

# The Mathematics and Statistics of Infectious Disease Outbreaks

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L9: Univariate outbreak detection<sup>1</sup>

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<sup>1</sup>LaMo: 2020-08-06 @ 15:53:31

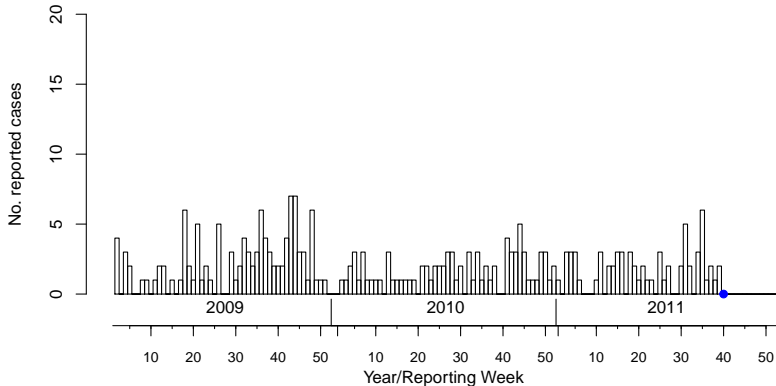
# Overview

- 1 Monitoring of univariate count data time series
  - Statistical Framework for Aberration Detection
  - Simple Algorithm for Ad-Hoc Detection
  - Farrington algorithm and beyond
- 2 A System for Automated Outbreak Detection in Germany
- 3 Discussion

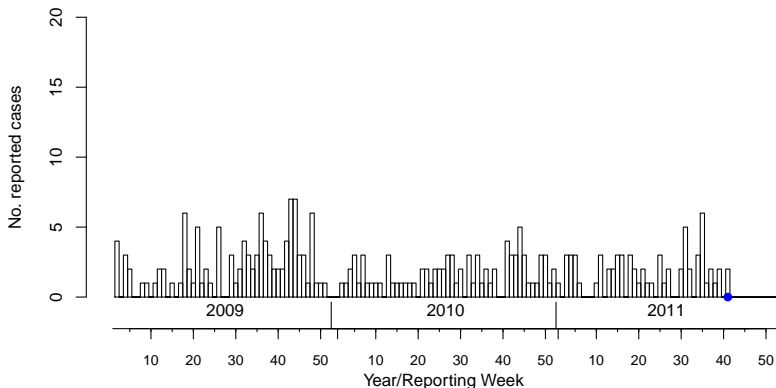
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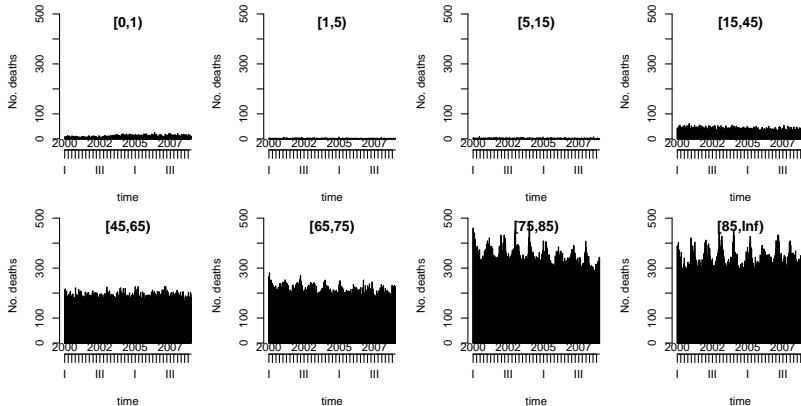


## Example – The EuroMOMO project (1)

- European monitoring of excess mortality for public health action (EuroMOMO)
- Aim: develop and strengthen real-time monitoring of mortality across Europe in order to enhance the management of serious public health risks such as pandemic influenza, heat waves and cold snaps
- Main outcome of mortality monitoring: excess mortality
- In this course: Focus on monitoring aspect

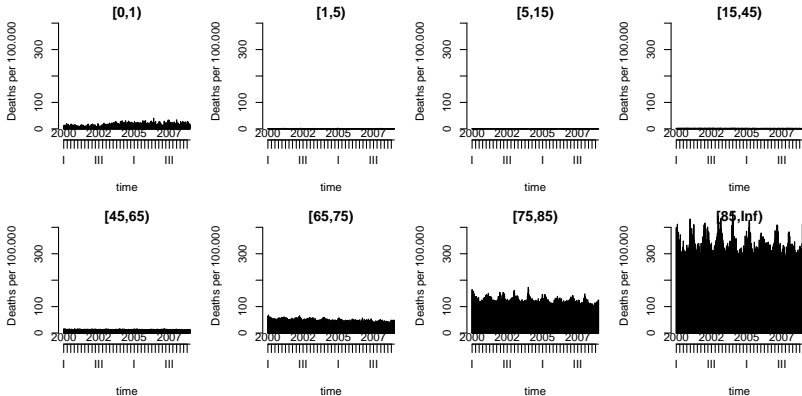
## Example – The EuroMOMO project (2)

Weekly danish mortalities 2000-2008 in 8 age-groups as provided by Statens Serum Institute (Höhle and Mazick, 2010).



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## Statistical Framework for Aberration Detection (2)

- The detectors are initially only based on the one-step-ahead predictive distribution at each time point (Shewhart-like control chart):
  - Let  $G(y_s | y_1, \dots, y_{s-1}; \theta)$  be the distribution of  $Y_s$  in case everything is in-control.
  - If the actual observed value  $Y_s = y_s$  is extreme in  $G$ , this is evidence against things being in-control.
  - The alarm threshold  $a_{1-\alpha, s}$  at each time point is calculated as the  $(1 - \alpha)$ 'th quantile of the predictive distribution. If  $y_s > a_{1-\alpha, s}$  then we have an alarm.
- This can be generalized to more sequential control charts accumulating information, e.g. cumulative sum (CUSUM) methods.



## Intermezzo: Estimation, prediction and uncertainty

- Data  $\mathbf{y}$  are the observed value of a random variable  $\mathbf{Y}$  characterized by a parametric model with density  $f(\mathbf{y}; \boldsymbol{\theta})$ .
- Aim: predict the value of a random variable  $\mathbf{Z}$ , which, conditionally on  $\mathbf{Y} = \mathbf{y}$  has distribution function  $G(\mathbf{z}|\mathbf{y}; \boldsymbol{\theta})$ , *depending on  $\boldsymbol{\theta}$* .
- Simplest form of the prediction problem:

$$Y_1, \dots, Y_n \stackrel{\text{iid}}{\sim} f(y; \boldsymbol{\theta}),$$

and the task is to predict  $Z = Y_{n+1}$ .

- In *time series 1-step-ahead prediction* the observations are correlated and the aim is to predict  $\mathbf{Z} = Y_{n+1}$ .

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## Example: Predicting a new $N(\mu, \sigma^2)$ observation (1)

- Let  $Y_1, \dots, Y_n \stackrel{\text{iid}}{\sim} N(\mu, \sigma^2)$  with unknown  $\mu$  and  $\sigma^2$ . Then

$$\frac{Y_{n+1} - \bar{Y}}{s \sqrt{1 + \frac{1}{n}}} \sim t(n-1),$$

where  $\bar{Y} = \frac{1}{n} \sum_{i=1}^n Y_i$  and  $s^2 = \frac{1}{n-1} \sum_{i=1}^n (Y_i - \bar{Y})^2$  are the sample mean and sample variance of  $\mathbf{Y}$ , respectively.

- A  $(1 - 2\alpha) \cdot 100\%$  two-sided **prediction interval** (PI) is thus given by

$$\bar{Y} \pm t_{1-\alpha}(n-1) \cdot s \cdot \sqrt{1 + \frac{1}{n}}.$$

## Example: Predicting a new $N(\mu, \sigma^2)$ observation (2)

- A *plug-in*  $(1 - 2\alpha) \cdot 100\%$  two-sided **prediction interval** for  $Y_{n+1}$  is:

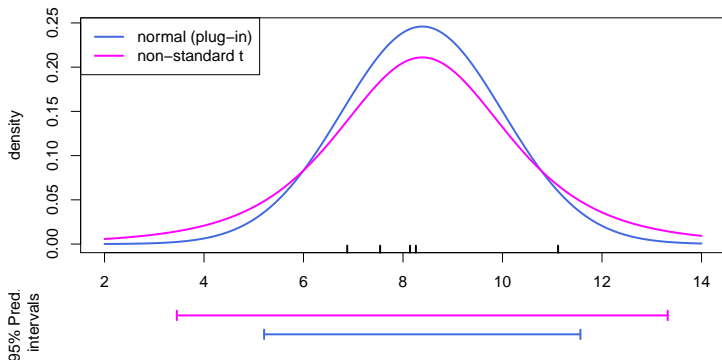
$$\bar{Y} \pm z_{1-\alpha} \cdot s.$$

- Both of these are not to be confused with a  $(1 - 2\alpha) \cdot 100\%$  two-sided **confidence interval** for  $\mu$ :

$$\bar{Y} \pm z_{1-\alpha} \cdot \frac{s}{\sqrt{n}}.$$

## Example: Predicting a new $N(\mu, \sigma^2)$ observation (3)

- Illustration: PIs based on  $n = 5$  observations from  $N(\mu, \sigma^2)$ .



- For  $n = 5$  the 95% plug-in PI corresponds to a 85% PI. The 95% CI for  $\mu$  is 7.2–9.6, which only corresponds to a 46% PI.

## Summary: Ad-Hoc Outbreak Detection Algorithm

- Predict value  $y_s$  at time  $s = (s^w, s^y)$  using a set of reference values from window of size  $2w + 1$  up to  $b$  years back.
- Let  $n = b(2w + 1)$  and compute threshold as the upper 97.5% quantile of the predictive distribution for  $y_s$ , i.e.

$$a_{0.975,s} = \bar{y} + t_{0.975}(n-1) \cdot s \cdot \sqrt{1 + \frac{1}{n}}.$$

- Sound alarm, if  $y_s > a_{0.975,s}$ .

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# Challenges of surveillance data

Issues making the statistical modelling and monitoring of surveillance time series a challenge:

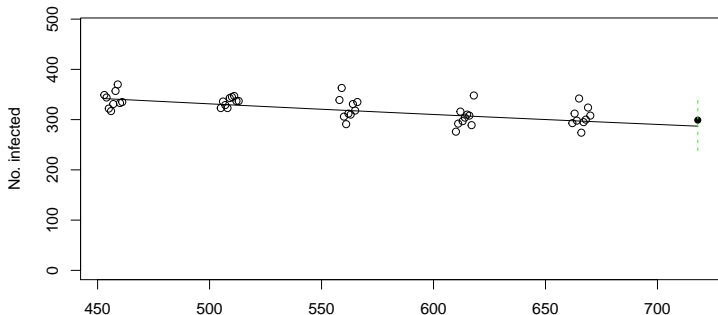
- Lack of clear case definitions
- Under-reporting and reporting delays
- Often no denominator data
- Seasonality
- Low number of reported cases
- Presence of past outbreaks
- Existence of concurrent “explanatory” processes



## Farrington algorithm (1) – basic model

- Predict value  $y_s$  at time  $s = (s^w, s^y)$  using a set of reference values from window of size  $2w + 1$  up to  $b$  years back.

Prediction at time  $t=718$  with  $b=5, w=4$



- Fit overdispersed Poisson generalized linear model (GLM) to the  $b(2w + 1)$  reference values where  $E(y_t) = \mu_t$ ,  $\text{Var}(y_t) = \phi \cdot \mu_t$  with  $\log \mu_t = \alpha + \beta t$  and  $\phi > 0$ .

## Farrington algorithm (2) – outbreak detection

Predict and compare:

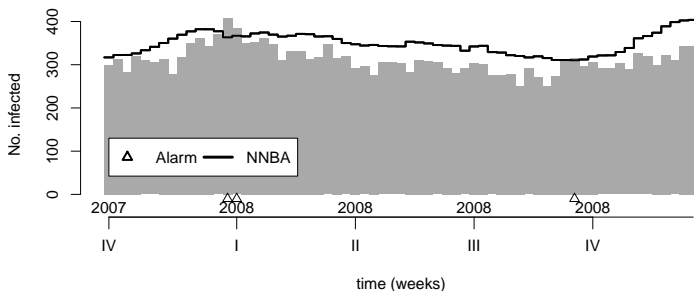
- An approximate  $(1 - \alpha)$  one-sided prediction interval for  $y_s$  based on the GLM has upper limit
$$a_{1-\alpha,s} = \hat{\mu}_s + z_{1-\alpha} \cdot \sqrt{\text{Var}(y_s - \hat{\mu}_s)}$$
- If the observed  $y_s$  is greater than  $a_{1-\alpha,s}$ , then flag  $s$  as outbreak

Refinements of the algorithm include:

- Computation of the prediction interval on a transformed scale
- Use a re-weighted fit with weights based on Anscombe residuals in order to correct for outliers
- Low count protection

## Application: Danish mortality data (age group 75-84 years)

- Results of the old and improved Farrington algorithm, respectively, with  $w = 4$ ,  $b = 5$  and  $\alpha = 0.005$  starting at W40-2007:



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## System Design

- Salmon, Schumacher, and Höhle (2016) describes a system integrating outbreak detection algorithms into the epidemiological workflow

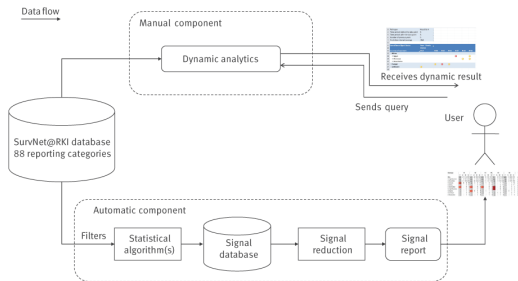


Figure source: Salmon, Schumacher, and Höhle (2016)

- Example of using machine learning methods for the more than 30,000 time series

## Application on Salmonella Montevideo 2009-2010

Results from the extended Farrington procedure using last five years as reference values:

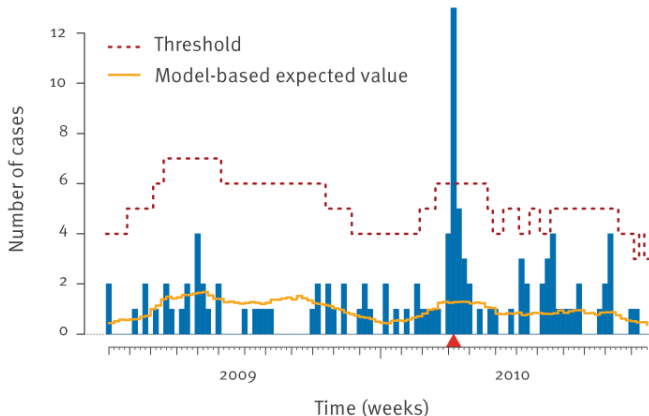


Figure source: Salmon, Schumacher, and Höhle (2016)

# Salmonella Report for W41–46 of 2013

## Weekly Report at National Level:

Serotype	Week 41				Week 42				Week 43				Week 44				Week 45				Week 46			
	$y_t$	$o_t$	$\mu_t$	$U_t$	$y_t$	$o_t$	$\mu_t$	$U_t$	$y_t$	$o_t$	$\mu_t$	$U_t$	$y_t$	$o_t$	$\mu_t$	$U_t$	$y_t$	$o_t$	$\mu_t$	$U_t$	$y_t$	$o_t$	$\mu_t$	$U_t$
Salmonella, all serotypes	466	27	512	691	373	23	485	650	370	16	461	620	356	15	439	601	411	8	417	580	290	14	390	540
S. Typhimurium	107	2	151	221	103	1	145	214	108	2	140	208	106	5	134	202	142	4	127	191	90	4	120	181
S. Enteritidis	158	11	154	230	123	12	142	212	115	11	131	194	84	4	124	189	80	1	116	182	62	2	107	168
S. Infantis	25	6	9	18	16	3	8	17	8	1	8	18	10	-	8	17	2	-	7	17	5	-	7	16
S. Derby	4	NA	5	11	2	NA	5	11	7	NA	5	11	3	NA	5	11	4	NA	5	11	1	-	5	11
S. Manhattan	7	NA	0	2	4	NA	0	2	4	NA	0	2	3	NA	0	2	3	NA	0	2	NA	NA	0	2
S. Typhimurium, monophasic	2	NA	0	2	2	NA	0	2	2	NA	0	2	6	NA	0	2	5	NA	0	3	3	NA	0	3
S. Agona	2	NA	1	4	7	4	1	4	2	1	1	4	3	2	1	4	1	NA	1	4	3	2	1	4
S. Virchow	4	NA	3	8	1	NA	3	8	3	NA	3	7	1	NA	3	7	5	1	3	7	1	NA	3	7
S. Muenchen	3	NA	1	4	3	NA	1	4	NA	NA	1	4	3	NA	1	4	2	NA	1	4	NA	NA	1	4

Table source: Salmon, Schumacher, and Höhle (2016)

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## Discussion

- The presented methods are implemented in the R package *surveillance* (Salmon, Schumacher, and Höhle, 2016)
- Developing, maintaining and improving automatic outbreak detection systems is an interdisciplinary activity!
  - Even more work could be put into user adaptation.
  - Delay adjusted monitoring (Salmon, Schumacher, Stark, et al., 2015)
- The system proved to be a good insurance against missing anything important – see e.g. Gertler et al. (2015)

# Literature I



Gertler, Maximilian et al. (2015). “Outbreak of cryptosporidium hominis following river flooding in the city of Halle (Saale), Germany, August 2013”. In: *BMC Infectious Diseases* 15.1, p. 88. ISSN: 1471-2334. DOI: 10.1186/s12879-015-0807-1. URL: <http://www.biomedcentral.com/1471-2334/15/88>.



Höhle, M. and A. Mazick (2010). “Aberration detection in R illustrated by Danish mortality monitoring”. In: *Biosurveillance: A Health Protection Priority*. Ed. by T. Kass-Hout and X. Zhang. CRC Press, pp. 215–238.



RKI (2012). “Salmonella Newport-Ausbruch in Deutschland und den Niederlanden, 2011”. In: *Epidemiologisches Bulletin* 20. Available as [http://www.rki.de/DE/Content/Infekt/EpidBull/Archiv/2012/Ausgaben/20\\_12.pdf](http://www.rki.de/DE/Content/Infekt/EpidBull/Archiv/2012/Ausgaben/20_12.pdf), pp. 177–184.

## Literature II



Salmon, M., D. Schumacher, and M. Höhle (2016). “Monitoring Count Time Series in R: Aberration Detection in Public Health Surveillance”. In: *Journal of Statistical Software* 70.10. Also available as vignette of the R package *surveillance*. DOI: [10.18637/jss.v070.i10](https://doi.org/10.18637/jss.v070.i10).



Salmon, M., D. Schumacher, K. Stark, and M. Höhle (2015). “Bayesian outbreak detection in the presence of reporting delays”. In: *Biometrical Journal* 57.6. <http://dx.doi.org/10.1002/bimj.201400159>, pp. 1051–1067.