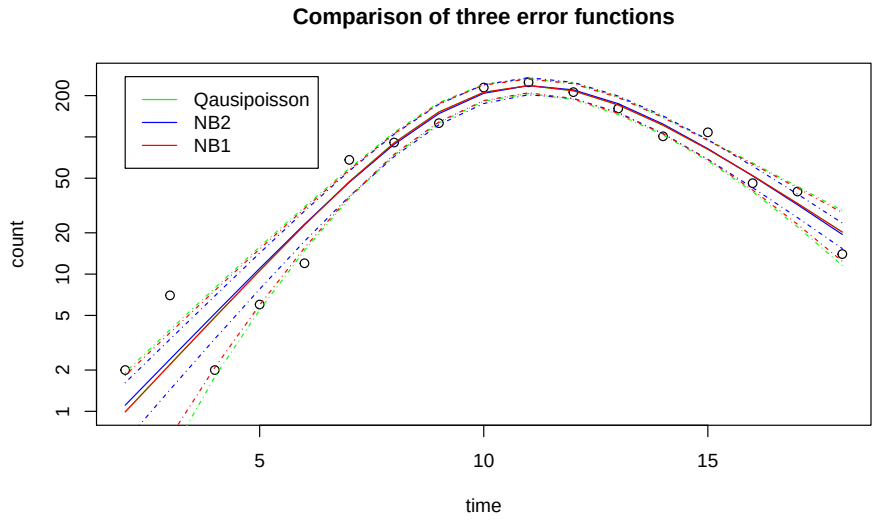
Then, we can fit:

```
ff2 <- fitsir(harbin2, dist="quasipoisson", type="death", method="BFGS")
ff3 <- fitsir(harbin2, dist="nbinom", type="death")
ff4 <- fitsir(harbin2, dist="nbinom1", type="death", hessian.opts=list(r=6))
```

For `nbinom1`, `hessian.opts=list(r=6)` was used because default Hessian calculation is not stable.

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
```

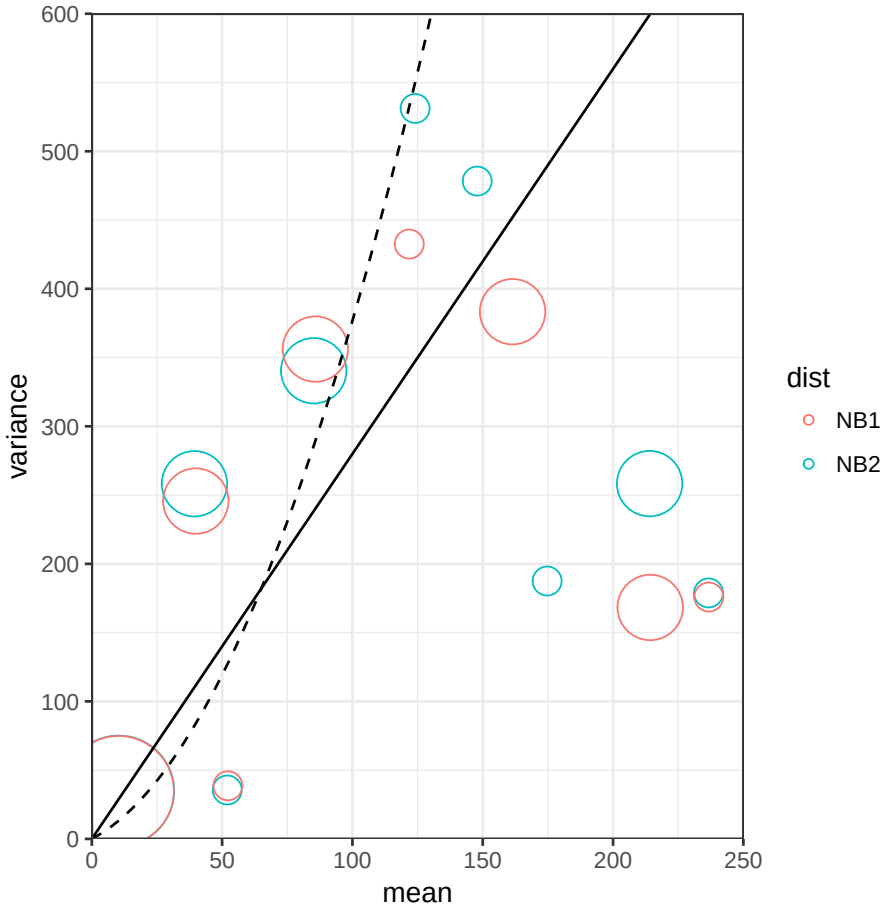


All these three fits give us very similar expected trajectories as well as confidence intervals. However, if we compare their log-likelihoods, we find that NB1 gives us the best fit.

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

## $QP
## 'log Lik.' -71.73737 (df=4)
##
## $NB2
## 'log Lik.' -67.67033 (df=4)
##
## $NB1
## 'log Lik.' -64.63234 (df=4)
```

To understand why NB1 fits better than NB2, we can look at the mean variance relationship (we disregard quasipoisson).



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, hessian.opts = ..1, gr = gradfun, control = control)
##
## Coefficients:
##                    R0          r     infper         i0         I0
## Estimate   1.8636e+00 7.9803e-01 1.0822e+00 3.5142e-04 7.0094e-01
```

```
## Std. Error 4.0990e-01 7.3250e-02 4.2853e-01 1.3284e-04 2.2963e-01
##                    S0       N
## Estimate   1.9939e+03 1994.62
## Std. Error 3.6691e+02  366.91
##
## -2 log L: 129.2647
```

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.