workshop vignette

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This vignette summarises the findings from the *100 days and 100 lines of code* workshop, hosted in December 2022 by Epiverse-TRACE.

This document is a draft, the final version will be published on Epiverse's blog after it has been reviewed by other Epiverse members and workshop participants * Participants who have contributed so far: Sara Hollis, Anne Cori, Geraldine Gomez, Juan Daniel Umana, David Santiago Quevedo, Chaoran Chen, and John Lees

What should the first 100 lines of code written during an epidemic look like?

To answer this question, we invited 40 experts, including academics, field epidemiologists, and software engineers, to take part in a 3-day workshop, where they discussed the current challenges, and potential solutions, in data analytic pipelines used to analyse epidemic data. In addition to highlighting existing technical solutions and their use cases, presentations on best practices in fostering collaboration across institutions and disciplines set the scene for the subsequent workshop scenario exercises.

What R packages and tools are available to use during an epidemic?

To investigate this in a similar setting to what an outbreak response team would experience, workshop participants were divided into groups, and asked to develop a plausible epidemic scenario, that included:

- A situation report, describing the characteristics of the epidemic
- A linelist of cases and contact tracing data, by modifying provided datasets containing simulated data
- A set of questions to address during the analytic process

Groups then exchanged epidemic scenarios and analysed the provided data to answer the questions indicated the previous group, as if they were a response team working to solve an outbreak. Details about each of these outbreak scenarios and the analytic pipelines developed by the groups are summarised in this vignette.

Simulating epidemic data

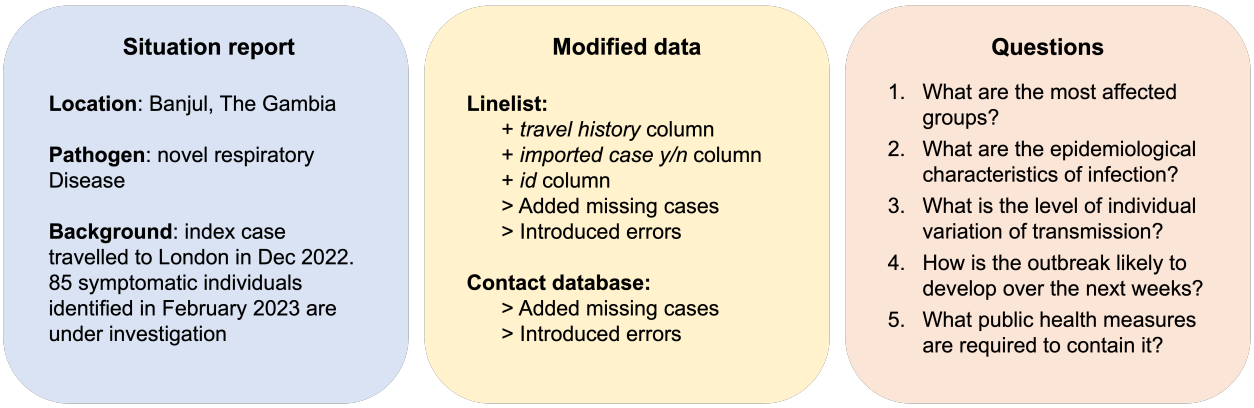
Before the workshop, a fictitious dataset was created, which consisted of a linelist and contact tracing information.

To generate linelist data, the package `bpmodels` was used to generate a branching process network. Cases were then transformed from the model output to a linelist format. To add plausible hospitalisations and deaths, delay distributions for SARS-CoV were extracted from `epiparameter`.

To create the contact tracing database, a random number of contacts was generated for each of the cases included in the linelist. These contacts were then assigned a category of *became case*, *under follow up* or *lost to follow up*, at random.

- Through this workshop, we identified the need for a tool to simulate outbreak data in a linelist format, to test analysis methods and other packages while having control over the characteristics of the test data. For this purpose, an R package is currently in progress, see simulist.

Scenario 1: Novel respiratory disease in The Gambia



Analytic pipeline for scenario 1 (analysed by group 2)

- Data cleaning
  - `linelist` to standardise date format
  - `cleanr` from previous Hackathon
- Delay distributions
  - `fitdisrplus` to fit parameteric distributions to scenario data
  - `epiparameter` to extract delay distributions from respiratory pathogens
  - `EpiNow2` to fit reporting delays
  - `EpiEstim` / `coarseDataTools` to estimate generation time/serial interval of disease
  - `epicontacts`
  - `mixdiff` to estimate delay distributions and correct erroneous dates at the same time (still under development)
- Population demographics
  - Would like to have had access to an R package similar to `ColOpenData`
- Risk factors of infection
  - Used R4epis as a guide on how to create two-way tables and perform Chi-squared tests
- Severity of disease
  - `datadelay` for CFR calculation
  - Implementation of method developed by AC Ghani, 2005 to estimate CFR
- Contact matching
  - `diyar` to match and link records
  - `fuzzyjoin` to join contact and case data despite misspellings or missing cell contents

- Epi curve and maps
  - Used `incidence` and `incidence2` for incidence calculation and visualisation
  - `raster` to extract spatial information from library of shapefiles
- Reproduction number
  - `APEestim`
  - `bayEStim`
  - `earlyR`
  - `epicontacts`
  - `epidemia`
  - `epiFilter`
  - `EpiNow2`
  - `EpiEstim`
  - `R0`
  - `outbreaker2`
  - Used this comparison table to choose the most appropriate package.
- Superspreading, by using these resources:
  - `fitdistrplus`
  - `epicontacts`
- Epidemic projections
  - `incidence` R estimation using a loglinear model
  - `projections` using Rt estimates, SI distributions and overdispersion estimates
- Transmission chains and strain characterisation
  - IQtree and nextclade to build a maximum likelihood tree and mannually inspect it
  - Advanced modelling through phylodynamic methods, using tools like BEAST

Data analysis step	Challenges
Data cleaning	Not knowing what packages are available for this purpose
Delay distributions	Dealing with right truncation Accounting for multiple infectors
Population demographics	Lacking tools that provide information about population by age, gender, etc.
Risk factors of infection	Distinguishing between risk factors vs detecting differences in reporting frequencies among groups
Severity of disease	Knowing the prevalence of disease (denominator) Right truncated data Varying severity of different strains
Contact matching	Missing data Misspellings
Epicurve and maps	NA dates entries not included Reporting levels varying over time
Offspring distribution	Right truncation Time varying reporting efforts Assumption of a single homogeneous epidemic Importation of cases
Forecasting	Underlying assumption of a given R distribution, e.g., single trend, homogeneous mixing, no saturation

Scenario 2: Outbreak of an unidentified disease in rural Colombia

Situation report

Location: Ibague, Colombia

Pathogen: unspecified

Background: suspected link to a zoonotic reservoir, since early cases were farmers.
Envoy is colourblind and unable to deal with complex visual information

Modified data

Linelist:
+ *travel to rural area* column
+ *case occupation* column
+ *notification date* column
+ *notification delay* column
> Added missing cases
> Introduced errors

Contact database: no changes

Questions

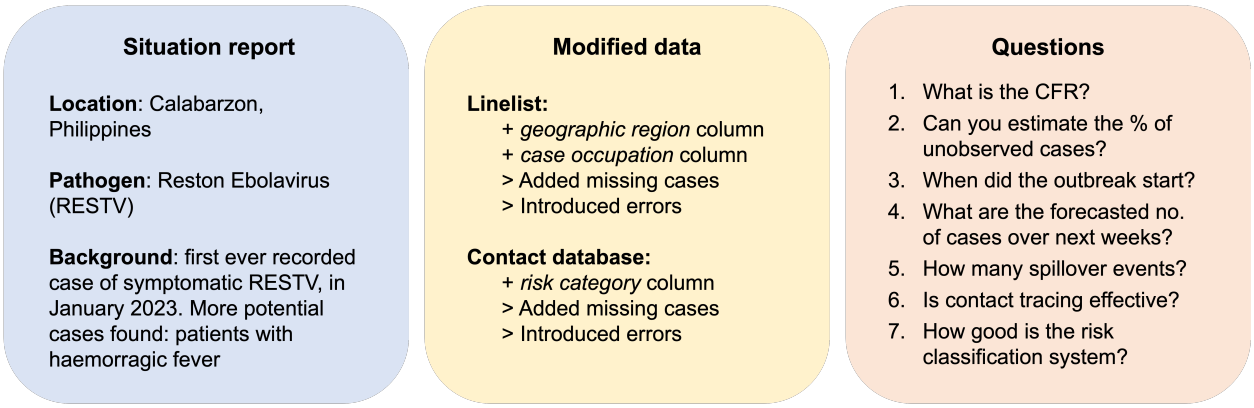
1. Have there been exposures to a zoonotic reservoir?
2. How transmissible is the disease?
3. What are the hospital bed requirements for next weeks?
4. What is the attack rate and the no. of deaths we expect?
5. Can you reconstruct transmission chains?

Analytic pipeline for scenario 2 (analysed by group 3)

- Data cleaning: manually, using R (no packages specified), to
  - Fix data entry issues in columns *onset_date* and *gender*
  - Check for missing data
  - Check sequence of dates: symptom onset → hospitalisation → death
- Data anonymisation to share with partners
  - `fastlink` for probabilistic matching between cases contacts, based on names, dates, and ages
- Case demographics
  - `apyramid` to stratify data by age, gender, and health status
- Reproductive number calculation, by using two approaches:
  - Manually, by calculating the number of cases generated by each source case, data management through `dplyr` and `data.table`
  - Using serial interval of disease, through `EpiEstim` or `EpiNow2`
- Severity of disease
  - Manual calculation of CFR and hospitalisation ratio
- Projection of hospital bed requirements
  - `EpiNow2` to calculate average hospitalisation duration and forecasting
- Zoonotic transmission of disease
  - Manual inspection of cases' occupation
  - Use of IQtree and `ggtree` to plot phylogenetic data
- Superspreading
  - `epicontacts`
- Calculation of attack rate
  - Unable to calculate, given the lack of seroprevalence data

Data analysis step	Challenges
Data anonymisation	Dealing with typos and missing data when generating random unique identifiers
Reproduction number	Right truncation Underestimation of cases due to reporting delays
Projection of hospital bed requirements	Incomplete data (missing discharge date) Undocumented functionality in R packages used
Zoonotic transmission	Poor documentation Unavailability of packages in R Differentiation between zoonotic transmission and risk factors- need for population data
Attack rate	Not enough information provided

Scenario 3: Reston Ebolavirus in the Philippines



Analytic pipeline for scenario 3 (analysed by group 4)

- Data cleaning
  - Importing data with `rio`, `readxl`, `readr`, or `openxlsx`
  - Rename variables with `janitor`
  - Initial data checks with `pointblank`, `assertr`, `compareDF`, or `skimr`
  - Vertical data checks with `matchmaker`, `lubridate`, or `parsedate`
  - Horizontal data checks with `hmatch`, `assertr`, or `queryR`
  - Detect duplicates with `janitor` and `tidyverse`
  - Checking for consistency with `dplyr`, or `powerjoin`
  - Translation with `matchmaker`
- Delay distributions
  - `fitdistrplus` to fit parameteric distributions to epidemic data
- Case demographics
  - `apyramid` to stratify data by age, gender, and health status
  - `ggplot2` to visualise data
- Outbreak description
  - `sitrep` to generate reports
- Visualisation of geographic data
  - `sf` for static maps
  - `leaflet` for interactive maps

- Generation of tables
  - `gtsummary` for static tables
  - `janitor` for interactive tables
- Severity of disease
  - `EpiNow2` and `survival` to calculate CFR
- Attack rate
  - `gadm` function to get population data
  - `epitabulate` to describe data
  - `sf` and `ggplot2` to plot data
- Forecasting
  - `EpiEstim`
  - `EpiNow2`
  - `bpmodels`
- Spillover events
  - By cross-referencing contact data with occupations
- Effectiveness of contact tracing
  - By calculating the proportion of case follow-ups and comparing the delay of disease exposure to the follow-up delay
- Transmission trees
  - `epicontacts`
  - `ggplot2`

Data analysis step	Challenges
Detection of outliers	No known tools to use
Severity of disease	Censoring
Spillover events	Missing data

Scenario 4: Emerging avian influenza in Cambodia

Situation report

Location: Phnom Penh, Cambodia

Pathogen: emerging avian influenza

Background: outbreak started in a small rural community of poultry farmers in Cambodia. Cases now also reported in the capital

Modified data

Linelist:
+ *outcome* column
+ *origin* column
+ *exposure* column
> Added missing cases
> Introduced errors

Contact database: no changes

Questions

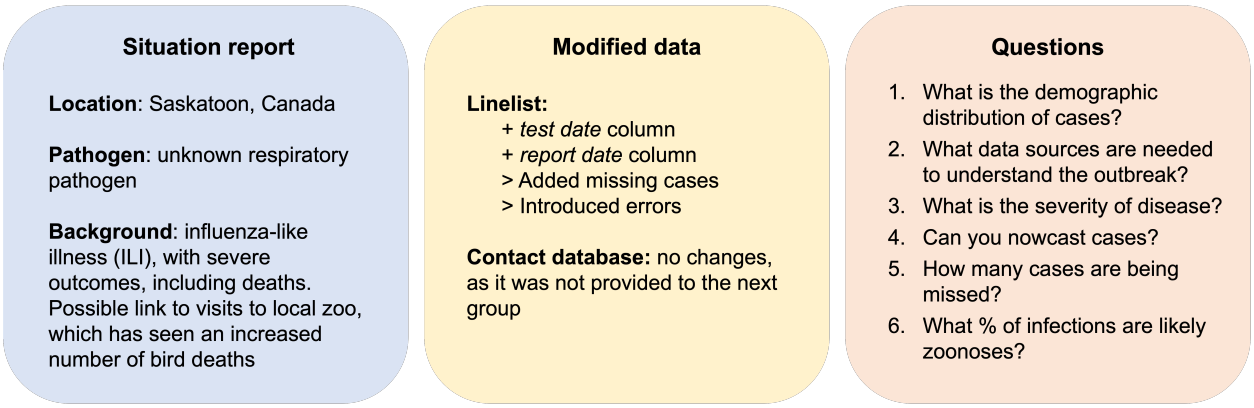
1. What are the % of human vs zoonotic transmission?
2. What is the epidemic potential?
3. Is the outbreak contained by the implemented measures?
4. What is the severity of disease?
5. Can underreporting be estimated?
6. Are more hospital beds needed?
7. Should they cull poultry farms?

Analytic pipeline for scenario 4 (analysed by group 5)

- Data cleaning
  - tidyverse
  - `readxl` to import data
  - `dplyr` to remove names
  - `lubridate` to standardise date formats
  - Manually scanning through excel to check for errors
- Reproduction number
  - `EpiEstim`
- Severity of disease
  - Manually using R to detect missing cases
  - `epiR` to check for data censoring

Data analysis step	Challenges
Data cleaning	No available R packages specific for epidemic data
Reproduction number	Difficulty finding parameter estimations in the literature
Serial interval	Lack of a tool to check for parameter estimates
Severity	Missing cases Need for an R package for systematic censoring analysis

Scenario 5: Outbreak of respiratory disease in Canada



Analytic pipeline for scenario 5 (analysed by group 1)

- Define project structure
  - Defining the script's structure with `cookiecutter`, `reportfactory`, and `orderly`
  - Ensuring reproducibility of the analysis with iRODS and Git
  - Working in a group with GitHub
- Data cleaning
  - Importing data with `readr` or `rio`
  - Checking for errors with `linelist`, `janitor`, `parsedate`, `matchmaker`, or `lubridate`
  - `janitor` to eliminate duplicates
  - `naniar` to check for missing data

  - `epitrix` to anonymise data
- Delay distributions
  - `epitrix`
  - `fitdistrplus` to fit parameteric distributions to scenario data
- Case demographics
  - `apyramid` to stratify data by age, gender, and health status
- Nowcasting
  - `incidence2` to visualise incidence from linelist data
  - `epiparameter` to extract infectious disease parameter data
  - `EpiEstim` or `EpiNow2` for Rt calculation
- Severity of disease
  - Calculation of hospitalisation and mortality rates- no R package specified
- Zoonotic transmission
  - `forecast`
- Generation of reports
  - `incidence` for static reports
  - Quarto and R markdown for dashboards

Data analysis step	Challenges
Project structure	Working simultaneously on the same script and managing parallel tasks Anticipating future incoming data in early pipeline design
Data cleaning	Large amount of code lines used on (reasonably) predictable cleaning (e.g. data sense checks) Omitting too many data entries when simply removing *NA* rows Non standardised data formats Implementing rapid quality check reports before analysis
Delay distributions	Identifying the best method to calculate, or compare functionality of tools Need to fit multiple parametric distributions and return best, and store as usable objects
Severity of disease	Censoring and truncation Underestimation of mild cases Need database of age/gender pyramids for comparisons
Forecasts	Need option for fitting with range of plausible pathogen serial intervals and comparing results Changing reporting delays over time Matching inputs/outputs between packages
Zoonotic transmisison	Need for specific packages with clear documentation How to compare simple trend-based forecasts

What next?

Scenarios developed by the *100 days* workshop participants illustrate that there are many commonalities across proposed analytics pipelines, which could support interoperability across different epidemiological questions. However, there are also several remaining gaps and challenges, which creates an opportunity to build on existing work to tackle common outbreak scenarios, using the issues here as a starting point. This will also require consideration of wider interactions with existing software ecosystems and users of outbreak analytics insights. We are therefore planning to follow up this vignette with a more detailed perspective article discussing potential for broader progress in developing a 'first 100 lines of code'.