L04 Latencies and Delays¹

Michael Höhle¹

¹Department of Mathematics, Stockholm University, Sweden

** m hoehle

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Statistical Methods in Infectious Disease Epidemiology Epidemiology, Biostatistics and Prevention Institute University of Zurich, Switzerland



Outline

- Back-calculation method
 - Back-projection for the 2011 STEC/HUS outbreak
 - Discussion and Extensions

2 Nowcasting

Overview

- Back-calculation method
 - Back-projection for the 2011 STEC/HUS outbreak
 - Discussion and Extensions

2 Nowcasting

STEC/HUS Outbreak in Germany 2011 (1)

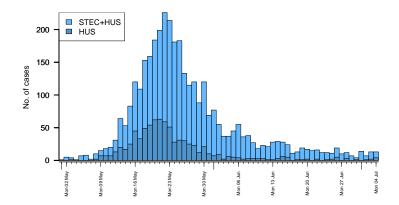
 Outbreak of Shiga toxin-producing E. coli (STEC) O104:H4 in Germany May–July 2011 associated with sprouts

	STEC	HUS
N (% of total)	2987 (78)	855 (22)
Median age (years)	46	42
Female (%)	58	68
Deaths	18	35
Case-fatality-ratio (%)	0.6	4.1

- Hemolytic-uremic syndrome (HUS) is a disease characterized by hemolytic anemia, thrombocytopenia and acute kidney failure.
- HUS can be a complication of an STEC infection.
- Onset of HUS occurs a median of 5 days (IQR: 4–7) days after onset of the STEC related diarrhea.

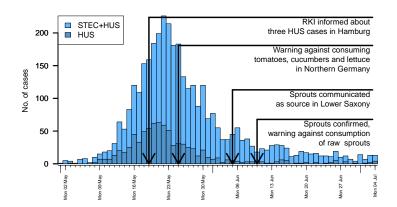
STEC/HUS Outbreak in Germany 2011 (2)

 Retrospective curve illustrating the onset of diarrhea of confirmed patients per day (where available: STEC 2715, HUS 783



STEC/HUS Outbreak in Germany 2011 (2)

 Retrospective curve illustrating the onset of diarrhea of confirmed patients per day (where available: STEC 2715, HUS 783



Example: STEC/HUS Outbreak in Germany 2011 (3)

- However, during the outbreak the situation is not as clear.
- Incubation period and reporting delays complicate real-time tracking of key indicators for detecting epidemic trends.
- Illustration: Day of hospitalization of HUS cases and the day the HUS case arrives at the RKI

[Animated curve of reporting delay of HUS cases]

Focus on implication of time lags

Time lags during the STEC outbreak, e.g.,

- the delay between exposure to the disease and onset of diarrhea in cases
- the inherent reporting delay present in any public health surveillance system

Goal of back-projection:

Infer exposure times of HUS patients from the retrospective epidemic curve of diarrhea onsets in order to reconstruct the infection curve.

Goal of nowcasting:

Extrapolate currently available counts by taking the reporting delay from the past into account. Add uncertainty indication to this extrapolation.

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Motivation for back-projection

- There is a time delay between time of infection and the onset of the disease. This time delay is often denoted *incubation time*.
- Usually, only onset of disease can be observed. Examples:
 - Time to AIDS onset after HIV infection
 - Onset of diarrhea after consumption of sprouts (STEC/HUS)
- Let D be a discrete random variable describing the delay in number of time units. Assuming this delay is constant over time let $f(d), d = 0, 1, 2, \ldots$, be the PMF of D.

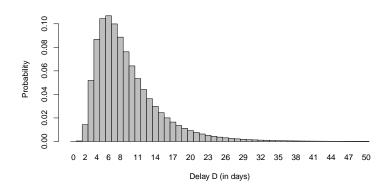
Back-projection

Interest is often in the time of exposure of individuals, but data is only available about their time of disease onset

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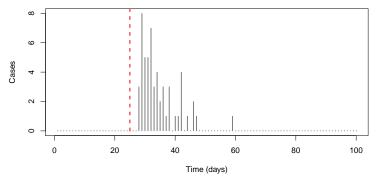
Incubation time as a random variable

• Example: D as discretized version of a log-normal distribution with $\log \mu = 2$, $\log \sigma = 0.6$ and $d_{\rm max} = 50$.



Example 1: Point source outbreak at time t_0

- Assume a point source is active on day $t_0=25$ infecting a total of n=55 individuals and f_D as in the previous example.
- The following time series for disease onsets is observed:

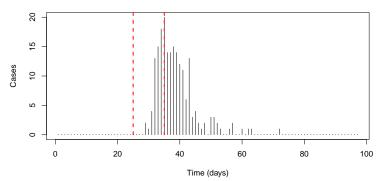


 To identify the possible source, interest is in inferring infection times from the onset times.

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Example 2: Point source during an interval

- Assume a point source is active for l days from day t_0 on infecting a total of n individuals, where individuals are equally likely to be infected within $[t_0, t_0 + l 1]$.
- Example $t_0 = 25$, l = 10 and n = 200.



Simple back-projection methods (1)

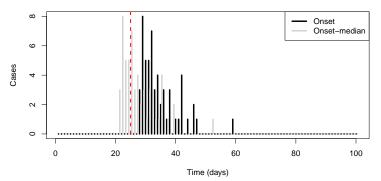
- Method 1: Determine the exposure interval by subtracting the shortest incubation time from the first case and the longest incubation from the last case of the epidemic curve
- R-code for outbreak Examples 1 & 2

```
subtract.minmax <- function(y, d.pmf,eps=1e-3) {
   exposure.left <- head(which(y>eps),n=1) - ((0:d.max)[head(which(d.pmf>eps),n=1)])
   exposure.right <- tail(which(y>eps),n=1) - ((0:d.max)[tail(which(d.pmf>eps),n=1)])
   structure( c(exposure.left,exposure.right-exposure.left),names=c("t0","l"))
}
subtract.minmax(y.ts, d.pmf)
## t0 1
## 26 1
subtract.minmax(y.l.ts, d.pmf)
## t0 1
## 27 13
```

Simple back-projection methods (2)

Method 2: Subtract the median incubation time from each onset.

```
subtract.median <- function(y,d.pmf) {
   d.median <- (0:length(d.pmf)-1)[which(cumsum(d.pmf)>0.5)][1]
   structure(c(tail(y,n=-d.median),rep(0,d.median)),names=names(y))
}
subtract.median(y.ts,d.pmf)
```



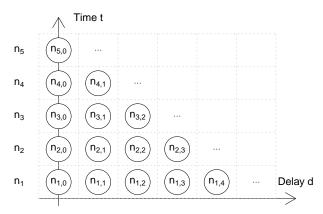
 This method is not recommendable since it ignores the order of events in the epidemic curve.

Non-parametric back-projection by Becker et al.

- Becker et al. proposed a non-parametric back-projection method for discrete time interval data.
- Their motivating application was a back-projection of AIDS cases to HIV incidence (before the use of antiretroviral therapy).
- The method differs from the the individual based continuous time parametric back-calculation of Brookmeyer et al.
- However, it equally presumes a fixed and known incubation time distribution.

Model and notation (1)

 $n_{t,d}$ – Number of individuals exposed in interval t = 1, ..., T having an incubation of time d (i.e. observed at time t + d)



 y_t – The observed number of incident cases in interval t

$$y_t = \sum_{i=M}^{L} n_{i,t-i}, \quad t=1,\ldots,T.$$

Model and notation (2)

 n_t – Number of individuals infected in interval t, i.e.

$$n_t = \sum_{d=0}^{\infty} n_{t,d}.$$

• Assume $n_t \sim \text{Po}(\lambda_t)$ and as a consequence

$$n_{t,d} \sim \text{Po}(f(d)\lambda_t),$$

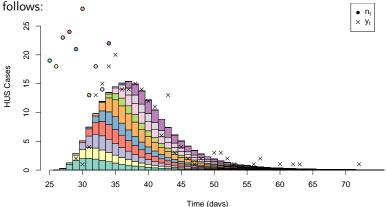
where $f(\cdot)$ is the PMF of the incubation time.

• As a consequence $y_t \sim Po(\mu_t)$, where

$$\mu_t = \sum_{i=1}^t E(n_{i,t-i}) = \sum_{i=1}^t f(t-i)\lambda_i.$$

Model and notation (3)

• The convoluted μ_t from the previous foil can be illustrated as



• Thus backprojection is the inverse problem of deducing the λ_t 's given the observed y_t 's.

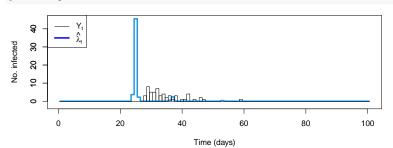
Implementation in surveillance

Code:

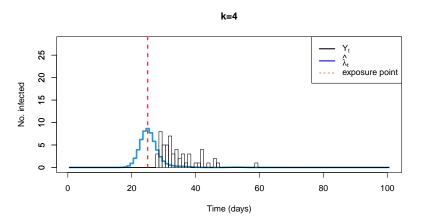
```
#Create vector with incubation time PMF values on (0,...,d_max)
incu.pmf <- c(0, (plnorm(1:d.max,logmu,logsd) - plnorm(0:(d.max-1),logmu,logsd))/plno
#Create sts object
require("surveillance")
sts <- new("sts",epoch=1:length(y.ts),observed=matrix(y.ts,ncol=1))
#Backproject using the method by Becker et al. (1991)
bp.control <- list(k=0,eps=1e-3,iter.max=100,verbose=TRUE,eq3a.method="C")
sts.bp.k0 <- backprojNP(sts, incu.pmf=incu.pmf, control=bp.control)</pre>
```

• Plotting code:

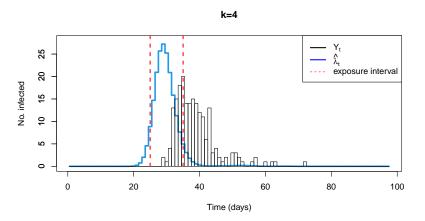
```
plot(sts.bp.k0,xaxis.labelFormat=NULL)
```



Back-projection for outbreak Example 1



Back-projection for outbreak Example 2

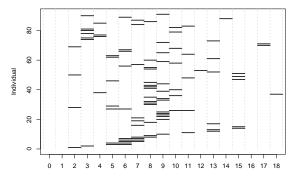


Uncertainty of the estimates

- Problem: The non-parametric back-projection (NPBP) does not provide any measures of uncertainty for the estimate $\hat{\lambda}$
- Two sources of uncertainty exists:
 - Sampling variation in the observed y_t
 - Uncertainty in the estimation of the incubation time

Estimation of the incubation time (1)

 Determination of the incubation time PMF from 91 cases with a well known exposure time (foreign cases, restaurant cluster, etc.)

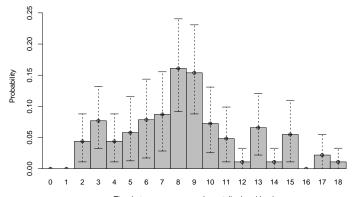


Time between exposure and onset diarrhea (days)

Goal: Non-parametric estimate of the probability mass function

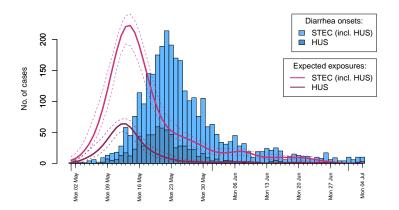
Estimation of the incubation time (2)

ullet Estimated PMF using Turnbull's method (Turnbull) for interval censored data and point-wise 95% CIs by the percentile method on R=999 additional bootstrap samples



Back-projection for the 2011 STEC/HUS outbreak (4)

 Werber et al. (2013) refines the incubation time estimation by using a Weibull interval censored regression model adjusting for age, sex and HUS in 114 symptomatic adults from six cohorts.



Discussion

- The non-parametric method needs no underlying assumptions about the mode of transmission (person to person, point source, etc.).
- During an outbreak one should choose T such that the incidence cases observed at time y_T are reliable (i.e. sufficiently complete), i.e. T should not be too close to "now".
- A good recent review of back-projection methods can be found in Egan et al.

Outline

- Back-calculation method
- 2 Nowcasting

Nowcasting – what's the situation?

- Opposite to forecasting, we just want to know what the situation is "now" during an outbreak, i.e. in a ideal setup of no reporting delay

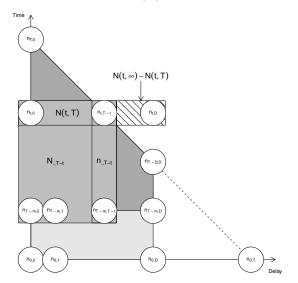
 → nowcasting.
- The term is basically a revival of what has been extensively studied as reporting delay during the AIDS/HIV epidemic, see
 e.g. Kalbfleisch et al. and Harris.
- Nowcasting was used for real-time tracking daily hospitalizations during the 2009 A/H1N1 influenza (Donker et al.).
- There is a close connection between nowcasting and claims reserving in actuarial sciences (England et al.).

Nowcasting Notation (1)

- Let $n_{t,d}$ be the number of cases which occur on day t and become available with a delay of d days, where $t=0,\ldots,T$ with T being now and $d=0,\ldots,D$.
- Problem: $n_{t,d}$ is unknown when d > T t see reporting triangle
- $N(t,T) = \sum_{d=0}^{\min(T-t,D)} n_{t,d}$ is the number of cases which occured on t and who are reported until time T
- Aim of nowcasting: predict the total number of cases, i.e.

$$N(t,\infty) = \sum_{d=0}^{\infty} n_{t,d} = \sum_{d=0}^{D} n_{t,d}.$$

Nowcasting Notation (2) – Reporting triangle



Nowcasting Methods (1)

- Alternative: The reporting delay for an event follows a distribution with probability mass function $f(d) = f_d$, d = 0, 1, ..., D.
- We will assume time homogeneity of the delay distribution
- Let $F(d) = \sum_{x=0}^{d} f(x)$ be the CDF of the delay distribution.
- Lawless presents the following nowcast procedure

$$\hat{N}(t,\infty) = \frac{N(t,T)}{\hat{F}(T-t)},$$

where the CDF F is estimated taking the right-truncation of the data into account, for example by using the reverse time hazard function.

Nowcasting Methods (2)

Alternative model in Donker et al.

$$N(t, T) \sim \operatorname{Bin}\left(N(t, \infty), \hat{F}(T - t)\right)$$

• In this model inference is about estimating the size parameter in a binomial distribution, i.e.

$$\hat{N}(t,\infty) = \underset{n \geq N(t,T)}{\arg \max} \left\{ f_{\mathsf{Bin}}(n,\hat{F}(T-t)) \right\}$$

Nowcasting Methods (3)

• The counts of the reporting triangle can also be thought of as an incomplete contingency table with

$$n_{t,d} \sim \text{Po}(\lambda_t \cdot f_d), \quad t = 0, \dots, T, \ 0 \le d \le \min(T - t, D),$$

where λ_t is the expected number of new events occurring at time t.

- Altogether, T + D + 2 parameters are to be estimated.
- The above presentation lends itself to log-linear modeling, i.e. with parametric, semi-parametric or non-parametric linear predictor

$$\log \mu_{t,d} = \log(\lambda_t) + \log(f_d) = s(t; \beta) + v(d; \theta),$$

where $E(n_{t,d}) = \mu_{t,d}$.

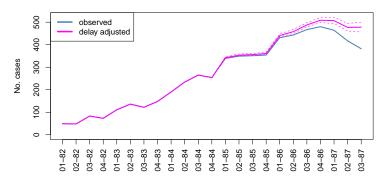
Example: AIDS registry data from the CDC (1)

 Zeger et al. contains an analysis of 6190 homosexual AIDS cases classified by quarter of diagnosis and the number of quarters between diagnosis and report to the CDC

```
##
             165 35 NA NA NA NA NA NA NA NA NA NA
## 01-87 317
               80 54 13 NA NA NA NA NA NA NA NA NA
## 04-86 353
                        14 NA NA NA NA NA NA NA
## 03-86 345
                  35 18 10
                             6 NA NA NA NA NA NA
## 02-86 313
                  29 15 10
                                7 NA NA NA NA NA
## 01-86 294
                  27 10 13
                                    NA NA NA NA NA
## 04-85 216
                  23 21 10
## 03-85 206
               58
                 36
## 02-85 215
                                               NA NA
                  26
                     19 15
## 01-85 188
                 36 22
                                                O NA
## 04-84 159
               36
## 03-84 149
                  26 16 10
## 02-84 140
               51
                  16 12
## 01-84 119
              41
                      4
## 04-83
          94
               26
## 03-83
          80
               24
## 02-83
          97
## 01-83
          67
## 04-82
          52
              10
## 03-82
          59
               11
## 02-82
          36
## 01-82
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```

Example: AIDS registry data from the CDC (2)

- The model is an instance of a generalized linear model, which can be fitted in R using the function glm
- Point estimate for the delay adjusted $N(t, \infty)$'s in the AIDS example (+ pointwise predictive distributions).



Discussion

- In practice the delay distribution often time-inhomogeneous. In this situation a proportional hazards model for the reverse time hazard function can be used (Kalbfleisch et al.; Pagano et al.).
- Back-projection based on registry data for an ongoing epidemic is often to be seen concurrently with delay adjustments (Brookmeyer et al.; Zeger et al.; Kalbfleisch et al.).

Literature I

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Literature II

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- Harris, J. E. "Reporting Delays and the Incidence of AIDS". <u>JASA</u> 85, no. 412 (1990): 915–924.
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Literature III



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Turnbull, Bruce W. "The Empirical Distribution Function with Arbitrarily Grouped, Censored and Truncated Data".

Journal of the Royal Statistical Society. Series B (Methodological) 38, no. 3 (1976): pp. 290–295. ISSN: 00359246.

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Literature IV



Zeger, S. L., L. C. See, and P. J. Diggle. "Statistical methods for monitoring the AIDS epidemic". Stat Med 8, no. 1 (Jan. 1989): 3–21.