Temporal Scale Estimation for Oversampled Network Cascades: Theory, Algorithms, and Experiments

Abram Magner
University at Albany, SUNY
AMAGNER@ALBANY.EDU

Carolyn Kaminski
University at Albany, SUNY
CKAMINSKI@ALBANY.EDU

Petko Bogdanov
University at Albany, SUNY
PBOGDANOV@ALBANY.EDU

Abstract

Spreading processes on graphs arise in a host of application domains, from the study of online social networks to viral marketing to epidemiology. Various discrete-time probabilistic models for spreading processes have been proposed. These are used for downstream statistical estimation and prediction problems, often involving messages or other information that is transmitted along with infections caused by the process. It is thus important to design models of cascade observation that take into account phenomena that lead to uncertainty about the process state at any given time. We highlight one such phenomenon – temporal distortion – caused by a misalignment between the rate at which observations of a cascade process are made and the rate at which the process itself operates, and argue that failure to correct for it results in degradation of performance on downstream statistical tasks. To address these issues, we formulate the clock estimation problem in terms of a natural distortion measure. We give a clock estimation algorithm, which we call FastClock, that runs in linear time in the size of its input and is provably statistically accurate for a broad range of model parameters when cascades are generated from the independent cascade process with known parameters and when the underlying graph is Erdős-Rényi. We further give empirical results on the performance of our algorithm in comparison to the state of the art estimator, a likelihood proxy maximization-based estimator implemented via dynamic programming. We find that, in a broad parameter regime, our algorithm substantially outperforms the dynamic programming algorithm in terms of both running time and accuracy.

Keywords: independent cascade, spreading processes, estimation, contagion, diffusion, temporal resolution

1. Introduction

There are a variety of well-established and simple probabilistic generative models for graphs and infectious processes that run over these graphs. In this work we specifically focus on models for spreading processes on networks such as the diffusion of innovation Montanari and Saberi (2010), information Bakshy et al. (2012) and misinformation Shin et al. (2018) in social networks. Accurate estimation of model parameters of such processes based on observational data is essential for a variety of important applications: from product marketing and social network recommendations to studying financial markets and detecting insurgent networks and limiting misinformation. At the same time, accurate modeling critically depends on our ability to account for major sources of uncertainty induced by the manner in which observational data about such evolving processes is acquired.
Discrete-time diffusion process models. Several well-studied information diffusion models assume a discrete timeline in which at every time step nodes participate in the diffusion process (i.e., get “infected”) based on influence from network neighbors who got infected in past time steps. For example, according to the independent cascade model Kempe et al. (2003) infected nodes have one chance to infect their neighbors, while in the linear threshold model nodes get infected when a critical fraction of their neighbors have been infected in any prior time steps.

It is important for our subsequent discussion to note what “discrete-time” means in the context of a process running in the real world, about which we would like to draw statistical inferences based on observations at potentially arbitrary physical time points. We think of a diffusion process as running in continuous time, so that, in principle, a vertex infection may occur at any time \( t \in \mathbb{R} \). A discrete-time process model posits the existence of a sequence of (possibly random) time steps \( 0 \leq \tau_0 < \tau_1 < \ldots, \tau_j \in [0, \infty) \), and specifies the probability distribution of the process state at each time \( \tau_{j+1} \) conditioned on the state of the process at time \( \tau_j \). Each such conditional distribution is invariant to the actual values of the \( \tau_j \). In this sense, we can think of a discrete-time process model as a partial specification of a continuous-time process model whose state evolves according to a discrete-valued variable.

The need to account for temporal distortion. One major source of uncertainty that is overwhelmingly overlooked in current literature is a misalignment of time points at which we observe a discrete-time process trajectory with the time points at which the state variables governing the process evolve. Here, an observation of a process at a particular time consists of the current state (infected or not) of every node. The aforementioned misalignment may be, for example, due to drawing observations at a higher rate than that at which the cascade process itself operates. This leads to what we call temporal distortion in process observations. Correcting for this distortion is the main focus of this paper. We illustrate this phenomenon with a concrete example, Example 1, that shows the deleterious effect of uncorrected temporal distortion on a downstream statistical estimation task.

Example 1 (Temporal distortion affects downstream statistical inference)

Consider a cascade generated by the independent cascade model Kempe et al. (2003) on a graph \( G \) with \( n \) vertices, with edge transmission parameter \( p_n = 1 \) and probability of infection from an external source \( p_e = 0 \). Assume that \( G \) is a complete binary tree and that the infection starts at the root node. We recall that this model runs in discrete time, with physical timesteps \( t_0 = 0 < t_1 < \ldots < t_N \), with \( t_j \in \mathbb{R} \) for all \( j \), producing infected vertex sets \( S_j \subseteq [n] = \{1, \ldots, n\} \), for each \( j \in \{0, \ldots, N\} \). That is, \( S_j \) is the set of vertices infected in the physical time interval \((t_{j-1}, t_j]\). In each time interval \((t_{j-1}, t_j]\), the set of active vertices (those vertices that can transmit infections across edges) is \( S_{j-1} \). Let us suppose that the infection times of vertices infected in a given time interval are uniformly distributed in that interval. For this example, we choose physical observation times \( t'_0 = 0, t'_1, \ldots, t'_{2N+1} \) with \( t'_{2j} = t_j \) and \( t'_{2j+1} = \frac{t_{j+1} + t_{j+2}}{2} \) for each \( j \). Thus, our view of the cascade consists of a sequence of infected sets \( \hat{S}_j, j \in \{0, 1, \ldots, 2N + 1\} \).

Consider the problem of doubling time prediction: given cascade observations up to/including a time \( t \in \mathbb{R} \) in which \( m \) vertices are infected, the task is to predict an interval \([a, b]\) such that, with probability at least \( 1 - \delta \), for some fixed parameter \( \delta > 0 \), the physical time of the \( 2m \)-th infection event lies in \([a, b]\).

If temporal distortion is not accounted for, so that we incorrectly assume that the process timesteps occur at times \( t'_j \), we have an inaccurate knowledge of the set of active vertices at
any given time. This has the following effect on doubling time prediction at times \( t = t'_{2j+1} \): at these times, approximately \( \sum_{k=0}^{2j} 2k + 2^{2j+1} = 2^{2j+1} \) vertices are infected, and we believe that approximately \( 2^{2j+1} \) vertices are active (when, in fact, only \( O\left(\frac{2^j}{j}\right) \) vertices are active). We would thus predict that the doubling time is exactly \( t'_{2(j+1)} \), despite the fact that the number of vertices infected at this time is exactly \( \sum_{k=0}^{2(j+1)} 2k = 2^{2(j+1)+1} - 2^j = 2^{2j+2} - 1 = 2^{2j+2} - 1 < 2^{2j+2} \). Thus, failure to account for temporal distortion in this setting leads to substantial and, in this setting, avoidable inaccuracy.

More realistic empirical experiments in DiTursi et al. (2017, 2019) confirm that accounting for temporal distortion can, in practical settings, improve performance on doubling time prediction and several other downstream statistical tasks.

More generally, temporal distortion degrades statistical performance on problems where model parameters are dependent on knowledge of the infectious sets of vertices (the so-called active vertices mentioned in the example) at given times. Correction for temporal distortion, which is the main focus of the present paper, is thus an important problem.

Prior work. The general topic of analysis of cascades has received a large amount of attention, both from theoretical and empirical perspectives. There are many cascade models, with features depending on application domains. E.g., the independent cascade (IC) and linear threshold (LT) models were popularized in Kempe et al. (2003) for the application of influence maximization. This problem continues to be studied Lee et al. (2016); Abbe et al. (2017). Variations on the influence maximization problem that have time-critical components and, thus, may be sensitive to temporal perturbation in the sense that we study here, have also been studied Chen et al. (2012); Ali et al. (2019). These models are also used outside the context of influence maximization, e.g., in the modeling of the spread of memes on social networks Adamic et al. (2016).

Statistical prediction tasks involving cascades have also been asked. For instance, the cascade doubling time prediction task was considered in Cheng et al. (2014). Other works propose models in which a piece of information, such as a message, an opinion, or a viral genome, is transmitted along with the infection of a node Eletreby et al. (2020); De et al. (2016); Park et al. (2020). For such statistical problems, statistical inferences about the transmitted information can be disrupted by inaccurate estimation of the set of infectious vertices at a given time, further motivating the consideration of methods for correcting for temporal distortion.

In DiTursi et al. (2017) (see also followup work in DiTursi et al. (2019)), the authors formulated a version of the problem of clock recovery (equivalent to temporal distortion correction studied here) from adversarially temporally perturbed cascade data as a problem of maximization of a function of the clock that serves as a proxy (in particular, an upper bound) for the log likelihood of the observed cascades. They proposed a solution to this problem via a dynamic programming algorithm. While the dynamic programming algorithm is an exact solution to their formulation of the problem, it has a running time of \( \Theta(n^4) \), where \( n \) is the total number of vertices in the graph on which the observed cascade runs, which is prohibitively expensive for graphs of moderate to large size. Furthermore, their formulation of the problem makes no comparison with the ground truth clock, and thus there are no theoretical guarantees or empirical evaluations of the accuracy of their estimator (which we call the maximum likelihood proxy (MLP) estimator) as an approximation to the ground truth clock. In contrast, the present work gives a rigorous formulation of the problem as one of statistical
estimation of the ground truth clock from observed cascades. We compare our proposed algorithm and estimator with the MLP estimator in this framework in terms of both accuracy and running time.

Our contributions In the present work, we propose an approximation formulation of the clock recovery problem, allowing us to quantify the proximity of estimated clocks to the ground truth in a principled manner. Our formulation is general, covering arbitrary varying observation rates. However, our algorithms, theorems, and experiments are specific to the oversampling case, wherein observations are made at a higher rate than that at which the spreading process operates. We leave estimators for the more complicated general case to future work.

We propose a novel estimation algorithm, which we call FastClock, that runs in time linear in the size of the cascade. We rigorously prove that, under natural conditions on the input graph and cascade parameters, the FastClock estimator produces a clock whose distance to the ground truth is vanishingly small as the size of the graph tends to infinity. Our guarantees on FastClock hold for a broad range of the parameter of the Erdős-Rényi graph model.

We bolster our theoretical results via experiments on synthetic graphs and cascades. We find that the FastClock estimator empirically outperforms the dynamic programming-based estimator from DiTursi et al. (2017) in these experimental conditions in terms of accuracy and running time.

Organization of the paper In Section 2, we give a precise formulation of the problem and introduce notation. In Section 3, we state the FastClock algorithm and the main theoretical results. We give proof sketches (and, where noted, full proofs) in Section 4. Section 5 gives empirical results comparing FastClock and the DP algorithm implementing the MLP estimator. We conclude in Section 6. Full proofs of all results are given in the appendix.

2. Problem formulation and notation

Our goal in this section is to formulate the problems of clock estimation and spreading process history reconstruction from a temporally perturbed cascade observation. As mentioned in the introduction, our formulation is quite general and covers temporal distortion arising from arbitrarily varying observation rates. Since this general case is algorithmically and statistically more complicated (in particular, while our proposed algorithm succeeds at clock estimation, the more relevant problem of history reconstruction is more difficult), we then focus on the oversampling case. In this case, our general problem formulation can be replaced by a simpler one, and the two problems of clock estimation and spreading process history reconstruction become equivalent.

2.1. General formulation

We fix a graph $G$ on the vertex set $[n] = \{1, ..., n\}$, and we define the timeline of length $N$, for any number $N \in \mathbb{N}$, to be the set $\llbracket N \rrbracket = \{0, 1, ..., N\}$. The first ingredient of our framework is a cascade model.

**Definition 1 (Cascade model)** A (discrete-time) cascade model $\mathcal{C}(N)$ is a probability distribution on sequences $(S_0, S_1, ..., S_N)$ of disjoint subsets of vertices of $G$. We think of $S_t$, $t \in \{0, ..., N\}$ as the set of vertices infected in timestep $t$. We call any such sequence an infection sequence, and we write $|S| = N + 1$.

As mentioned in the introduction, we think of a discrete-time cascade as running in continuous, physical time, so that the $j$th timestep begins at some physical time $t_{j-1}$ and ends at physical time
and every vertex \( v \in S_j \) is infected at some physical time in the interval \( (t_{j-1}, t_j] \). Note, however, that physical times are not formally part of the logical framework, and our models have no explicit dependence on them. We introduce them only to aid intuition.

Next, we define our observation model, which formalizes our notion of temporal perturbations. To do this, we need the notion of a *clock*. Intuitively, a clock encodes the number of *observations* of the cascade made during each cascade timestep. For us, an observation of a cascade at some physical time \( t \) consists of the set of nodes that have been infected at or before time \( t \). We will talk about the \( k \)th observation to occur, \( k \geq 0 \), as having index \( k \).

**Definition 2 (Clock)** A clock \( C \) on a timeline \([N]\) is a map \( C : [N] \to \mathbb{Z}_{\geq 0} \). Equivalently, it is a tuple of \( N + 1 \) non-negative integers \((C(0), \ldots, C(N))\), where \( C(j) \) intuitively gives the number of observations made in the physical time interval \((t_{j-1}, t_j] \). The size \( |C| \) of \( C \) is given by

\[
|C| = \sum_{j=0}^{N} C(j). \tag{1}
\]

It will be convenient to introduce more notation regarding clocks:

- For a clock \( C \), let the \( j \)th partial sum of \( C \) be given by \( \sum_{k=0}^{j} C(k) \), and denote it by \( C(0 : j) \). This is the number of observations made prior to the \( j \)th cascade timestep.
- Let \( M_C : [N] \to 2^{[N]} \) be given as follows: \( M_C(j) = \{C(0 : j-1) + 1, \ldots, C(0 : j)\} \). In other words, \( M_C(j) \) is the set of observation indices that occur during the time interval \((j-1, j] \), according to \( C \).

The following definition captures the notion of an infection sequence \( S' \) that could arise from observing a ground truth infection sequence \( S \) according to a schedule dictated by a clock \( C \).

**Definition 3 (Clock-consistent observation of an infection sequence)** Fix two infection sequences \( S = (S_0, \ldots, S_N) \) and \( S' = (S'_0, \ldots, S'_N) \) and a clock \( C \) on \([N]\) with size \( |C| = N' \). We say that \( S' \) is an observation of \( S \) that is consistent with \( C \) if, for each ground truth timestep \( t \in [N] \),

\[
S_t = \bigcup_{t' \in M_C(t)} S'_t. \tag{2}
\]

In other words, \( S'_j \) can be interpreted as encoding \( j \)th observation of the infection sequence given by \( S \), according to the schedule dictated by \( C \).

As an easy consequence of this definition, if \( S' \) is an observation of \( S \) consistent with any clock \( C \), then \( C \) is the unique clock for which this is true.

**Example 2 (Infection sequences, clocks, clock-consistent observations)** Consider a graph \( G \) on the vertex set \([n] = [10] \). One possible infection sequence on \( G \) is

\[
S = (S_0, S_1, S_2) = (\{2, 8, 10\}, \{1, 3, 4, 7, 9\}, \{6\}). \tag{3}
\]
This encodes a sequence of infections occurring in three timesteps — i.e., on the timeline \([2]\). In particular, we may think of \(S_1\) as encoding that vertices 1, 3, 4, 7, 9 are all infected during timestep 1, but the order in which they are infected is not encoded.

One possible example clock on the timeline \([2]\) is \(C = (C_0, C_1, C_2) = (0, 4, 1)\). This encodes that 0 observations are made in timestep 0, 4 are made in timestep 1, and 1 is made in timestep 2.

An example infection sequence \(\hat{S}\) that is an observation of \(S\) consistent with \(C\) is as follows:

\[
\hat{S} = (\hat{S}_0, \hat{S}_1, \hat{S}_2, \hat{S}_3, \hat{S}_4) = (\{2, 7, 8, 10\}, \{1, 9\}, \{3, 4\}, \{\}, \{6\})
\]

Note that \(\hat{S}\) is necessarily an infection sequence on the timeline \([0 + 4 + 1 - 1]\) = \([4]\).

We finally come to the definition of a temporal distortion model.

**Definition 4 (Temporal distortion model)** A temporal distortion model is a conditional probability distribution \(P(\cdot | S)\) on infection sequences, parameterized by infection sequences \(S\) (which we think of as being the ground truth infection sequences), such that \(P(S' | S) > 0\) only if \(S'\) is an observation of \(S\) consistent with some clock.

In other words, a temporal distortion model is a probabilistic generative model for observations of an infection sequence.

2.2. Specialization to the oversampling regime

In this work, we will focus without much further comment on oversampling temporal distortion models, which are models resulting in observations according to clocks with \(C(j) > 0\) for all \(j\). Intuitively, this covers the case where observations are made at a higher rate than that at which the process itself operates. In the oversampling regime, we can simplify the definition of a clock:

**Definition 5 (Clock (oversampling case))** An (oversampling) clock \(C\) on the timeline \([N]\) with size \(N' + 1\) is a partition of \([N']\) into \(N + 1\) subintervals. We call the \(j\)th such subinterval, for \(j = 0\) to \(N\), the \(j\)th observation interval.

In the above definition, we think of \([N]\) as the ground truth timeline and \([N']\) as the observation timeline. An oversampling clock partitions the observation timeline into subintervals, each corresponding to a single ground truth timestep.

**Example 3 (Oversampling clock)** Consider the timeline \([5]\) (here, \(N' = 5\)). An example of an oversampling clock is

\[
C = \{[0, 2], [3, 3], [4, 5]\}.
\]

This is equivalent to the following clock on \([2]\), with \(N = 2\), in the sense of Definition 2:

\[
C = (3, 1, 2).
\]

An infection sequence \(S\) naturally induces a partial order on the set of vertices: namely, for two vertices \(a, b\), \(a < b\) if and only if \(a \in S_i, b \in S_j\) for some \(i < j\). Similarly, a clock on an infection sequence, in the sense of Definition 5, induces a partial order.
We will consider two clocks $C_0, C_1$ to be equivalent with respect to a given observed infection sequence $S$ if they induce the same partial order. The reason for this is that two equivalent clocks separate vertices in the same way into a sequence of time steps. We will sometimes abuse terminology and use “clock” to mean “clock equivalence class”.

We next define a distortion function on clock equivalence classes. This will allow us to measure how far a given estimated clock is from the ground truth. Note that given an observed infection sequence $S$, a clock cannot reverse the order of any pair of events, so that the standard Kendall $\tau$ distance between partial orders is not appropriate here.

**Definition 6 (Distortion function on clock pairs)** Consider two clocks $C_0, C_1$ with respect to an observed infection sequence $S$. We define $\text{Dis}_{C_0, C_1}(i, j)$ to be the indicator that the clocks $C_0$ and $C_1$ order vertices $i$ and $j$ differently (i.e., that the partial order on vertices induced by $C_0$ orders $i$ and $j$ and the partial order induced by $C_1$ does not, for $b$ equal to either 0 or 1). If the clocks in question are clear from context, we may drop the subscript.

We define the following distortion measure on clock pairs:

$$d_S(C_0, C_1) = \frac{1}{\binom{n}{2}} \sum_{i<j} \text{Dis}_{C_0, C_1}(i, j). \quad (7)$$

We finally come to the general problem that we would like to solve:

**Definition 7 (Clock estimation/Spreading process history reconstruction)** Fix a graph $G$, a cascade model $C(G, T)$, and an oversampling temporal distortion model $T$. An infection sequence $S \sim C(G, T)$ is generated on $G$. Finally, an observed infection sequence $\hat{S}$ with $|\hat{S}| = N + 1$ is generated according to $T$, with implicit clock $\hat{C}$. Our goal is to produce an estimator $\hat{C} = \hat{C}(\hat{S})$ of $C$ so as to minimize $\mathbb{E}[d_\hat{S}(C, \hat{C})]$. This is called the clock estimation problem.

We call the problem of estimating $S$ the spreading process history reconstruction problem. An estimated oversampling clock $\hat{C}$ induces an estimate $\hat{S}$ of $S$, so that clock estimation and spreading process history reconstruction are equivalent in the oversampling case.

We note that the above definition implicitly assumes knowledge of the parameters of the cascade model. Estimation of these parameters has been studied in the literature. Furthermore, we note that knowledge of the initial conditions of the cascade is necessary in order to achieve an expected estimation error that tends to 0 in general. We thus assume that the number of initially infected vertices is given to us. Under mild additional assumptions on the model (e.g., that $S_0$ consists of $\Theta(1)$ vertices chosen uniformly at random, and that the graph is sparse, so that $S_0$ is an independent set with high probability), the initial set $S_0$ can be inferred with high probability.

**Specific cascade models.** Having laid out the general framework for temporal distortion models, we specify a few example cascade models for our problem. Our approach generalizes beyond these two, as we will explain after the statement of our algorithm.

We first define the independent cascade (IC) process. We fix a graph $G$, an initial infection set $S_0$ of vertices in $G$ (given by elements of $[n] = \{1, \ldots, n\}$), and probability parameters $p_n$ and $p_e$. Here, $p_n$ denotes the probability of transmission of an infection across an edge, and $p_e$ denotes the probability of infection from an external source.

Step $j + 1$ of the IC process proceeds as follows: for each node $v$ in $S_j$ and each uninfected neighbor $w$, $v$ attempts to infect $w$, succeeding with probability $p_n$, independent of anything else.
Next, each uninfected node is independently infected with probability \( p_e \). The set of nodes infected in step \( j + 1 \) is denoted by \( S_{j+1} \). The process terminates either after a specified number of steps, after all nodes are infected, or when \( S_{j+1} = \emptyset \) and \( p_e = 0 \).

The linear threshold (LT) process works as follows: for every node \( v \) in \( G \), a threshold \( \theta_v \) is drawn independently from some known distribution on \([0, 1]\). Some initial subset \( S_0 \) of vertices is infected, and, in each subsequent timestep, vertex \( v \) is infected if either it has already been infected or the fraction of its neighbors that are infected exceeds \( \theta_v \).

3. Main results: Algorithm, approximation and running time guarantees

In this section, we present our proposed algorithm (Algorithm 1) for clock estimation, which we call FastClock. It takes as input a graph \( G \), an observed infection sequence \( \hat{S} = (\hat{S}_0, \ldots, \hat{S}_N) \), and the parameters \( \theta \) of the cascade model, including the initial infection set \( S_0 \) (see our discussion of this assumption in the previous section). The output of the algorithm is an estimated clock \( \hat{C} \), which takes the form of a sequence of interval endpoints \( \hat{t}_0, \hat{t}_1, \ldots, \hat{t}_\hat{N} \in [\lfloor N \rfloor] \), for some \( \hat{N} \) and is an estimate of the ground truth clock \( C \) specified by \( t_0, \ldots, t_N \).

Our algorithm proceeds by iteratively computing the estimate \( \hat{t}_j \). In the \((j + 1)\)-st iteration, to compute \( \hat{t}_{j+1} \), it chooses the size of the next interval of the clock so as to match as closely as possible the expected number of newly infected nodes in the next timestep. We will prove that the resulting clock estimate is very close, in terms of \( d_{\hat{S}}(\cdot, \cdot) \), to the ground truth clock, using concentration inequalities.

In particular, the correctness of FastClock is based on the following intuition: if we manage to correctly estimate \( t_0, \ldots, t_j \), then we can estimate the conditional expected number of vertices infected in the \((j + 1)\)-st timestep of the process (i.e., \( |S_{j+1}| \)). We can show a conditional concentration result for \( |S_{j+1}| \) around its expectation. Thus, we output as our next clock interval endpoint \( \hat{t}_{j+1} \) the smallest integer \( t \geq \hat{t}_j \) for which the number of vertices in \( \bigcup_{k=\hat{t}_j+1}^t \hat{S}_k \) does not exceed its conditional expectation, corrected by a small quantity. This quantity is determined by the concentration properties of the random variable \( |S_{j+1}| \) conditioned on the state of the process given by \( \hat{S}_0, \ldots, \hat{S}_j \). We choose the threshold to be such that, under this conditioning, the number of vertices infected in the next process timestep is slightly less than it with probability tending exponentially to 1. Our approximation analysis illustrate that the approximation quality depends on the graph structure and the model parameters.

The significance of the approximation and running time results (Theorems 8 and 9 below) is that oversampling temporal distortion under natural conditions can be quickly corrected for with provably high accuracy using relatively simple expected value calculations. While our approximation theorem is formally stated for the IC model, the conclusions hold as long as the number of infected nodes in the next cascade timestep, conditioned on the current state of the process, is well-concentrated and as long as the expected number of such nodes is immune to small errors in the estimation of the process state. These are both functions of the cascade model and of the structure of the graph \( G \) on which the cascade runs: our results hold when the graph is an expander with appropriate parameters (which is implied by our Erdős-Rényi stipulation in the approximation theorem).

As long as the expected number of nodes infected in the next timestep can be calculated efficiently, the FastClock algorithm can be adapted to a wide variety of cascade models.
3.1. The FastClock algorithm

Before we define our algorithm we introduce some necessary notation. For an infection sequence \( \hat{S} \) and a timestep index \( t \in |\hat{S}| \), define \( \sigma_t(\hat{S}) \) to be the \( \sigma \)-field generated by the event that the first \( t \) infection sets of the cascade process are given by \( \hat{S}_0, \hat{S}_1, ..., \hat{S}_t \). That is, the event in question is that \( \hat{S}_0 = \hat{S}_0, ..., \hat{S}_t = \hat{S}_t \). We also define \( \mu_t(\hat{S}) \) to be \( \mu_t(\hat{S}) = \mathbb{E}[|S_{t+1}| \mid \sigma_t(\hat{S})] \). The algorithm is given in Algorithm 1.

**Algorithm 1: FastClock**

**Data:** Graph \( G \), cascade model parameters \( \theta \), observed infection sequence \( \hat{S} = (\hat{S}_0, ..., \hat{S}_N) \)

**Result:** An estimated clock \( \hat{C} \).

// An initially empty list for the estimated clock.
1. Set \( \hat{C} = () \);

// \( t \): index of the next estimated clock interval, i.e., \( t \) is an index in \( S \), the un-distorted infection sequence.
// \( t_{\text{obs}} \): the index in \( \hat{S} \) of the beginning of the next estimated clock interval
2. Set \( t = 1 \), \( t_{\text{obs}} = \min\{j \leq N : |\cup_{k=0}^j \hat{S}_k| = S_0\} \);

// \( \hat{S} \): the estimated infection sequence approximating the ground truth sequence \( S \).
3. Set \( \hat{S}_0 = \cup_{k=0}^{t_{\text{obs}}} \hat{S}_k \);
4. Append \( t_{\text{obs}} \) to \( \hat{C} \);
5. while \( t_{\text{obs}} \neq N \) do

    // Compute the expected number \( \mu_t \) of infected nodes in a single step of the cascade process, starting from the state of the process estimated so far.
6. Set \( \mu_t = \mathbb{E}[|S_{t+1}| \mid \sigma_t(\hat{S}_0, \hat{S}_1, ..., \hat{S}_t)] \);
7. Set
   \[
   t'_{\text{obs}} = t_{\text{obs}} + \max \left\{ \Delta \mid \sum_{i=t_{\text{obs}}+1}^{t_{\text{obs}}+\Delta} |\hat{S}_i| \leq \mu_t \cdot (1 + \mu_t^{-1/3}) \right\} \tag{8}
   \]
8. Append \( t'_{\text{obs}} \) to \( \hat{C} \);
9. Set \( \hat{S}_t = \cup_{i=t_{\text{obs}}+1}^{t'_{\text{obs}}} \hat{S}_i \);
10. Set \( t = t + 1 \);
11. Set \( t_{\text{obs}} = t'_{\text{obs}} \);
12. end
13. return \( \hat{C} \);

After an initialization, the main loop in FastClock (Steps 5-11) iteratively determines the first infection event in the next step of the process, by estimating the expected number of nodes \( \mu_t \) to be infected next (Step 6). The key step in this process is the computation of \( \mu_t \) which we discuss next.
Computing $\mu_t(\tilde{S})$ in the IC model. Let us be more precise in specifying how to compute $\mu_t(\tilde{S}) = \mathbb{E}[|S_{t+1}| \mid \sigma_t(\tilde{S})]$ in the independent cascade model. A node can be infected in one of two ways: through external factors (governed by $p_e$) or via transmission from a vertex in $\tilde{S}_t$ through an edge. In the latter case, the node must lie in the frontier set $\mathcal{F}_t(\tilde{S})$, defined as follows: $\mathcal{F}_t(\tilde{S})$ is the set $\mathcal{N}(\tilde{S}_t) \setminus \bigcup_{j=0}^t \tilde{S}_j$; i.e., it is the set of neighbors of $\tilde{S}_t$ that we believe to be uninfected at the beginning of cascade timestep $t$.

For a set of vertices $W \subseteq [n]$ and a vertex $v \in [n]$, let $\deg_W(v)$ denote the number of edges incident on $v$ that are also incident on vertices in $W$. We have, by linearity of expectation,

$$\mu_t(\tilde{S}) = \sum_{v \in [n]} \Pr[v \text{ gets infected at time } t \mid \sigma_t(\tilde{S})]$$

$$= \sum_{v \not\in \mathcal{F}_t} \Pr[v \text{ gets infected at time } t \mid \sigma_t(\tilde{S})] + \sum_{v \in \mathcal{F}_t} \Pr[v \text{ gets infected at time } t \mid \sigma_t(\tilde{S})]$$

$$= \sum_{v \in \mathcal{F}_t \cup \bigcup_{j=0}^t \tilde{S}_j} \Pr[v \text{ gets infected at time } t \mid \sigma_t(\tilde{S})] + \sum_{v \in \mathcal{F}_t} \Pr[v \text{ gets infected at time } t \mid \sigma_t(\tilde{S})]$$

$$= p_e \cdot \left(n - |\mathcal{F}_t| - \sum_{j=0}^t |\tilde{S}_j|\right) + \sum_{v \in \mathcal{F}_t} (p_e + (1-p_e)(1-(1-p_n)^{\deg_{\tilde{S}_t}(v)})).$$

A similar expression can be derived for the more general case where transmission probabilities across edges may differ from each other.

The calculation of the summation $\sum_{j=0}^t |\tilde{S}_j|$ can be performed efficiently by keeping track of its value in the $t$-th iteration of the loop of the algorithm. In the $t$-th iteration, the value of the summation is updated by adding $|\tilde{S}_t|$ to the running total. Note also that this estimation will be the only difference in our algorithm when applied to alternative cascade models such as the linear threshold model.

3.2. Approximation guarantee for FastClock

Our first theorem gives an approximation guarantee for FastClock in the case of the IC model. It is subject to a few assumptions about the temporal distortion model, the parameters of the cascade model and those of the graph model from which $G$ is sampled, which we state next. It is, however, important to note that FastClock itself does not assume anything about the graph.

Assumption 1 (Assumption on the temporal distortion model) No observed infection set $\hat{S}_i$ has too few vertices compared to the ground truth infection set $S_j$ from which it came. In particular, this means that, for all $i$, the width of each observation interval $C_i$ is bounded above by a constant, and there is some absolute constant $\epsilon > 0$ such that, for each $j \in C_i$,

$$|\hat{S}_j| \geq \epsilon \sum_{k \in C_i} |\hat{S}_k|.$$

Note that we do not assume anything else about the distribution of vertices in these observation intervals. Furthermore, this assumption can be somewhat relaxed to hold with high enough probability.
Assumption 2 (Assumptions on random graph model parameters) We assume that $G \sim G(n, p)$ (i.e., that $G$ is sampled from the Erdős-Rényi model), where $p$ satisfies the following relation with the ground truth number of cascade timesteps $T$: \[ p = o\left(n^{-\frac{T}{T+1}}\right) \quad \text{and} \quad p \geq C \log n/n, \] for some $C > 1$. The former condition may be viewed as a constraint on $T$, for a given choice of $p$. It is natural in light of the fact that, together with our assumptions on $p_n$ and $p_e$ below, it implies that the cascade does not flood the graph, in the sense of infecting a $\Theta(1)$-fraction of nodes. Many cascades in practice do not flood the graph in this sense.

The latter condition implies that the graph is connected with high probability.

Regarding parameters of the IC process, we assume that $p_n$ is some fixed positive constant and that $p_e = o(p)$. Our results also hold if $p_n$ is different for every edge $e$ (so that $p_n = p_n(e)$), provided that there are two positive constants $0 < c_0, c_1 < 1$ such that for every edge $e$, $p_n(e) \in [c_0, c_1]$.

The assumption that $p_n$ is constant with respect to $n$ is natural in the sense that, for many infectious processes, the probability of transmission from one node to another should not depend on the number of nodes.

The assumption on $p_e$, the probability of infection from an external source, is reasonable when the cascade is overwhelmingly driven by network effects, rather than external sources.

Theorem 8 (Main FastClock approximation theorem) Suppose that Assumptions 1 and 2 hold. We have, with probability at least $1 - e^{-\Omega(np)}$,

\[ d_{\hat{S}}(C, \hat{C}) = O((np)^{-1/3}), \quad (14) \]

where we recall that $S$ is an infection sequence generated by the cascade model, $C$ is the ground truth clock, $\hat{S}$ is the observed infection sequence generated by the temporal distortion model, and $\hat{C}$ is the output of FastClock.

3.3. Running time analysis

We have a strong guarantee on the running time of FastClock in the independent cascade case.

Theorem 9 (Running time of FastClock) The FastClock algorithm for the independent cascade model runs in time $O(N + n + m)$, where $m$ is the number of edges in the input graph.

Thus, the running time of FastClock is asymptotically much smaller than that of the dynamic programming estimator from DiTursi et al. (2017).

4. Proof sketches

In this section, we primarily give proof sketches (except where subsection headers indicate full proofs). Full proofs of all results are given in the appendix.

4.1. Sketch of proof of Theorem 8

The proof of Theorem 8 employs an auxiliary result (Theorem 11 in the appendix, which we call the FastClock utility theorem) stating that with high probability, for every $i$, the intersection of the ground truth infection sequence element $S_i$ with the estimated infection sequence element $\hat{S}_i$ is
asymptotically equivalent in cardinality to \( S_i \) itself. We prove this theorem by induction on the infection sequence element index \( i \), which requires a careful design of the inductive hypothesis.

Given the utility theorem, the required upper bound on the distortion \( d_{\hat{S}}(C, \hat{C}) \) follows by summing over all possible pairs \( S_i, S_j \) of infection sequence elements in \( S \), the ground truth infection sequence, then summing over all vertex pairs \( u \in S_i, v \in S_j \). This inner sum can be approximated using the utility theorem.

4.2. Full proof of Theorem 9

We analyze the worst-case running time of FastClock as follows: initialization takes \( O(1) \) time. The dominant contribution to the running time is the while loop. Since \( t_{\text{obs}} \) is initially 0 and increases by at least 1 in each iteration, the total number of iterations is at most \( N \). The remaining analysis involves showing that each vertex and edge is only processed, a constant number of times, in \( O(1) \) of these loop iterations, so that the running time is at most \( O(N + n + m) \), as claimed.

In particular, the calculation of \( \mu_t \) in every step involves a summation over all edges from currently active vertices to their uninfected neighbors, along with a calculation involving the current number of uninfected vertices (which we can keep track of using \( O(1) \) calculations per iteration of the loop). A vertex is only active in a single iteration of the loop. Thus, each of these edges is only processed once in this step. The calculation of \( t'_{\text{obs}} \) entails calculating a sum over elements of \( \hat{S} \) that are only processed once in all of the iterations of the loop. The calculation of all of the \( |\hat{S}_i| \) can be done as a preprocessing step via an iteration over all \( n \) vertices of \( G \). Finally, the calculation of \( F_{t+1} \) entails a union over the same set of elements of \( \hat{S} \) as in the calculation of the maximum, followed by a traversal of all edges incident on elements of \( \hat{S}_{t+1} \) whose other ends connect to uninfected vertices. These operations involve processing the vertices in \( \hat{S}_{t+1} \) (which happens only in a single iteration of the loop, and, thus, with the preprocessing step of calculating the \( |\hat{S}_i| \), only a constant number of times in the entire algorithm). The edges leading to elements of \( F_{t+1} \) from elements of \( \hat{S}_{t+1} \) are traversed at most twice in the loop: once in the building of \( F_{t+1} \) and once in the next iteration in the calculation of \( \mu_t \).

This implies that each vertex and edge is only processed \( O(1) \) times in the entire algorithm. This leads to the claimed running time of \( O(N + n + m) \), which completes the proof.

5. Empirical results on synthetic graphs

In this section, we present empirical results on synthetic graphs and cascades. Our goal is to confirm the theoretical guarantees of FastClock and compare it to the dynamic programming (DP) algorithm optimizing a proxy of the maximum likelihood for observed cascades proposed by DiTursi et al. (2017). Our comparative analysis focuses on (i) distance of the estimated clock from the ground truth clock (see Definition 6) and (ii) empirical running time of both techniques.

We generate synthetic graphs using both the Erdős–Rényi and the Stochastic Block Model. We then generate synthetic cascades on each graph using the independent cascade (IC) model. We employ the obtained cascade sequence \( S \) as the ground truth infection sequence, and create corresponding distorted (disaggregated) sequences \( \hat{S} \) by “stretching” each ground truth time step of \( S \). Specifically, to obtain a sample of a distorted observation sequence \( \hat{S} \), we distribute the activated nodes in the ground truth time steps to \( l \) corresponding time steps, where each node is placed in one of these \( l \) timesteps uniformly at random. Here, \( l \) is an integer \( \text{stretch} \) factor greater than 1. This implicitly specifies a clock \( C \) on the stretched timeline, which we would like to infer (we note that
While all of our experiments involve a uniformly stretched timeline, our theoretical contributions are more general. We then employ both \textit{FastClock} and DP to estimate the ground truth clock from $\hat{S}$. We draw 50 samples for each setting and report average and standard deviation for both running time and quality of estimations for each setting.

\textbf{Experiments on Erdős–Rényi graphs.} We first experiment with Erdős–Rényi to confirm the theoretical behavior of our estimator and compare its running time and quality to the DP baseline. We report the results in Figure 1. With increasing graph size \textit{FastClock}'s distance from the ground truth clock diminishes (as expected based on Theorem 8), while that of DP increases (Fig. 1(a)). Note that DP optimizes a proxy to the cascade likelihood and in our experiments tend to over-aggregate the timeline which for large graph sizes results in incorrect recovery of the ground truth clocks. Similarly, \textit{FastClock}'s quality is better than that of DP for varying on $p_n$ (Fig. 1(c)), graph density (Fig. 1(e)) and stretch factor for the cascades (Fig. 1(g)), with distance from ground truth close to 0 for regimes aligned with the key assumptions we make for our main results (Assumptions 1,2). In addition to superior quality, \textit{FastClock}'s running time scales linearly with the graph size and is orders of magnitude smaller than that of DP for sufficiently large instances (Figs. 1(b), 1(d), 1(f), 1(h)).

\textbf{Experiments on Stochastic Block Model (SBM) graphs.} We would also like to understand the behavior of our estimator on graphs with communities where the cascade may cross community boundaries. To this end, we experiment with SBM graphs varying the inter-block connectivity and virality ($p_n$) of the cascades and report results in Fig. 2. As the cross-block connectivity increases and approaches that within blocks (i.e. the graph structure approaches ER-graph) \textit{FastClock}'s quality improves and is significantly better than that of DP (Fig. 2(a)). When, however, the transmission


Figure 2: Comparison of the distance and runtime of the estimated clocks by FastClock and the baseline DP from DiTursi et al. (2017) on Stochastic Block Model graphs (default parameters: $n = 5000$, two blocks/communities of sizes $n/\sqrt{n}$ and $n - n/\sqrt{n}$, $p_n = 10^{-7}$, stretch $l = 2$). (a),(b): Varying inter-block connectivity ($p_n = 0$.1) where a setting of 0.2 makes the graph equivalent to an Erdős–Rényi graph with $p = 0.2$. (c),(d): Varying infection probability $p_n$ (inter-block connectivity is set to 0.01).

Probability $p_n$ is high, coupled with sparse inter-block connectivity, FastClock’s estimation quality deteriorates beyond that of DP (Fig. 2(e)). This behavior is due to the relatively large variance of $\mu_t$ when the cascade crosses a sparse cut in the graph with high probability. This challenging scenario opens an important research direction we plan to explore in future work.

6. Conclusions and future work

We have formulated a statistical estimation framework for the problem of recovery of all states of a discrete-time cascade from temporally distorted observation sequences. In the case of oversampling clocks, we showed that temporal distortion can be corrected with high accuracy and low computational cost, subject to certain natural constraints on the structure of the underlying graph and on the cascade model: in essence, these must be such that the graph is an expander with appropriate parameters; that, conditioned on an estimated current state of the process at any time, the expected number of vertices infected in the next timestep is immune to small errors in the estimated state; and that the number of vertices infected in the next timestep is well-concentrated around its conditional expected value. We empirically showed that the FastClock algorithm is superior in accuracy and running time to the current state of the art dynamic programming algorithm. Furthermore, unlike this baseline, FastClock comes with theoretical accuracy guarantees. Our results are formally stated for the independent cascade model, but they very likely hold for a broad class of other models, including the linear threshold model.

We intend to pursue further work on this problem: most pressingly, our empirical results and intuition derived from our theorems indicate that FastClock may not perform accurately when the graph contains very sparse cuts (so that it is not an expander graph). Further work is needed to determine whether accuracy and computational efficiency can be achieved for such graphs. Furthermore, our method relies on knowledge of the parameters of the cascade process. We intend to investigate the extent to which this assumption can be relaxed.

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Appendix A. Glossary of notation

Here we collect the notation that is used in the main body of the paper and in the proofs in the appendix.

1. $\mathcal{N}(S)$: Neighborhood of the set $S$ of vertices in a given graph.

2. $S = (S_0, S_1, ..., S_T)$ – An infection sequence generated by a cascade model with $T + 1$ timesteps. Each $S_j$ is a subset of vertices, and $S_i \cap S_j = \emptyset$ for $i \neq j$. We denote by $|S|$ the number of timesteps of $S$: $T + 1$. We think of $S$ as the ground truth infection sequence.

3. $\hat{S} = (\hat{S}_0, \hat{S}_1, ..., \hat{S}_N)$ – An observation of an infection sequence that has been temporally distorted by a clock.

4. $C$ – The ground-truth clock in our estimation problem.

5. $\hat{C}$ – The clock estimated by our algorithm.

6. $\tilde{S}$ – The estimate of the original infection sequence $S$ induced by our estimate $\hat{C}$ of the clock $C$ applied to the observed infection sequence $\hat{S}$.

7. $\sigma_t(S)$, for an infection sequence $S$ and a timestep index $t \in |S|$ – The $\sigma$-field generated by the event that the first $t$ infection sets of the IC process are given by $S_0, ..., S_t$.

8. $\mu_t(S)$, for an infection sequence $S$ and a timestep index $t \in |S|$ – $\mathbb{E}[|S_{t+1}| \mid \sigma_t(S)]$. This is the expected number of vertices infected in the $t + 1$st timestep, given the infection sequence up to and including timestep $t$.

9. $N$ – The index of the last observed infection set. That is, $|\tilde{S}| = N + 1$. 
10. $T$ – The index of the last ground truth infection set. That is, $|S| = T + 1$.
11. $n$ – The size of the graph.
12. $p_n$ – The probability in the IC model of transmission across an edge in a single timestep.
13. $p_e$ – The probability of infection of a vertex in a single timestep by a non-network source.
14. $R(S, i)$ – For an infection sequence $S$ and an index $i$, define the $i$th running sum to be
   \[ R(S, i) = \bigcup_{j \leq i} S_j. \] (15)
15. $F(S, i)$ – For an infection sequence $S$ and an index $i \in \{0, 1, \ldots, |S|\}$, define the $i$th frontier set to be
   \[ F(S, i) = N(S_i) \setminus R(S, i). \] (16)
The $i$th frontier with respect to $S$ is the set of neighbors of vertices infected in timestep $i$ that have not infected by the end of timestep $i$.
16. $\mathcal{CF}(S, i)$ – The candidate frontier set at the end of timestep $i$ in infection sequence $S$. That is, this is
   \[ \mathcal{CF}(S, i) = [n] \setminus R(S, i). \] (17)
   Note that $F(S, i) \subseteq \mathcal{CF}(S, i)$.
17. $\mathcal{CCF}(S, \tilde{S}, i, j)$ – The common candidate frontier:
   \[ \mathcal{CCF}(S, \tilde{S}, i, j) = \mathcal{CF}(S, i) \cap \mathcal{CF}(\tilde{S}, j). \] (18)

Appendix B. Proofs
In this section, we give full proofs of all results.

B.1. Proof of Theorem 8
To prove the main FastClock approximation theorem, we start by characterizing the growth of $\mu_i(S)$ and $|S_i|$ as a function of $n$ and $i$. Note that this is a result about the independent cascade process, not the FastClock algorithm.

Lemma 10 (Growth of $\mu_i(S)$ and $|S_i|$) We have that, with probability at least $1 - e^{-np}$, for all $i \leq T$,
\[ \mu_i(S) = \Theta((np)^{i+1}), \] (19)
where the $\Theta(\cdot)$ is uniform in $i$. Furthermore, with probability at least $1 - e^{-np}$, we have
\[ |S_i| = \Theta((np)^i) \] (20)
for every $i$.

Proof We prove this by induction on $i$ and use the formula (12) throughout.
**Base case** \((i = 0)\): In the base case, we are to verify that \(\mu_0(S) = \Theta(np)\). The first term of (12) is non-negative and at most \(p \cdot n\). By our assumption, we have that \(p = o(p_n)\), implying that the first term is \(o(np)\). Thus, it remains for us to show that the second sum is \(\Theta(np)\). The dominant contribution comes from the second term of each term of the sum:

\[
\sum_{v \in \mathcal{F}_0(S)} (p_e + (1 - p)(1 - (1 - p_n)))^{\deg_S_0(v)} = \Theta(\sum_{v \in \mathcal{F}_0(S)} 1 - (1 - p_n)^{\deg_S_0(v)})
\]

(21)

\[
= \Theta(|\mathcal{F}_0(S)| + \sum_{v \in \mathcal{F}_0(S)} (1 - p_n)^{\deg_S_0(v)}).
\]

(22)

In the final expression above, the remaining sum is lower bounded by 0 and upper bounded by \(|\mathcal{F}_0(S)|\), since each term is between 0 and 1. Thus, we have shown that, with probability exactly 1,

\[
\mu_0(S) = \Theta(|\mathcal{F}_0(S)|) + o(np).
\]

(23)

Since \(|\mathcal{F}_0(S)|\) is the set of uninfected neighbors of all vertices in \(S_0\), and, by assumption, \(|S_0| = \Theta(1)\), we have that with probability at least \(1 - e^{-np}\),

\[
|\mathcal{F}_0(S)| = \Theta(np).
\]

(24)

Thus, we have

\[
\mu_0(S) = \Theta(np)
\]

(25)

with probability \(\geq 1 - e^{-np}\). Conditioning on this event (which is only an event dealing with the graph structure), we have that \(|S_1| \sim \text{Binomial}(\Theta(np), p_n)\), and a Chernoff bound gives us that with probability \(1 - e^{-\Omega(np)}\), \(|S_1| = \Theta(np)\), as desired. This completes the proof of the base case.

**Induction** \((i > 0, \text{ and we verify the inductive hypothesis for } i)\): We assume that \(\mu_j(S) = \Theta((np)^{j+1})\) and \(|S_{j+1}| = \Theta((np)^{j+1})\) for \(j = 0, 1, \ldots, i - 1\). We must verify that it holds for \(j = i\), with probability at least \(1 - e^{-np}\). As in the base case, the first term of (12) is \(O(np) \ll np \ll (np)^{i+1}\). It is, therefore, negligible with probability 1. The second term again provides the dominant contribution and is easily seen to be \(\Theta(|\mathcal{F}_i(S)|)\), just as in the base case. Thus, it remains to show that \(|\mathcal{F}_i(S)| = \Theta((np)^{i+1})\) with probability at least \(1 - e^{-\Omega(np)}\), which implies the desired result for \(\mu_i(S)\). The inductive hypothesis implies that \(|S_i| = \Theta((np)^i)\), and the number of uninfected vertices is \(n - \sum_{j=0}^{i} |S_j| = n - \Theta((np)^{i+1})\). Since \(i \leq T - 1\), this is asymptotically equivalent to \(n\).

Now, conditioned on the first \(i\) elements of \(S\), the \(i\)th frontier \(|\mathcal{F}_i(S)| \sim \text{Binomial}(n \cdot (1 - o(1)), 1 - (1 - p)^{|S_i|})\). Thus, with probability at least \(1 - e^{-\Omega((np)^i)}\), we have

\[
|\mathcal{F}_i(S)| = \Theta(n \cdot (1 - (1 - p)^{|S_i|})).
\]

(26)

Now,

\[
1 - (1 - p)^{|S_i|} = 1 - (1 - p)^{(np)^i}.
\]

(27)

Since \(p = o(1)\), we have

\[
1 - (1 - p)^{(np)^i} \sim 1 - e^{-p^{i+1}n^i}
\]

(28)
From (68) below, we have that
\[ p^{i+1}n^i = o(1). \]  
(29)

This implies that
\[ 1 - e^{-p^{i+1}n^i} = 1 - (1 - p^{i+1}n^i)(1 + O(p^{i+1}n^i)) = p^{i+1}n^i(1 + o(1)). \]  
(30)

Thus, with probability at least \( 1 - e^{-\Omega((np)^i)} \),
\[ |F_i(S)| = \Theta((np)^{i+1}), \]  
(31)

which implies that
\[ \mu_i(S) = \Theta((np)^{i+1}). \]  
(32)

By concentration of \(|S_i|\), we then have that with probability at least \( 1 - e^{-\Omega(\mu_i(S))} \),
\[ |S_i| = \Theta((np)^{i+1}), \]  
(33)

as desired.

**Completing the proof**  Let \( G_i \) be the event that the inductive hypothesis holds for index \( i = 0, 1, \ldots, T - 1 \). Then we have
\[ \Pr[\bigcap_{i \geq 0} G_i] = \Pr[G_0] \cdot \prod_{i \geq 1} \Pr[G_i \mid \bigcap_{j=0}^{i-1} G_j] \geq \prod_{i=0}^{T-1} (1 - e^{-\Omega((np)^i)}) (1 - e^{-\Omega(np)}). \]  
(34)

This completes the proof.

Next, we state and prove a utility theorem (Theorem 11 below). To state it, we need some notation: our estimated clock \( \hat{C} \) induces an estimate \( \tilde{S} \) of the ground truth infection sequence \( S \). In particular, \( \tilde{S} \) is the unique infection sequence such that distorting \( \tilde{S} \) according to \( \hat{C} \) yields \( \hat{S} \) as an observed infection sequence.

**Theorem 11 (Main FastClock analysis utility theorem)**  We have that with probability \( 1 - e^{-\Omega(np)} \), for every \( i \leq T - 1 \),
\[ |S_i \cap \tilde{S}_i| = |S_i| \cdot (1 - O((np)^{-1/3})). \]  
(35)

We will prove this theorem by induction on \( i \). The inductive hypothesis needed is subtle, as a naive hypothesis is too weak. To formulate it and to prove our result, we need some notation: for an infection sequence \( W \), we define the \( i \)th running sum to be
\[ R(W, i) = \bigcup_{j=0}^{i} W_j. \]  
(36)
We define the **frontier** and **running sum discrepancy sets** as follows:

\[ \Delta F(S, \hat{S}, i, j) = F_i(S) \triangle F_j(\hat{S}) \]  
\[ \Delta R(S, \hat{S}, i, j) = R(S, i) \triangle R(\hat{S}, j), \]

where \( \triangle \) denotes the symmetric difference between two sets.

We define the **candidate frontier** at timestep \( i \) in infection sequence \( S \) to be

\[ CF(S, i) = [n] \setminus R(S, i). \]  

This is the set of vertices that are not yet infected after timestep \( i \).

We define the **common candidate frontier** to be

\[ CCF(S, \hat{S}, i, j) = CF(S, i) \cap CF(\hat{S}, j). \]

With this notation in hand, we define the following inductive hypotheses:

1. There is a small discrepancy between the running sums of the true and estimated clocks:

\[ ||R(S, i) - |R(\hat{S}, i)||| \leq f_1(n, i), \]

where we set, with foresight, \( f_1(n, i) = \mu_i - 1(S)^{66} = o(\mu_i - 1(S)^{2/3}) \).

2. There is a small discrepancy between \( S_i \) and \( \hat{S}_i \):

\[ 1 - \frac{|S_i \cap \hat{S}_i|}{|S_i|} \leq f_2(n, i), \]

where we set, with foresight, \( f_2(n, i) = D \cdot \mu_i - 1(S)^{-1/3} \), for some large enough absolute constant \( D \).

We will use these to prove Theorem 11. The base case and inductive steps are proven in Propositions 13 and 14 below. First, we start by proving an upper bound (Theorem 12) on the following difference:

\[ |\mu_i(S) - \mu_i(\hat{S})|. \]

In essence, the upper bound says that at any given clock time step, the expected number of nodes infected in the next timestep is almost the same according to both the true and estimated clock. This will later be used verify the two inductive hypotheses stated above.

**Theorem 12 (Upper bound on (43))** Granted the inductive hypotheses explained above, we have that

\[ |\mu_i(S) - \mu_i(\hat{S})| \leq p\mu_i - 1(S)^{2/3}\mu_i(S), \]

with probability \( \geq 1 - e^{-\Omega(\mu_i(S))} \).
This decomposition holds for the following reason: let decompose it as follows:

\[ \Delta \text{ is a member of at least one of } R \]

member of \( R \) or \( \tilde{R} \). We will show that it must be a \( \Delta \) cannot be a member of the frontier discrepancy set. Thus, it one of these). If it were a member of both, then it would not be a member of either frontier, so it could not be a member of the frontier discrepancy set. This implies that \( v \in \Delta R(S, \tilde{S}, i, i) \). This directly implies the claimed decomposition (49).

We now compute the expected value of each term of the right-hand side of (49), where the expectation is taken with respect to the graph \( G \). After upper bounding the expectations, standard concentration inequalities will complete our claimed bound on the size of the frontier discrepancy set.

In the first term, the size of the intersection of the frontier discrepancy with the running sum discrepancy is simply the number of vertices in the running sum discrepancy set that have at least one edge to some vertex in \( S_i \) (here we assume, without loss of generality, that \(|R(S, i)| \leq |R(\tilde{S}, i)|\)). Using linearity of expectation, the expected number of such vertices is

\[ \mathbb{E}[|\Delta F(S, \tilde{S}, i, i) \cap \Delta R(S, \tilde{S}, i, i)|] = |\Delta R(S, \tilde{S}, i, i)| \cdot (1 - (1 - p)^{|S_i|}). \]

Here \((1 - (1 - p)^{|S_i|})\) is the probability that, for a fixed vertex \( w \in \Delta R(S, \tilde{S}, i, i) \), there is at least one edge between \( w \) and some vertex in \( S_i \).

We compute the expected value of the second term of (49) as follows.
We claim that

\[ \Delta F(S, \tilde{S}, i, i) \cap \mathbb{C} \mathbb{F}(S, \tilde{S}, i, i) \subseteq \mathbb{C} \mathbb{F}(S, \tilde{S}, i, i) \cap (\mathcal{N}(\Delta R(S, \tilde{S}, i, i)) \setminus \mathcal{N}(S_i)). \]  

(51)

To show this, let \( v \in \Delta F(S, \tilde{S}, i, i) \cap \mathbb{C} \mathbb{F}(S, \tilde{S}, i, i) \). The fact that \( v \) is in the frontier discrepancy set means that it has an edge to exactly one of \( S_i, \tilde{S}_i \). This implies that it has an edge to the running sum discrepancy set. Recalling that we assumed wlog that \( |R(S, i)| \leq |R(\tilde{S}, i)| \), we must have that \( \Delta R(S, \tilde{S}, i, i) \cap S_i = \emptyset \), and so we must also have that there are no edges from \( v \) to \( S_i \). This completes the proof of the claimed set inclusion. This implies that

\[ \mathbb{E}[|\Delta F(S, \tilde{S}, i, i) \cap \mathbb{C} \mathbb{F}(S, \tilde{S}, i, i)|] \leq \mathbb{E}[|\mathbb{C} \mathbb{F}(S, \tilde{S}, i, i) \cap (\mathcal{N}(\Delta R(S, \tilde{S}, i, i)) \setminus \mathcal{N}(S_i))|]. \]

(52)

As above, the expectation is taken with respect to the random graph \( G \).

For a single vertex in the common candidate frontier, the probability that it lies in the frontier discrepancy set is thus at most

\[ (1 - (1 - p)^{|\Delta R(S, \tilde{S}, i, i)|}) \cdot (1 - p)^{|S_i|}. \]

(53)

Thus, using linearity of expectation, the expected size of the second term in (49) is upper bounded by

\[ \mathbb{E}[|\Delta F(S, \tilde{S}, i, i) \cap \mathbb{C} \mathbb{F}(S, \tilde{S}, i, i)| | \sigma_i(S)] \leq |\mathbb{C} \mathbb{F}(S, \tilde{S}, i, i)| \cdot (1 - (1 - p)^{|\Delta R(S, \tilde{S}, i, i)|}) \cdot (1 - p)^{|S_i|}. \]

(54)

Combining (50) and (54) and defining \( q = 1 - p \), we have the following expression for the expected size of the frontier discrepancy set:

\[ \mathbb{E}[|\Delta F(S, \tilde{S}, i, i)|] = |\Delta R(S, \tilde{S}, i, i)| \cdot (1 - q^{|S_i|}) \]

(55)

\[ + |\mathbb{C} \mathbb{F}(S, \tilde{S}, i, i)| \cdot (1 - q^{|\Delta R(S, \tilde{S}, i, i)|}) \cdot q^{|S_i|}. \]

(56)

We would like this to be \( O(\mathbb{E}[|\mathbb{F}_i(S)| | \sigma_i(S)]) \). Note that \( \mathbb{E}[|\mathbb{F}_i(S)| | \sigma_i(S)] \) can be expressed as follows:

\[ \mathbb{E}[|\mathbb{F}_i(S)| | \sigma_i(S)] = (|\Delta R(S, \tilde{S}, i, i)|

+ |\mathbb{C} \mathbb{F}(S, \tilde{S}, i, i)|) \cdot (1 - q^{|S_i|}). \]

(58)

The intuition behind (55) being \( O(\mathbb{E}[|\mathbb{F}_i(S)| | \sigma_i(S)]) \) is as follows: the \( \Delta R \) term is exactly the same as in (58). However, this term is negligible compared to the common candidate frontier term in both expected values. The second term, (57), can be asymptotically simplified as follows: we have

\[ 1 - q^{|\Delta R(S, \tilde{S}, i, i)|} = 1 - (1 - p)^{|\Delta R(S, \tilde{S}, i, i)|} \approx 1 - (1 - p) \cdot |\Delta R(S, \tilde{S}, i, i)| \]

(60)

\[ = p \cdot |\Delta R(S, \tilde{S}, i, i)| \]

(61)

(62)
\[= p|S_i| \cdot \frac{\Delta R(S, \tilde{S}, i, i)}{|S_i|} \]

\[\sim (1 - q|S_i|) \cdot \frac{\Delta R(S, \tilde{S}, i, i)}{|S_i|}.\]

Here, we have used the following facts:

- For the first asymptotic equivalence, we used the fact that \(p|\Delta R(S, \tilde{S}, i, i)| = o(1)\). More precisely, we have from the inductive hypothesis that

\[|\Delta R(S, \tilde{S}, i, i)| = o(\mu_{i-1}(S)^{0.66}) = o((np)^{i-0.66})\],

so we have

\[p|\Delta R(S, \tilde{S}, i, i)| = o(p^{0.66i+1}n^{0.66i}) = o(n^{-T/(T+1) + 0.66i/(T+1)}),\]

which is polynomially decaying in \(n\).

- For the second asymptotic equivalence, we used the fact that \(p|S_i| = o(1)\). More precisely, this comes from the fact that

\[p|S_i| = O(p(np)^i) = O(p^{i+1}n^i).\]

Now, we use the fact that \(p = o(n^{-\frac{T}{T+1}})\):

\[p^{i+1}n^i = o(n^{-\frac{T}{T+1}(i+1)+i}),\]

from our assumption on the growth of \(p\). Now, we need to show that the exponent is sufficiently negative and bounded away from 0.

\[-\frac{T}{T+1}(i + 1) + i = \frac{-T \cdot (i + 1) + i \cdot (T + 1)}{T + 1} = \frac{-T + i}{T + 1} \leq \frac{-1}{T + 1}.\]

We have used the fact that \(i \leq T - 1\). Now, the constraints that we imposed on \(p\) imply that \(T = o(\log n)\), so

\[n^{-\frac{T}{T+1}} = e^{-\log n} = o(1),\]

as desired, since the exponent tends to \(-\infty\) as \(n \to \infty\).

Let us be more precise about what we proved so far. We have

\[\mathbb{E}[|\Delta F(S, \tilde{S}, i, i)| \mid \sigma_i(S)] \sim (1 - q|S_i|) \cdot |\mathcal{CF}(S, \tilde{S}, i, i)| \cdot \left(\frac{|\Delta R|}{|\mathcal{CF}|} + \frac{|\Delta R|}{|S_i|} q|S_i|\right).\]
We have that
\[ \frac{\mathbb{E}[\Delta F_i \mid \sigma_i(S)]}{\mathbb{E}[|\mathcal{F}_i| \mid \sigma_i(S)]} \sim \frac{\mid \Delta R \mid_{\mathcal{C}C\mathcal{F}} + \mid \Delta R \mid_{\mathcal{C}C\mathcal{F}} \cdot q^{|S_i|}}{1 + \mid \Delta R \mid_{\mathcal{C}C\mathcal{F}}}. \]  
(73)

This can be simplified as follows:
\[ \frac{\mathbb{E}[\Delta F_i \mid \sigma_i(S)]}{\mathbb{E}[|\mathcal{F}_i| \mid \sigma_i(S)]} \sim \frac{\mid \Delta R \mid_{\mathcal{C}C\mathcal{F}} + \mid \Delta R \mid_{\mathcal{C}C\mathcal{F}} \cdot q^{|S_i|}}{1 + \mid \Delta R \mid_{\mathcal{C}C\mathcal{F}}} = \frac{\mid \Delta R \mid \cdot \left(1 + \frac{\mid \mathcal{C}C\mathcal{F}\mid q^{|S_i|}}{\mid \mathcal{C}C\mathcal{F}\mid + \mid \Delta R \mid}\right)}{\mid \mathcal{C}C\mathcal{F}\mid + \mid \Delta R \mid}. \]  
(74)

This can be upper bounded as follows, by distributing in the numerator and upper bounding \( \mid \Delta R \mid \) by \( \mid \Delta R \mid + \mid \mathcal{C}C\mathcal{F}\mid \) in the numerator of the resulting first term:
\[ \frac{\mid \Delta R \mid \cdot \left(1 + \frac{\mid \mathcal{C}C\mathcal{F}\mid q^{|S_i|}}{\mid \mathcal{C}C\mathcal{F}\mid + \mid \Delta R \mid}\right)}{\mid \mathcal{C}C\mathcal{F}\mid + \mid \Delta R \mid} \leq 1 + \frac{\mid \Delta R \mid \cdot \mid \mathcal{C}C\mathcal{F}\mid q^{|S_i|}}{\mid \mathcal{C}C\mathcal{F}\mid (\mid \mathcal{C}C\mathcal{F}\mid + \mid \Delta R \mid)}. \]  
(75)

We can further upper bound by noticing that \( \mid \mathcal{C}C\mathcal{F}\mid + \mid \Delta R \mid \geq \mid \mathcal{C}C\mathcal{F}\mid \), so
\[ \frac{\mathbb{E}[\Delta F_i \mid \sigma_i(S)]}{\mathbb{E}[|\mathcal{F}_i| \mid \sigma_i(S)]} \leq 1 + \frac{\mid \Delta R \mid}{\mid S_i \mid}. \]  
(76)

Now, by our inductive hypothesis, we know that \( \mid \Delta R \mid_i = o(\mu_{i-1}(S)^{0.66}) \), and by concentration, we know that \( \mid S_i \mid = \Theta(\mu_{i-1}(S)) \). Thus, we have
\[ \frac{\mathbb{E}[\Delta F_i \mid \sigma_i]}{\mathbb{E}[|\mathcal{F}_i| \mid \sigma_i]} \leq 1 + \frac{\mid \Delta R \mid}{\mid S_i \mid} = 1 + o(\mu_{i-1}(S)^{-(1-0.66)}) = O(1). \]  
(77)

Thus,
\[ \mathbb{E}[\Delta F(S, \tilde{S}, i, i) \mid \sigma_i(S)] = O(\mathbb{E}[|\mathcal{F}_i(S)| \mid \sigma_i(S)]). \]  
(78)

Now, remember that our goal is to show that \( \mid \Delta F(C, \tilde{C}, i, i) \mid = O(\mathbb{E}[|\mathcal{F}_i(C)|]) \) with high probability, conditioned on \( \sigma_i(S) \). This follows from the expectation bound above and the fact that the size of the frontier in both clocks is binomially distributed, so that standard concentration bounds apply. This results in the following:
\[ p_c \mid \Delta F_i \mid = O(p_c |\mathcal{F}_i|) \]  
(79)

with conditional probability at least \( 1 - e^{-\Omega((np)^{1})} \).

**Upper bounding (46) by \( o(p_c |R(S, i)|) \):** To upper bound (46), we note that
\[ \sum_{j=0}^{i} |S_j| = |R(S, i)|, \]  
(80)

and an analogous identity holds with \( \tilde{S} \) in place of \( S \). Moreover,
\[ \mid R(S, i) - R(\tilde{S}, i) \mid = \mid \Delta R(S, \tilde{S}, i, i) \mid. \]  
(81)
Thus, we have

\[(46) = p_e |\Delta R(S, \tilde{S}, i, i)| \leq p_e f_1(n, i), \tag{82}\]

where the inequality is by the inductive hypothesis. We want this to be \(o(p_e \cdot |R(S, i)|)\), which means that we want \(|\Delta R(S, \tilde{S}, i, i)| = o(|R(S, i)|)\). This is follows from the inductive hypothesis.

In particular, we know that \(|R(S, i)| \geq |S_i|\), since \(S_i \subset R(S, i)\). Furthermore, we have by the inductive hypothesis that \(|\Delta R(S, \tilde{S}, i, i)| = o(\mu_{i-1}(S)^{0.66} = o(|S_i|^{0.66})\). Thus, we have

\[p_e |\Delta R(S, \tilde{S}, i, i)| = o(p_e |R(S, i)|), \tag{83}\]

with (conditional) probability 1, as desired.

Upper bounding (47) by \(\sum_{v \in \mathbb{F}_i(S)} Q(i, S, v)p_{\mu_{i-1}^2(S)}\): To upper bound (47), we apply the triangle inequality and extend both sums to \(v\) in \(\mathbb{F}_i(S) \cup \mathbb{F}_i(\tilde{S})\). This results in the following upper bound:

\[(47) \leq \sum_{v \in \mathbb{F}_i(S) \cup \mathbb{F}_i(\tilde{S})} |Q(i, S, v) - Q(i, \tilde{S}, v)|. \tag{84}\]

To proceed, we will upper bound the number of nonzero terms in (84). Each nonzero term can be upper bounded by 1, since \(Q(i, S, v), Q(i, \tilde{S}, v)\) are both probabilities. We will show that the number of nonzero terms is at most \(O(|\mathbb{F}_i(S)|p \cdot \mu_{i-1}^{2/3}(S))\) with high probability.

We write

\[
Q(i, S, v) - Q(i, \tilde{S}, v) = p_e + (1 - p_e)(1 - (1 - p_n)^{\text{deg}_S(v)}) - p_e - (1 - p_e)(1 - (1 - p_n)^{\text{deg}_{\tilde{S}_i}(v)}) = (1 - p_e)((1 - p_n)^{\text{deg}_S(v)} - (1 - p_n)^{\text{deg}_{\tilde{S}_i}(v)}). \tag{85}\]

Thus, a term in the sum (84) is nonzero if and only if \(\text{deg}_S(v) \neq \text{deg}_{\tilde{S}_i}(v)\). This happens if and only if \(v\) has at least one edge to some vertex in \(\tilde{S}_i - S_i\). Thus, our task reduces to figuring out how many vertices \(v\) there are that connect to some element of \(\tilde{S}_i - S_i\). The expected number of such vertices is

\[|\mathbb{F}_i(S) \cup \mathbb{F}_i(\tilde{S})| \cdot (1 - q^{|\tilde{S}_i - S_i|}). \tag{86}\]

This is an upper bound on the contribution of (47). We thus have

\[(47) \leq |\mathbb{F}_i(S) \cup \mathbb{F}_i(\tilde{S})| \cdot (1 - q^{|\tilde{S}_i - S_i|}). \tag{87}\]

Next, we show that \(|\mathbb{F}_i(S) \cup \mathbb{F}_i(\tilde{S})| = O(|\mathbb{F}_i(S)|)\). To do this, we apply the results from upper bounding (45). In particular,

\[|\mathbb{F}_i(S) \cup \mathbb{F}_i(\tilde{S})| = |\mathbb{F}_i(S) \cap \mathbb{F}_i(\tilde{S})| + |\Delta \mathbb{F}(S, \tilde{S}, i, i)| \leq |\mathbb{F}_i(S)| + |\Delta \mathbb{F}(S, \tilde{S}, i, i)| = O(|\mathbb{F}_i(S)|). \tag{88}\]
Next, we show that $1 - q^{\tilde{S}_i - S_i} = p \mu_{i-1}^{2/3}(S)$. We can write

$$q^{\tilde{S}_i - S_i} = (1 - p)^{|\tilde{S}_i - S_i|} \sim e^{-p|\tilde{S}_i - S_i|},$$

(91)

provided that $p \cdot |\tilde{S}_i - S_i| = o(1)$. Now from the inductive hypothesis, $|\tilde{S}_i - S_i| = O(|S_i|^{2/3})$, and from Lemma 10, we know that $|S_i| = O((np)^i)$. Then we have that

$$1 - q^{\tilde{S}_i - S_i} \leq 1 - e^{-O(p(np)^{2/3})}.$$  

(92)

In order for this second term to be $1 - o(1)$, it is sufficient to have that

$$p^{i+1}n^i = o(1).$$

(93)

This happens if and only if

$$p^{i+1} = o(n^{-i}) \iff p = o(n^{-i+1}).$$

(94)

This is guaranteed by our assumption that $p = o(n^{-\frac{i}{i+1}})$. Thus,

$$1 - q^{\tilde{S}_i - S_i} \leq 1 - e^{-O(p(np)^{2/3})} \sim p \mu_{i-1}^{2/3}(S).$$

(95)

We have shown that

$$(47) = O(\|F_i(S)\|p \mu_{i-1}^{2/3}(S)).$$

(96)

Next, we show that $\sum_{v \in F_i(S)} Q(i, S, v) = \Omega(\|F_i(S)\|)$. We have

$$Q(i, s, v) \geq 1 - (1 - p_n)^{\deg_{S_i}(v)}.$$  

(97)

Since the sum is over $v \in F_i(S)$, this implies that $\deg_{S_i}(v) \geq 1$. So

$$Q(i, C, v) \geq 1 - (1 - p_n) = p_n = \Omega(1).$$

(98)

Thus,

$$\sum_{v \in F_i(S)} Q(i, C, v) \geq \|F_i(S)\| \cdot p_n = \Omega(\|F_i(S)\|).$$

(99)

Thus, we have shown that

$$(47) \leq \text{const} \cdot \sum_{v \in F_i(C)} Q(i, C, v) \cdot (1 - q^{\tilde{C}_i - C_i}) = \text{const} \sum_{v \in F_i(C)} Q(i, C, v)p \mu_{i-1}^{2/3}(C),$$

(100)

with conditional probability at least $1 - e^{-\Omega((np)^i)}$.  

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Completing the proof  We combine (100), (79), and (83) to complete the proof.

So we have that the difference between $\mu_i(C)$ and $\mu_i(\hat{C})$ is negligible in relation to $\mu_i(C)$.

Now, the next two propositions give the base case and inductive step of the proof of Theorem 11.

**Proposition 13 (Base case of the proof of Theorem 11)** We have that, with probability 1,

$$|\Delta R_0| = |\Delta R(S, \tilde{S}, 0, 0)| = 0,$$

and

$$|\tilde{S}_0 \triangle S_0| = 0.$$  \hspace{1cm} (101)

**Proof** This follows directly from the assumed initial conditions. \hfill \square

**Proposition 14 (Inductive step of the proof of Theorem 11)** Assume that the inductive hypotheses (41) and (42) hold for $i$. Then we have the following:

$$|\tilde{S}_{i+1} \triangle S_{i+1}| \leq |\Delta R_i| = |\Delta R(S, \tilde{S}, i, i)| = o(\mu_{i-1}(S)^{2/3}) = o(\mu_i(S)^{2/3}).$$  \hspace{1cm} (103)

Equivalently,

$$1 - \frac{|\tilde{S}_{i+1} \cap S_{i+1}|}{|S_i|} = o(\mu_i(S)^{2/3}).$$  \hspace{1cm} (104)

Furthermore,

$$|\Delta R_{i+1}| \leq |\Delta R_i| \leq o(\mu_{i-1}(S)^{2/3}) = o(\mu_i(S)^{2/3}).$$  \hspace{1cm} (105)

In other words, both inductive hypotheses are satisfied for $i+1$. This holds with probability at least $1 - e^{-\Theta(\mu_i(C))}$.

**Proof** To prove this, we first need a few essential inequalities.

- By definition of the algorithm,

  $$|\tilde{S}_{i+1}| \leq \mu_i(\tilde{S})(1 + \mu_i(\tilde{S})^{-1/3}),$$

  with probability 1.  \hspace{1cm} (106)

- We will also need to prove an upper bound on $|\tilde{S}_{i+1}| - |S_{i+1}|$. In particular, we will show that with probability at least $1 - e^{-\Theta(\mu_i(S))}$,

  $$|\tilde{S}_{i+1}| \leq |S_{i+1}| \cdot (1 + O(\mu_i(S)^{-1/3})).$$

  We show this as follows. From Theorem 12,

  $$\mu_i(\tilde{S}) \leq \mu_i(S)(1 + p\mu_{i-1}(S)^{2/3}),$$
with probability $\geq 1 - e^{-\Omega(\mu_i(S))}$. This implies, via (106), that

$$|\tilde{S}_{i+1}| \leq \mu_i(S) \cdot (1 + p\mu_{i-1}(S)^{2/3} \cdot (1 + O(\mu_i(S)^{-1/3})).$$

By concentration of $|S_{i+1}|$, with probability at least $1 - e^{-\Omega(\mu_i(S))}$, this is upper bounded as follows:

$$|\tilde{S}_{i+1}| \leq |S_{i+1}|(1 + O(|S_{i+1}|^{-1/2 + const}))(1 + p\mu_{i-1}(S)^{2/3}(1 + O(\mu_i(S)^{-1/3})).$$

Now, we can see from (68) that this is equal to the desired upper bound. We have thus shown (107).

Now, with the preliminary inequalities proven, we proceed to prove the proposition. We split into two cases:

- $S_{i+1}$ begins before $\tilde{S}_{i+1}$ (in other words, $|R(S,i)| < |R(\tilde{S},i)|$).

  In this case, we will show (i) that $S_{i+1}$ must end before $\tilde{S}_{i+1}$ (i.e., that $|R(S,i+1)| \leq |R(\tilde{S},i+1)|$) with high probability, (ii) that

$$\Delta R_{i+1} = 0,$$

and (iii) that

$$|\tilde{S}_{i+1} \triangle S_{i+1}| \leq |\Delta R_i|.$$

To show that (i) is true, we note that because $S_{i+1}$ begins before $\tilde{S}_{i+1}$, $S_{i+1}$ consists of an initial segment $\tilde{S}_j, \tilde{S}_{j+1}, \ldots, \tilde{S}_{j_2}$ with total cardinality $|\Delta R_i|$, ending in an observation endpoint (specifically, the one corresponding to $R(\tilde{S},i)$), followed by a segment $\hat{S}_{j_2+1}, \ldots, \hat{S}_{j_3}$ of total cardinality $|S_{i+1}| - |\Delta R_i|$, again ending in an observation endpoint. This is true by definition of $\Delta R_i$. The second segment begins at the same point as $\tilde{S}_{i+1}$ (that is, $R(\tilde{S},i) = \bigcup_{j=0}^{j_2+1} \tilde{S}_j$), and we know that it has cardinality

$$|S_{i+1}| - |\Delta R_i| \leq |S_{i+1}| \leq \mu_i(S)(1 + \mu_i(S)^{-1/2 + const}) \leq \mu_i(\tilde{S})(1 + \mu_i(\tilde{S})^{-1/3}),$$

by concentration of $|S_{i+1}|$. The last inequality follows from the fact that $\mu_i(S) = \Theta(\mu_i(\tilde{S}))$. Thus, the second segment of $S_{i+1}$ must be contained in $\tilde{S}_{i+1}$, by (106), by definition of the FastClock algorithm, as desired.

This has the following implication: we can express $|\Delta R_{i+1}|$ as

$$|\Delta R_{i+1}| = |\tilde{S}_{i+1}| - (|S_{i+1}| - |\Delta R_i|) \leq \mu_i(S)^{-1/3} + |\Delta R_i|.$$  

We have used (107). Since, by the inductive hypothesis, we have $|\Delta R_i| = o(\mu_{i-1}(C)^{0.66})$, and since this is $o(|C_{i+1}|)$, we have that

$$|\Delta R_{i+1}| = 0,$$

by Assumption 1 that no observation interval has too few vertices. This follows because, if $\Delta R_{i+1}$ were nonempty, then it would contain an observation interval (i.e., $\tilde{S}_j$ for some $j$)
with cardinality at most \( o(|S_{i+1}|) \) that is a subset of \( S_{i+1} \). This contradicts Assumption 1. Thus, we have established (ii).

We next show (iii). We have

\[
|\tilde{S}_{i+1} \triangle S_{i+1}| \leq |\Delta R_i|,
\]

by the fact that \( |\tilde{S}_{i+1} \triangle S_{i+1}| = |\Delta R_i| + |\Delta R_{i+1}| \).

- **Or** \( S_{i+1} \) begins after or at the same time as \( \tilde{S}_{i+1} \) (in other words, \( |R(S, i)| \geq |R(\tilde{S}, i)| \)).

In this case, we will show (i) that

\[
|\Delta R_{i+1}| = 0,
\]

and (ii) that

\[
|\tilde{S}_{i+1} \triangle S_{i+1}| \leq |\Delta R_i|.
\]

This is because of the following identity:

\[
|\tilde{S}_{i+1}| = |\Delta R_i| + |S_{i+1}| + |\Delta R_{i+1}|I_{i+1},
\]

where

\[
I_{i+1} = \begin{cases} 
1 & \text{if } S_{i+1} \text{ stops before } \tilde{S}_{i+1} \\
-1 & \text{otherwise}
\end{cases}
\]

This is a consequence of the following derivation, which relies on the definitions of all involved terms.

\[
|\Delta R_i| + |S_{i+1}| + |\Delta R_{i+1}|I_{i+1} = \sum_{k=0}^{i} |S_k| - \sum_{k=0}^{i} |\tilde{S}_k| + |S_{i+1}| + \sum_{k=0}^{i+1} |S_k| - \sum_{k=0}^{i+1} |\tilde{S}_k| |I_{i+1}|
\]

\[
= \sum_{k=0}^{i} |S_k| - \sum_{k=0}^{i} |\tilde{S}_k| - \left( \sum_{k=0}^{i+1} |S_k| - \sum_{k=0}^{i+1} |\tilde{S}_k| \right)
\]

\[
= |\tilde{S}_{i+1}|.
\]

Rearranging (116) to solve for \( |\Delta R_{i+1}| \), we have that

\[
|\Delta R_{i+1}| = ||\tilde{S}_{i+1}| - |\Delta R_i| - |S_{i+1}||
\]

\[
\leq ||\tilde{S}_{i+1}| - |S_{i+1}|| + |\Delta R_i|
\]

\[
= ||\tilde{S}_{i+1}| - |S_{i+1}|| + o(\mu_{i-1}(S)^{2/3})
\]

\[
\leq O(\mu_i(S)^{-1/3}) + o(\mu_{i-1}(S)^{2/3})
\]

\[
= o(\mu_i(S)).
\]

Here, we have used the triangle inequality and the inductive hypothesis on \( |\Delta R_i| \), followed by the inequality (107).
Since $|\Delta R_{i+1}| = o(\mu_i(C))$, it must be 0 because of Assumption 1, which verifies the inductive hypothesis on $|\Delta R_{i+1}|$.

Furthermore, this implies that

$$|\tilde{S}_{i+1} \triangle S_{i+1}| \leq |\Delta R_i|,$$

which verifies the inductive hypothesis on $|\tilde{S}_{i+1} \triangle S_{i+1}|$.

The inductive hypotheses follow directly from the above.

We can now prove the utility theorem, Theorem 11.

**Proof [Proof of Theorem 11]** Let $B_i$ denote the bad event that either inductive hypothesis fails to hold at step $i$. We will lower bound

$$\Pr[\bigcap_{i=0}^{T-1} \neg B_i].$$

By the chain rule, we have

$$\Pr[\bigcap_{i=0}^{T-1} \neg B_i] = \Pr[\neg B_0] \prod_{i=1}^{T-1} \Pr[\neg B_i \mid \bigcap_{j=0}^{i-1} \neg B_j].$$

From Proposition 14, Proposition 13, and Lemma 10, this is lower bounded by

$$\prod_{i=1}^{T-1} (1 - e^{-D(\text{np})^{i+1}}) = \exp \left( \sum_{i=1}^{T-1} \log \left( 1 - e^{-D(\text{np})^{i+1}} \right) \right)$$

$$= \exp \left( - \sum_{i=1}^{T-1} e^{-D(\text{np})^{i+1}} \cdot (1 + o(1)) \right)$$

$$= 1 - e^{-\Omega(\text{np})}.$$

Now, the event that none of the bad events hold implies the claim, which completes the proof.

We can now prove the main result, Theorem 8.

**Proof [Proof of Theorem 8]** Let us recall the definition of $d_{\hat{S}}(C, \hat{C})$. We have

$$d_{\hat{S}}(C, \hat{C}) = \frac{1}{2} \sum_{i<j} \text{Dis}_{C, \hat{C}}(i, j).$$

What we need is an upper bound on this quantity in terms of the error term $f(n) = (\text{np})^{-1/3}$ in Theorem 11. To this end, we partition the sum according to vertex membership in clock intervals as follows:

$$\left(\begin{array}{c}n \\ 2\end{array}\right) d_{\hat{S}}(C, \hat{C}) = \sum_{k_1=1}^{[S]} \sum_{i<j \in S_{k_1}} \text{Dis}_{C, \hat{C}}(i, j) + \sum_{k_1=1}^{[S]} \sum_{k_2=k_1+1}^{[S]} \sum_{i \in S_{k_1}} \sum_{j \in S_{k_2}} \text{Dis}_{C, \hat{C}}(i, j).$$
In the first sum, \(i\) and \(j\) are \textit{not} ordered by \(C\), because they lie in the same set in \(S\). We consider the corresponding set in \(\tilde{S}\). From the theorem, at least \(\left(\frac{|C_{k_1}|(1-f(n))}{2}\right)\) vertex pairs from \(S_{k_1}\) are correctly placed together in \(\tilde{S}\). Furthermore, at least
\[
|S_{k_1}| \cdot (1 - f(n)) \cdot \sum_{k_2 = k_1 + 1}^{S} (1 - f(n))|S_{k_2}|
\]
(126)
pairs of vertices with one vertex in \(S_{k_2}\) are correctly placed in different intervals. So the number of correctly ordered/unordered vertex pairs is at least
\[
\sum_{k_1 = 1}^{|S|} \left(\frac{|S_{k_1}|^2 \cdot (1 - f(n))^2}{2} + \sum_{k_2 = k_1 + 1}^{|S|} |S_{k_1}| |S_{k_2}| (1 - f(n))^2\right) \sim \left(\frac{n}{2}\right) \cdot (1 - f(n))^2.
\]
(127)
Since \(f(n) = o(1)\), this is asymptotically equal to \(\left(\frac{n}{2}\right) \cdot (1 - 2f(n))\).

This completes the proof.

### B.2. Proof of Theorem 9

We analyze the worst-case running time of FastClock as follows: initialization takes \(O(1)\) time. The dominant contribution to the running time is the \textit{while} loop. Since \(t_{obs}\) is initially 0 and increases by at least 1 in each iteration, the total number of iterations is at most \(N\). The remaining analysis involves showing that each vertex and edge is only processed, a constant number of times, in \(O(1)\) of these loop iterations, so that the running time is at most \(O(N + n + m)\), as claimed.

In particular, the calculation of \(\mu_t\) in every step involves a summation over all edges from currently active vertices to their uninfected neighbors, along with a calculation involving the current number of uninfected vertices (which we can keep track of using \(O(1)\) calculations per iteration of the loop). A vertex is only active in a single iteration of the loop. Thus, each of these edges is only processed once in this step. The calculation of \(t'_{obs}\) entails calculating a sum over elements of \(\hat{S}\) that are only processed once in all of the iterations of the loop. The calculation of all of the \(|\hat{S}_t|\) can be done as a preprocessing step via an iteration over all \(n\) vertices of \(G\). Finally, the calculation of \(F_{t+1}\) entails a union over the same set of elements of \(\hat{S}\) as in the calculation of the maximum, followed by a traversal of all edges incident on elements of \(\hat{S}_{t+1}\) whose other ends connect to uninfected vertices. These operations involve processing the vertices in \(\hat{S}_{t+1}\) (which happens only in a single iteration of the loop, and, thus, with the preprocessing step of calculating the \(|\hat{S}_t|\), only a constant number of times in the entire algorithm). The edges leading to elements of \(F_{t+1}\) from elements of \(\hat{S}_{t+1}\) are traversed at most twice in the loop: once in the building of \(F_{t+1}\) and once in the next iteration in the calculation of \(\mu_t\).

This implies that each vertex and edge is only processed \(O(1)\) times in the entire algorithm. This leads to the claimed running time of \(O(N + n + m)\), which completes the proof.