**Supporting Information File 1: model used for outbreak detection**

To detect abnormalities in outbreaks, we compared four algorithms implemented in the R “Surveillance” package. All the algorithms are based on the same idea, which is the use of the number of cases observed during the previous years for a given week to construct an expected (“predictive”) distribution of the number of cases observed for the current year and the corresponding week. The algorithms can be divided into 3 steps:

*Step 1*: Construction of a predictive distribution from a set of reference values for the number of reported cases for the current week of the year , using the reported cases from the previous years

* + the previous weeks before in the current year
  + the weeks around in the previous years

Let be the number of reported cases during weekof the current year and be the number of reported cases during week for the th  year in the past (1). We have:

*Step 2:* The number of cases observed is considered abnormal (aberrations) for the current year and current week ≥ 95th percentile of this distribution.

*Step 3:* We considered an alarm only if multiple aberrations occurred (more than two aberrations in 4 weeks).

* We compared several methods to construct the predictive distributions from the reference values . First, the Centers for Diseases Control and Prevention (CDC) method, which use a simple Gaussian model. Second, the Farrington method, which uses a quasi-Poisson distribution. Third, the Robert Koch Institute (RKI) method, which assumes a Gaussian or a Poisson based on the mean of the cases counts for the previous years. Finally, we also used a Bayesian approach, assuming a negative-binomial distribution with parameters estimated through a Bayesian procedure (2). We compared the models with the following parameters :
  + - = 1, 2, 3, 4, 5, 6, 7, and 8
    - = 1, 2, 3 and 4
    - = 1, 2, 3 and 4

A detailed description of each method can be found in the references given above.

* For each Province, the optimal algorithm and set of parameters was selected using the Euclidean distance between the sensitivity and 1-specificity, with a real major outbreak defined according to expert-based thresholds.

References:

1. Hohle M, Riebler A, Paul M. The R-Package ’surveillance’ [Internet]. CRAN R-project; 2015 [cited 2015 Oct 23]. Available from: https://cran.r-project.org/web/packages/surveillance/vignettes/surveillance.pdf

2. Monitoring Count Time Series in R: Aberration Detection in Public Health Surveillance | Salmon | Journal of Statistical Software. [cited 2018 Sep 26]; Available from: https://www.jstatsoft.org/article/view/v070i10