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## Towards an open-source, unified platform for disease outbreak analysis

Disease outbreak analysis is a rapidly expanding methodological field, with a number of statistical methods being developed to harness the potential of diverse epidemiological and genetic data. Unfortunately, few of these approaches are widely available to the community as computer software, and a unified platform for the analysis of disease outbreaks is still lacking. Being free, open-source, and hosting the largest collection of tools for data analysis, the R software appears as an ideal host for the development of such platform. As a matter of fact, R is hosting a growing number of R packages for infectious disease epidemiology, such as surveillance, for analysing surveillance data and outbreak detection, R0, TreePar and EpiEstim for reproduction number estimation, and outbreaker for transmission tree reconstruction.

To ensure coherence between these different approaches and promote further developments, basic tools for storing and handling outbreak data are also needed. In order to fill this gap, a community of epidemiologists, statisticians and bioinformaticians has developed the R package OutbreakTools. This software, created during a hackathon for the analysis of disease outbreaks in R (<http://sites.google.com/site/hackoutwiki/>), provides classes for a flexible and coherent representation of outbreak data, alongside procedures to manipulate, summarize and visualize these data.

After giving an overview of some leading-edge R tools for infectious disease epidemiology, we introduce the main features of OutbreakTools, and discuss the future of R as a platform for the analysis of outbreak data. We also discuss the possibility of exploiting this platform for designing powerful yet user-friendly tools for Public Health agencies.