



Time invariant analysis of epidemics with EpiCompare

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Abstract

We present **EpiCompare**, an R package that supplants and enhances current infectious disease analysis pipelines and encourages comparisons across models and epidemics. A major contribution of this work is the set of novel *time-invariant* tools for model and epidemic comparisons - including time-invariant prediction bands. **EpiCompare** embraces R's *tidy* coding style to make adoption of the package easier and analysis faster. This paper provides an overview of both the tools in and intuition behind **EpiCompare** and a thorough demonstrating of the tools through a detailed example of a full data analysis pipeline.

Keywords: keywords, not capitalized, Java.

1. Introduction

The recent (and on-going) COVID-19 global pandemic has galvanized public interest in understanding more about infectious disease modeling and has highlighted the usefulness of research in the area of infectious disease epidemiology. Infectious diseases inflict enormous burdens on the world: millions of lives lost and trillions of dollars spent yearly. Infectious disease models typically attempt to do one or more of the following: 1) predict the spread of current and future epidemics (e.g. flu prediction [Biggerstaff *et al.* 2016](#)), 2) analyze past and current epidemics to increase scientific knowledge (e.g. historical measles outbreaks [Neal and Roberts 2004](#)), and 3) forecast or project epidemic scenarios under pre-specified parameters (e.g. [Ferguson *et al.* 2020](#)). At the same time, descriptive statistics and visualizations from universities, many branches and levels of government, and news organizations are an important first step of the process [as has been seen in the current COVID-19 epidemic](#) ([Dong *et al.*](#)

2020; CDC 2021; The Washington Post 2021).¹

With the many visualization and exploratory tools, models and modeling paradigms, and reviews and comparisons in the literature and through the MIDAS (Models of Infectious Disease Agent Study) network (MIDAS Network 2021), this field has a lot of devices to aid an individual practitioner decide the correct approach. For example, R packages such as **surveillance**, **EpiModel**, and **pomp** have all made significant steps in standardizing the flow of the data analysis pipeline for epidemic modeling through digitizing data sets, making accessible statistical models, and providing a plethora of educational material for both coding novices and experts alike (Meyer *et al.* 2017; Jenness *et al.* 2018; King *et al.* 2016).

At the same time, analysis packages often only address a specific portion of the analysis pipeline, ~~for instance focusing on certain types of models. These modeling tools, which~~ usually require learning package-specific syntax, and often don't provide easy ways to compare and assess their models on new data. Moreover, exploring, ~~and modeling and comparing~~ epidemics require transforming and *tidying* data in different ways. To fill these gaps, we present our R package **EpiCompare**. Our package's primary focus is to aid and advance research in the area of comparison and assessment of epidemic and epidemiological models. In Figure 1, we illustrate the data analysis pipeline of infectious diseases as 1) data pre-processing, 2) exploratory data analysis (EDA), 3) modeling and simulating, 4) post-processing, and 5) comparison and assessment; where each previous part of the pipeline influences the next. **EpiCompare** provides tools to aids practitioners in all areas of this pipeline.

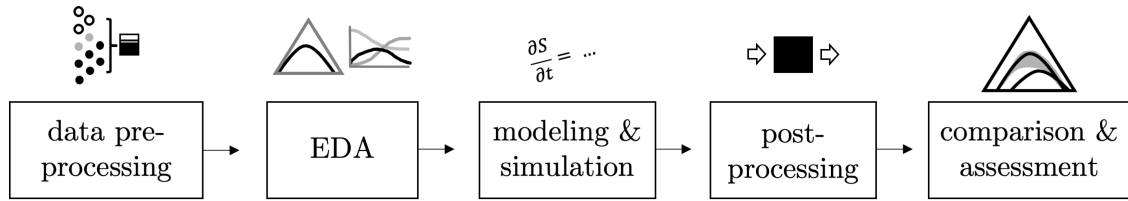


Figure 1: An idealized epidemiological data analysis pipeline.

EpiCompare also emphasizes the value of analyzing epidemics in a *time-invariant* way. Epidemics, despite by definition being a process that evolves over time, often need to be compared in a way not constrained to initial times or time scales to understand the processes at play. Time-invariant analysis can also make it easier to compare state-space models in a more global, holistic fashion. ~~Moreover, m~~ Many current time-dependent comparison tools for state-space models (e.g. SIR models) ~~highlight~~ examine the proportion of individuals in each state (at a given time) in a piece-wise / marginal fashion. ~~These This~~ approaches may reduce the amount of connections that can be seen, similar to projections of a multidimensional distribution onto a single axis at a time. Tools in **EpiCompare** give the user the ability to extend their toolkit to evaluate epidemics within a time-invariant lens. The goal of **EpiCompare** is not to supplant existing infectious disease modeling tools and software but, rather, is a concerted effort

¹[Ben says: probably should have a conclusion sentence here - seems to end abruptly. *This is less so the case now.]

to create standard and fair comparisons among models developed for disease outbreaks and outbreak data.

This paper is broken up into the following sections; section 2 motivates and showcases tools of time-invariant analysis, section 3 presents an outline of how **EpiCompare** aids a practitioner in every step of the pipeline and section 4 provides a **thorough** demonstrating of the tools through a detailed example of a full data analysis pipeline.

2. Motivation and tools for time-invariant analysis

EpiCompare delivers *time-invariant* analysis by (1) taking a global, not marginal view of how epidemics move through populations and (2) by treating full epidemics as filamental trajectories. The following section aims to highlight the strengths of *time-invariant analysis* and define the mathematical foundations that **EpiCompare**'s tools stand upon.

Mathematically, epidemics are complex objects. They can be hard to assess and compare to one another due to the differences in the diseases, the location where the outbreak occurs, how the affected population reacts, and the time ~~related~~**related** features (including start of the epidemic, speed of infection and more). Time-invariant analysis makes different epidemics easier to compare by removing many time dependent aspects of an epidemic. ~~Instead,~~ **Time-invariant analysis** focuses on the global pattern of an epidemic, via filamental trajectories, and emphasizes the number of lives affected. [Ben wants to try this sentence again.]

2.1. Motivating time-invariant analysis through the reproduction number R_0

Time-invariant analysis, as it appears in **EpiCompare**, **bypasses** many difficulties **in** comparing different epidemics. With time-invariant analysis, comparing the decades-long outbreak of HIV in the US to a 10 day outbreak of norovirus on a cruise ship is **still** possible. Time-dependent problems can arise when estimating epidemiological parameters, including the reproduction number R_0 . ~~We will use R_0 to motivate the usefulness of time-invariant analysis in this section.~~²

R_0 is probably the most famous ~~time-invariant~~ numerical summary of an epidemic and is often associated with the Susceptible-Infectious-Recovered (SIR) model (Hethcote 2000). R_0 is ~~a one-number summary of a disease and is defined as the expected number of infections caused by a single infector who is added to a completely susceptible population (Anderson and May 1992).~~ **This definition has no mention of time and hence means that R_0 is a time-invariant parameter. Yet R_0 is estimated with time-baseddependent data, which can make it a difficult quantity to estimate. For example, Gallagher *et al.* (2020) demonstrate how R_0 can be sensitive to time-baseddependent parameters such as the beginning and end of an epidemic, two quantities that generally arehard to define precisely.** ~~do not have precise definitions.~~ To demonstrate the difficulty of discerning R_0 in ~~a~~³ **another** time-dependent analysis, we first introduce Kermack and McKendrick (1927)'s SIR model. This model captures the transitions from one state to the next as a system of ordinary differential equations, where N is the total number of individuals, β is the rate of infection, and γ is the rate of recovery,

²I don't think this is a necessary sentence. I still think it adds value to the story and I'm not sure people really read section titles that are long.

³I change this so we don't confused readers that we're going show the impact in tools beyond just the estimation itself.

$$\begin{aligned}
 S'(t) &= -\frac{\beta S(t)I(t)}{N} \\
 I'(t) &= \frac{\beta S(t)I(t)}{N} - \gamma I(t) \\
 R'(t) &= \gamma I(t).
 \end{aligned}
 \tag{1}$$

From this model, the reproduction number is the ratio of the infection rate to the recovery rate, $R_0 = \beta/\gamma$, aka the ratio of the infection rate compared to the recovery rate. From this definition, given Since β and γ are both rates, it should be clear that the ratio of the two, R_0 , is a time-invariant quantity.⁴ Once R_0 is estimated, practitioners can infer important epidemic quantities such as the total number of infections or the percent of a population needed to be vaccinated to stop the sustained spread of an epidemic. Moreover, R_0 allows us to compare different diseases and different instances of outbreaks on the same scale.⁵

[Ben says: It's unclear to me why we have a subtitle here - isn't it just more motivation of time-invariant analysis with R_0 ? Also, I feel like the story is weak here. The point is to leverage R_0 to show the value of time-invariant analysis - this seems a bit more like just discussing properties of R_0 . In the follow rewrite I use "[]" and "]" to indicate that this is a section from your earlier draft.] [Shannon says: Tried to tie this better to the previous part since it's no longer a new section. also highlighted tie to time-invariant analysis and R_0 . I also wanted to bring the punch line (overlapping epidemics = same r_0) closer to the beginning so those who don't want to slog through mathematical details can get the takeaway.] Shannon tries again in blue

[Ben says: this paragraph needs to still be looked at. Also I'm not sure why this particular paragraph was c Time-invariant analysis helps practitioners to more easily compare R_0 from different outbreaks.

For example, consider two epidemics generated from the Kermack and McKendrick SIR equations. The first epidemic has parameters $\beta_1, \gamma_1 = (0.8, 0.4)$ and the second has $\beta_2, \gamma_2 = (0.64, 0.32)$. Both epidemics have populations of 1000 people with 10 individuals initially infected. Additionally note that the two reproduction numbers are the same for each epidemic, $R_0 = 2 = 0.8/0.4 = 0.64/0.32$. We plot the epidemics with traditional *state vs. time* plots⁶. In Fig. 2 we show the time-based paths for the S , I , and R states for the first 15 days of observed data. In this time-variant view, we may believe that epidemic 1 has a larger R_0 than epidemic 2 because the peak of infection occurs more quickly than in Epidemic 2. On the other hand, we may believe epidemic 2 has a larger R_0 because it's unclear if the number of infections in that epidemic has not yet peaked at time 15. In this time-variant view, we cannot determine if one epidemic has larger value of R_0 ⁷.

Since R_0 is an important value, it would be helpful to have more intuitive ways of comparing one R_0 to another. Usually numerical summaries of R_0 are presented, which while overall very helpful, may be confusing when presented along side epidemic data that are visualized in a traditional, time-dependent manner.

For example, consider two epidemics generated from the Kermack and McKendrick SIR equations where both have the same value of R_0 . The first epidemic has parameters $\beta_1, \gamma_1 =$

⁴I am trying to make it look like we are not repeating ourselves by saying R_0 is time-invariant.

⁵cool facts about r_0 , but not the central point

⁶This sentecne is out of place / doesn't connect with the other sentences.

⁷This sentnce doesn't connect wit previous examples.

(0.8, 0.4) and the second has $\beta_2, \gamma_2 = (0.64, 0.32)$. Both epidemics have populations of 1000 people with 10 individuals initially infected. An analysis may present an estimate of $\hat{R}_0 = 2$ alongside state vs. time plots like those shown in Figure 2. The paths of the epidemics in the state vs. time view seem to differ from one another including having different infection peaks. From these traditional time-based plots, there is no intuitive way to conclude that these two epidemics have the same value of R_0 .

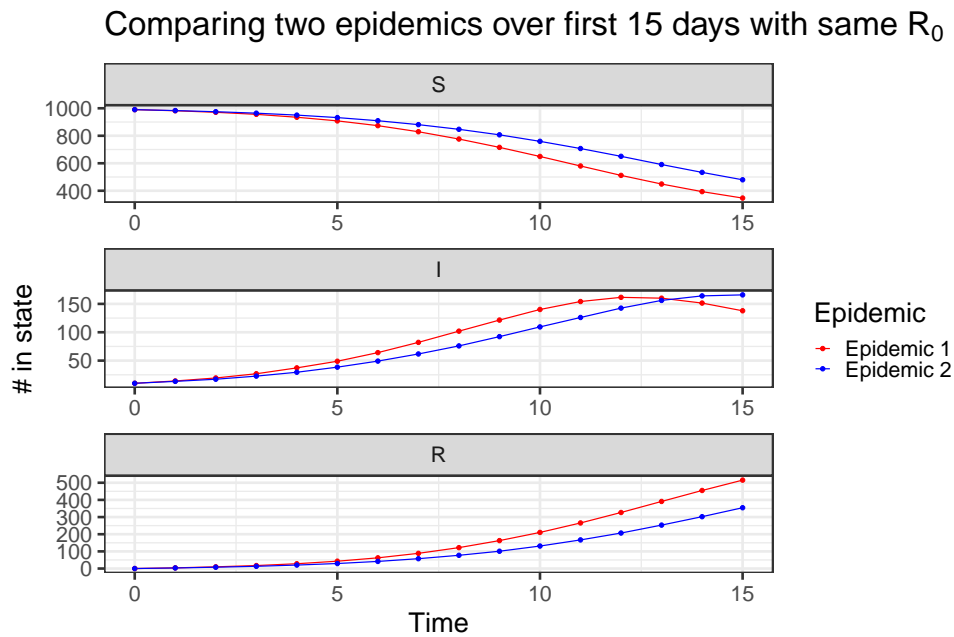


Figure 2: Example of two epidemics with different β and γ parameters but the same initial reproduction number $R_0 = 2$. Both epidemics are generated from models with $N = 1000$ individuals with $S(0) = 990$ and $I(0) = 10$.

EpiCompare provides a time-invariant tool to visualize these epidemics in a more intuitive manner, at least in regards to comparing values of R_0 . A time-invariant approach to visualizing epidemics, in comparison, allows us to directly compare R_0 from a single plot. For every time point t we have a point $(S(t), I(t), R(t))$, so we can treat epidemics as a trajectory in this three-dimensional space, as we visual in the left subplot of Figure ??, so we can visualize the trajectory of the epidemic in three-dimensional space (see Fig. 3 (left)). For state space models like in our example, given the constraint that $S(t) + I(t) + R(t)$ is always equal to N (the total population size), we can visual these point in a two-dimesional *ternary* plot, as seen in Figure 3 (right). In Fig. 3 we plot the filamental trajectories of the two epidemics in a time-invariant view. We will explain how and why this works shortly. The important takeaway is that in this time-invariant view, it is apparent that these epidemics are on “the same path.” In this case, this indicates that two epidemics have the same value of R_0 .

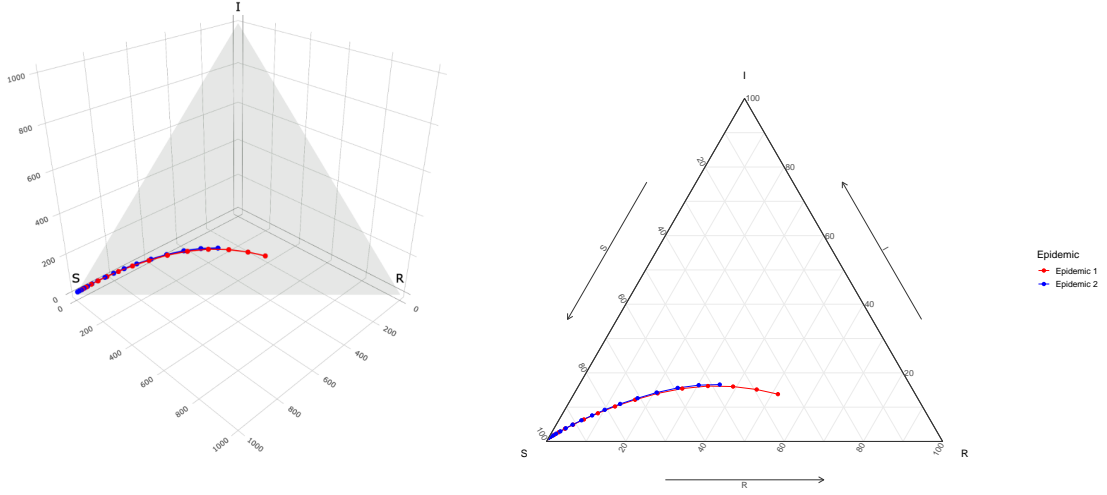


Figure 3: Left: trajectory of epidemic in three-dimensional space, plotting $(S(t), I(t), R(t))$. Right: the gray-shaded region and epidemic trajectory shown from (left) now shown in two-dimensional space. This is more commonly known as a ternary plot.

Underlying our time-invariant visualization that allowed for the comparison of R_0 in Fig. 3 is the treatment of the epidemic as a single filamental trajectory in the state space. The reason why we can visually compare R_0 in Fig. 3 is because of the time-invariant nature of the filamental trajectory associated with an epidemic. A filamental trajectory can be mathematically viewed as a set of points in space that have an ordering, and that all points on the line between these ordered points are also contained in the geometric object. For a SIR epidemic, we can represent the associated filamental trajectory ψ as

$$\psi = \{(S(t), I(t), R(t)) : S, I, R \geq 0, S + I + R = N\}_{t \in [0, T]},$$

where a mapping $\xi : s \rightarrow \mathbb{R}$ that is strictly monotonically increasing would not change the definition of ψ , i.e. $\psi_\xi \equiv \psi$ where :

$$\psi_\xi = \{(S(\xi(s)), I(\xi(s)), R(\xi(s))) : S, I, R \geq 0, S + I + R = N\}_{s \in [0, T]}.$$

[Ben says: removed this paragraph now] Since the number of individuals in each state is non-negative and the sum over the three states for a given time point sums to N , then all points in ψ will lay in a two-dimensional triangular plane in three-dimensional space. We can then which can be visualize the full filamental trajectory in a two-dimensional ternary plot. As a result, we can visualize the full filamental trajectory of an epidemic in a single ternary plot 2d plot and ultimately R_0 . [Shannon says: Show pic here?]⁸

[This section could be a bit less wordy. But generally good.] We visualize the two epidemics in a global, ternary view in Figure 3. Without getting into too much detail of the intricacies of this plot, we immediately see the points of the two filaments ψ seem to form the same

⁸Which? 3d space one? But I'm leaning against it now. 3d never looks good in a paper.

trajectory. Now, it is much clearer that ~~Model epidemic 2~~ is following the same trajectory as ~~Model epidemic 1~~ but is not as far along in the infection process.

~~As suggested a few paragraphs back,~~ The filamental trajectories in Fig. 3 seem to overlap, and we may suspect that something is fundamentally linking these two different epidemics together. Mathematically, we can show this fundamental link turns is R_0 . Let our two epidemics be presented as $\{(S_1(t), I_1(t), R_1(t))\}_{t \geq 0}$, $\{(S_2(s), I_2(s), R_2(s))\}_{s \geq 0}$ respectively. As with the example, assume both models have the same initial values $(S(0), I(0), R(0))$, and let $R_0 = \frac{\beta_1}{\gamma_1} = \frac{\beta_2}{\gamma_2}$ where β_i and γ_i are the average infection rate and recovery rate, respectively, for SIR model $i = 1, 2$. And define $a > 0$ to be the relative scalar such that $\beta_2 = a\beta_1$ if and only if $\gamma_2 = a\gamma_1$.

Theorem 1. *Let there be two SIR models as described above. Then for all $t > 0$ there exists an $s > 0$ such that $(S_1(t), I_1(t), R_1(t)) = (S_2(s), I_2(s), R_2(s))$. Moreover, $s = \frac{1}{a}t$.*

The proof of Theorem 1 relies on a fairly recent result from Harko *et al.* (2014) and is shown in detail in Proof 4.7. The consequence of Theorem 1 is that for two SIR models that have the same initial percent of individuals in each state and R_0 then for every point on the epidemic path of the first SIR model ~~is also~~ can be mapped to a point on the epidemic path of the second SIR model. In other words, the two epidemics form the same filamental trajectory. For SIR models with similar initial state percentages, time-invariant analysis allows practitioners to compare values of R_0 at a glance.

2.2. Time-invariant analysis beyond R_0 and Kermack's and McKendrick SIR Models⁹

Through the R_0 example, we see that treating epidemics like filamental trajectories embedded in a lower dimensional space allows us to better more fully compare the overall structure of the epidemic and see how the population is directly impacted. Time-invariant tools that can be useful even when the underlying generative model for the epidemic is unknown or have more than three epidemic states.

New paragraph Viewing epidemics as filamental trajectories provides a lot new ways to compare and examine epidemics in a time-invariant manner. \ben{For completed?}epidemics that have ended, one way to examine their filamental trajectories is to ~~redefine~~represent the filamental trajectory as a finite sequence of equally spaced points. ~~finite sequence of points on the filamental trajectory that are equally spaced (i.e. equa-distance between pairs of ordered points).~~ For epidemics that have "played" themselves out, one way to represent their filamental trajectories to avoid confusion stemming from impacts of temporal structure is to define them as a sequence of points their trajectory with equi-distance between each point [Shannon says: are we missing a few words in this definition?]. This representation induces a natural distance between this type of representation between epidemics, specifically:

$$d_{\text{equi-distance}}(\psi_1, \psi_2) = \int_{s \in [0,1]} (\psi'_1(s) - \psi'_2(s))^2 ds$$

where $\psi'_i(s)$ the point along ψ_1 that is s fraction of $|\psi_1|$ distance away from the start of ψ_i .¹⁰

⁹Probably will need to change this title...

¹⁰I think you're trying to say something about a distance based on the equally space points. Some clarifying questions: is ψ' the derivative? Does proportion make more sense than fraction? or simply $\frac{|\psi|}{s}$? It's only naturally time-invariant if we have a well defined ending point, right?

This distance is naturally time-invariant, and can be plugged into multiple distance-based assessment tools to examine the overall “extremeness” of points, including pseudo-density estimators and depth/local depth functions (for examples see Ciollaro *et al.* 2016; Geenens and Nieto-Reyes 2017). These extremeness estimators can be very useful when comparing between a set of simulation a set of simulated epidemics and the true epidemic. Moreover these extremeness estimators, and does not constrain the number of states of the model, though we recommend projecting the points into the unit simplex¹¹ (by making all values the proportion of the population in the given state).

New paragraph: If the set of epidemics that one is examining have only gone through a single cycle of the outbreak If one a practitioner is interested in understanding an epidemics through a single cycle realization of their outbreak (before the population of individuals have become susceptible again), then additional time-invariant tools, including prediction regions can be leveraged awk sentence¹². In these settings, EpiCompare goes we go a step further and treats epidemics more like geometric filaments (i.e. filamental trajectories without an ordering of points) than filamental trajectories. In EpiCompare, we create prediction regions that contain a the top $(1 - \alpha)$ proportion of simulated curves by defining geometric regions defined by the union of small geometric? filaments around the subset of simulations (subset grouped by measures like the above pseudo-density estimates or depth estimates). These regions look at show where in the state-space we expect the epidemic to traverse, and. Additionally, we can compare prediction regions defined by different models using many set difference distances the Hausdorff why Hausdorff specifically? distance as well as examining how well the truth epidemic matches the simulations by examining if the epidemic’s trajectory lies within the prediction region. All these mentioned? geometric structures and distance notations apply to epidemics with any number of states, and at the end of Section 3 we also highlight how these prediction regions can aid in visual comparisons for epidemics with 3 states (like the SIR models).

3. Overview of EpiCompare

In this section, we present the tools implemented in EpiCompare and explain how they aid in the data analysis pipeline. In Figure 4, we show how our package’s functions fit into the data analysis pipeline introduced in Figure 1. All front-facing functions in EpiCompare are aimed to be as user-friendly as possible. We also focus on providing the user “tidyverse” style functions, that encourage piping objects from one function to the next and follow clear “verb” naming schemes (Wickham *et al.* 2019). Although users can incorporate EpiCompare into any step in the data analysis pipeline, there are two primary points of entry. The first point of entry is the very beginning with pre-processing and visualizing raw data, and the second point of entry is after modeling and simulation. Figure 4 captures these different paths, and we highlight how to leverage EpiCompare functionalities in the subsections below.

Data pre-processing

The first step of most data analysis is “cleaning” the raw data so it can be explored. Before data can be explored, they must be collected. Sometimes individual records are collected,

¹¹I’m not sure we’ve talked about this before... I don’t think we have but am wondering if we’re getting in the weeds

¹²{What are we predicting if the epidemic is done? Update 4/6: I’m satisfied.}



Figure 4: How **EpiCompare** supplements and aids in the epidemiological data analysis pipeline.

with times of different states of the epidemic (infection, recovery, etc.) as well as individual information like network structure, location, and sub-population information. Other data collections focus on aggregate counts of individuals in each epidemic state. In fact, many times only the number of new infections at each time step (e.g. weekly case counts) is observed. In this setting, compartment totals (amounts of individuals in each state) are then imputed from those case counts and using other information about the disease and the population of interest. In **EpiCompare**, we focus on understanding the overall impact of an outbreak at the aggregate/population level, which allows for streamlined examination of overall trends of an epidemic.

To help the practitioner examine epidemics from an aggregate/population lens, we provide a function called `agents_to_aggregate()`. This function transforms data about individual/agents' initial entry into each state (e.g. start of infection, start of recovery, etc.) to an aggregate view of how many individuals were in a state at a given time. Researchers, including [Rvachev and Longini \(1985\)](#); [Anderson and May \(1992\)](#); [Worby et al. \(2015\)](#), often are interesting in more granular trends that can be detected by aggregation, conditional on subpopulations (e.g. subpopulations defined by age or sex). By combining the function `dplyr::group_by()` and `agents_to_aggregate()`, **EpiCompare** provides group level aggregation.

Besides aiding subpopulation analysis, `agents_to_aggregate()` can accommodate a wide range of information about each individual. In fact, this function can account for infinitely many states. This functionality allows the practitioner to aggregate information relative to common states (e.g. "Susceptible", "Infectious", and "Recovered") as well as more complex states (e.g. "Exposed", "iMmune", "Hospitalized"). Additionally, `agents_to_aggregate()` permits indicators for death/exit and birth/entry dates. Overall, this function is a powerful tool for pre-processing data.

Exploratory data analysis (EDA)

In the early stages of a project, familiarizing oneself with the data usually means figuring out useful combinations of visualizations and numerical summaries of the data both at population and subpopulation level. An expert coder can start with `agents_to_aggregate()` to successfully accomplish exploratory data analysis (EDA) in many ways. **EpiCompare** also includes tools that allow a novice coder to rapidly explore data, provided there are three unique epidemiological states (like in the SIR model). Building on `ggplot2` and `ggtern` packages, **EpiCompare**'s `geom_aggregate()` provides a way to explore how different subpopulations experience of an epidemic ([Wickham 2016](#); [Hamilton and Ferry 2018](#)). The function `geom_aggregate()` provides a visualization tool to holistically examine aggregate level information across different subpopulations by visualizing each subpopulation's epidemic trajectory in the three-dimensional state space. Visualization tools for three-state models were developed because SIR models are some of the most common and basic epidemic state-based models and our three-dimensional simplex representation of these epidemics emphasizes a time-invariant representation of the data (for a refresher see [Section 2](#)).

Model fitting and simulations

After getting a sense of what a past or current epidemic looks like with EDA, the next step in the data analysis pipeline is often model fitting and/or simulation. While **EpiCompare** does not focus on fitting models to data, we do provide some flexible functions for simulation of basic discrete-time epidemic-state models. These functions simulate individual-level informa-

tion based on practitioner estimated transition rates between states and can be combined with `agents_to_aggregate()` to view these simulations through an aggregate lens. The function `simulate_SIR_agents()` simulates a basic SIR epidemic with user inputs for the number of simulations, the initial number in each state, the infection and recovery parameters (β, γ), and the total number of discrete time steps. Beyond SIR models, the function `simulate_agents()` takes as input a user-specified state-transition matrix and other epidemic parameters to allow the user to create simulations for an outbreak with *any* number of states and any number of transitions among them. This flexibility in states can be used to also reflect group-based dynamics. Both of these functions allow users to explore the space of models in an intuitive way without getting bogged down by too much mathematical detail. For consistency, we have made output from `simulate_agents()` and `simulate_SIR_agents()` compatible with `agents_to_aggregate()` so aggregate information may easily be accessed.

Post-processing

If practitioners wish to compare models-to-observations or even models-to-models, they need to post-process their models and simulations to disseminate the results in an easily digestible format. In **EpiCompare**, we provide (1) functions to standardize simulation and model output from external packages and (2) a function to transform standardized simulation and model output into a format amenable to time-invariant analysis.

Modeling and simulation output can be very complex objects, and as a result, a number of epidemic modeling R packages return a special class. The special classes often contain a plethora of information about residuals, model diagnostics, input parameters, and more. While incredibly useful, these special classes can be difficult for novice coders to handle. To this end, **EpiCompare** provides a series of fortify-style methods, called `fortify_aggregate()` which transform output from infectious disease modeling and simulation packages like **pomp** and **EpiModel** into tidy-styled data frames which contain information about the total number of individuals in each state at a given time, for a given simulation. These fortify functions have output that is consistent with that of `agents_to_aggregate()`. These standardized outputs can then be piped to summaries, tables, and plots.

Because epidemic data is stored in a temporal way, we provide the function, `filament_compression()`, to transform temporally defined epidemics to their filamental representations. These filaments can then be fairly compared to one another or passed to further time-invariant analysis tools described below.

Comparisons and assessment

The last step of the data analysis pipeline often ends with plots, tables, and summary statistics that are used to assess model performance and compare across models or simulations. In **EpiCompare** we provide a set of comparison and assessment tools for model and simulation results that extend beyond the standard performance metrics (e.g. mean squared error or AIC) and into the lens of time-invariant analysis. We have found that these tools are specifically applicable for situations where only one season or cycle of an epidemic has occurred or is the object of interest.

The first set of tools surround the creation of prediction regions. We can create a prediction regions from model simulations to examine if our model simulations capture the true epidemic trajectory. We do so in a time-invariant way and utilizing filamental representations of the model simulations and the true epidemic. For three-state epidemic models, we provide the `ggplot/ggtern` extension `geom_prediction_band()` which creates a prediction region around

the top $1 - \alpha$ proportion of the simulations. In this visual setting, comparing this prediction region to the true epidemic trajectory can be done by eye. In **EpiCompare**, we also provide these prediction regions for epidemic models with more than three states. The functions `create_convex_hull_structure()` and `create_delta_ball_structure()` create different geometric representations of prediction regions for any dimensional state-based model. For both of these geometric structures, we provide functions to check if a path is contained (`contained()`). We can also use these prediction regions to visually or mathematically compare how similar two sets of simulations are. In **EpiCompare** we provide the `hausdorff_dist()` function to calculate the Hausdorff distance between multiple prediction regions, when visual comparison is not possible.

We also provide functions to calculate the “extremeness” of a true epidemic trajectory compared to simulated epidemics via the equi-distance filamental trajectory representation as mentioned in Section 2.2.] We provide implementations of a few distance-based score functions that capture how “reasonable” an epidemic is relative to other epidemics, and these scores can be turned into an extremeness measure with `mean(sim_scores > truth_score)`. [Specifically, functions like `distance_pseudo_density_function()` can calculate a pseudo-density estimate of the true epidemic relative to simulated ones. Functions `distance_depth_function()` and `local_distance_depth_function()` provide depth scores that suggest how geometrically central an epidemic is to simulations.

4. A tour of EpiCompare

I have substantially overhauled section 4. The older versions are kept after the entirety of this section but note that much of the text (but not the structure) of this section is different. I’ve tried to better motivate why we use the `epicompare` functions to answer our questions of interest.

UPDATE 6/11/2021. I am now adding overall goals of section and each subheading. Additionally there are a few updates from last draft (unmarked since you didn’t comment on last draft).

SECTION GOALS:

The main goal of this section is to show how a person can use **EpiCompare** in a real data analysis. With that said my primary focus is on **EpiCompare** and not the data analysis – a point I think you may be having an issue with. I’ve given this some thought and believe that the data analysis is a means for an end to us – showing off **EpiCompare**. That said again, I’ve made some changes in the first paragraph below.

To accomplish this main goal, I shadow the data analysis pipeline we have introduced and show how `epicompare` can be used in the steps.

The secondary goals are figuring out useful information about this measles outbreak.

[[NEWEST TEXT

[[sub-section goal: outline goal of section – how to use `epicompare` in a real situation

To conclude our paper, we demonstrate how **EpiCompare** streamlines the data analysis process with a case study of a measles outbreak in 1861-1862 Germany. With the help of **EpiCompare**, we can answer important questions such as is a SIR model a good fit for the data, does the outbreak spread differently within the different school classes of the children, and can


```

+   rename(time = t, S = X0, I = X1, R = X2)
R>
R>
R> ggplot(hagelloch_sir, aes(x = S, y = I, z = R)) +
+   coord_tern() +
+   geom_path() +
+   labs(x = "S", y = "I", z = "R",
+        title = "Time invariant view of Hagelloch measles outbreak") +
+   theme_sir(base_size = 24)

```

Time invariant view of Hagelloch measles outbreak

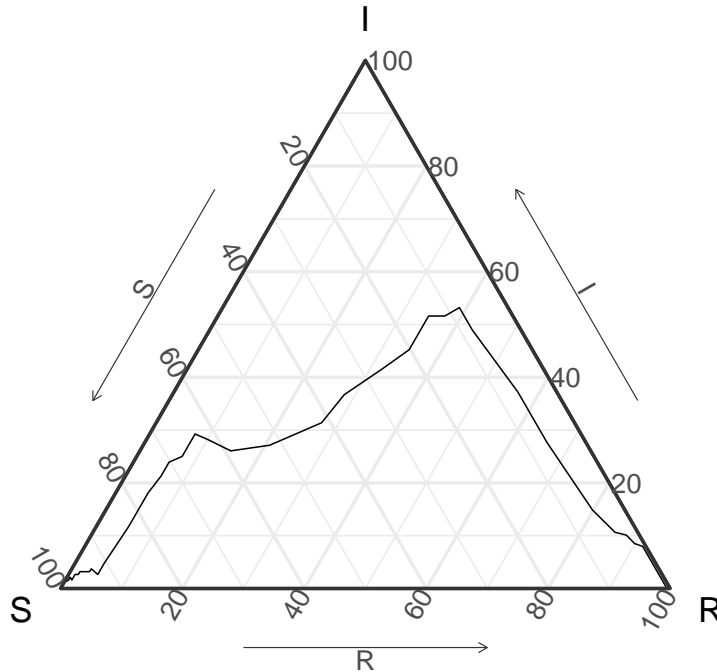


Figure 5: Time invariant view of the Hagelloch epidemic where we view the individuals in Susceptible, Infectious, or Recovered states. We see there are two peaks of infection (the vertical axis).

In Figure 9, we can focus on the infections over time by analyzing the vertical axis. Specifically, we see two peaks of infection. This is interesting because the SIR model, which is sometimes used to model the spread of measles, generally has one defined peak of infection. We may wonder if the two peaks in the observed data may be due to random noise or if a model more complex than the simple SIR is needed to adequately capture these two peaks.

With regards to our goal of identifying interesting subgroups with different infection behavior, previous study tells us that measles outbreaks are often associated with children within the same grade level, and we examine if this is the case here. By combining the **dplyr** function `facet_wrap()` with `geom_aggregate()` we can easily analyze this scenario,

```
R> haggelloch_raw %>%
+   ggplot(aes(y = tI, z = tR, color = CL)) +
+   geom_aggregate(size = 2) + coord_tern() +
+   labs(x = "S", y = "I", z = "R",
+        color = "Class") +
+   scale_color_brewer(palette = "Dark2") +
+   facet_wrap(~CL)
```

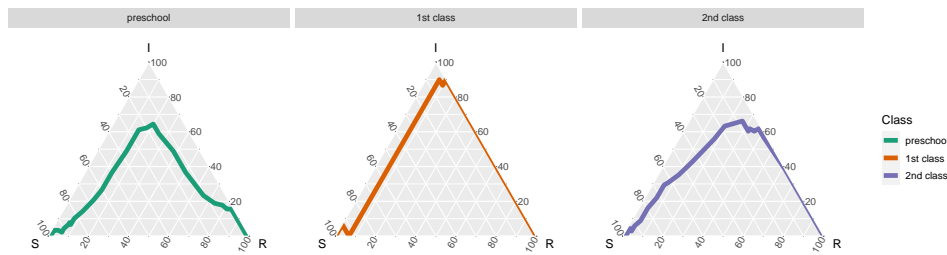


Figure 6: Time invariant outbreak curves for the three class groups. The pre-school class has a distinct peak of infection whereas the peak infection point for the other two classes are less well defined.

Immediately in Fig. 10, we see that time invariant infection curve is different for the pre-school class compared to the 1st class. In the 1st class, we see about 95% of the class become infected and less than 10% of them having recovered, which may be indicative of a super-spreading event. This suspicion is further supported in that 26 of the 30 1st class students have been reportedly infected by the same individual. We now have some evidence that class structure may play a role in the spread of infection. We can further analyze this claim with modeling and simulation.

4.3. Modeling and Simulation

[[The goal is to ‘test’ (although not formally) whether our observations from EDA are correct. We want to see whether SIR model is a good fit and whether including these found sub-groups helps model fit]]

We now use modeling and simulation to informally test whether the baseline SIR model is a good fit for the data and whether incorporating a network-based structure dependent on the class of the children improves model fit.

We first try to model the Hagelloch data with a baseline stochastic SIR model, which we refer to as the ‘simple SIR.’ In our full vignette ([available online](#)), we show how to fit this simple SIR model via maximum likelihood, a common approach used to fit parameters, and simulate from the model with those best fit parameters. Our function `simulate_agents()` (or `simulate_SIR_agents()`) generates individual level data according to discrete-time multinomial draws, which depend on the number of individuals in each state at the previous time step and a matrix of transition probabilities. For example, the below code generates 100 simulations of an outbreak of a disease with one initial infector in a population of $n = 188$ individuals, a scenario analogous to the actual outbreak.


```

R> trans_mat <- matrix(c("X0 * (1 - X1 * par1 / N)", "X0 * X1 * par1 / N", "0",
+                         "0", "X1 * (1 - par2)", "par2 * X1",
+                         "0", "0", "X2"), byrow = TRUE, nrow = 3)

R> set.seed(2020)
R>
R> best_params <- c("beta" = .36, "gamma" = .13)
R> ## This is the SIR representation
R>
R> rownames(trans_mat) <- c("S", "I", "R")
R> init_vals <- c(187, 1, 0)
R> par_vals <- c(par1 = best_params[1], par2 = best_params[2])
R> max_T <- 55
R> n_sims <- 100
R>
R> agents <- simulate_agents(trans_mat,
+                           init_vals,
+                           par_vals,
+                           max_T,
+                           n_sims,
+                           verbose = FALSE)

R> agg_model <- agents %>% group_by(sim) %>%
+   agents_to_aggregate(states = c(I, R)) %>%
+   mutate(Type = "Simple SIR")

```

The result of our simulation is the object `agents` which is a 18800×5 data frame, which details the time of entry into the *S*, *I*, and *R* states for a given simulation.

To fit a more complex SIR model with a network structure, we use the package **EpiModel** (Jenness *et al.* 2018). The below code sets up a network of individuals (which includes class as a variable) and then simulates infection and recovery over this network.

```

R> library(EpiModel)
R> ## WARNING: Will take a minute or two
R>
R> set.seed(42)
R> nw <- network.initialize(n = 188, directed = FALSE)
R> nw <- set.vertex.attribute(nw, "group", rep(0:2, each = 90, 30, 68))
R> formation <- ~edges + nodematch("group") + concurrent
R> target.stats <- c(200, 300, 200)
R> coef.diss <- dissolution_coefs(dissolution = ~offset(edges), duration = 5)
R> est1 <- netest(nw, formation, target.stats, coef.diss, edapprox = TRUE)
R>
R> param <- param.net(inf.prob = 0.1, act.rate = 5, rec.rate = 0.1)
R> status.vector <- c(rep(0, 90), rep(0, 30), rep(0, 67), 1)
R> status.vector <- ifelse(status.vector == 1, "i", "s")

```

```
R> init <- init.net(status.vector = status.vector)
R> control <- control.net(type = "SIR", nsteps = 55,
+                          nsims = 100, epi.by = "group")
R> epimodel_sir <- netsim(est1, param, init, control)
```

The output of this network model is `epimodel_sir`, an object of class `netsim`, which contains a plethora of modeling information. In the following section, we will use the capabilities of **EpiCompare** to streamline the process of comparing the two models contained in the objects `agg_model` (the simple SIR) and `epimodel_sir` (the network SIR model).

4.4. Post-processing and comparison

[[Finally we want to answer the questions in our analysis by comparing the models to the data and the models to each other]].

Ultimately we want to compare the models to the data and the models to one another to answer our questions of interest. The **EpiCompare** function `fortify_aggregate()` takes in an object from specialized classes of modeling output (like those made by `netsim()`) and transforms it into a tidy-style data frame.

```
R> fortified_net <- fortify_aggregate(epimodel_sir,
+                                   states = c("s.num", "i.num", "r.num")) %>%
+   mutate(Type = "EpiModel SIR",
+          sim = as.numeric(gsub("sim", "", sim)))
```

With the two modeling objects both in the same format, we can then compare the models side-by-side. The results are shown in Figure 11, where a 90% prediction region is estimated for the two models and the actual data are plotted as black dots. For the Simple SIR model, we see that while the prediction region covers the data fairly well, the prediction region clearly misses the second peak of infection. This indicates that the simple SIR is not a good fit to our data, even after incorporating noise. We also see that the prediction region is very large, covering up a large area of the ternary plot. Together, this indicates that the simple SIR model produces a biased model with a large amount of variance. On the other hand, for the EpiModel network model, we see that the prediction region covers the data quite well and takes up less area compared to the simple SIR. With **EpiCompare**, we see that the model using the class structure is a better fit to the outbreak than the simple SIR model.

```
R> both_models <- bind_rows(agg_model, fortified_net)
R>
R> g <- ggplot() + geom_prediction_band(data = both_models %>% filter(t != 0) %>%
+   mutate(Type = factor(Type, levels = c("Simple SIR",
+                                          "EpiModel SIR"))),
+   aes(x = X0, y = X1, z = X2,
+       sim_group = sim, fill = Type),
+   alpha = .5,
+   conf_level = .90)
```

```

R> g + geom_path(data = both_models %>% filter(t != 0) %>%
+               mutate(Type = factor(Type, levels = c("Simple SIR",
+               "EpiModel SIR"))),
+               aes(x = X0, y = X1, z = X2, group = paste(Type, sim)),
+               alpha = .3, col = "gray40") +
+   coord_tern() + theme_sir(base_size = 24) +
+   geom_point(data = hagelloch_sir,
+               aes(x = S, y = I, z = R), col = "black") +
+   labs(title = "Simple SIR model",
+         subtitle = "90% Prediction band and original data",
+         x = "S", y = "I", z = "R") +
+   scale_fill_manual(values = c("#006677", "#AA6600")) +
+   facet_wrap(~Type) +
+   theme(legend.position = "bottom")

```

Simple SIR model

90% Prediction band and original data

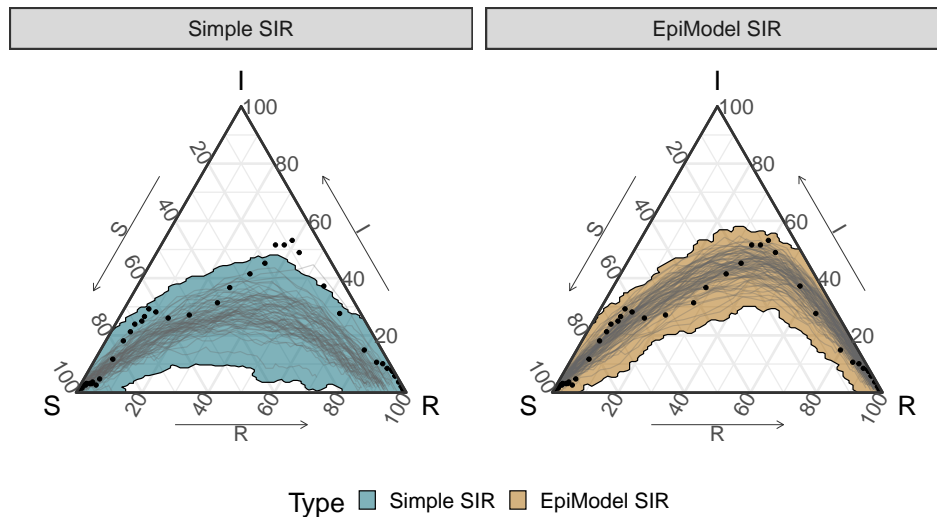


Figure 7: Original Hagelloch SIR data (black) along with 90% prediction band and actual simulation paths from the Simple SIR and the EpiModel SIR models.

Although the prediction region generated by the network model covers the observed data well visually, that does not mean that individual filaments generated from the network model are good fits to the observed data. We can further examine the model fits by incorporating these filaments into our visualization. In Fig. 11 we show the individual filaments generated from the two sets of models as gray lines. Examining these, we see that the individual lines typically only have one defined peak, whereas the data certainly looks like it has two distinct peaks, a feature possibly caused by our speculated super-spreader event.

We can also examine these filaments quantitatively by using functions that take the distance between the filaments with the observed data. In the below code, we transform the simulations to a more computationally-friendly format with the function `filament_compression()`.

Following that, we calculate the distance between the simulated filaments and the observed filament with the function `dist_matrix_innersq_direction()` and calculate the probability of the truth with respect to those simulations with the function `compare_new_to_rest_via_distance()`. The estimated pseudo-density of the observed epidemic (relative to the simulations from either model) is much less likely than **any** of the simulations (reported in Table 6). This indicates that neither of two SIR models are good fits to the data at the filament level.

```
R> simple_sir <- both_models %>% filter(Type == "Simple SIR") %>%
+   rename(S = "X0", I = "X1", R = "X2") %>%
+   select(Type, sim, t, S, I, R)
R>
R> hagelloch_sir2 <- hagelloch_sir %>%
+   rename(t = "time") %>%
+   mutate(Type = "true observation",
+           sim = 0) %>%
+   select(Type, sim, t, S, I, R)

R> #-- after cleaning up and combining --
R> all_together_df <- rbind(simple_sir,
+                           hagelloch_sir2)
```

Table 2: Top and bottom 2 rows of `all_together_df`, combining both simulated epidemics and the true epidemic.

Type	sim	t	S	I	R
Simple SIR	1	0	188	0	0
Simple SIR	1	1	187	1	0
true observation	0	54	1	0	187
true observation	0	55	1	0	187

```
R> compression_df <- all_together_df %>% group_by(Type, sim) %>%
+   filament_compression(data_columns = c("S", "I", "R"),
+                           number_points = 20)
R>
R> tdmat <- compression_df %>%
+   dist_matrix_innersq_direction(
+     position = c(1:length(compression_df))[
+       names(compression_df) %in% c("S", "I", "R")],
+     tdm_out = T)
R>
R> simple_sir_true_obs_info <- tdmat %>%
+   compare_new_to_rest_via_distance(
+     new_name_id = data.frame(Type = "true observation", sim = 0),
+     distance_func = distance_pseudo_density_function,
+     sigma = "20%")
```

Table 3: The extremeness of the true simulations based on comparing pseudo-density estimates between true vs simulated curves

Type	simulations-based estimated pseudo-density	proportion of simulations with lower estimated pseudo-density
Simple SIR	0.0036733	0.00
EpiModel SIR	0.0118283	0.03

In conclusion, **EpiCompare** allows us to fully examine this outbreak at every step in the data analysis pipeline (see Fig. 4) in a streamlined fashion. With EDA, we saw evidence that class structure may be important in the spread of measles. We then compared a baseline simple SIR model to a more complicated SIR model which incorporated a network structure which included the class structure. Based on the prediction regions generated from these models, we saw that the network model fit the data better than the simple SIR model. However, when we examined the individual filaments generated by the network model, we found that the data are unlikely to be generated from such a model. For further analysis, we would recommend looking into models that can more accurately capture super-spreading events based on the observation that one child was allegedly responsible for nearly all of his classmates' infections. Overall, this analysis demonstrates how **EpiCompare** aids in the data analysis pipeline for both novice and expert practitioners and coders alike.

]]

[[NEWER TEXT

¹³ To conclude our paper, we demonstrate the capabilities of **EpiCompare** with a complete data analysis of a measles outbreak in 1861-1862 Germany. Specifically, we demonstrate how tools in **EpiCompare** can be used in each step of the data analysis pipeline ¹⁴ (see Figure 1) ¹⁵. Additionally, we highlight how time-invariant analysis (see Section 2) can be used to enhance understanding of an outbreak ¹⁶.

¹⁷ Before demonstrating **EpiCompare**, we provide some context for the measles outbreak presented here. ¹⁸ The data was originally organized by Pfeilsticker (1863), later made visible by Oesterle (1992), and made available in an R by Meyer *et al.* (2017). This data set includes a rich collection of features including household location, class level, and alleged infector ID, and is an ideal testing ground for methodology in infectious disease epidemiology Neal and

¹³[Ben says: Generally I found this whole section to be pretty passive and not well motivated on why we'd actually do the analysis.]

¹⁴[Ben says: based on an earlier read of this section, I might suggest something like "and streamline the analysis process" - is that a selling point you want to highlight?] check out new re-write. new goal is to motivate question of hagelloch and then show how epicompare helps

¹⁵[Ben says: It's unclear why you want to highlight the figure again - could you be clearer on that? / what does it add to the conv/ why should they reference it?]

¹⁶[Ben says: I'm not sure this is necessary to state. Additionally - is it really true do we highlight this?]

¹⁷[Ben says: The data introduction could be another subsection. Why does it fit better here?. Other comment: This paragraph is pretty rambling. It is unclear what you want someone to take away from it. I might suggest highlight the fact that the data is "an ideal testing group for methodology".]

¹⁸[Ben says: this first sentence is pretty sign-post-y yet it only relates to the next few sentences. Update so it's less sign-post-y.]

Roberts (2004); Britton *et al.* (2011); Groendyke *et al.* (2012); Becker *et al.* (2016)¹⁹. In this data set, there are 188 children who became infected with the measles over the course approximately 90 days.

]]

[[LESS NEW TEXT

Finally, in this section we show how tools from **EpiCompare** can be used in each step of the data analysis pipeline shown in Fig. 1. We analyze an outbreak of measles in the town of Hagelloch, Germany from 1861-1862, a data set organized by Pfeilsticker (1863). The data was later made visible by Oesterle (1992) and made available in an R by Meyer *et al.* (2017). This data set includes a rich collection of features and is an ideal testing ground for methodology in infectious disease epidemiology Neal and Roberts (2004); Britton *et al.* (2011); Groendyke *et al.* (2012); Becker *et al.* (2016).²⁰

]]

[[OLD TEXT

²¹In this section, we highlight many of the tools available in **EpiCompare**. As previously discussed, these tools include data cleaning; visualization; modeling and simulation; post-processing; and comparison and model assessment, in accordance with the data analysis pipeline (Fig. 1). We show a full data analysis from beginning to end that can be accomplished in a streamlined and standardized manner via **EpiCompare**.]]

4.5. Pre-processing and EDA

²²The Hagelloch data include a rich set of features at the individual level, and the tools in **EpiCompare** help with pre-processsing and EDA. Recorded features include household members, school level, household locations, date of first symptoms (prodromes), date of measles rash, and even the alleged infector. A subset of the data is shown in Table 1. For example,²³ with **EpiCompare**, we can easily pre-process the data to obtain the empirical cumulative incidence function with respect to the measles rash appearance (variable ERU) with the following tidy-style function, `agents_to_aggregate()`. The function `agents_to_aggregate()` is a key component of **EpiCompare**, allowing the user to easily switch from an individual-level (i.e. an agent) view lens of a disease to an aggregate level lens. For example²⁴, the below code shows how we can convert the agent data to a cumulative incidence plot of the measles rash, in order to see how the disease spread through the population over time. We can then compare the cumulative incidence of the rash to the cumulative incidence of the prodromes, i.e. the initial²⁵ symptoms²⁶. We do this with the below code, and a part of the cumulative incidence

¹⁹[Ben says: This citation doesn't make sense - should it be "citep"?]

²⁰The old first paragraph from data and exploratory analysis paragraph was combined with the intro as a better lead-in to what's going on.

²¹[Ben says: Shannon, would you mind reading this whole section over again once we've finished edits for section 2 and 3? This initial paragraph seems to be stating section 3's story.]

²²[Ben says: The first two sentences is very similar to the data paragraph in the section above. Given it's not really connecting the 2 sections I suggest a rewrite - could move some of this stuff above.]

²³[Ben says: I'm unclear of what this is actually an example of.]

²⁴[Ben says: Same comment as before.]

²⁵[Ben says: please be clearer on what these could be given you comparing them to start of the rash - which seems like an early symptom to me...]

²⁶[Ben says: This action in the analysis pipeline is unmotivated - which naturally makes me want to ask

data output is shown in Table 4. The argument `integer_time_expansion` indicates whether we should include all time points in the recorded range of the data or only when there is a change in the incidence.

```
R> cif_rash <- haggelloch_raw %>%
+   mutate(time_of_rash = as.numeric(ERU - min(PRO, na.rm = TRUE))) %>%
+   agents_to_aggregate(states = time_of_rash,
+                       integer_time_expansion = FALSE) %>%
+   mutate(type = "Rash")
```

Table 4: Turning the individual-level information from the Hagelloch data to an aggregate view of the cumulative incidence of the measles rash in the population over time.

Time	# Susceptible	# Total rash appearances
0	188	0
4	187	1
7	186	2
9	185	3
12	183	5

One possible question of interest is the duration between initial onset of prodromes and the appearance of the measles rash²⁷. Since `agents_to_aggregate()` outputs a tidy-style data frame, it is a simple task to plot the two sets of incidence curves on the same graph (Fig. 8).

```
R> cif_prodromes <- haggelloch_raw %>%
+   mutate(time_of_PRO = as.numeric(PRO - min(PRO, na.rm = TRUE))) %>%
+   agents_to_aggregate(states = time_of_PRO,
+                       integer_time_expansion = FALSE) %>%
+   mutate(type = "Pro")
```

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```
R> plot_df <- bind_rows(cif_rash, cif_prodromes)
R>
R> ggplot(data = plot_df,
+   aes(x = t, y = X1, col = type)) +
+   geom_step() +
+   labs(title = "Cumulative incidence of measles appearance",
+   x = "Time (days relative to first prodrome appearance)",
+   y = "Cumulative incidence of event") +
+   coord_cartesian(xlim = c(0, 55)) +
+   scale_color_manual(values = c("blue", "red"))
```

"why would I do this?"]

²⁷[Ben says: You don't give a good definition of prodromes above, and you only use the name twice. Is this a super common term in Epi? I find it a bit taxing on the reader to remember what this is referring to.]

²⁸I'm confused why Figure 5 is included. What is the conclusion you'd like to take away? / Why do people create plots like this?

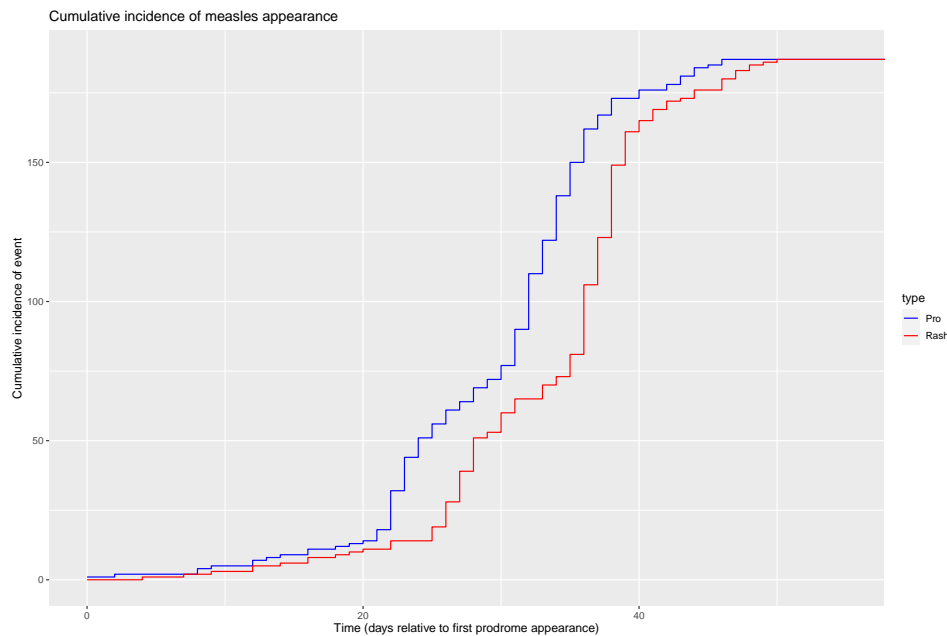


Figure 8: Empirical cumulative incidence functions of prodrome (symptom) onset and measles rash appearance. We see that there is approximately a constant lag between the two curves.

The real power of `agents_to_aggregate()` lies in its ability to aggregate over any number of pre-specified states. For example, the Hagelloch data sets contains two columns, `tI` and `tR`, the time of infection and recovery, respectively of each individual. We can then²⁹ plot the SIR values through a time-invariant lens using `ggplot2` and `ggtern` functions (as shown in Fig. 9) or with our custom `geom`, `geom_aggregate`, which takes the raw agent data as input.

```
R> hagelloch_sir <- hagelloch_raw %>%
+   agents_to_aggregate(states = c(tI, tR),
+                           min_max_time = c(0, 55)) %>%
+   rename(time = t, S = X0, I = X1, R = X2)
R>
R>
R> ggplot(hagelloch_sir, aes(x = S, y = I, z = R))+
+   coord_tern() +
+   geom_path() +
+   labs(x = "S", y = "I", z = "R",
+         title = "Time invariant view of Hagelloch measles outbreak") +
+   theme_sir(base_size = 24)
```

²⁹[Ben says: using "then" here captures a very progression step of analysis but I stopped here and asked "what is this following" - and the previous "step" occurred a paragraph back and wasn't described as a direct progression but just a possible thing to do.]

Time invariant view of Hagelloch measles outbreak

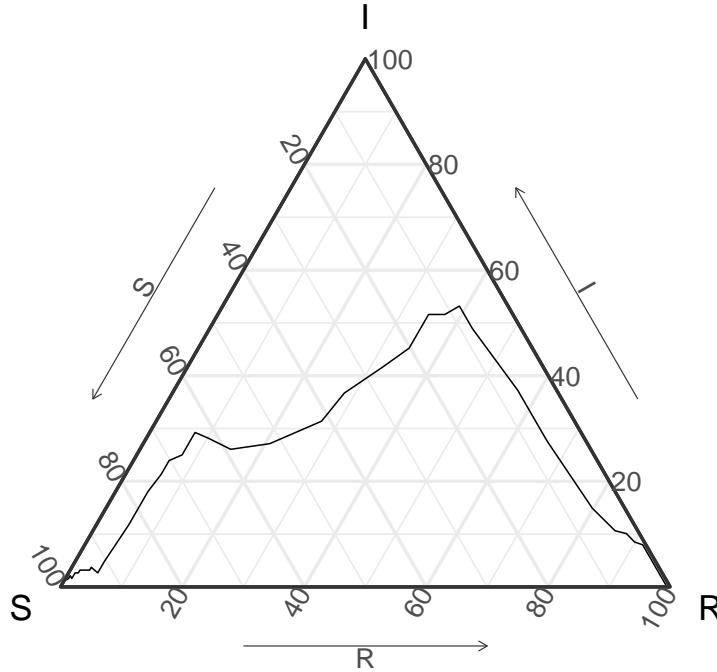


Figure 9: Time invariant view of the Hagelloch epidemic where we view the individuals in Susceptible, Infectious, or Recovered states. We see there are two peaks of infection (the vertical axis).

³⁰Moreover, we can look at the outbreaks of the disease by group within `agent_to_aggregate()` or `geom_aggregate()`. This allows us to examine differences among the different groups of individuals. For example, we show the time invariant outbreak by class level in Figure 10. Immediately, we see that time invariant infection curve is different for the pre-school class compared to the 1st class. In the 1st class, we see about 95% of the class become infected and less than 10% of them having recovered, which may be indicative of a super-spreading event. This suspicion is further confirmed in that 26 of the 30 1st class students have been reportedly infected by the same individual.

```
R> hagelloch_raw %>%
+   ggplot(aes(y = tI, z = tR, color = CL)) +
+   geom_aggregate(size = 2) + coord_tern() +
+   labs(x = "S", y = "I", z = "R",
+        color = "Class") +
+   scale_color_brewer(palette = "Dark2") +
+   facet_wrap(~CL)
```

³⁰I found this paragraph very unmotivated. I recommend first arguing why we might care to look into the class subpopulation grouping. And maybe comment that this is a common desire for practitioners.

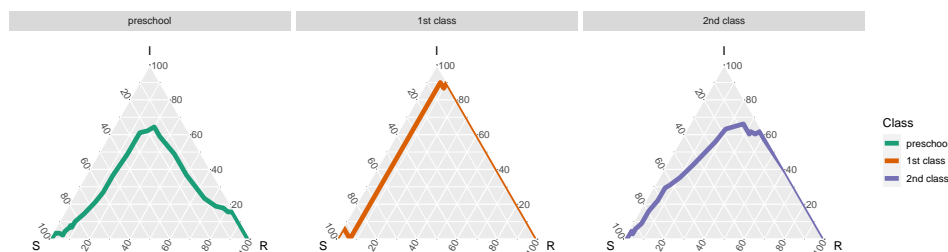


Figure 10: Time invariant outbreak curves for the three class groups. The pre-school class has a distinct peak of infection whereas the peak infection point for the other two classes are less well defined.

Along with multiple epidemic states, the function `agents_to_aggregate()` can also be extended to populations with vital dynamics (e.g. birth and death) and examples of this are shown in the package vignette. In summary, `agents_to_aggregate()` is a multi-purpose workhorse that may be leveraged to convert individual level records into aggregate information that may be more useful for some forms of epidemic modeling such as compartment modeling.³¹

4.6. Modeling and simulation

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Up to this point, we have used **EpiCompare** in the context of observed data.³³ We also want to compare statistical models, and **EpiCompare** aids in that process via a simple yet flexible individual-level simulator, conversion tools for popular epidemic model packages, and model assessments. We demonstrate an example³⁴ here.

We first try to model the Hagelloch data with a stochastic SIR model, which we refer to as the ‘simple SIR’.³⁵ In our full vignette (available online), we show how to fit this simple SIR model via maximum likelihood and simulate from the model with those best fit parameters³⁶. Our function `simulate_agents()`^{footnote{[Ben Should somethings be said about the simulation_SIR_agents() function?]}} generates individual level data according to discrete time multinomial draws, which depend on the number of individuals in each state at the previous time step and a matrix of transition probabilities. For example, the below code generates 100 simulations of an outbreak of a disease with one initial infector in a population of $n = 188$ individuals.

```
R> trans_mat <- matrix(c("X0 * (1 - X1 * par1 / N)", "X0 * X1 * par1 / N", "0",
+                        "0", "X1 * (1 - par2)", "par2 * X1",
+                        "0", "0", "X2"), byrow = TRUE, nrow = 3)
```

```
R> set.seed(2020)
```

```
R>
```

³¹Is this not just a repeat of section 3?

³²section headings to align with our pipeline

³³[Ben says: Why?]

³⁴[Ben says: to me this whole section is 1 example - as such this wording is confusing to me.]

³⁵[Ben says: could / should this be thought of as a “base” model?]

³⁶[Ben says: should you highlight that this is a common approach?]

```

R> best_params <- c("beta" = .36, "gamma" = .13)
R> ## This is the SIR representation
R>
R> rownames(trans_mat) <- c("S", "I", "R")
R> init_vals <- c(187, 1, 0)
R> par_vals <- c(par1 = best_params[1], par2 = best_params[2])
R> max_T <- 55
R> n_sims <- 100
R>
R> agents <- simulate_agents(trans_mat,
+                             init_vals,
+                             par_vals,
+                             max_T,
+                             n_sims,
+                             verbose = FALSE)

R> agg_model <- agents %>% group_by(sim) %>%
+   agents_to_aggregate(states = c(I, R)) %>%
+   mutate(Type = "Simple SIR")

```

The result of our simulation is the object `agents` which is a 18800×5 data frame, which details the time of entry into the *S*, *I*, and *R* states for a given simulation.³⁷ Before we examine the results of this simple SIR model, we will also examine another, more sophisticated SIR model, this time from the package **EpiModel** (Jenness *et al.* 2018). Briefly, this model first fits a contact network to the set of individuals, where the class of the child is a covariate³⁸. The model then simulates a SIR-epidemic on that network.

```

R> library(EpiModel)
R> ## WARNING: Will take a minute or two
R>
R> set.seed(42)
R> nw <- network.initialize(n = 188, directed = FALSE)
R> nw <- set.vertex.attribute(nw, "group", rep(0:2, each = 90, 30, 68))
R> formation <- ~edges + nodematch("group") + concurrent
R> target.stats <- c(200, 300, 200)
R> coef.diss <- dissolution_coefs(dissolution = ~offset(edges), duration = 5)
R> est1 <- netest(nw, formation, target.stats, coef.diss, edapprox = TRUE)
R>
R> param <- param.net(inf.prob = 0.1, act.rate = 5, rec.rate = 0.1)
R> status.vector <- c(rep(0, 90), rep(0, 30), rep(0, 67), 1)
R> status.vector <- ifelse(status.vector == 1, "i", "s")
R> init <- init.net(status.vector = status.vector)
R> control <- control.net(type = "SIR", nsteps = 55,

```

³⁷[Ben says: please motivate - through model comparison?]

³⁸[Ben says: Make this connect better to the problem at hand - why do you think you should build this bigger model?]

```
+               nsims = 100, epi.by = "group")
R> epimodel_sir <- netsim(est1, param, init, control)
```

The output of this model is `epimodel_sir`, an object of class `netsim`, which contains a plethora of modeling information.³⁹

4.7. Post-processing and comparison

The next step is to compare the simple SIR model to the EpiModel SIR model. We provide⁴⁰ the function `fortify_aggregate()`, which can take objects from specialized classes of modeling output (like those made by `netsim()`) and transform it into a tidy-style data frame.

```
R> fortified_net <- fortify_aggregate(epimodel_sir,
+                                   states = c("s.num", "i.num", "r.num")) %>%
+   mutate(Type = "EpiModel SIR",
+          sim = as.numeric(gsub("sim", "", sim)))
```

We can then analyze the results of the two models side by side as time-invariant⁴¹ epidemic curves. The results are shown in Figure 11, where a 90% prediction band is estimated from the delta ball⁴² method for each of the two models. For the Simple SIR model, we see that the data generally covers the data fairly well but clearly misses the second peak of infection⁴³. We also see that the prediction band is very large, covering up a large area of the ternary plot. On the other hand, for the EpiModel network model, we see that the prediction band covers the data quite well and takes up less area.

```
R> both_models <- bind_rows(agg_model, fortified_net)
R>
R>
R> g <- ggplot() + geom_prediction_band(data = both_models %>% filter(t != 0) %>%
+   mutate(Type = factor(Type, levels = c("Simple SIR",
+                                         "EpiModel SIR"))),
+   aes(x = X0, y = X1, z = X2,
+        sim_group = sim, fill = Type),
+   alpha = .5,
+   conf_level = .90)
```

[Ben says: In figure 8 I changed the order of the facets given we talk about the simple model first and its more like the "base" model. I think the title should be changed?]

```
R> g +   geom_path(data = both_models %>% filter(t != 0) %>%
+   mutate(Type = factor(Type, levels = c("Simple SIR",
```

³⁹[Ben says: what's the point for this sentence. It also doesn't flow/ connect to previous and later text.]

⁴⁰[Ben says: the phrase "We provide" is very passive / distance from the current demonstration at hand. Moreover section 3 already phrases things this way.]more of sentence 2 of ben than 1.

⁴¹[Ben says: this isn't a clear phrase here - what are you trying to say?]

⁴²[Ben says: this has never been discussed anyway.]

⁴³[Ben says: This could be better motivated with talk of model fit...]

```

+                                     "EpiModel SIR"))),
+       aes(x = X0, y = X1, z = X2, group = paste(Type, sim)),
+       alpha = .3, col = "gray40") +
+     coord_tern() + theme_sir(base_size = 24) +
+     geom_point(data = hagelloch_sir,
+       aes(x = S, y = I, z = R), col = "black") +
+     labs(title = "Simple SIR model",
+       subtitle = "90% Prediction band and original data",
+       x = "S", y = "I", z = "R") +
+     scale_fill_manual(values = c("#006677", "#AA6600")) +
+     facet_wrap(~Type) +
+     theme(legend.position = "bottom")

```

Simple SIR model

90% Prediction band and original data

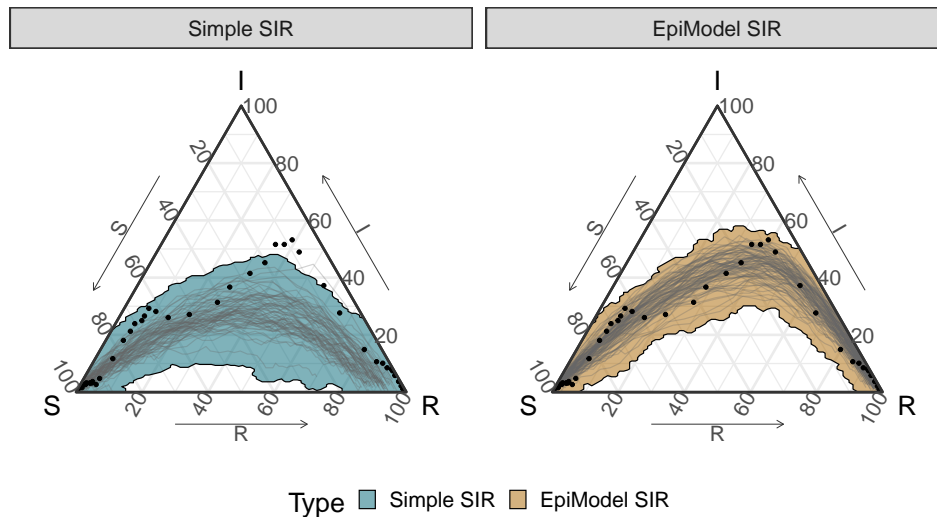


Figure 11: Original Hagelloch SIR data (black) along with 90% prediction band and actual simulation paths from the Simple SIR and the EpiModel SIR models.

However, both models are not a good fit to the filamental path as opposed to the individual points in (S, I, R) -space. This can be⁴⁴ captured with the set of simulations both models predict (gray lines), which all generally have a single defined peak of infection whereas the data certainly looks like it has two distinct peaks, likely caused by our assumed super-spreader event. This observation is backed up⁴⁵ by the below analysis that demonstrates that the estimated pseudo-density of the observed epidemic (relative to the simulations from either model) is much less likely than **any** of the simulations (reported in Table 6)⁴⁶ In conclusion, **EpiCompare** makes it clear that, at a glance, 1) the EpiModel network model is a better fit than the Simple SIR model, and 2) the fit is only good at the ~~geometric filamental level~~ as

⁴⁴[Ben says: this is a very passive way to say such things. Try being more direct.]

⁴⁵[Ben says: describe this?]

⁴⁶Ben, do we want to add another sentence or two explaining the two columns in the table? The second one I think makes sense to me but not the first.

opposed to the epidemic trajectory filamental level: individual point level as opposed to the geometric filamental level.⁴⁷

```
R> #-- after cleaning up and combining --
R> all_together_df <- rbind(simple_sir,
+                           hagelloch_sir2)
```

Table 5: Top and bottom 2 rows of `all_together_df`, combining both simulated epidemics and the true epidemic.

Type	sim	t	S	I	R
Simple SIR	1	0	188	0	0
Simple SIR	1	1	187	1	0
true observation	0	54	1	0	187
true observation	0	55	1	0	187

```
R> compression_df <- all_together_df %>% group_by(Type, sim) %>%
+   filament_compression(data_columns = c("S", "I", "R"),
+                           number_points = 20)

R> tdm_mat <- compression_df %>%
+   dist_matrix_innersq_direction(
+     position = c(1:length(compression_df))[,
+       names(compression_df) %in% c("S", "I", "R")],
+     tdm_out = T)
R>
R> simple_sir_true_obs_info <- tdm_mat %>%
+   compare_new_to_rest_via_distance(
+     new_name_id = data.frame(Type = "true observation", sim = 0),
+     distance_func = distance_pseudo_density_function,
+     sigma = "20%")
```

Table 6: The extremeness of the true simulations based on comparing pseudo-density estimates between true vs simulated curves

Type	simulations-based estimated pseudo-density	proportion of simulations with lower estimated pseudo-density
Simple SIR	0.0036733	0.00
EpiModel SIR	0.0149686	0.02

⁴⁷[Ben says: how would this look with the time plots? Do we add value here?]

⁴⁸Overall, **EpiCompare** aids in the data analysis pipeline for both novice and expert practitioners and coders alike. These tools encourage model and simulation exploration of many of the existing and well-supported packages that already exist, and side-by-side comparison thereof. Finally, we hope that practitioners will consider using time-invariant analysis when trying to assess and compare epidemics and epidemic models.

A. Appendix

A.1 Proof of Theorem 1

Proof. Harko *et al.* (2014) provide an analytical solution for the Kermack and McKendrick equations (Eq. (1)) by reparameterizing the ODEs so that $\mathcal{S}(u) = S(t)$, $\mathcal{I}(u) = I(t)$, and $\mathcal{R}(u) = R(t)$ for $0 < u_T < 1$ with

$$\begin{aligned}\mathcal{S}(u) &= S(0)u \\ \mathcal{I}(u) &= N - R(0) + NR_0^{-1} \log u - S(0)u \\ \mathcal{R}(u) &= R(0) - NR_0^{-1} \log u,\end{aligned}\tag{2}$$

and u and t are related by the following integral,

$$\begin{aligned}t &= \int_u^1 \frac{N}{\beta\tau(N - R(0) + R_0^{-1} \log \tau - S(0)\tau)} d\tau \\ &= \int_u^1 \frac{1}{\beta f(S(0), R(0), N, R_0, \tau)} d\tau \\ &= \int_u^1 \frac{1}{\beta f(\tau)} d\tau,\end{aligned}$$

where we have made the denominator of the integral a function of N , the initial values, R_0 , and τ , which we further condense to $f(\tau)$ for brevity. Then for a given t we want to find s such that $(S_1(t), I_1(t), R_1(t)) = (S_2(s), I_2(s), R_2(s))$. Or equivalently, for a fixed u want to find v such that $\mathcal{S}_1(u) = \mathcal{S}_2(v)$ and then the corresponding t and s are given by

$$\begin{aligned}t &= \int_u^1 \frac{1}{\beta_1 f(\tau)} d\tau \\ s &= \int_v^1 \frac{1}{\beta_2 f(\tau)} d\tau.\end{aligned}$$

Note that since the equations in Eq. (2) are functions of the initial values and R_0 , then $u = v$.

⁴⁸I think this paragraph captures some good goals, but I don't think we've done some of this. For example - we don't really highlight novice/expert usage, and we don't highlight side-by-side comparisons of models.

We then can find a relation for s ,

$$\begin{aligned} s &= \int_u^1 \frac{1}{\beta_2 f(\tau)} d\tau \\ &= \int_u^1 \frac{1}{a\beta_1 f(\tau)} d\tau \\ &= \frac{1}{a} \int_u^1 \frac{1}{\beta_1 f(\tau)} d\tau \\ &= \frac{1}{a} t. \end{aligned}$$

□

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