

Delay Network Tomography Using a Partially Observable Bivariate Markov Chain

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Abstract—Estimation of link delay densities in a computer network, from source–destination delay measurements, is of great importance in analyzing and improving the operation of the network. In this paper, we develop a general approach for estimating the density of the delay in any link of the network, based on continuous-time bivariate Markov chain modeling. The proposed approach also provides the estimates of the packet routing probability at each node, and the probability of each source–destination path in the network. In this approach, the states of one process of the bivariate Markov chain are associated with nodes of the network, while the other process serves as an underlying process that affects statistical properties of the node process. The node process is not Markov, and the sojourn time in each of its states is phase-type. Phase-type densities are dense in the set of densities with non-negative support. Hence, they can be used to approximate arbitrarily well any sojourn time distribution. Furthermore, the class of phase-type densities is closed under convolution and mixture operations. We adopt the expectation-maximization (EM) algorithm of Asmussen, Nerman, and Olsson for estimating the parameter of the bivariate Markov chain. We demonstrate the performance of the approach in a numerical study.

Index Terms—Delay network tomography, bivariate Markov chain, EM algorithm.

I. INTRODUCTION

NETWORK tomography aims at estimating internal parameters of a computer network from some measurements taken from accessible nodes or links of the network. Network tomography was pioneered by Vanderbei and Iannone [34] and Vardi [35]. In [34], the rate of traffic over source-destination pairs of the network was estimated from aggregated traffic counts at input and output nodes. In [35], the rate of traffic over source-destination pairs was estimated from traffic counts on some links of the network. Both formulations led to similar sets of under-determined linear equations of the form $V = AU$ where $V = \text{col}\{V_1, \dots, V_q\}$ is a column vector of say q traffic count measurements, $U = \text{col}\{U_1, \dots, U_c\}$ is a column vector of say c traffic variables of interest, $c > q$, and $A = \{a_{ij}\}$ is a $q \times c$ zero-one routing matrix with $a_{ij} = 1$ if U_j contributes

to V_i , and $a_{ij} = 0$ otherwise. In [35], V represents traffic over links, and U represents traffic over source-destination pairs, which is modeled as a vector of independent Poisson random variables. It was shown in [35] that the unknown source-destination rates are identifiable provided that A does not contain duplicate columns or zero columns. A Bayesian solution to the rate estimation problem of [35] was developed in [31]. Similar tomography problems arise in other networks such as road and rail networks [31], as well as in image deblurring [30], [36].

In this paper we study another aspect of network tomography, namely, estimation of the density of link delay from overall source-destination delay measurements. We do not distinguish between queuing, propagation, processing, and transmission delays, and model the total delay on each link [4]. Estimation of propagation delay was studied in [17]. It was shown that propagation delay satisfies a set of under-determined equations similar to those described above, and the maximum entropy principle was invoked in estimating that delay. Propagation link delay was also estimated using compressed sensing in [16].

In estimating the density of link delay, we assume a network with random routing. Under this regime, there are multiple routes for each source-destination pair, and routes are chosen according to some distribution. We do not impose any particular structure, such as tree-structure, on the network. In a deterministic routing regime, there exists a single path for each source-destination pair. This regime was implicitly assumed in our above description of the work in [34] and [35]. Clearly, the deterministic routing regime is a particular case of a random routing regime. Hence, our approach applies to the two routing strategies. Both deterministic and random routing regimes were studied in [35].

We model traffic over the network as a continuous-time bivariate Markov chain, see, e.g., [15]. A bivariate Markov chain Z comprises a pair of random processes (X, S) which are jointly Markov. The nodes of the network are represented by the states of the X -chain. The S -chain plays the role of an auxiliary underlying process. While (X, S) is Markov, the individual process X or S alone need not be Markov. We do not constrain X to be Markov, and thus allow the sojourn time in each state to deviate from the exponential density characteristic of Markov chains. The distribution of the sojourn time in each of the X -states is phase-type. The family of phase-type distributions includes mixtures of convolutions of exponential distributions. Phase-type densities are dense in

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the set of densities with support on the non-negative real line. This means that any sojourn time density is either phase-type or it can be approximated arbitrarily well by a phase-type density. The sojourn time in a given X -state, prior to jumping to a specific next X -state, represents the link delay. The link delay in a bivariate Markov chain has a matrix exponential distribution, which generalizes the phase-type distribution [18]. The proposed approach for estimating the density of link delay allows great modeling flexibility, and it does not necessitate any assumption regarding the form of the density of the link delay. We note that the proposed approach also provides the packet routing distribution at each node, and the probability of each source-destination path. Both can be efficiently calculated.

An intuitive explanation for the phase-type distribution, is that each transition in the X -chain may involve several transitions of the S -chain and hence of the bivariate Markov chain $Z = (X, S)$. On a given path in the state space of Z , the sojourn times are independent exponentially distributed, and hence the sojourn time of the X -chain is the convolution of exponential distributions. When all possible paths are considered, the density of the sojourn time of the X -chain is a mixture of convolutions of exponential distributions.

In the proposed approach, the parameter of the bivariate Markov chain is estimated from a sequence of independent source-destination delay measurements. The estimated parameter is then used to calculate analytically the matrix exponential distribution of each link delay, the routing distribution, and the probability of each source-destination path. Estimation of the parameter of the bivariate Markov chain is performed using the expectation-maximization (EM) approach. We adopt the EM algorithm developed by Asmussen *et al.* [2], for estimating the parameter of a transient Markov chain with a single absorbing state, from a sequence of independent absorbing times. We use a fundamental standard result from Van Loan [33] to significantly speed up the EM algorithm of [2]. The resulting EM algorithm is explicit in the E-step and the M-step, and no numerical integration is required. Conditions for identifiability of the parameter of the bivariate Markov chain in this problem are not known. It was shown in [2] that the initial distribution of the transient Markov chain may not be identifiable. Nevertheless, the approach is useful in fitting a parametric model to the measurements, when such measurements were not necessarily produced by the model.

Estimation of link delay density from source-destination delay measurements has attracted significant research interest over the years. We mention here a few representative ideas. Some schemes rely on active network tomography in which test probes are transmitted across the network (see, for example, [6], [8], [12], [14], [19]–[21], [25], [29], [32]), and the references therein. Various models for the link delay density were used. Discrete models were studied, for example, in [8], [19], and [20]. Mixture models were studied, for example, in [6], [19], [29], and [39]. Conditions for identifiability of the discrete models were given in [19]. Identifiability of exponential link delay density was established in [39]. In [8] a Markov model was assumed to capture spatial dependencies among delays on various links in a tree-structured

network. Two other related aspects of network tomography include estimation of link loss rate from source-destination loss measurements (see e.g., [5], [9], [11], [13]), and topology identification from source-destination measurements (see, e.g., [7], [10], [26]).

The work in [39] on parametric link delay density estimation is directly related to our approach. In [39], a single source-destination path of a network was studied, and the density of the delay on each link on that path was assumed to be a mixture of exponential densities. Delays on different links on the path were assumed statistically independent. The delay link density was estimated using the EM algorithm and the moment generating function of the exponential density. This model is a particular case of our approach when it is applied to a single source-destination path of the network. In our approach, link delays are not statistically independent, and the density of each link delay is phase-type. A similar comparison could be made between our approach and the approach of [8].

The plan for the remainder of this paper is as follows. In Section II we provide some background material on bivariate Markov chains. In Section III we detail the application of the bivariate Markov chain model to delay network tomography. In Section IV we summarize the EM algorithm for estimating the model's parameter from source-destination delay measurements. In Section V we discuss application of the proposed approach to model a fixed source-destination path in a network. In Section VI we provide the results of a numerical study. Some concluding remarks are provided in Section VII.

II. BIVARIATE MARKOV CHAINS

In this section we summarize some results from the theory of bivariate Markov chains which are relevant to this work. A recent review of bivariate Markov chains may be found in [15]. Throughout this paper, a random variable is denoted by a capital letter, the range or the alphabet of a random variable is denoted by a blackboard bold capital letter, and values that the random variable take are denoted by lower case letters. For example, we may have a random variable X with range \mathbb{X} and values $x \in \mathbb{X}$. We use P generically to denote probability functions such as probability measures and conditional probability measures. We use p generically to denote densities such as probability mass functions and probability density functions. When these functions depend on a parameter ϕ , we use P_ϕ and p_ϕ , respectively. For example, when X is a discrete random variable, the probability of the event $\{X = x\}$ is denoted by $P_\phi(X = x) = p_\phi(x)$. In another example, when T is a continuous random variable representing a time instant or duration, we denote its density by $p_\phi(t)$. Thus, the identity of the random variable is implicit in the notation of the density, where in the above examples $p_\phi(x)$ is the density of the random variable X , and $p_\phi(t)$ is the density of the random variable T . We also use $P_\phi(T \in dt)$ to express the probability of the event $\{T \in [t, t + dt)\}$ for an infinitesimal interval dt . In our notation system, this probability is given by $P_\phi(T \in dt) = p_\phi(t)dt$. The transition matrix of the bivariate Markov chain is denoted by bold capital letter \mathbf{P}_t , in order to distinguish it from the scalar probability measure P_ϕ .

Let $Z = \{Z(t), t \geq 0\}$ denote a continuous-time finite-state homogeneous irreducible bivariate Markov chain defined on a given probability space. We use P to denote a probability measure on that space. The bivariate Markov chain comprises a pair of random processes, say $Z = (X, S)$, which are *jointly* Markov. The individual process X or S alone need not be Markov. We assume without loss of generality that the state space of X is $\mathbb{X} = \{1, 2, \dots, d\}$, and that the state space of S is $\mathbb{S} = \{1, 2, \dots, r\}$, for some finite d and r . The state space of Z is given by $\mathbb{Z} = \mathbb{X} \times \mathbb{S}$. We assume that the states $\{(a, i) \in \mathbb{Z}\}$ of the bivariate Markov chain are ordered lexicographically.

The transition probability of the bivariate Markov chain is given by $P(Z(t) = (b, j) \mid Z(0) = (a, i))$ for any $t \geq 0$ and any $(a, i), (b, j) \in \mathbb{Z}$. We denote the transition matrix of Z by \mathbf{P}_t and assume that \mathbf{P}_t is standard, i.e., \mathbf{P}_t approaches the identity matrix as $t \rightarrow 0$. The matrix \mathbf{P}_t is continuous and differentiable at $t = 0$. The derivative of \mathbf{P}_t at $t = 0$ is the infinitesimal *generator* of the bivariate Markov chain given by

$$G = \lim_{t \downarrow 0} \frac{1}{t} (\mathbf{P}_t - I). \quad (1)$$

The off-diagonal elements of G are non-negative, and the diagonal elements are non-positive. If the diagonal elements of G are finite, then each row of G sums to zero. This assumption is made throughout this paper. The transition matrix satisfies Kolmogorov's forward and backward equations, whose unique solution is given by

$$\mathbf{P}_t = e^{Gt}. \quad (2)$$

Let $G = \{g_{ab}(ij); (a, i), (b, j) \in \mathbb{Z}\}$. For sufficiently small t ,

$$\begin{aligned} P(Z(t) = (b, j) \mid Z(0) = (a, i)) \\ = \begin{cases} g_{ab}(ij)t + o(t), & (a, i) \neq (b, j) \\ 1 + g_{aa}(ii)t + o(t), & (a, i) = (b, j). \end{cases} \end{aligned} \quad (3)$$

Assume that the bivariate Markov chain enters state (a, i) at some time which we denote as $t = 0$. Let ΔT_{ai} denote the sojourn time of the bivariate Markov chain in state (a, i) until it transits to another state. This sojourn time is exponentially distributed with rate given by $-g_{aa}(ii)$. Thus,

$$P(\Delta T_{ai} > \tau \mid Z(0) = (a, i)) = e^{g_{aa}(ii)\tau}, \quad \tau \geq 0. \quad (4)$$

When the chain is in state (a, i) and a jump occurs at some time t , the probability that the chain jumps to $(b, j) \neq (a, i)$ is given by

$$P(Z(t) = (b, j) \mid Z(t-) = (a, i)) = -g_{ab}(ij)/g_{aa}(ii). \quad (5)$$

Recall that the states $\{(a, i) \in \mathbb{Z}\}$ are ordered lexicographically. The generator matrix G may be partitioned into $r \times r$ sub-matrices such that $G = \{G_{ab}; a, b \in \mathbb{X}\}$ where $G_{ab} = \{g_{ab}(ij); i, j \in \mathbb{S}\}$. For this partition, the order of each G_{aa} is r . A more interesting bivariate Markov chain is obtained when each X -state is associated with a possibly different number of S -states. Suppose that the X -state a is

associated with r_a S -states, given without loss of generality by $\mathbb{S}_a = \{1, 2, \dots, r_a\}$. Then, the state space of Z is given by

$$\mathbb{Z} = \bigcup_{a=1}^d \{(a, i), i \in \mathbb{S}_a\}. \quad (6)$$

The generator matrix G may now be partitioned into sub-matrices $\{G_{ab}; a, b \in \mathbb{X}\}$, where $G_{ab} = \{g_{ab}(ij); i \in \mathbb{S}_a, j \in \mathbb{S}_b\}$. The order of each G_{aa} is r_a . We shall encounter such partition in Eq. (23).

We assume that in addition to G , all diagonal matrices $\{G_{aa}\}$ are irreducible. This assumption guarantees that for every $a \in \mathbb{X}$, G_{aa} is non-singular, and that the elements of $-G_{aa}^{-1}$ and of $e^{G_{aa}t}$ are all positive for every $t > 0$. The S -chain is Markov if and only if the order r_a , and the matrix $\sum_{b=1}^d G_{ab}$, are independent of a for every $a \in \mathbb{X}$ [3]. In that case, $\sum_{b=1}^d G_{ab}$ is the generator matrix of the S -chain. A similar condition can be stated for the X -chain to be Markov upon re-partitioning of G .

The bivariate Markov chain is a Markov jump process with right continuous piecewise constant sample paths and a finite number of jumps in each finite interval. As such, the bivariate Markov chain is strong Markov, i.e., the Markov property holds for stopping times. This result could be applied to jumps of the X process, which constitute a subset of the jumps of the Z process.

Let ϕ denote the parameter of the bivariate Markov chain. Under the usual parametrization, $\phi = \{\nu, G\}$ where ν is the initial distribution of the bivariate Markov chain and G is its generator. In a more general setup, both ν and G may be functions of a parameter ϕ of a relatively small dimension. Also, when ν is the stationary distribution of the process, then it is a function of G . Let P_ϕ denote a probability measure of the process.

Suppose that the bivariate Markov chain is sampled at the jump points of the X -chain. Suppose that the arbitrary time origin at $t = 0$ coincides with a jump of X . This technical condition guarantees that the first positive sojourn time of X is distributed like any other sojourn time of that process. For $k = 0, 1, 2, \dots$, let T^k denote the time of the $k + 1$ st jump of X . Let $X_k = X(T^k)$, $S_k = S(T^k)$, and $Z_k = (X_k, S_k)$. We refer to $\{Z_k\}$ as the *sampled bivariate Markov chain*. For $k = 1, 2, \dots$, let $T_k = T^k - T^{k-1}$ denote the sojourn time of X in state X_{k-1} . Let $T_0 = 0$. The resulting process $\{(T_k, Z_k)\}_{k=0}^\infty$ is a Markov renewal process for which

$$\begin{aligned} P_\phi(T_k \leq t, Z_k = z_k \mid T_{k-1} = t_{k-1}, \\ Z_{k-1} = z_{k-1}, \dots, T_1 = t_1, Z_1 = z_1, Z_0 = z_0) \\ = P_\phi(T_k \leq t, Z_k = z_k \mid Z_{k-1} = z_{k-1}). \end{aligned} \quad (7)$$

Let $p_\phi(t_k, z_k \mid z_{k-1})$ denote the density obtained by differentiating the rhs of (7) w.r.t. t , where t_k is a realization of the sojourn time T_k and z_k is a realization of Z_k . Since the sample path $\{X(t), t \in [0, t^n]\}$ is uniquely determined by the random variables $\{(X_0, T_1), (X_1, T_2), \dots, (X_{n-1}, T_n), X_n\}$, its likelihood function follows from the joint density of these random variables, or as the marginal density of $\{(Z_0, T_1), (Z_1, T_2), \dots, (Z_{n-1}, T_n), Z_n\}$. Using the

Markov renewal property in (7) we obtain

$$p_\phi(x(t), t \in [0, t^n]) = \sum_{s_0, \dots, s_n} p_\phi(z_0) \prod_{k=1}^n p_\phi(t_k, z_k | z_{k-1}). \quad (8)$$

Let $f_{ij}^{ab}(t; \phi) = p_\phi(t_k, z_k | z_{k-1})$ when $t_k = t$, $z_{k-1} = (a, i)$, and $z_k = (b, j)$. Using homogeneity of the bivariate Markov chain Z , this density can be evaluated as

$$f_{ij}^{ab}(t; \phi) = \frac{\partial}{\partial t} P_\phi(T_1 \leq t, Z_1 = (b, j) | Z_0 = (a, i)). \quad (9)$$

Define the *transition density matrix* by

$$f^{ab}(t; \phi) = \{f_{ij}^{ab}(t; \phi); i, j = 1, \dots, r\}. \quad (10)$$

Then from [22, Proposition 1],

$$f^{ab}(t; \phi) = e^{G_{aa}t} G_{ab}, \quad a \neq b, \quad t \geq 0. \quad (11)$$

Furthermore, $e^{G_{aa}t}$ is a transition matrix with the (i, j) element given by

$$P_\phi(T_1 > t, S(t) = j | Z(0) = (a, i)). \quad (12)$$

Let $\nu_{ai} = P_\phi(Z_0 = (a, i))$, and define

$$\begin{aligned} \nu_a &= (\nu_{a,1}, \nu_{a,2}, \dots, \nu_{a,r}) \\ \nu &= (\nu_1, \dots, \nu_d) \end{aligned} \quad (13)$$

where ν represents the initial distribution of Z . The likelihood function in (8) can now be rewritten as

$$p_\phi(x(t), t \in [0, t^n]) = \nu_{x_0} \left\{ \prod_{l=1}^n f^{x_{l-1}x_l}(t_l; \phi) \right\} \mathbf{1} \quad (14)$$

where $\mathbf{1}$ denotes a column vector of all ones.

The likelihood function (14) can be calculated using forward or backward recursions as follows. Let the row vector

$$L(k; \phi) = \nu_{x_0} \prod_{l=1}^k f^{x_{l-1}x_l}(t_l; \phi) \quad (15)$$

define the forward density for $k \geq 1$, and note that

$$L(k; \phi) = L(k-1; \phi) f^{x_{k-1}x_k}(t_k; \phi) \quad (16)$$

where $L(0; \phi) = \nu_{x_0}$. Next, let the column vector

$$R(k; \phi) = \prod_{l=k}^n f^{x_{l-1}x_l}(t_l; \phi) \mathbf{1}, \quad (17)$$

with $R(n+1; \phi) = \mathbf{1}$, define the backward density, and note that

$$R(k; \phi) = f^{x_{k-1}x_k}(t_k; \phi) R(k+1; \phi). \quad (18)$$

The likelihood function is given by

$$p_\phi(x(t), t \in [0, t^n]) = L(k-1; \phi) R(k; \phi) \quad (19)$$

where k may be chosen arbitrarily to be any integer between 1 and $n+1$. The forward and backward recursions must be scaled to improve their numerical stability, see [15, Sec. 3.4].

Returning to the sampled bivariate Markov chain, integrating (11) over t gives the transition probabilities

$$P_\phi(Z_k = (b, j) | Z_{k-1} = (a, i)) = [-G_{aa}^{-1} G_{ab}]_{ij}. \quad (20)$$

Define the matrix

$$D_{ab} = \begin{cases} -G_{aa}^{-1} G_{ab}, & a \neq b \\ \mathbf{0}, & a = b. \end{cases} \quad (21)$$

The transition matrix of the sampled bivariate Markov chain is given by the block matrix $D = \{D_{ab}, a, b = 1, \dots, d\}$. The sampled bivariate Markov chain has one closed set of recurrent, possibly periodic, states, while the remaining states are transient [15, Lemma 3]. A state (b, j) is recurrent if and only if it corresponds to a non-zero column of G_{ab} for some $a \neq b$. Hence, the transition matrix D has a unique stationary distribution with zero entries for the transient states. When ν satisfies $\nu = \nu D$ then it constitutes the stationary distribution of D . The sampled bivariate Markov chain is stationary if and only if it is initialized with the stationary distribution.

Let $\nu_{ai}^k = P_\phi(Z_k = (a, i))$ for $k = 0, 1, \dots$ where $\nu_{ai}^0 = \nu_{ai}$. Define ν_a^k and ν^k analogously to ν_a and ν in (13), respectively. We have

$$\nu_b^k = \sum_{a=1}^d \nu_a^{k-1} D_{ab}. \quad (22)$$

When the sampled bivariate Markov chain is initialized with its stationary distribution, then ν_b^k is independent of k and it follows from the solution of $\nu = \nu D$.

III. PARTIALLY OBSERVABLE BIVARIATE MARKOV CHAIN

In this section we describe the proposed model for estimating link delay densities, routing probabilities, and the probability of any source-destination path in an unstructured network with random routing regime. We also discuss some important relevant properties of the model.

We model traffic over the network as a bivariate Markov chain $Z = (X, S)$. The states of the X -chain represent the nodes of the network, and the S -chain serves as an auxiliary background process. We designate a subset of the state space \mathbb{X} as source/intermediate states, and the remaining states as destination states. This partition is made purely for accounting purposes. A packet entering a randomly chosen source state will propagate to a destination state through intermediate states using random routing. This means that at each node the packet will be routed to one of the subsequent nodes, which will be chosen according to some distribution. Upon leaving the destination state, the process will re-start from a randomly chosen source state, and a new packet will propagate through random routing to its destination state, and so on. Effectively, a source/intermediate node is represented by a non-absorbing state, while a destination state may be seen as an absorbing state with a reset loop.

The S -chain serves as an underlying process that helps the X -chain attain some desirable statistical properties. In particular, in a bivariate Markov chain, the density of the sojourn time in each X -state is phase-type, and that density may be far more general than the exponential density. We shall specify that density shortly. In the proposed model, we only measure the overall delay from source to destination, and have no access to either X or S . We therefore refer to the model as a partially observable bivariate Markov chain.

Suppose that the source/intermediate states are $\mathbb{X}_1 = \{1, \dots, d_1\}$ for some $d_1 < d$, and that the destinations states are $\mathbb{X}_2 = \{d_1 + 1, \dots, d\}$ where clearly $\mathbb{X} = \mathbb{X}_1 \cup \mathbb{X}_2$. The matrix G can be expressed as $\{G_{ab}, a, b \in \mathbb{X}\}$, where, for $a, b \in \mathbb{X}_1$, $G_{ab} = \{g_{ab}(ij), i, j = 1, \dots, r\}$ are $r \times r$ matrices; for $a \in \mathbb{X}_2, b \in \mathbb{X}_1$, $G_{ab} = \text{row}\{g_{ab}(1j), j = 1, \dots, r\}$ are $1 \times r$ row vectors; for $a \in \mathbb{X}_1, b \in \mathbb{X}_2$, $G_{ab} = \text{col}\{g_{ab}(i1), i = 1, \dots, r\}$ are $r \times 1$ column vectors; and for $a, b \in \mathbb{X}_2$, G_{ab} is a scalar. The generator G of the bivariate Markov chain may be partitioned according to the class of possible source/intermediate states and the class of possible destination states as follows:

$$G = \left(\begin{array}{ccc|ccc} G_{11} & \cdots & G_{1,d_1} & & & \\ \vdots & & \vdots & h_1 & \cdots & h_{d_2} \\ G_{d_1,1} & \cdots & G_{d_1,d_1} & & & \\ \hline & & e_1 & -\xi_1 & & \\ & & \vdots & & \ddots & \\ & & e_{d_2} & & & -\xi_{d_2} \end{array} \right) \quad (23)$$

where $\{h_l, l = 1, \dots, d_2\}$ are $rd_1 \times 1$ column vectors with $d_2 = d - d_1$, $\{e_l, l = 1, \dots, d_2\}$ are $1 \times rd_1$ row vectors, and $\{\xi_l\}$ are positive scalars. For $l = 1, \dots, d_2$, we have $h_l = \text{col}\{G_{a,d_1+l}, a = 1, \dots, d_1\}$, $e_l = \text{row}\{G_{d_1+l,b}, b = 1, \dots, d_1\}$, and $\xi_l = -G_{d_1+l,d_1+l}$.

We may conceptually rewrite G as

$$G = \left(\begin{array}{c|c} H_{cc} & H_{cd} \\ \hline H_{dc} & H_{dd} \end{array} \right) \quad (24)$$

where the subscripts c and d are associated with source/intermediate states and with destination states, respectively. For a network with given topology, if no physical link exists between a pair of source/intermediate nodes, say $a, b \in \mathbb{X}_1$, then the corresponding sub-matrix G_{ab} of the model is null. Similarly, elements of H_{cd} corresponding to non-existent links from any node $a \in \mathbb{X}_1$ to any node $b \in \mathbb{X}_2$ should be null. A similar comment can be made about elements of H_{dc} . A well known property of the EM algorithm is that it preserves null values of the parameter.

The sub-matrix H_{dd} is diagonal since traffic does not flow from one destination node to another destination node. Since $\{\xi_i\}$ are positive scalars, the sojourn time associated with the i th destination state is exponential with mean sojourn time of $1/\xi_i$. By choosing sufficiently large $\{\xi_i\}$, we can diminish the sojourn time in each destination state, so that the return to a source node may be considered instantaneous.

Recall that ν denotes the initial distribution of the sampled bivariate Markov chain. Since the bivariate Markov chain cannot start in a destination state,

$$\nu = (\nu_1, \dots, \nu_{d_1}, \mathbf{0}, \dots, \mathbf{0}). \quad (25)$$

We define $\mu = (\nu_1, \dots, \nu_{d_1})$.

The sojourn time of the process in each of the X -states is phase-type [22]. For $X_0 = x_0$, with $x_0 \in \mathbb{X}$, the phase-type

density is obtained using (11) and (21) as follows:

$$\begin{aligned} p_\phi(t | x_0) &= \frac{\sum_{s_0, z_1: x_1 \neq x_0} p_\phi(z_1, t | z_0) p_\phi(z_0)}{\sum_{x_1: x_1 \neq x_0} \sum_{s_0, s_1} p_\phi(z_1 | z_0) p_\phi(z_0)} \\ &= \frac{\sum_{x_1: x_1 \neq x_0} \nu_{x_0} e^{G_{x_0 x_0} t} G_{x_0 x_1} \mathbf{1}}{\sum_{x_1: x_1 \neq x_0} \nu_{x_0} D_{x_0 x_1} \mathbf{1}} \\ &= -\bar{\nu}_{x_0} e^{G_{x_0 x_0} t} G_{x_0 x_0} \mathbf{1}, \end{aligned} \quad (26)$$

where we have used $\sum_{x_1: x_1 \neq x_0} G_{x_0 x_1} \mathbf{1} = -G_{x_0 x_0} \mathbf{1}$, $\sum_{x_1: x_1 \neq x_0} D_{x_0 x_1} \mathbf{1} = \mathbf{1}$, and $\bar{\nu}_{x_0} = \nu_{x_0} / (\nu_{x_0} \mathbf{1})$ denotes the initial conditional distribution of the S -states associated with x_0 , given that $X_0 = x_0$. Note that when $x_1 \in \mathbb{X}_2$, the terms $D_{x_0 x_1} \mathbf{1}$ and $G_{x_0 x_1} \mathbf{1}$ become the subvectors $D_{x_0 x_1}$ and $G_{x_0 x_1}$, respectively. These subvectors follow from the corresponding subvectors of $h_{x_1-d_1}$. When $X_k = a$ for some $k > 0$, the sojourn time density is given by (26) with ν_{x_0} replaced by ν_a^k from (22), and $\bar{\nu}_{x_0}$ is replaced by $\bar{\nu}_a^k = \nu_a^k / (\nu_a^k \mathbf{1})$. The family of phase-type densities is dense in the family of densities with non-negative support [37]. This means that every sojourn time density is either phase-type or it can be approximated arbitrarily well by a phase-type density. The number of phases of the phase-type sojourn time density (26) equals the number of states in \mathbb{S}_{x_0} . Increasing that number improves the approximation of the true sojourn time density.

The parameter ϕ of the bivariate Markov chain may be estimated from K independent source-destination delay measurements using the EM algorithm. We adopt the EM algorithm developed in [2] for estimating the parameter of a univariate Markov chain from K independent absorbing times. In the Markov chain of [2], all states but one are transient, and the exceptional state is absorbing. The EM algorithm will be detailed in Section IV.

Once the parameter of the bivariate Markov chain is estimated, the density of each link delay may be evaluated as follows. Suppose that $X_0 = x_0$ and $X_1 = x_1$, $x_0, x_1 \in \mathbb{X}_1$. For the link connecting these nodes we have from (11) and (21),

$$\begin{aligned} p_\phi(t | x_0, x_1) &= \frac{\sum_{s_0, s_1} p_\phi(z_1, t | z_0) p_\phi(z_0)}{\sum_{s_0, s_1} p_\phi(z_1 | z_0) p_\phi(z_0)} \\ &= \frac{\nu_{x_0} e^{G_{x_0 x_0} t} G_{x_0 x_1} \mathbf{1}}{\nu_{x_0} D_{x_0 x_1} \mathbf{1}}. \end{aligned} \quad (27)$$

When $x_1 \in \mathbb{X}_2$, the terms $G_{x_0 x_1} \mathbf{1}$ and $D_{x_0 x_1} \mathbf{1}$ in (27) are replaced by $G_{x_0 x_1}$ and $D_{x_0 x_1}$, respectively. The density in (27) is a matrix exponential density [18]. The family of matrix exponential densities contains all phase-type densities.

Given the estimated parameter of the bivariate Markov chain, we can also calculate the packet routing distribution under the random routing regime. This is the probability that a packet will reach state x_1 once it has left state x_0 . Suppose $x_0, x_1 \in \mathbb{X}_1$. For $Z_0 = (x_0, s_0)$ and $Z_1 = (x_1, s_1)$ we have from (21),

$$\begin{aligned} p_\phi(x_1 | x_0) &= \frac{\sum_{s_0, s_1} p_\phi(z_1 | z_0) p_\phi(z_0)}{\sum_{x_1} \sum_{s_0, s_1} p_\phi(z_1 | z_0) p_\phi(z_0)} \\ &= \frac{\nu_{x_0} D_{x_0 x_1} \mathbf{1}}{\sum_{x_1} \nu_{x_0} D_{x_0 x_1} \mathbf{1}} = \frac{\nu_{x_0} D_{x_0 x_1} \mathbf{1}}{\nu_{x_0} \mathbf{1}}. \end{aligned} \quad (28)$$

Note that we need not restrict the sum over x_1 to $x_1 \neq x_0$ since $D_{x_0 x_0} = \mathbf{0}$. When $x_1 \in \mathbb{X}_2$, the term $D_{x_0 x_1} \mathbf{1}$ is replaced by $D_{x_0 x_1}$. Similarly to (26), Eqs. (27) and (28) could also be used to evaluate $p_\phi(t \mid x_k, x_{k+1})$ and $p_\phi(x_{k+1} \mid x_k)$, respectively, for any $k > 0$. Assuming $X_k = a$, this can be accomplished by replacing ν_{x_0} and $\bar{\nu}_{x_0}$ by ν_a^k and $\bar{\nu}_a^k$, respectively. Alternatively, we could use the stationary distribution ν which follows from $\nu = \nu D$. In our numerical study described in Section VI we have opted for the latter approach in order to obtain “steady state” link delay density and routing probability estimates.

Finally, we note that the probability of a source-destination path $\{x_0, \dots, x_n\}$, where $x_0, \dots, x_{n-1} \in \mathbb{X}_1$ and $x_n \in \mathbb{X}_2$, can be obtained as follows:

$$\begin{aligned} p_\phi(x_0, \dots, x_n) &= \sum_{s_0, \dots, s_n} p_\phi(z_0) p_\phi(z_1 \mid z_0) \cdots p_\phi(z_n \mid z_{n-1}) \\ &= \nu_{x_0} D_{x_0 x_1} D_{x_1 x_2} \cdots D_{x_{n-1} x_n}. \end{aligned} \quad (29)$$

IV. THE EM ALGORITHM

In this section we detail the EM algorithm for estimating the parameter ϕ of the bivariate Markov chain described in Section III, from K independent source-destination delay measurements $Y = \{Y_1, Y_2, \dots, Y_K\}$. The EM algorithm is derived along the lines of the approach developed in [2]. The parameter ϕ constitutes the off-diagonal elements of H_{cc} , the elements of H_{cd} , and the initial distribution μ . The elements of H_{dd} are set as detailed in the paragraph following (24). For H_{dc} , we choose $\{e_i = \xi_i \mu, i = 1, \dots, d_2\}$, so that the initial distribution of the bivariate Markov chain remains μ after bouncing from any destination state in \mathbb{X}_2 . We do not assume any particular topology for the network, and hence, we do not constrain any of the sub-matrices of the H_{cc} , H_{cd} , and H_{dc} portions of the generator G to be null. See also comments following Eq. (24).

The EM algorithm generates a sequence of parameter estimates with increasing likelihood, unless a fixed point is reached, in which case, the parameter estimate and its likelihood remain constant. Every fixed point of the EM algorithm is a stationary point of the likelihood function characterized by zero derivative. Conditions for reaching a fixed point may be found in [38] but are not easy to verify. The performance of the EM algorithm depends on the initial guess of the parameter value since the likelihood function is usually rather complex and has multiple local maxima. We shall elaborate on the choice of the initial estimate in Section VI.

The likelihood of the observation sequence is evaluated at the end of each iteration, and its value is used to judge the quality of the estimate. The likelihood function is commonly used in a stopping criterion for the EM algorithm. For example, the algorithm could be stopped if the relative increase in likelihood values in two consecutive iterations falls below a given threshold. Alternatively, the algorithm could be stopped after a certain number of iterations if the rate of increase of the likelihood is low. This stopping criterion was adopted in this paper where the EM algorithm was limited to 1000 iterations. It is well known that the EM algorithm has slow convergence rate [23].

Let $\tilde{Z}_k = \{Z(t), 0 \leq t \leq Y_k\}$ denote the bivariate Markov chain defined in the interval $[0, Y_k]$. The complete statistic for the EM algorithm is given by $\{(\tilde{Z}_k, Y_k), k = 1, \dots, K\}$. Let ϕ_ι denote the estimate of the parameter ϕ of the bivariate Markov chain at the end of the ι th iteration of the EM algorithm. Since the observations are assumed independent, the estimate $\phi_{\iota+1}$ is obtained from maximization of the EM auxiliary function as follows:

$$\phi_{\iota+1} = \operatorname{argmax}_\phi \sum_{k=1}^K E_{\phi_\iota} \{\log p_\phi(Y_k, \tilde{Z}_k) \mid Y_k\}, \quad (30)$$

where E_{ϕ_ι} denotes expectation under P_{ϕ_ι} . The density $p_\phi(\tilde{Z}_k, Y_k)$ was derived by Albert in [1, Th. 3.1]. Substituting that density in (30), and carrying out the maximization, yield the EM iteration for estimating ϕ as detailed below.

Assume that for a given k , $Y_k = y_k$. Let $M_{ij}^{ab}(y_k)$ denote the number of jumps from state (a, i) to state (b, j) in $[0, y_k]$, and let $D_i^a(y_k)$ denote the total sojourn time of the bivariate Markov chain in state (a, i) in $[0, y_k]$. Let

$$\begin{aligned} \hat{M}_{ij}^{ab}(y_k) &= E_{\phi_\iota} \{M_{ij}^{ab}(Y_k) \mid Y_k = y_k\} \\ \hat{D}_i^a(y_k) &= E_{\phi_\iota} \{D_i^a(Y_k) \mid Y_k = y_k\} \end{aligned} \quad (31)$$

denote the conditional mean estimates of $M_{ij}^{ab}(y_k)$ and $D_i^a(y_k)$, respectively. At the end of the $(\iota + 1)$ st iteration, the new estimate of the initial distribution of the bivariate Markov chain is given by

$$\hat{\nu}_{ai} = \frac{1}{K} \sum_{k=1}^K P_{\phi_\iota}(Z(0) = (a, i) \mid Y_k = y_k), \quad (32)$$

and the new estimate of the generator is given by

$$\hat{g}_{ab}(ij) = \frac{\sum_{k=1}^K \hat{M}_{ij}^{ab}(y_k)}{\sum_{k=1}^K \hat{D}_i^a(y_k)}, \quad (b, j) \neq (a, i). \quad (33)$$

When $a, b \in \mathbb{X}_1$, then (33) applies to $i, j = 1, \dots, r$. When $a \in \mathbb{X}_1$, and $b \in \mathbb{X}_2$, then (33) applies to $i = 1, \dots, r$ and $j = 1$.

The essence of the EM algorithm is the evaluation of the conditional probability in (32) and the conditional mean estimates in (31). These estimates are derived in the propositions below. The key to the derivation is (11), which implies that for any $a \in \mathbb{X}_1$ and any $b \in \mathbb{X}_2$,

$$\begin{aligned} P_{\phi_\iota}(Y_k \in dy_k, Z(y_k) = (b, j) \mid Z(0) = (a, i)) \\ = \mathbf{1}_{ai}' e^{H_{cc} y_k} H_{cd} \mathbf{1}_{bj} dy_k, \end{aligned} \quad (34)$$

where $Y_k \in dy_k$ means that $Y_k \in [y_k, y_k + dy_k)$ for an infinitesimal interval dy_k of Y_k , and $\mathbf{1}_{ai}$ is a unit column vector of suitable dimension with a one in the (a, i) position and zeros elsewhere. Another important relation, similar to (12), is given by

$$P_{\phi_\iota}(Z(t) = (a, i), t \leq Y_k) = \mu e^{H_{cc} t} \mathbf{1}_{ai}. \quad (35)$$

This relation can be proved similarly to [22, Proposition 1].

Proposition 1: The initial distribution estimate $\hat{\nu}_{ai}$, $a \in \mathbb{X}_1$, in (32) is given by

$$\hat{\nu}_{ai} = \frac{1}{K} \sum_{k=1}^K \frac{\nu_{ai} \mathbf{1}_{ai}' e^{H_{cc} y_k} H_{cd} \mathbf{1}}{\mu e^{H_{cc} y_k} H_{cd} \mathbf{1}}. \quad (36)$$

Proof: Multiplying (34) by ν_{ai} and summing over all (b, j) we obtain,

$$P_{\phi_l}(Y_k \in dy_k, Z(0) = (a, i)) = \nu_{ai} \mathbf{1}'_{ai} e^{H_{cc} y_k} H_{cd} \mathbf{1} dy_k. \quad (37)$$

Summing (37) over all (a, i) we obtain,

$$P_{\phi_l}(Y_k \in dy_k) = \mu e^{H_{cc} y_k} H_{cd} \mathbf{1} dy_k. \quad (38)$$

The ratio of the probabilities in (37) and (38) gives $P_{\phi_l}(Z(0) = (a, i) \mid Y_k = y_k)$, and the result follows from (32). \square

Proposition 2: The total sojourn time estimate $\hat{D}_i^a(y_k)$, $a \in \mathbb{X}_1$, in (31) is given by

$$\hat{D}_i^a(y_k) = \frac{\int_0^{y_k} [\mu e^{H_{cc} t} \mathbf{1}_{ai}] [\mathbf{1}'_{ai} e^{H_{cc}(y_k - t)} H_{cd} \mathbf{1}] dt}{\mu e^{H_{cc} y_k} H_{cd} \mathbf{1}}. \quad (39)$$

Proof: To evaluate $\hat{D}_i^a(y_k)$, define the indicator function

$$\varphi_{ai}(t) = \begin{cases} 1, & Z(t) = (a, i) \\ 0, & \text{otherwise} \end{cases} \quad (40)$$

and note that

$$D_i^a(Y_k) = \int_0^{Y_k} \varphi_{ai}(t) dt. \quad (41)$$

Hence, using Bayes rule, we obtain,

$$\begin{aligned} \hat{D}_i^a(y_k) &= E \left\{ \int_0^{Y_k} \varphi_{ai}(t) dt \mid Y_k = y_k \right\} \\ &= \int_0^{y_k} P_{\phi_l}(Z(t) = (a, i), t \leq Y_k \mid Y_k = y_k) dt \\ &= \frac{1}{P_{\phi_l}(Y_k \in dy_k)} \int_0^{y_k} P_{\phi_l}(Z(t) = (a, i), t \leq Y_k) \\ &\quad \cdot P_{\phi_l}(Y_k \in dy_k \mid Z(t) = (a, i), t \leq Y_k) dt. \end{aligned} \quad (42)$$

From (34), we have,

$$P_{\phi_l}(Y_k \in dy_k \mid Z(t) = (a, i), t \leq Y_k) = \mathbf{1}'_{ai} e^{H_{cc}(y_k - t)} H_{cd} \mathbf{1} dy_k, \quad (43)$$

and $P_{\phi_l}(Y_k \in dy_k)$ is given in (38). Substituting (35), (43), and (38) in (42) completes the proof. \square

Proposition 3: The estimate $\hat{M}_{ij}^{ab}(y_k)$ of the number of jumps from state (a, i) to state (b, j) , $a \neq b$, given the measurement y_k , is given as follows:

a) For $a, b \in \mathbb{X}_1$ and $i, j \in \{1, \dots, r\}$,

$$\begin{aligned} \hat{M}_{ij}^{ab}(y_k) &= \frac{\int_0^{y_k} [\mu e^{H_{cc} t} \mathbf{1}_{ai}] g_{ab}(ij) [\mathbf{1}'_{bj} e^{H_{cc}(y_k - t)} H_{cd} \mathbf{1}] dt}{\mu e^{H_{cc} y_k} H_{cd} \mathbf{1}}. \end{aligned} \quad (44)$$

b) For $a \in \mathbb{X}_1$, $i = 1, \dots, r$; and $b \in \mathbb{X}_2$, $j = 1$, we have using $l = b - d_1$,

$$\hat{M}_{ij}^{ab}(y_k) = \frac{[\mu e^{H_{cc} y_k} \mathbf{1}_{ai}] [\mathbf{1}'_{ai} h_l]}{\mu e^{H_{cc} y_k} H_{cd} \mathbf{1}}. \quad (45)$$

Proof: The number of jumps in Part a) is given by

$$M_{ij}^{ab}(y_k) = \lim_{\epsilon \rightarrow 0} \sum_{l=0}^{\lfloor y_k/\epsilon \rfloor - 1} \varphi_{ai}(l\epsilon) \varphi_{bj}((l+1)\epsilon) \quad (46)$$

where $\lfloor \cdot \rfloor$ denotes the floor function, and $\varphi_{ai}(t)$ is defined in (40). Since the number of jumps in any finite interval is finite, the conditional expected value of (46) is given by

$$\begin{aligned} \hat{M}_{ij}^{ab}(y_k) &= \lim_{\epsilon \rightarrow 0} \sum_{l=0}^{\lfloor y_k/\epsilon \rfloor - 1} P_{\phi_l}(Z(l\epsilon) = (a, i), \\ &\quad Z((l+1)\epsilon) = (b, j), (l+1)\epsilon \leq Y_k \mid Y_k = y_k) \\ &= \frac{1}{P_{\phi_l}(Y_k \in dy_k)} \lim_{\epsilon \rightarrow 0} \sum_{l=0}^{\lfloor y_k/\epsilon \rfloor - 1} \epsilon [P_{\phi_l}(Z(l\epsilon) = (a, i), l\epsilon \leq Y_k) \\ &\quad \cdot \frac{1}{\epsilon} P_{\phi_l}(Z((l+1)\epsilon) = (b, j) \mid Z(l\epsilon) = (a, i), (l+1)\epsilon \leq Y_k) \\ &\quad \cdot P_{\phi_l}(Y_k \in dy_k \mid Z((l+1)\epsilon) = (b, j), (l+1)\epsilon \leq Y_k)]. \end{aligned} \quad (47)$$

The result in (44) is obtained by substituting (38) into the first term of (47), using a similar argument as in (35) for the second term, using (2) and

$$\lim_{\epsilon \downarrow 0} \frac{e^{G\epsilon} - I}{\epsilon} = G, \quad (48)$$

for the third term, applying (43) to the fourth term, and interpreting the resulting sum as a Riemann integral.

For Part b), the bivariate Markov chain transits from (a, i) to $(b, 1)$ only in its last jump occurring at time $Y_k = y_k$. Hence,

$$M_{i1}^{ab}(y_k) = \lim_{\epsilon \rightarrow 0} \varphi_{ai}(y_k - \epsilon) \varphi_{b1}(y_k). \quad (49)$$

The conditional mean estimate of $M_{i1}^{ab}(y_k)$ is given by

$$\begin{aligned} \hat{M}_{i1}^{ab}(y_k) &= \lim_{\epsilon \rightarrow 0} P(Z(y_k - \epsilon) = (a, i), Z(y_k) = (b, 1) \mid Y_k = y_k) \\ &= \frac{1}{P_{\phi_l}(Y_k \in dy_k)} \lim_{\epsilon \rightarrow 0} [P_{\phi_l}(Z(y_k - \epsilon) = (a, i)) \\ &\quad \cdot P_{\phi_l}(Y_k \in dy_k, Z(y_k) = (b, 1) \mid Z(y_k - \epsilon) = (a, i))]. \end{aligned} \quad (50)$$

Using (38), (35), and (34), in (50) yields,

$$\hat{M}_{i1}^{ab}(y_k) = \lim_{\epsilon \rightarrow 0} \frac{[\mu e^{H_{cc}(y_k - \epsilon)} \mathbf{1}_{ai}] [\mathbf{1}'_{ai} e^{H_{cc}\epsilon} h_l]}{\mu e^{H_{cc} y_k} H_{cd} \mathbf{1}}, \quad (51)$$

which is equivalent to (45). \square

The integrals in (39) and (44) can be efficiently evaluated using Van Loan's approach [33, Th. 1]. Rearranging terms in (44) (and similarly in (39)), we are interested in evaluating

$$J(y) = \int_0^y e^{H_{cc}(y-t)} \cdot H_{cd} \mathbf{1} \mu \cdot e^{H_{cc} t} dt. \quad (52)$$

Define

$$C = \begin{pmatrix} H_{cc} & H_{cd} \mathbf{1} \mu \\ \mathbf{0} & H_{cc} \end{pmatrix}, \quad (53)$$

and evaluate e^{Cy} . Then, $J(y)$ is the upper right block of e^{Cy} . The matrix exponential is usually calculated using Padé approximation, which requires $O(r^3)$ operations for a matrix of order r [24]. This approach for evaluating (52) is significantly faster than the approach used in [2] which relies on Runge-Kutta numerical integration [28].

Algorithm 1: EM Algorithm for Estimating the Bivariate Markov Chain Parameter**Data:** Source-destination observations $\{Y_1, \dots, Y_K\}$;**Result:** A high likelihood estimate $\hat{\phi}$ of the parameter ϕ of the bivariate Markov chain, which comprises $\{\nu_a, a = 1, \dots, d_1\}$, $\{g_{ab}(ij) \in H_{cc}\}$, and $\{g_{ab}(i1) \in H_{cd}\}$;**Initialization:** Set an initial estimate $\hat{\phi} \leftarrow \phi_0$;Evaluate the likelihood $\delta(0)$ of the initial estimate using (54); Set $\iota \leftarrow 1$, $\iota_{max} \leftarrow 1000$;**while** $\iota \leq \iota_{max}$ **do** Use Proposition IV.1 to evaluate $\hat{\nu}_{ai}$; Use Propositions IV.2 and IV.3 to evaluate $\hat{D}_i^a(y_k)$ and $\hat{M}_{ij}^{ab}(y_k)$, respectively; Use the estimates in (33) to obtain a new estimate of $\{\hat{g}_{ab}(ij)\}$; Evaluate the likelihood $\delta(\iota)$ of the new parameter estimate ϕ_ι using (54); Update parameter estimate: $\hat{\phi} \leftarrow \phi_\iota$, $\iota \leftarrow \iota + 1$;**end**

The likelihood of the observation sequence follows from (38) and is given by

$$P_{\phi_\iota}(Y_1 \in dy_1, \dots, Y_K \in dy_K) = \prod_{k=1}^K \mu e^{H_{cc} y_k} H_{cd} \mathbf{1}_{dy_k}. \quad (54)$$

A formal statement of the EM algorithm is given as Algorithm 1.

V. SINGLE PATH MODELING

In this section we discuss delay estimation on a single source-destination path, which is of particular interest in a computer network. We attribute a bivariate Markov chain to that path, and estimate the parameter of the model from multiple source-destination delay measurements. Modeling of traffic on a single source-destination path is simpler than modeling traffic over the entire network, it provides more intuitive results, and it will be used to compare our approach with previous work such as that in [39]. In addition, this approach could be applied to a network with deterministic routing, i.e., all packets for a given source-destination pair follow a single path.

Suppose that the nodes on the single source-destination path of interest are numbered consecutively, say $\{1, \dots, d\}$, where node 1 is the source node, node d is the destination node, and nodes $\{2, \dots, d_1\}$, $d_1 = d - 1$, are intermediate nodes. The generator of the bivariate Markov chain model is given by

$$G = \left(\begin{array}{cc|c} G_{11} & G_{12} & \mathbf{0} \\ & \ddots & \\ & & G_{d_1-1, d_1-1} & G_{d_1-1, d_1} \\ & & & G_{d_1, d_1} \\ \hline \xi_1 \nu_1 & \mathbf{0} & h_1 & -\xi_1 \end{array} \right) \quad (55)$$

where all matrices in the upper left block of G , which we previously referred to as H_{cc} , have the same order r , ξ_1 is

a scalar, and the dimension of the row vector ν_1 and of the column vector h_1 equals that order. The initial distribution is given by

$$\nu = (\nu_1, \mathbf{0}, \dots, \mathbf{0}, 0). \quad (56)$$

The delay on a given link coincides with the sojourn time of the X -chain in the state from which the link originates, since only one X -state is reachable from any given X -state. Thus, the source-destination delay is the sum of the X -state sojourn times.

In this model, a packet entering the root node will wander in the state space of the auxiliary S -chain, until it leaves the X -state 1 and moves to the next X -state 2. There it will wander again in the state space of the S -chain, until it moves to the X -state 3, and so on. Each jump of the S -chain while the X -chain is at rest, is also a jump of the Z -chain, and the sojourn time in each state of Z is exponentially distributed. The link delay could thus be the sum of exponentially distributed delays, mixtures of such delays, etc. The density of the link delay in a bivariate Markov chain is known to be phase-type [15], of which mixtures of convolutions of exponential densities is a particular case. It is also important to note that link delays in this model are statistically dependent as expected in a real network.

Estimation of the parameter of this model from independent source-destination delay measurements can be done using the EM algorithm of Section IV. The algorithm applies for estimating the initial distribution ν_1 , the off-diagonal elements of H_{cc} , and the elements of h_1 . As in the unstructured network, ξ_1 is set a priori as a large positive number, and $e_1 = \xi_1 \nu_1$ guarantees that the initial distribution of the bivariate Markov chain remains ν_1 after bouncing from the destination X -state d .

When the matrices $\{G_{aa}\}$ are diagonal, the density of the sojourn time in a given X -state, say $X_k = a$, follows from (26) and is given by

$$p_\phi(t | a) = \sum_{i=1}^r -\bar{\nu}_a^k(i) g_{aa}(ii) e^{g_{aa}(ii)t} \quad (57)$$

where $\bar{\nu}_a^k(i)$ denotes the i th component of $\bar{\nu}_a^k$ defined shortly after Eq. (26). This is a mixture of exponential densities with parameters $\{g_{aa}(ii), i = 1, \dots, r\}$. Thus, when the path is modeled as a bivariate Markov chain with diagonal matrices $\{G_{aa}\}$, each link delay is a mixture of exponential densities, but link delays on the path are not statistically independent. A mixture of exponential densities link delay model was used in [39], under the assumption that various link delays are statistically independent. In the single path context, this model is a special case of the bivariate Markov chain model for which the block matrices $\{G_{aa}\}$ are diagonal and the block matrices $\{G_{a, a+1}\}$ satisfy $G_{a, a+1} = -G_{aa} \mathbf{1}_{\nu_{a+1}} / (\nu_{a+1} \mathbf{1})$ when $a \in \mathbb{X}_1$, and $G_{d_1, d_1+1} = -G_{d_1, d_1} \mathbf{1}$, where $\nu = \{\nu_b, b \in \mathbb{X}\}$ is the stationary distribution of the sampled bivariate Markov chain given below (22).

VI. NUMERICAL RESULTS

In this section we present numerical results, obtained using MATLAB, aimed at assessing the performance of the bivariate

Markov chain as a model for estimating parameters of a network such as link delay density and routing probabilities. We study modeling of unstructured networks with random routing regime, as well as modeling of single paths in a network. We do not assume any specific topology in the unstructured network, except for the partition of the nodes into source/intermediate nodes and destination nodes. Thus, we do not constrain any of the sub-matrices in the H_{cc} , H_{cd} , and H_{dc} portions of the generator G of the bivariate Markov chain to be null. This generator is given in (23). In modeling a single source-destination path in a network, the generator of the bivariate Markov chain is given by (55). We compare our results for the single path modeling with the mixture model approach of [39].

A. Unstructured Networks

We tested our approach on data generated by a relatively high order bivariate Markov chain, which simulated data generated by a network. We refer to this model as the “true” model. We have used a bivariate Markov chain with $d_1 = 8$ source/intermediate states, $d_2 = 8$ destination states, and $r = 10$ for each source/intermediate state. The entries of the initial distribution vector μ were chosen by first sampling a uniform distribution on $[0, 1]$, and then normalizing its components so that $\mu \mathbf{1} = 1$. The entries of the generator G of the bivariate Markov chain in (23) were chosen as follows. The off-diagonal elements of the sub-matrix H_{cc} , and the elements of H_{cd} , were drawn randomly by sampling a uniform distribution on $[0, 100]$ where the value of 100 was set arbitrarily. For $i = 1, \dots, d_2$, we have assigned $\xi_i = 10^5$. This value of ξ_i guarantees a negligible sojourn time with a mean of 10^{-5} seconds in each destination state. Furthermore, for $i = 1, \dots, d_2$, we chose $e_i = \mu \cdot 10^5$. In generating the data Y , the bivariate Markov chain was initialized according to μ . It then evolved through the states within $\mathbb{X}_1 \times \mathbb{S}$, and incurred an exponentially distributed sojourn time in each visited state. When a destination state was reached, the total sojourn time was recorded, and the chain bounced back to an initial state in accordance with e_1 . We allowed the process to proceed in this manner until we recorded $K = 5000$ source-destination delays $\{Y_k\}$ which constituted the data Y .

Next, we used the source-destination delay data Y generated from the high order bivariate Markov chain to estimate a relatively low order bivariate Markov chain with $d_1 = d_2 = 8$ and $r = 4$ using the EM algorithm from Section IV. The estimated parameter was used to infer the link delay density estimate from Eq. (27), the routing distribution from Eq. (28), and the density of the overall source-destination path delay from Eq. (38). These estimates were compared against similar estimates obtained from the known parameter of the higher order true model of $r = 10$. We have initialized the EM algorithm by randomly generating off-diagonal elements of H_{cc} and all elements of H_{cd} , as explained above, except that here the non-negative elements of these matrices were drawn from a uniform distribution on $[0, 150]$. By sampling from a distribution with larger support, we have reduced the dependency of the initial value of the parameter on its actual

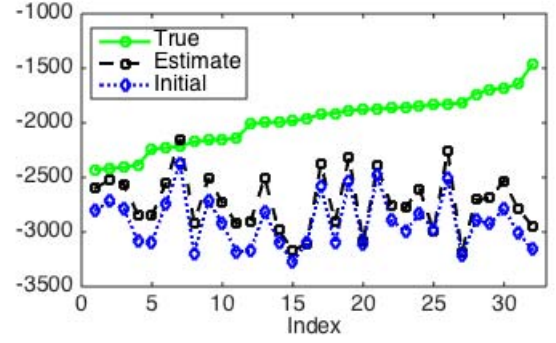


Fig. 1. Diagonal elements of H_{cc} depicted in ascending order.

value. Furthermore, it appears reasonable to choose the initial value of the parameter from a broader distribution rather than from a narrower distribution, which could exclude typical values of the true parameter. Similarly, the elements of μ were drawn from a uniform distribution on $[0, 1]$ and were subsequently normalized. We have observed that the likelihood of the estimated model increased rather slowly from one EM iteration to the other. Hence, we have limited the EM algorithm to 1000 iterations in estimating the parameter of the model.

In comparing the true and estimated densities, we have evaluated the Kullback-Leibler divergence between the two densities as follows. For densities f and g the divergence is given by

$$D_{KL}(f||g) = \int_0^\infty f(v) \log \frac{f(v)}{g(v)} dv, \quad (58)$$

which can be approximated using standard numerical integration techniques. We have designated f as the true density and g as the estimated density.

Before turning to the presentation of our link delay estimation results, we demonstrate the accuracy of the parameter estimation procedure, by estimating the parameter of a partially observable bivariate Markov chain with generator (23) and $d_1 = d_2 = 8$, $r = 4$, from source-destination delay data generated by the *same* bivariate Markov chain. The parameter of the bivariate Markov chain was randomly generated as described above, and the EM algorithm was initialized and terminated as described above. Since the generator G contains a relatively large number of entries, and estimation of each individual entry is typically difficult, we present here only aggregated values of the estimated entries. In particular, Fig. 1 shows plots of the true and estimated 32 diagonal elements of H_{cc} as obtained in our study. Fig. 1 demonstrates that the estimation procedure, starting from an initial parameter, results in an estimate that is closer to the true parameter with respect to the diagonal elements. Despite the relatively inaccurate parameter estimate, the derived estimates of the source-destination and link delay densities turn out to achieve reasonably good accuracy, as will be seen shortly. Theoretical performance bounds for parameter estimation from partially observable bivariate Markov chain are not known.

In the remaining experiments described in this and in subsection VI-B, we used the data Y generated by the high order bivariate Markov chain with $r = 10$, and applied the EM

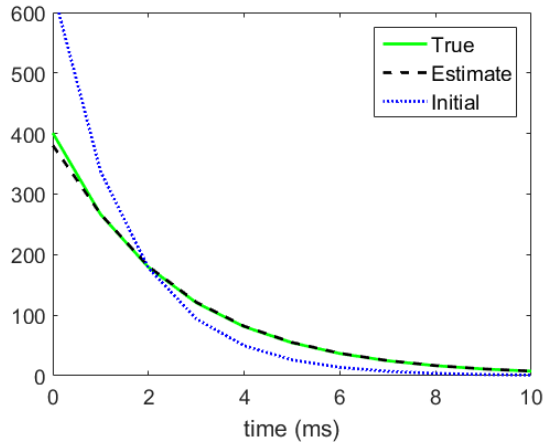


Fig. 2. Overall source-destination delay densities.

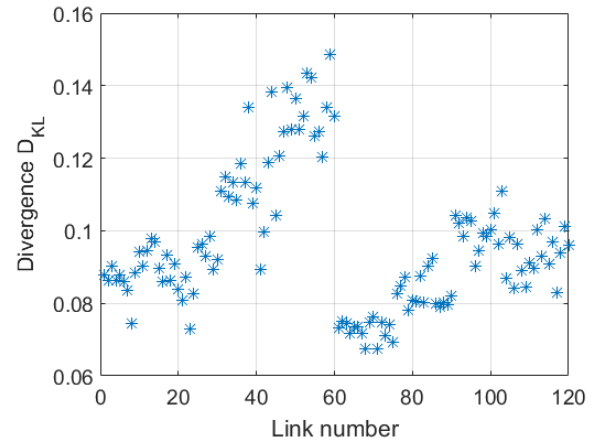


Fig. 4. Divergence values for estimated link delay densities.

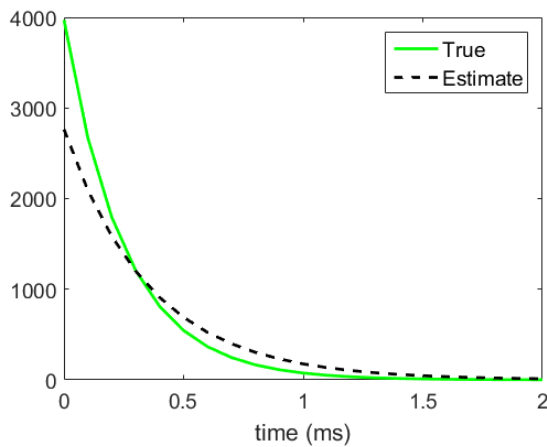


Fig. 3. Delay density for a typical link: no. 116.

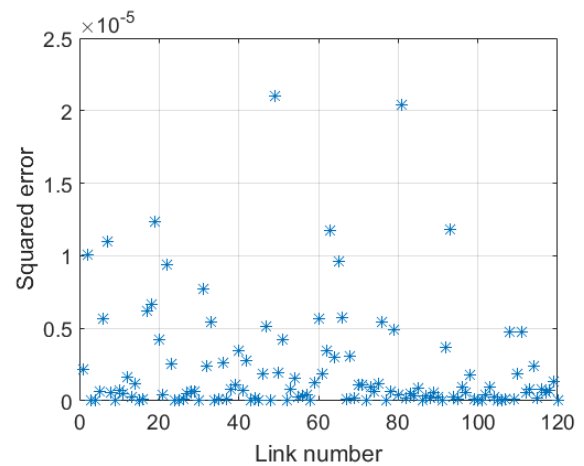


Fig. 5. Squared error for estimated packet routing probabilities on the various links.

algorithm to estimate the partially observed bivariate Markov chain of order $r = 4$. Fig. 2 shows plots of the density of the overall source-destination delay, corresponding to $P_\phi(Y_k \in dy_k)$ in (38), when ϕ is the initial parameter, and when ϕ is the estimated parameter. Clearly, the true and estimated densities are in very good agreement. The estimated divergence value for the true and estimated densities in Fig. 2 was found to be $1.02 \cdot 10^{-5}$.

Next, we compare the link delay density estimates obtained from the true and estimated parameters. In the proposed model there are $d_1^2 - d_1 = 56$ links connecting states within \mathbb{X}_1 , $d_1 d_2 = 64$ links connecting source/intermediate states to destination states, and a similar number of 64 links connecting destination states to source/intermediate states. We are only interested in the first two sets of links, which total 120 links. Fig. 3 depicts the true and estimated link delay densities for one of the links. Fig. 4 shows the divergence values for all 120 link delay estimates. We have also evaluated the packet routing probabilities using (28). Fig. 5 depicts the squared error between the true and estimated packet routing probability for each link.

We also studied the sensitivity of our approach to the model order r . We have repeated our experiments using $r = 1, 2, 3$, and compared with the results obtained using $r = 4$. Lowering

the order from $r = 4$ to $r = 1$ had negligible effect on the estimation accuracy of the overall source-destination delay density as presented in Fig. 2. Lowering the order, however, impacted the quality of the link delay estimation. As expected, the quality improved as the order r was increased from 1 to 4. Fig. 6 demonstrates the results for link number 116. The divergence values corresponding to $r = 1, 2, 3, 4$ were, respectively, 0.686, 0.316, 0.180, and 0.061.

B. Single Path Modeling

In this section we demonstrate the workings of our approach in modeling traffic on a single source-destination path of a network. We consider a path with 5 nodes given by $\{1, 2, 3, 4, 5\}$. Traffic on the given path was modeled as a high order bivariate Markov chain with $d = 5$ and $r = 10$. In this case, $d_1 = 4$ and $d_2 = 1$.

The initial distribution and generator of the high order bivariate Markov chain were generated randomly as in the unstructured network. The value of ξ_1 in (55) was set to 10^5 as before. This model was used to generate $K = 5000$ source-destination delay measurements $Y = \{Y_1, \dots, Y_K\}$. The data was used to train a low order bivariate Markov chain with

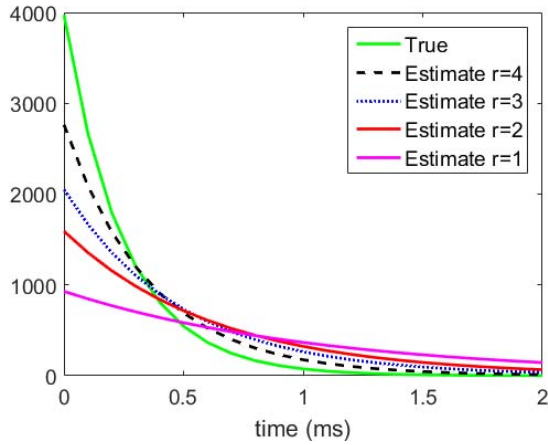
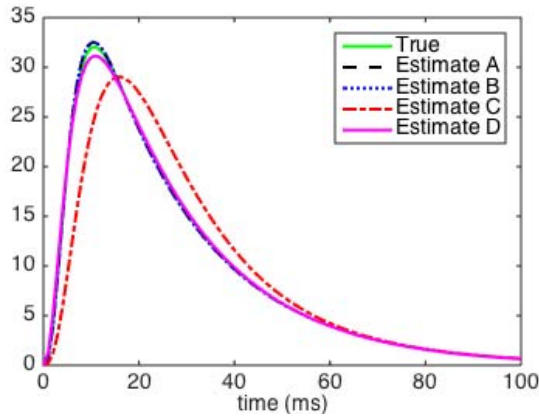
Fig. 6. Delay density estimates for link no. 116 using varying order r .

Fig. 7. Overall source-destination delay densities in a single route.

$d = 5$ and $r = 4$. The EM algorithm was initialized similarly as was done for the unstructured network. The estimated parameter was used in (26) to estimate the link delay, and in (38) to estimate the source-destination path delay.

We compared four different approaches to obtaining an estimate of the parameter of the bivariate Markov chain. In approach A, the estimate was obtained using a partially observable bivariate Markov chain with the generator structure shown in (55). In approach B, the estimate was also obtained using the partially observable bivariate Markov chain with the structure shown in (55), except that here the matrices $\{G_{aa}\}$ were diagonal. The link-delay density estimate provided by this model is the mixture density (57). This model does not assume that the delays on various links are independent and hence provides an upper bound on the performance of [39]. The estimate in C was obtained using the mixture fitting approach of [39] by specializing the implementation of the EM algorithm as discussed at the end of Section V. The estimates in approach D were obtained using the partially observable bivariate Markov chain with the general generator structure given in (23).

In Fig. 7, the overall source-destination delay densities are plotted for the estimates obtained by the four approaches. Note that source-destination delay density achieves its maximum

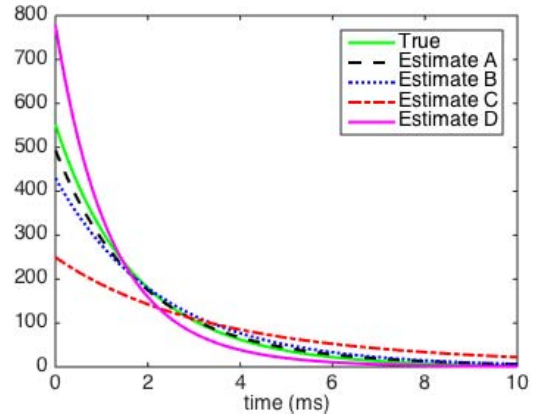


Fig. 8. Link delay densities for the first link on the given route.

TABLE I
DIVERGENCE BETWEEN TRUE AND ESTIMATED
DENSITIES ON THE GIVEN ROUTE

	$D_{KL} - A$	$D_{KL} - B$	$D_{KL} - C$	$D_{KL} - D$
Source-dest.	$6.33 \cdot 10^{-5}$	$7.20 \cdot 10^{-5}$	0.0399	$4.80 \cdot 10^{-4}$
Link no. 1	0.0146	0.0250	0.2657	0.0462
Link no. 2	0.0627	0.0039	0.1011	0.0343
Link no. 3	0.0166	0.0066	0.1950	0.0689
Link no. 4	0.0144	0.0057	0.0322	14.9156

away from time 0, in contrast to the delay densities shown in Figs. 2 and 3. We also remark that a link delay density with this shape, say for a link starting from node a , could be obtained using a bivariate Markov chain with generator such that the submatrix G_{aa} has a structure similar to that in (55). All four approaches appear to provide a reasonable approximation of the source-destination delay density. The first row of Table I gives the approximate divergence values between the true source-destination delay density and each of the estimated densities. Approaches A and B provide delay density estimates of comparable accuracy. Estimate A results in a slightly more accurate source-destination delay density estimate and link 1 delay density estimate, whereas estimate B results in somewhat better link delay estimates for links 2-4. In principle, approach A should lead to the most accurate estimate, as it models the link delays using a general phase-type distribution, but its associated parameter contains more elements to be estimated. Approaches B and C both assume a link delay model based on mixtures of exponentials. As expected, estimate C is less accurate than estimate B, due to the further assumption of statistical independence among the link delays. Approach D ignores the single path structure of the network and consequently, the generator of the bivariate Markov chain contains significantly more elements to be estimated. As a result, for the same number of samples and EM iterations, estimate D is less accurate than estimate A, particularly with respect to the link 4 delay density. Table I provides the divergence values between the true and estimated delay densities for the four links.

Fig. 8 depicts plots for the true and estimated link delay densities for the first link on the source-destination route. Comparing the estimates obtained by the bivariate Markov

chain model and the mixture model of [39], when the EM for each model is initialized in a similar manner, we see from Fig. 8 and Table I that estimates A and B are better than estimate C.

VII. COMMENTS

We developed a fairly general approach to estimate the density of the total delay on a link in a computer network from source-destination delay measurements. Our approach is based on fitting traffic over the network with a continuous-time bivariate Markov chain. This model implies that the link delay is fitted with a parametric matrix exponential delay density. This family of densities is dense in the family of densities with non-negative support and it includes phase-type densities as well as mixtures of convolutions of exponential densities. We studied link delay in networks with random routing as well as link delay on a single route of the network. We demonstrated the performance of the proposed approach using numerical examples and compared some of our results with the mixture density fitting approach of [39]. One possible extension of the work presented here is to consider bivariate Markov chains with finite support phase-type distributions [27]. Such models could improve the estimation of the link delay densities which naturally have finite support.

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