

Food products identified as source of a foodborne disease outbreak by a fast and robust likelihood estimation

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Abstract

Identifying a specific product causing a foodborne disease outbreak can be difficult, especially when dealing with large amounts of suspicious food items and weak epidemiological evidence. A previously described likelihood model (Norström et al. 2015), improved within the OHEJP NOVA project, helps to prioritize food products that should be sampled for laboratory analysis. It is the aim of our study to integrate this approach into state of the art tracing software FoodChain-Lab (FCL; <https://foodrisklabs.bfr.bund.de/foodchain-lab>) developed at BfR to facilitate outbreak investigations.

The model improved by Kausrud et al. in R (Ihaka and Gentleman 1996) uses wholesale data, the distribution of disease cases and census data to sort food items by their estimated likelihood to be the source of an outbreak. We developed a fast and secure intuitive software module using the Web Assembly technology (Haas et al. 2017) allowing professionals to embed the module easily into other applications.

We integrated the module into the FCL web application for tracing (FCL Web; <https://fcl-portal.bfr.berlin>) to provide an intuitive and user-friendly solution. This solution combines a simple data input with extended data wrangling to make the calculation of the NOVA model as easy as possible. Since the model can be executed directly inside the web browser and therefore does not rely on any server environment, the possibility of data leakage can be highly reduced. The implementation of the advanced likelihood model into FCL Web increase the availability of this model and provides investigators easy, fast and reliable usage to improve outbreak investigation workflows.

Keywords

foodborne outbreak investigation, FoodChain-Lab, web application, model, WebAssembly

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Conflicts of interest

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