

**PHYLOGENETIC ESTIMATION OF CONTACT NETWORK PARAMETERS
WITH APPROXIMATE BAYESIAN COMPUTATION**

by

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Abstract

Models of the spread of disease in a population often make the simplifying assumption that the population is homogeneously mixed, or is divided into homogeneously mixed compartments. However, human populations have complex structures formed by social contacts, which can have a significant influence on the rate [and pattern](#) of epidemic spread. Contact ~~network models~~ [networks](#) capture this structure by explicitly representing each contact that could possibly lead to a transmission. [Contact network models parameterize the structure of these networks, but . . .](#)

We developed a method based on approximate Bayesian computation (ABC) for estimating structural parameters of the contact network underlying an observed viral phylogeny. The method combines adaptive sequential Monte Carlo for ABC, Gillespie simulation for propagating epidemics through networks, and a [previously developed](#) kernel-based tree similarity score. [Our method offers the potential to quantitatively investigate contact network structure from phylogenies derived from viral sequence data, as a complementary approach to traditional epidemiological investigation.](#)

We used the method to ~~fit~~ [investigate](#) the Barabási-Albert network model. [This model incorporates the mechanism of preferential attachment observed in real world social and sexual networks, whereby individuals with a higher number of connections attract new contacts at an elevated rate \(“the rich get richer”\).](#) ~~to simulated transmission trees and applied it to viral phylogenies estimated from six real-world HIV sequence datasets.~~ Using simulated data, we found that the strength of preferential attachment and the number of infected nodes in the network could often be accurately estimated. On the other hand, the mean degree of the network, as well as the total number of nodes, appeared to be weakly or non-identifiable with ABC.

Finally, the Barabási-Albert model was fit to six real-world HIV datasets. We observed substantial heterogeneity in the parameter estimates on real datasets, with point estimates for the preferential attachment power ranging from 0.06 to 1.05. [Point estimates of the strength of preferential attachment were higher in injection drug user populations, potentially indicating. . .](#) ~~These results underscore the importance of considering contact structures when performing phylodynamic inference.~~

Preface

The initial idea to use approximate Bayesian computation (ABC) to infer contact network model parameters was Dr. Poon's, based on his previous work using ABC to infer parameters of population genetic models. The tree kernel was originally developed by Dr. Poon, but the version used here was implemented by me to improve computational efficiency. The idea to apply sequential Monte Carlo was mine, but Dr. Alexandre Bouchard-Côté made me aware of the adaptive version used in this work. Dr. Sarah Otto suggested the experiments involving a network with a heterogeneous α parameter and peer-driven sampling. Dr. Richard Liang provided guidance in the development of the Gillespie simulation algorithm and statistical advice. The *netabc* program, and all supplementary analysis programs, were written by me.

A version of chapter 2 has been submitted for publication with the title “Reconstructing network parameters from viral phylogenies.” An oral presentation entitled “Phylogenetic inference of contact network parameters with kernel-ABC” was given based on chapter 2 to the 23rd HIV Dynamics and Evolution meeting on April 25, 2016, in Woods Hole, Massachusetts, USA (the presentation was delivered remotely).

Use of the BC data is in accordance with an ethics application that was reviewed and approved by the UBC/Providence Health Care Research Ethics Board (H07-02559).

[Source code for the *netabc* program is freely available at <https://github.com/rmcclosk/netabc> under the GPL-3 license. Scripts to run all computational experiments, as well as the source code for this thesis, are available at <https://github.com/rmcclosk/thesis>.](https://github.com/rmcclosk/netabc)

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List of Symbols

I number of infected nodes in a contact network at the time of transmission tree sampling.

N total number of nodes in a contact network.

α preferential attachment power parameter in Barabási-Albert networks.

γ exponent of power-law degree distribution in scale-free networks.

λ decay factor meta-parameter for tree kernel.

σ radial basis function variance meta-parameter for tree kernel.

m number of edges added per vertex when constructing a Barabási-Albert network.

List of Abbreviations

ABC approximate Bayesian computation.

AIC Akaike information criterion.

ANOVA analysis of variance.

BA Barabási-Albert.

ER Erdős-Rényi.

ERGM exponential random graph model.

ESS expected sample size.

GLM generalized linear model.

GSL GNU scientific library.

GTR generalized time-reversible.

HIV human immunodeficiency virus.

HMM hidden Markov model.

HPD highest posterior density.

IDU injection drug users.

IQR interquartile range.

IS importance sampling.

kPCA kernel principal components analysis.

kSVR kernel support vector regression.

LTT lineages-through-time.

MAP maximum *a posteriori*.

MCMC Markov chain Monte Carlo.

MH Metropolis-Hastings.

ML maximum likelihood.

MSM men who have sex with men.

nLTT normalized lineages-through-time.

pdf probability density function.

POSIX Portable Operating System Interface.

SARS severe acute respiratory syndrome.

SI susceptible-infected.

SIR susceptible-infected-recovered.

SIS sequential importance sampling.

SMC sequential Monte Carlo.

SVM support vector machine.

SVR support vector regression.

TasP treatment as prevention.

WS Watts-Strogatz.

Acknowledgements

Chapter 1

Introduction

1.1 Objective

The spread of a disease is most often modelled by assuming either a homogeneously mixed population [1, 2], or a population divided into a small number of homogeneously mixed groups [3]. This assumption, also called *mass action* [4], or *panmixia*, implies that any two individuals in the same compartment are equally likely to come into contact making transmission possible at some predefined rate. Although this provides a reasonable approximation in many cases [5], the error introduced by assuming a panmictic population can be substantial when significant contact heterogeneity exists in the underlying population [6–8]. Contact network models provide an alternative to compartmental models which do not require the assumption of panmixia. In addition to more accurate predictions, the parameters of the networks themselves may be of interest from a public health perspective. For example, certain vaccination strategies may be more or less effective in curtailing an epidemic depending on the underlying network’s degree distribution [9, 10]. Phylodynamic methods, [which link viruses’ evolutionary and epidemiological dynamics](#), have been used to fit many different types of models to phylogenetic data [11, 12]. However, these models generally assume a panmictic population. The primary objective of this work is *to develop a method to fit contact network models, [and thereby relax the assumption of homogeneous mixing](#), in a phylodynamic framework.*

[In this work, we take a Bayesian approach: our goal is to estimate the posterior distribution on model parameters given our data,](#)

$$\Pr(\theta | T) = \frac{\Pr(T | \theta) \Pr(\theta)}{\Pr(T)},$$

[where \$\Pr\(T | \theta\)\$ is the likelihood, \$\Pr\(\theta\)\$ is the prior, and \$\Pr\(T\)\$ is the marginal probability of \$T\$ which acts as a normalizing constant on the posterior \(see appendix A for a review of mathematical modeling and Bayesian inference, including definitions of these concepts\). As we shall show \(see section 2.1.4\), estimating this distribution presents computational challenges beyond those usually encountered in Bayesian inference. Both the likelihood \$\Pr\(T | \theta\)\$ and the normalizing constant \$\Pr\(T\)\$ seem to be intractable, which rules out the use of most common maximum likelihood and Bayesian methods.](#)

Calculating the likelihood of the parameters of a contact network model seems likely to be an intractable problem. We have not proven this is the case, but some intuition can be provided by examining the process involved in the likelihood calculation. Consider a contact network model with parameters θ and an estimated transmission tree T with n tips. In general, we do not know the labels of the internal nodes of T , only the labels of its tips. To fit this model using likelihood-based methods, we must calculate the likelihood of θ , that is, $\Pr(T | \theta)$. Let \mathcal{G} be the set of all possible contact networks, and \mathcal{N} be the set of all possible labellings of the internal nodes of T . We can write the likelihood as

$$\begin{aligned}\Pr(T | \theta) &= \sum_{v \in \mathcal{N}} \Pr(T, v | \theta) \\ &= \sum_{G \in \mathcal{G}} \sum_{v \in \mathcal{N}} \Pr(T, v | G, \theta) \Pr(G | \theta) \\ &= \sum_{G \in \mathcal{G}} \sum_{v \in \mathcal{N}} \Pr(T, v | G) \Pr(G | \theta),\end{aligned}\tag{1.1}$$

the last equality following from the fact that T and v depend only on G , not on θ . Although $\Pr(T, v | G)$ and $\Pr(G | \theta)$ may individually be straightforward to calculate, the number of possible directed graphs on N nodes is $2^{N(N-1)}$ [13], larger if the nodes and edges in the graph may have different labels or attributes. Hence, the number of terms in the sum is at least exponential in n , as there must be at least n nodes in the network. In addition, eq. (1.1) assumes that T is complete, meaning that all infected individuals were sampled. This is rarely the case in practice—most often, we only have access to a subset of the infected individuals. In this case, the likelihood calculation becomes even more complex, because we must also sum over all possible complete trees.

Depending on the network model studied, it is possible that eq. (1.1) could be simplified into a tractable expression. An alternative to likelihood-based methods, which could be applied to any network model, is provided by approximate Bayesian computation (ABC) [14–17]. All of the ingredients required to apply ABC to this problem are readily available. Simulating networks is straightforward under a variety of models. Epidemics on those networks, and the corresponding transmission trees, can also be easily simulated. As mentioned above, contact networks can profoundly affect transmission tree shape. Those shapes can be compared using a highly informative similarity measure called the “tree kernel” [18]; [similar kernel functions have been demonstrated to work well as distance functions in ABC \[19\]](#). ABC can be implemented with several algorithms, but sequential Monte Carlo (SMC) has advantages over others, [including improved accuracy in low-density regions and parallelizability \[20\]](#). A recently-developed adaptive algorithm requiring minimal tuning on the part of the user makes SMC an even more attractive approach [21]. In summary, our method to infer contact network parameters will combine the following: stochastic simulation of epidemics on networks, the tree kernel, and adaptive ABC-SMC. [Our method will expand on the framework developed by \[22\], who combined ABC with the tree kernel to infer parameters of population genetic models from viral phylogenies using Markov chain Monte Carlo \(MCMC\).](#)

Empirical studies of sexual contact networks have found that these networks tend to be scale-free [23–26], meaning that their degree distributions follow a power law (although there has been some

disagreement, see [6, 27]). Preferential attachment has been postulated as a mechanism by which scale-free networks could be generated [28]. The Barabási-Albert (BA) model [28] is one of the simplest preferential attachment models, which makes it a natural choice to explore with our method. The second aim of this work is *to use simulations to investigate the parameters of the Barabási-Albert model, including whether they have a detectable impact on tree shape, and whether they can be accurately recovered using ABC*.

Due to its high global prevalence and fast mutation rate, human immunodeficiency virus (HIV) is one of the most commonly-studied viruses in a phylodynamic context. Consequently, a large volume of HIV sequence data is publicly available, more than for any other pathogen, and including sequences sampled from diverse geographic and demographic settings. At the time of this writing, there were 635,400 HIV sequences publicly available in GenBank, annotated with 172 distinct countries of origin. Since HIV is almost always spread through either sexual contact or sharing of injection drug supplies, the contact networks underlying HIV epidemics are driven by social dynamics and are therefore likely to be highly structured [26]. Moreover, since no cure yet exists, efforts to curtail the progression of an epidemic have relied on preventing further transmissions through measures such as treatment as prevention (TasP) and education leading to behaviour change. The effectiveness of this type of intervention can vary significantly based on the underlying structure of the network and the particular nodes to whom the intervention is targeted [29, 30]. Due to this combination of data availability and potential public health impact, HIV is an obvious context in which our method could be applied. Therefore, the third and final aim of this work is *to apply ABC to fit the Barabási-Albert model to existing HIV outbreaks*.

To summarize, this work has three objectives. First, we will develop a method which uses ABC to infer parameters of contact network models from observed transmission trees. Second, we will use simulations to characterize the parameters of the BA network model in terms of their effect on tree shape and how accurately they can be recovered with ABC. Finally, we will apply the method to fit the BA model to several real-world HIV datasets.

The remainder of this background chapter is organized in four sections. The first section introduces phylogenies and transmission trees, which are the input data from which our method aims to make statistical inferences. This section also introduces phylodynamics, a family of methods that, like ours, aim to infer epidemiological parameters from evolutionary data. The second section focuses on contact networks and network models, whose parameters we are attempting to infer. The relationship between contact networks and transmission trees is also discussed. The third and fourth sections introduce SMC and ABC respectively, which are the two algorithmic components of the method we will implement. In particular, ABC refers to the general approach of using simulations to replace likelihood calculations in a Bayesian setting, while SMC is a particular algorithm which can be used to implement ABC.

1.2 Phylogenetics and phylodynamics

1.2.1 Phylogenetic trees

In evolutionary biology, a *phylogeny*, or *phylogenetic tree*, is a graphical representation of the evolutionary relationships among a group of organisms or species (generally, *taxa*) [31]. The *tips* of a phylogeny, that is, the nodes without any descendants, correspond to *extant*, or observed, taxa. The *internal nodes* correspond to their common ancestors, [usually extinct \(although occasionally the internal nodes may be observed as well, eg. \[32\]\)](#). The edges or *branches* of the phylogeny connect ancestors to their descendants. Phylogenies may have a *root*, which is a node with no descendants distinguished as the most recent common ancestor of all the extant taxa [33]. When such a root exists, the tree is referred to as being *rooted*; otherwise, it is *unrooted*. The structural arrangement of nodes and edges in the tree is referred to as its *topology* [34].

The branches of the tree may have associated lengths, representing either evolutionary distance or calendar time between ancestors and their descendants. The term “evolutionary distance” is used here imprecisely to mean any sort of quantitative measure of evolution, such as the number of differences between the DNA sequences of an ancestor and its descendant, or the difference in average body mass or height. A phylogeny with branch lengths in calendar time units is often referred to as *time-scaled*. In a time-scaled phylogeny, the internal nodes can be mapped onto a timeline by using the tips of the tree, which usually correspond to the present day, reference points [35]. The corresponding points on the timeline are called *branching times*, and the rate of their accumulation is referred to as the *branching rate*. Rooted trees whose tips are all the same distance from the root are called *ultrametric* trees [36]. These concepts are illustrated in fig. 1.1.

1.2.2 Transmission trees

In epidemiology, a *transmission tree* is a graphical representation of an epidemic’s progress through a population [37]. Like phylogenies, transmission trees have tips, nodes, edges, and branch lengths. However, rather than recording an evolutionary process (speciation), they record an epidemiological process (transmission). The tips of a transmission tree represent the removal by sampling of infected hosts, while internal nodes correspond to transmissions from one host to another. Transmission trees generally have branch lengths in units of calendar time, with branching times indicating times of transmission. The root of a transmission tree corresponds to the initially infected patient who introduced the epidemic into the network, also known as the *index case*. The internal nodes may be labelled with the donor of the transmission pair, if this is known. The tips of the tree, rather than being fixed at the present day, are placed at the time at which the individual was removed from the epidemic, such as by death, recovery, isolation, behaviour change, or migration [38]. Consequently, the transmission tree may not be ultrametric, but may have tips located at varying distances from the root. Such trees are said to have *heterochronous* taxa [39], in contrast to the *isochronous* taxa found in most phylogenies of macro-organisms. A transmission tree is illustrated in fig. 1.2 (right). The object on the right of the figure is called a *contact network*, which depicts the entire susceptible population along with all possible

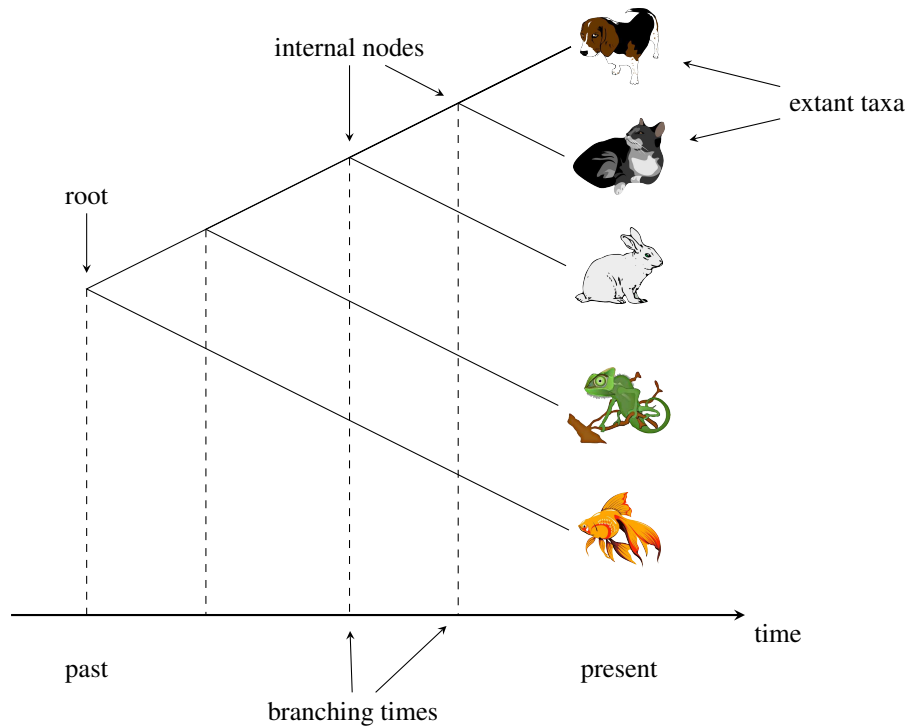


Figure 1.1: Illustration of a rooted, ultrametric, time-scaled phylogeny. The tips of the tree, which represent extant taxa, are placed at the present day on the time axis. Internal nodes, representing extinct common ancestors to the extant taxa, fall in the past. The topology of the tree indicates that cats and dogs are the most closely related pair of species, whereas fish is most distantly related to any other taxon in the tree.

routes of disease transmission. Contact networks, and their relationships to transmission trees, will be discussed further in section 1.3.

Each infected individual in an epidemic may appear at nodes of the transmission tree more than once. This is different from the transmission *network*, in which each infected individual appears exactly once, and edges are in one-to-one correspondence with transmissions [8, 40]. The distinction between the two objects is illustrated in fig. 1.2. However, since transmission networks generally have no cycles (unless re-infection occurs), they are trees in the graph theoretical sense, and hence are sometimes also referred to as transmission trees [e.g. 41]. In this work, we reserve the term “transmission tree” for the objects depicted on the right side of fig. 1.2, following e.g. [38]. The term “transmission network” is taken to mean the subgraph of the contact network along which transmissions occurred, following e.g. [8, 40].

Since transmission trees are essentially a detailed record of an epidemic’s progress, they contain substantial epidemiological information. As a basic example, the lineages-through-time (LTT) plot [35], which plots the number of lineages in a phylogeny against time, can be used to quantify the incidence of new infections over the course of an epidemic [42]. However, in all but the most well-studied of epidemics, transmission trees are not possible to assemble through traditional epidemiological methods [40]. The time and effort to conduct detailed interviews and contact tracing of a sufficient number

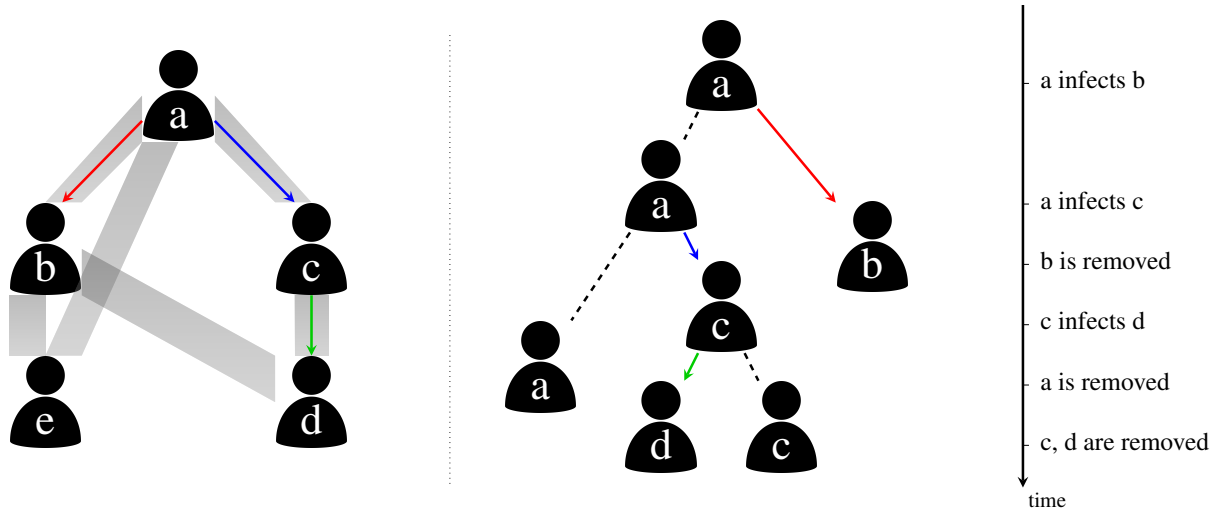


Figure 1.2: Illustration of epidemic spread over a contact network, and the corresponding transmission tree. (Left) A contact network with five hosts, labelled *a* through *e*. Thick shaded edges indicate symmetric contacts among the hosts. The transmission network is indicated by coloured arrows. The epidemic began with node *a*, who transmitted to nodes *b* and *c*. Node *c* further transmitted to node *d*. Node *e* was not infected. (Right) The transmission tree corresponding to this scenario, with a timeline of transmission and removal times.

of infected individuals is usually prohibitive, and may additionally be confounded by misreporting and other challenges [43]. However, it turns out that for viral epidemics, some of the epidemiological information contained in the transmission tree leaves a mark on the viral genetic material circulating in the population. A family of methods called *phylodynamics* [44] addresses the challenge of estimating epidemiological parameters from viral sequence data [12].

1.2.3 Phylodynamics: linking evolution and epidemiology

The basis of phylodynamics is the fact that, for RNA viruses, epidemiological and evolutionary processes occur on similar time scales [39]. In fact, these two processes interact, such that it is possible to detect the influence of host epidemiology on the evolutionary history of the virus as recorded in an *inter-host viral phylogeny*. Phylodynamic methods aim to detect and quantify the signatures of epidemiological processes in these phylogenies [11, 12], which relate one representative viral genotype from each host in an infected population. These methods have been used to investigate parameters such as transmission rate, recovery rate, and basic reproductive number [11, 12]. The majority of phylodynamic studies attempt to infer the parameters of an epidemiological model for which the likelihood of an observed phylogeny can be calculated. Most often, this is some variation of the birth-death [45, 46] or coalescent [47, 48] models. These methods either assume the viral phylogeny is known, as we do in this work, or (more commonly) integrate over phylogenetic uncertainty in a Bayesian framework. Phylogenetic inference is a complex topic which we shall not discuss here; see *e.g.* [49] for a full review.

Due to the relationship between the aforementioned processes, there is a degree of correspondence between viral phylogenies and transmission trees [37, 41, 50, 51]. In particular, the transmission process

is quite similar to *allopatric speciation* [52], where genetic divergence follows the geographic isolation of a sub-population of organisms. Thus, transmission, which is represented as branching in the transmission tree, causes branching in the viral phylogeny as well [53]. Similarly, the removal of an individual from the transmission tree causes the extinction of their viral lineage in the phylogeny. Consequently, the topology of the viral phylogeny is sometimes used as a proxy for the topology of the transmission tree [54]. Modern likelihood-based methods of phylogenetic reconstruction [e.g. 55, 56] produce unrooted trees whose branch lengths measure genetic distance in units of expected substitutions per site. On the other hand, transmission trees are rooted, and have branches measuring calendar time [11]. Therefore, estimating a transmission tree from a viral phylogeny requires the phylogeny to be rooted and time-scaled. Methods for performing this process include root-to-tip regression [57–59], which we apply in this work, and least-square dating [60]. Alternatively, the tree may be rooted separately with an outgroup [61] before time-scaling.

A caveat of estimating transmission trees in this manner is that the correspondence between the topologies of the viral phylogeny and transmission tree is far from exact [37, 62]. Due to intra-host diversity, the viral strain which is transmitted may have split from another lineage within the donor long before the transmission event occurred. Hence, the branching point in the viral phylogeny may be much earlier than that in the transmission tree. Another possibility is that one host transmitted to two or more recipients in one order, but the transmitted lineages originated within the donor in a different order. In this case, the topology of the transmission tree and the viral phylogeny will be mismatched. In practice, this discordance has not proven an insurmountable problem: for example, Leitner et al. [63] and Paraskevis et al. [64] were able to accurately recover known transmission trees using viral phylogenies. The problem of accurately estimating transmission trees is an ongoing area of research [32, 54, 65–68]. For example, Hall, Woolhouse, and Rambaut [54] developed a Bayesian method to jointly estimate a transmission tree and viral phylogeny by combining models of agent-based transmission, within-host population dynamics, and sequence evolution.

1.2.4 Tree shapes

To perform phylodynamic inference, we must be able to extract quantitative information from viral phylogenies. What is informative about a phylogeny, beyond the demographic characteristics of the individuals it relates, is its *shape*. The shape of a phylogeny has two components: the topology, and the distribution of branch lengths [69]. Methods of quantifying tree shape fall into two categories: summary statistics, and pairwise measures. Summary statistics assign a numeric value to each individual tree, while pairwise measures quantify the similarity between pairs of trees.

One of the most widely used tree summary statistics is Sackin’s index [70], which measures the imbalance or asymmetry in a rooted tree. For the i th tip of the tree, we define N_i to be the number of branches between that tip and the root. The unnormalized Sackin’s index is defined as the sum of all N_i . It is called unnormalized because it does not account for the number of tips in the tree. Among two trees having the same number of tips, the least-balanced tree will have the highest Sackin’s index. However, among two equally balanced trees, the larger tree will have a higher Sackin’s index. This

makes it challenging to compare balances among trees of different sizes. To correct this, Kirkpatrick and Slatkin [71] derive the expected value of Sackin's index under the Yule model [72]. Dividing by this expected value normalizes Sackin's index, so that it can be used to compare trees of different sizes. An example of a pairwise measure is the normalized lineages-through-time (nLTT) [73], which compares the LTT [35] plots of two trees. Specifically, the two LTT plots are normalized so that they begin at (0,0) and end at (1,1), and the absolute difference between the two plots is integrated between 0 and 1. In the context of infectious diseases, the LTT is related to the prevalence [42], so large values may indicate that the trees being compared were produced by different epidemic trajectories [73].

Poon et al. [18] developed an alternative pairwise measure which applies the concept of a *kernel function* to phylogenies. Kernel functions, originally developed for support vector machines (SVMs) [74], compare objects in a space \mathcal{X} by mapping them into a feature space \mathcal{F} of high or infinite dimension via a function ϕ . The similarity between the objects is defined as

$$K(x, x') = \langle \phi(x), \phi(x') \rangle,$$

that is, the inner product of the objects' representations in the feature space. Computing $\phi(x)$ may be computationally prohibitive due to the dimension of \mathcal{F} . The utility of a kernel function K is that it is constructed in such a way that it can compute the inner product without explicitly computing $\phi(x)$. The kernel function developed in [18] will henceforth be referred to as the *tree kernel*. This kernel maps trees into the space of all possible possible *subset trees*, which are subtrees that do not necessarily extend all the way to the tips. The subset-tree kernel was originally developed for comparing parse trees in natural language processing [75] and did not incorporate branch length information. The version developed by Poon et al. [18] includes a radial basis function to compare the differences in branch lengths, thus incorporating both the trees' topologies and their branch lengths in a single similarity score.

The kernel score of a pair of trees, denoted $K(T_1, T_2)$, is defined as a sum over all pairs of nodes (n_1, n_2) , where n_1 is a node in T_1 and n_2 is a node in T_2 . Following Poon et al. [18], let $N(T)$ denote the set of all nodes in T , $nc(n)$ be the number of children of node n , c_n^j be the j th child of node n , and l_n be the vector of branch lengths connecting node n to its $nc(n)$ children. Furthermore, let $nl(n)$ be the number of children of n which are leaves (we always have $nl(n) \leq nc(n)$). The production rule of n is the pair $(nc(n), nl(n))$. That is, if two nodes have the same number of children and among these, the same number of leaves, then they have the same production rule. Let $k_G(x, y)$ be a Gaussian radial basis function of the vectors x and y ,

$$k_G(x, y) = \exp\left(-\frac{1}{2\sigma} \|x - y\|_2^2\right),$$

where $\|\cdot\|_2$ is the Euclidean norm and σ is a variance parameter. The tree kernel is defined as

$$K(T_1, T_2) = \sum_{n_1 \in N(T_1)} \sum_{n_2 \in N(T_2)} \Delta(n_1, n_2), \quad (1.2)$$

where

$$\Delta(n_1, n_2) = \begin{cases} \lambda & n_1 \text{ and } n_2 \text{ are leaves} \\ \lambda k_G(l_{n_1}, l_{n_2}) \prod_{j=1}^{\text{nc}(n_1)} (1 + \Delta(c_{n_1}^j, c_{n_2}^j)) & n_1 \text{ and } n_2 \text{ have the same} \\ & \text{production rule} \\ 0 & \text{otherwise.} \end{cases}$$

The parameter λ in the above expression, is called the *decay factor* [76], and takes a value between 0 and 1. Without this parameter, terms in the sum 1.2 corresponding to large subset trees with the same topology would be similarly large and tend to dominate the kernel score. λ penalizes Δ more strongly as the number of recursive calls increases, which downweights the largest matching substructures and allows smaller matches to contribute more to the kernel score. In this work, we refer to the parameters λ and σ as *meta-parameters*, to avoid confusing them with model parameters we are trying to estimate.

When evaluating the tree kernel, it is helpful to reorder the children of each internal node such that the larger of the two subtrees is on the right-hand side. If the two subtrees have equal sizes, then the child with the longer branch length can be put on the right-hand side. This operation is referred to as *ladderizing*. Since the ordering of children is arbitrary in phylogenies, this operation ensures that a maximal number of matching subset trees are counted by the tree kernel without making meaningful changes to the trees.

The tree kernel was later shown to be highly effective in differentiating trees simulated under a compartmental model with two risk groups of varying contact rates [22]. In that paper, Poon used the tree kernel as the distance function in approximate Bayesian computation (ABC) (see section 1.5), to fit epidemiological models to observed trees.

1.3 Contact networks

1.3.1 Overview

Epidemics spread through populations of hosts through *contacts* between those hosts. The definition of contact depends on the mode of transmission of the pathogen in question. For an airborne pathogen like influenza, a contact may be simple physical proximity, while for human immunodeficiency virus (HIV), contact could be via unprotected sexual relations or blood-to-blood contact (such as through needle sharing). A *contact network* is a graphical representation of a host population and the contacts among its members [8, 77, 78]. The *nodes* in the network represent hosts, and *edges* or *links* represent contacts between them. A contact network is shown in fig. 1.2 (left). Contact networks are a particular type of *social network* [79, 80], which is a network in which edges may represent any kind of social or economic relationship. Social networks are frequently used in the social sciences to study phenomena where relationships between people or entities are important [for a review see 81].

Edges in a contact networks may be *directed*, representing one-way transmission risk, or *undirected*, representing symmetric transmission risk. For example, a network for an airborne epidemic would use undirected edges, because the same physical proximity is required for a host to infect or to become in-

fect. However, an infection which may be spread through blood-to-blood contact through transfusions would use directed edges, since the recipient has no chance of transmitting to the donor. Directed edges are also useful when the transmission risk is not equal between the hosts, such as with HIV transmission among men who have sex with men (MSM), where the receptive partner carries a higher risk of infection than the insertive partner [82]. In this case, a contact could be represented by two directed edges, one in each direction between the two hosts, with the edges annotated by what kind of risk they imply [81]. An undirected contact network is equivalent to a directed network where each contact is represented by two symmetric directed edges. The *degree* of a node in the network is how many contacts it has. In directed networks, we may make the distinction between *in-degree* and *out-degree*, which count respectively the number incoming and outgoing edges. The *degree distribution* of a network denotes the probability that a node has any given number of links. The set of edges attached to a node are referred to as its *incident* edges.

Epidemiological models most often assume some form of contact homogeneity. The simplest models, such as the susceptible-infected-recovered (SIR) model [5], assume a completely homogeneously mixed population, where every pair of contacts is equally likely. More sophisticated models partition the population into groups with different contact rates between and among each group [83]. However, these models still assume that every possible contact between a member of group i and a member of group j is equally likely. This assumption is clearly unrealistic for the majority of human communities and can lead to errors in predicted epidemic trajectories when there is substantial heterogeneity present [6, 84, 85]. Contact networks provide a way to relax this assumption by representing individuals and their contacts explicitly. It is important to note that, although panmixia is an unrealistic modelling assumption, it has not proven a substantial hurdle to epidemic modelling in practice [5]. Using this assumption, researchers have been able to derive estimates of the transmission rate and the basic reproductive number of various outbreaks, which have agreed with values obtained by on-the-ground data collection [86]. Therefore, if one is interested only in these population-level variables, the additional complexity of contact network models may not be warranted. Rather, these models are most useful when we are interested in properties of the network itself, such as centrality, structural balance, and transitivity [81].

From a public health perspective, knowledge of contact networks has the potential to be extremely useful. On a population level, network structure can dramatically affect the speed and pattern of epidemic spread [e.g. 7, 87]. For example, epidemics are expected to spread more rapidly in networks having the “small world” property, where the average path length between two nodes in the network is relatively low [88]. Some sexually transmitted infections would not be expected to survive in a homogeneously mixed population, but their long-term persistence can be explained by contact heterogeneity [5, 89]. Hence, the contact network can provide an idea of what to expect as an epidemic unfolds. In terms of actionable information, the efficacy of different vaccination strategies may depend on the topology of the network [8–10, 90]. On a local level, contact networks can be informative about the groups or individuals who are at highest risk of acquiring or transmitting infection who would therefore benefit most from public health interventions [29, 30].

Contact networks are a challenging type of data to collect, requiring extensive epidemiological in-

vestigation in the form of contact tracing [8, 40, 43, 78]. Therefore, it has been necessary to explore less resource-intensive alternatives which still contain information about population structure. For instance, it is possible to obtain limited information about the contact network by individual interviews without contact tracing. Variables which can be estimated in this fashion are referred to as *node-level* measures [81]. One of the most well-studied of these is the degree distribution mentioned above, which can theoretically be estimated by simply asking each person how many contacts they had in some interval of time. However, the degree distributions often observed in real-world sexual networks are heavy-tailed [23–25], so dense or respondent-driven sampling [91] would be needed to capture the high-degree nodes characterizing the tail of the distribution.

An alternative approach has been the analysis of other types of network, which can be directly estimated with phylogenetic methods from viral sequence data. Some work focuses on the *phylogenetic network*, in which two nodes are connected if the genetic distance between their viral sequences is below some threshold. Primarily, this work has focused on the detection of *phylogenetic clusters*, which are groups of individuals whose viral sequences are significantly more similar to each other’s than to the general population’s. The phylogenetic network is informative about “hotspots” of transmission and can be used to identify demographic groups to whom targeted interventions are likely to have the greatest effect [92]. However, this network may show little to no agreement with contact data obtained through epidemiological methods [93–95] and therefore may be a poor proxy for the contact network. Other studies [96] have investigated the *transmission network*, which is the subgraph of the contact network consisting of infected nodes and the edges that led to their infections [40] (fig. 1.2, left). It is possible to estimate the transmission network phylogenetically, although the methods required for doing so are more sophisticated than for estimating the phylogenetic network [96]. These studies again mostly focus on clustering and also on degree distributions.

Other statistical methods have been developed to infer contact network parameters strictly from the timeline of an epidemic, using neither genetic data nor reported contacts. Britton and O’Neill [97] developed a Bayesian method to infer the p parameter of an Erdős-Rényi (ER) network, along with the transmission and removal rate parameters of the susceptible-infected (SI) model, using observed infection and optionally removal times. However, it was designed for only a small number of observations, and was unable to estimate p independently from the transmission rate. Groendyke, Welch, and Hunter [98] significantly updated and extended the methodology of Britton and O’Neill and applied it to a measles outbreak affecting 188 individuals. They were able to obtain a much more informative estimate of p , although this data set included both symptom onset and recovery times for all individuals and was unusual in that the entire contact network was presumed to be infected. Volz [87] developed differential equations describing the dynamics of the SIR model on a wide variety of random networks defined by their degree distributions. Although the topic of estimation was not addressed in the original paper, Volz’s method could in principle be used to fit such models to observed epidemic trajectories, similar to what is done with the ordinary SIR model. Volz and Meyers [84] later extended the method to dynamic contact networks and applied it to a sexual network relating 99 individuals investigated during a syphilis outbreak.

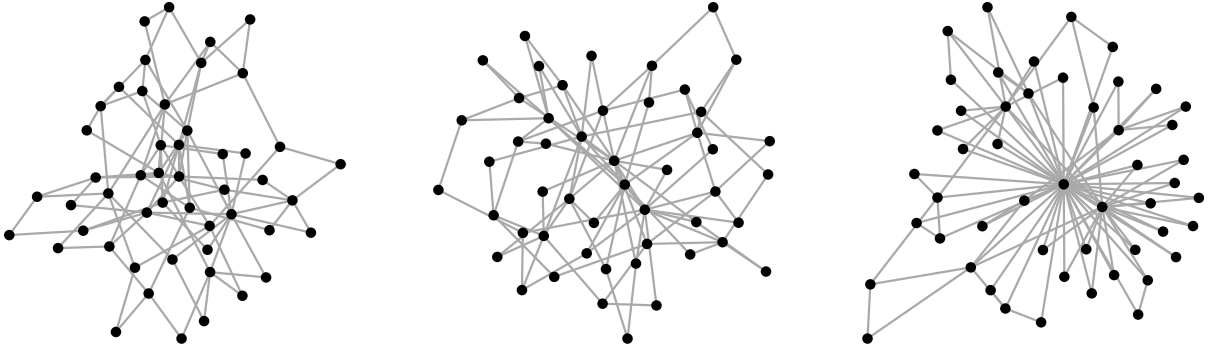


Figure 1.3: Examples of Barabási-Albert networks with preferential attachment power $\alpha = 0$ (left), 1 (centre), and 2 (right). All networks have $N = 50$ nodes and were constructed with $m = 2$ edges per vertex. When $\alpha = 0$, attachments are formed at random and most nodes have low degree. When $\alpha = 1$, preferential attachment is linear and several higher-degree nodes are observable. When $\alpha = 2$, preferential attachment is quadratic and nearly every vertex is attached to a small number of hub nodes.

1.3.2 Scale-free networks and preferential attachment

A *scale-free* network is one whose degree distribution follows a power law, meaning that the number of nodes in the network with degree k is proportional to $k^{-\gamma}$ for some constant γ [28]. Scale-free networks are characterized by a large number of nodes of low degree, with relatively few “hub” nodes of very high degree. Epidemiological surveys have indicated that human sexual networks tend to be scale-free [23–26]. Interestingly, many other types of network, including computer networks [89], biological metabolic networks [99], and academic co-author networks [100], also have the scale-free property.

Several properties of scale-free networks are relevant in epidemiology. The high-degree hub nodes are known as *superspreaders* [101], which have been postulated to contribute in varying degree to the spread of diseases such as HIV [38] and severe acute respiratory syndrome (SARS) [102]. Scale-free networks have no epidemic threshold [89], meaning that diseases with arbitrarily low transmissibility [can persist have a chance, however small, of persisting](#) at low levels indefinitely. This is in contrast with homogeneously mixed populations, in which transmissibility below the epidemic threshold would result in exponential decay in the number of infected individuals and eventual extinction of the pathogen [5].

One mechanism which has been shown to lead to scale-free networks is *preferential attachment* [28, 103]. The simplest preferential attachment model is known as the Barabási-Albert (BA) model after its inventors [28]. Under this model, networks are formed by starting with a small number m_0 of nodes. New nodes are added one at a time until there are a total of N in the network. Each time a new node is added, $m \geq 1$ edges are added from it to other nodes in the graph. In the original formulation, the partners of the new node are chosen with probability linearly proportional to their degree. However, Barabási and Albert suggest extending the model such that the probability of choosing a partner of degree d is proportional to $d^\alpha + 1$ for some constant α , and we use this extension here. When $m = 1$, the network takes on the distinctive shape of a tree, that is, it does not contain any cycles. Cycles are present in the network for all other m values. Examples of BA networks with three different values of the preferential attachment power α are shown in fig. 1.3.

There has been some contention over the idea that contact networks are scale-free. Handcock and Jones [27] fit several stochastic models of partner formation to empirical degree distributions derived from population surveys of sexual behaviour. They found that a negative binomial distribution, rather than a power law, was the best fit to five out of six datasets, although the difference in goodness of fit was extremely small in four out of these five. Bansal, Grenfell, and Meyers [6] found that an exponential distribution, rather than a power law, was the best fit to degree distributions of six social and sexual networks.

1.3.3 Relationship between network structure and transmission trees

The contact network underlying an epidemic constrains the shape of the transmission network, which in turn determines the topology of the transmission tree relating the infected hosts (fig. 1.2). The index case who introduces the epidemic into the network becomes the root of the tree. Each time a transmission occurs, the lineage corresponding to the donor host in the tree splits into two, representing the recipient lineage and the continuation of the donor lineage. Figure 1.2 illustrates this correspondence. It must be emphasized that, although the order and timing of transmissions determines the tree topology uniquely, the converse does not hold. That is, for any given topology, there are in general many transmission networks which would lead to that topology. In other words, it is impossible to distinguish who transmitted to whom from a transmission tree alone [104].

A number of studies have made progress in quantifying the relationship between contact networks and transmission trees. O’Dea and Wilke [105] simulated epidemics over networks with four types of degree distribution. They then estimated the Bayesian skyride [106] population size trajectory in two ways: from the phylogeny, using MCMC; and from the incidence and prevalence trajectories, using the method developed by Volz et al. [53]. The concordance between the two skyrides, as well as the relationship between the skyride and prevalence curve, was qualitatively different for each degree distribution. Leventhal et al. [107] investigated the relationship between transmission tree imbalance and several epidemic parameters under four contact network models and found that these relationships varied considerably depending on which model was being considered. The authors also investigated a real-world HIV phylogeny and found a level of imbalance inconsistent with a randomly mixing population. Welch [108] simulated transmission trees over networks with varying degrees of community structure. They found that transmission trees simulated under networks with low clustering could not generally be distinguished from those simulated under highly clustered networks and concluded that contact network clusters do not affect transmission tree shape. However, more recently, Villandre et al. [109] investigated the correspondence between contact network clusters and transmission tree clusters and did find a moderate correspondence between the two in some cases. Goodreau [110] combined a dynamic contact network model with a model of within-host viral evolution to simulate viral phylogenies over eight types of contact network. Estimates of prevalence and effective population size were calculated for each simulated phylogeny under three models of epidemic growth. The author found that estimates for networks with a small high-risk subgroup and networks involving commercial sex workers were substantially different than estimates for random networks or networks with segregated equal-risk groups.

1.4 Sequential Monte Carlo

1.4.1 Overview and notation

Recall that the primary objective of our work is to develop a statistical inference method for estimating contact network parameters from transmission trees. In particular, for a network model with parameters θ and an input transmission tree T , we are interested in the *posterior distribution*

$$\Pr(\theta | T) = \frac{\Pr(T | \theta) \Pr(\theta)}{\Pr(T)}. \quad (1.3)$$

As outlined in section 1.1, both the likelihood $\Pr(T | \theta)$ and the normalizing constant $\Pr(T)$ are likely computationally intractable. Hence, rather than computing the posterior distribution analytically, we will approximate it using a *Monte Carlo* approach. The fundamental idea behind Monte Carlo methods is succinctly expressed by Liu, Chen, and Logvinenko [111]:

Monte Carlo’s view of the world is that any probability distribution π , regardless of its complexity, can always be *represented* by a discrete sample from it. By “represented”, we mean that any computation of expectations using π can be replaced to an acceptable degree of accuracy by using the empirical distribution resulting from the discrete sample.

In other words, if we are able to sample enough points from a distribution of interest, we will be able to make reasonably accurate statements about the distribution itself. For example, the expected value of the distribution can be estimated by the sample’s population mean. The reason Monte Carlo methods will be useful in this work is that algorithms exist for obtaining samples from distributions, including as the aforementioned posterior, that are analytically intractable and from which direct sampling is not possible (for a review see [112]). Sequential Monte Carlo (SMC) [113–115] is one such algorithm.

SMC is also known as the *particle filter*. Rather than sampling points one at a time from the target distribution, SMC considers a population of points or “particles”, here denoted $\{x^{(k)}\}$. The particles are associated with weights, $\{w(x^{(k)})\}$. These weighted particles are a representation for the target distribution. For example, the expected value of the distribution is approximated by

$$\frac{1}{n} \sum_{k=1}^n x^{(k)} w(x^{(k)}),$$

where n is the number of particles. Initially, the particles do not represent the target distribution but rather a more tractable distribution from which direct sampling is straightforward. The word “sequential” is used to describe the iterative process of perturbation, resampling, and reweighting applied to the particles in such a way that they converge, collectively, to a sample from the target.

In this work, the distribution of interest is the posterior distribution 1.3. The particles are particular values of the parameters θ of the contact network model being studied. If we were taking a typical Bayesian Monte Carlo approach to this problem, the particles would end up weighted by their posterior probability and distributed in such a way that the weighted population was a reasonable representation

of $\Pr(\theta \mid T)$. This turns out to be not straightforward in our case, as we will address in [section 1.5](#). For now, nothing is lost by ...

[The goal of this section of the introduction is to describe an algorithm called the SMC sampler \[116\], which forms the basis of the adaptive ABC-SMC algorithm we apply toward the main objective of this work. We begin by describing sequential importance sampling \(SIS\), which is a precursor to SMC that samples from a sequence of distributions defined on spaces of increasing dimension. We then describe SMC itself, which extends SIS with a resampling step to fight particle degeneracy. Finally, we outline the SMC sampler, which allows SMC to be applied to sequences of distributions all defined on the same space. This terminology will become clear as the methods are described.](#)

SMC is the name for a family of statistical inference methods that rely on approximating probability distributions of interest with large collections of *particles*, here denoted $\{x^{(k)}\}$ [113–115]. These collections or *populations* are constructed to form a *Monte Carlo approximation* to some distribution of interest π , meaning that the empirical distribution of the particles converges in distribution to π as the population size gets large [111]. The word *sequential* is used because the particle populations are modified in an iterative fashion over time, for example, to incorporate new evidence.

To fully describe SMC, we will introduce some notation and terminology. The definitions of these terms will become clearer as they are used. For a sequence x_1, \dots, x_d , we will write \mathbf{x}_i to mean the partial sequence x_1, \dots, x_i . The subscript $^{(k)}$ will be used to indicate the k th particle in a population. To ease the notational burden we will omit the superscripts and subscripts on the weight functions w .

We define a *Markov kernel* as the continuous analogue of the transition matrix in a finite-state Markov model. For some spaces X and Y , $K : X \times Y \rightarrow [0, 1]$ such that

$$\int_Y K(x, y) dy = 1 \quad (1.4)$$

for all $x \in X$. This is an “operational” definition of Markov kernel which will be suitable for our purposes. A more rigorous definition can be found in *e.g.* [117]. Note that Markov kernels have nothing to do with the kernel functions defined in [section 1.2.4](#), other than sharing a name (the word “kernel” is ubiquitous in mathematics).

1.4.2 Sequential importance sampling

Sequential importance sampling (SIS) [118] [is a particle-based method](#) whose aim is to sample from a distribution π on an high-dimensional space, say $\pi(\mathbf{x}) = \pi(x_1, \dots, x_d)$. The basis of SIS is importance sampling (IS), which is a method of estimating summary statistics of distributions which are known only up to a normalizing constant, and therefore cannot be sampled from directly. That is, if π is such a distribution and f is any real-valued function, IS is concerned with estimating

$$\pi(f) = \int f(x) \pi(x) dx = \int f(x) \frac{\gamma(x)}{Z} dx,$$

where the integral is over the space on which π is defined, $\gamma(x)$ is known pointwise, and $Z = \int \gamma(x)dx$ is the unknown normalizing constant. Suppose we have at hand another distribution η , called the *importance distribution*, from which we are able to sample. Define the *importance weight* as the ratio $w(x) = \gamma(x)/\eta(x)$. We can write the expectation of interest as

$$\int f(x)\pi(x)dx = \frac{1}{Z} \int w(x)f(x)dx. \quad (1.5)$$

Since η can be sampled from exactly, and γ and f can both be evaluated pointwise, the integral $\int w(x)f(x)dx$ can be approximated by a Monte Carlo estimate. Moreover, the normalizing constant Z can be expressed in terms of the importance weight and distribution, $Z = \int w(x)\eta(x)dx$. Therefore, we have all the ingredients we need to obtain an estimate of $\pi(f)$ using eq. (1.5). Although this is a simple and elegant approach, the drawback is that the variance of the estimate is proportional to the variance of the importance weights [115], which may be quite large if η and γ are very different. Therefore, the practical use of IS on its own is limited, since it depends on finding an importance distribution similar to π , which we usually know very little about *a priori*.

The objective of SIS is to build up an importance distribution η for π sequentially. By the general product rule, $\pi(\mathbf{x})$ can be decomposed as

$$\pi(\mathbf{x}) = \pi(x_1)\pi(x_2 | x_1) \cdots \pi(x_{d-1} | \mathbf{x}_{d-2})\pi(x_d | \mathbf{x}_{d-1}).$$

This decomposition is natural in many contexts, particularly for on-line estimation. For example, in a stateful model like an hidden Markov model (HMM), x_i may represent the state at time i , with $\pi(\mathbf{x})$ being the posterior distribution over possible paths. The importance distribution η for π will be constructed using a similar decomposition,

$$\eta(\mathbf{x}) = \eta(x_1)\eta(x_2 | x_1) \cdots \eta(x_{d-1} | \mathbf{x}_{d-2})\eta(x_d | \mathbf{x}_{d-1}).$$

The importance weights for η can be written recursively as

$$w(\mathbf{x}_i) = \frac{\pi(\mathbf{x}_i)}{\eta(\mathbf{x}_i)} = \frac{\pi(x_i | \mathbf{x}_{i-1})\pi(\mathbf{x}_{i-1})}{\eta(x_i | \mathbf{x}_{i-1})\eta(\mathbf{x}_{i-1})} = \frac{\pi(x_i | \mathbf{x}_{i-1})}{\eta(x_i | \mathbf{x}_{i-1})} \cdot w(\mathbf{x}_{i-1}). \quad (1.6)$$

Thus, we can choose $\eta(x_i | \mathbf{x}_{i-1})$ such that the variance of the importance weights is as small as possible at every step, eventually arriving at a full importance distribution. This choice is made on a problem-specific basis, taking any available information about $\pi(x_i | \mathbf{x}_{i-1})$ into account (see *e.g.* [115, 119] for many examples). One potential choice for $\eta(x_i | \mathbf{x}_{i-1})$ is simply $\pi(x_i | \mathbf{x}_{i-1})$, if it is possible to compute. In a Bayesian setting, the prior distribution may be used. The exact form of $\eta(x_i | \mathbf{x}_{i-1})$ which minimizes the variance of the weights is called the *optimal kernel* [120], the name deriving from the fact that $k(x_i, \mathbf{x}_{i-1}) = \eta(x_i | \mathbf{x}_{i-1})$ is a Markov kernel. In some applications, it is possible to approximate the optimal kernel or even compute it explicitly.

The recursive definition 1.6 suggests an algorithm for obtaining a sample from η and using it to

[obtain an approximate sample from \$\pi\$ by IS](#) (algorithm 1). We begin with n “particles”, which have been sampled from the importance distribution $\eta(x_0)$ for $\pi(x_0)$. The particles are updated and reweighted d times, corresponding to the d elements of the decomposition of π . At the i th step, each particle is extended to include x_i drawn according to the chosen $\eta(x_i | \mathbf{x}_{i-1})$, and the importance weights are recalculated and normalized.

Algorithm 1 Sequential importance sampling.

```

for  $k = 1$  to  $n$  do
    Sample  $x_1^{(k)}$  from  $\eta(x_1)$                                 ▷ Initialize the  $k$ th particle
     $w^{(k)} \leftarrow \pi(x_1^{(k)}) / \eta(x_1^{(k)})$ 
end for
for  $i = 2$  to  $d$  do
    for  $k = 1$  to  $n$  do
        Sample  $x_i^{(k)}$  from  $\eta(x_i | \mathbf{x}_{i-1}^{(k)})$                     ▷ Extend the  $k$ th particle
         $w(\mathbf{x}_i^{(k)}) \leftarrow [\pi(x_i^{(k)} | \mathbf{x}_{i-1}^{(k)}) / \eta(x_i^{(k)} | \mathbf{x}_{i-1}^{(k)})] \cdot w(\mathbf{x}_{i-1}^{(k)})$ 
    end for
    Normalize the weights so that  $\sum w = 1$ 
end for

```

1.4.3 Sequential Monte Carlo

The importance distribution η constructed with SIS is merely an approximation to π , and may be a fairly poor one in practice depending on the application. Try as we might to keep the variances of the weights low, the cumulative errors at each sequential step tend to push many of the weights to very low values [113]. This results in a poor approximation to π , since only a few particles retain high importance weights after all d sequential steps, [a problem known as *particle degeneracy*](#). To mitigate this problem, [Gordon, Salmond, and Smith \[118\] introduced technique they called the *bootstrap filter*, which involves a resampling of the population of particles after each sequential step in accordance with their importance weights](#). A similar idea, termed *particle rejuvenation*, was proposed by Liu and Chen [121]. These approaches cause particles with high importance weights to be replicated in the population, while particles with low weights may be removed. After each resampling step, the importance weights for all particles are set equal.

[The resampling step was formally integrated with SIS by Doucet, Godsill, and Andrieu \[113\] to form the first SMC algorithm \(algorithm 2\)](#). Rather than resample at every step as the bootstrap filter proposed, the authors use a criterion based on the expected sample size (ESS) the particle population to determine when resampling is necessary. The ESS of the population of particles is defined as

$$\text{ESS}(w) = \frac{n}{1 + \text{Var}(w)},$$

where n is the number of particles in the population. When the ESS drops below the threshold [\(conventionally \$n/2\$ \[115\]\)](#), particles are resampled according to their importance weights. This results in the removal of

Algorithm 2 Sequential Monte Carlo [113].

```
for  $k = 1$  to  $n$  do
    Sample  $x_1^{(k)}$  from  $\eta(x_1)$  ▷ Initialize the  $k$ th particle
     $w^{(k)} \leftarrow \pi(x_1^{(k)}) / \eta(x_1^{(k)})$ 
end for
for  $i = 2$  to  $d$  do
    for  $k = 1$  to  $n$  do
        Sample  $x_i^{(k)}$  from  $\eta(x_i \mid \mathbf{x}_{i-1}^{(k)})$  ▷ Extend the  $k$ th particle
         $w(\mathbf{x}_i^{(k)}) \leftarrow [\pi(x_i^{(k)} \mid \mathbf{x}_{i-1}^{(k)}) / \eta(x_i^{(k)} \mid \mathbf{x}_{i-1}^{(k)})] \cdot w(\mathbf{x}_{i-1}^{(k)})$ 
    end for
    if  $\text{ESS}(w) < T$  then ▷  $T$  is a user-defined threshold
        Resample the particles according to  $w$ 
        for  $k = 1$  to  $n$  do
             $w^{(k)} \leftarrow 1/n$ 
        end for
    end if
end for
```

low-weight particles from the population, and also equalizes all the weights. Various resampling strategies beyond the basic sampling with replacement have been proposed [122], but we will not discuss those here.

1.4.4 The sequential Monte Carlo sampler

The SIS and SMC algorithms described above aim to sample from a high-dimensional distribution $\pi(x)$, by sequentially sampling from d distributions of lower but increasing dimension. Del Moral, Doucet, and Jasra [116] developed an *SMC sampler* with an alternative objective: to sample sequentially from d distributions π_1, \dots, π_d , all of the same dimension and defined on the same space. The π_i are assumed to form a related sequence, such as posterior distributions attained by sequentially considering new evidence. As with SIS, we assume that $\pi_i(x) = \gamma_i(x) / Z_i$, where γ_i is known pointwise and the normalizing constant Z_i is unknown.

Both algorithms involve progression through a sequence of related distributions. For SIS, these distributions are lower-dimensional marginals of the target distribution, while for the SMC sampler, they are of the same dimension and constitute a smooth progression from an initial to a final distribution. In both cases, the neighbouring distributions in the sequence are related to each other in some way, and we can take advantage of that relationship to create a sequence of importance distributions alongside the sequence of targets. In SIS, the neighbouring marginals $\pi(\mathbf{x}_i)$ and $\pi(\mathbf{x}_{i+1})$ were related by the conditional density $\pi(x_i \mid \mathbf{x}_{i-1})$, which we used to inform the importance distribution. In SMC, the relationship between subsequent distributions is less explicit, but it is assumed that they are related closely enough that an importance distribution for π_i can be easily transformed into one for π_{i+1} . In particular, the sequence

of importance distributions η_i is constructed as

$$\eta_i(x') = \int \eta_{i-1}(x) K_i(x, x') dx, \quad (1.7)$$

where K_i is a Markov kernel and the integral is over the space on which the π_i are defined. The choice of K_i should be based on the perceived relationship between π_{i-1} and π_i . Del Moral, Doucet, and Jasra [116] propose the use of a MCMC kernel with equilibrium distribution π_i . That is,

$$K_i(x, x') = \max \left(1, \frac{q(x', x) \pi_i(x)}{q(x, x') \pi_i(x')} \right),$$

where $q(x, x')$ is a proposal function such as a Gaussian distribution centred at x [from which \$x'\$ is drawn](#) (see ??).

Although this method of building up η appears straightforward, the drawback is that the importance distribution itself becomes intractable. In particular, evaluating $\eta_i(x)$ involves a i -dimensional integral of the type in eq. (1.7). As it is necessary to evaluate $\eta(x)$ pointwise to perform IS, this construction appears to have defeated the purpose of providing an importance distribution for each π_i . Del Moral, Doucet, and Jasra [116] overcome this problem with two “artificial” objects. First, they propose the existence of *backward* Markov kernels $L_{i-1}(x_i, x_{i-1})$. For now, these kernels are arbitrary; they will later be precisely defined on a problem-specific basis. Second, the authors define an alternative sequence of target distributions

$$\tilde{\pi}_i(\mathbf{x}_i) = \pi_i(x_i) \prod_{k=1}^{i-1} L_k(x_{k+1}, x_k)$$

of increasing dimension. This brings us back to the setting described above in section 1.4.2, namely of building up an importance distribution of dimension d sequentially through lower-dimensional distributions. We can write $\tilde{\pi}_i$ in terms of $\tilde{\pi}_{i-1}$ by noticing that

$$\frac{\tilde{\pi}_i(\mathbf{x}_i)}{\tilde{\pi}_{i-1}(\mathbf{x}_{i-1})} = \frac{\pi_i(x_i) \prod_{k=1}^{i-1} L_k(x_{k+1}, x_k)}{\pi_{i-1}(x_{i-1}) \prod_{k=1}^{i-2} L_k(x_{k+1}, x_k)} = \frac{\pi_i(x_i) L(x_i, x_{i-1})}{\pi_{i-1}(x_{i-1})},$$

and hence

$$\tilde{\pi}_i = \frac{\pi_i(x_i) L(x_i, x_{i-1})}{\pi_{i-1}(x_{i-1})} \cdot \tilde{\pi}_{i-1}.$$

Therefore, the importance weights for these new targets are defined recursively as

$$w(\mathbf{x}_i) = \frac{\tilde{\pi}_i(\mathbf{x}_i)}{\eta_i(\mathbf{x}_i)} \quad (1.8)$$

$$= \frac{\tilde{\pi}_{i-1}(\mathbf{x}_{i-1}) \pi_i(x_i) L(x_i, x_{i-1})}{\eta_{i-1}(\mathbf{x}_{i-1}) \pi_{i-1}(x_{i-1}) K_i(x_{i-1}, x_i)} \quad (1.9)$$

$$= w(\mathbf{x}_{i-1}) \cdot \frac{\pi_i(x_i) L_{i-1}(x_i, x_{i-1})}{\pi_{i-1}(x_{i-1}) K_i(x_{i-1}, x_i)} \quad (1.10)$$

$$\propto w(\mathbf{x}_{i-1}) \cdot \frac{\gamma_i(x_i) L_{i-1}(x_i, x_{i-1})}{\gamma_{i-1}(x_{i-1}) K_i(x_{i-1}, x_i)}. \quad (1.11)$$

The final key piece of information is to notice that, because the L_i are Markov kernels, π_i is simply the marginal in \mathbf{x}_{i-1} of $\tilde{\pi}$. Therefore, a sample from $\tilde{\pi}_i$ automatically gets us a sample from π_i , by considering only the i th component of \mathbf{x}_i . These are all the ingredients we need to apply SIS. The sequences of kernels L and K should be chosen based on the problem at hand to minimize the variance in the importance weights as well as possible. For a fixed choice of K_i , the backward kernels L_i which minimize this variance are called the *optimal* backward kernels. The full SMC sampler algorithm is presented as algorithm 3. A resampling step is applied whenever the ESS of the population drops too low, as discussed in the previous section.

Algorithm 3 Sequential Monte Carlo sampler of Del Moral, Doucet, and Jasra [116].

```

for  $k = 1$  to  $n$  do
  Sample  $x_1^{(k)}$  from  $\eta_1(x_1)$  ▷ Initialize the  $k$ th particle
   $w^{(k)} \leftarrow \gamma_1(x_1^{(k)}) / \eta_1(x_1^{(k)})$ 
  Normalize the weights so that  $\sum w = 1$ 
end for
for  $i = 2$  to  $d$  do
  for  $k = 1$  to  $n$  do
    Sample  $x_i^{(k)}$  from  $K(x_{i-1}^{(k)}, x_i)$  ▷ Extend the  $k$ th particle
     $w^{(k)} \leftarrow w^{(k)} \cdot \frac{\gamma_i(x_i) L_{i-1}(x_i, x_{i-1})}{\gamma_{i-1}(x_{i-1}) K_i(x_{i-1}, x_i)}$ 
  end for
  Normalize the weights so that  $\sum w = 1$ 
  if  $\text{ESS}(w) < T$  then ▷  $T$  is a user-defined threshold
    Resample the particles according to  $w$ 
    for  $k = 1$  to  $n$  do
       $w^{(k)} \leftarrow 1/n$ 
    end for
  end if
end for

```

1.5 Approximate Bayesian computation

[sequential Monte Carlo, and the SMC sampler, were developed for sampling from distributions which can be evaluated up to a normalizing constant. TODO](#)

[This section is organized as follows. First, we formalize the concept of a mathematical model and discuss what it means to “fit” such models to data and how this is typically accomplished. Second, we introduce approximate Bayesian computation \(ABC\), which was designed for situations like the one we face in this work where the most commonly used means of fitting models cannot be applied. Finally, we describe algorithms which can be used to implement ABC, including a variant of SMC.](#)

1.5.1 Overview of ABC

Most mathematical models are amenable to fitting via one or both of the approaches, maximum likelihood (ML) or Bayesian inference, discussed above. However, there are some, particularly in the domain of population genetics [17, 123], for which calculation of either the likelihood or the product of the likelihood and the prior may be infeasible. For example, one or both of these quantities may be expressible only as an intractable integral. ABC is designed for such cases, where standard likelihood-based techniques for model fitting cannot be applied.

Ordinarily, Bayesian inference targets the posterior distribution $f(\theta | y)$. That is, in the Bayesian framework, model parameters with higher posterior density are “better” in the sense that they offer a more credible explanation for the observed data. Approximate Bayesian computation offers an alternative metric for parameter credibility, namely the similarity of simulated datasets to the observed data. If datasets simulated under the model closely resemble the real data, it follows that the model is a reasonable approximation to the real-world process generating the observed data. More formally, suppose we have a distance measure ρ defined on the space of all possible data our model could generate. ABC aims to sample from the joint posterior distribution of model parameters and simulated datasets z which are within some small distance ε of the observed data y ,

$$\pi_\varepsilon(\theta, z | y) = \frac{\pi(\theta)f(z | \theta)\mathbb{I}_{A_{\varepsilon,y}}(z)}{\int_{A_{\varepsilon,y} \times \Theta} \pi(\theta)f(z | \theta) d\theta}.$$

Here, $A_{\varepsilon,y}$ is an ε -ball around y with respect to ρ , Θ is the space of all possible model parameters, and \mathbb{I} is the indicator function [124]. As we shall see in the next section, this distribution can be sampled from exactly. The word “approximate” derives from the assumption that, for a suitably chosen distance ρ and a small enough ε , the marginal in z of this distribution approximates the posterior of interest [124]. That is,

$$\int \pi_\varepsilon(\theta, z | y) dz \approx f(\theta | y).$$

The distribution $\pi_\varepsilon(\theta, z | y)$ is variously referred to as the *ABC target distribution* or the ABC approximation to the posterior. The intuition for why this approximation might be reasonable comes from the fact that, when $\varepsilon = 0$, the ε -ball around y should contain only y itself, hence the integral on the left is exactly equal to the posterior. Thus, by taking ε small, we should attain something close to the posterior if ρ captures the similarity between datasets reasonably well. However, the accuracy of the ABC approximation depends heavily on the choice of distance function [125, 126].

In many applications (eg. [16, 127]), ρ is defined as $\rho(S(\cdot), S(\cdot))$ where S is a function which maps data points into a vector of summary statistics. In the context of ABC, a summary statistic S is called *sufficient* if

$$f(\theta | y) = f(\theta | S(y)).$$

That is, sufficiency implies that the data can be replaced with the summary statistic without losing any information about the posterior distribution [128]. For most problems, it is not possible to find sufficient summary statistics [128]. A number of sophisticated methods have been developed for selecting and

[weighting summary statistics based on various optimality criteria \[125, 126, and references therein\].](#)

Summary statistics can be useful if the data are high-dimensional or of a complex type, but they are not strictly necessary. For instance, if the data are numeric and of low dimension, the distance function may simply be the Euclidean distance [129]. [Park et al. \[19\] proposed the use of a kernel function \(defined in section 1.2.4\) in place of a distance function. The authors referred to their approach as “double-kernel ABC” due to the use of a second kernel function to compute the weights of the particles. The work by Poon \[22\], upon which ours is based, employed a similar approach, replacing the likelihood ratio in Bayesian MCMC with a ratio of kernel scores.](#)

1.5.2 Algorithms for ABC

Algorithms for performing ABC fall into one of three categories: rejection, MCMC, and SMC [124]. To simplify the notation, we shall restrict the descriptions of these algorithms to the case of one simulated dataset per parameter particle (the meaning of this will become clear shortly). The extension to multiple datasets per particle is straightforward and will be given at the end of the section. We use the variable x to refer to the pair (θ, z) , so that the ABC target distribution can be written $\pi_\varepsilon(x | y)$.

Rejection ABC is the simplest method, and also the one which was first proposed [14, 15]. The algorithm, outlined in algorithm 4, repeats the following steps until a desired number of samples from the target distribution are obtained. Parameter values θ are sampled according to the prior distribution $\pi(\theta)$. Then, a simulated dataset z is generated from the model with the sampled parameter values. By definition, the probability density of obtaining the particular dataset z is $f(z | \theta)$. Finally, the parameters are sampled if the distance of z from the observed data y is less than ε , that is, with probability $\mathbb{I}_{A_{\varepsilon,y}}(z)$. Putting this all together, the parameters θ are sampled with probability proportional to

$$\pi(\theta)f(z | \theta)\mathbb{I}_{A_{\varepsilon,y}}(z),$$

which is exactly the numerator of the ABC target distribution. Thus, θ represents an unbiased sample from the approximate posterior.

Algorithm 4 Rejection ABC.

```

loop
  Draw  $\theta$  according to  $\pi(\theta)$ 
  Simulate a dataset  $z$  from the model with parameters  $\theta$ 
  if  $\rho(y, z) < \varepsilon$  then
    Sample  $\theta$ 
  end if
end loop

```

Rejection ABC is easy to understand and implement, but it is not generally computationally feasible. If the posterior is very different from the prior, a very large number of samples may need to be taken in order to find a simulated dataset which is close to z . The inefficiency is compounded by the curse of dimensionality - the measure of the ε -ball around y decreases exponentially with the number of

dimensions. ABC-MCMC (algorithm 5) was designed to overcome these hurdles [130]. The approach is similar to ordinary Bayesian MCMC (??), except that a distance cutoff replaces the likelihood ratio. That is, the transition probability between states x and x' is defined as

$$\min \left(1, \frac{\pi(\theta')q(\theta', \theta)}{\pi(\theta)q(\theta, \theta')} \cdot \mathbb{I}_{A_{\varepsilon,y}}(z') \right).$$

Algorithm 5 ABC-MCMC.

Draw θ according to $\pi(\theta)$

loop

 Propose θ' according to $q(\theta, \theta')$

 Simulate a dataset \mathbf{z}' according to the model with parameters θ

 Accept $\theta \leftarrow \theta'$ with probability $\min \left(1, \frac{\pi(\theta')q(\theta', \theta)}{\pi(\theta)q(\theta, \theta')} \cdot \mathbb{I}_{A_{\varepsilon,y}}(z') \right)$

end loop

Some of the same computational inefficiencies arise with ABC-MCMC as with rejection. For example, in regions of low posterior density, the probability to simulate a dataset proximal to the observed data is low. Various strategies have been developed to mitigate this, including reducing the tolerance level ε as the chain progresses [131].

The most recently developed class of algorithm for ABC is ABC-SMC [129, 132]. As with ABC-MCMC, the algorithm is a straightforward modification of an existing Bayesian inference method, in this case the SMC sampler (section 1.4.4). The sequence of target distributions is defined as $\pi_i = \pi_{\varepsilon_i}(x | y)$ for a decreasing sequence of tolerances ε_i . The intention is for the algorithm to progress smoothly through a sequence of target distributions which ends at the ABC approximation to the posterior. As discussed in section 1.4.4, the choices of the kernels K and L is problem-specific, and so appropriate kernels must be chosen for ABC. Several options have been proposed [21, 129, 132].

All the algorithms discussed in this section can be straightforwardly extended to sample from the joint distribution

$$\pi_{\varepsilon}(\theta, z_1, \dots, z_M | y),$$

which is equivalent to associating M simulated datasets to each parameter particle instead of just one. The simulated dataset z is replaced by $z = z_1, \dots, z_M$, and the indicator function for the ε -ball around y is replaced by

$$\sum_{k=1}^M \mathbb{I}_{A_{\varepsilon,y}}(z_k).$$

For ABC-MCMC and ABC-SMC, the proposal distribution $q(\theta, \theta')f(z | \theta')$ is replaced by

$$q_i(\theta, \theta') \prod_{k=1}^M f(z_k | \theta').$$

1.6 Summary

Our method integrates the four distinct research areas just described: phylogenetics, contact networks, sequential Monte Carlo, and approximate Bayesian computation. The first two topics together form the problem domain. Phylogenetic data is the input to our method, while estimates of the parameters of contact network models are the desired output. The latter two topics define the algorithm and statistical framework that our inference method will use.

Chapter 2

Reconstructing contact network parameters from viral phylogenies

[In this chapter, we will address the three research aims of this thesis introduced in section 1.1. First, in section 2.1, we describe *netabc*, a computer program that implements an approximate Bayesian computation-based algorithm to fit contact network models to phylogenetic data. We also provide a justification for the use of ABC for this problem by arguing that the likelihood functions required to fit these models by more conventional means are likely to be computationally intractable. Second, in section 2.2, we perform a simulation study to investigate the Barabási-Albert network model, which uses a preferential attachment mechanism to generate networks with the power law degree distributions observed in real world social and sexual networks. We progress through two exploratory analyses testing the identifiability of the model's parameters, and conclude by testing *netabc*'s ability to recover the parameters from simulated transmission trees. Third, in section 2.3, we apply *netabc* to fit the BA model to six real world HIV datasets, with the understanding of the model parameters' identifiability gained through the simulation experiments. We conclude the chapter with a unified discussion of the three research aims, including interpretation of the results of both the simulated and real data experiments, as well as an examination of the limitations of our approach and opportunities for future investigation.](#)

2.1 *Netabc*: a computer program for estimation of contact network parameters with kernel-assisted ABC

Netabc is a computer program to perform statistical inference of contact network parameters from an estimated transmission tree using ABC. [As discussed in section 1.1, the principal statistical algorithm used by *netabc* is adaptive ABC-SMC \[21\]. In addition, there are two supplementary components which are specific to the domain of phylogenetics and contact networks: Gillespie simulation \[133\], to simulate transmission trees on contact networks; and the tree kernel \[18\], which is used as the distance function in ABC to compare transmission trees \[22\] \(see section 1.5\). We give a high-level overview of the program here, before describing these components in detail. *Netabc* takes as input an estimated transmission tree,](#)

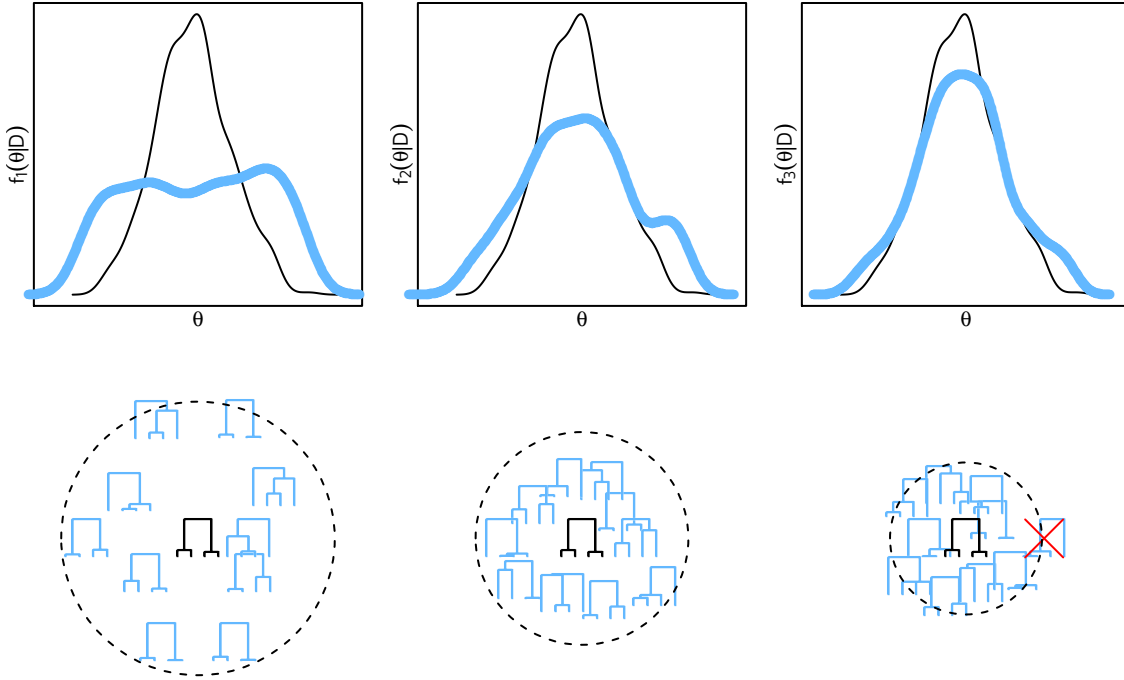


Figure 2.1: Graphical schematic of the ABC-SMC algorithm implemented in *netabc*. Particles are initially drawn from their prior distributions, making the initial population a Monte Carlo approximation to the prior. At each iteration, particles are perturbed, and a distance threshold around the true tree contracts. Particles are rejected, and eventually resampled, when all their associated simulated trees lie outside the threshold. As the algorithm progresses, the population smoothly approaches a Monte Carlo approximation of the ABC target distribution, which is assumed to resemble the posterior.

which can be derived from a viral phylogeny by rooting and time-scaling as described in section 1.2.3 or estimated by other methods [32, 54, 65–68]. We variously refer to this estimated transmission tree as the observed tree, input tree, or true tree.

As described in section 1.4, *netabc* keeps track of a population of particles $x^{(k)}$, each of which contains particular parameter values $\theta^{(k)}$ for the [contact network](#) model we are trying to fit [to the input tree](#). A small number of contact networks $z^{(k)}$ are generated under the model for each particle, in accordance with that particle’s parameters. An epidemic is simulated over each of these networks using Gillespie simulation, and by keeping track of its progress, a transmission tree is obtained. Thus, each particle becomes associated with several simulated transmission trees. These trees are compared to the input tree using the tree kernel. Particles are weighted according to the similarity of their associated simulated trees with the true tree, with more similar trees receiving higher weights. The particles are iteratively perturbed to explore the parameter space, and particles with simulated trees too distant from the true tree are periodically dropped and resampled. Once a convergence criterion is attained, the final set of particles is used as a Monte Carlo approximation to the target distribution of ABC, which is assumed to resemble the posterior distribution on model parameters (see section 1.5). A graphical schematic of this algorithm is given in fig. 2.1.

Netabc is written in the C programming language. The *igraph* library [134] is used to generate and

store contact networks and phylogenies. Judy arrays [135] are used for hash tables and dynamic programming matrices. The GNU scientific library (GSL) [136] is used to generate random draws from probability distributions, and to perform the bisection step in the adaptive ABC-SMC algorithm. Parallelization is implemented with Portable Operating System Interface (POSIX) threads [137]. In addition to the *netabc* binary to perform kernel-assisted ABC, we provide three additional stand-alone utilities: *treekernel*, to calculate the tree kernel; *nettree*, to simulate a transmission tree over a contact network; and *treestat*, to compute various summary statistics of phylogenies. The programs are freely available at <https://github.com/rmcclosk/netabc>.

To check that our implementation of Gillespie simulation was correct, we reproduced Figure 1A of Leventhal et al. [107] (our fig. A.1), which plots the imbalance of transmission trees simulated over four network models at various levels of pathogen transmissibility. Our implementation of adaptive ABC-SMC was tested by applying it to the same mixture of Gaussians used by Del Moral, Doucet, and Jasra [21] to demonstrate their method (originally used by Sisson, Fan, and Tanaka [129]). We were able to obtain a close approximation to the function (see fig. A.2), and attained the stopping condition used by the authors in a comparable number of steps. To check that the algorithm would converge to a bimodal distribution, we also applied it to a mixture of two Gaussians with means ± 4 and variances 1. The algorithm was able to recover both peaks (fig. A.3).

2.1.1 Simulation of transmission trees over contact networks

The simulation of epidemics, and the corresponding transmission trees, over contact networks is performed in *netabc* using the Gillespie simulation algorithm [133]. This method has been independently implemented and applied by several authors [e.g. 95, 98, 105, 107, 109]. Groendyke, Welch, and Hunter [98] published their implementation as an *R* package, but since the SMC algorithm is quite computationally intensive, we chose to implement our own version in *C* [as part of netabc](#).

Let $G = (V, E)$ be a directed contact network. We assume the individual nodes and edges of G follow the dynamics of the SIR model [2]. Each directed edge $e = (u, v)$ in the network is associated with a transmission rate β_e , which indicates that, once u becomes infected, the waiting time until u infects v is distributed as $\text{Exponential}(\beta_e)$. Note that v may become infected before this time has elapsed, if v has other incoming edges. v also has a removal rate γ_v , so that the waiting time until removal of v from the population is $\text{Exponential}(\gamma_v)$. Removal may correspond to death or recovery with immunity, or a combination of both, but in our implementation recovered nodes never re-enter the susceptible population. We define a *discordant edge* as an edge (u, v) where u is infected and v has never been infected.

To describe the algorithm, we introduce some notation and variables. Let $\text{in}(v)$ be the set of incoming edges to v , and $\text{out}(v)$ be the set of outgoing edges from v . Let I be the set of infected nodes in the network, R be the set of removed nodes, and S be the remaining susceptible nodes, and D be the set of discordant edges in the network. Let β be the total transmission rate over all discordant edges, and γ be

the total removal rate of all infected nodes,

$$\beta = \sum_{e \in D} \beta_e, \quad \gamma = \sum_{v \in I} \gamma_v.$$

The variables S , I , R , D , β , and γ are all updated as the simulation progresses. When a node v becomes infected, it is deleted from S and added to I . Any formerly discordant edges in $\text{in}(v)$ are deleted from D , and edges in $\text{out}(v)$ to nodes in S are added to D . If v is later removed, it is deleted from I and added to R , and any discordant edges in $\text{out}(v)$ are deleted from D . At the time of either infection or removal, the variables β and γ are updated to reflect the changes in the network. Since these updates are straightforward, we do not write them explicitly in the algorithm.

The Gillespie simulation algorithm is given as Algorithm 2.1.1. The transmission tree T is simulated along with the epidemic. We keep a map called *tip*, which maps infected nodes in I to the tips of T . The simulation continues until either there are no discordant edges left in the network, or we reach a user-defined cutoff of time (t_{\max}) or number of infections (I_{\max}). We use the notation $\text{Uniform}(0, 1)$ to indicate a number drawn from a uniform distribution on $(0, 1)$, and likewise for $\text{Exponential}(\lambda)$. The combined number of internal nodes and tips in T is denoted $|T|$.

Algorithm 6 Simulation of an epidemic and transmission tree over a contact network

```

infect a node  $v$  at random, updating  $S$ ,  $I$ ,  $D$ ,  $\beta$  and  $\gamma$ 
 $T \leftarrow$  a single node with label 1
 $\text{tip}[v] \leftarrow 1$ 
 $t \leftarrow 0$ 
while  $D \neq \emptyset$  and  $|I| + |R| < I_{\max}$  and  $t < t_{\max}$  do
   $s \leftarrow \min(t_{\max} - t, \text{Exponential}(\beta + \gamma))$ 
  for  $v \in \text{tip}$  do
    extend the branch length of  $\text{tip}[v]$  by  $s$ 
  end for
   $t \leftarrow t + s$ 
  if  $t < t_{\max}$  then
    if  $\text{Uniform}(0, \beta + \gamma) < \beta$  then
      choose an edge  $e = (u, v)$  from  $D$  with probability  $\beta_e/\beta$  and infect  $v$ 
       $\text{tip}[v] \leftarrow |T| + 1$  ▷ add new tips to tree and tip array
       $\text{tip}[u] \leftarrow |T| + 2$  ▷ corresponding to  $u$  and  $v$ 
      add tips with labels  $(|T| + 1)$  and  $(|T| + 2)$  to  $T$ 
      connect the new nodes to  $\text{tip}[v]$  in  $T$ , with branch lengths 0
    else
      choose a node  $v$  from  $I$  with probability  $\gamma_v/\gamma$  and remove  $v$ 
      delete  $v$  from  $\text{tip}$ 
    end if
    update  $S$ ,  $I$ ,  $R$ ,  $D$ ,  $\beta$ , and  $\gamma$ 
  end if
end while

```

2.1.2 Phylogenetic kernel

The tree kernel developed by Poon et al. [18] provides a comprehensive similarity score between two phylogenetic trees, via the dot-product of the two trees' feature vectors in the space of all possible subset trees with branch lengths (see section 1.2.4). Because the branch lengths are continuous, there are infinitely many possible subset trees; hence, the feature space is infinite-dimensional. The kernel was implemented using the fast algorithm developed by Moschitti [76]. First, the production rule of each node, which is the total number of children and the number of leaf children, is recorded. The nodes of both trees are ordered by production rule, and a list of pairs of nodes sharing the same production rule is created. These are the nodes for which the value of the tree kernel must be computed - all other pairs have a value of zero. The pairs to be compared are then re-ordered so that the child nodes are always evaluated before their parents. Due to its recursive definition, ordering the pairs in this way allows the tree kernel to be computed by dynamic programming. The complexity of this implementation is $O(|T_1||T_2|)$ for the two trees T_1 and T_2 being compared.

The tree kernel cannot be used directly as a distance measure for ABC, since it is maximized, not minimized, when the two trees being compared are the same. Therefore, we defined the distance between two trees as

$$\rho(T_1, T_2) = 1 - \frac{K(T_1, T_2)}{\sqrt{K(T_1, T_1)K(T_2, T_2)}},$$

which is a number between 0 and 1 that is minimized when $T_1 = T_2$. This is similar to the normalization used by Poon et al. [18] and Collins and Duffy [75].

2.1.3 Adaptive sequential Monte Carlo for Approximate Bayesian computation

We implemented the adaptive SMC algorithm for ABC developed by Del Moral, Doucet, and Jasra [21]. This algorithm is similar to the reference ABC-SMC algorithm described in section 1.5.2, except that the sequence of tolerances ε_i is automatically determined rather than specified in advance. The tolerances are chosen such that the ESS of the particle population, which indicates the quality of the Monte Carlo approximation (see section 1.4.2), decays at a controlled rate. A sudden precipitous drop in ESS would indicate that only a small number of particles had non-zero importance weights, which would result in a very poor Monte Carlo approximation to the target distribution. This situation is referred to as the “collapse” of the approximation, also known as particle degeneracy (see section 1.4.3) and is mitigated by the adaptive approach. A single parameter ~~α (not to be confused with the BA model parameter)~~ controls the decay rate. In the original paper of Del Moral, Doucet, and Jasra [21], the parameter is called α , but to avoid confusion with the BA parameter of the same name, we will refer to it here as α_{ESS} . The tolerance ε_i is chosen to satisfy

$$\text{ESS}(w_i) = \alpha_{\text{ESS}} \text{ESS}(w_{i-1}),$$

where, w_i is the vector of weights at the i th step. Note that, since w_i depends on ε_i , this equation solves for the updated weights and the updated tolerance simultaneously. As pointed out by Del Moral, Doucet, and

Jasra [21], the equation has no analytic solution, but can be solved numerically by bisection. The forward kernels K_i are taken to be MCMC kernels with stationary distributions π_{ε_i} and proposal distributions

$$q_i(\theta, \theta') \prod_{k=1}^M \Pr(z_i^{(k)'} | \theta'),$$

where θ is the vector of model parameters and z_k are M datasets simulated according to θ' . In our implementation, q is either a Gaussian proposal for continuous parameters, or a Poisson proposal for discrete parameters. For the Poisson proposals, the number of steps to move the particle is drawn from a Poisson distribution, and the direction in which to move the particle is chosen uniformly at random. For both proposals, the variance was set equal to twice the empirical variance of the particles, following [21, 132]. The backwards kernels are

$$L_{i-1}(x', x) = \frac{\pi_n(x) K(x, x')}{\pi_n(x')}.$$

When substituted into eq. (1.11), the forward kernels $K(x, x')$ and densities $\pi_n(x') = \pi_{\varepsilon_n}(x')$ cancel out, and we are left with the weight update

$$\begin{aligned} w_i(x) &\propto w_{i-1}(x) \frac{\pi_n(x | y)}{\pi_{i-1}(x | y)} \\ &= w_{i-1}(x) \frac{\pi(x) \pi_i(y | x)}{\pi(x) \pi_{i-1}(y | x)} \\ &= w_{i-1}(x) \frac{\sum_{k=i}^M \mathbb{I}_{A_{\varepsilon_i, y}}(z_k)}{\sum_{k=i}^M \mathbb{I}_{A_{\varepsilon_{i-1}, y}}(z_k)}. \end{aligned}$$

In other words, when the distance threshold ε_{i-1} is contracted to ε_i , the particles' weights are multiplied by the proportion of simulated datasets that are still inside the new threshold. The user may specify a final tolerance ε , or a final acceptance rate of the MCMC kernel, and the algorithm will be stopped when either of these termination conditions is reached. The latter condition stops the algorithm when the particles are not moving around very much, implying little change in the estimated target.

2.1.4 Justification for approach

We present here a non-rigorous justification for the use of ABC for the problem at hand, as opposed to more frequently-used approaches for fitting mathematical models (see appendix A). Consider a contact network model with parameters θ , and an estimated transmission tree T . Taking a Bayesian approach, our aim is to obtain a sample from the posterior distribution on the model's parameters given our data,

$$\Pr(\theta | T) = \frac{\Pr(T | \theta) \Pr(\theta)}{\Pr(T)}.$$

For all but the simplest models, the normalizing constant $\Pr(T)$ is an intractable integral. What we shall argue here is that, in contrast to most commonly studied mathematical models, the likelihood $\Pr(T | \theta)$ is also likely to be intractable in our case.

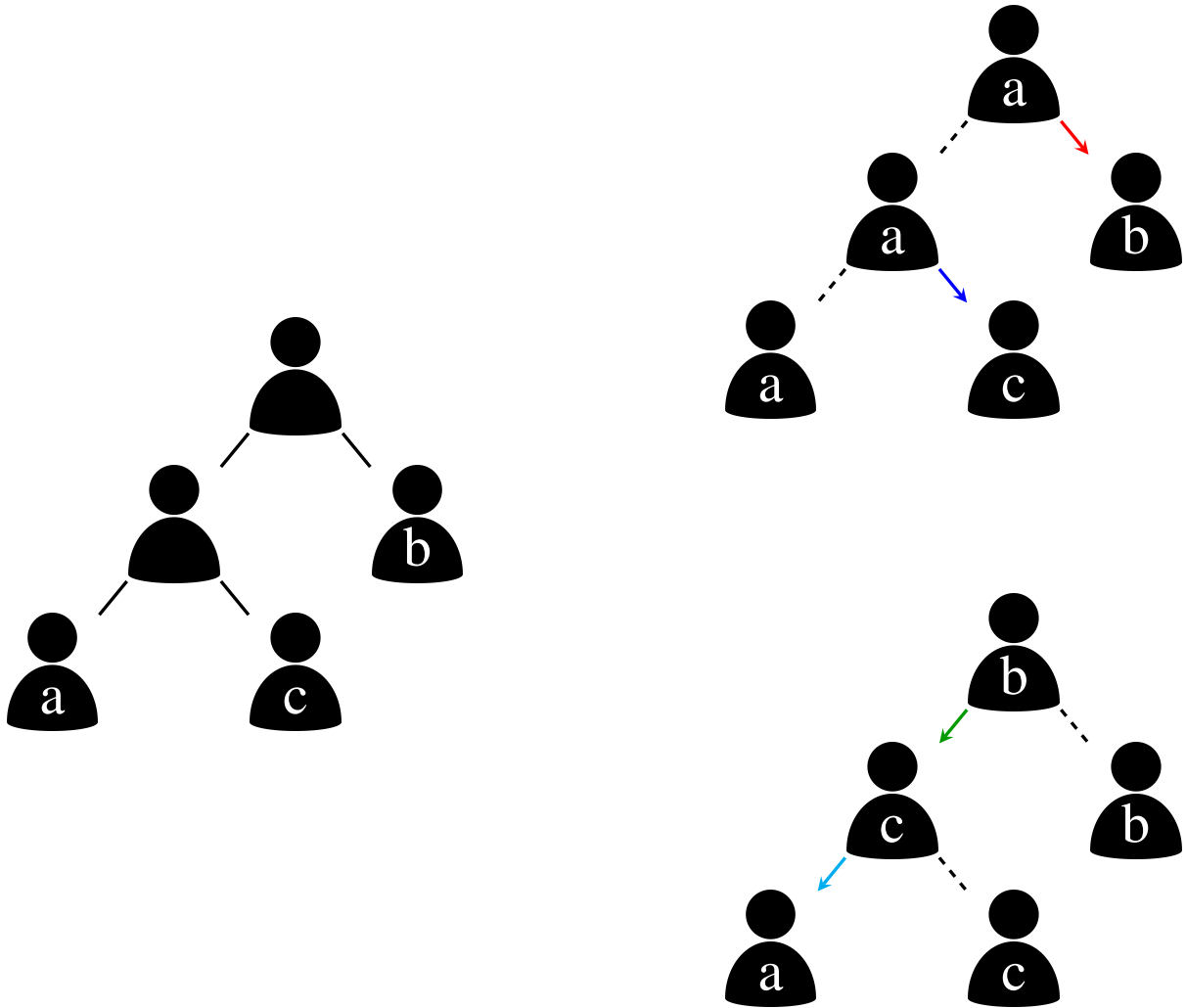


Figure 2.2: Illustration of an estimated transmission tree without labels (left) and two possible underlying complete transmission trees with labels (right). In the top right scenario, the epidemic began with node *a* who transmitted first to *b* and then to *c*. In the bottom right scenario, *b* was the index case; *b* infected *c*, who went on to infect *a*. A transmission tree estimated from a viral phylogeny would have the same topology and tip labels in both cases.

As discussed in section 1.2.2, the internal nodes of transmission trees represent transmission events, and are labelled with the donor in the associated transmission pair. However, when we estimate a transmission tree from viral sequence data, we generally only know the labels of the tips of the tree, not the labels of the internal nodes. In viral phylogenies, the transmissions are at least partially preserved through the evolutionary relationships among the viruses, but the directionality of those transmissions is unknown. Thus, a single estimated transmission tree can correspond to many possible pathways of the epidemic through the network. Figure 2.2 illustrates this concept for a simple transmission tree with three tips. When calculating a likelihood given a transmission tree, we must sum over all possible labellings of the internal nodes. Let \mathcal{N} be the set of such labellings. Then

$$\Pr(T \mid \theta) = \sum_{\nu \in \mathcal{N}} \Pr(T, \nu \mid \theta). \quad (2.1)$$

A contact network model assigns a probability to each possible contact network. Transmission trees are realized over particular contact networks, not over the model itself. Therefore, we must also sum over all contact networks which could be generated by the model. Let \mathcal{G} be the set of all possible contact networks. Summing eq. (2.1) over \mathcal{G} gives

$$\Pr(T \mid \theta) = \sum_{G \in \mathcal{G}} \sum_{\nu \in \mathcal{N}} \Pr(T, \nu \mid G, \theta) \Pr(G \mid \theta). \quad (2.2)$$

This can be simplified somewhat by noticing that, given a specific contact network, the labelled transmission tree depends only on that network and not on the model that generated it. That is, $\Pr(T, \nu \mid G, \theta) = \Pr(T, \nu \mid G)$, and

$$\Pr(T \mid \theta) = \sum_{G \in \mathcal{G}} \Pr(G \mid \theta) \sum_{\nu \in \mathcal{N}} \Pr(T, \nu \mid G) \quad (2.3)$$

Under the assumption that both transmission and removal are Poisson processes, calculating $\Pr(T, \nu \mid G)$ can be accomplished by a straightforward modification of the Gillespie simulation algorithm (section 2.1.1). Rather than choosing transmission or removal events according to their probabilities, the events would be deterministically chosen based on the transmission tree and the probabilities of each event would be multiplied together. Assuming efficient data structures for storing lists of nodes and edges, the complexity of this calculation would be $O(|T|)$. The number of possible labellings of internal nodes of T is easily seen to be $2^{(|T|-1)/2}$ by noticing that each of the $(|T|-1)/2$ internal nodes must be labelled with the same label as either its right child or its left child. Although exponential calculations of this nature can often be simplified on trees using dynamic programming (e.g.[138]), it cannot be straightforwardly applied in this case because the subtrees' probabilities depend on the existing epidemic progress (their parents and siblings). Hence, calculating the inner sum over labels may take time $O(2^{(|T|-1)/2})$.

The outer sum, over all contact networks, is also difficult to evaluate in general. There are $2^{N(N-1)}$ directed graphs on N nodes [13]. There must be at least as many nodes in the contact network as the number of tips in the tree, which is $(|T|+1)/2$. Of course, it is very likely that there are more nodes

in the network than observed tips because some individuals are never infected and/or some infected individuals are never sampled. The complexity of calculating $\Pr(G \mid \theta)$ is obviously dependent on the particular model being investigated. For the BA model, we might have to sum over all possible orders in which the nodes could be added, and all assignments of edges to the nodes which generated them. However, even in the unlikely case that calculating $\Pr(G \mid \theta)$ can be done in constant time, the sum 2.3 still has at least $O(2^{|T|^2})$ terms.

We have shown that both the normalizing constant $\Pr(T)$ and the likelihood $\Pr(T \mid \theta)$ are likely computationally prohibitive to calculate. If this is the case, the problem of fitting contact network models to phylogenies seems to be of the *doubly-intractable* type [139], which would imply that these models are not amenable to neither ML nor Bayesian inference techniques. Although both methods are able to cope with an intractable normalizing constant (for example, by local search for ML or Bayesian MCMC), neither can avoid the intractable likelihood calculations. This justifies the use of ABC, which is a likelihood-free method.

We have not proven here that eq. (2.3) is impossible to calculate in polynomial time - it could be possible to algebraically simplify the sum into a tractable expression. Furthermore, under certain models, a large proportion of \mathcal{G} may have zero probability, which would enable the simplification of the outer sum on a model-specific basis. It should also be noted that extensions of Bayesian MCMC have been developed for doubly-intractable problems [139, 140], which might be adaptable to the problem at hand. These have not been as widely used as ABC, nor are they as easily parallelizable as SMC.

2.2 Analysis of Barabási-Albert model with synthetic data

2.2.1 Methods

Using synthetic data, we investigated four parameters related to the Barabási-Albert (BA) contact network model, denoted N, m, α, I (see section 1.3.2). The first three of these are parameters of the model itself, while I is related to the simulation of transmission trees over the network. However, we will refer to all four as BA parameters. N denotes the total number of nodes in the network, or equivalently, susceptible individuals in the population. When a node is added to the network, m new undirected edges are added incident to it, and are attached to existing nodes of degree k with probability proportional to $k^\alpha + 1$ (section 1.3.2). To simulate transmission trees over a BA network, we allowed an epidemic to spread until I nodes were infected, and sampled a transmission tree at that time. The α parameter is unitless, while m has units of edges or connections per vertex, and N and I both have units of nodes or individuals.

Our investigation comprised three sets of computational experiments aimed at determining which of these parameters could be estimated from phylogenetic data, and with what degree of accuracy. First, we performed an exploratory analysis using a tree kernel-based classifier to determine which of the four BA parameters might be identifiable from tree shapes when all others were held fixed. This analysis was also used to validate our choice of the tree kernel as a distance function for ABC, by evaluating two further classifiers based on other tree summary statistics from the literature. Second, we used grid

search to investigate the accuracy and precision of marginal parameter estimates, again holding all but one parameters of the model fixed. Finally, we applied the full ABC-SMC algorithm to jointly estimate the four parameters of the BA model simultaneously.

We assumed that all contacts had symmetric transmission risk, which was implemented by replacing each undirected edge in the network with two directed edges (one in each direction). Nodes in our networks followed simple SI dynamics, meaning that they became infected at a rate proportional to their number of infected neighbours, and never recovered. We did not consider the time scale of the transmission trees in these simulations, only their shape. Therefore, the transmission rate along each edge in the network was set to 1, the removal rate of each node was set to 0, and all transmission trees' branch lengths were scaled by their mean. The *igraph* library's implementation of the BA model [134] was used to generate the graphs. The analyses were run on Westgrid (<https://www.westgrid.ca/>) and a local computer cluster. With the exception of our own programs, all analyses were done in *R*, and all packages listed below are *R* packages. Code to run all simulation-based experiments is freely available at <https://github.com/rmcclosk/thesis>.

Classifiers for BA model parameters based on tree shape

Our first computational experiment was designed as an exploratory analysis of the four BA model parameters defined above: α , I , m , and N . The objective of this experiment was to determine whether any of the four parameters were identifiable from the shape of the transmission tree, as quantified by the tree kernel. Each of the BA model parameters was varied one at a time, while holding the other parameters at fixed, known values. Contact networks were generated according to each set of parameter values, and transmission trees were simulated over the networks. We then evaluated how well a classifier based on the tree kernel could differentiate the trees simulated under distinct parameter values. If the classifier's cross-validation accuracy was high, this could be taken as an indication that the parameter in question was identifiable in the range of values considered. A caveat of this preliminary analysis is that, since all parameters but one were held at known values, nothing could be said about the identifiability of combinations of parameters; this issue will be explored later by jointly estimating all parameters with ABC (??).

In addition to testing for identifiability, a secondary objective of this analysis was to validate the use of the tree kernel as a distance measure for ABC in our context. As discussed in section 1.5, the choice of distance function is extremely important for the accuracy of the ABC approximation to the posterior. Therefore, we evaluated two additional tree statistics in the same manner as we evaluated the tree kernel (that is, by constructing and testing a classifier). First, we considered Sackin's index [70], which measures the degree of imbalance or asymmetry in a phylogeny (see section 1.2.4). Sackin's index is widely used for characterizing phylogenies [141] and has been demonstrated to vary between transmission trees simulated under different contact network types [107]. Sackin's index does not take branch lengths into account, considering only the tree's topology. The other statistic we considered was the normalized lineages-through-time (nLTT) [73], which compares two trees based on normalized distributions of their branching times (see ??). In contrast with Sackin's index, the nLTT does not

[explicitly consider the trees' topologies, but it does use their normalized branch lengths. While the nLTT is a newly developed statistic not yet in widespread use, the unnormalized LTT \[35\] was the basis of seminal early work extracting epidemiological information from phylodynamics \[42\]. We expected the tree kernel to classify the BA parameters more accurately than either Sackin's index or the nLTT, since the tree kernel takes both topology and branch lengths into account.](#)

This experiment involved a large number of variables that were varied combinatorially. For ease of exposition, we will describe a single experiment first, then enumerate the values of all variables for which the experiment was repeated. The parameters of the tree kernel, λ and σ (section 1.2.4), will be referred to as *meta-parameters* to distinguish them from the parameters of the BA model.

The attachment power parameter α was varied among three values: 0.5, 1.0, and 1.5. For each value, the *sample_pa* function in the *igraph* package was used to simulate 100 networks, with the other parameters set to $N = 5000$ and $m = 2$. This step yielded a total of 300 networks. An epidemic was simulated on each network using our *nettree* binary until $I = 1000$ nodes were infected, at which point 500 of them were sampled to form a transmission tree. A total of 300 transmission trees were thus obtained, comprised of 100 trees for each of the three values of α . The trees were “ladderized” so that the subtree descending from the left child of each node was not smaller than that descending from the right child. Summary statistics, such as Sackin's index and the ratio of internal to terminal branch lengths, were computed for each simulated tree using our *treestat* binary. The trees were visualized using the *ape* package [142]. [Both the tree kernel and the nLTT are pairwise statistics, and the SVMs classifiers we used to investigate them operate on pairwise distance matrices.](#) Our *treekernel* binary was used to calculate the value of the kernel for each pair of trees, with the meta-parameters set to $\lambda = 0.3$ and $\sigma = 4$. These values were stored in a symmetric 300×300 kernel matrix. Similarly, we computed the nLTT statistic between each pair of trees using our *treestat* binary, and stored them in a second 300×300 matrix.

To investigate the identifiability of α from tree shape, we constructed classifiers for α based on the three tree shape statistics discussed above. First, we used the *kernelab* package [143] to create a kernel support vector regression (kSVR) classifier using the computed kernel matrix. Second, we used the *e1071* package [144] to create an ordinary support vector regression (SVR) classifier using the pairwise nLTT matrix. Finally, we performed an ordinary linear regression of α against Sackin's index. Each of these classifiers was evaluated with 1000 two-fold cross-validations. We also performed a kernel principal components analysis (kPCA) projection of the kernel matrix, and used it to visualize the separation of the different α values in the tree kernel's feature space. A schematic of this experiment is presented in fig. 2.3.

Similar experiments were performed with the values shown in table 2.1. The other three BA parameters, namely N , m , and I , were each varied while holding the others fixed. The experiments for α , m , and N were repeated with three different values of I . All experiments were repeated with trees having three different numbers of tips. Kernel matrices were computed for all pairs of the meta-parameters $\lambda = \{0.2, 0.3, 0.4\}$ and $\sigma = \{1/8, 1/4, 1/2, 1, 2, 4, 8\}$.

varied parameter	N	α	m	I	tips	λ	σ
N	3000, 5000, 8000	1.0	2	500, 1000, 2000	100, 500, 1000	0.2, 0.3, 0.4	$\frac{1}{8}, \frac{1}{4}, \frac{1}{2}, 1, 2, 4, 8$
α	5000	0.5, 1.0, 1.5	2	500, 1000, 2000	100, 500, 1000	0.2, 0.3, 0.4	$\frac{1}{8}, \frac{1}{4}, \frac{1}{2}, 1, 2, 4, 8$
m	5000	1.0	2, 3, 4	500, 1000, 2000	100, 500, 1000	0.2, 0.3, 0.4	$\frac{1}{8}, \frac{1}{4}, \frac{1}{2}, 1, 2, 4, 8$
I	5000	1.0	2	500, 1000, 2000	100, 500	0.2, 0.3, 0.4	$\frac{1}{8}, \frac{1}{4}, \frac{1}{2}, 1, 2, 4, 8$

Table 2.1: Values of parameters and other variables used in tree kernel simulation experiments. Each row corresponds to one of the BA model parameters. One kernel matrix was created for every combination of values except the one indicated in the “varied parameter” column, which was varied when producing simulated trees.

parameter	grid values	test values	N	α	m	I	tips
N	1050, 1125, ..., 15000	1000, 3000, ..., 15000	-	1.0	2	1000	100, 500, 1000
α	0, 0.01, ..., 2	0, 0.25, ..., 2	5000	-	2	1000	100, 500, 1000
m	1, 2, ..., 6	1, 2, ..., 6	5000	1.0	-	1000	100, 500, 1000
I	500, 525, ..., 5000	500, 1000, 1500, 2000	5000	1.0	2	-	100, 500

Table 2.2: Variables and BA parameter values used for grid search experiments. Trees were simulated under the test values, and compared to a grid of trees simulated under the grid values. Kernel scores were used to calculate point estimates and credible intervals for the test values.

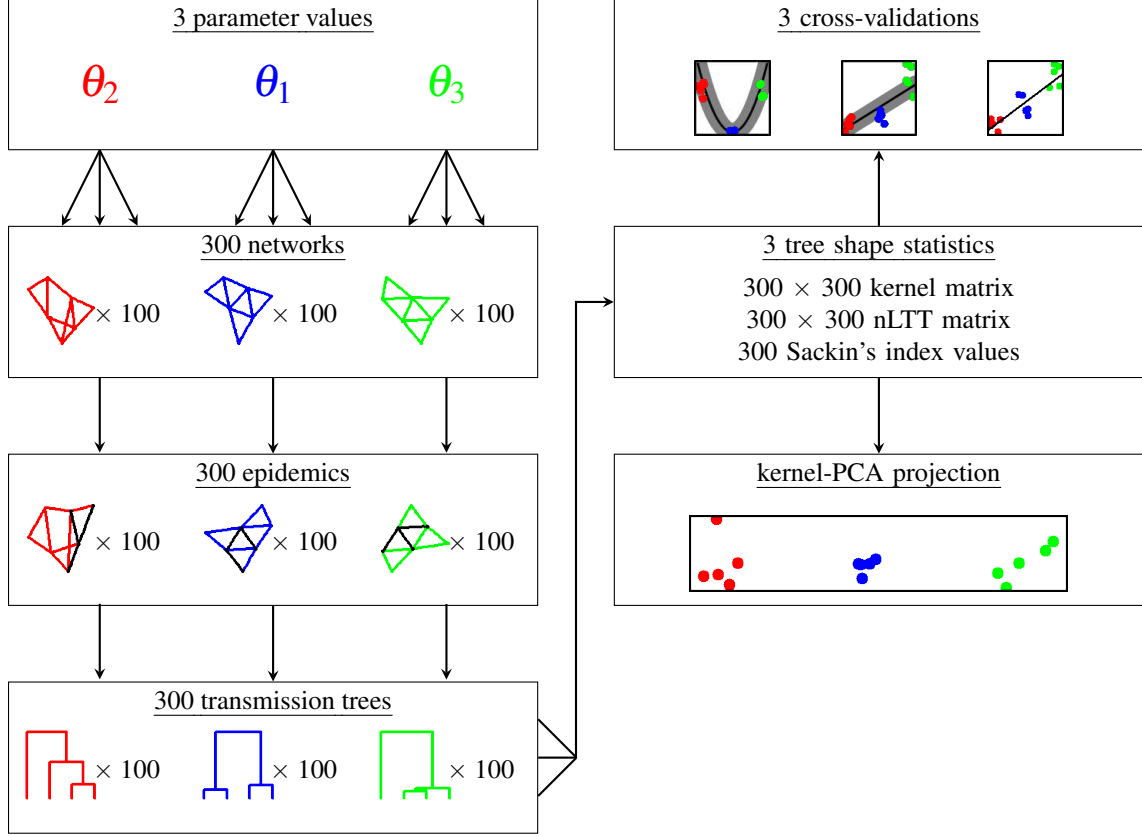


Figure 2.3: Schematic of experiments designed to investigate the impact of variations in BA model parameters on transmission tree shapes. The parameters of the BA model were varied one at a time while holding all others fixed. Transmission trees were simulated under three different values of each parameter, then compared pairwise using the tree kernel. Classifiers were constructed for each parameter, and their accuracy was evaluated by cross-validation. Kernel-PCA projections were used to visually examine the separation of the trees in the feature space defined by the tree kernel.

Grid search

The previous experiment was an exploratory analysis intended to determine which of the BA parameters were identifiable, and whether the tree kernel could potentially be used to distinguish different parameter values when all others were held fixed. In this experiment, which was still of an exploratory nature, we continued to consider one parameter at a time while fixing the other three. However, rather than checking for identifiability, we were now interested in quantifying the accuracy and precision of kernel score-based estimates. This was done by examining the distribution of kernel scores on a grid of parameter values, when trees simulated according to those values were compared with a single simulated test tree. This experiment did not involve the full ABC-SMC algorithm, nor did we continue to use Sackin's index or the nLTT.

As in the previous section, we will begin by describing a single experiment, and then list the variables for which similar experiments were performed. We varied α along a narrowly spaced grid of

values: 0, 0.01, ..., 2. For each value, fifteen networks were generated with *igraph*, and transmission trees were simulated over each using *nettree*. These trees will be referred to as “grid trees”. Next, one further test tree was simulated with the test value $\alpha = 0$. Both the grid trees and the test tree had 500 tips, and were simulated with the other BA parameters set to [the known values](#) $N = 5000$, $m = 2$, and $I = 1000$. The test tree was compared to each of the grid trees using the tree kernel, with the meta-parameters set to $\lambda = 0.3$ and $\sigma = 4$, using the *trekernel* binary. The median kernel score was calculated for each grid value, and the scores were normalized such that the area under the curve was equal to 1. ~~The grid value with the highest median kernel score was taken as the point estimate for the test value~~ [A point estimate for the test value was obtained by calculating the weighted mean of the grid values with the kernel scores as weights](#), and a 95% credible interval was obtained using the *hpd* function in the *TeachingDemos* package [145].

Each experiment of the type just described was repeated ten times with the same test value. Similar experiments were performed for each of the four BA parameters, with several test values and trees of varying sizes. The variables are listed in table 2.2. A graphical schematic of the grid search experiments is shown in fig. 2.4. [We emphasize that these experiments were marginal in nature; that is, the each parameter was varied and estimated individually while holding the others at known, fixed values.](#)

Approximate Bayesian computation

[Our final simulation-based experiment was designed to test the full ABC-SMC algorithm by jointly estimating the four parameters of the BA model. In contrast to the previous two experiments, we did not inform the algorithm of any of the true parameter values.](#)

We simulated three trees each under a variety of parameter values and ran the *netabc* program to estimate posterior distributions for the parameters. The parameter values and priors used are listed in table 2.3. The tree kernel meta-parameters were set to $\lambda = 0.3$ and $\sigma = 4$. The SMC algorithm was run with 1000 particles, five sampled datasets per particle, and the α_{ESS} parameter (not to be confused with the BA preferential attachment parameter, see section 2.1.3) set to 0.95. The algorithm was stopped when the acceptance rate of the Metropolis-Hastings (MH) kernel dropped below 1.5%, the same criterion used by Del Moral, Doucet, and Jasra. Approximate marginal posterior densities for each parameter were calculated using the *density* function in *R* applied to the final weighted population of particles. ~~Credible intervals were obtained for each parameter using the *HPDinterval* function in the *coda* package [146].~~ [Posterior means obtained for each parameter using the *wtd.mean* function in the *Hmisc* package \[147\]. Credible intervals were obtained using the *hpd* function in the *TeachingDemos* package \[145\].](#)

[To evaluate the effects of the true parameter values on the accuracy of the posterior mean estimates, we analysed the \$\alpha\$ and \$I\$ parameters individually using generalized linear models \(GLMs\). The response variable was the error of the point estimate, and the predictor variables were the true values of \$\alpha\$, \$I\$, and \$m\$. We did not test for differences across true values of \$N\$, because \$N\$ was not varied in these simulations. The distribution family and link function for the GLMs were chosen as Gaussian and inverse, respectively, by examination of residual plots and Akaike information criterion \(AIC\). The](#)

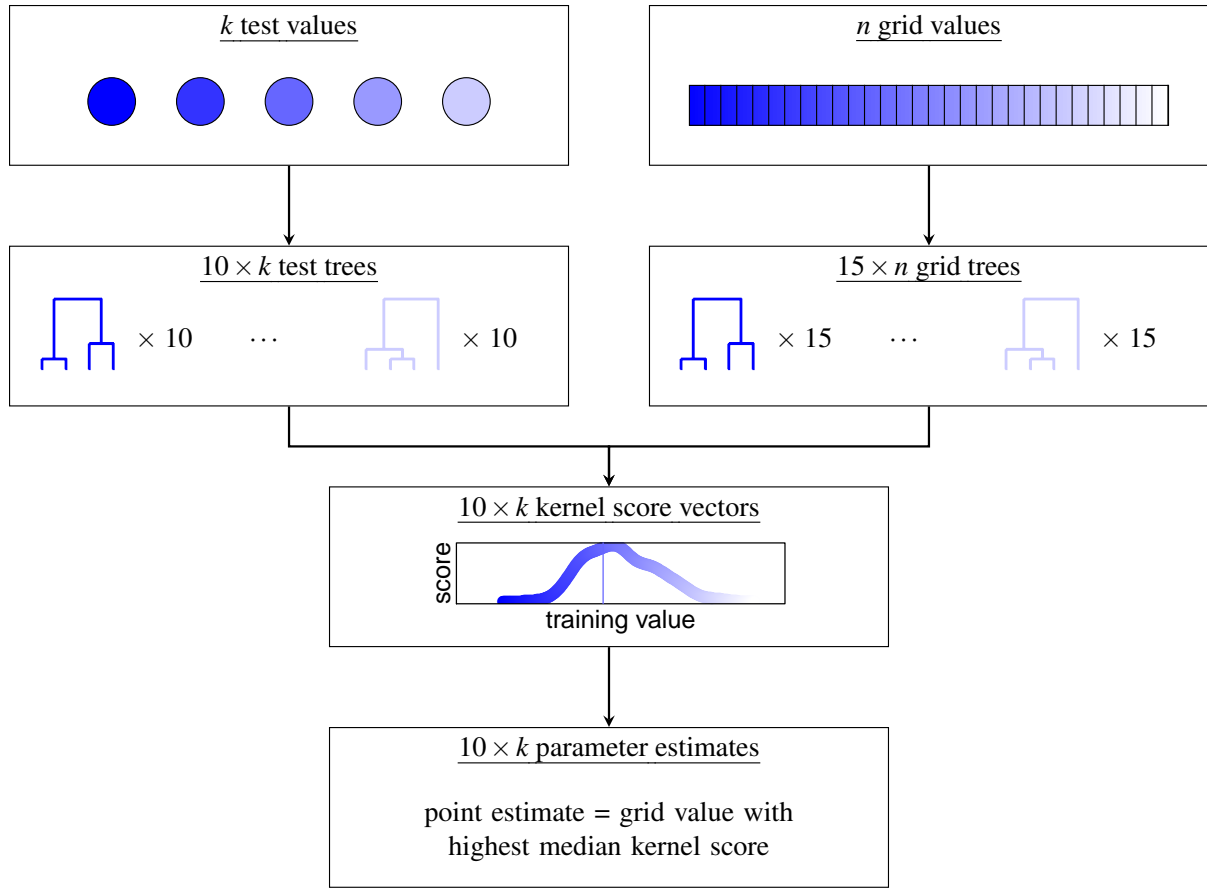


Figure 2.4: Graphical schematic of grid search experiments used to investigate BA model parameters. Trees were simulated along a narrowly spaced grid of values of one parameter (“grid trees”) [with all other parameters fixed to known values](#). Separate trees were simulated for a small subset of the grid values (“test trees”), [also holding the other parameters fixed](#). Each test tree was compared to every grid tree using the tree kernel, and the resulting kernel scores were normalized to resemble a probability density from which the mode and 95% highest density interval were calculated.

[p-values of the estimated GLMs coefficients were corrected using Holm-Bonferroni correction \[148\] with \$n = 6\$ \(two GLMs with three predictors each\). Because there was clearly little to no identifiability of the \$N\$ and \$m\$ parameters with ABC \(see Results in next section\), we did not construct GLMs for those parameters.](#)

Two further experiments were performed to address potential sources of error. To evaluate the effect of model misspecification in the case of heterogeneity among nodes, we generated a network where half the nodes were attached with power $\alpha = 0.5$ and the other half with power $\alpha = 1.5$. The other parameters for this network were $N = 5000$, $I = 1000$, and $m = 2$. To investigate the effects of potential sampling bias [149], we simulated a transmission tree where the tips were sampled in a peer-driven fashion, rather than at random. That is, the probability to sample a node was twice as high if any of that node’s network peers had already been sampled. The parameters of this network were $N = 5000$, $I = 2000$, $m = 2$, and $\alpha = 0.5$.

parameter or variable	test values	prior
N	5000	Uniform(500, 15000)
α	0, 0.5, 1, 1.5, 2	Uniform(0, 2)
m	2, 3, 4	DiscreteUniform(1, 5)
I	1000, 2000	Uniform(500, 5000)
tips	500	-

Table 2.3: Variables and BA parameter values used for ABC validation experiments. Trees were simulated under the test values, and kernel-assisted ABC was used to re-estimate posterior distributions for the BA parameters without training.

2.2.2 Results

Classifiers for BA model parameters based on tree shape

Trees simulated under different values of α were visibly quite distinct (fig. 2.5). In particular, higher values of α produce networks with a small number of highly connected nodes, which, once infected, are likely to transmit to many other nodes. This results in a more unbalanced, ladder-like structure in the phylogeny, compared to networks with lower α values. None of the other three parameters produced trees that were as easily distinguished from each other (figs. A.4 to A.6). Sackin’s index, which measures tree imbalance, was significantly correlated with all four parameters (for α , I , m , and N respectively: Spearman’s rho = 0.85, -0.12 , -0.13 , 0.09; p -values $<10^{-5}$, 0.003, $<10^{-5}$, $<10^{-5}$). The ratio of internal to terminal branch lengths was negatively correlated with α and I , and positively correlated with m and N (Spearman’s rho -0.84 , -0.69 , 0.1, 0.18; all $p < 10^{-5}$).

Figure 2.6 shows kPCA projections of the simulated trees onto the first two principal components of the kernel matrix. The figure shows only the simulations with 500-tip trees and 1000 infected nodes. The three α and I values considered are well separated from each other in feature space. On the other hand, the three N values overlap significantly, and the three m values are virtually indistinguishable. Similar observations can be made for other values of I and the number of tips (figs. A.11 to A.14). The values of I and N separated more clearly with larger numbers of tips, and in the case of N , with larger epidemic sizes (figs. A.12 and A.14).

Accuracy of the kSVR classifiers varied based on the parameter being tested (fig. 2.7, left). Classifiers based on two other tree statistics, the nLTT and Sackin’s index, generally exhibited worse performance than the tree kernel, although the magnitude of the disparity varied between the parameters (fig. 2.7, centre and right). The results were largely robust to variations in the tree kernel meta-parameters λ and σ , although accuracy varied between different epidemic and sampling scenarios (figs. A.7 to A.10).

When classifying α , the kSVR classifier had an average R^2 of 0.92, compared to 0.56 for the nLTT-based SVR, and 0.75 for the linear regression against Sackin’s index. There was little variation about the mean for different tree and epidemic sizes. No classifier could accurately identify the m parameter in any epidemic scenario, with average R^2 values of 0.12 for kSVR, 0.01 for the nLTT, and 0.06 for Sackin’s index. Again, there was little variation in accuracy between epidemic scenarios, although the

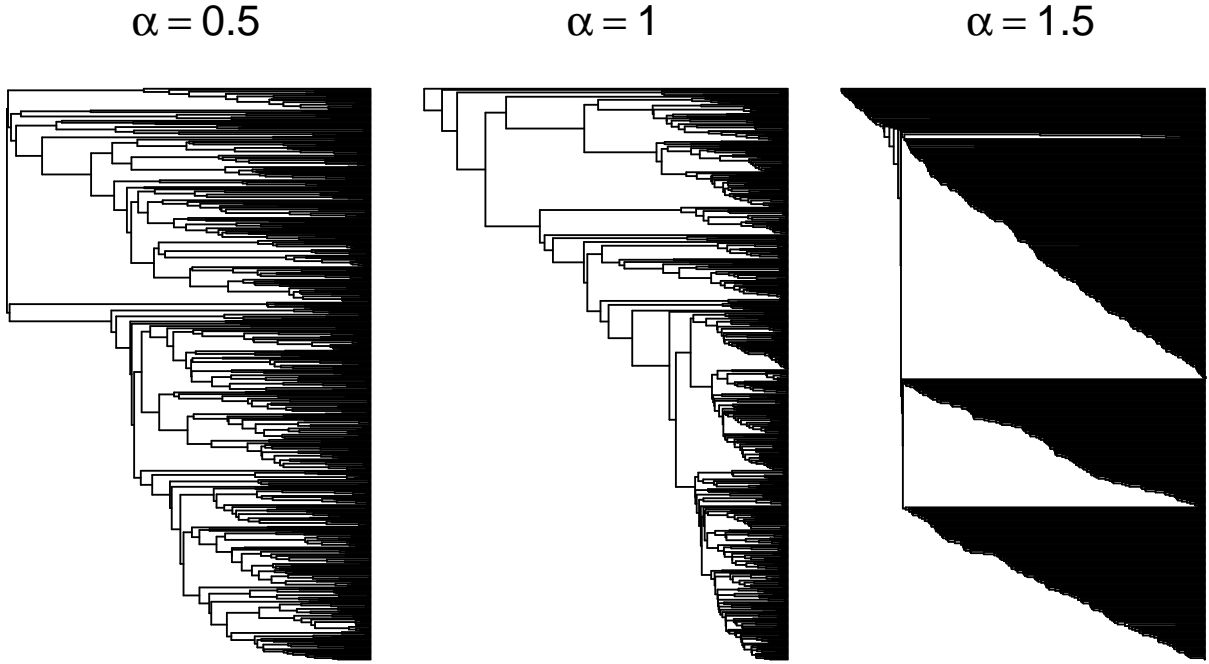


Figure 2.5: Simulated transmission trees under three different values of BA parameter α . Epidemics were simulated on BA networks of 5000 nodes, with α equal to 0.5, 1.0, or 1.5, until 1000 individuals were infected. Transmission trees were created by sampling 500 infected nodes. Higher α values produced networks with a small number of highly-connected nodes, resulting in highly unbalanced, ladder-like trees.

accuracy of the kSVR was slightly higher on 1000-tip trees (average R^2 0.01, 0.11, 0.32 for 100, 500, and 1000 tips respectively).

The accuracy of classifiers for I varied significantly with the number of tips in the tree. For 100-tip trees, the average R^2 values were 0.7, 0.55, and 0.02 for the tree kernel, nLTT, and Sackin's index respectively. For 500-tip trees, the values increased to 0.93, 0.83, and 0.07. Finally, the performance of classifiers for N depended heavily on the epidemic scenario. The R^2 of the kSVR classifier ranged from 0.08 for the smallest epidemic and smallest sample size, to 0.82 for the largest. Likewise, R^2 for the nLTT-based SVR ranged from 0.01 to 0.54. Sackin's index did not accurately classify N in any scenario, with an average R^2 of 0.03 and little variation between scenarios.

Marginal parameter estimates with grid search

~~The accuracy of grid search estimates largely paralleled that of the kSVR classifiers.~~ Figure 2.8 shows point estimates and 95% highest density intervals for each of the BA parameters, for one replicate experiment with 500-tip trees. Plots showing the point estimates for all replicates can be found in figs. A.19 to A.22. For all parameters except m , the error of point estimates was negatively correlated with the number of sampled tips in the tree (for α , I , and N respectively: Spearman's $\rho = -0.22, -0.51, -0.16$; p -values $4 \times 10^{-4}, < 10^{-5}, 0.01$). The 95% highest density intervals obtained for all parameters were extremely wide, occupying $> 75\%$ of the grid in all cases (fig. 2.8).

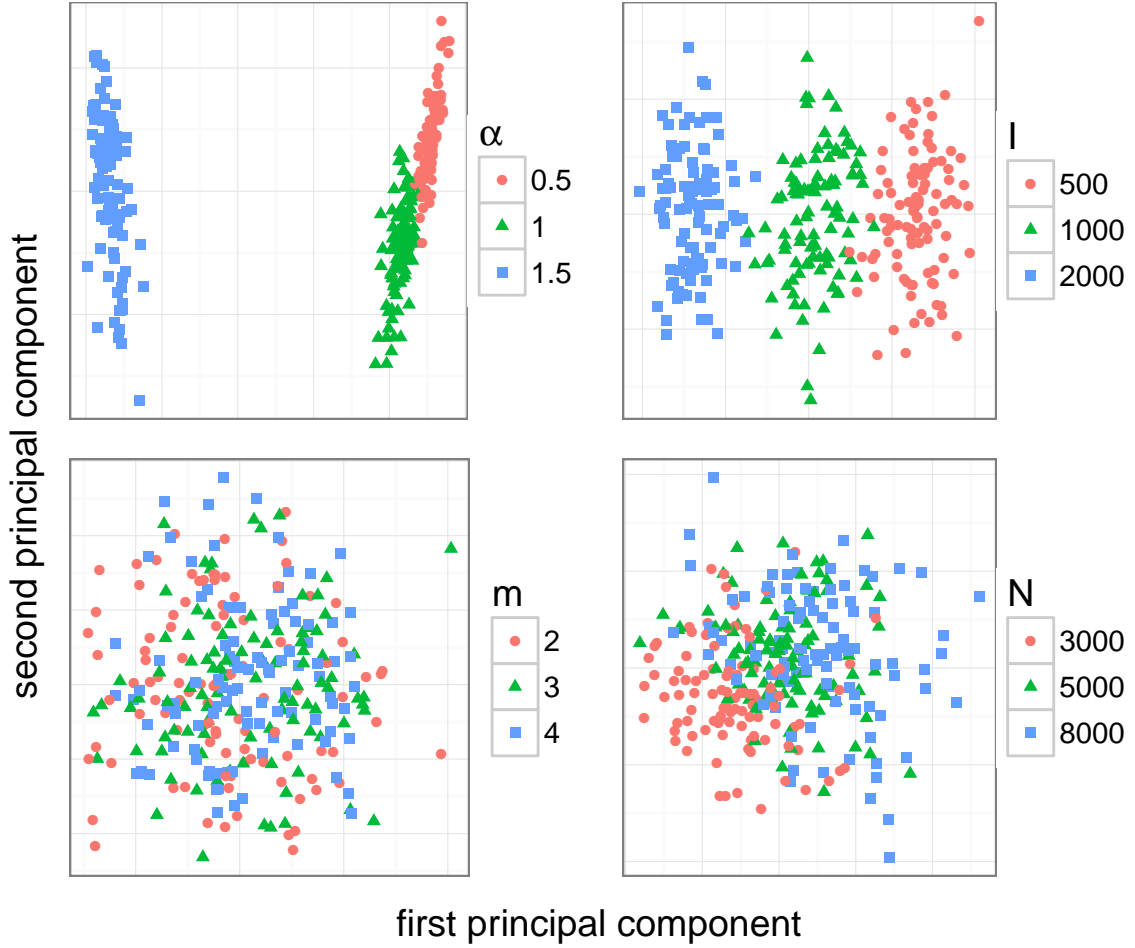


Figure 2.6: Each parameter of the BA model was individually varied to produce 300 simulated trees. Kernel matrices were formed from all pairwise kernel scores among each set of 300 trees. The trees were projected onto the first two principal components of the kernel matrix calculated using kPCA. All trees had 500 tips. The parameters not being varied were set to $\alpha = 1$, $I = 1000$, $m = 2$, and $N = 5000$. The tree kernel meta-parameters were $\lambda = 0.3$ and $\sigma = 4$.

Similar to the results obtained in the previous experiment, the α and I parameters were estimated with comparably high accuracy, while the other two parameters were less identifiable. Across all replicates, R^2 values for the correlations between the estimated and true values were 0.91, 0.91, 0.25, and 0.54 for α , I , m , and N respectively. The mean absolute errors of the point estimates were 0.14, 310, 1.31, and 2419, representing 7%, 8%, 26%, and 17% of the respective grids.

Qualitatively, three of the parameters (excluding N) exhibited weak identifiability within particular sections of the grid. The interquartile ranges (IQRs) for α were nearly identical for the values $\alpha \leq 1$, spanning approximately [0-1.3]. Similarly, the IQRs for $\alpha > 1$ were all approximately [0.7-2] (fig. 2.8). The distributions of kernel scores for these groups of values were also qualitatively similar (fig. A.15), although the value $\alpha = 1.25$ exhibited a more pronounced peak in kernel scores around the true value.

For I , the IQRs were nearly identical for the values $I \leq 2000$ (approximately [500,3800]), and for the values $I > 3000$ (approximately [1600-5000]). Kernel score distributions for all I values exhibited

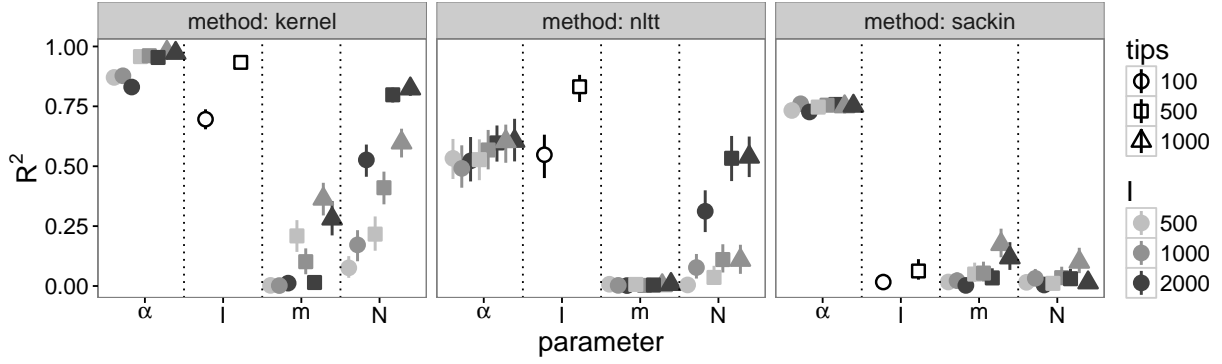


Figure 2.7: Cross-validation accuracy of kernel-SVR classifier (left), SVR classifier using nlTT (centre), and linear regression using Sackin's index (right) for BA model parameters. Kernel meta-parameters were set to $\lambda = 0.3$ and $\sigma = 4$. Each point was calculated based on 300 simulated transmission trees over networks with three different values of the parameter being tested, assuming perfect knowledge of the other parameters. Vertical lines are empirical 95% confidence intervals based on 1000 two-fold cross-validations. [The classifiers for \$I\$ were not evaluated with 1000-tip trees, because one of the tested \$I\$ values was 500, and it is not possible to sample a tree of size 1000 from 500 infected individuals.](#)

a similar rounded shape (fig. A.16), although this was most pronounced for values near the upper and lower extremes of the grid.

[The IQRs for \$m\$ were distinct for \$m = 1\$ and 2, but were similar for all values of \$m > 2\$ \(approximately \[2-6\]\). The kernel score distribution for \$m = 1\$ was distinct from the others, having a large peak at \$m = 1\$, while the others exhibited a valley at \$m = 1\$ and were mostly flat everywhere else \(fig. A.17\).](#)

[The IQRs for \$N\$ did not form any obvious groups like the other parameters' IQRs \(fig. 2.8\). The kernel score distribution for \$N = 1000\$ was distinct, having a peak at the true value \(fig. A.18\). The distributions for \$N > 1000\$ were all relatively similar, having a valley at the low end of the grid and being mostly flat everywhere else.](#)

~~The α parameter was the most accurately estimated, with point estimates having an average deviation of 0.14 from the true value, on a grid from 0 to 2. The error of point estimates varied significantly between true values of α (one-way analysis of variance (ANOVA), $p < 10^{-5}$). In particular, errors were lower for the values $\alpha = 1.0$ and 1.25 than for the other values (average errors 0.03 for $\alpha = 1.0$ or 1.5 vs. 0.17 for $\alpha \neq 1.0$ or 1.5), and this difference was significant (Wilcoxon rank-sum test, $p < 10^{-5}$, fig. A.19). These two values exhibited different qualitative behaviour than the other values in terms of the distribution of kernel scores along the grid (fig. A.15). In particular, there was a pronounced peak in scores around the true value, in contrast to the other values where the scores were flat around the true value. The effect was most obvious for the value $\alpha = 1.25$.~~

Joint parameter estimates with *netabc*

Figure 2.9 shows ~~maximum-a-posteriori (MAP)~~ [posterior mean](#) point estimates of the BA model parameters obtained with kernel-assisted ABC on simulated data. The estimates shown correspond only to the

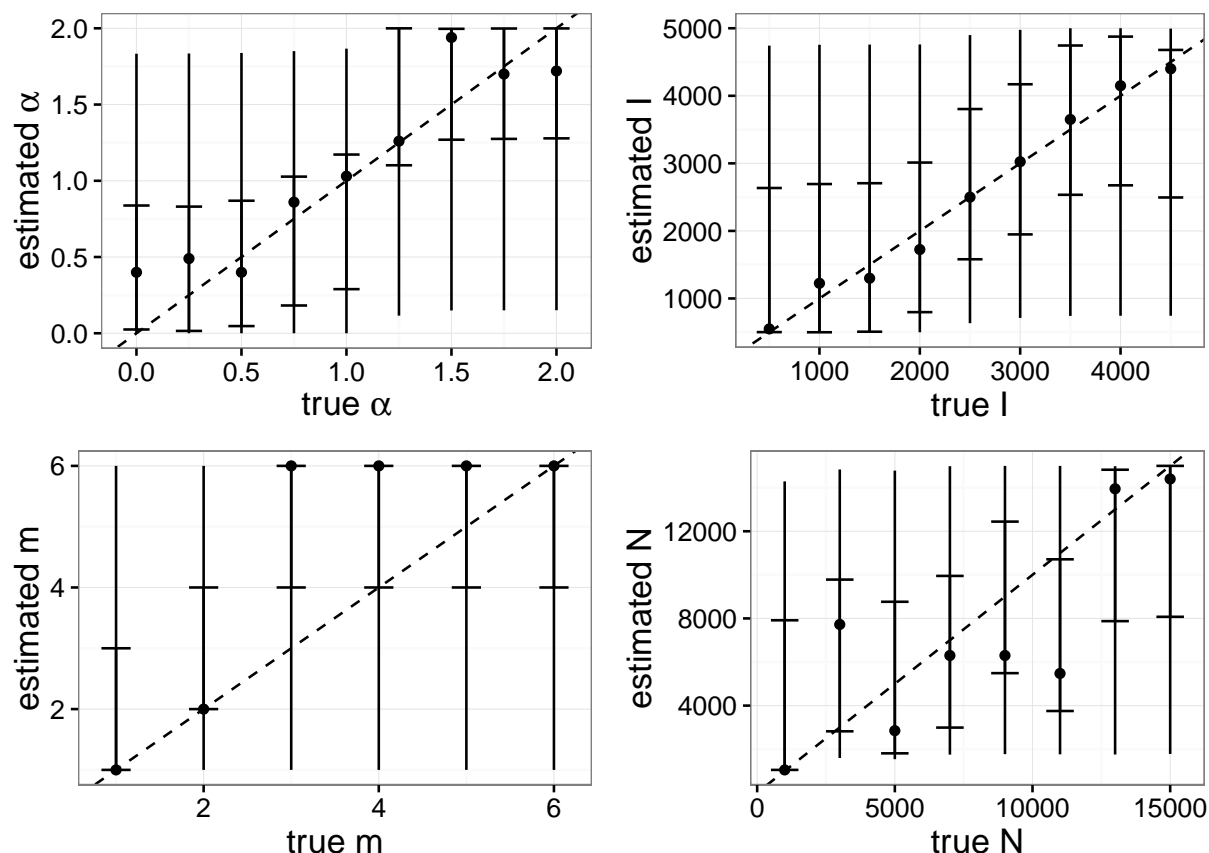


Figure 2.8: Point estimates (center lines) and 75% (boxes) and 95% (whiskers) highest density intervals for each BA model parameter, obtained using grid search. Networks and transmission trees were simulated over a grid of values for each parameter while holding the others fixed. For a subset of the grid values (x -axis), test networks and trees were created and compared to each tree on the grid using the tree kernel. The kernel scores along the grid were normalized to resemble a probability distribution, from which the mode and highest density interval were calculated. Shown values correspond to one replicate experiment, with trees of size 500.

simulations where the m parameter was set to 2, however the results for $m = 3$ and $m = 4$ were similar (figs. A.23 and A.24). Average boundaries of 95% highest posterior density (HPD) intervals are given in table 2.6.

Across all simulations, the median [IQR] absolute errors of the parameter estimates obtained with *netabc* were 0.11 [0.03 - 0.25] for α , 492 [294 - 782] for I , 1 [0 - 1] for m , and 4153 [3660 - 4489] for N . These errors comprised, respectively, 6%, 11%, 17%, and 29% of the regions of nonzero prior density. Average HPD interval widths were 0.68, 2454, 3.01, and 12046, representing 34%, 55%, 50%, and 83% of the nonzero prior density regions. Point estimates of I were upwardly biased: I was overestimated in 69 out of 72 simulations (4%). The estimates for m and N were similar across all simulations (median [IQR] point estimates 3 [3 - 3] and 9153 [8660 - 9489]) regardless of the true values of any of the BA parameters.

To analyse the effects of the true parameter values on the accuracy our estimates of α and I , we fitted one GLMs for each of these two parameters, with error rate as the dependent variable and the true parameter values as independent variables. Since the estimates of m and N were roughly equal across all simulations (figs. 2.9, A.23 and A.24), GLMs were not fitted for these parameters. The estimated coefficients are shown in tables 2.4 and 2.5. For the parameters α , I , and N , the GLM were fitted using the inverse link function. That is, if p is the true value of the parameter and \hat{p} is a random variable representing our estimate of the parameter, the GLM posits a relationship of the form

$$\mathbb{E}(|p - \hat{p}|) = (\beta_0 + \beta_\alpha \alpha + \beta_I I + \beta_m m)^{-1},$$

where the β 's are coefficients to be fitted. If the true value α , say, is increased by one, the *inverse* of the expected absolute error will increase by β_α . If β_α is positive, it means that the absolute error decreases as the true value of α increases.

Parameter	Estimate	Standard error	p -value
(Intercept)	2	0.6	0.01
α	10	2	$<10^{-5}$
I	-3×10^{-4}	2×10^{-4}	0.7
m	0.5	0.2	0.01

Table 2.4: Parameters of a fitted GLM relating error in estimated α to true values of BA parameters. GLM was fitted with a Gaussian distribution and inverse link function. Coefficients are interpretable as additive effects on the inverse of the mean error.

Parameter	Estimate	Standard error	p -value
(Intercept)	0.004	5×10^{-4}	$<10^{-5}$
α	-0.001	2×10^{-4}	$<10^{-5}$
I	-4×10^{-7}	2×10^{-7}	0.05
m	-7×10^{-5}	8×10^{-5}	1

Table 2.5: Parameters of a fitted GLM relating error in estimated I to true values of BA parameters. GLM was fitted with a gaussian distribution and inverse link function. Coefficients are interpretable as additive effects on the inverse of the mean error.

The GLM analysis indicated that the error in estimates of α decreased with larger true values of α ($p < 10^{-5}$) and m ($p = 0.01$) but was not significantly affected by I (table 2.4). Qualitatively, α seemed to be only weakly identifiable between the values of 0 and 0.5 (fig. 2.9). The error in the estimated prevalence I was slightly lower for smaller values of α ($p < 10^{-5}$) and I ($p = 0.05$), but was not significantly affected by the true value of m (table 2.5).

~~The accuracy of the parameter estimates obtained with kernel-assisted ABC paralleled the results from the kSVR classifier. Of the four parameters, α was the most accurately estimated, with point estimates having a median [IQR] absolute error of 0.11 [0.03–0.25]. The errors when the true value of α was zero were significantly greater than those for the other values (Wilcoxon rank-sum test, $p = 0$). Errors in estimating α did not vary across the true values of m or I (both one-way ANOVA).~~

Estimates for I were relatively accurate, with point estimate errors of 492 [294–782] individuals. These errors were significantly higher when the true value of α was at least 1 (Wilcoxon rank-sum test, $p=0$) and when the true value of I was 2000 ($p<10^{-5}$). The true value of m did not affect the estimates of I (one-way ANOVA).

The m parameter was estimated correctly in 37 % of simulations barely better than random guessing. The true values of the other parameters did not significantly affect the estimates of m (both one-way ANOVA).

Finally, the total number of nodes N was consistently over-estimated by about a factor of two (error 4153 [3660–4489] individuals). No parameters influenced the accuracy of the N estimates (all one-way ANOVA).

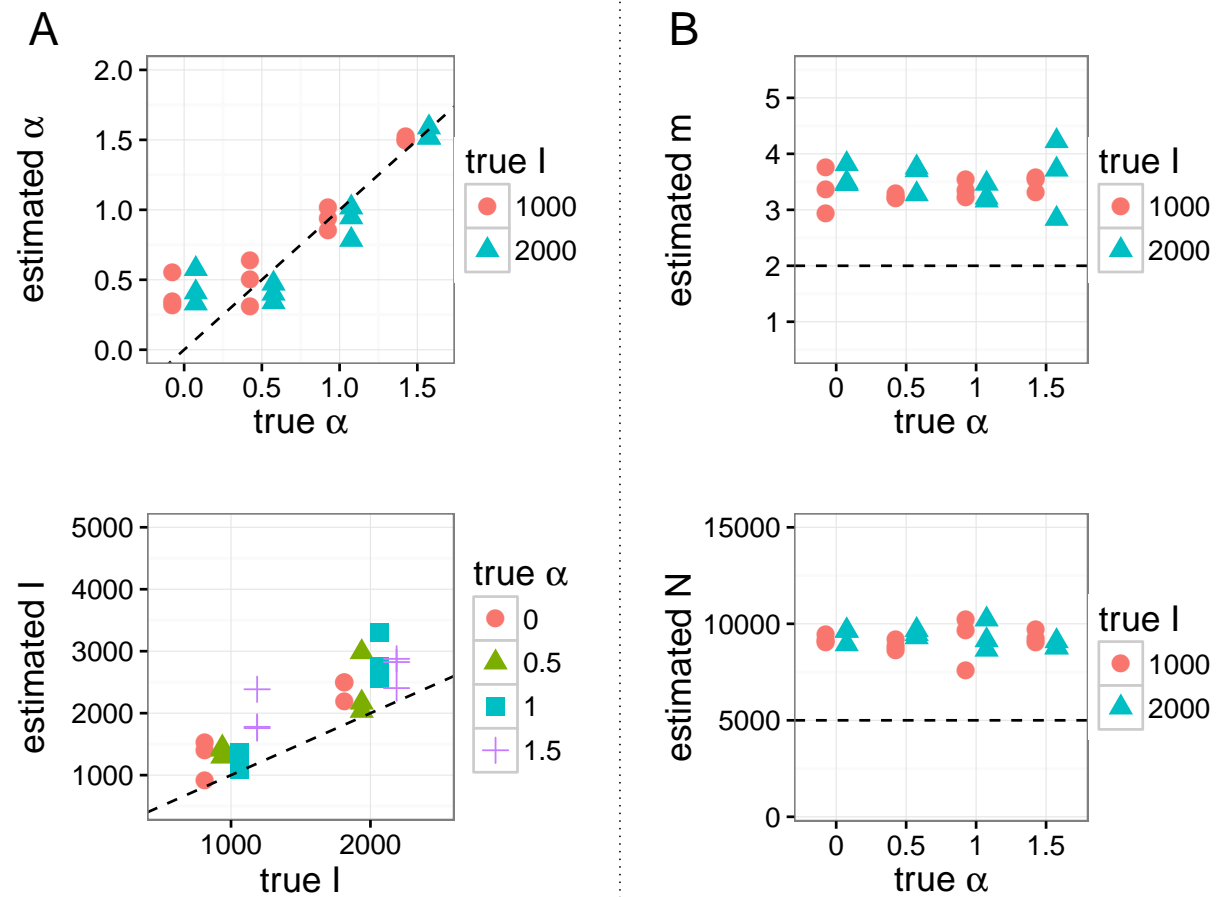


Figure 2.9: Posterior mean point estimates for BA model parameters obtained by running *netabc* on simulated data, for simulations with $m = 2$. Dashed lines indicate true values. (A) Estimates of α and I which were varied in these simulations against known values. (B) Estimates of m and N which were held fixed in these simulations at the values $m = 2$ and $N = 5000$.

The dispersion of the ABC approximation to the posterior also varied between the parameters, with narrower HPD intervals for the parameters with more accurate point estimates (table 2.6). Figure 2.10

Parameter	True value	Mean point estimate	Mean HPD lower bound	Mean HPD upper bound
α	0.0	0.36	0.01	0.81
	0.5	0.43	0.04	0.83
	1.0	0.90	0.51	1.09
	1.5	1.52	1.26	1.81
I	1000	1450.36	651.28	2592.05
	2000	2622.61	1114.37	4080.61
m	2	2.96	2.00	5.00
	3	3.04	2.04	4.96
	4	3.17	1.88	5.00
N	5000	9041.75	2613.88	14659.82

Table 2.6: Average posterior mean point estimates and 95% highest posterior density (HPD) interval widths for BA model parameter estimates obtained with kernel-assisted ABC. Three transmission trees were simulated under each combination of the listed parameter values, and the parameters were estimated with kernel-assisted ABC without training.

shows the distributions for one simulation. Equivalent plots for one replicate simulation with each studied parameter combination can be found in figs. A.35 to A.58. HPD intervals around α and I were often narrow relative to the region of nonzero prior density, whereas the intervals for m and N were more widely dispersed.

To test the effect of model misspecification, we simulated one network where the nodes exhibited heterogeneous preferential attachment power (half 0.5, the other half 1.5), with $m = 2$, $N = 5000$, and $I = 1000$. The posterior mean [95% HPD] estimates for each parameter were: α , 1.03 [0.67 - 1.18]; I , 1474 [511 - 2990]; m , 3 [1 - 5]; N , 9861 [3710- 14977]. The approximate posterior distributions for this simulation are shown in fig. A.26. To test the effect of sampling bias, we sampled one transmission tree in a peer-driven fashion, where the probability to sample a node was twice as high if one of its peers had already been sampled. The parameters for this experiment were $N = 5000$, $m = 2$, $\alpha = 0.5$, and $I = 2000$. The estimated values were α , 0.3 [0 - 0.63]; I , 2449 [1417 - 3811]; m , 3 [2 - 5]; N , 9132 [2852 - 14780]. The approximate posterior distributions are shown in fig. A.27. Both of these results were in line with estimates obtained on other simulated datasets (table 2.6), although the estimate of peer-driven sampling for α was somewhat lower than typical.

2.3 Application to real world HIV data

2.3.1 Methods

[The synthetic data experiments presented in the previous section demonstrated that the \$\alpha\$ and \$I\$ parameters, and to a lesser extent the \$N\$ parameter, had measurable impacts on tree shape and were identifiable with kernel-assisted ABC. Therefore, our next step was to use *netabc* to estimate the parameters of the BA model for real world HIV epidemics.](#) Because the BA model assumes a single connected contact network, it is most appropriate to apply to groups of individuals who are epidemiologically related.

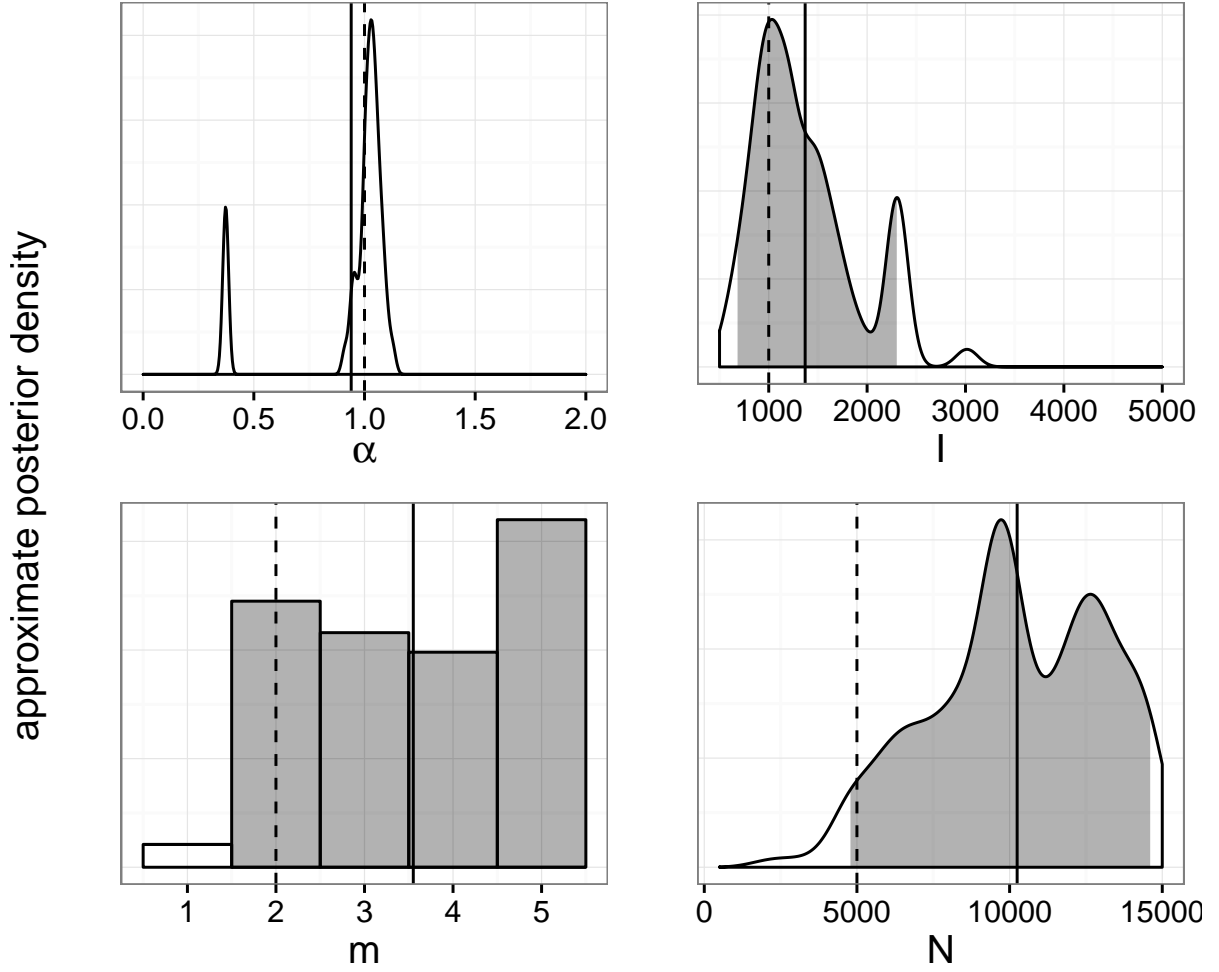


Figure 2.10: Marginal posterior distributions of BA model parameters estimated with kernel-assisted ABC for a single simulated transmission tree. Dotted lines indicate true values, solid lines indicate posterior mean point estimates, and shaded areas show 95% highest posterior density intervals.

Therefore, we searched for published HIV datasets which originated from existing clusters, either phylogenetically or geographically defined. In addition, we analysed an in-house dataset sampled from HIV-positive individuals in British Columbia, Canada (the “BC data”). The datasets are summarized in table 2.7.

We downloaded all sequences associated with each published study from GenBank. For the Novitsky et al. [152] data, each *env* sequence was aligned pairwise to the HXB2 reference sequence (GenBank accession number K03455), and the hypervariable regions were clipped out with *BioPython* version 1.66+ [155]. Sequences were multiply aligned using *MUSCLE* version 3.8.31 [156], and alignments were manually inspected with *Seaview* version 4.4.2 [157]. Phylogenies were constructed from the nucleotide alignments by approximate maximum likelihood using *FastTree2* version 2.1.7 [55] with the generalized time-reversible (GTR) model [158]. Transmission trees were estimated by rooting and time-scaling the phylogenies by root-to-tip regression, using a modified version of Path-O-Gen (distributed

Reference	Sequences (n)	Location	Risk group	Gene
Wang et al. [30]	173	Beijing, China	MSM	<i>pol</i>
Cuevas et al. [150]	287	Basque Country, Spain	mixed	<i>pol</i>
Novitsky et al. [151]	180	Mochudi, Botswana	HET	<i>env</i>
Novitsky et al. [152]				
Li et al. [153]	280	Shanghai, China	MSM	<i>pol</i>
Niculescu et al. [154]	136	Romania	IDU	<i>pol</i>
unpublished	399	British Columbia, Canada	IDU	<i>pol</i>

Table 2.7: Characteristics of published HIV datasets analyzed with *netabc*. Abbreviations: MSM, men who have sex with men; HET, heterosexual; IDU, injection drug users. The Novitsky et al. [151] and Novitsky et al. [152] data were sampled from a primarily heterosexual risk environment but did not explicitly exclude other risk factors.

as part of BEAST [159]) as described previously [22].

Three of the datasets [152, 153, and the BC data] were initially much larger than the others, containing 1265, 1299, and 7923 sequences respectively. To ensure that the analyses were comparable, we reduced these to a number of sequences similar to the smaller datasets. For the Li et al. and BC datasets, we detected clusters of size 280 and 399 respectively using a patristic distance cutoff of 0.02 as described previously [92]. Only sequences within these clusters were carried forward. For the Novitsky et al. [152] data, no large clusters were detected using the same cutoff, so we analysed a subtree of size 180 chosen arbitrarily.

Empirical studies of contact networks often report the exponent γ of the power law degree distribution. To compare our results to the literature, we simulated 100 networks each according to the MAP parameter estimates obtained for each investigated dataset. The power-law exponent γ was calculated for each network using the *fit.power.law* function in *igraph*, with the ‘R.mle’ implementation. The median of the 100 γ values was taken as a point estimate for the associated dataset.

For all datasets, we used the priors $\alpha \sim \text{Uniform}(0, 2)$ and N and I jointly uniform on the region $\{n \leq N \leq 10000, n \leq I \leq 10000, I \leq N\}$, where n is the number of tips in the tree (see table 2.7). Since the value $m = 1$ produces networks with no cycles, which we considered fairly implausible, we ran one analysis with the prior $m \sim \text{DiscreteUniform}(1, 5)$, and one with the prior $m \sim \text{DiscreteUniform}(2, 5)$. The other parameters to the SMC algorithm were the same as used for the simulation experiments, except that we used 10000 particles instead of 1000 to increase the accuracy of the estimated posterior. This was computationally feasible due to the small number of runs required for this analysis.

2.3.2 Results

We applied kernel-assisted ABC to five published HIV datasets (table 2.7), and found substantial heterogeneity among the parameter estimates (figs. 2.11 and A.28). Plots of the marginal posterior distributions for each dataset are shown in figs. A.30 to A.34. Two of the datasets (Wang et al. [30] and Niculescu et al. [154]) had estimated α values near unity for the prior allowing $m = 1$ (MAP estimates [95% HPD] 0.76 [0.07 - 1.34] and 0.61 [0.01 - 1.02] respectively). The MAP estimates did not change appreciably

Dataset	Estimated γ
mixed/Spain (Cuevas et al. 2009)	2.09
MSM/China (Li et al. 2015)	2.09
IDU/Romania (Niculescu et al. 2015)	2.20
IDU/Canada (unpublished)	2.16
HET/Botswana (Novitsky et al. 2013 & 2014)	2.49
MSM/China (Wang et al. 2015)	2.15

Table 2.8: Estimated power law exponents for six HIV datasets based on maximum *a priori* estimates of BA model parameters. 100 networks were simulated using *MAP* parameter estimates obtained with *netabc*. The power law exponent γ was estimated for each, and the median of those estimates was used as a point estimate for the corresponding dataset.

when $m = 1$ was disallowed by the prior, although the credible interval of the Niculescu et al. [154] data was narrower (0.07 - 1.34). When $m = 1$ was permitted, the Cuevas et al. [150] and Li et al. [153] both had low estimated α values (0.31 [0 - 0.73] and 0.38 [0.01 - 0.8]). However, the MAP estimates increased when $m = 1$ was not permitted, although the HPD intervals remained roughly the same (0.55 [0.01 - 0.93] and 0.5 [0.07 - 0.94]). The Novitsky et al. [152] data had a fairly low estimated α for both priors on m (0.5 for $m \geq 1$; 0.34 for $m \geq 2$). However, the confidence interval was much wider when $m = 1$ was allowed ([0.03 - 1.61] for $m \geq 1$ vs. [0 - 0.73] for $m \geq 2$).

For all the datasets except Novitsky et al., estimated values of I were below 2000 when $m = 1$ was allowed, with relatively narrow HPD intervals compared to the nonzero prior density region (Cuevas et al., 943 [287 - 2093]; Niculescu et al., 1032 [136 - 2851]; Li et al., 1437 [365 - 2897]; Wang et al., 872 [173 - 2119]). The Novitsky et al. data was the outlier, with a very high estimated I , and HPD interval spanning almost the entire prior region (5586 [187 - 8806]). The I estimates and HPD intervals were generally robust to the choice of prior on m , with slightly narrower HPD intervals (compare figs. 2.11 and A.28).

The MAP estimate of m was equal to 1 for all but the Novitsky et al. data, when this value was allowed. However, the upper bound of the HPD interval was different for each dataset (Niculescu et al., 5; Wang et al., 4; Li et al., 1; Cuevas et al., 2). When $m = 1$ was disallowed, the MAP for all datasets was either 2 or 3, with HPD intervals spanning the entire prior region. The estimates for the total number of nodes N were largely uninformative for all samples, with almost all MAP estimates greater than 7500 and HPD intervals spanning almost the entire nonzero prior density region. The only exception was the Li et al. data, for which the MAP estimate was lower (6049) when $m = 1$ was allowed.

To make our analyses comparable to the existing network literature, we estimated values of the power law exponent γ for each of the datasets investigated. The results are summarized in table 2.8. All of the estimated exponents were in the range $2 \leq \gamma \leq 2.5$, which is on the lower end of the range $2 \leq \gamma \leq 4$ reported in the literature.

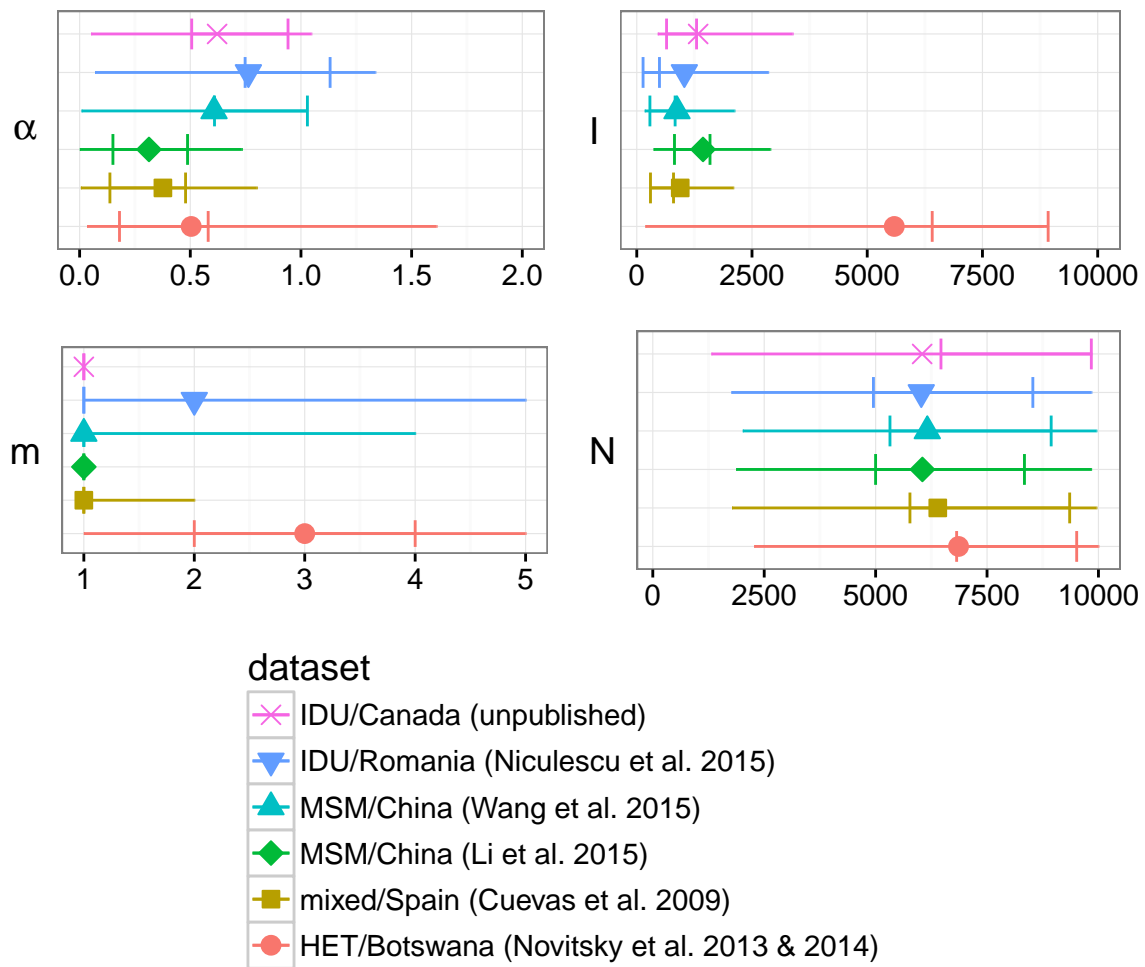


Figure 2.11: Maximum *a posteriori* point estimates and 95% HPD intervals for parameters of the BA network model, fitted to six HIV datasets with *netabc*. Legend labels indicate risk group and country of origin. Abbreviations: IDU, injection drug users; MSM, men who have sex with men; HET, heterosexual.

2.4 Discussion

2.4.1 *Netabc*: uses, limitations, and possible extensions

Contact networks can have a strong influence on epidemic progression, and are potentially useful as a public health tool [29, 30]. Despite this, few methods exist for investigating contact network parameters in a phylodynamic framework [although see 87, 96, 98, 107, 160, for related work]. Kernel-ABC is a model-agnostic method which can be used to investigate any quantity that affects tree shape [22]. In this work, we developed *netabc*, a method based on kernel-ABC to infer the parameters of a contact network model. The method is general, meaning that it can be used to infer parameters of any network model, as long as it allows simulated networks can be easily generated. We have included generators for the BA model discussed here, as well as the ER and Watts-Strogatz (WS) network models. Instructions for adding additional models are available in the project’s online documentation. We have made *netabc* publicly available at github.com/rmcclosk/netabc under a permissive open source license, to encourage other researchers to apply and extend our method.

Several alternative network models and modelling frameworks have been developed which may provide useful future targets for kernel-assisted ABC. Waring models [27, 161] are a more flexible type of preferential attachment model which permit a subset of attachments to be formed non-preferentially. These models were used by Brown et al. [96] to characterize the transmission network in the United Kingdom. Exponential random graph models (ERGMs) [162] are a flexible and expressive parameterization of contact networks in terms of statistics of network features such as pairs and triads. Goodreau [110] evaluated the effect of several different ERGM parameterizations on transmission tree shape and effective population size. The author suggested the use of ERGMs as a general framework for estimation of epidemiological quantities related to HIV transmission. Except for a few special cases, simulating a network according to an ERGM generally requires MCMC, which would be too computationally intensive to integrate into *netabc* as it currently stands. To fit ERGM with kernel-assisted ABC, one possibility would be to consider the network itself as a parameter to be modified by the MCMC kernel. Other network modelling frameworks include the partnership-centric formulation developed by Eames and Keeling [163] and the log-linear adjacency matrix parameterization applied by Morris [78].

The two-step process of simulating a contact network and subsequently allowing an epidemic to spread over that network carries with it the assumption that the contact network is static over the duration of the epidemic. Clearly this assumption is invalid, as people make and break partnerships on a regular basis. Addressing the impact of this simplifying assumption is outside the scope of this work. However, the same assumption is made by most studies using contact network models in an epidemiological context [6, 40]. In principle, kernel-assisted ABC could be adapted to dynamic contact networks by using a method such as that developed by Robinson, Cohen, and Colijn [164] to simulate such a network, while concurrently simulating the spread of an epidemic.

It is important to note that *netabc* takes a transmission tree as input, rather than a viral phylogeny. In reality, true transmission trees are not available and must be estimated; these estimates are often based on the viral phylogeny. Although this has been demonstrated to be a fair approximation [e.g. 63], and

is frequently used in practice [e.g. 38], the topologies of a viral phylogeny and transmission tree can differ significantly [37, 54] due to within-host evolution and the sampling process. We have left the estimation of a transmission tree up to the user. In theory, it is possible to incorporate the process by which a viral phylogeny is generated along with a transmission tree into our method, for example by simulating within-host dynamics. [Indeed, progress has very recently been demonstrated on this front in a talk by Giardina, who have independently developed in a method similar to ours to fit contact network models to phylogenetic data that additionally incorporates a within-host evolutionary model.](#) Although this may be an avenue for future extension, we felt that it would obscure the primary purpose of this work, which is to study contact network parameters. In addition, there are a number of different methods available for inferring transmission trees [32, 54, 65, 66, 68], some of which incorporate geographic and/or epidemiological data not accommodated by our method. We therefore felt it would be best to allow researchers to use their own preferred method of constructing a transmission tree.

Our implementation of SMC uses a simple multinomial scheme to sample particles from the population according to their weights. Several other sampling strategies have been developed [122], and it is possible that the use of a more sophisticated technique might increase the algorithm’s accuracy. Finally, the ABC-SMC algorithm is computationally intensive, taking about a day when run on 20 cores in parallel with the settings described in the methods section. Implementing parallelization using MPI, rather than POSIX threads as we have done here, would allow the program to be run over a larger number of cores on multiple CPUs in parallel.

2.4.2 Analysis of Barabási-Albert model with synthetic data

The preferential attachment power α had a very strong influence on tree shape in the range of values we considered (figs. 2.5 and 2.6). Although the tree kernel was the most effective classifier for α , a Sackin’s index of tree imbalance performed nearly as well (fig. 2.7). This result was intuitive: high α values produce networks with few well-connected “superspreader” nodes which are involved in a large number of transmissions, resulting in a highly unbalanced ladder-like tree structure (fig. 2.5). There was no observable bias in the estimates of α obtained with *netabc*, however the variation in these estimates was higher for $\alpha < 1$ than for $\alpha \geq 1$ (fig. 2.9 and table 2.6). The relationship between α and the power law exponent γ may explain this result (fig. A.25). The γ values associated with $\alpha = 0$ and $\alpha = 0.5$ are nearly identical (about 2.28 for $\alpha = 0$ and 2.33 for $\alpha = 0.5$ with $N = 5000$ and $m = 2$). In other words, the degree distributions of networks with $\alpha < 1$ are similar to each other, which may result in similarity of corresponding transmission trees as well.

The I parameter, representing the prevalence at the time of sampling, was also generally identifiable, although it was slightly over-estimated for both cases we considered with kernel-assisted ABC. The dynamics of the SI model, and the coalescent process [47], offer a potential explanation for the identifiability of I . In our simulations, we assumed that all discordant edges shared the same transmission rate, so that the waiting time until the next transmission in the entire network was always inversely proportional to the number of discordant edges. In the initial phase of the epidemic, when I is small, each new transmission results in many new discordant edges. Hence, there is an early exponential growth

phase, producing many short branches near the root of the tree. As the epidemic gets closer to saturating the network, the number of discordant edges decays, causing longer waiting times. The distribution of coalescence times in the tree should therefore be informative about I [53]. This information is captured by the tree kernel, and also by the nLTT statistic, which both performed quite well in classifying I (fig. 2.7).

The number of nodes in the network, N , exhibited the most variation in terms of its effect on tree shape. There was almost no difference between trees simulated under different N values when the number of infected nodes I was small. There is an intuitive explanation for this result, namely that adding additional nodes does not change the edge density or overall shape of a BA network. This can be illustrated by imagining that we add a small number of nodes to a network after the epidemic simulation has already been completed. It is possible that none of these new nodes attains a connection to any infected node. Thus, running the simulation again on the new, larger network could produce the exact same transmission tree as before. On the other hand, when I is large relative to N , the coalescent dynamics discussed above also apply. That is, the waiting times until the next infection increase, resulting in longer coalescence times toward the tips. The relative accuracy of the nLTT in these situations (figs. 2.7 and A.10) corroborates this hypothesis, as the nLTT uses only information about the coalescence times. When all BA parameters were simultaneously estimated with kernel-assisted ABC, N was nearly always over-estimated by approximately a factor of two (fig. 2.9 and table 2.6). One factor which may have contributed to this bias was our choice of prior distribution. Since the prior for I and N was jointly uniform on a region where $I \leq N$, more prior weight was assigned to higher N values. Another contributing factor relates to the dynamics of the SI model and the coalescent process.

I and N were both systematically over-estimated by *netabc*, although the bias was more severe for N than for I . The number of infected individuals follows a logistic growth curve under the SI model. This kind of growth curve has three qualitative phases: a slow ramp-up, an exponential growth phase, and a slow final phase when the susceptible population is almost depleted. The waiting times until the next transmission, which determine the coalescence times in the tree, are dependent on the growth phase of the epidemic. Therefore, we hypothesize that it is the growth phase at the time of sampling which most affects tree shape, rather than the specific values of I or N . To investigate this hypothesis, we simulated transmission trees over networks on a grid of I and N values in the region of uniform prior density. We fit logistic growth curves to the proportion of infected individuals over time, and calculated the first and second derivatives of these curves at the time of transmission tree sampling. These derivatives give us an indication of the growth rates of the epidemics at the time of sampling. As shown in fig. 2.12, there are bands along which both derivatives are similar which contain the values we tested. These bands span mostly higher values of N and I than the true values. Therefore, if N and I are free to vary (as is the case in kernel-assisted ABC), and our hypothesis is true, both parameters will tend to be overestimated due to being less identifiable within their own band. However, when N is fixed at 5000, the derivatives vary substantially along the I -axis, which explains why the grid search estimates of I were accurate and unbiased (fig. A.20).

The m parameter, which controls the number of connections added to the network per vertex, did not

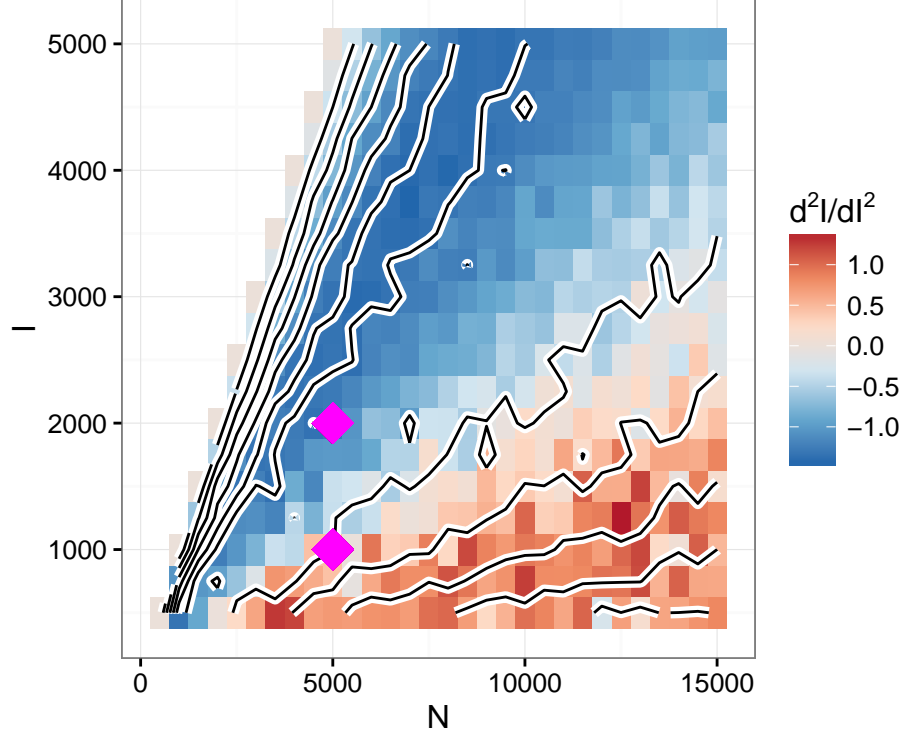


Figure 2.12: First and second derivatives of epidemic growth curves at time of sampling for various values of I and N . Networks were simulated under the BA model with $\alpha = 1.0$, $m = 2$, and N varied along the values shown on the x -axis. Transmission trees were sampled at the time when I nodes were infected (y -axis). Logistic growth curves were fit to epidemic trajectories derived from the transmission trees, and their first and second derivatives were calculated at the time of sampling. Contours show first derivatives, while colours indicate second derivatives. Values of I and N used in simulation experiments with kernel-assisted ABC are indicated by diamonds.

have a measurable impact on tree shape and was not identifiable with kernel-ABC. The exception to this was the value $m = 1$, which produces networks without cycles whose associated trees were more easily distinguished. However, all the analyses presented here did not take the absolute size of the transmission trees into account, as the branch lengths were rescaled by their mean. Because higher m values imply higher edge density, an epidemic should spread more quickly for higher m than lower m with the same per-edge transmission probability. Hence, considering the absolute height of the trees may improve our method's ability to reconstruct m .

In addition to the tree height, many summary statistics have been developed to capture particular details of tree shape. Two of these, Sackin's index and the ratio of internal to terminal branch lengths, were correlated with every BA parameter. Classifiers based on Sackin's index and the nLTT similarity measure performed well in some cases, though poorly in others. ABC is often applied using a vector of summary statistics [124, 166], rather than a kernel-based similarity score as we have done here. Methods have been developed to select an optimal combination of summary statistics for a given inference task [167]. Hence, an avenue for future improvement of our method may be the inclusion of additional summary statistics to supplement the tree kernel. In addition, all four parameters were more accurately

classified when the number of tips in the transmission trees was larger, underscoring the importance of adequate sampling for accurate phylodynamic inference.

For the more identifiable parameters, the credible intervals attained from the marginal ABC target distributions were much narrower than those obtained through grid search, while point estimates were of comparable accuracy. This was likely due to the fact that SMC employs importance sampling to approximate the posterior distribution, while grid search simply calculates a distance metric which may not have any resemblance to the posterior. Admittedly, our method of finding credible intervals from kernel scores along the grid, namely by normalizing the scores to resemble a probability distribution, was somewhat ad hoc, which may also have played a role. Regardless, this result indicates that there is benefit to applying the more sophisticated method, even if values for some of the parameters are known *a priori*, and especially if credible intervals are desired on the parameters of interest.

As noted by Lintusaari et al. [168], uniform priors on model parameters may translate to highly informative priors on quantities of interest. We observed a non-linear relationship between the preferential attachment power α and the power law exponent γ (fig. A.25). Therefore, placing a uniform prior on α between 0 and 2 is equivalent to placing an informative prior that γ is close to 2. Therefore, if we were primarily interested in γ rather than α , a more sensible choice of prior might have a shape informed by fig. A.25 and be bounded above by approximately $\alpha = 1.5$. This would uniformly bound γ in the region $2 \leq \gamma \leq 4$ commonly reported in the network literature [23–25, 96]. We note however that Jones and Handcock [169] estimated γ values greater than four for some datasets, in one case as high as 17, indicating that a wider range of permitted γ values may be warranted.

The combination of method, model, and priors we employed did not produce perfect estimates of any of the parameters. The estimates of α were the most accurate, although the variance of the estimates was high and the confidence intervals were wide for $\alpha < 1$ (table 2.6 and figs. 2.9, A.23 and A.24). The estimates of N and I were both biased, and the estimates of m were largely uninformative. Despite these issues, a major result of our investigation is that some contact network parameters have a measurable impact on tree shape which can be used to perform statistical inference. Further refinements to *netabc*, as well as the use of more sophisticated network models, may improve the accuracy and precision of these estimates.

2.4.3 Application to real world HIV data

Our investigation of published HIV datasets indicated heterogeneity in the contact network structures underlying several distinct local epidemics. When interpreting these results, we caution that the BA model is quite simple and most likely misspecified for these data. In particular, the average degree of a node in the network is equal to $2m$, and therefore is constrained to be a multiple of 2. Furthermore, we considered the case $m = 1$, where the network has no cycles, to be implausible and therefore assigned it zero prior probability in one set of analyses. This forced the average degree to be at least four, which may be unrealistically high for sexual networks. The fact that the estimated values of α differed substantially for three datasets depending on whether or not $m = 1$ was allowed by the prior is further evidence of this potential misspecification. However, we note that for two of the datasets, the estimated values of

α did not change much between priors, and the estimates of I were robust to the choice of prior for all datasets studied. More sophisticated models, for example models incorporating heterogeneity in node behaviour, are likely to provide a better fit to these data.

With respect to the preferential attachment power α , the six datasets analysed fell into two categories (fig. 2.11). First, we estimated a preferential attachment power close to 1, indicating linear preferential attachment, for the BC data and the outbreaks studied by Niculescu et al. [154] and Wang et al. [30]. These values were robust to specifying different priors for m . All three datasets were sampled from populations in which we would expect a high degree of epidemiological relatedness: Niculescu et al. [154] studied a recent outbreak among Romanian injection drug users (IDU), Wang et al. sampled acutely infected MSM in Beijing, China, and the BC data constituted a phylogenetic IDU cluster. These are all contexts in which we would expect some of the assumptions of the BA model, such as a connected network, relatively high mean degree, and preferential attachment dynamics, to hold.

The remaining three datasets (Cuevas et al. [150], Novitsky et al. [152], and Li et al. [153]) had estimated values of α below 0.5 when $m = 1$ was included in the prior, but these were not robust to changing the prior to exclude $m = 1$. For the Cuevas et al. data, model misspecification is likely partially responsible. While the authors found that a large proportion of the samples were epidemiologically linked, these were mainly in small local clusters rather than the single large component postulated by the BA model. In addition, the mixed risk groups in the dataset would be unlikely to significantly interact, further weakening any global preferential attachment dynamics. The dataset studied by Novitsky et al. [152] originated from a densely sampled population where the predominant risk factor was believed to be heterosexual exposure. Although the MAP estimate of α was almost unchanged when the value $m = 1$ was excluded from the prior, the confidence interval shrank substantially.

The posterior mean estimates for the real world HIV datasets corresponded to power law exponents γ between 2.09 and 2.49. TODO

The estimates of the prevalence I were largely robust to the choice of prior on m (figs. 2.11 and A.28). Niculescu et al. [154] reported that 494 new HIV infections were diagnosed among the studied population (IDUs in Bucharest) during the study period. Our estimate of the prevalence was higher (X), although the 95% HPD interval did contain the value 494. In addition, it is not unreasonable that a substantial fraction of the HIV-positive individuals in an IDU population could be undiagnosed, given that these populations are often marginalized.

The individuals sampled by Wang et al. [30] were recruited by following a prospective cohort of 2000 MSM in Beijing, China. Of the 2000, 179 new infections were identified during the study period. This number is much lower than the estimated prevalence of X obtained with *netabc*, however the authors did not claim to have sampled the entire sexual network. In a nationwide survey, Wu et al. [170] estimated that there were 24,198 MSM living in Beijing, of whom 5.7%, or 1379, were HIV-infected, which is within the 95% confidence interval of our estimate of I .

Li et al. [153] studied an MSM population in Shanghai, China. Despite the apparent similarity to the context of the Wang et al. [30] study, the estimated HIV prevalence of the Li et al. data was higher (X). The aforementioned survey [170] estimated that there were 14,511 MSM living in Shanghai, with an

HIV prevalence of 6.8% or approximately 987 individuals. This was within the 95% confidence interval of the estimate obtained with *netabc*. It is worth noting that Li et al. claimed that there were 80,000 MSM living in Shanghai, which is a significantly different estimate than that obtained by Wu et al. [170].

Cuevas et al. [150] reported that 620 newly infected and 1500 chronically infected patients had been sampled during the study period, for a total of 2120. This is substantially greater than the point estimate of X we obtained with ABC, even without considering the likely possibility that there were more infected than sampled individuals. Again, this error may in part be due to model misspecification, which highlights the importance of selecting a model appropriate to the dataset at hand.

Our use of the BA model makes several simplifying assumptions. First, we assume homogeneity across the network with respect to node behaviour and transmission risk. In reality, the attraction to high-degree nodes seems likely to vary among individuals, as does their risk of transmitting or contracting the virus. We have also assumed that all transmission risks are symmetric, which is clearly false for all known modes of HIV transmission, and that infected individuals never recover but remain infectious indefinitely. These assumptions were made for the purpose of keeping the model as simple as possible, since this is the very first attempt to fit a contact network model in a phylodynamic context. However, the Gillespie simulation algorithm built into *netabc* can handle arbitrary transmission and removal rates which need not be homogeneous across the network. Moreover, it is possible to use ABC to fit a model which relaxes some or all of these assumptions, which may be a fruitful avenue for future investigation. Despite the possible misspecification, our estimates of the power law exponent γ were within the range of values reported in the literature (table 2.8).

Chapter 3

Conclusion

Due to the rapid advancement of nucleotide sequencing technology, viral sequence data have become increasingly feasible to collect on a population level. Through phylodynamic methods, these data offer a window into epidemiological processes which would otherwise be virtually impossible to study on a realistic scale.

This thesis developed *netabc*, a computer program implementing a statistical inference method for contact network parameters from viral phylogenetic data. *Netabc* brings together the areas of viral phylodynamics and network epidemiology, which have only intersected in a very limited fashion thus far [40]. The use of kernel-ABC, a likelihood-free method, makes it possible to fit network models to phylogenies without calculating intractable likelihoods.

Although phylodynamic methods have been developed to fit a wide variety of epidemiological models to phylogenetic data assuming homogeneous mixing [48, 171], our method is able to fit models not requiring this assumption. We believe this capability will be of broad interest to the molecular evolution and epidemiology community, as it widens the field of epidemiological parameters which may be investigated through viral sequence data. In addition, the characterization of local contact networks could be valuable from a public health perspective, such as for investigating optimal vaccination strategies [8–10, 90]. This information could assist in curtailing current epidemics, as well as preventing future epidemics of different diseases over the same contact network.

The particular model we have investigated uses a preferential attachment mechanism to generate scale-free networks resembling real-world social and sexual networks [23–25]. Of the four parameters we considered, the preferential attachment power α was the most readily estimable. Estimating α with traditional epidemiological methods is challenging due to the requirement of sampling the high-degree nodes making up the tail of the power law distribution, although approaches such as respondent-driven sampling [91] may be effective.

In closing, *netabc* combines phylodynamics, contact network epidemiology, approximate Bayesian computation, and sequential Monte Carlo to provide a source of insight into network structures complementary to traditional epidemiology.

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Appendix A

Mathematical models, likelihood, and Bayesian inference

A *mathematical model* is a formal description of a hypothesized relationship between some observed data, x and outcomes y . A *parametric* model defines a family of possible relationships between data and outcomes, parameterized by one or more numeric parameters θ . A *statistical* model describes the relationship between data and outcomes in terms of probabilities. Statistical models define, either explicitly or implicitly, the probability of observing y given x and, if the model is parametric, θ . Note that it is entirely possible to have no data x , only observed outcomes y . In this case, a model would describe the process by which y is generated.

To illustrate these concepts, consider the well-known linear model. For clarity, we will restrict our attention to the case of one-dimensional data and outcomes where $x = \{x_1, \dots, x_n\}$ and $y = \{y_1, \dots, y_n\}$ are vectors of real numbers. The linear model postulates that the outcomes are linearly related to the data, modulo some noise introduced by measurement error, environmental fluctuations, and other external factors. Formally, $y_i = \beta x_i + \varepsilon_i$, where β is the slope of the linear relationship, and ε_i is the error associated with measurement i . We can make this model a statistical one by hypothesizing a distribution for the error terms ε_i ; most commonly, it is assumed that they are normally distributed with variance σ . In mathematical terms, $y_i \sim \beta x_i + \mathcal{N}(0, \sigma^2)$, where “ \sim ” means “is distributed as”. We can see from this formulation that the model is parametric, with parameters $\theta = (\beta, \sigma)$. Moreover, we can write down the probability density π of observing outcome y_i given the parameters,

$$\pi(y \mid \beta, \sigma) = \prod_{i=1}^n f_{\mathcal{N}(0, \sigma^2)}(y_i - \beta x_i),$$

where $f_{\mathcal{N}(0, \sigma^2)}$ is the probability density of the normal distribution with mean zero and variance σ^2 . Note that we are treating the x_i as fixed quantities and therefore have not conditioned the probability density on x . Also, we have assumed that all the y_i are independent.

For a general model, the probability density of y given the parameters θ is also known as the *likelihood*, written \mathcal{L} , of θ . That is, $\mathcal{L}(\theta \mid y) = f(y \mid \theta)$ for the model’s probability density function (pdf)

f . The higher the value of the likelihood, the more likely the observations y are under the model. Thus, the likelihood provides a natural criterion for fitting the model parameters: we want to pick θ such that the probability density of our observed outcomes y is as high as possible. The parameters that optimize the likelihood are known as the *ML* estimates, denoted $\hat{\theta}$. That is,

$$\hat{\theta} = \arg \max_{\theta} \mathcal{L}(\theta | y).$$

ML estimation is usually performed with numerical optimization. In the simplest terms, many possible values for θ are examined, $\mathcal{L}(\theta | y)$ is calculated for each, and the parameters that produce the highest value are accepted. Many sophisticated numerical optimization methods exist, although they may not be guaranteed to find the true ML estimates if the likelihood function is multi-modal.

ML estimation makes use only of the data and outcomes to estimate the model parameters θ . However, it is frequently the case that the investigator has some additional information or belief about what θ are likely to be. For example, in the linear regression case, the instrument used to measure the outcomes may have a well-known margin of error, or the sign of the slope may be obvious from previous experiments. The Bayesian approach to model fitting makes use of this information by codifying the investigator's beliefs as a *prior distribution* on the parameters, denoted $\pi(\theta)$. Instead of considering only the likelihood, Bayesian inference focuses on the product of the likelihood and the prior, $f(y | \theta)\pi(\theta)$. Bayes' theorem tells us that this product is related to the *posterior distribution* on θ ,

$$f(\theta | y) = \frac{f(y | \theta)\pi(\theta)}{\int f(y | \theta)\pi(\theta)d\theta}. \quad (\text{A.1})$$

In principle, $f(y | \theta)\pi(\theta)$ can be optimized numerically just like $\mathcal{L}(\theta | y)$, which would also optimize the posterior distribution. The resulting optimal parameters are called the MAP estimates. However, from a Bayesian perspective, θ is not a fixed quantity to be estimated, but rather a random variable with an associated distribution (the posterior). Therefore, the MAP estimate by itself is of limited value without associated statistics about the posterior distribution, such as the mean or credible intervals. Unfortunately, to calculate such statistics, it is necessary to evaluate the normalizing constant in the denominator of eq. (A.1), which is almost always an intractable integral.

A popular method for circumventing the normalizing constant is the use of MCMC to obtain a sample from the posterior distribution. MCMC works by defining a Markov chain ~~whose states are indexed by possible model parameters. The transition probability from state θ_1 to state θ_2 is taken to be~~ on the space of possible model parameters. The transition density from parameters θ_1 to θ_2 is taken to be

$$\min \left(1, \frac{f(y | \theta_2)\pi(\theta_2)q(\theta_2, \theta_1)}{f(y | \theta_1)\pi(\theta_2)q(\theta_1, \theta_2)} \right),$$

where $q(\theta, \theta')$ is a symmetric *proposal distribution* used in the algorithm to generate the chain. The stationary distribution of this Markov chain is equal to the posterior distribution on θ . Therefore, if a long enough random walk is performed on the chain, the distribution of states visited will be a Monte Carlo approximation of $f(\theta | y)$, from which we can calculate statistics of interest. Actually performing this

random walk is straightforward and can be accomplished via the Metropolis-Hastings algorithm [172, 173] (algorithm A.1).

Algorithm A.1 Metropolis-Hastings algorithm for Markov chain Monte Carlo.

Draw θ according to the prior $\pi(\theta)$

loop

Propose θ' according to $q(\theta, \theta')$

Accept $\theta \leftarrow \theta'$ with probability $\min\left(1, \frac{f(y | \theta')\pi(\theta')q(\theta, \theta')}{f(y | \theta)\pi(\theta)q(\theta', \theta)}\right)$

end loop

Appendix B

Additional plots

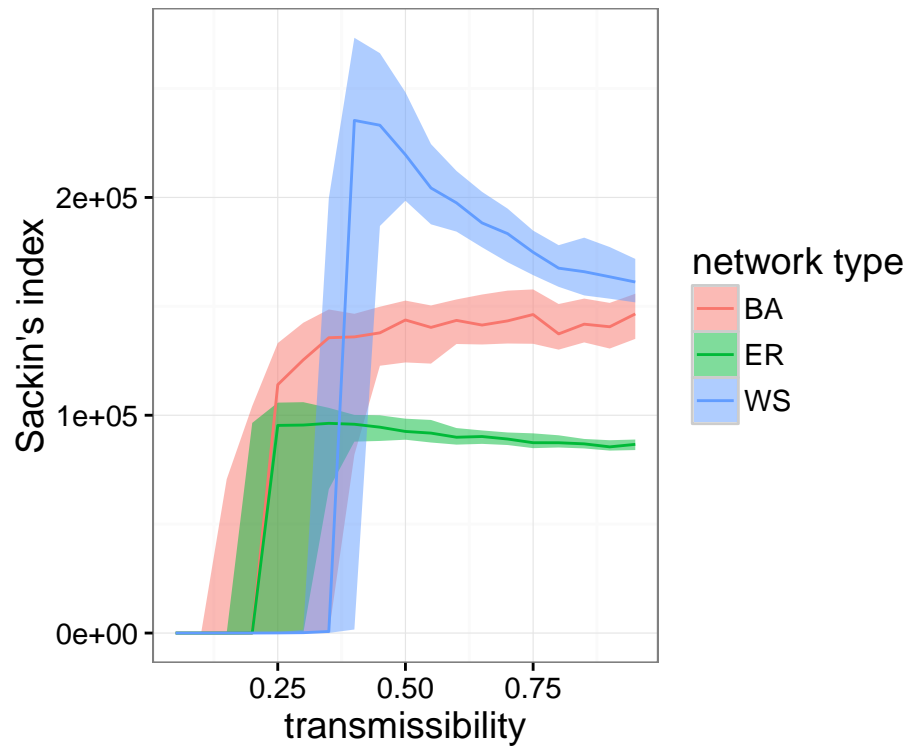


Figure A.1: Reproduction of Figure 1A from Leventhal *et al.* (2012) used to check the accuracy of our implementation of Gillespie simulation. Transmission trees were simulated over three types of network, with pathogen transmissibility varying from 0 to 1. Sackin's index was calculated for each simulated transmission tree. Lines indicate median Sackin's index values, and shaded areas are interquartile ranges.

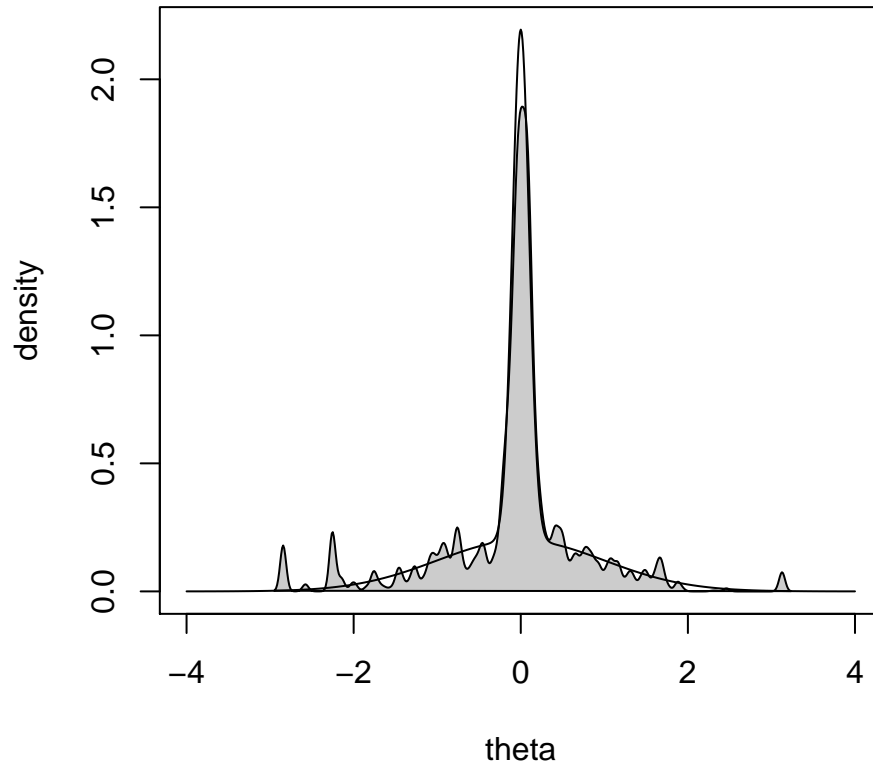


Figure A.2: Approximation of mixture of Gaussians used by Del Moral *et al.* (2012) and Sisson *et al.* (2009) to test SMC. Solid black line indicates true distribution. Grey shaded area shows ABC approximation obtained with our implementation of adaptive ABC-SMC, using 10000 particles with one simulated data point per particle.

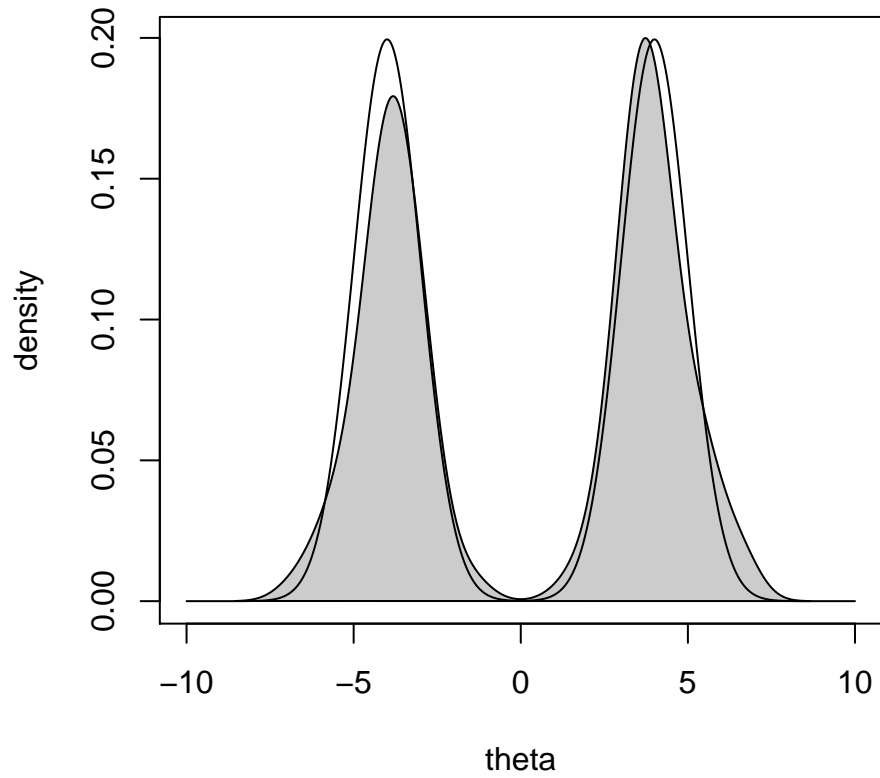


Figure A.3: Approximation of mixture of two Gaussians used to test convergence of SMC algorithm to a bimodal distribution. Solid black line indicates true distribution. Grey shaded area shows ABC-SMC approximation obtained with our implementation, using 10000 particles with one simulated data point per particle.

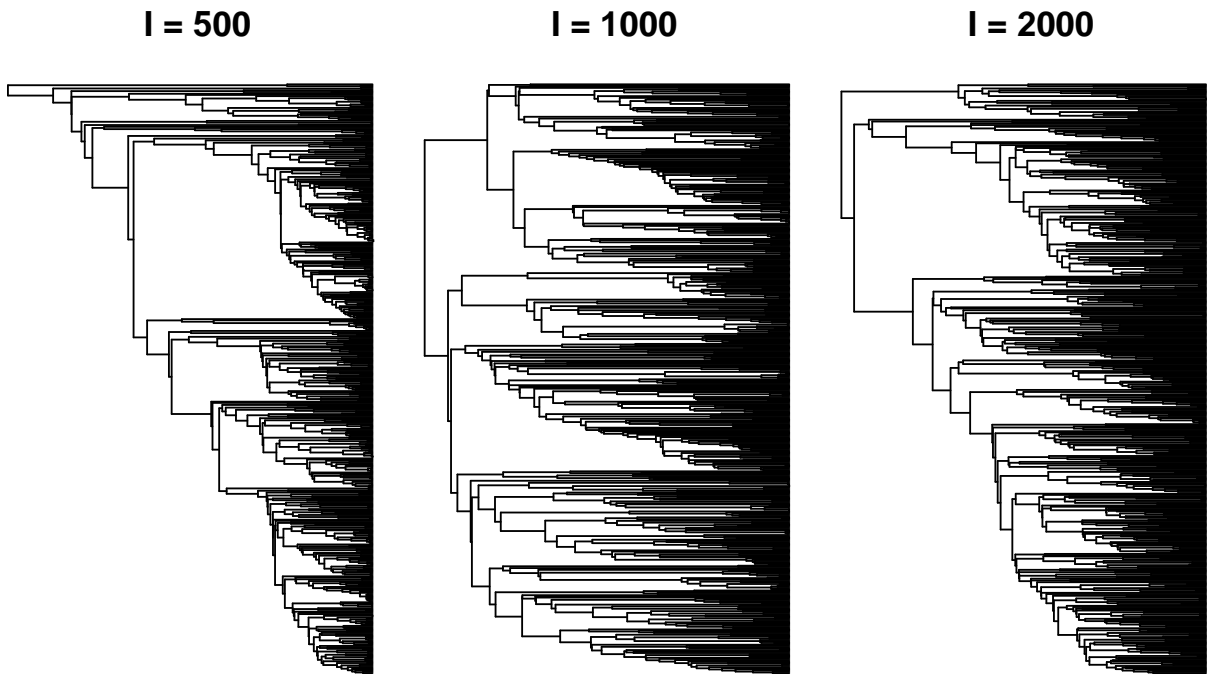


Figure A.4: Simulated transmission trees under three different values of BA parameter I . Epidemics were simulated on BA networks with parameters $\alpha = 1.0$, $m = 2$, and $N = 5000$. Epidemics were simulated until $I = 500$, 1000 , or 2000 nodes were infected. Transmission trees were created by sampling 500 infected nodes. For higher I values, the network was closer to saturation at the time of sampling, resulting in longer terminal branches as the waiting time until the next transmission increased.

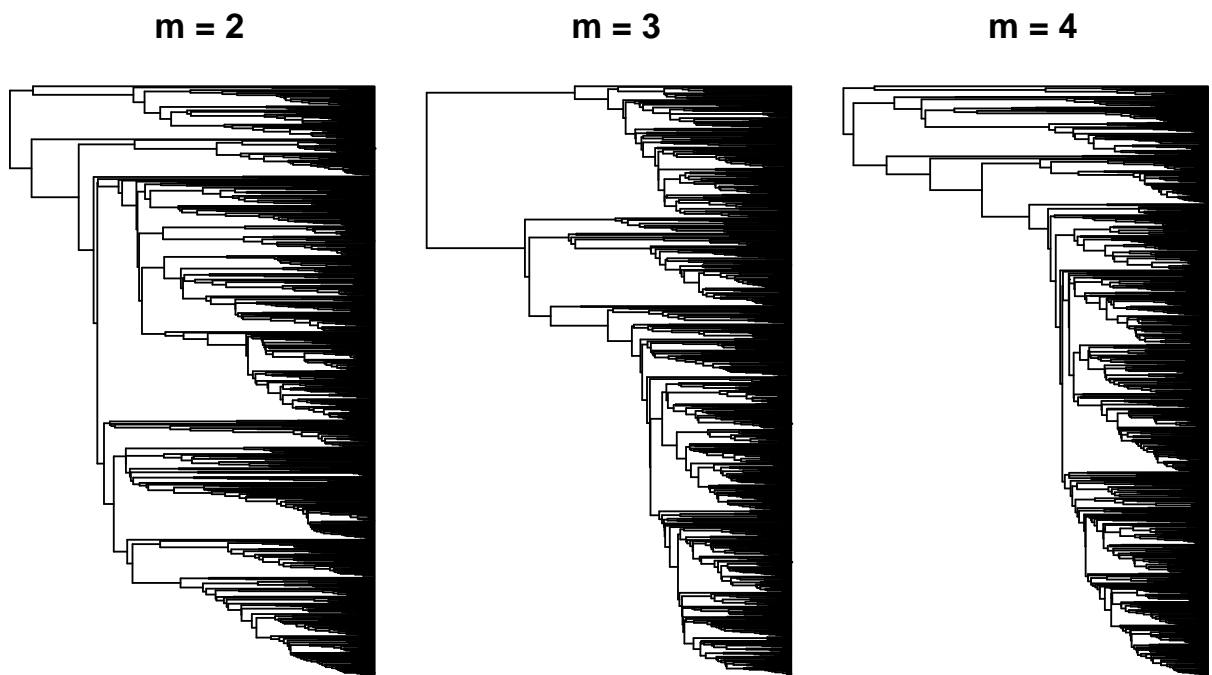


Figure A.5: Simulated transmission trees under three different values of BA parameter m . Epidemics were simulated on BA networks with parameters $\alpha = 1.0$, $N = 5000$, and $m = 2, 3$, or 4 . Epidemics were simulated until $I = 1000$ nodes were infected. Transmission trees were created by sampling 500 infected nodes.

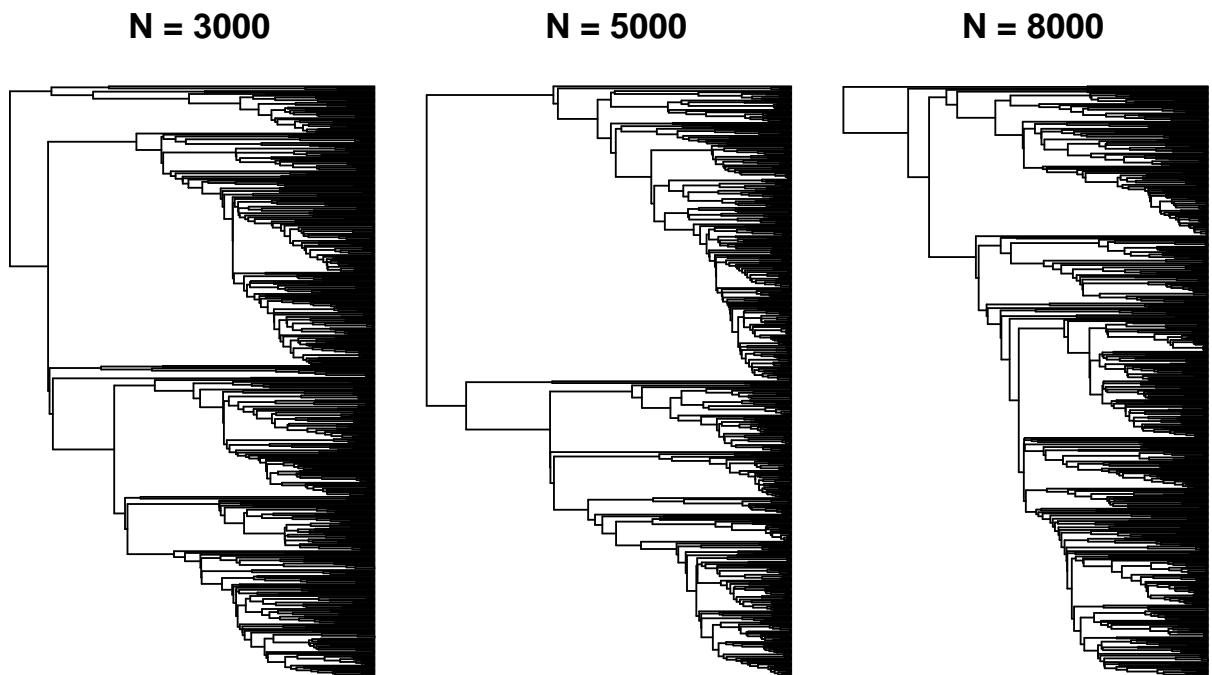


Figure A.6: Simulated transmission trees under three different values of BA parameter N . Epidemics were simulated on BA networks with parameters $\alpha = 1.0$, $m = 2$, and $N = 3000$, 5000 , or 8000 . Epidemics were simulated until $I = 1000$ nodes were infected. Transmission trees were created by sampling 500 infected nodes. For lower N values, the network was closer to saturation at the time of sampling, resulting in longer waiting times until the next transmission and longer terminal branch lengths.

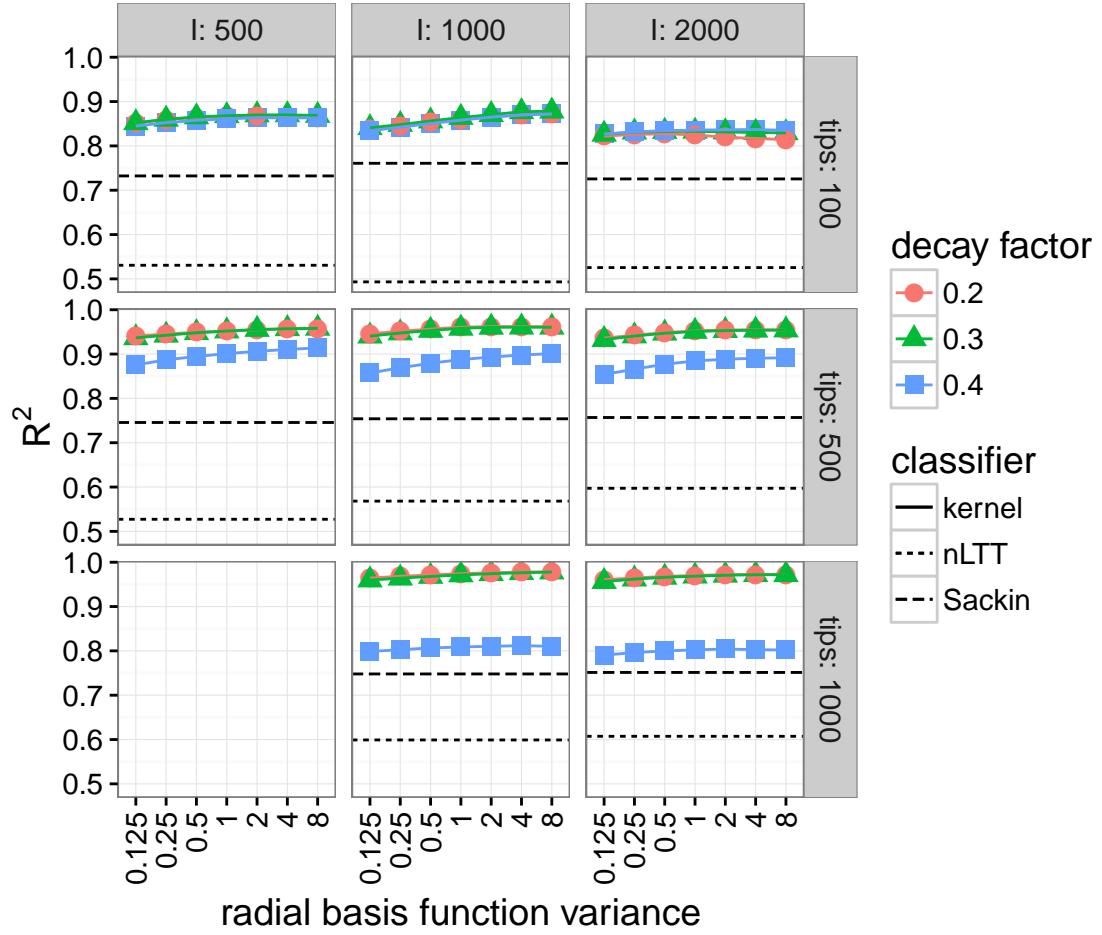


Figure A.7: Cross validation accuracy of classifiers for BA model parameter α for eight epidemic scenarios. Solid lines and points are R^2 of tree kernel kSVR under various kernel meta-parameters. Dashed and dotted lines are R^2 of linear regression against Sackin's index, and SVR using nLTT.

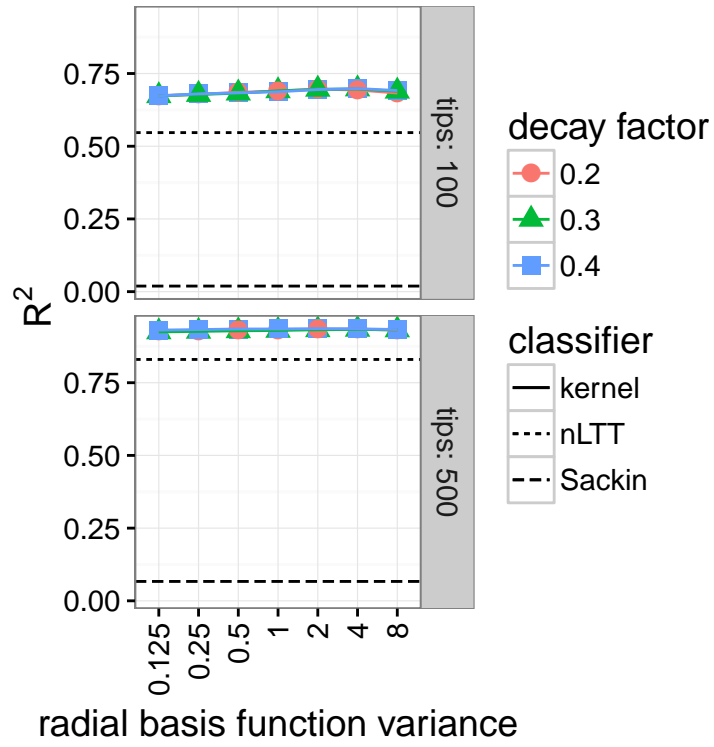


Figure A.8: Cross validation accuracy of classifiers for BA model parameter I for eight epidemic scenarios. Solid lines and points are R^2 of tree kernel kSVR under various kernel meta-parameters. Dashed and dotted lines are R^2 of linear regression against Sackin's index, and SVR using nLTT.

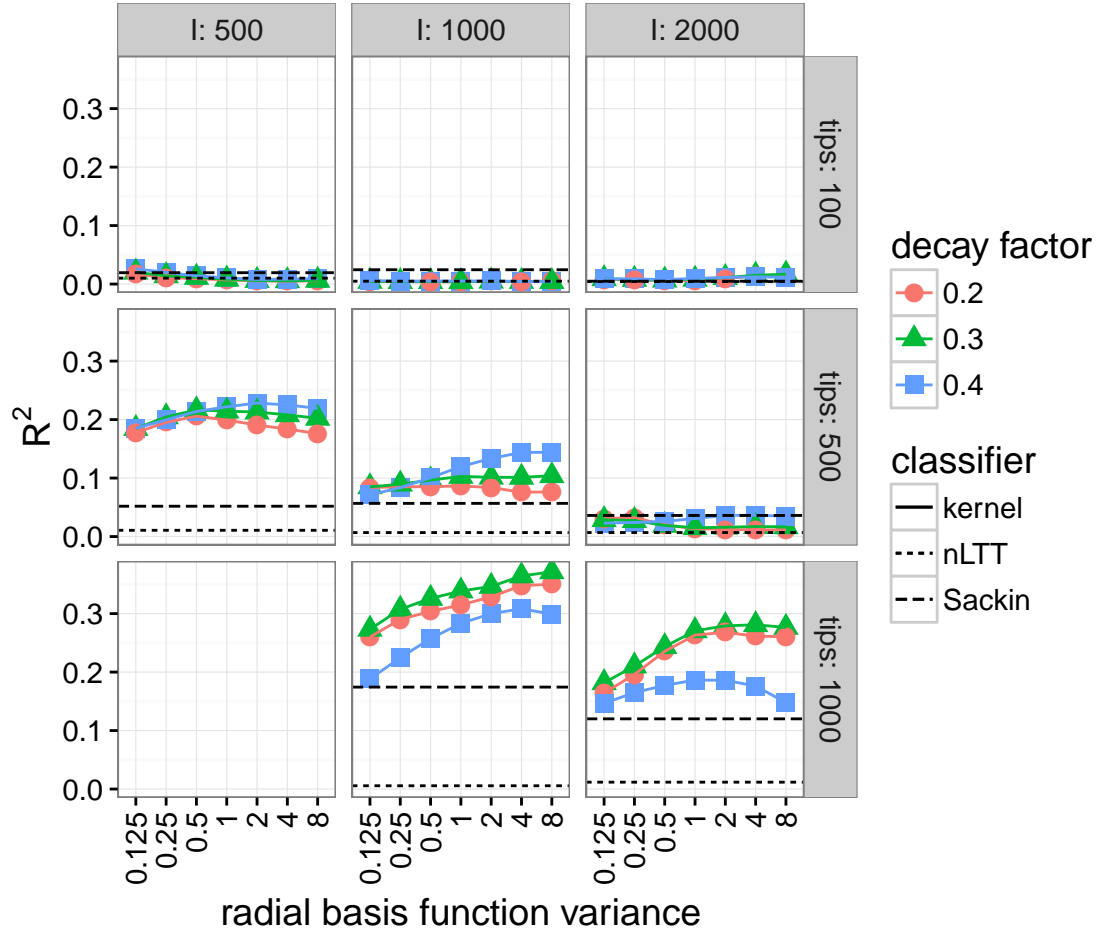


Figure A.9: Cross validation accuracy of classifiers for BA model parameter m for eight epidemic scenarios. Solid lines and points are R^2 of tree kernel kSVR under various kernel meta-parameters. Dashed and dotted lines are R^2 of linear regression against Sackin's index, and SVR using nLTT.

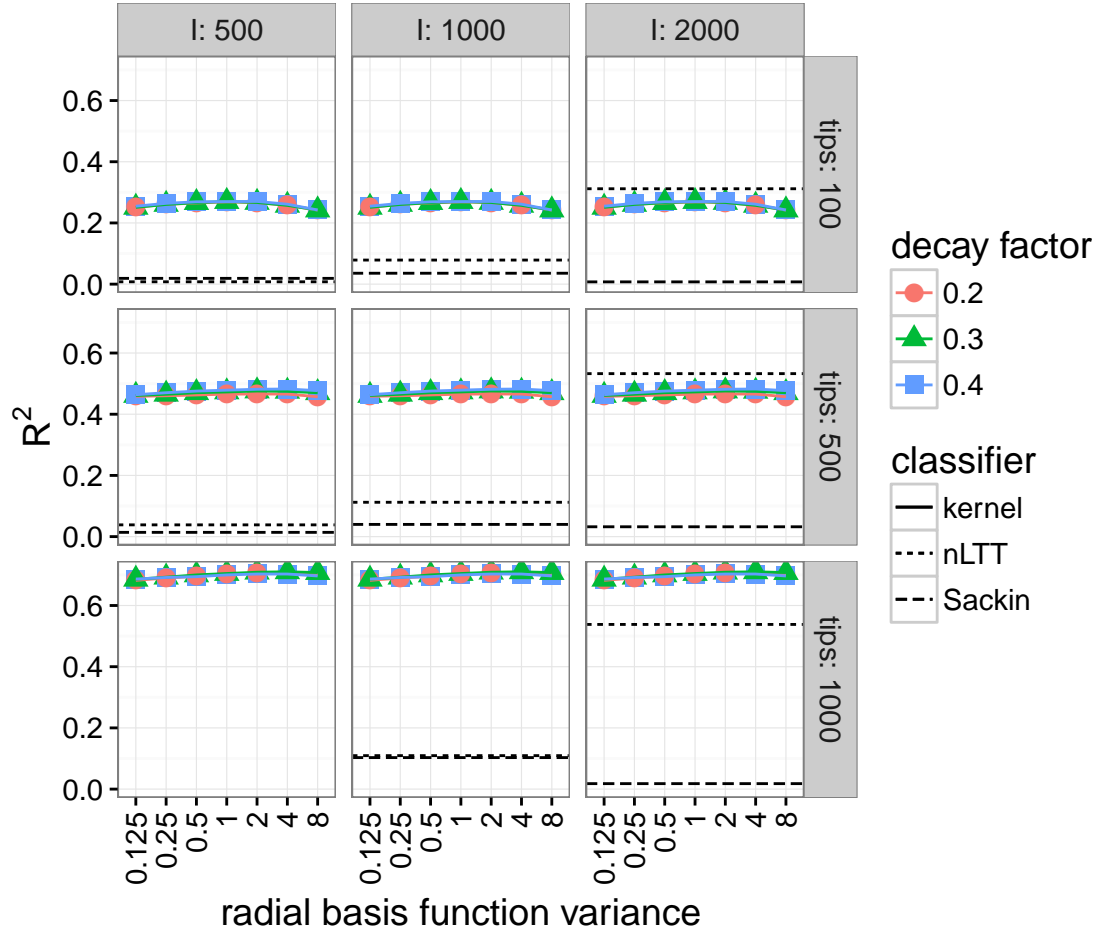


Figure A.10: Cross validation accuracy of classifiers for BA model parameter N for eight epidemic scenarios. Solid lines and points are R^2 of tree kernel kSVR under various kernel meta-parameters. Dashed and dotted lines are R^2 of linear regression against Sackin's index, and SVR using nLTT.

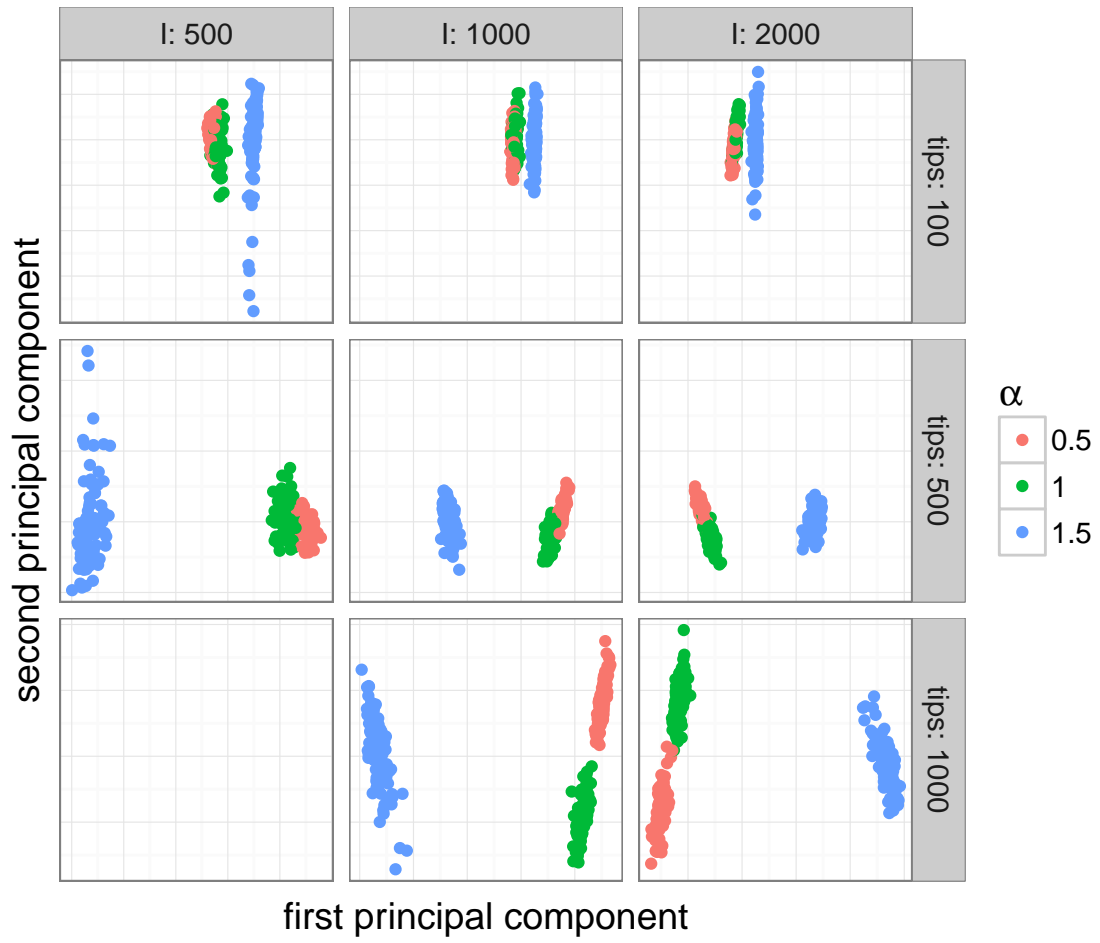


Figure A.11: Kernel principal components projection of trees simulated under three different values of BA parameter α , for eight epidemic scenarios.

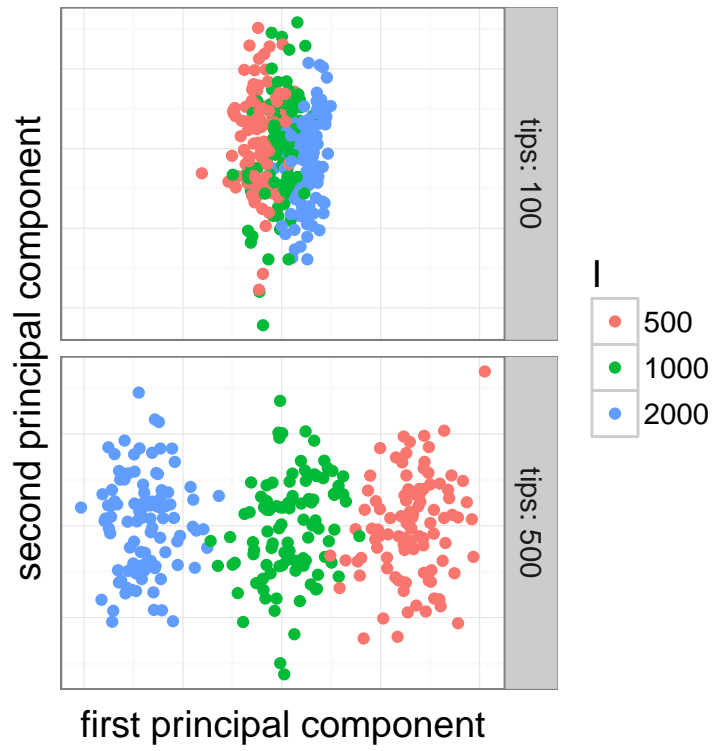


Figure A.12: Kernel principal components projection of trees simulated under three different values of BA parameter I , for eight epidemic scenarios.

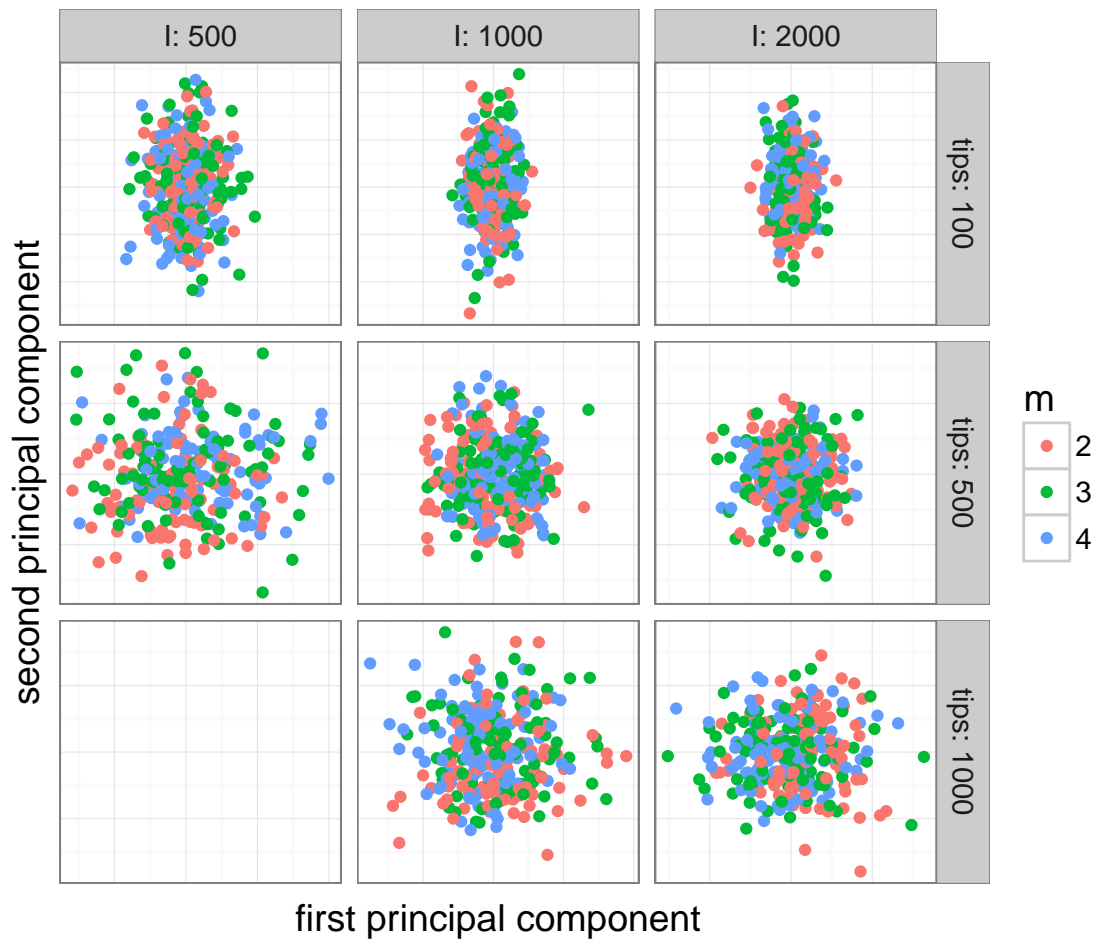


Figure A.13: Kernel principal components projection of trees simulated under three different values of BA parameter m , for eight epidemic scenarios.

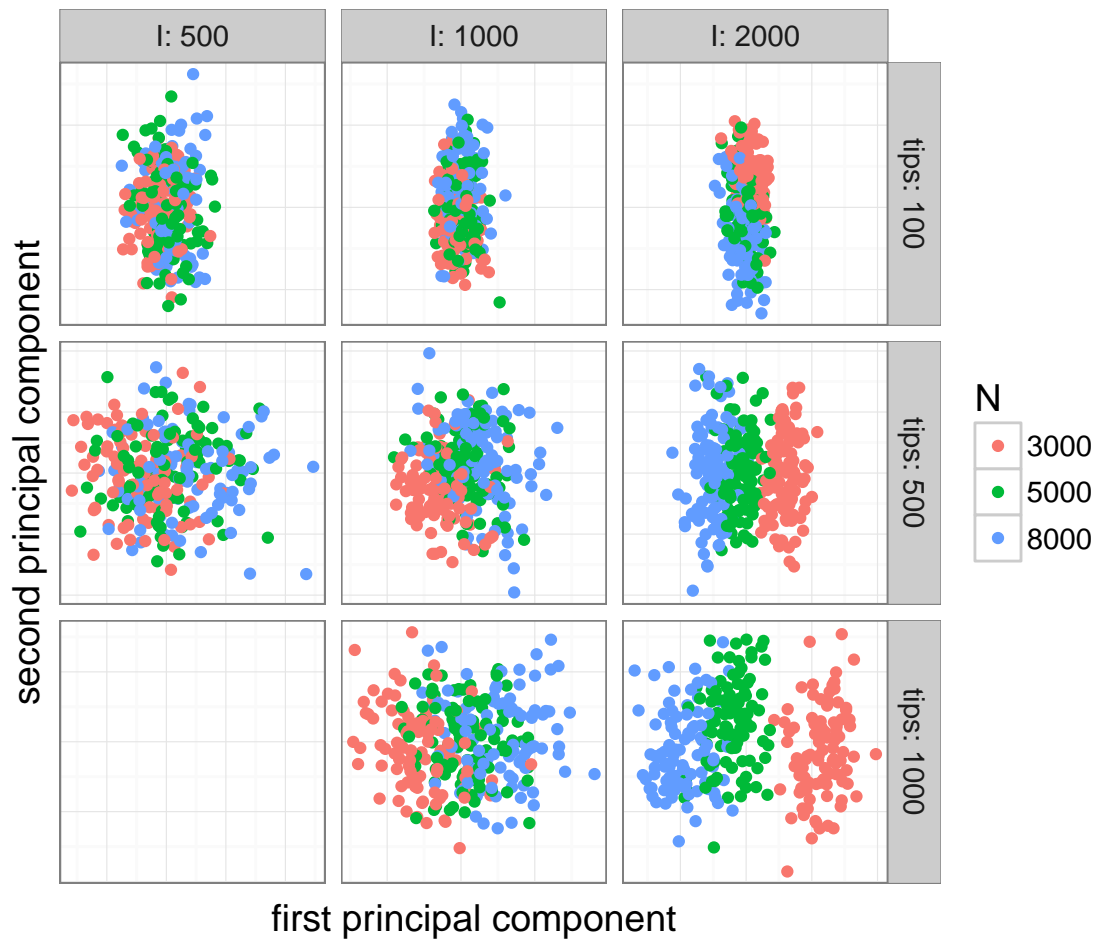


Figure A.14: Kernel principal components projection of trees simulated under three different values of BA parameter N , for eight epidemic scenarios.

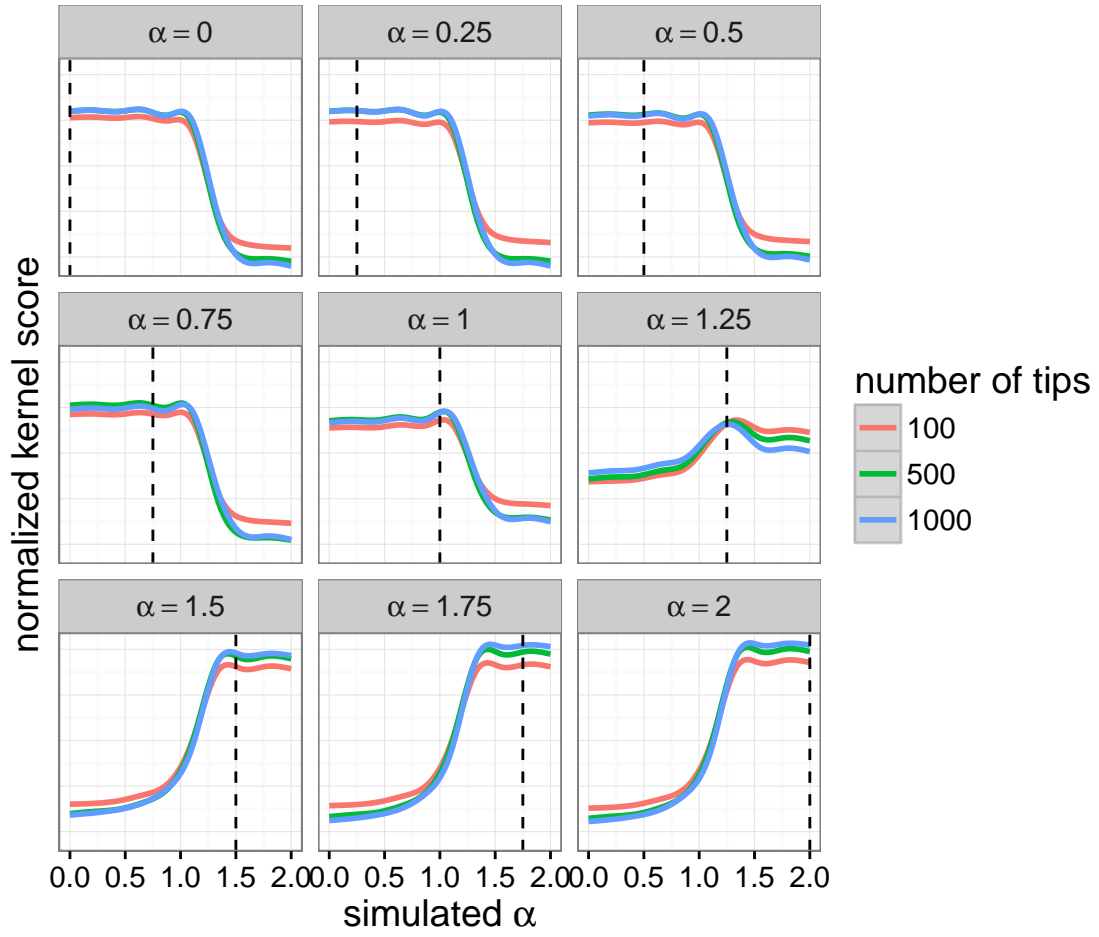


Figure A.15: Grid search kernel scores for testing trees simulated under various α values. The other BA parameters were fixed at $I = 1000$, $N = 5000$, and $m = 2$.

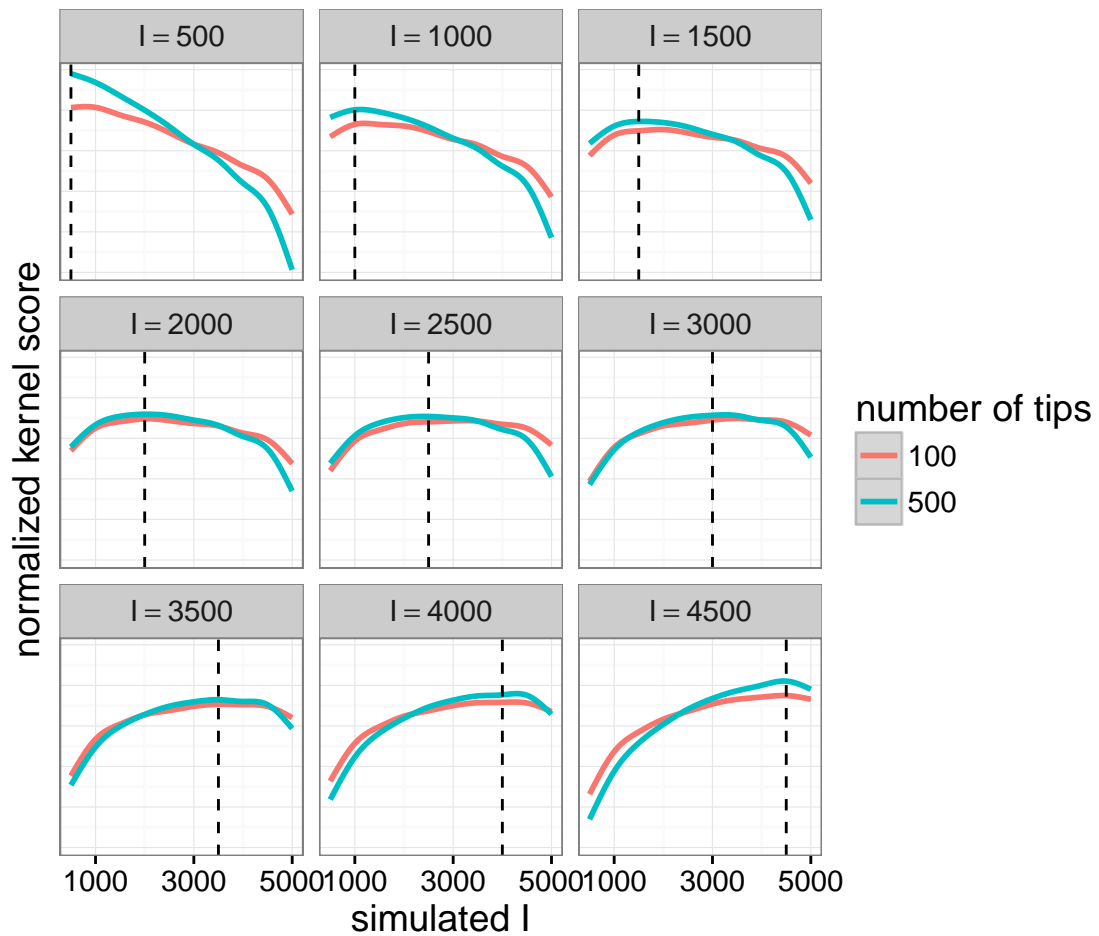


Figure A.16: Grid search kernel scores for testing trees simulated under various I values. The other BA parameters were fixed at $\alpha = 1.0$, $N = 5000$, and $m = 2$.

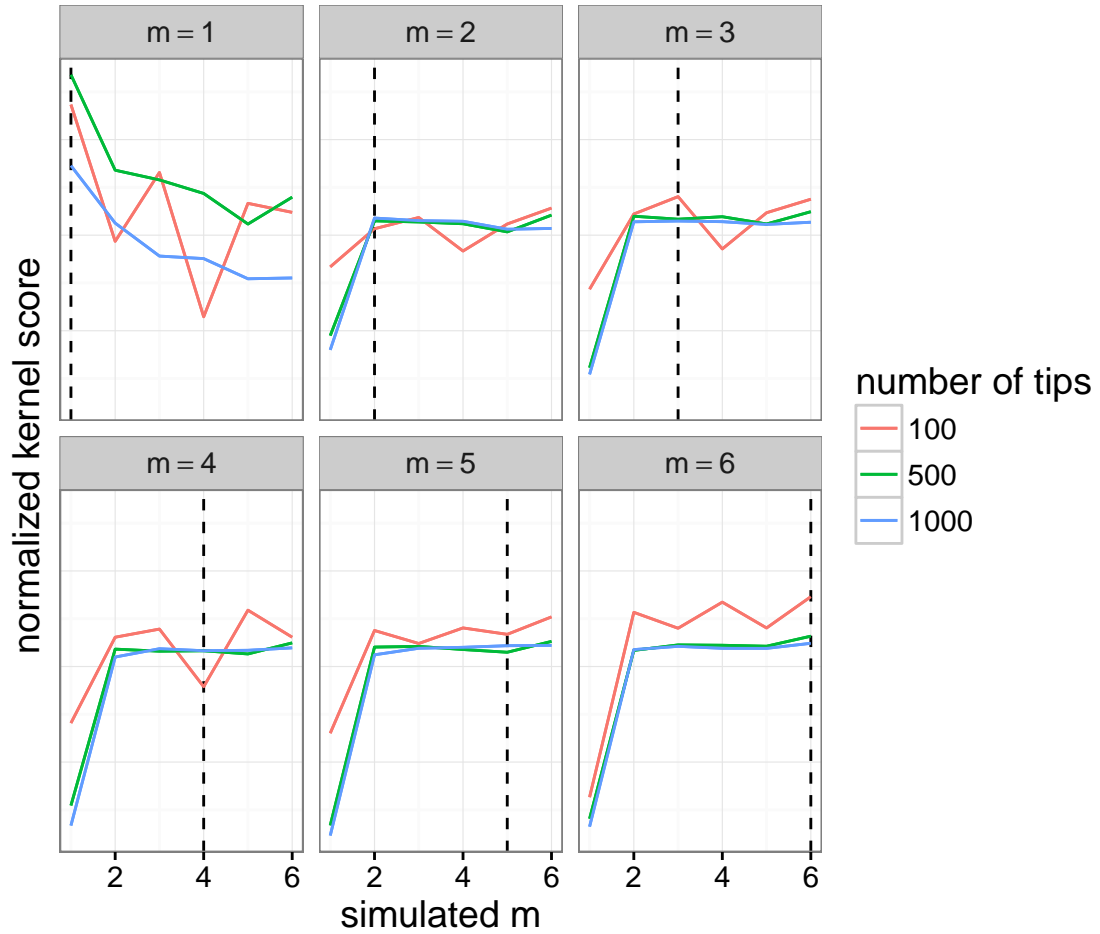


Figure A.17: Grid search kernel scores for testing trees simulated under various m values. The other BA parameters were fixed at $\alpha = 1.0$, $I = 1000$, and $N = 5000$.

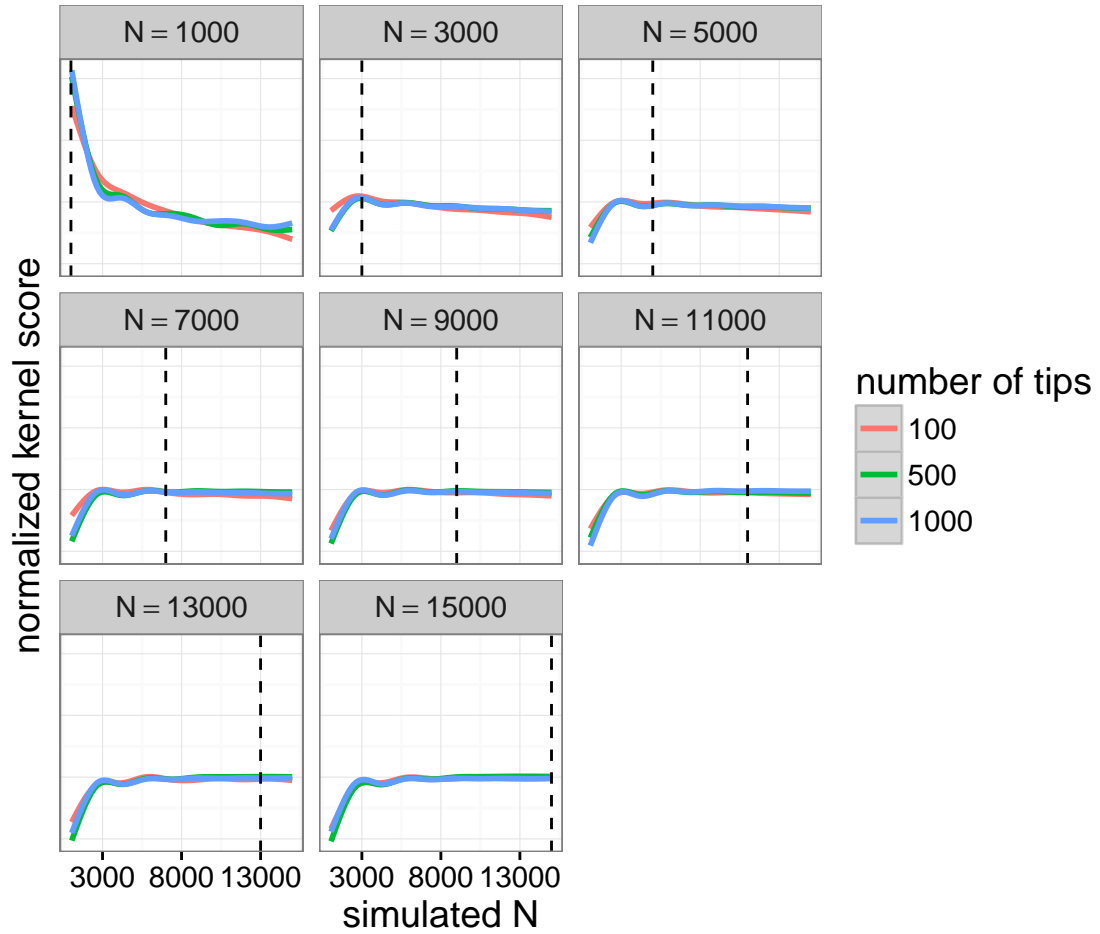


Figure A.18: Grid search kernel scores for testing trees simulated under various N values. The other BA parameters were fixed at $\alpha = 1.0$, $I = 1000$, and $m = 2$.

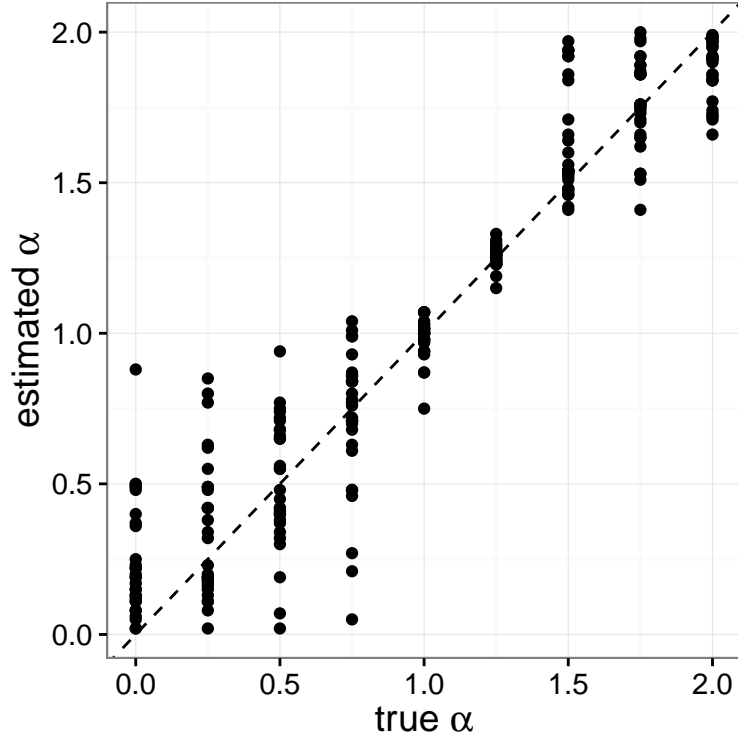


Figure A.19: Point estimates of preferential attachment power α of Barabási-Albert network model, obtained on simulated trees with kernel-score-based grid search. Test trees were simulated according to several values of α (x-axis) with other model parameters fixed at $m = 2$, $N = 5000$, and $I = 1000$. The test trees were compared to trees simulated along a narrowly spaced grid of α values using the tree kernel, with the same values of the other parameters. The grid value with the highest median kernel score was taken as a point estimate for α (y-axis).

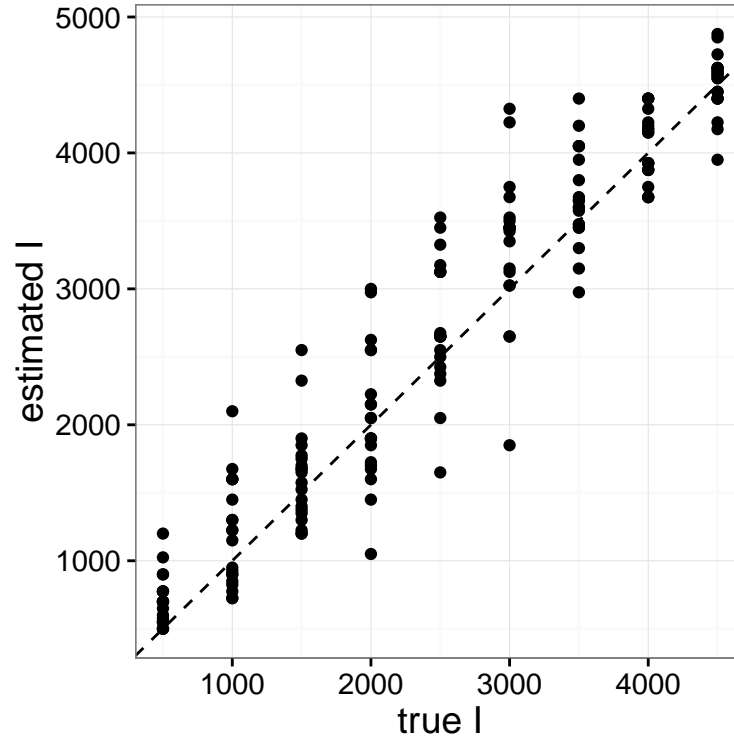


Figure A.20: Point estimates of prevalence at time of sampling I of Barabási-Albert network model, obtained on simulated trees with kernel-score-based grid search. Test trees were simulated according to several values of I (x -axis) with other model parameters fixed at $\alpha = 1$, $m = 2$, and $N = 5000$. The test trees were compared to trees simulated along a narrowly spaced grid of I values using the tree kernel, with the same values of the other parameters. The grid value with the highest median kernel score was taken as a point estimate for I (y -axis).

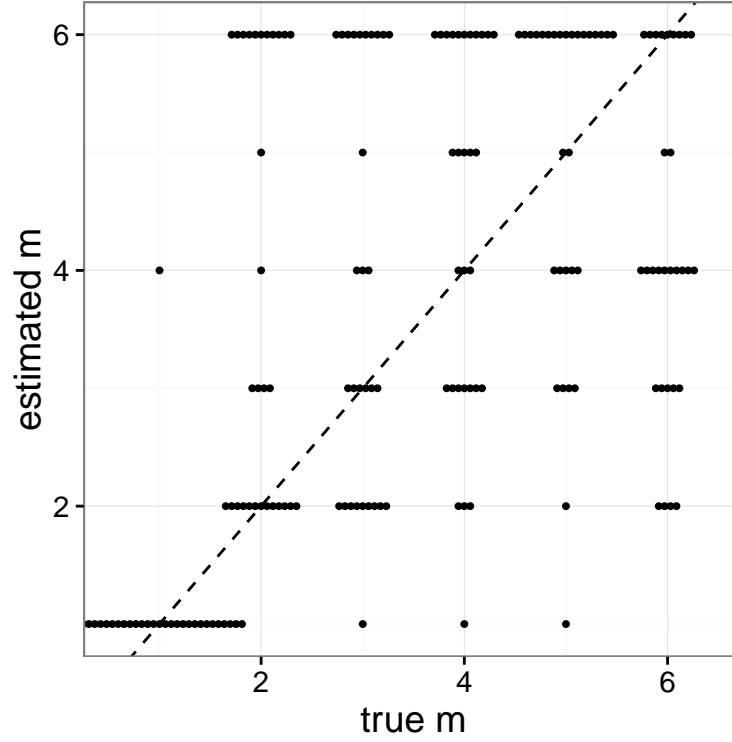


Figure A.21: Point estimates of number of edges per vertex m of Barabási-Albert network model, obtained on simulated trees with kernel-score-based grid search. Test trees were simulated according to several values of m (x -axis) with other model parameters fixed at $\alpha = 1$, $I = 1000$, and $N = 5000$. The test trees were compared to trees simulated along a narrowly spaced grid of m values using the tree kernel, with the same values of the other parameters. The grid value with the highest median kernel score was taken as a point estimate for m (y -axis).

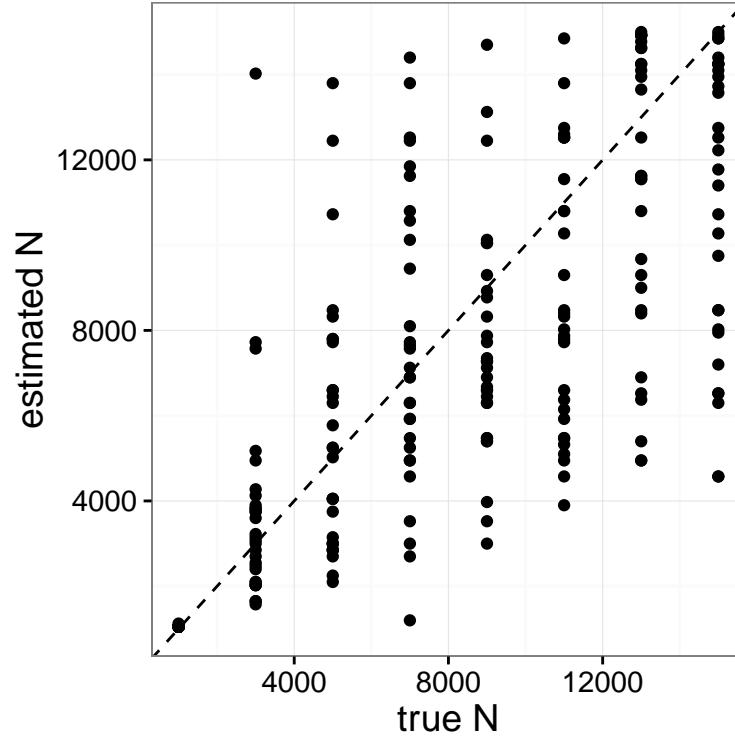


Figure A.22: Point estimates of number of edges per vertex N of Barabási-Albert network model, obtained on simulated trees with kernel-score-based grid search. Test trees were simulated according to several values of N (x -axis) with other model parameters fixed at $\alpha = 1$, $m = 2$, and $I = 1000$. The test trees were compared to trees simulated along a narrowly spaced grid of N values using the tree kernel, with the same values of the other parameters. The grid value with the highest median kernel score was taken as a point estimate for m (y -axis).

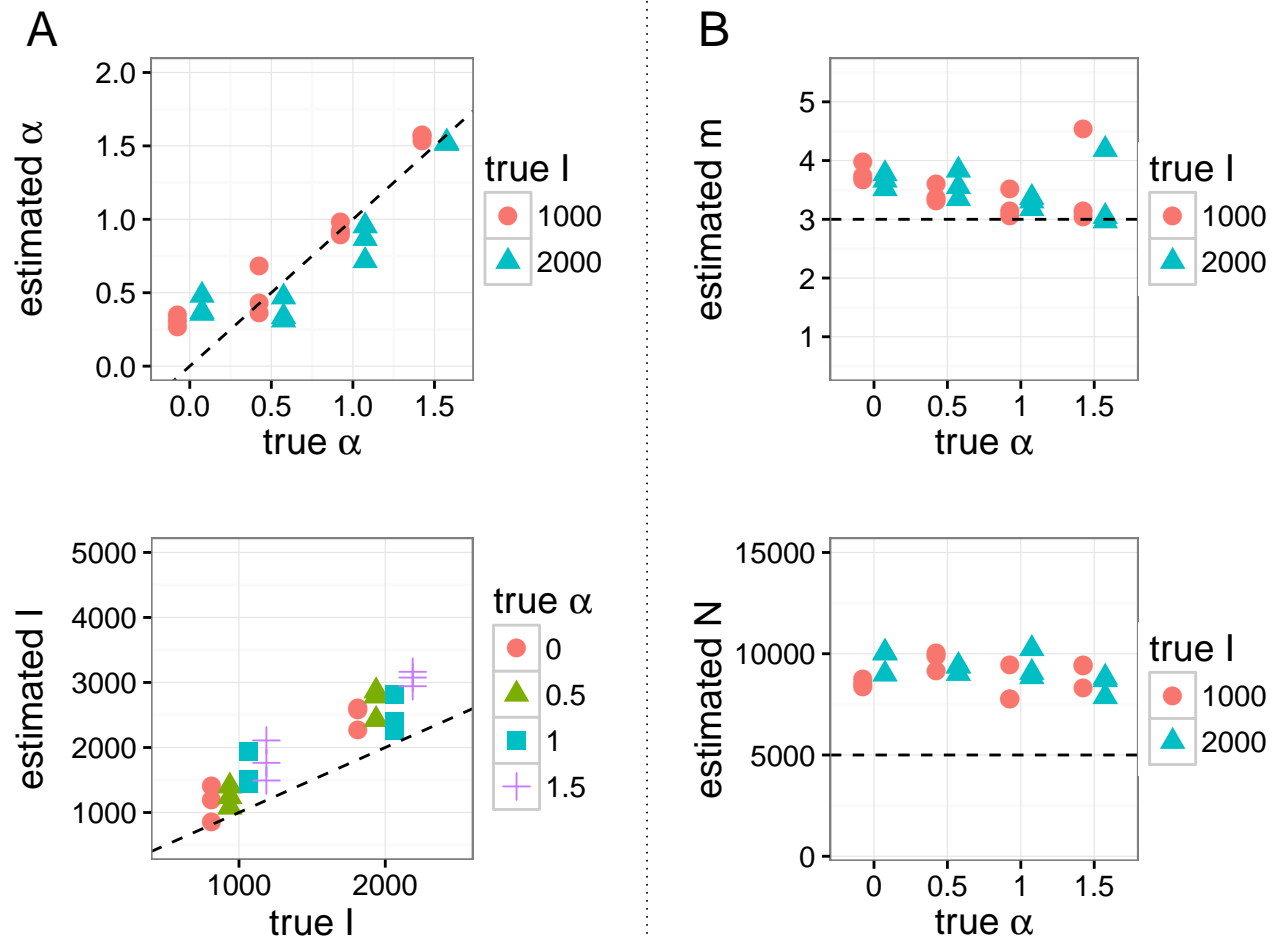


Figure A.23: Maximum *a posteriori* point estimates for BA model parameters obtained by running *netabc* on simulated data, for simulations with $m = 3$. Dashed lines indicate true values. (A) Estimates of α and I which were varied in these simulations against known values. (B) Estimates of m and N which were held fixed in these simulations at the values $m = 3$ and $N = 5000$.

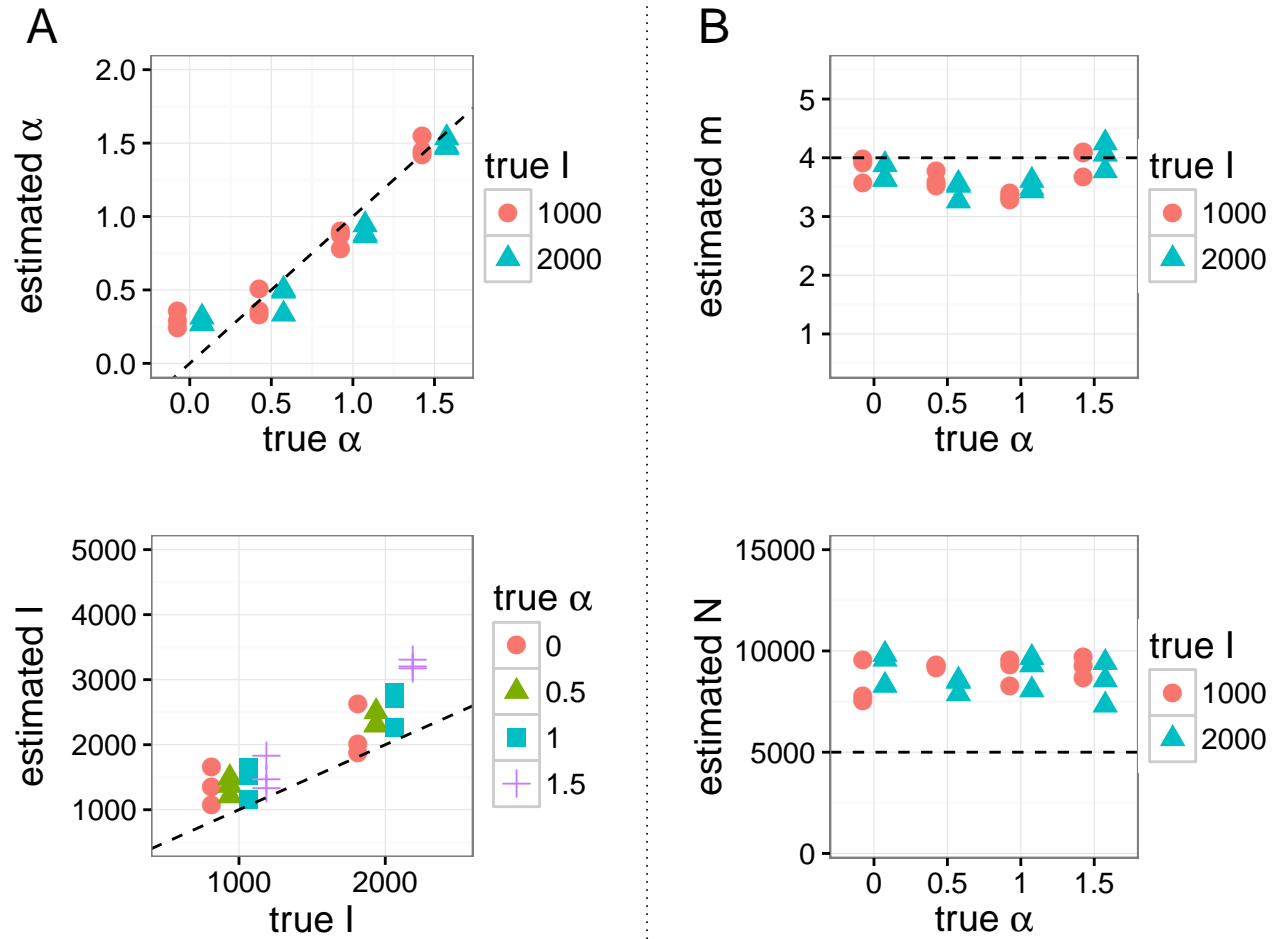


Figure A.24: Maximum *a posteriori* point estimates for BA model parameters obtained by running *netabc* on simulated data, for simulations with $m = 4$. Dashed lines indicate true values. (A) Estimates of α and I which were varied in these simulations against known values. (B) Estimates of m and N which were held fixed in these simulations at the values $m = 4$ and $N = 5000$.

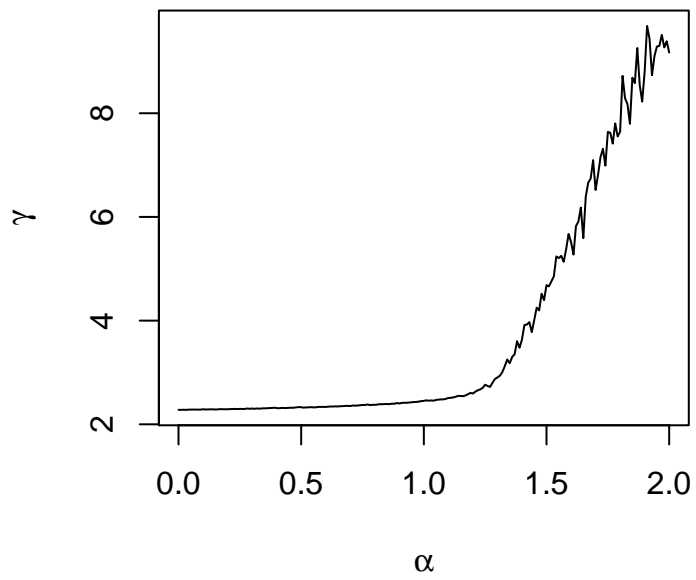


Figure A.25: Relationship between preferential attachment power parameter α and power law exponent γ for networks simulated under the BA network model with $N = 5000$ and $m = 2$.

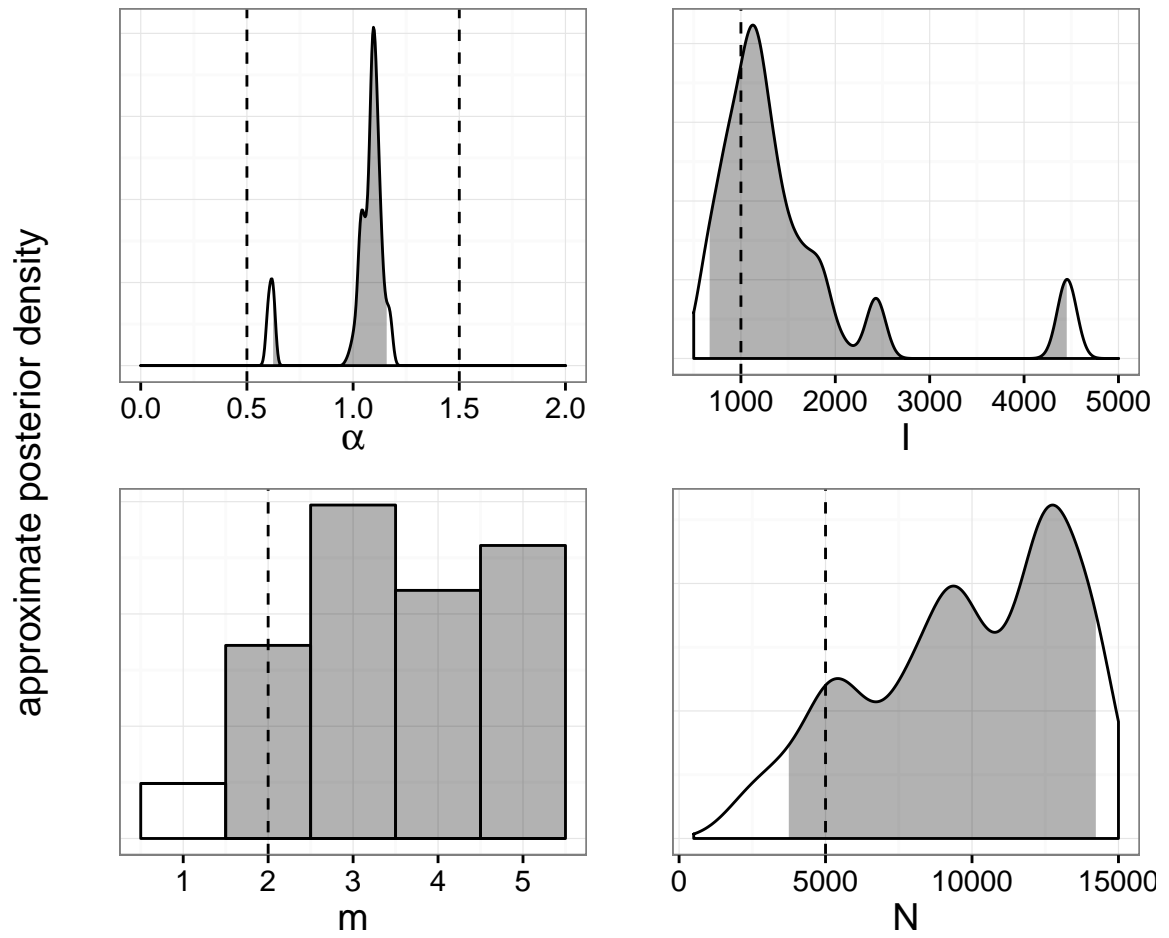


Figure A.26: Approximate marginal posterior distributions of Barabási-Albert model parameters obtained using kernel-assisted ABC for a network with heterogeneous node behaviour. Half of the nodes were attached with $\alpha = 0.5$, and the other half with $\alpha = 1.5$ (vertical dashed lines, top left). Other parameter values were $m = 2$, $I = 1000$, and $N = 5000$ (vertical dashed lines, other than top left). Shaded areas indicate 95% highest posterior density intervals.

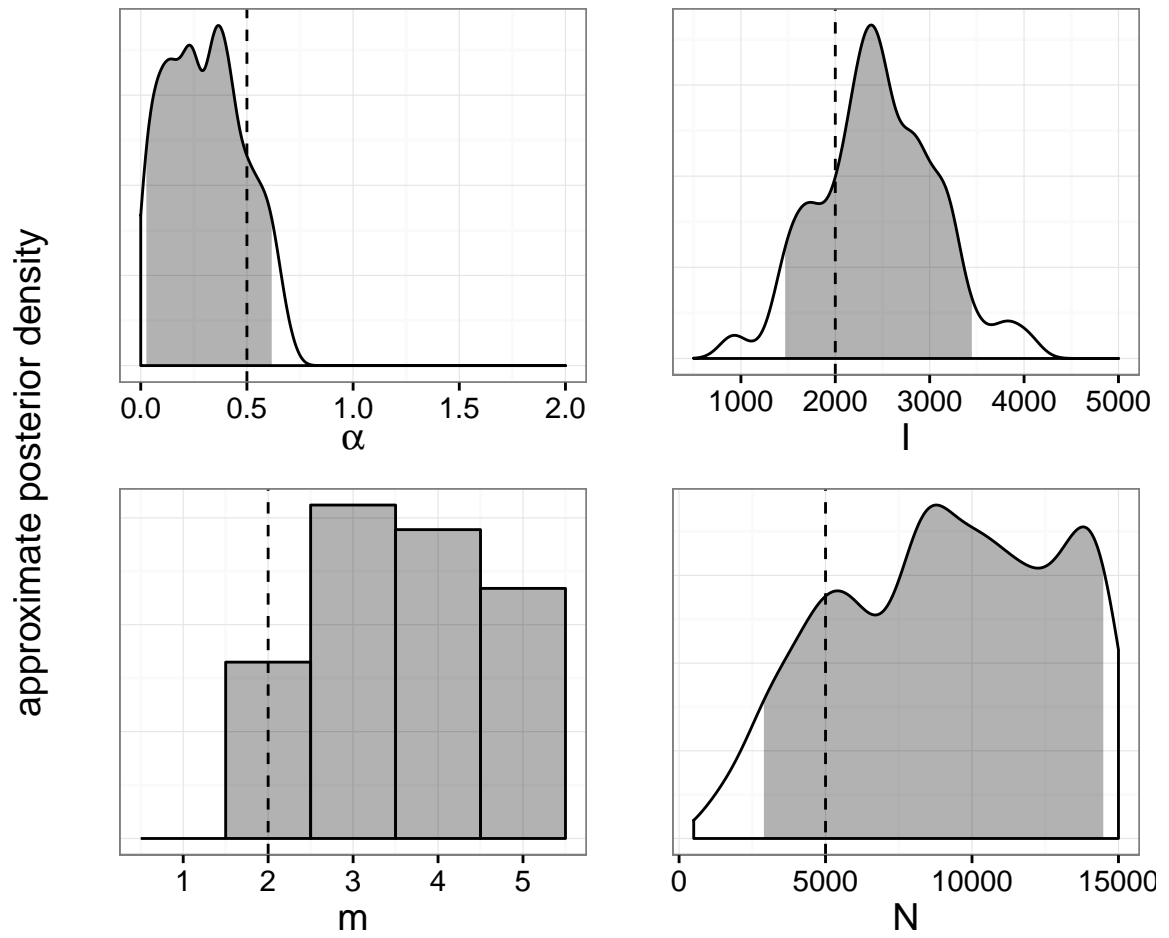


Figure A.27: Approximate marginal posterior distributions of Barabási-Albert model parameters obtained using kernel-assisted ABC for a network with peer-driven sampling. An epidemic was simulated in the usual fashion, but rather than being sampled at random, infected nodes were sampled with a probability two times higher if they had any sampled neighbours in the contact network. Vertical dashed lines indicate true parameter values, and shaded areas indicate 95% highest posterior density intervals.

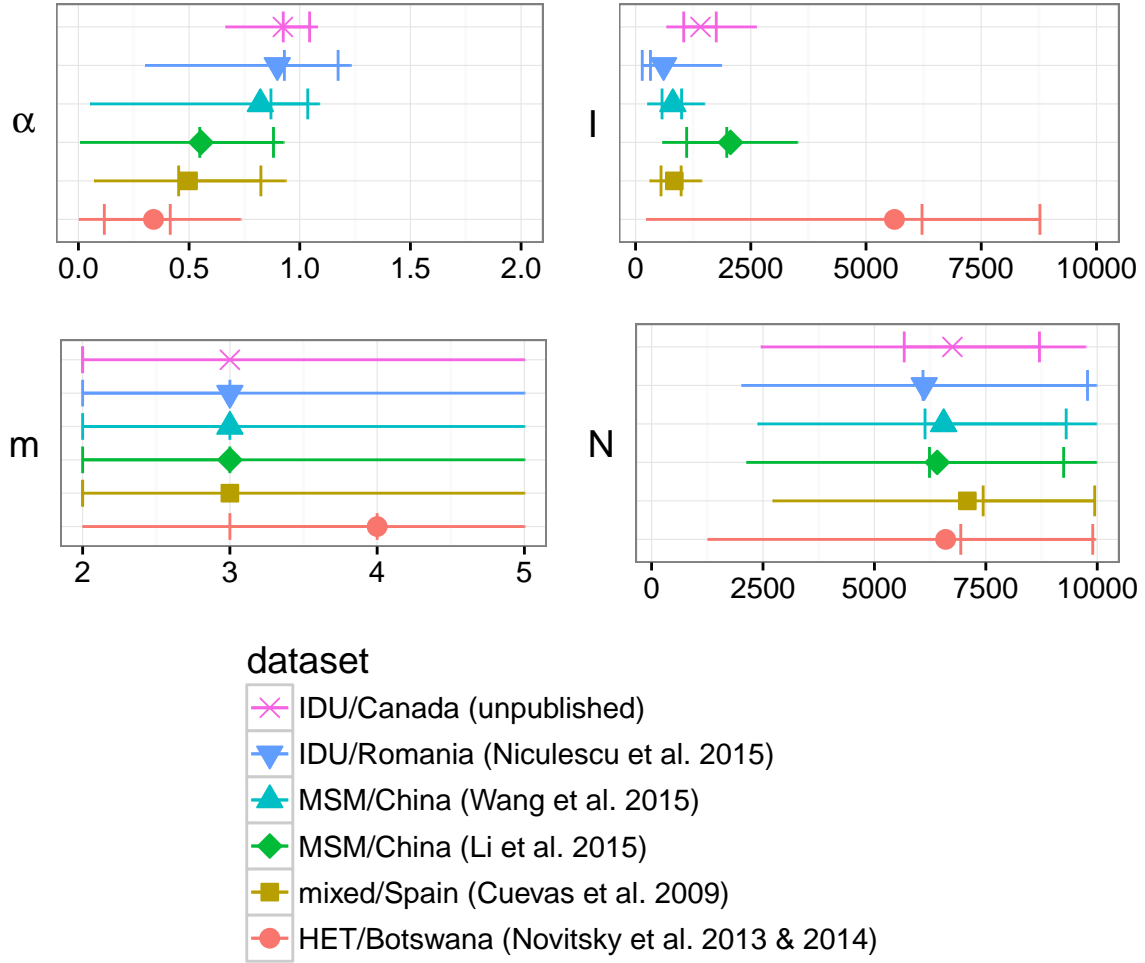


Figure A.28: Maximum *a posteriori* point estimates and 95% HPD intervals for parameters of the BA network model, fitted to five published HIV datasets with *netabc* using the prior $m \sim \text{DiscreteUniform}(2, 5)$. x -axes indicate regions of nonzero prior density. In particular, the prior on m was $\text{DiscreteUniform}(2, 5)$.

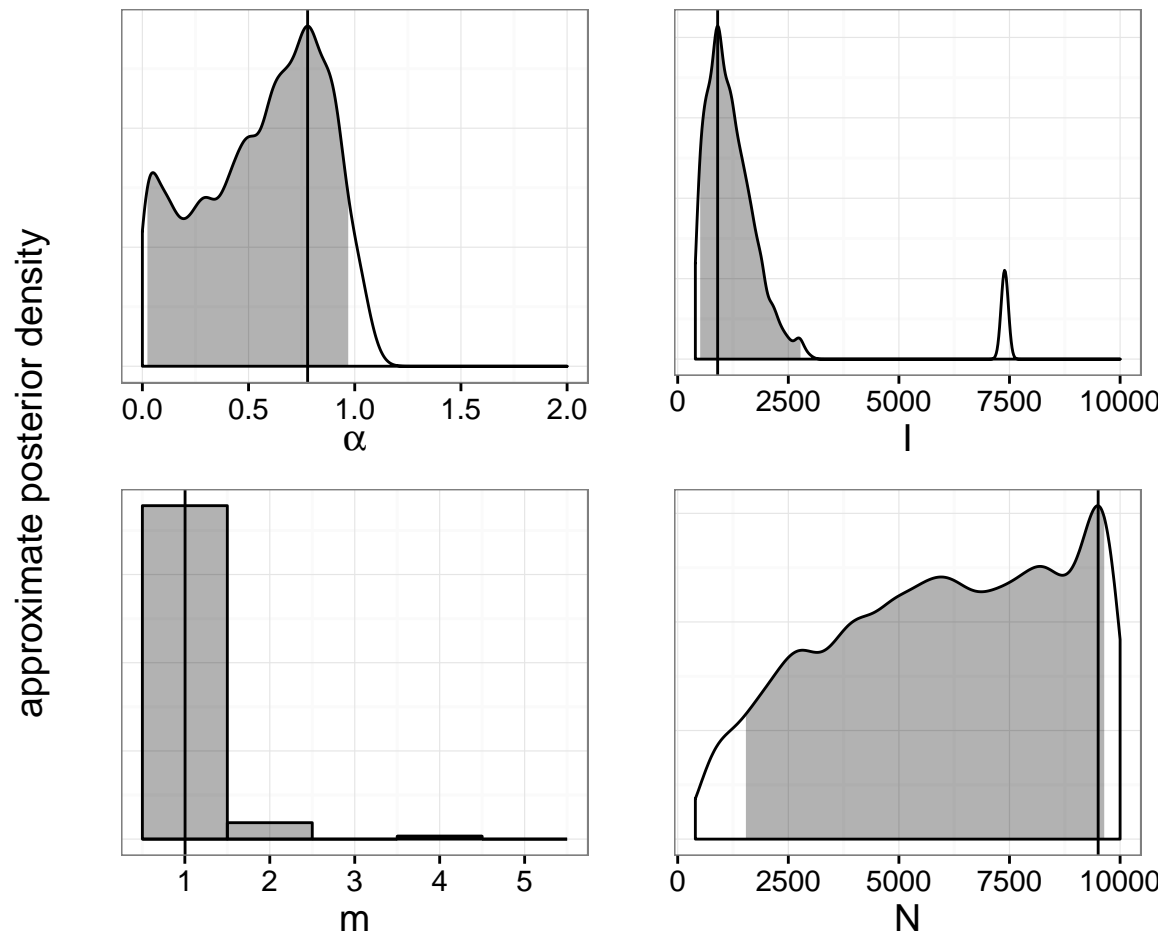


Figure A.29: Approximate marginal posterior distributions of BA model parameters for BC data. Vertical lines indicate maximum *a posteriori* estimates, and shaded areas are 95% highest posterior density intervals. *x*-axis indicates regions of nonzero prior density.

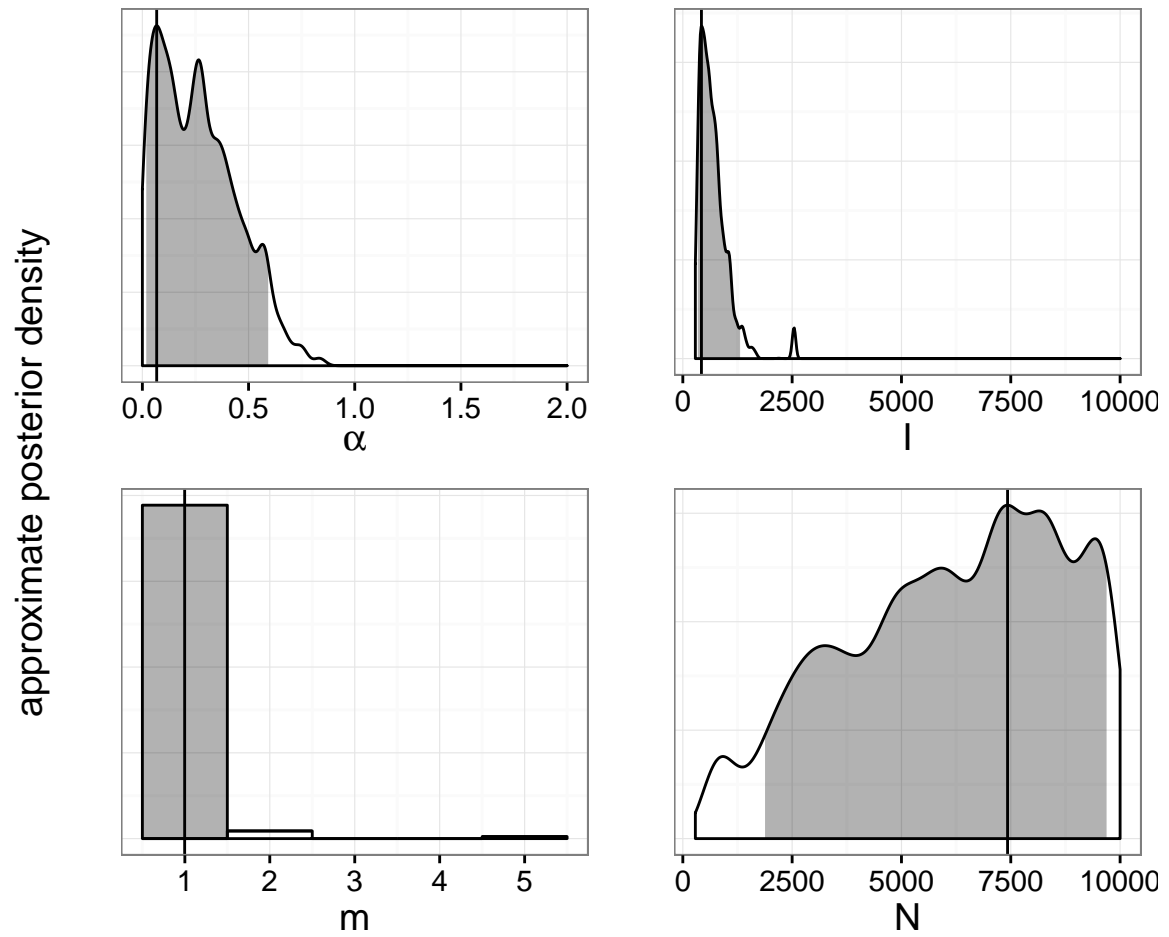


Figure A.30: Approximate marginal posterior distributions of BA model parameters for Cuevas et al. [150] data. Vertical lines indicate maximum *a posteriori* estimates, and shaded areas are 95% highest posterior density intervals. x-axis indicates regions of nonzero prior density.

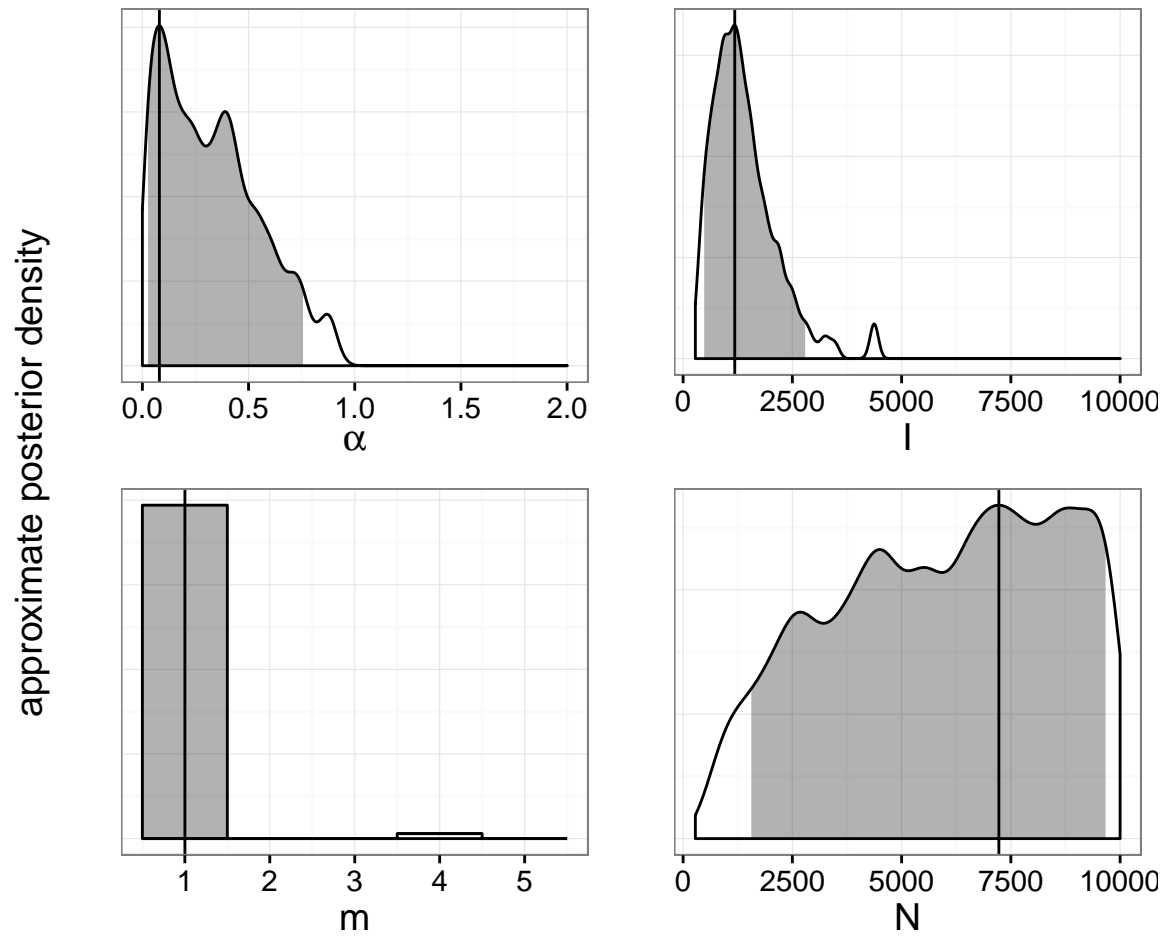


Figure A.31: Approximate marginal posterior distributions of BA model parameters for Li et al. [153] data. Vertical lines indicate maximum *a posteriori* estimates, and shaded areas are 95% highest posterior density intervals. x -axis indicates regions of nonzero prior density.

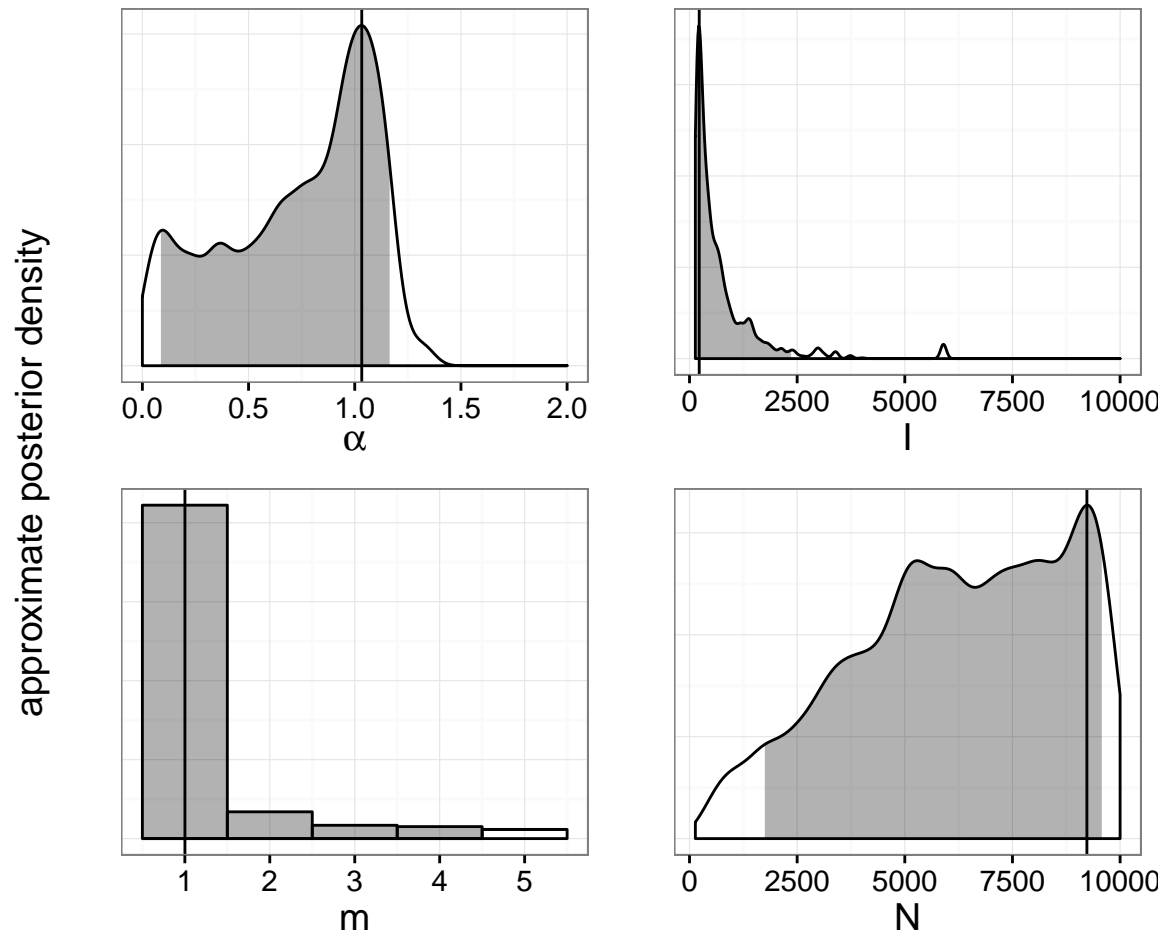


Figure A.32: Approximate marginal posterior distributions of BA model parameters for Niculescu et al. [154] data. Vertical lines indicate maximum *a posteriori* estimates, and shaded areas are 95% highest posterior density intervals. x -axis indicates regions of nonzero prior density.

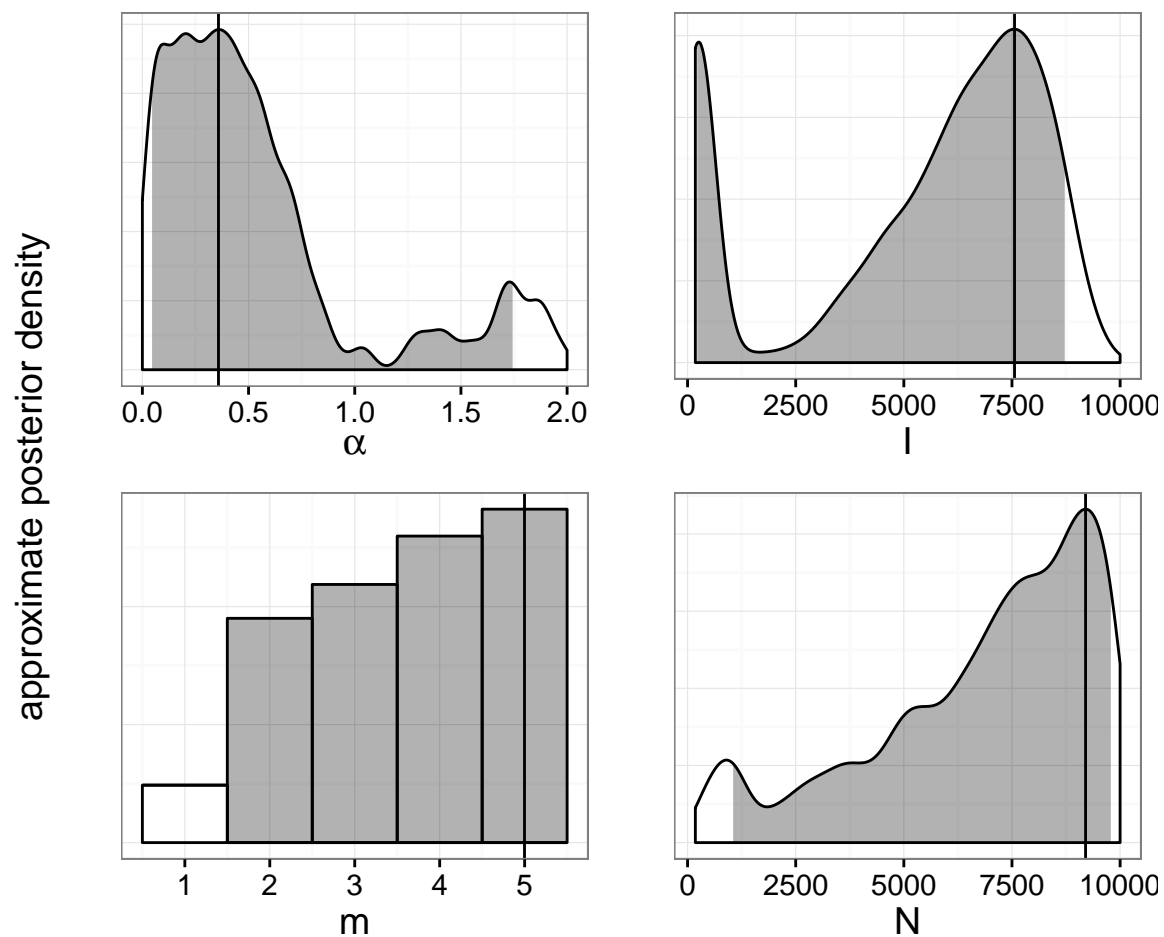


Figure A.33: Approximate marginal posterior distributions of BA model parameters for Novitsky et al. [151] and Novitsky et al. [152] data. Vertical lines indicate maximum *a posteriori* estimates, and shaded areas are 95% highest posterior density intervals. *x*-axis indicates regions of nonzero prior density.

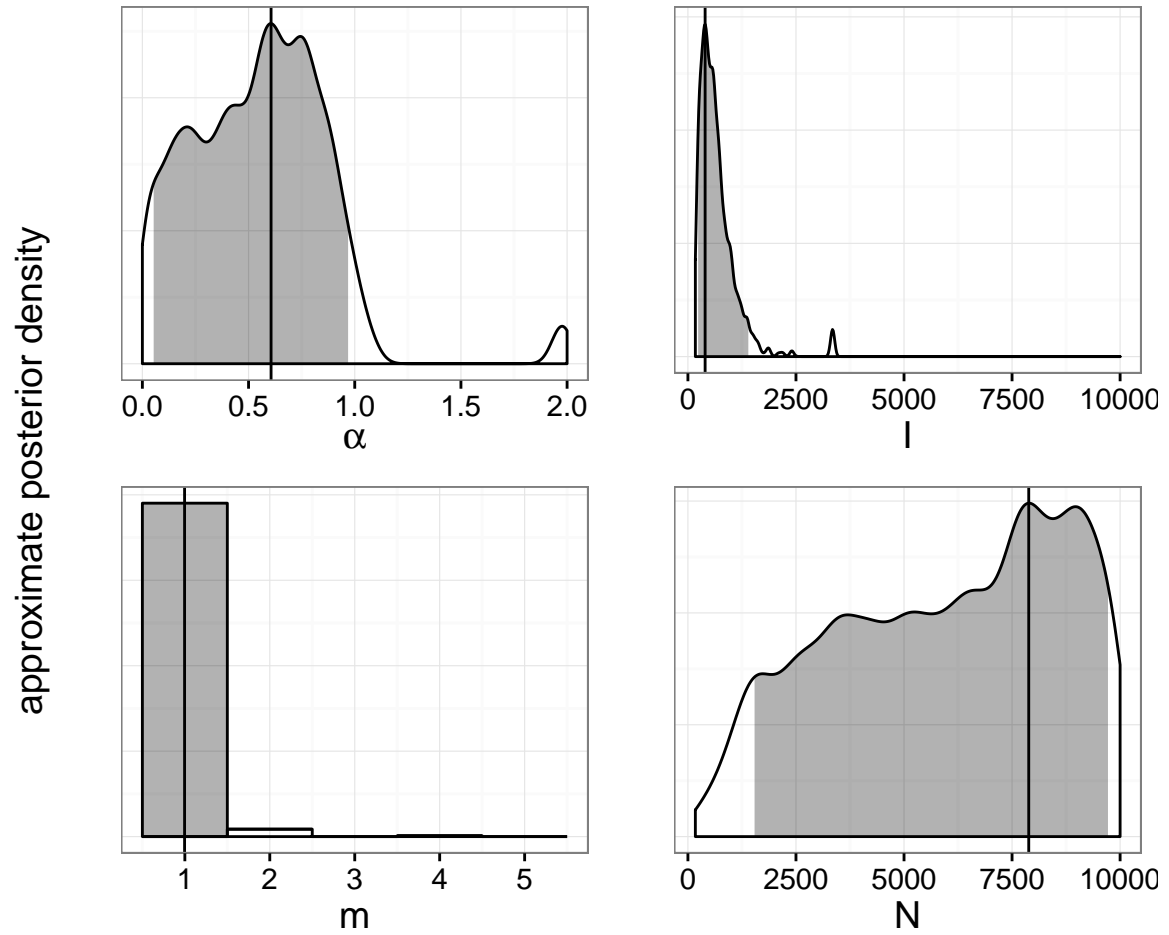


Figure A.34: Approximate marginal posterior distributions of BA model parameters for Wang et al. [30] data. Vertical lines indicate maximum *a posteriori* estimates, and shaded areas are 95% highest posterior density intervals. *x*-axis indicates regions of nonzero prior density.

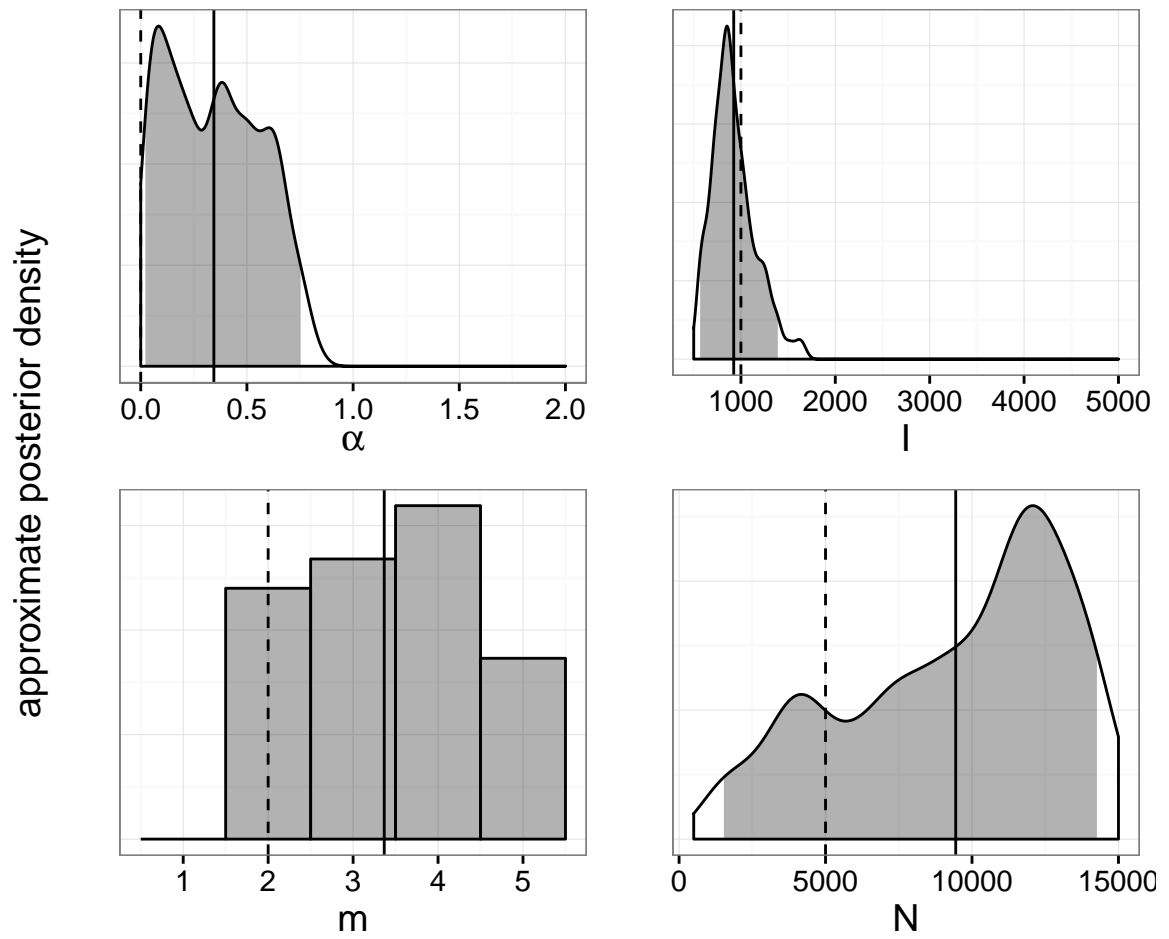


Figure A.35: Approximate marginal posterior distributions of BA model parameters obtained by applying *netabc* to a simulated transmission tree with BA parameter values $\alpha = 0.0$, $I = 1000$, $m = 2$, and $N = 5000$. Vertical dashed lines indicate true values. Shaded areas are 95% highest posterior density intervals. x -axes indicate regions of nonzero prior density.

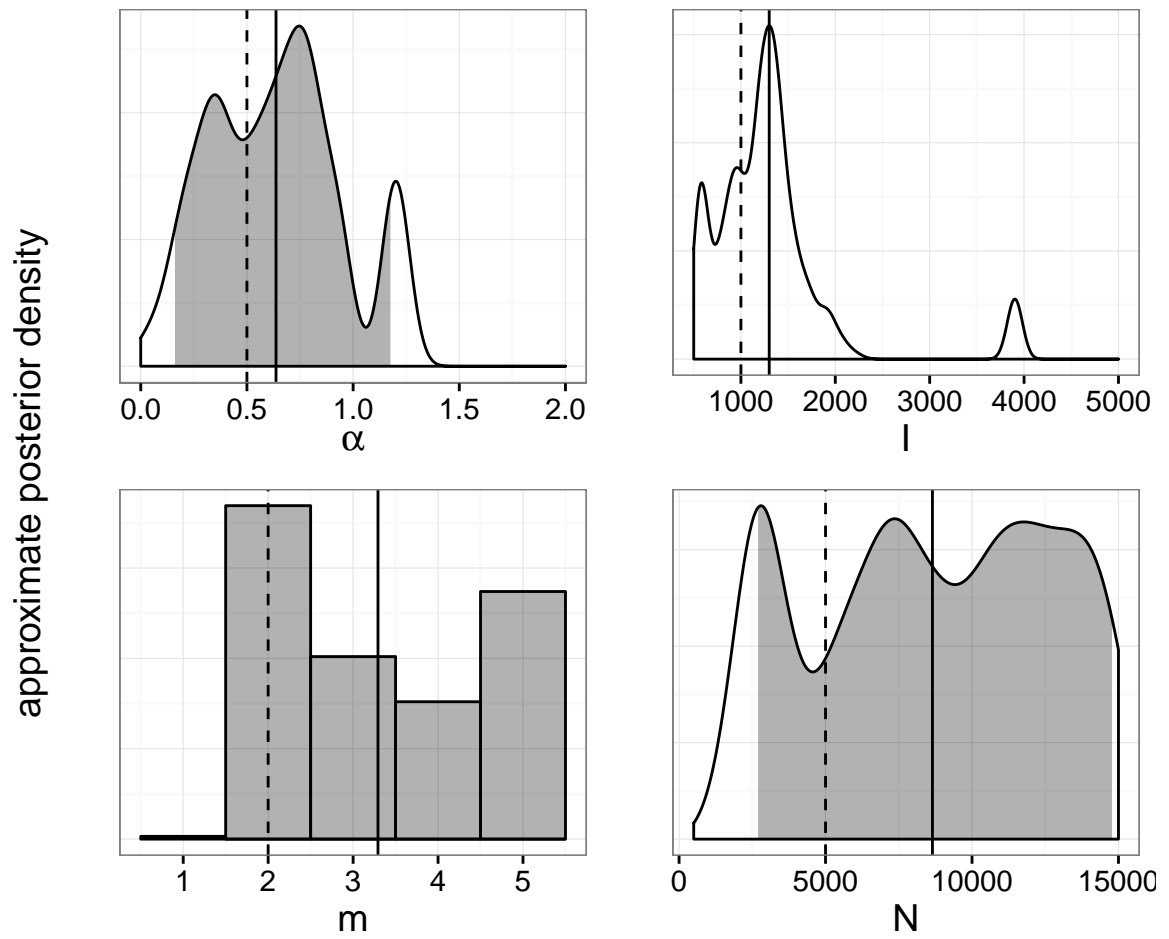


Figure A.36: Approximate marginal posterior distributions of BA model parameters obtained by applying *netabc* to a simulated transmission tree with BA parameter values $\alpha = 0.5$, $I = 1000$, $m = 2$, and $N = 5000$. Vertical dashed lines indicate true values. Shaded areas are 95% highest posterior density intervals. x -axes indicate regions of nonzero prior density.

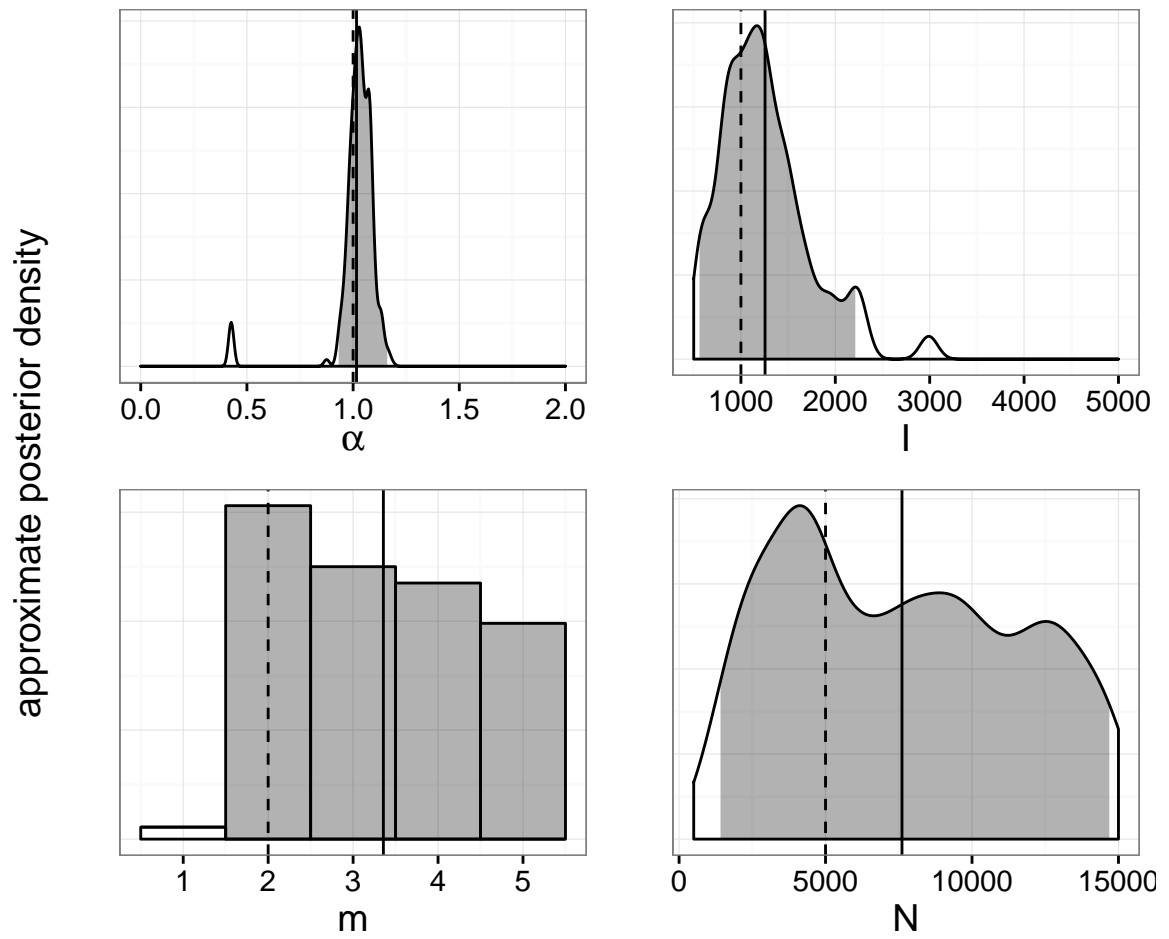


Figure A.37: Approximate marginal posterior distributions of BA model parameters obtained by applying *netabc* to a simulated transmission tree with BA parameter values $\alpha = 1.0$, $I = 1000$, $m = 2$, and $N = 5000$. Vertical dashed lines indicate true values. Shaded areas are 95% highest posterior density intervals. x -axes indicate regions of nonzero prior density.

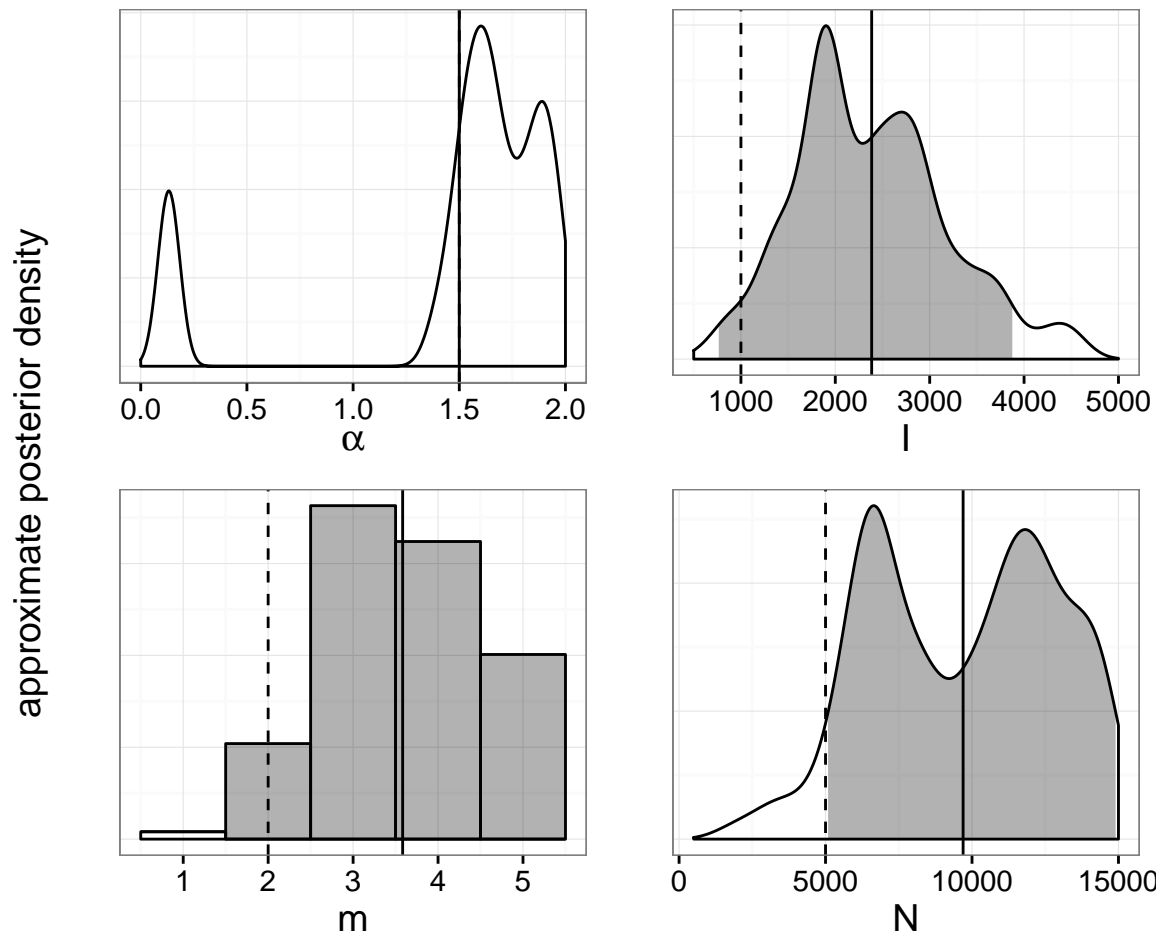


Figure A.38: Approximate marginal posterior distributions of BA model parameters obtained by applying *netabc* to a simulated transmission tree with BA parameter values $\alpha = 1.5$, $I = 1000$, $m = 2$, and $N = 5000$. Vertical dashed lines indicate true values. Shaded areas are 95% highest posterior density intervals. x -axes indicate regions of nonzero prior density.

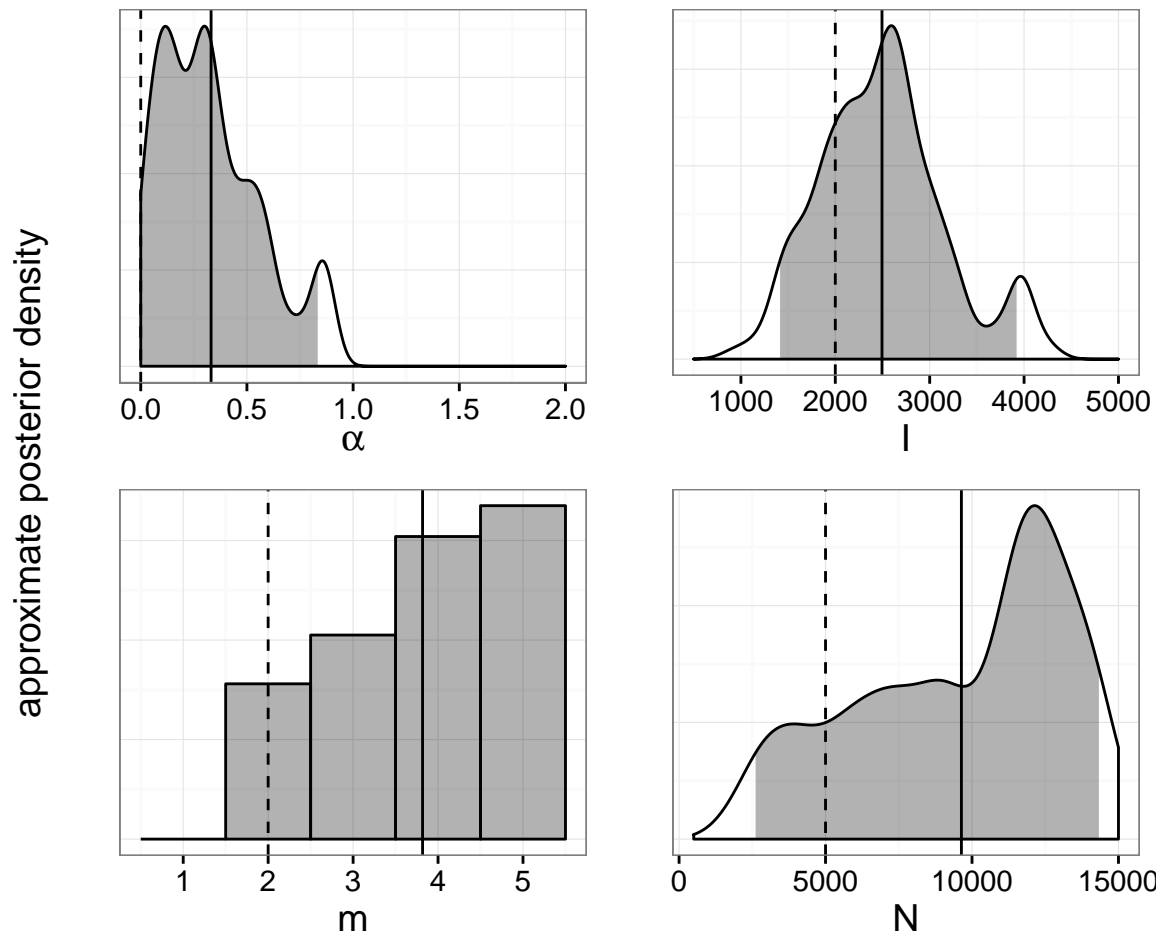


Figure A.39: Approximate marginal posterior distributions of BA model parameters obtained by applying *netabc* to a simulated transmission tree with BA parameter values $\alpha = 0.0$, $I = 2000$, $m = 2$, and $N = 5000$. Vertical dashed lines indicate true values. Shaded areas are 95% highest posterior density intervals. x -axes indicate regions of nonzero prior density.

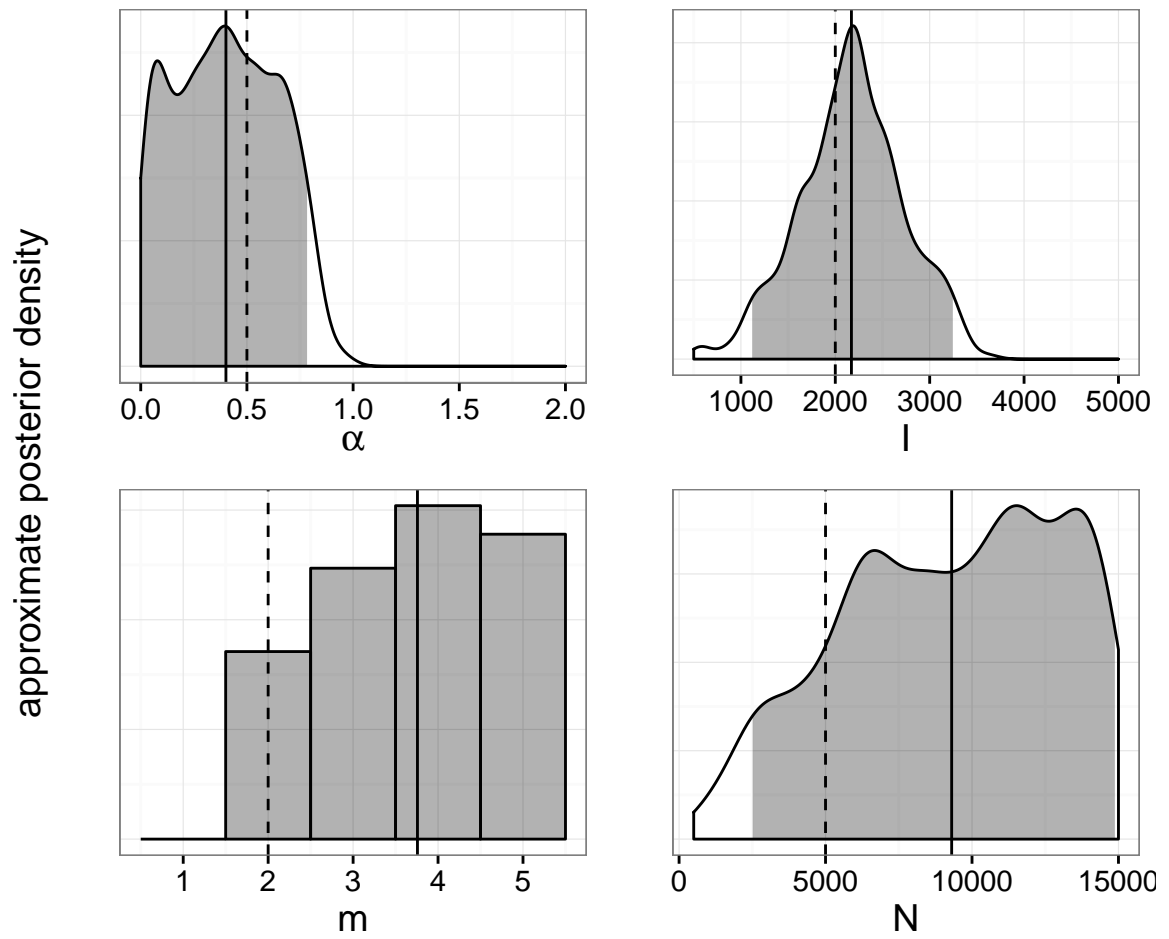


Figure A.40: Approximate marginal posterior distributions of BA model parameters obtained by applying *netabc* to a simulated transmission tree with BA parameter values $\alpha = 0.5$, $I = 2000$, $m = 2$, and $N = 5000$. Vertical dashed lines indicate true values. Shaded areas are 95% highest posterior density intervals. x -axes indicate regions of nonzero prior density.

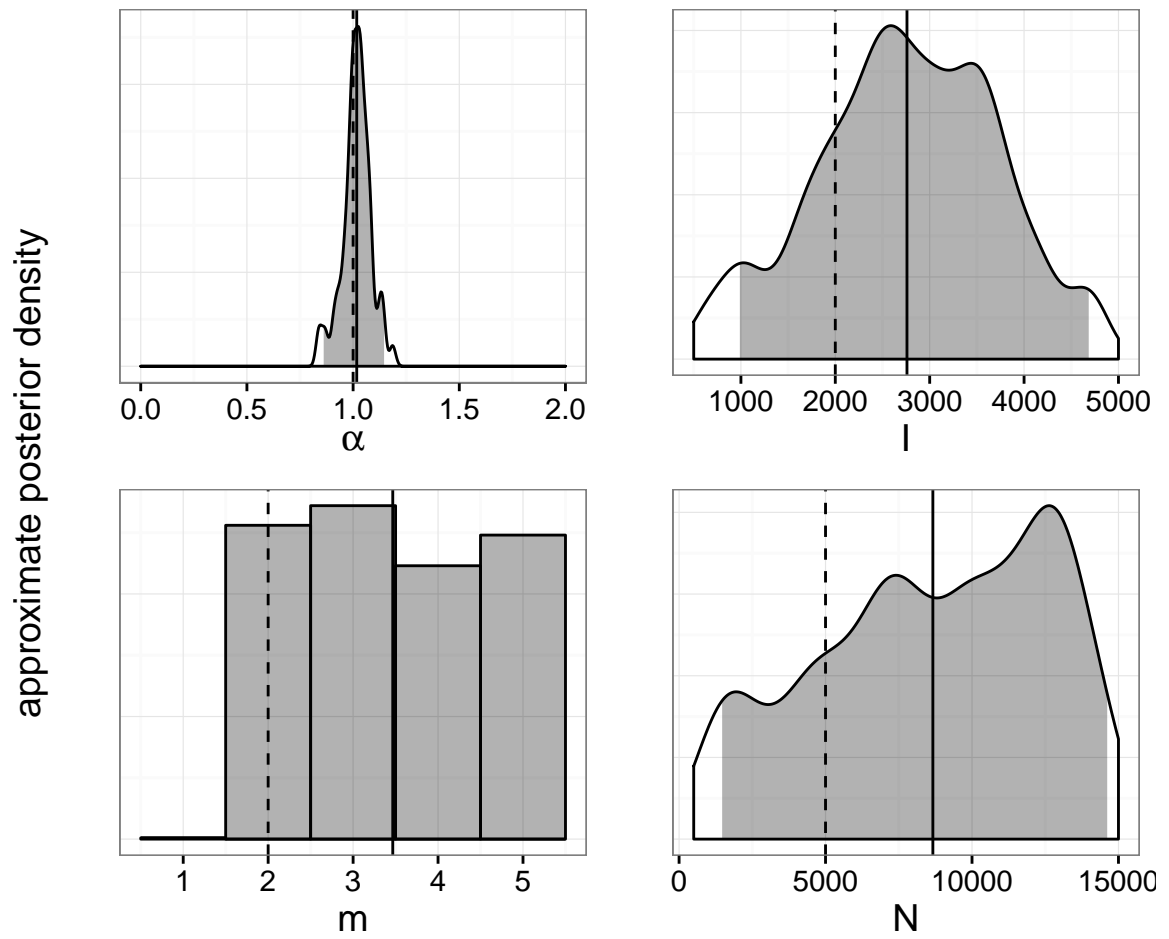


Figure A.41: Approximate marginal posterior distributions of BA model parameters obtained by applying *netabc* to a simulated transmission tree with BA parameter values $\alpha = 1.0$, $I = 2000$, $m = 2$, and $N = 5000$. Vertical dashed lines indicate true values. Shaded areas are 95% highest posterior density intervals. x -axes indicate regions of nonzero prior density.

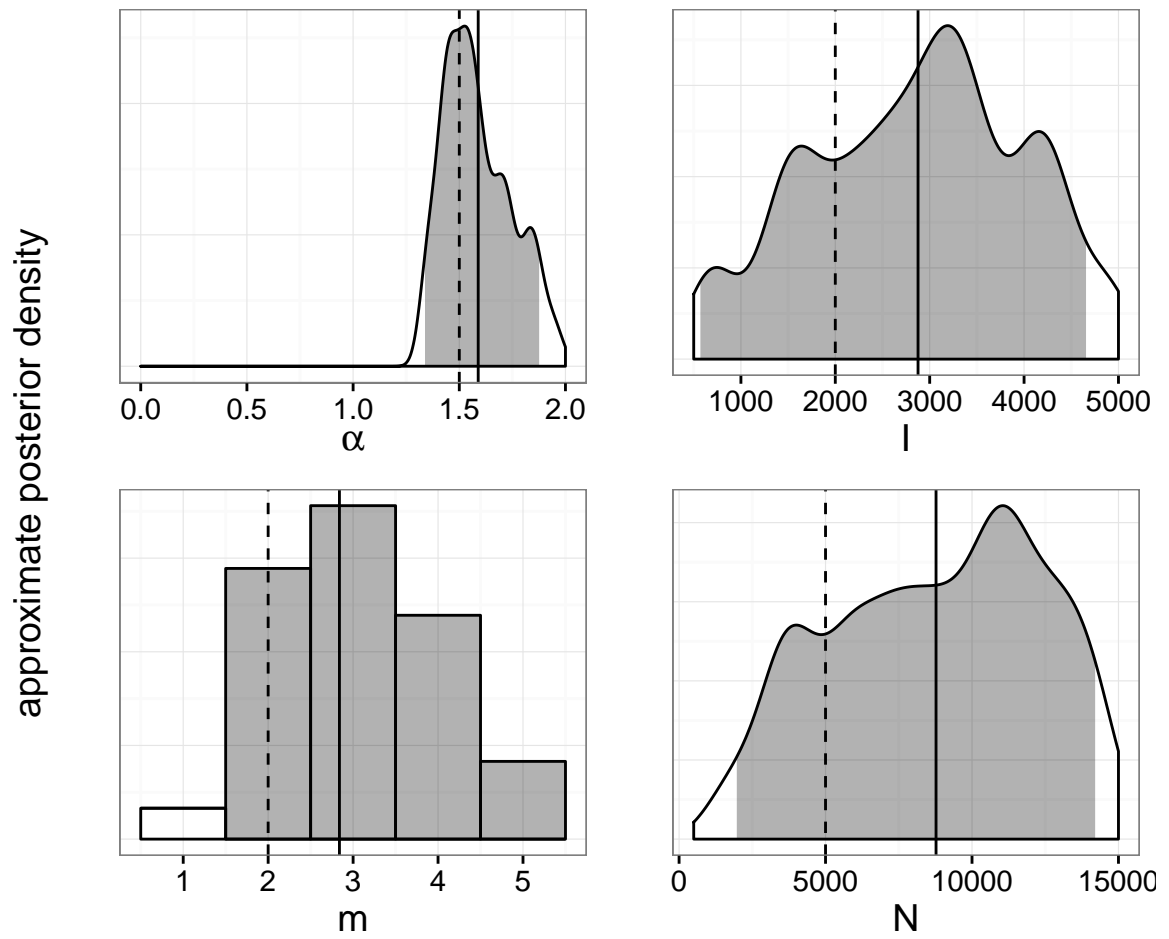


Figure A.42: Approximate marginal posterior distributions of BA model parameters obtained by applying *netabc* to a simulated transmission tree with BA parameter values $\alpha = 1.5$, $I = 2000$, $m = 2$, and $N = 5000$. Vertical dashed lines indicate true values. Shaded areas are 95% highest posterior density intervals. x -axes indicate regions of nonzero prior density.

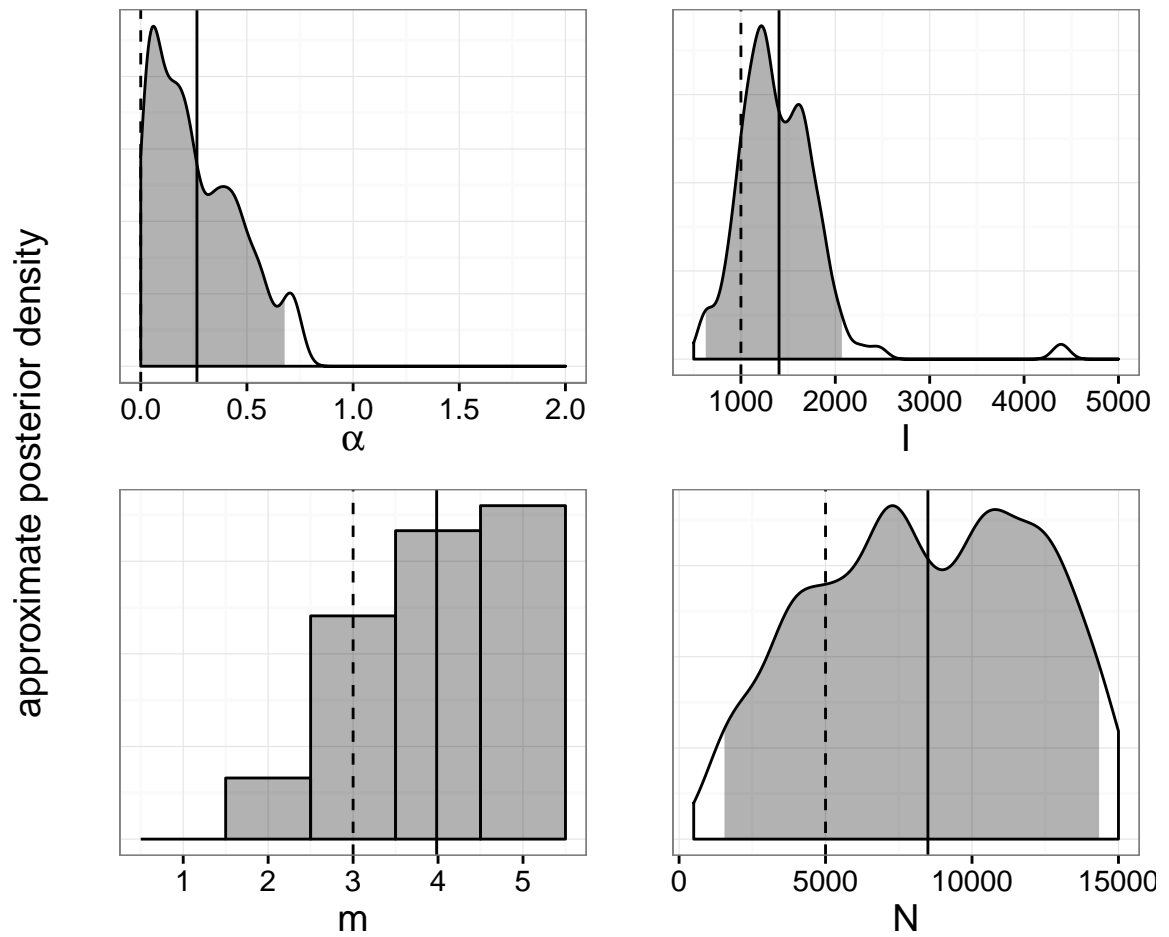


Figure A.43: Approximate marginal posterior distributions of BA model parameters obtained by applying *netabc* to a simulated transmission tree with BA parameter values $\alpha = 0.0$, $I = 1000$, $m = 3$, and $N = 5000$. Vertical dashed lines indicate true values. Shaded areas are 95% highest posterior density intervals. x -axes indicate regions of nonzero prior density.

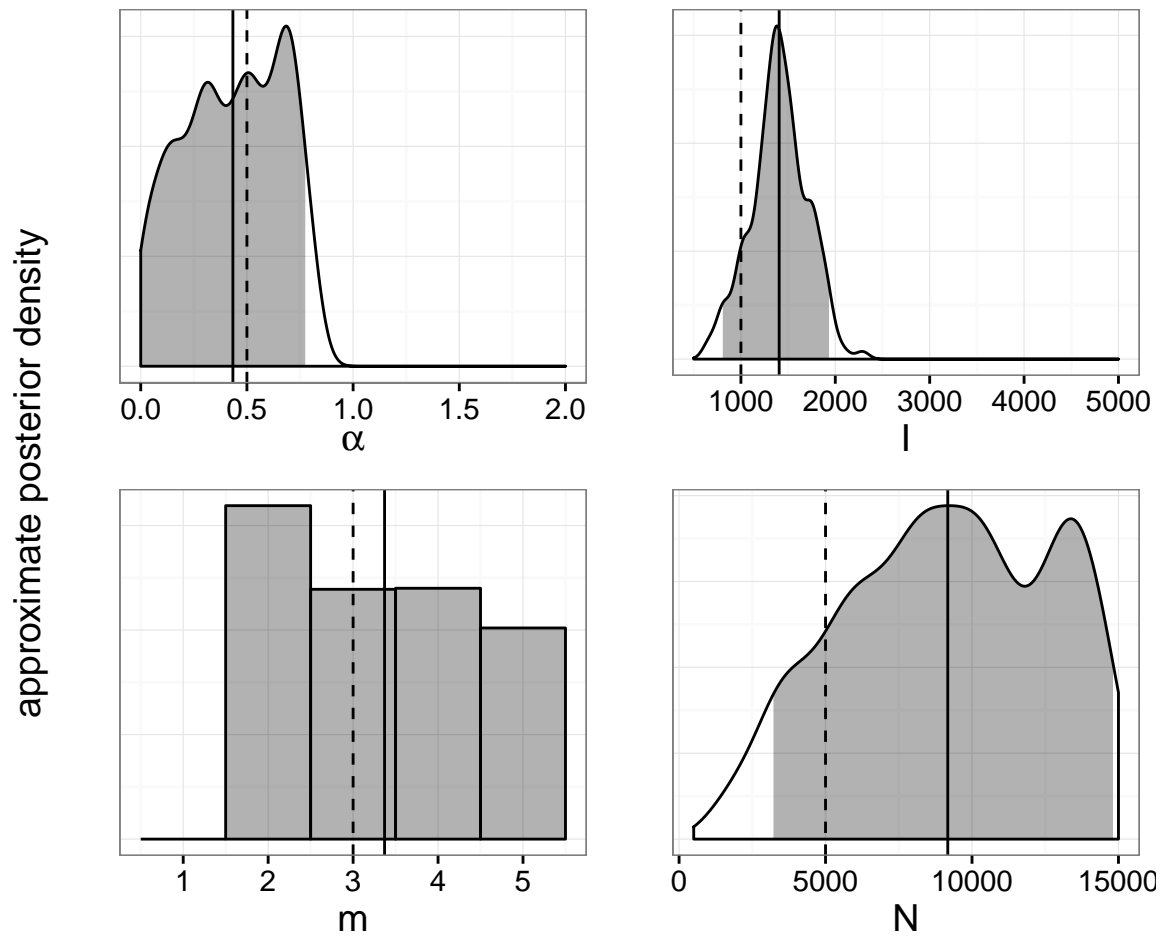


Figure A.44: Approximate marginal posterior distributions of BA model parameters obtained by applying *netabc* to a simulated transmission tree with BA parameter values $\alpha = 0.5$, $I = 1000$, $m = 3$, and $N = 5000$. Vertical dashed lines indicate true values. Shaded areas are 95% highest posterior density intervals. x -axes indicate regions of nonzero prior density.

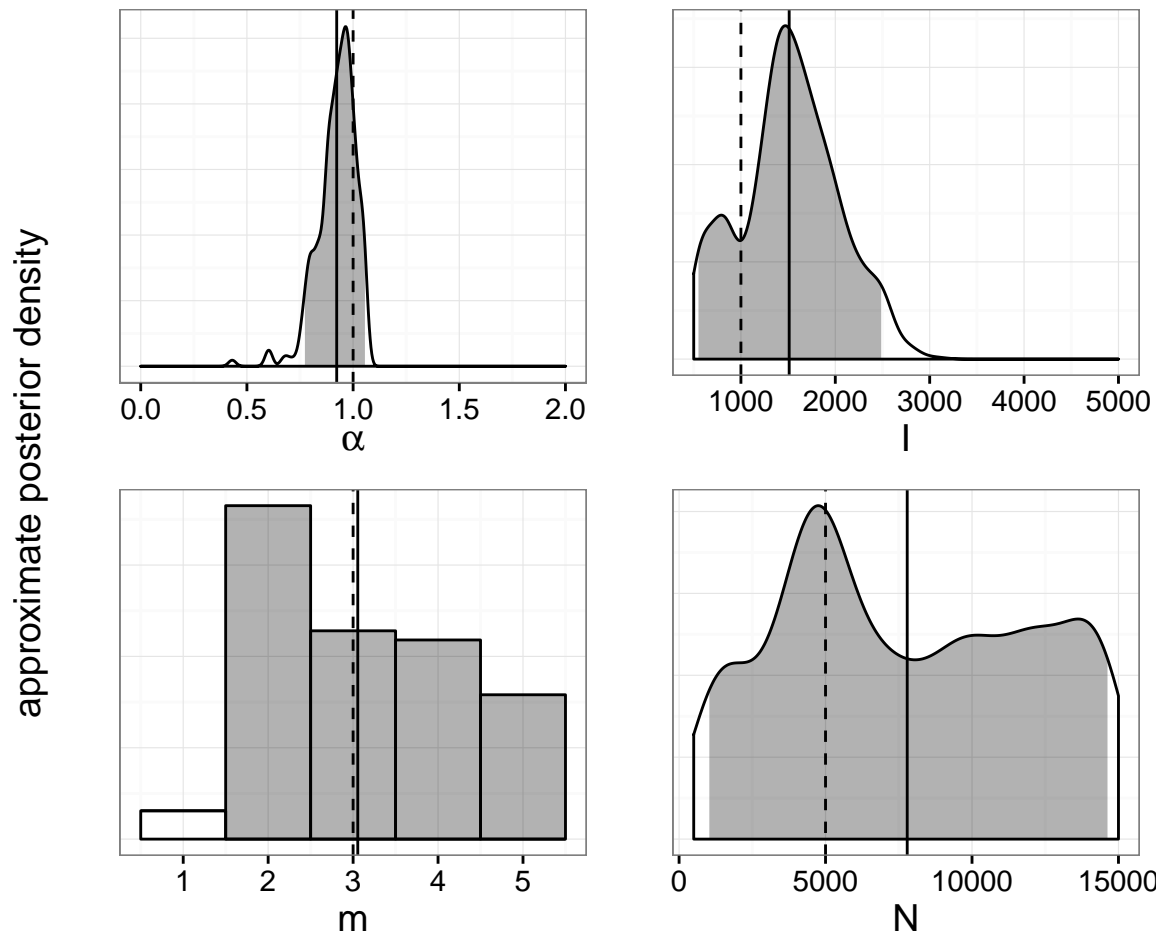


Figure A.45: Approximate marginal posterior distributions of BA model parameters obtained by applying *netabc* to a simulated transmission tree with BA parameter values $\alpha = 1.0$, $I = 1000$, $m = 3$, and $N = 5000$. Vertical dashed lines indicate true values. Shaded areas are 95% highest posterior density intervals. x -axes indicate regions of nonzero prior density.

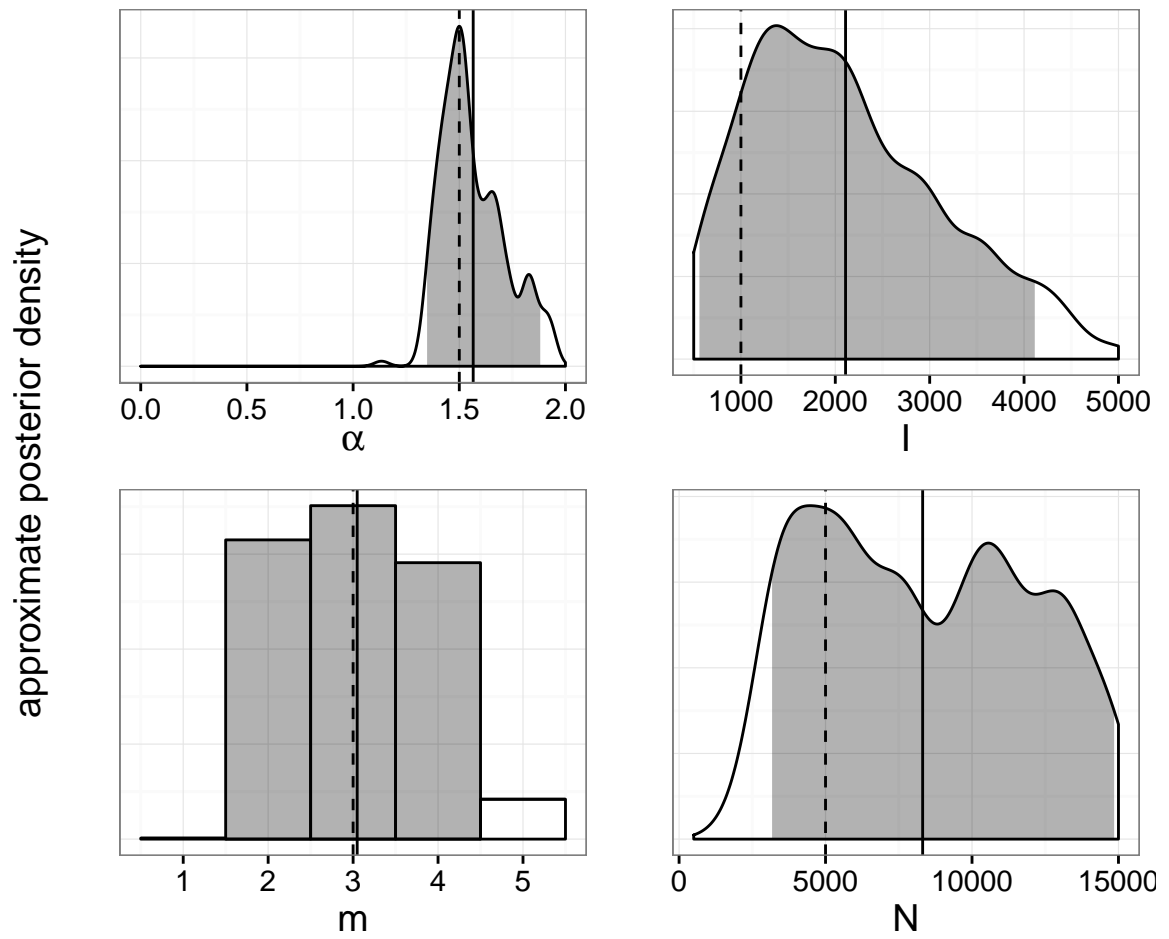


Figure A.46: Approximate marginal posterior distributions of BA model parameters obtained by applying *netabc* to a simulated transmission tree with BA parameter values $\alpha = 1.5$, $I = 1000$, $m = 3$, and $N = 5000$. Vertical dashed lines indicate true values. Shaded areas are 95% highest posterior density intervals. x -axes indicate regions of nonzero prior density.

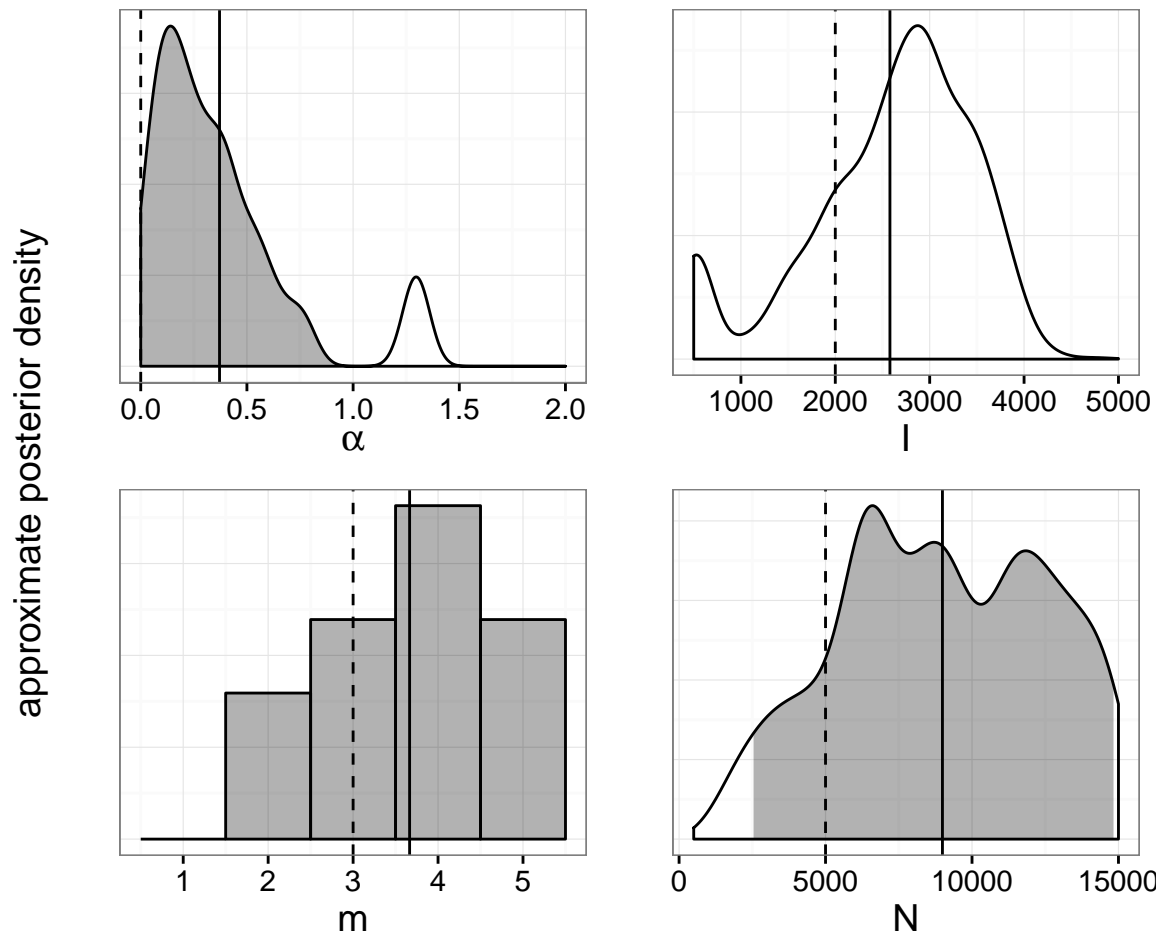


Figure A.47: Approximate marginal posterior distributions of BA model parameters obtained by applying *netabc* to a simulated transmission tree with BA parameter values $\alpha = 0.0$, $I = 2000$, $m = 3$, and $N = 5000$. Vertical dashed lines indicate true values. Shaded areas are 95% highest posterior density intervals. x -axes indicate regions of nonzero prior density.

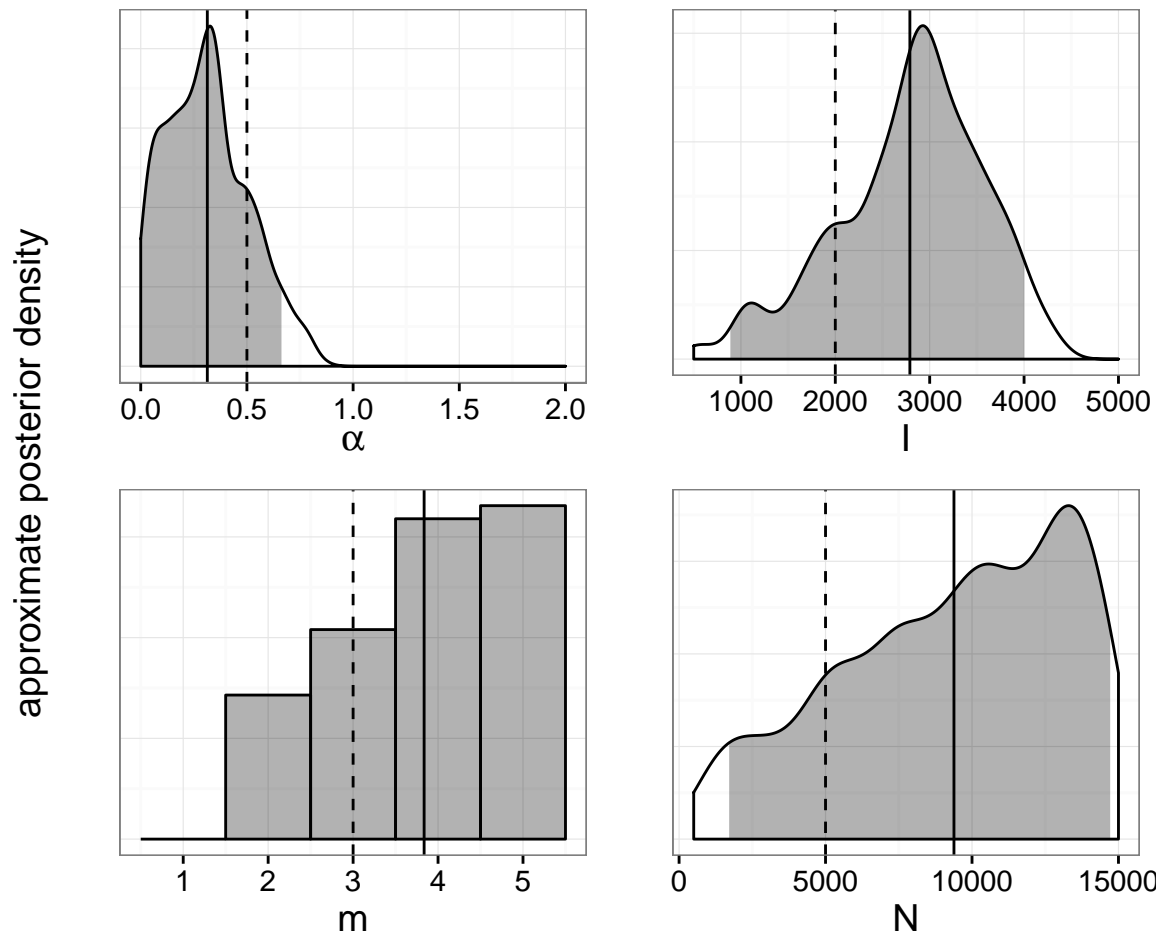


Figure A.48: Approximate marginal posterior distributions of BA model parameters obtained by applying *netabc* to a simulated transmission tree with BA parameter values $\alpha = 0.5$, $I = 2000$, $m = 3$, and $N = 5000$. Vertical dashed lines indicate true values. Shaded areas are 95% highest posterior density intervals. x -axes indicate regions of nonzero prior density.

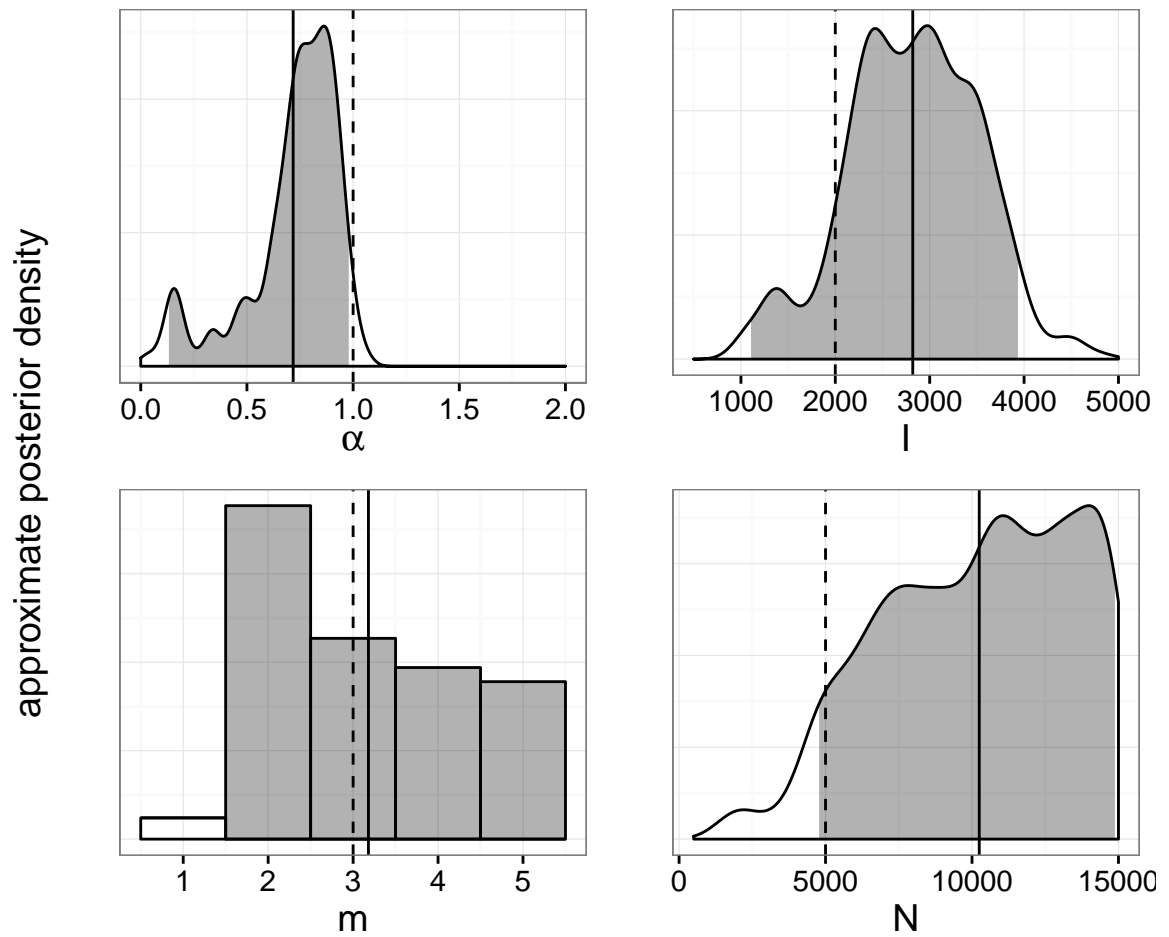


Figure A.49: Approximate marginal posterior distributions of BA model parameters obtained by applying *netabc* to a simulated transmission tree with BA parameter values $\alpha = 1.0$, $I = 2000$, $m = 3$, and $N = 5000$. Vertical dashed lines indicate true values. Shaded areas are 95% highest posterior density intervals. x -axes indicate regions of nonzero prior density.

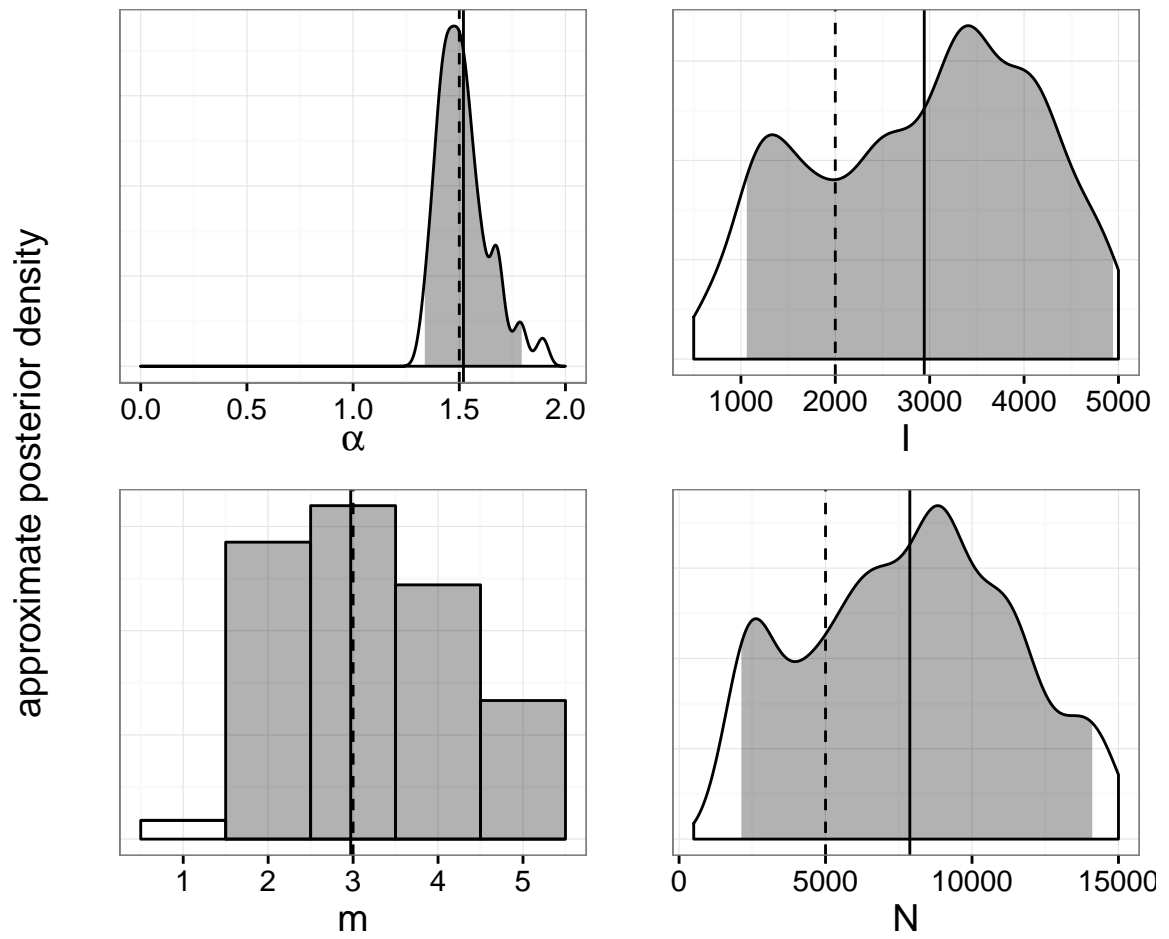


Figure A.50: Approximate marginal posterior distributions of BA model parameters obtained by applying *netabc* to a simulated transmission tree with BA parameter values $\alpha = 1.5$, $I = 2000$, $m = 3$, and $N = 5000$. Vertical dashed lines indicate true values. Shaded areas are 95% highest posterior density intervals. x -axes indicate regions of nonzero prior density.

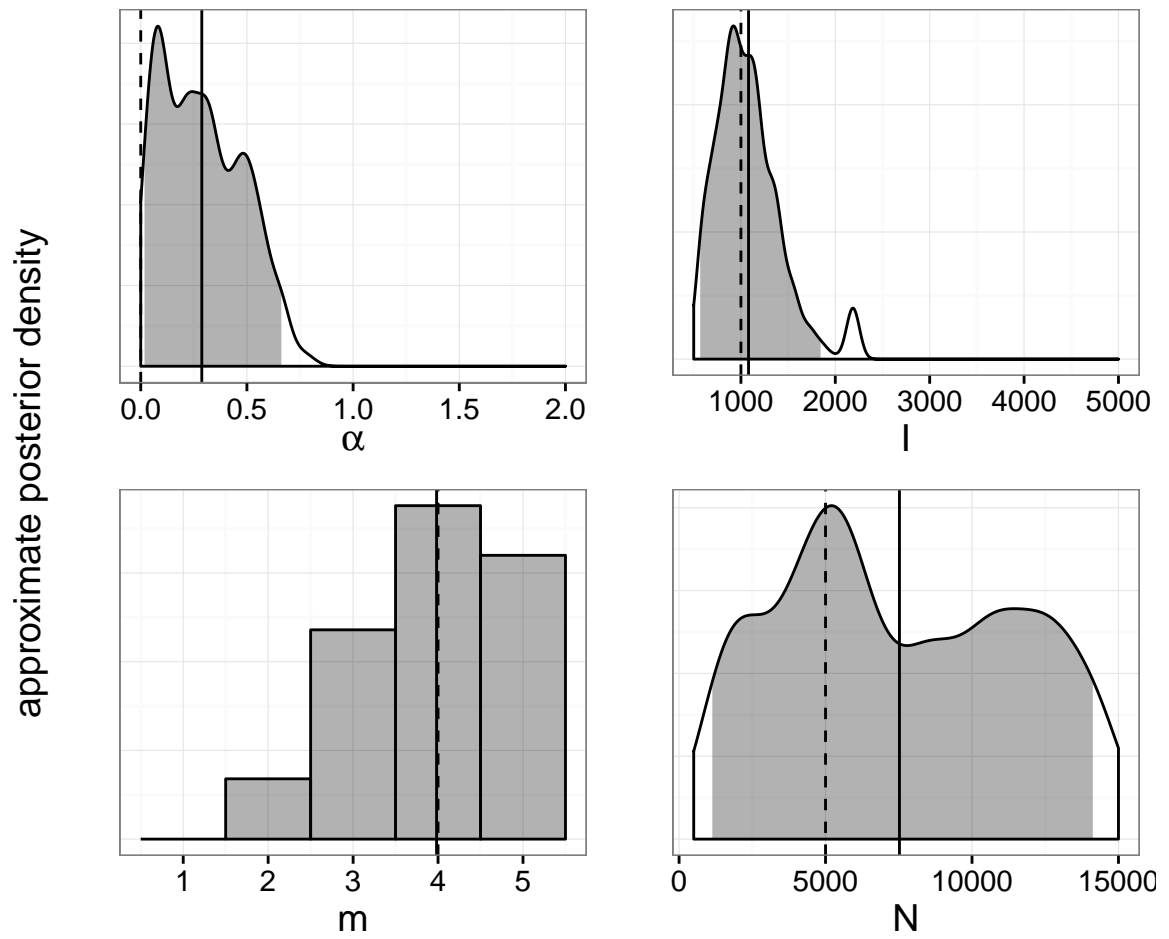


Figure A.51: Approximate marginal posterior distributions of BA model parameters obtained by applying *netabc* to a simulated transmission tree with BA parameter values $\alpha = 0.0$, $I = 1000$, $m = 4$, and $N = 5000$. Vertical dashed lines indicate true values. Shaded areas are 95% highest posterior density intervals. x -axes indicate regions of nonzero prior density.

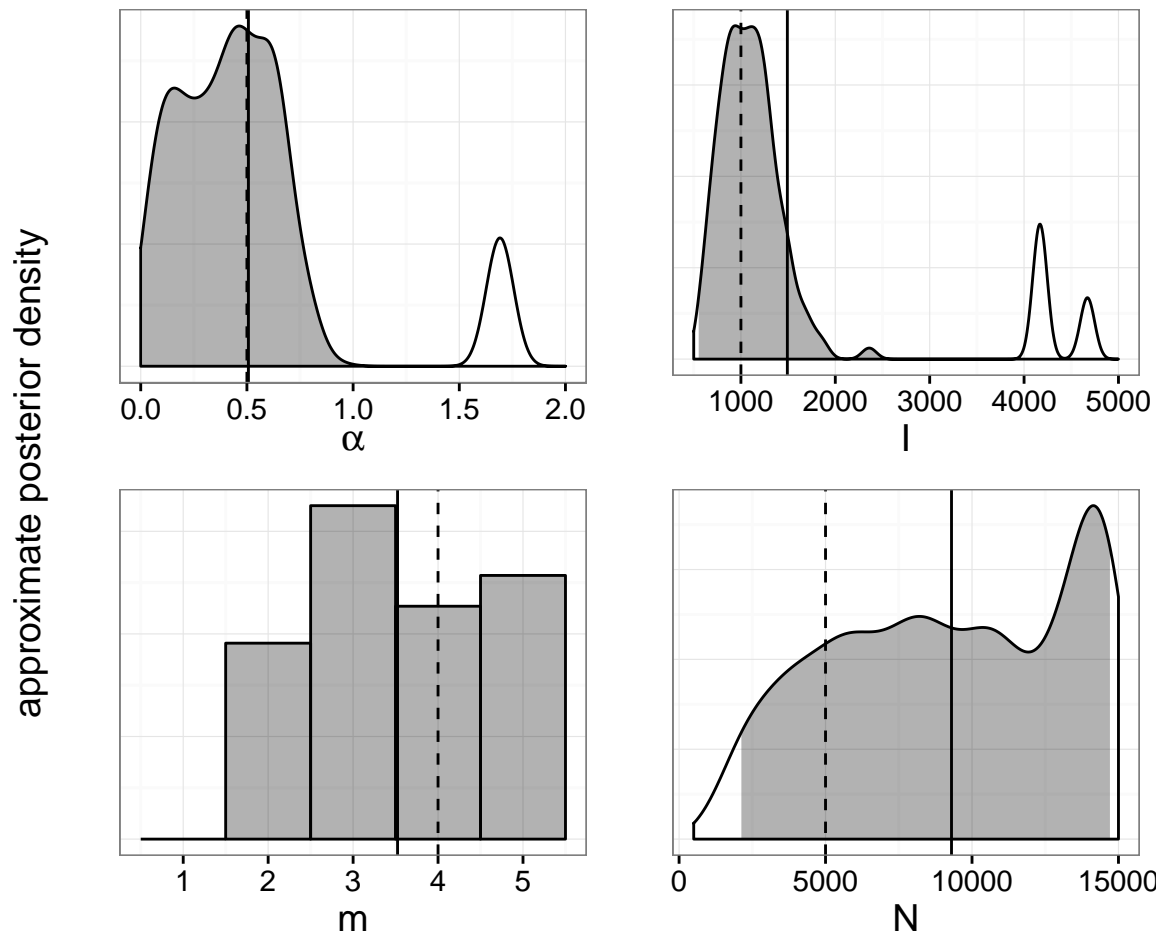


Figure A.52: Approximate marginal posterior distributions of BA model parameters obtained by applying *netabc* to a simulated transmission tree with BA parameter values $\alpha = 0.5$, $I = 1000$, $m = 4$, and $N = 5000$. Vertical dashed lines indicate true values. Shaded areas are 95% highest posterior density intervals. x -axes indicate regions of nonzero prior density.

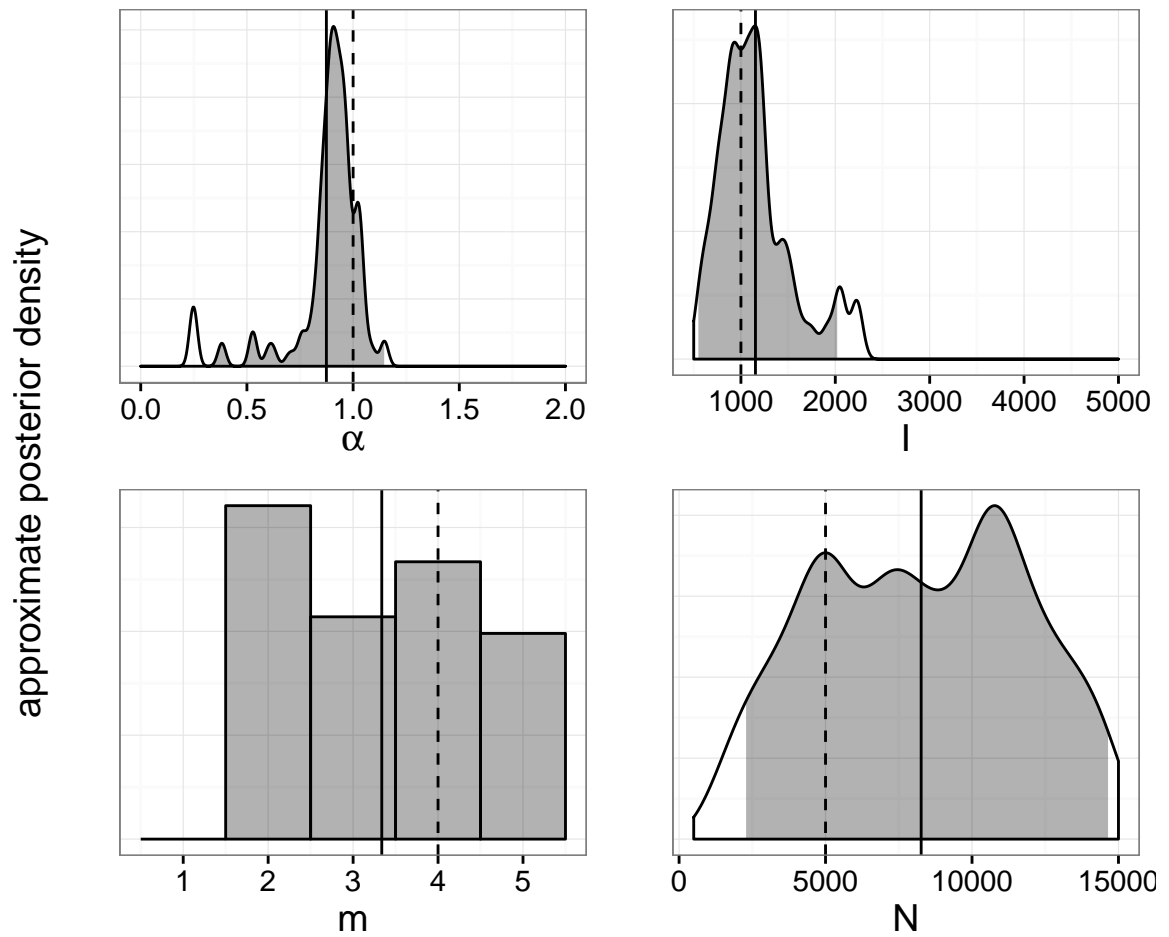


Figure A.53: Approximate marginal posterior distributions of BA model parameters obtained by applying *netabc* to a simulated transmission tree with BA parameter values $\alpha = 1.0$, $I = 1000$, $m = 4$, and $N = 5000$. Vertical dashed lines indicate true values. Shaded areas are 95% highest posterior density intervals. x -axes indicate regions of nonzero prior density.

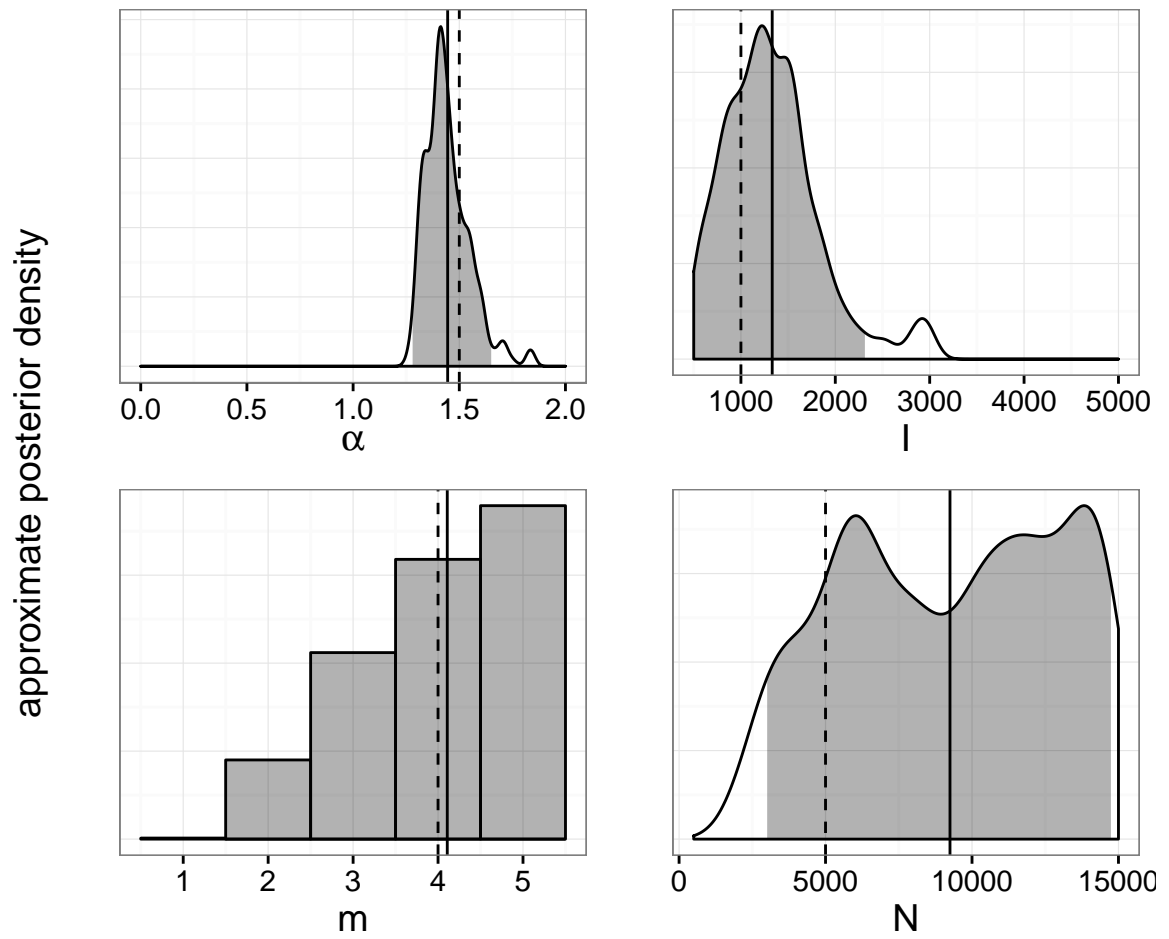


Figure A.54: Approximate marginal posterior distributions of BA model parameters obtained by applying *netabc* to a simulated transmission tree with BA parameter values $\alpha = 1.5$, $I = 1000$, $m = 4$, and $N = 5000$. Vertical dashed lines indicate true values. Shaded areas are 95% highest posterior density intervals. x -axes indicate regions of nonzero prior density.

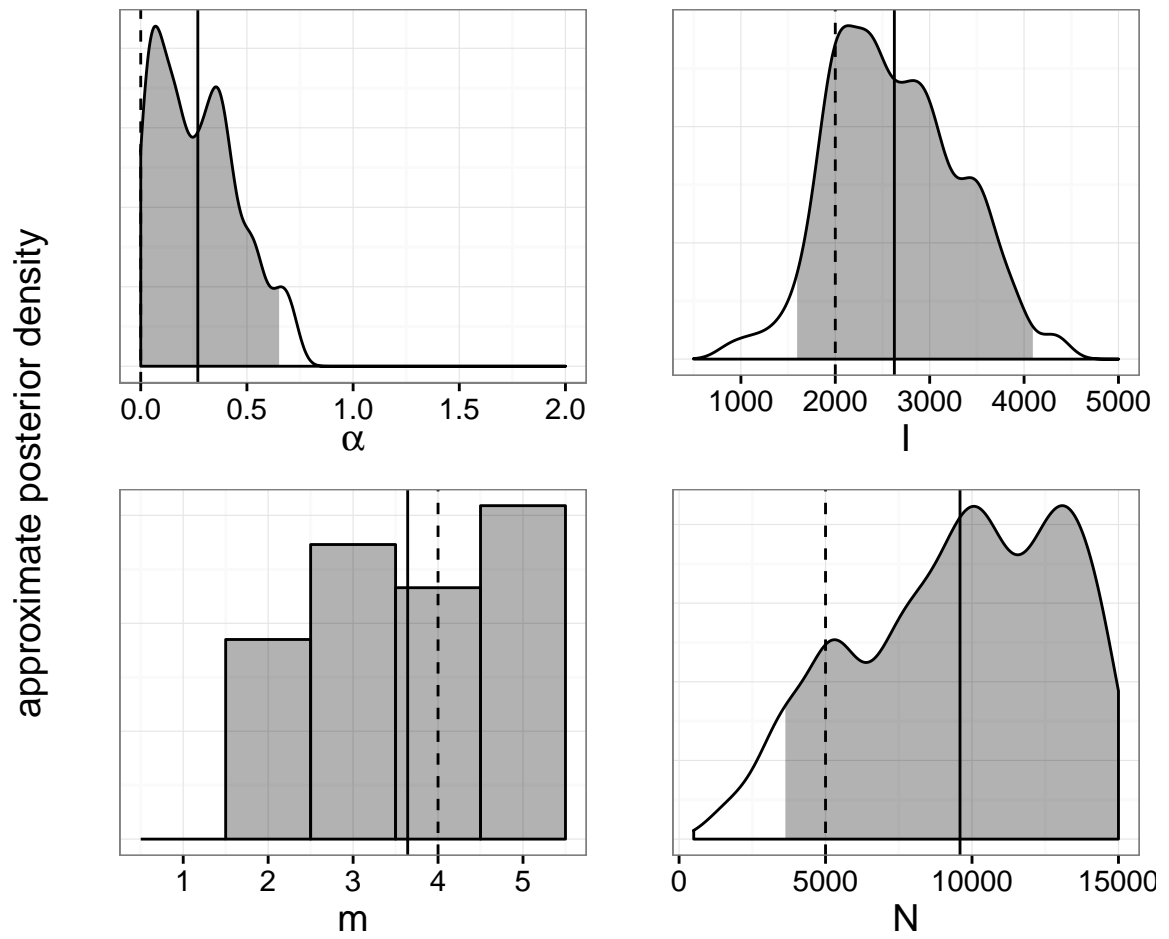


Figure A.55: Approximate marginal posterior distributions of BA model parameters obtained by applying *netabc* to a simulated transmission tree with BA parameter values $\alpha = 0.0$, $I = 2000$, $m = 4$, and $N = 5000$. Vertical dashed lines indicate true values. Shaded areas are 95% highest posterior density intervals. x -axes indicate regions of nonzero prior density.

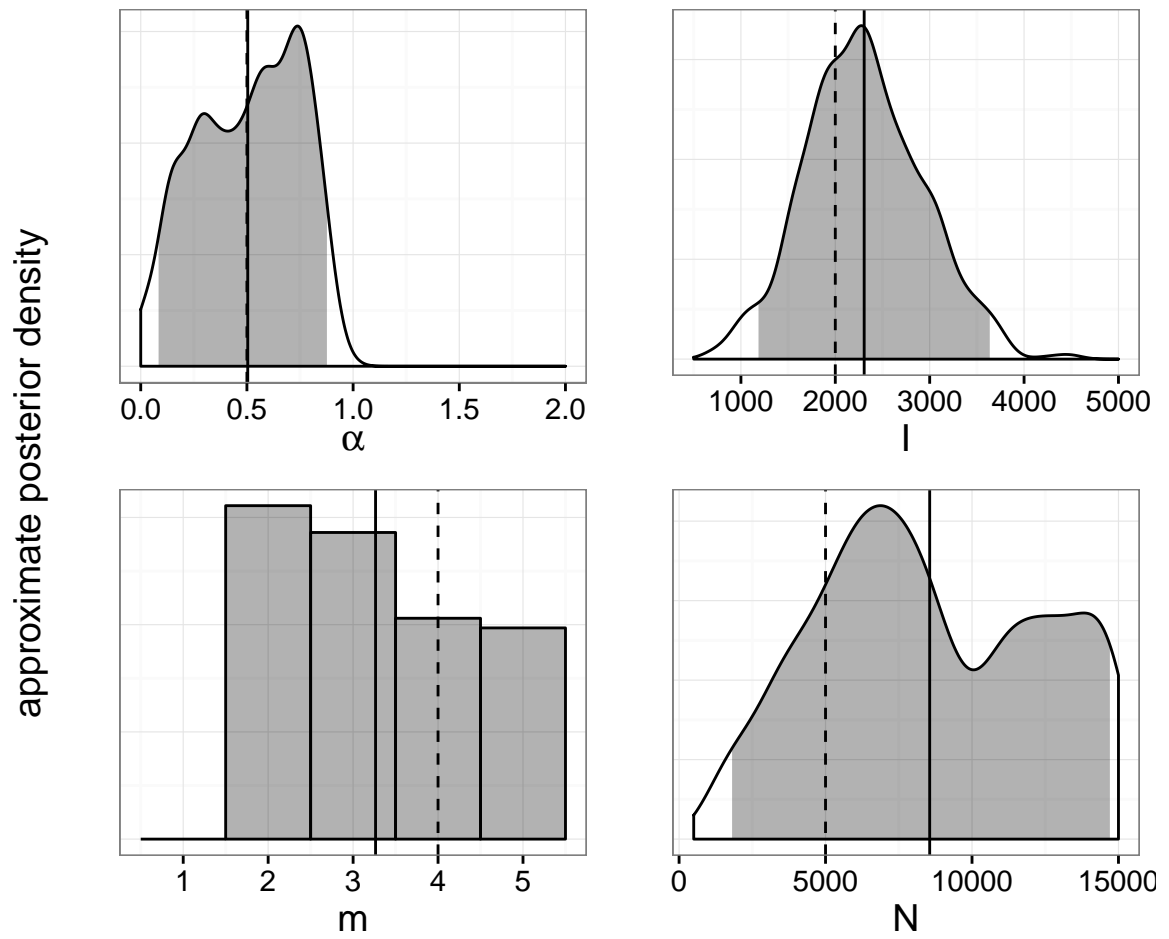


Figure A.56: Approximate marginal posterior distributions of BA model parameters obtained by applying *netabc* to a simulated transmission tree with BA parameter values $\alpha = 0.5$, $I = 2000$, $m = 4$, and $N = 5000$. Vertical dashed lines indicate true values. Shaded areas are 95% highest posterior density intervals. x -axes indicate regions of nonzero prior density.

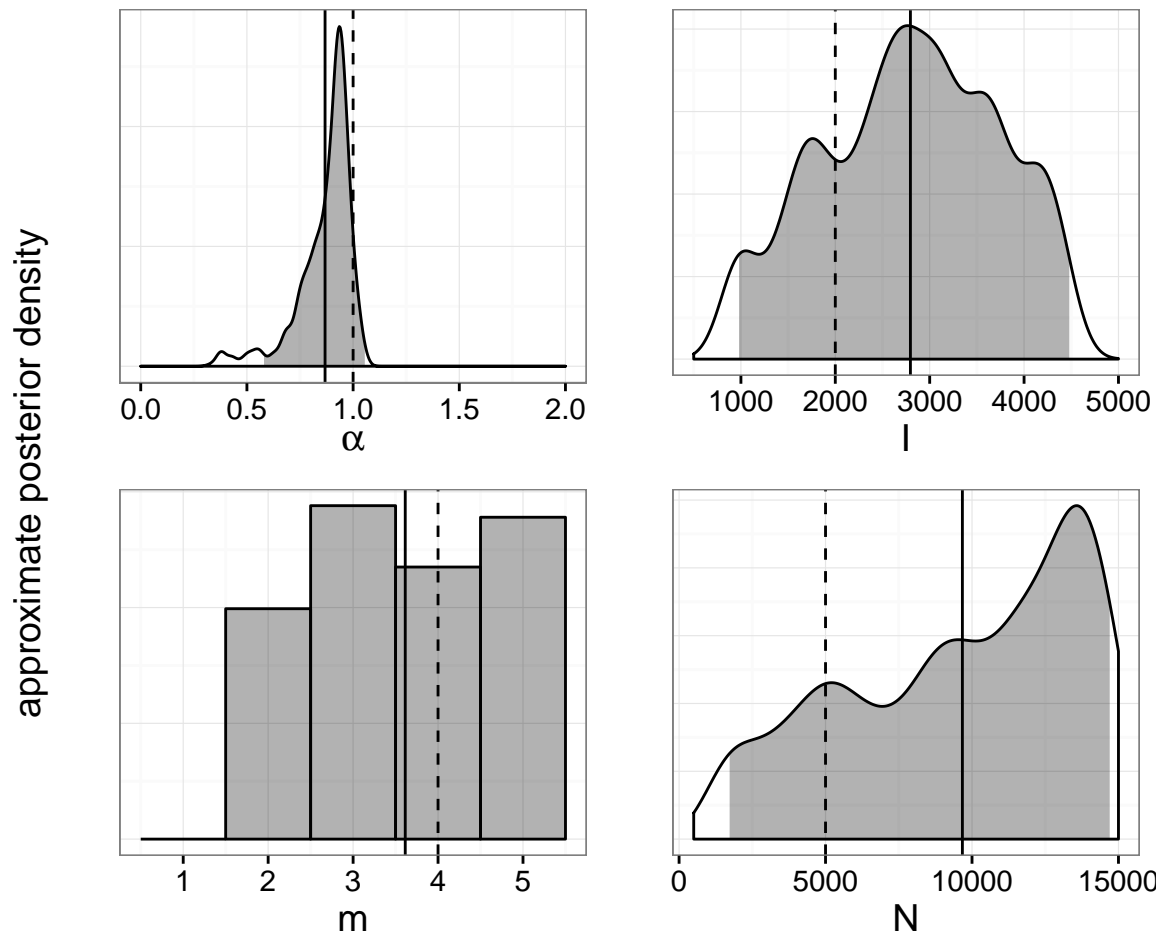


Figure A.57: Approximate marginal posterior distributions of BA model parameters obtained by applying *netabc* to a simulated transmission tree with BA parameter values $\alpha = 1.0$, $I = 2000$, $m = 4$, and $N = 5000$. Vertical dashed lines indicate true values. Shaded areas are 95% highest posterior density intervals. x -axes indicate regions of nonzero prior density.

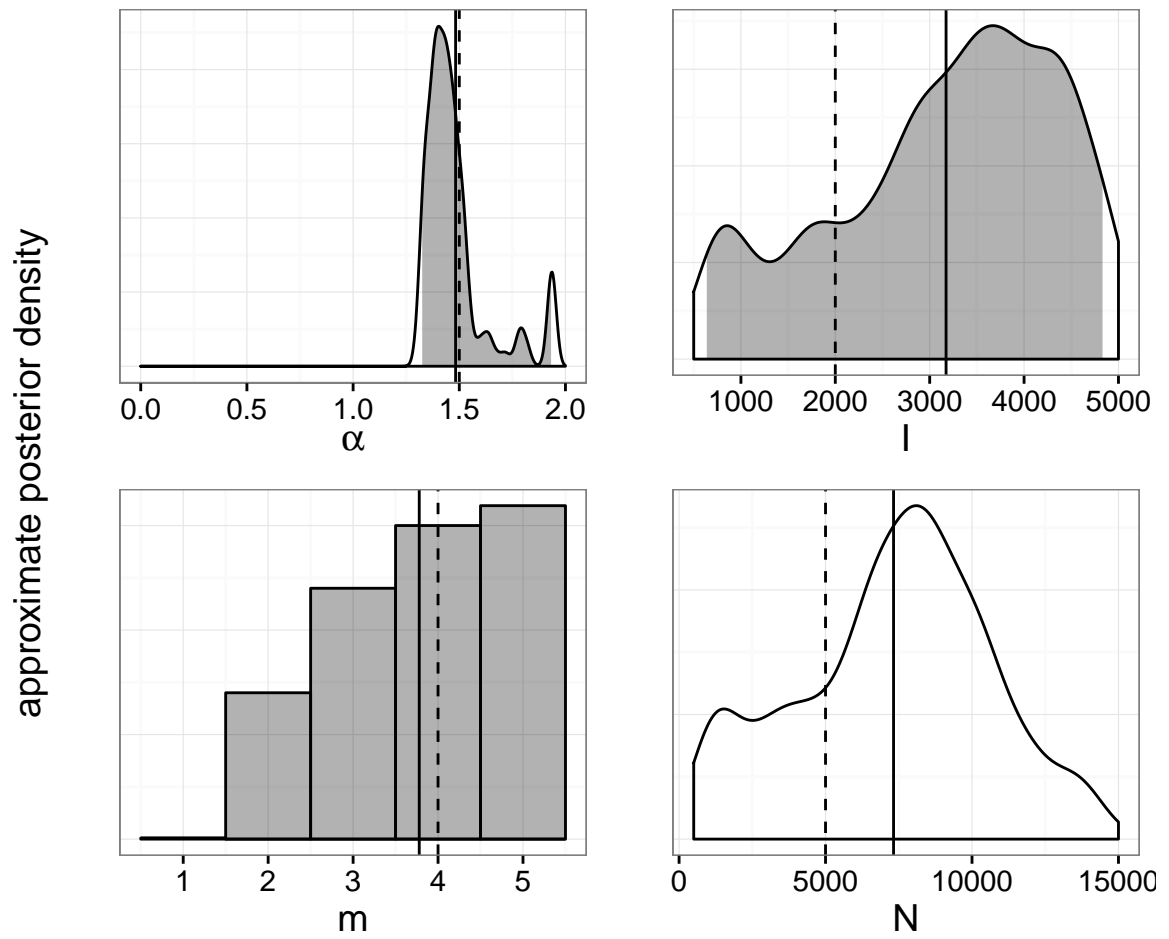


Figure A.58: Approximate marginal posterior distributions of BA model parameters obtained by applying *netabc* to a simulated transmission tree with BA parameter values $\alpha = 1.5$, $I = 2000$, $m = 4$, and $N = 5000$. Vertical dashed lines indicate true values. Shaded areas are 95% highest posterior density intervals. x -axes indicate regions of nonzero prior density.