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Improved Estimation of Tail Distribution of Link Delays by Using Networks Tomography Based on the Genetic Programming and the Importance Sampling

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1 Introduction

With today's fast growth of the Internet service, networks monitoring and inference need to deal with a large number of networks performance parameters, such as individual link loss rates and packet delays. Since the direct measurement of networks traffic is partly possible due to the collaboration of individual router and servers, the estimation of parameters can only be based on measurements made at a limited subset of computers. The term networks tomography or networks delay tomography is originated to illustrate the similarity between networks inference problems and medical tomography [1]-[7]. The networks delay tomography is defined as a method to estimate the networks performance especially on the internal nodes, which gives rise to inverse problems.

This paper deals with the improved estimation of tail distribution of intermediate link delays by using the networks tomography based on the Genetic Programming (GP) and the Importance Sampling (IS) [5]-[7]. Existing methods for solving inverse problems are proposed to cut the computational complexity by modifying the original likelihood maximization problems to Pseudo Likelihood Estimation (PLE) problems [1]-[4]. However, these estimation methods are usually focusing on the cases with fixed topology of networks, and are not applicable to networks where the topologies are unknown, for example, due to the dynamic routing and adopting several platforms whose internal structure is not disclosed.

In our previous works, we use the GP to estimate the networks topology which is assumed to be unknown simultaneously by employing the PLE to estimate link delay distribution [5]-[17]. The GP method is combined with the PLE method proposed by Liang and Yu which forms simple subproblems and ignores the dependence among the subproblems by keeping the balance between the computational complexity and the statistical efficiency for the parameter estimation [4][5]-[17] In our paper, the GP method is applied to improve the estimation of networks structure [5]-[7]. Since the networks having single root node and several internal nodes and end receivers can be regarded as a tree structure, it is possible to express the structure as an arithmetic expression where the operators correspond to internal nodes and the operands correspond to end receivers (these expressions are called individuals). Then, the GP method is applied to improve the estimation of networks topology by using the genetic operation on individuals. If the estimation of the networks topology and the link delay distribution are close to true values, then the fitness of the underlying individual will be very large.

However, the most meaningful analysis of link delay depends on the extreme values of delay distributions rather than whole functional form, which affects direct the packet losses in networks. Then we use the IS method to exploit effectively the data of broadcasting packets by using the transformation of distribution function so that the extreme shape (called tail) of the distribution can be figured out more precisely [21]-[23]. The IS method is widely used to estimate parameters in systems, such as the delay distribution in networks as well as fractal time series and surfaces.

We show examples with simulated data to illustrate the estimated tail delay distribution in intermediate links of networks. It is seen through simulation studies, the IS method remarkably improves the estimation of tail distribution in delay tomography compared to conventional Monte Carlo simulations.

In Section 2, we show the problem description. In section 3, we show the estimation of networks topology based on the GP method, and in Section, 4 we give the IS method for improving delay estimation. In Section 5, we show the application of the paper to artificially generated networks traffics.

2 Network Tomography and Estimation Problems in Networks

2.1 Link delay estimation and network tomography

We assume under a general network topology that a node represents a computer or a subnet (a collection of computers). A connection between any two nodes in the networks is called a path, which may consist of several links. A packet is a unit of data bits, and the information is exchanged by sending packets along a path from a source node to destination nodes.

In conventional works, it is assumed that the components such as characteristics of nodes and the networks topology affecting routing schemes are known [1]-[4]. However, in the paper, we assume that inside structures of the networks are unknown [5]-[7]. More precisely, each packet is sent from a single root node, and the delay time of packets spent between the transmission from the root node and thearrival at the terminal node (end receivers) is observed. In other words, under the multicast transmission scheme, the internal delay of probe packets exhausted within the end-to-end transmissions in networks is observed.

Even though the unknown structures (topologies) for nodes included in networks are assumed to be estimated by our method, we also assume that the kind of packet is restricted to one, and we do not introduce any priority among packets.

Generally, the connections among nodes are defined by using the routing table (scheme) including joins and splits of input nodes as well as a simple tandem connection of nodes. But we restrict ourselves to topologies of tree structures where the connection of nodes is represented by a hierarchical tree starting from a single root node and nodes are connected by branching to the terminal nodes. Then, we exclude the networks where several links are branched from an internal node and then are connected again to another destination nodes just by jumping the hierarchy of topology in tree structures. However, it is not difficult to extend the standard topology of networks treated in the paper to these special cases.

By considering the tree structure, end receivers are seemed to correspond to terminals such as personal computers, and then internal nodes of trees are seemed to correspond to switching facilities such as routers and hubs. In basic models, we assume that a node is composed of one input link and two output links. But the model is easily extended for cases of nodes having more than three output links by introducing dummy nodes with zero transmission delay.

Fig.1 shows an example of networks topology. In the figure, the symbol 0 corresponds to the root node from where packets are sent, and the symbol n_i stands for the end receivers. The two symbols A and B represent the internal nodes having two output links.

Let $X = (x_1, x_2, ..., x_J)'$ be a J-dimensional random vector, which reflects the networks dynamics such as link delays. Let $Y = (y_1, y_2, ..., y_I)'$ be an I-dimensional measurement vector at end receivers. For example, in Fig.1, the unknown vector (variable) X is needed to be estimated whose elements represent the delay time on each link, and the variable Y stand for the observation whose elements are representing accumulated delay time observed at end receivers n_1, n_2, n_3 for multicast packets sent from the root node. The goal of the networks tomography is to estimate X from the observed Y. The mathematical model in the problem is written as

$$Y = AX \tag{1}$$

where A is a routing matrix, determined by the networks topology and the routing table at each router in the networks. In conventional works the matrix A is assumed to be fixed under the fixed routing scheme and ignoring the possibility of dynamic routing. However, in our paper, we assume that the matrix A is unknown and must be estimated by the GP method. But, for simplicity, we also assume for a while that the element of the matrix A is 0 or 1 which means a deterministic routing is selected at the time of observation.

For example, the equation (1) for the networks in Fig.1 is represented as

$$\begin{pmatrix} y_{n1} \\ y_{n2} \\ y_{n3} \end{pmatrix} = \begin{pmatrix} 1 & 1 & 1 & 0 & 0 \\ 1 & 1 & 0 & 1 & 0 \\ 1 & 0 & 0 & 0 & 1 \end{pmatrix} \begin{pmatrix} x_A \\ x_B \\ x_{n1} \\ x_{n2} \\ x_{n3} \end{pmatrix}$$

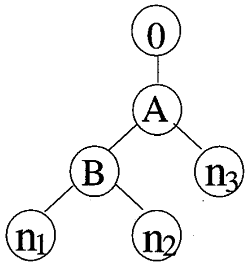

図 1: Example of networks structure

(2)

where y_{n1}, y_{n2}, y_{n3} are accumulated delay time at terminal nodes n_1, n_2, n_3, respectively, and $x_A, x_B, x_{n1}, x_{n2}, x_{n3}$ represent the delay time at nodes A, B, n_1, n_2, n_3 or at links connected to these nodes.

The estimation of X is an inverse problem. In a general networks tomography scenario, A is not a full-rank square matrix, where $I << J$, hence some constraints have to be introduced to ensure the identifiability of the model. Thus, we assume that all components of X are independent of each other, even though such an assumption does not hold strictly due to the temporal and spatial correlation among the network traffics. Therefore, we give a good first-step approximation by solving the problem. Under these assumptions we show the procedure to estimate X using Y. We assume each component of X denoted as x_j under a probability distribution.

Throughout the paper, we assume that the vector Y is observed at T consecutive time period of intervals, and X is estimated as corresponding unobserved networks performance quantity.

2.2 Subproblems with Pseudo Likelihood Estimation

For the problem of multicast delay inference through end-to-end traffic, the maximum likelihood method is usually infeasible because its likelihood function involves finding all possible internal delay vectors X, given an observed delay vector Y. Thus, the computational complexity of the problem grows at a nonpolynomial rate.

We can, however, apply the PLE approach to this problem, which is proposed by Liang and Yu [4]. In the PLE, the whole problem is divided into several subproblems, and the likelihood function is represented by the product of each likelihood function of subproblems. In this case, each row of the routing table matrix A corresponds to an end receiver in the multicast tree, and subproblems are formed by choosing two end receivers each time.

An example is depicted in Fig.2. From arbitrary multicast tree as illustrated in Fig 2 (a), we select an internal node at random, and then define only two end receivers connected to the internal node regarding them as the only attainable end receivers in the networks and neglecting other end receivers in this subproblem. The subnetworks obtained by generating subproblem

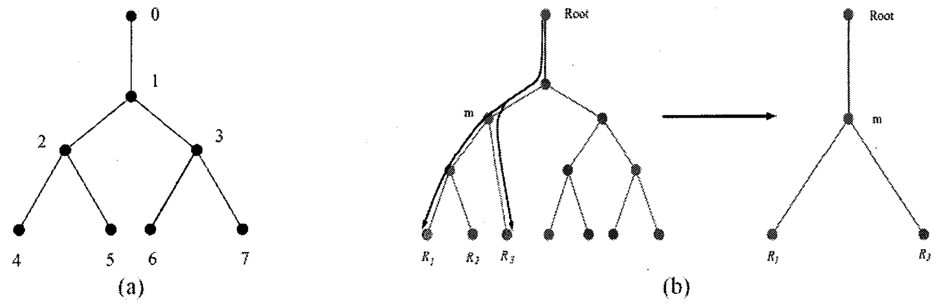

図 2: Example for obtaining subnetworks (a)original multicast tree, (b) selection of two end receivers, for PLE decomposition

is shown in Fig.2(b) in which each link delay is estimated based on the accumulated delay at terminal nodes. After calculating the log likelihood for these subnetworks, then we have comprehensive log likelihood for the while networks.

Subproblems are formed by selecting some pairs of rows from the routing matrix A. Namely, we select all possible pairs, but a subset can be judiciously chosen to reduce the computation.

Let S denote the set of subproblems by selecting all possible pairs of rows from the routing matrix A. Then, for each subproblem

$$Y^s = A^s X^s, s \in S \tag{3}$$

where X^s is the vector of networks dynamics involved in the subproblem, and A^s is the corresponding routing matrix, and Y^s is the corresponding observation of $s \in S$.

A discretizaton scheme is imposed on link-level delay in such a way that x_j takes finite possible values

$$x_j \in (0, q, 2q, \ldots, mq, \infty) \tag{4}$$

where q is the bin width and m is a constant. Assume q is known so that each x_j is a independent multinominal variables with $\theta_j = (\theta_{j0}, .\theta_{j1}, ..., \theta_{jm}, \theta_{j\infty})$.

$$\theta_{jl} = Prob(x_j = lq) \tag{5}$$

If the delay is infinite, it implies that the packet is lost during the transmission.

2.3 PLE algorithm

Maximizing the pseudo likelihood function in PLE leads to the ordinary maximizing procedure, but often the pseudo likelihood function cannot be solved analytically. Hence, a numerical optimization algorithm has to be adopted. The EM (Expectation Maximization) algorithm is well known method for maximizing the likelihood function numerically. We can use an pseudo-EM (an EM like algorithm) to maximize the pseudo likelihood function. In the EM algorithm, we do not optimize all of the parameters at the same time. At first, we optimize by parameters in group A by assuming that another group B of parameters are fixed so as to maximize the likelihood function. Then, at the next time we optimize by parameters in the group B by assuming that parameters in the group A are fixed.

For a given subproblem s, each component of X^s is an independent multi-nominal random variable, so that the log-likelihood function given the complete data for time t denoted as X_t^s $(X_1^s, X_2^s, \ldots, X_T^s)$ is obtained. For convenience, we denote jth element of X_t^s as x_{tj}^s.

Let $\theta_{jl}^{(k)}$ be the parameter estimate obtained in the kth step of pseudo-EM for jth element x_{tj}^s where $\theta_{jl} = P(x_{tj}^s = lq)$. Then, the Expectation Maximization algorithm is given as follows.

(Initial values)

The initial values of the pseudo-EM algorithm can be chosen arbitrarily. A uniform distribution, i.e., $\theta_{jl}^{(0)} = 1/(m+2)$ for all possible j and l is used as the starting point for the simulation study.

(E-step) Calculate next values

$$\hat{n}_{jl} = \sum_{s \in S} E_{\theta^{s(k)}} (\sum_{t=1}^{T} 1\{x_{tj}^s = lq | Y_t^s\}) \tag{6}$$

where $1\{\}$ is a function taking the value 1 (0) if the condition in the parenthesis is satisfied (not satisfied). The term $\hat{n}_{jl}$ means the expectation of the number of packets whose delay time on link j is equal to lq. The calculation is carried out as is shown on the right hand side of equation. Under the given observation Y_t^s, we sum up the expected number of packets satisfying the condition $x_{tj}^s = lq$ for all of the subproblems s, which is obtained by the forward-backward algorithm [1]-[4]. In the procedure, we assume that the delay distribution on each node expect the node j is fixed to the previous value at the time step k.

(M-step) Update $\theta^{(k)}$ as follows

$$\theta_{jl}^{(k+1)} = \frac{\hat{\eta}_{jl}}{\sum_{r \in R} \hat{n}_{jr}}, R = [0, 1, ..., m, \infty] \tag{7}$$

We iterate above two steps (E-step and M-step) until we can expect no further improvement of parameter estimations.

Consistency and asymptotic normality of the PLE method base on solving subproblems is shown by Liang and Yu under very general conditions [4]. Details are omitted here.

3 Network Topology Estimation by the GP

3.1 Basics of the GP

In the basic method of the networks tomography, we assume that the networks topology is known and fixed [1]-[4]. Then, we extend the model to the case where neigther the networks topology nor the delay distribution is known[5][6]. In our method, the networks topology is represented as a tree structure, and is regarded as an individual to be improved by the genetic operations [8]-[20].

For simplicity, at first we explain the GP procedure for the approximation of function in time series prediction. Any S-expression can be graphically depicted as a rooted point-labeled tree with ordered branches. The external points(leaves) of the tree is labeled with terminals, i.e., constants and variables $x(t-1), x(t-2)$. The root and internal nodes of the tree are labeled with the primitive function such as binomial operation $+, -, \times, /$. We employ the prefix representation to treat the tree. For example, for the function $x(t) = [6.43 \times x(t-1) - (x-2)] \times [x(t-3) - 3.54]$ generating the time series, we have the next prefix representation.

$$\times - 6.43x(t-1)x(t-2) - x(t-3)3.54 \tag{8}$$

The equation represented by using the prefix representation is called as an individual. The individual is interpreted based upon the stack operation. Since we know the values $x(t-1), x(t-2), x(t-3)$, we obtain the prediction for the individual $\hat{x}(t)$ by substituting these values in the prefix representation. The difference between the observed value $x(t)$ and the prediction $\hat{x}(t)$ reveals as the ability of the individual, then we define the fitness of the individual as the inverse of the prediction error.

StackCount

For checking the validity of underlying parse tree, the so-called stack count (denoted as *StackCount* in the paper) is useful [8]-[20]. The *StackCount* is the number of end-nodes that places on minus the number of intermediate nodes that takes off from the stack. At first we set zero to *StackCounrt*. By scanning the prefix representation from left to right, we add 1 to *StackCount* if we meet operands, otherwise (meet operators) subtract 1 from *StackCount*. The cumulative *StackCount* never becomes positive until we reach the end at which point the overall sum still needs to be 1.

crossover operation

The basic rule is that any two loci on the two parents genomes can serve as crossover points as long as the ongoing *StackCount* just before those points is the same. At first, we select a random location L_A on the individual A, and then calculate *StackCount* denoted as N_s to the location L_A (crosspoint). Then, we select the location L_B on the individual B which is a pair of crossover operation for individual A in such a way that the *StackCount* for B until the location L_B is equal to N_s. Generally, we have several candidates for the location L_B, and then select one of them at random. The crossover operation creates new offsprings by exchanging sub-trees between two parents. We generate two individual by combining former part of individual A (B) by latter part of individual B (A). By applying the genetic operations for two individuals selected in proportion to the fitness, we have offsprings with better fitness which are used to replace individuals with relatively small fitness.

mutation operation

The goal of the mutation operation is the reintroduction of some diversity in a population.

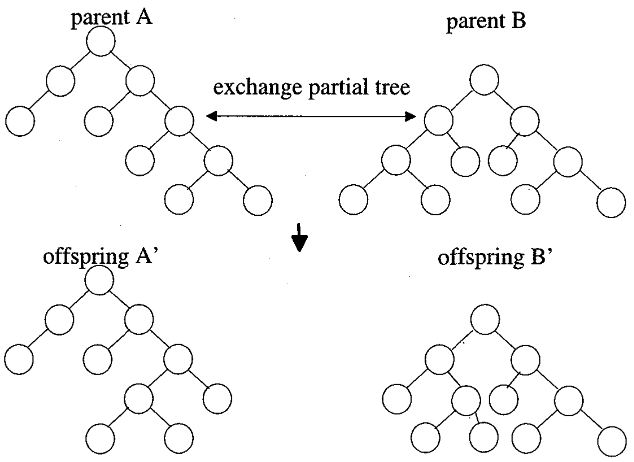

図 3: Example of crossover

Select at random a locus in a parse tree to which the mutation is applied, we replace it by another value corresponding to operators and operands.

3.2 Applying GP to topology estimation

The prefix representation for networks topology is obtained by changing the definition in arithmetic expressions by regarding the operands as end receivers, and operators as the internal nodes in the networks. For example, for the networks in Fig.1, we have the prefix representation as

$$A\ B\ n_1\ n_2\ n_3 \tag{9}$$

The *StackCount* used for arithmetic expressions is easily extended for representing networks topologies. At first we set zero to *StackCounrt*. By scanning the prefix representation from left to right, we add 1 to *StackCount* if we meet symbols denoting end receivers, otherwise (meet symbols for internal nodes) subtract 1 from *StackCount*.

We can apply the same GP operations (crossover and mutation operations) as arithmetic expressions for the individuals representing networks topologies by selecting crosspoints L_A and L_B for individuals A and B by considering appropriate *StackCount* numbers, and details are omitted here. Examples of crossover operation and mutation operation are shown in Fig.3 and Fig.4.

Since each individual in the GP corresponds to a realization of networks topology, then by applying the genetic operation, we can have more appropriate estimation of networks structure depending on the fitness of individuals. The fitness of individuals is defined by using the calculation of delay distribution at the end receivers based on the PLE. Once the networks topology is determined by interpreting the individual, the delay distribution on the end-nodes is calculated by the PLE. The fitness of an individual is defined as the inverse of estimation error for the delay

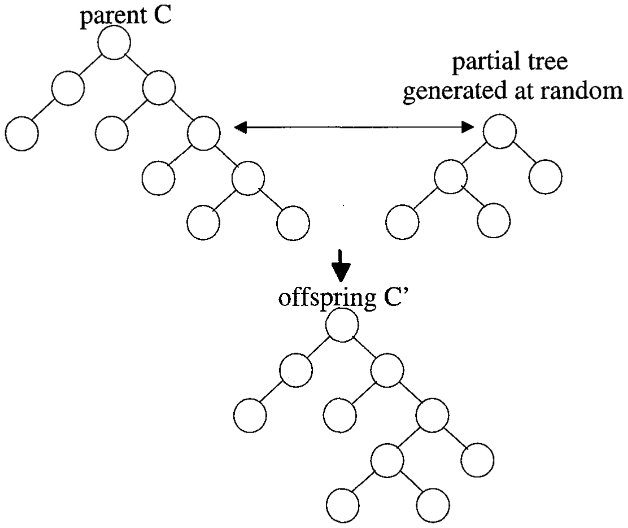

図 4: Example of mutation

distribution on end receivers.

delay distributions on end receivers

At first, we assume that we have a given delay distribution on the end receivers (denoted as d_T) as observations. These observations are able to be given as a set of numerical values. But in cases we postulate functional forms of delay distribution on internal nodes, we use the convolution to get the delay distributions on end receivers. Theoretically, we can calculate these values by using the convolution of delay distribution of each link which is placed on the rooting path beginning from the root node to the end receivers.

GP algorithm

We iteratively perform the following steps until the termination criterion has been satisfied.

(Step 1) generate initial population of individuals

Generate an initial population of random composition of possible internal nodes (operators) and end receivers(operands) for the problem at hand. The random tree must be syntactically correct program in the sense that the value of *StackCount* is 1.

(Step 2) Calculation of fitness of individuals

Execute the evaluation for each individual i (estimation of delay distribution at end receivers) in population by applying the PLE. By assuming the networks topology is identical to the tree given by the underlying individual i, we calculate link delay distribution (probabilistic distribution) on each link based on the PLE. Then, we compare the calculation (estimation) of delay distribution on end receivers (denoted as d_S) obtained by the GP and PLE methods with true value d_T. Then we define the fitness of individual i as the inverse of the square error between d_T and d_S where d_T is given observation of delay distribution at end receivers. Even though the estimation error between d_T and d_S is affected by the estimation error caused from the PLE itself, but it is ensured that the error comes from the irrelevant identification of topology heavily affects the estimation error. Then, we sort individuals according to the fitness S_i.

(Step 3) crossover operations

Select a pair of individuals chosen with a probability p_i based on the fitness. The probability p_i is defined for ith individual as follows.

$$p_i = (S_i - S_{min}) / \sum^{N} (S_i - S_{min}) \tag{10}$$

where S_{min} is the minimum value of S_i, and N is the population size. Then, create new individuals (offsprings) from the selected pair by genetically recombining randomly chosen parts of two existing individuals using the crossover operation applied at a randomly chosen crossover point while keeping the restriction for the *StackCount* for both individuals. Then, we gather these new offsprings in the pool P-B which is different from the initial pool P-A. Repeat the procedure several times, and we gather sufficient number of new offsprings necessary for the replacement of individuals. Then, we replace individuals in the pool P-A having lower fitness by individuals in the pool P-B.

(Step 4) mutation operations

To reintroduction some diversity in an population, we apply the mutation operation with a certain probability to an individual at random. value (a intermediate node (operator) or a end-node).

(Step 5) iterations

If the result designation is obtained by the GP (the maximum value of the fitness become larger than the prescribed value), then terminate the algorithm, otherwise go to Step 2. The procedure iterated from Step 2 through 4 is called a generation of the GP.

4 Importance Sampling for Improved Tail Estimation

4.1 IS for rare events

An important concept for quantifying networks performance is the loss in packets or large delay during a specified period duration of service [21]-[23]. For a given probability p, the tail distribution x_p is defined to be the $(1-p)$ th quantile of the distribution of link delay x.

$$P(x > x_p) = p \tag{11}$$

The computational cost required to obtain accurate Monte Carlo estimates of tail distribution is often enormous, since a large number of runs (packet delay evaluations) are required to obtain accurate estimates of the loss the distribution in the region of interest. Then we apply the IS by changing the measure for sampling (the change of delay distribution).

The IS is a particularly appropriate technique for rare event simulations. The standard simulation is inaccurate for estimating $P(x > x_p)$, while for large x_p few samples are obtained in the important region where $x \simeq x_p$. Effective IS should generate a disproportionally large number of samples in this region. We use the approximation $x_p \simeq a_0 + Q$ and select an IS technique that generates large values of $a_0 + Q$ with high probability. In fact, under the condition, the mean of $a_0 + Q$ equals x_p. For IS, we consider a change of measure in which the mean of x is changed from 0 to μ. Then, we have $P(x > x_p) = E[I(z > x_p)l(z)$ where $E(.)$ means the expectation under the IS distribution, and $l(z)$ is the likelihood ratio with new random variable z.

Under packet loss estimation, we denote

$$p_t = P(x > x_p) = \int_{x_p}^{\infty} f(x)dx \tag{12}$$

where the function $f(x)$ is the probability density function of packet delay x on a certain link using the PLE and GP methods in previous sections. Then, we introduce a distribution function to generate twisted random variable z as follows:

$$p_t = \int_{x_p}^{\infty} f^*(z)\frac{f(z)}{f^*(z)}dz \tag{13}$$

where the function $f^*(x)$ is the probability density function (called Importance Function) for the twisted variable z having higher probability in the region close to x_p and greater than x_p.

4.2 Determining Importance functions

Then, we define the Importance Function $f^*(x)$ which is used as an alternate density function or a biasing density function. Biasing by exponential twisting is most easily explained by means of derivation of statistical upper bounds on tail probability, and is widely used in various areas such as information theory [23].

The basic method of the exponential twisting is summarized as follows:

(1) function $f^*(x)$

The function $f^*(x)$ is defined as

$$f^*(x) = e^{sx-\mu(s)}f(x) \tag{14}$$

where the function $\mu(s) = \log M(s)$ is obtained from the moment generating function $M(s) = E\{\exp(sX)\}$ of $f(x)$.

(2) optimal value of s

If the functional form of $f(x)$ is given, then the optimal value of s is determined so that the two quantities are to be minimized.

$$I(s) = \int_{t}^{\infty} e^{-(sx-\mu(s))}f(x)dx \tag{15}$$

$$\bar{I}(s) = e^{-2(st-\mu(s))} \tag{16}$$

If we choose the function $f(x)$, an exponential density function $f(x) = \alpha e^{\alpha x}$, then we have optimal value of s as s_t

$$s_t = \alpha - \frac{1}{t} \tag{17}$$

For example, if we choose as $\alpha = 1$ and $p_t = 10^{-6}$, then we have $t = 13.81551$.

(3) approximation of density function

We assume that the estimated delay distribution $g(x)$ for delay time x on a link obtained by the proposed method based on the GP and PLE is numerically approximated by the exponential distribution function $f(x) = \alpha e^{-\alpha x}$. Since the parameters $\theta_{jt} = Prob(x_j = lq)$ in equation (5) is obtained for each bin as a discretized version of the function of $g(x)$, then we adopt the continuous function $f(x) = \alpha e^{-\alpha x}$ to approximate $g(x)$. We simply use the steepest descent algorithm to minimize the mean square error between $g(x)$ and $f(x)$ so that the parameter α is estimated.

(4) giving the gain of IS

We also denote the gain of IS as follows:

$$\tau = \frac{p_t(1-p_t)}{E^*\{1^2(X \geq t)l^2(X)\} - p_t^2} \tag{18}$$

It means the ratio of the sample sizes of standard Monte Carlo method and importance sampling method under the circumstance with the same estimator variances.

We can recognize the ability of the IS by a simple example. For a given exponential distribution $f(x)$ with $\alpha = 3$, we generate $M = 500000$ samples along the distribution. Then, we calculate the probability of rare event $p_t = P(x > x_p) = 10^{-6}$. We have the estimation for expected value of p_t ($E\{p_t\}$) and its variances ($V\{p_t\}$) as ($E\{p_t\} = 0.90001E^{-06}, V\{p_t\} = 1.46316E^{-12}$. On the other hand, we obtain estimation result by using the IS ($E\{p_t\} = 1.00180E^{-06}, V\{p_t\} = 9.92378E^{-17}$) with the sample size $M = 100000$. At the same time, we have the value τ for the example as $\tau = 54075.94$. The fact shows the ability of IS to increase the estimation result.

5 Applications

5.1 Estimation for artificially generated delay

In order to assess the performance of the PLE combined with the GP procedure for estimating the networks topology, model simulations are carried out on a four-level multi-cast tree depicted in Fig.5.We assume that the networks topology and the delay distributions of all internal nodes are given. Then, the estimation method of our paper is applied to obtain the networks topology and the delay distribution on the internal nodes. If the result of estimation of networks topology is the same as the original (given) structure and the estimation of delay distribution is close to the prescribed distribution, the method of the paper is proved to be appropriate for the delay tomography.

Followings are assumed to the networks topology and the delay distribution on the internal nodes. In Fig.4 the number 0 means the root node from which the packets are sent to the networks. The numbers from 1 through 6 mean the internal nodes, and the numbers from 7 through 13 are the end receivers where the accumulated delay of the packet are observed. It is assumed that the delay for packet are incurred in communication links between two adjacent nodes. For simplicity, the identical number of link is the same as the number of corresponding node connected to the lower node in the networks. The numbers written in parentheses in Fig.5 mean the average delay value of delay distribution on these links.

Followings are used for the simulation study.

Number of individuals:20

Delay distribution on links: exponential distribution having Mean value between 3 and 8.

Bin characteristics:$q = 1, m = 20$

Number of multicast delay measurement:5000 i.i.d data

After composing the tree structure of the networks based on an individual, we calculate the observation Y on end receivers by accumulating the link delay along the paths from the root node 0 to end receivers $7, 8, ..., 13$. Since we have seven end nodes, then we have seven dimensional with 5000 samples each. For the generation of packet delay, we generate random numbers corresponding to the delay distributions on links $0, 1, ..., 13$ as identically independent distributed numbers. Then, we sum up these delays along the path of packet, so that we can get the delay time on end nodes.

We apply our proposed method to estimate the networks topology and the distributional parameter to the networks in Fig.5. As a result of simulation, we get the same tree structure as the estimation of the GP procedure after seven generations of GP (the diagram depicting the convergence is omitted here). Fig.6 shows an example of estimated results on the link 7 compared with the original (given) distribution. Fig.7 shows the estimation of accumulated delay distribution on link 11 compared with the original (given) distribution. In these figures, the solid lines correspond to the original distribution, and the dashed lines mean the estimated distributions. Obviously, the results show that our suggested method works well. The result shows the GP procedure combined with the PLE provides us almost the same estimation for delay distribution. Furthermore, the networks topology is also estimated and identified by the GP procedure given in the paper.

5.2 Improved estimation by IS

Now, we examine the estimation of packet loss probability obtained by the IS method proposed in the paper by comparing the result obtained solely from the PLE outputs. Since the delay distribution on each link of artificially generated networks is known, it is easy to see the estimation error by two methods.

For simplicity, we compare the estimated probability of packet loss with true value. Since we know the original delay distribution of each link, we can obtain the marginal delay time x_p for which the delay time larger than x_p has the probability $p_t = 10^{-6}$ such as $P(x \geq x_p) = p_t$.

We prepare following two type of simulation studies for the same networks configuration.

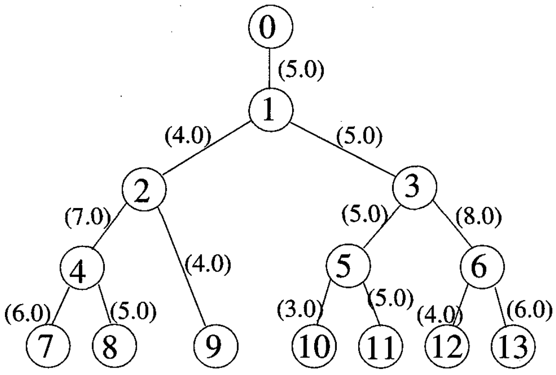

図 5: Example of given networks topology

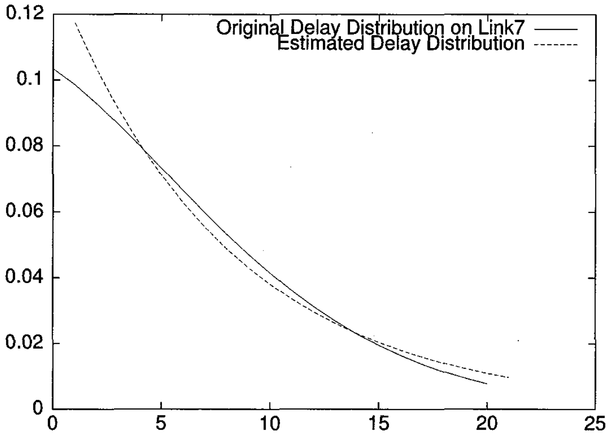

図 6: Example of estimation of delay distribution (link 7)

Case GP-PLE:

We use only the GP and PLE for the estimation of topology and delay distribution as a basic method, and no improvement using the IS is applied.

Case GP-PLE-IS:

We use the GP and PLE for the estimation of topology and delay distribution, and then apply the IS to improve the estimation of tail distribution.

In the estimation of tail distribution, we use 10000 samples of random numbers generated after identifying the distribution function $g(x)$ on each link. Table 1 shows examples of the expectation of packet loss probability p_t for which the quantile x_p of the distribution of link delay is realized, namely, $P(x > x_p) = p_t$. In the table, we also show the variance of p_t. Then, the estimation of p_t obtained from tail delay distribution compared with true distribution for several arbitrarily selected links. At the same time, to examine the stability of estimation, Table 2 shows the gain τ defined by equation (18). The Table 2 shows the ratio of the number of samples used for the GP-PLE scheme necessary to get the same estimation as the GP-PLE-IS scheme. If the

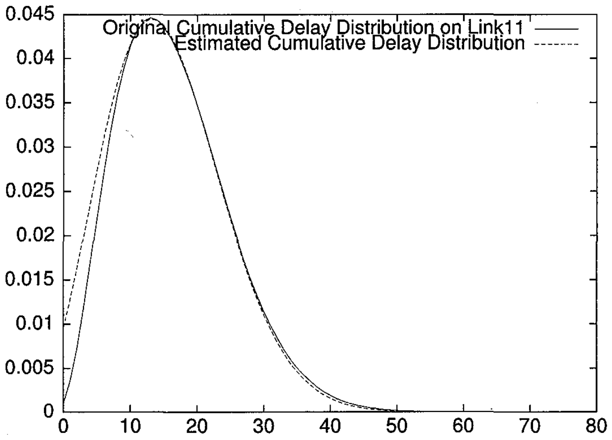

図 7: Example of estimation of accumulated delay distribution (link 11)

gains are large, we can attain the computational speed-up by the IS.

Seen from Table 1 and 2, the estimated p_ts obtained by the IS after applying GP and PLE are much more accurate than those obtained by standard Monte Carlo method after applying GP and PLE. It is also seen from the tables that large reductions of samples are realized for all the intermediate nodes by using the IS.

表 1: Estimates of $E\{p_t\}$ for tail distributions of several link delays(GP-PLE-IS)

links	$E\{p_t\}$(GP-PLE-IS)	$Var[p_t]$
No.2	1.004680E-06	6.029493E-16
No.4	9.828698E-07	1.173991E-15
No.6	9.568224E-07	5.974170E-16
No.7	9.967802E-07	1.72109E-15
No.8	9.920351E-07	8.46020E-16
No.11	9.998340E-07	8.93730E-16
No.13	9.987617E-07	7.206100E-16

5.3 Other networks and delay distribution

We apply the estimation method proposed in the paper to another networks configuration and delay distribution to asses the applicability of the method. We generate 100 different networks topologies and related delay distributions for each link having exponential distribution with mean value between 1.0 and 10.0. In these networks, we restricted ourselves to the cases where the maximum number of links on the paths from the root node to the end nodes is less than five. The restriction is substantial, otherwise the computation time of estimation grows

表 2: Values of τs for tail distributions of several link delays

links	$E\{\tau\}$
No.2	53955
No.4	55580
No.6	58832
No.7	54855
No.8	55100
No.11	54176
No.13	54375

very rapidly.

Among 100 simulated networks, we have 97 truly estimated topologies for the networks obtained by the GP method , and in 3 cases we fail to identify the topologies. Table 3 and Table 4 summarize the result of estimation of packet loss (obtained by GP-PLE-IS) compared with the basic estimation (GP-PLE). In the following tables, the symbols of L_I and L_T stand for the intermediate links and the terminal links, respectively. In Table 3, we show simply the mean value of estimation of packet loss probabilities p_t for link delay. In the table, we also show the variance of estimation of p_t for each links in 97 cases. In Table 4, the gain $E\{\tau\}$ given in equation (18) is shown as a mean value.

As is seen from the result, the estimation of tail distribution of link delay is sufficiently improved by using the IS compared to basic estimation with only the GP and PLE.

表 3: Estimates of mean value of $E\{p_t\}$(GP-PLE-IS)

links	$E\{p_t\}$	$Var[p_t]$
L_I	9.994234E-07	1.213233E-16
L_T	9.985642E-07	5.768534E-17

表 4: Values of mean τ

links	mean$[E\{\tau\}]$
L_I	56545
L_T	54345

5.4 Erlang type of delay distribution

For the study of dependency of type of probability distribution of link delays, we use the same 100 examples of tree structure used in previous section. By keeping the same networks topologies as previous 100 examples, then we change the delay distribution on links from exponential distribution with mean values ranging from 1 to 10 to the Erlang distribution E(k) with identical phase k but having the same mean values as the original exponential distribution to introduce more general types of delay distributions. Moreover, we change the phase of Erlang distribution simultaneously from $k = 2$ to $k = 7$ on every links.

Then, we must slightly change the definition of Importance Functions. The moment generating function $M(s)$ used for calculating $\mu(s) = \log M(s)$ in equation (14) is gives as

$$M(s) = \frac{\alpha^k}{(\alpha - s)^k} \tag{19}$$

Then, we estimate optimal s numerically for the IS method. At the same time, since the Erlang distribution has two parameters the mean value and the phase k, we must also used the steepest descent approximation to get these parameters.

The conditions for the simulation studies are the same as previous sections. We are interested in the identification of networks topologies and the mean value of estimation of tail distribution p_t on each link.

Among 100 simulated networks, we have 97 truly estimated topologies for the networks obtained by the GP method , and in 3 cases we fail to identify the topologies. The result is the same as examples in previous section. The fact means that the effectiveness of the GP method is mainly depends on the networks topologies themselves, and not on the delay distributions.

Table 5 and Table 6 summarize the result of estimation of packet loss (obtained by GP-PLE-IS) compared with the basic estimation (GP-PLE). In Table 5, we show simply the mean value of estimation of packet loss probabilities p_t for link delay in 97 cases. In Table 6, the gain $E\{\tau\}$ given in equation (18) is shown as a mean value. The results in Table 5 and 6 show that the estimation of p_t will become worse if the phase k grows . However, as is seen from the result, the estimation of tail distribution of link delay is sufficiently improved by using the IS compared to basic estimation with only the GP and PLE.

表 5: Estimatation of mean value of $E\{p_t\}$ along phase k

links	$E\{p_t\}, k = 2$	$k = 4$	$k = 6$
L_I	9.96742E-07	1.00344E-08	1.00332E-08
L_T	9.98654E-07	1.00342E-08	1.00353E-08

表 6: Values of mean τ along phase k

links	mean$[E\{\tau\}], k=2$	$k=4$	$k=6$
L_I	71720	88495	98969
L_T	72009	87998	98778

6 Conclusion

In this paper, we proposed a method for improving the estimation of tail distribution of link delay by using the networks tomography and the GP based on the IS method. We used the GP to estimate the networks topology which is assumed to be unknown simultaneously by employing the PLE for delay distribution. Each individual in the GP was the representation of networks topology, and then assigned the fitness by calculating the link delay estimation by using the PLE. The IS method is utilized to exploit the data for broadcasting packet by transforming the distribution functions. The simulation studies were shown for the artificially generated data.

The problems remain to be solved are the extension for various real world data and estimation of density function in a functional form, and the further research will be done by the authors.

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