simulist: An R package to simulate disease outbreak line list and contacts data

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Summary

Epidemic and pandemic preparedness and response requires robust analysis methods and a deep understanding of outbreak data. We introduce `simulist`, an open-source R package for simulating realistic infectious disease outbreak data. It is designed to allow users to generate data with specific disease outbreak characteristics by enabling flexible parameterisation of processes and variables, including epidemiological parameters (e.g. delay distributions), contact patterns and demographic information, to simulate two common datasets in outbreak settings: 1) line list data, and 2) contact tracing data. It also offers post-processing of line list data to replicate right-truncation of real-time outbreak data, as well as creating "messy" data with realistically incomplete and inconsistent values.

Statement of need

Synthetic data, which is generated by a known simulation process, is useful in many scenarios where a "ground truth" is required, including teaching concepts on data collection, data cleaning and data visualisation; and testing analysis methods for precision, adequacy and robustness. In the analysis of infectious disease outbreaks, termed *outbreak analytics* (Carter et al., 2021; Jombart, 2021; Polonsky et al., 2019), one of the most common forms of data is a line list. This is a tabular dataset where each row corresponds to a single case in the outbreak, recording information on person, place and time. Information for each case can include, but is not limited to, personal information (name, age, sex), key event dates (date of symptom onset, date of hospitalisation, date of outcome) (Figure 1), clinical outcomes, and geographic information (coordinates, administrative area). Understanding and characterising the transmissibility and severity of infectious disease outbreaks typically use line list data (Cori et al., 2017).

In the ecosystem of R packages for epidemiology, there are a range of tools for simulating and analysing line list data (Jombart et al., 2025), however, there are no stable, actively maintained and tested R packages that simulate epidemiologically realistic line list data[1]. The `simulist`

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[1]This was found from an unstructured scoping review we conducted of other outbreak simulation tools, documented here: https://epiverse-trace.github.io/simulist/#related-projects

R package offers functionality to simulate outbreak data (line list and contact tracing) with options for users to define the epidemiological and demographic characteristics of the outbreak (Figure 2), while also being designed on the principle of maximum interoperability with other related R packages, e.g. epicontacts (Campbell et al., 2017), epiparameter (Lambert et al., 2025), and cleanepi (Mané et al., 2024). Accepting epidemiological parameters directly from epiparameter, an R package with a library of parameter estimates from the literature, facilitates generating synthetic data with the characteristics of past outbreaks.

State of the field

The majority of outbreak analytics uses R (R Core Team, 2025). There are many R packages that help to answer common epidemiological questions in an outbreak (Tamayo Cuartero et al., 2025). These range from basic data wrangling and data science tools such as the tidyverse (Wickham et al., 2019), to advanced methods, for example nowcasting/forecasting of transmissibility (Abbott et al., 2020). Additionally, there are several initiatives that teach epidemiology using R tooling (Batra et al., 2021; Valle Campos & Minter, 2025), resulting in an active ecosystem of open-source tooling, teaching, and community engagement (Morgan & Pebody, 2022), for example the epinowcast community.

However, to our knowledge, there are no existing tools that offer an easy method to generate synthetic outbreak data, with a defined and highly customisable simulation model. The simulist R package, part of the Epiverse-TRACE ecosystem, aims to fill this niche by offering line list simulation functionality that includes: custom parameterisation of epidemiological delay distributions, population-wide or age-stratified hospitalisation and death risks, uniform or age-structured populations, constant or time-varying case fatality risks, and customisable proportions of case types and contact tracing follow-up. This is complemented by post-processing to enable emulation of real-time outbreak dynamics (e.g. right-truncation and outbreak snapshotting) and introducing realistic messiness to the data to mimic the types of issues encountered by people working with empirical outbreak data.

Key functions

simulist offers two modules of functionality: 1) simulation and 2) post-processing. In the simulation module there is a function for simulating a line list, a function for simulating contact tracing data, and a function for simulating both. Respectively, these output an outbreak line list (data.frame), a contact tracing dataset (data.frame), and lastly both an outbreak line list and contact tracing dataset that are linked (i.e. from the same outbreak) (list of data.frames). All simulation functions internally call a branching process model (Farrington, 2003) with the option of network-adjusted contact patterns. This accounts for the fact that choosing someone at random by following up a contact chooses individuals with a probability proportional to their number of contacts (Alexander & Day, 2010; Blumberg et al., 2014). No data are stored in the package, all outbreak data are generated upon calling a simulation function. All simulation functions can be run without requiring the user to specify any parameters (i.e. function arguments, see function documentation for defaults), but all functions offer a range of arguments to modify the characteristics of the outbreak data. The parameters that can be specified by the user are organised into two levels. The parameters that control the branching process, key epidemiological delays, risks, and demographic parameters are function arguments because they are more likely to be adjusted by users. Parameters thought to rarely require changing, except for advanced use cases, are passed to the function via a configuration list, to prevent the function signature being overly complex. A helper function is provided to automatically generate the configuration list with sensible defaults, and allow easy modification; this helper is called by default in the simulation functions.
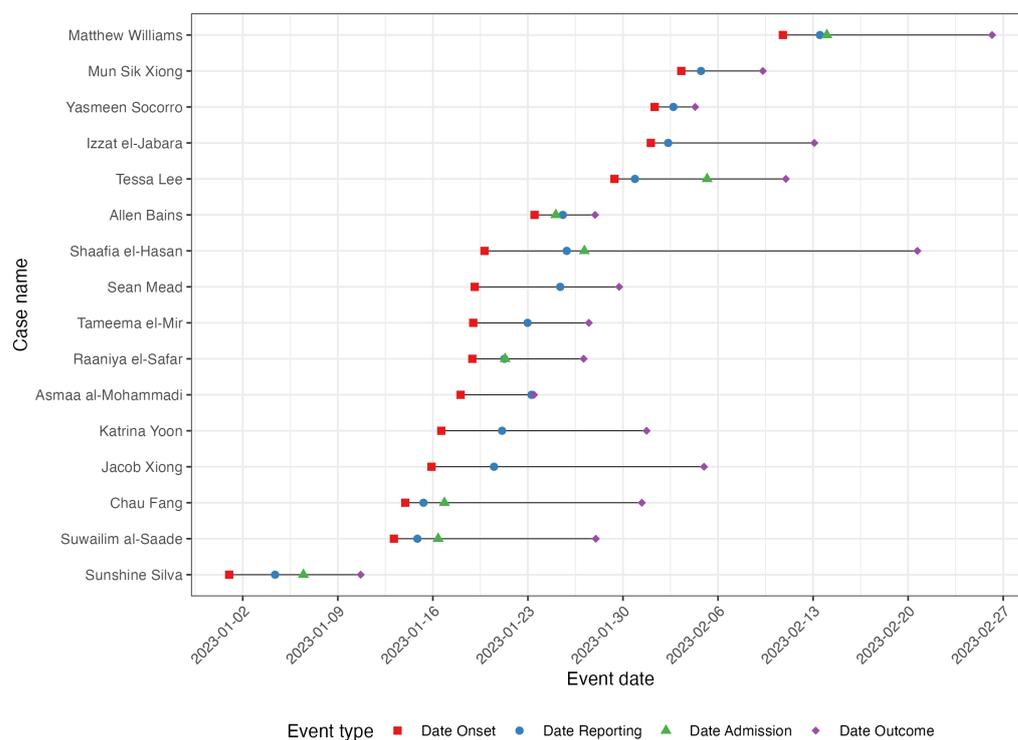
Figure 1: A connected dot plot of the timeline of events in a simulated line list. Data are simulated and all case names are randomly generated. See *Visualising simulated data vignette* at https://epiverse-trace.github.io/simulist/articles/vis-linelist.html or in R (`vignette("vis-linelist", package = "simulist")`) for more information.
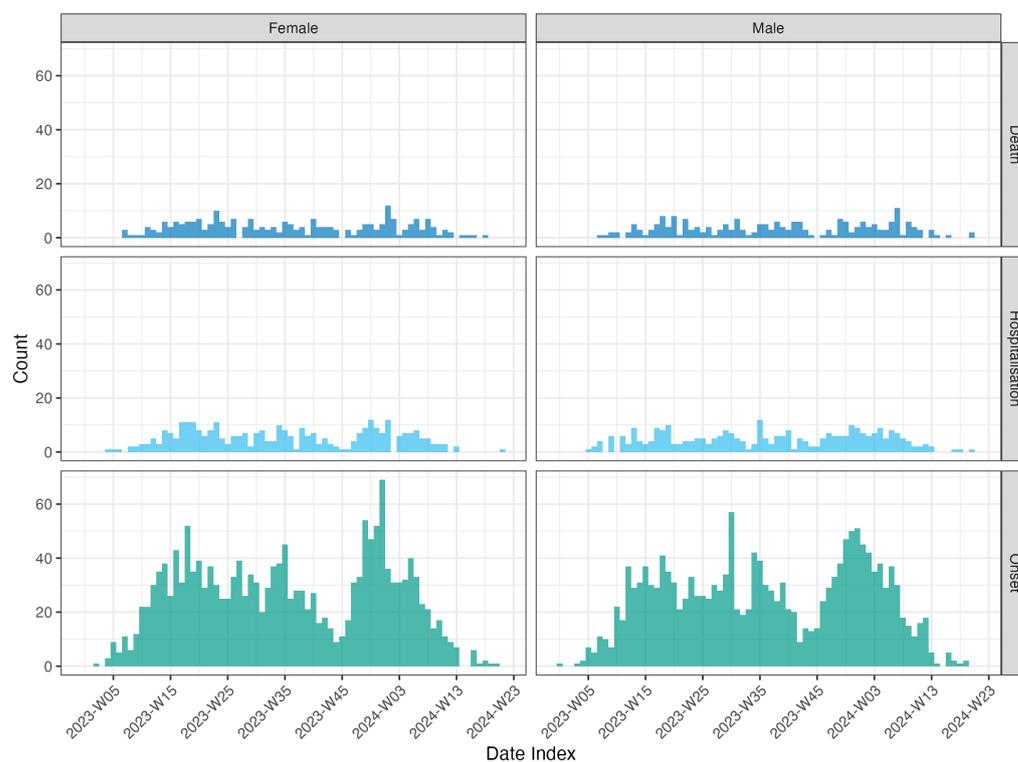
Figure 2: The weekly incidence of symptom onset, hospital admission and deaths facetted by sex for a simulated line list and aggregated and plotted with `incidence2` ([Taylor, 2020](#)). See *Visualising simulated data vignette* at https://epiverse-trace.github.io/simulist/articles/vis-linelist.html or in R (`vignette("vis-linelist", package = "simulist")`) for more information.
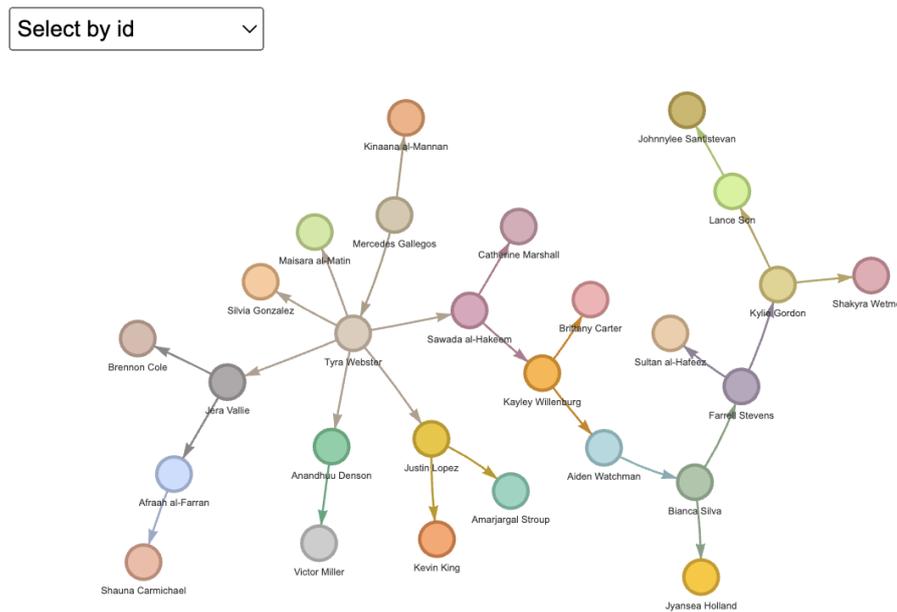
Figure 3: A simulated contact network (line list and contact tracing dataset), converted to an `<epicontacts>` object and plotted with `epicontacts` (this network is interactive when rendered in an IDE or online). See *Visualising simulated data vignette* at https://epiverse-trace.github.io/simulist/articles/vis-linelist.html or in R (`vignette("vis-linelist", package = "simulist")`) for more information.

Here we highlight some of the simulation functionality available:

Age-stratified hospitalisation and death risks: The outbreak simulation includes three risks: hospitalisation risk, death risk in hospital, and death risk outside of hospital, which all, by default, accept a single number to define the population risk. In many infectious disease outbreaks, risk is non-uniform across ages. `simulist` accepts risks stratified by age using a user-defined `data.frame`, so that any age-stratification can be specified. See the Age-stratified hospitalisation and death risks vignette for a complete explanation.

Age-structured population: The outbreak simulation in `simulist` assumes a uniform population age between a lower and upper limit (0 and 90 by default). However, to accurately generate synthetic data for outbreak scenarios where the population age structure is known, this can be input into the outbreak simulation, again using a user-defined `data.frame` to flexibly specify an arbitrary number of age groups and proportions. See the Age-structured population vignette for more details and a worked example.

Time-varying case fatality risk: In addition to the ability to age-stratify hospitalisation and death risks, as outlined above, it is also possible to vary the fatality risk through time in the outbreak simulation. This is set up to accept a user-defined R function that takes the baseline risk and the simulation time (t) and calculates the fatality risk at time t. This is again set up in such a way as to maximise flexibility to the users and allows continuously varying (monotonic and non-monotonic functions) or discrete step-wise functions. The aim of this functionality is to phenomenologically mimic vaccination or non-pharmaceutical interventions without mechanistically modelling these in the simulation model. See the Time-varying case fatality risk vignette for more explanation and examples.

Simulating empirical outbreak data: The outbreak simulation produces exact, standardised,

Lambert et al. (2026). simulist: An R package to simulate disease outbreak line list and contacts data. *Journal of Open Source Software*, *11*(119), 8781. https://doi.org/10.21105/joss.08781.

and complete data, hereafter referred to as *ideal* data. However, in reality, those working with line list data often encounter a myriad of issues where the data they have available differs from the *ideal* data. In `simulist`, we offer multiple post-processing functions that modify *ideal* line list data to include empirical characteristics. Currently, `simulist` post-processing functions can introduce 1) real-time outbreak data artifacts such as right-truncation, 2) inconsistent, missing, and duplicated data, so-called *messy* data, and 3) censor dates to the nearest time unit (e.g. day, week, etc.) as well as introduce a *weekend effect* where reporting is lower on weekends (Gallagher et al., 2025).

Other functionality is documented in the Get Started vignette and Wrangling simulated outbreak data vignette. All vignettes are included in the R package.

Package Design

The `simulist` package is developed around certain design principles: *interoperability* with other R packages for upstream (e.g. `epiparameter`) or downstream (e.g. `epicontacts`, see Figure 3) use; *ease of use* of functions (all simulation functions have sensible defaults for use out-of-the-box); and *transparency*, all design decisions are documented in the Design Principles vignette and help with developer onboarding. Simulation functions output a `data.frame` (or `list` of `data.frame`s) enabling users to easily transform and manipulate the data, for example with the tidyverse R packages; and post-processing functions are compatible with `data.frame` subclasses (e.g. `<tibble>` or `<data.table>`).

Other resources

`simulist` is documented through vignettes and function documentation, and is also included within Epiverse-TRACE open-source tutorials.

Availability

The `simulist` R package is open-source and licensed under MIT. The source code is available on GitHub. The package can be downloaded from CRAN, R-universe or GitHub. Code to reproduce figures in this paper can be found at the `simulist` GitHub repository.

Acknowledgements

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