A NEW MONTE CARLO METHOD FOR ESTIMATING EQUILIBRIUM NETWORK RELIABILITY PARAMETERS

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1. **Introduction**.

A network $\mathcal{N}$ is defined as a triple (V, E, T), where V is the set of vertices, E is the set of edges and T is a subset of V called the *terminal* set. The stochastic behavior of edge $e, e \in E$, is described by an alternating two-state Markov process. In this process, $p(e)$ is the stationary probability that the edge e is *up* and $q(e) = 1 - p(e)$ is the probability that e is *down*. $1/\lambda(e)$ and $1/\mu(e)$ are the corresponding mean up and down periods for edge $e \in E$ in this process. All edges are assumed to be stochastically independent. By the definition, the network $\mathcal{N}$ is *up* if all terminals in T are connected to each other. Otherwise, the network is in *down* state. Let T_{up} and T_{dn} be the mean equilibrium *up* and *down* periods for the whole network, respectively.

A new Monte Carlo method is suggested for estimating the stationary network availability $R = T_{up}/(T_{up} + T_{dn})$ and the so-called stationary *down* $\rightarrow$ *up* transition rate $\Phi = (T_{up} + T_{dn})^{-1}$. Having the estimates of R and Φ, one can easily estimate T_{up} and T_{dn}, which is a quite difficult task, especially for highly reliable networks.

2. **The Monte Carlo Sampling Scheme and the Edge Evolution Process**.

A general representation of the Monte Carlo sampling scheme is drawing "balls" ω from an "urn" which contains a "population" Ω of balls. The probability that a particular ω is chosen equals $p(\omega)$. A random variable Y is defined on Ω in such a way that it takes on the value $Y(\omega)$ on a particular ω. The quantity of interest θ is the mean value of Y:

$$\theta = E[Y] = \Sigma_{\omega \in \Omega} p(\omega) Y(\omega). \quad (1)$$

Monte Carlo means in fact estimation θ via its *sample mean*:

$$\hat{\theta} = N^{-1} \Sigma_{i=1}^{N} Y(\omega_i) \quad (2)$$

Obviously, $\hat{\theta}$ is an unbiased and consistent as $N \to \infty$ estimator of θ .

The heart of any Monte Carlo is defining the "urn" and the "balls". For a crude Monte Carlo, a "ball" is a binary vector whose components determine the state of each edge. In our method, ω is a *trajectory* in a special edge evolution process with closure . Its idea was originally suggested by M.Lomonosov in 1972 [1]. In this process, each edge e is initially down at $t = 0$ and is "born" at random instant $\eta(e)$ which is exponentially distributed with rate $\alpha(e) = -t_0^{-1} \log q(e)$. Once born, an edge remain "up" forever. The rate $\alpha(e)$ is chosen in such a way that the probability that the edge e is up at the instant t_0 coincides with the stationary probability $p(e) = 1 - q(e)$. This guarantees that the probability that all edges born on $[0, t_0]$ will connect all terminals in T, coincides with the equilibrium *up* probability of the original network. In other words, the static network reliability, i.e. the probability that the network is *up* in equilibrium, coincides with the probability that the edges born on $[0, t_0]$ in the evolution process constitute a network in which all terminals are connected to each other.

An efficient Monte Carlo for estimating R and Φ is based on introducing a Markov-type continuous - time process σ_t. Its states are, loosely speaking, the partitions of the graph $G = (V, E)$ arising in the above edge evolution process. A typical trajectory ω of σ_t starts at the partition σ_0 with no edges at all and terminates in a partition σ_k having the property that all terminals belong to one connected component of σ_k.

Since the definition of σ_t is the key issue for our Monte Carlo, let us describe it in more detail.

Given a graph $G = (V, E)$, a partition $\sigma = \{X_1, X_2, ..., X_r\}$ of V, where $X_i \cap X_j = \emptyset$ for $i \neq j$ and $\cup_{i=1}^{r} X_i = V$, is called *regular* (with respect to G) if each induced subgraph $G(X_i)$ is connected. Arbitrary set F of edges generates a regular partition $< F >= \{X_1, ..., X_r\}$ where X_i are the components of the spanning subgraph (V, F) (including isolated nodes, if any). Subsets F' and F'' are *equivalent* if $< F' >=< F'' >$. Identify every regular partition σ with the class of subsets F of E satisfying $< F >= \sigma$. Clearly, each such class is the collection of subsets of edges with a common closure.

For every regular σ, let its components be referred to as *supernodes* and $E(\sigma)$ denote the set of *external* edges, i.e. the edges between distinct supernodes. Put $\alpha(\sigma) = \Sigma_{e \in E(\sigma)} \alpha(e)$.

Regular partitions of V are partially ordered by the relation: $\sigma' < \sigma''$ when σ'' is obtained by merging components of σ'.

Denote by $F(t)$ the set of edges born on the interval $[0,t]$. Denote by $\sigma_t = \sigma$ the corresponding equivalence class, i.e. the equivalence class which exists at the instant t. Clearly, σ_t spends in σ a random exponentially distributed time with parameter $\alpha(\sigma)$. On leaving σ, σ_t jumps in one of its direct successors, say σ' which is obtained by merging exactly two super-nodes of σ, and chosen with probability $(\alpha(\sigma) - \alpha(\sigma'))/\alpha(\sigma)$. For addiional details see [2],[3],[4].

A *trajectory* ω of the random process σ_t is a sequence $\omega = (\sigma_0, \sigma_1, ..., \sigma_r)$, where σ_0 is a trivial partition into singletons, σ_i is a direct successor of σ_{i-1}, and σ_r is the first partition in the above sequence in which all terminals belong to one super-node. These ω - trajectories are the "balls" in our Monte Carlo scheme. Each ω is drawn from the urn with its probability

$$P(\omega) = \prod_{i=0}^{r-1} \frac{\alpha(\sigma_i) - \alpha(\sigma_{i+1})}{\alpha(\sigma_i)}. \quad (3)$$

Now, using the total probability formula, we represent

$P(\mathcal{N}$is up at $t_0) =$

$\Sigma_{\omega\in\Omega} p(\omega) P($to be up at $t_0|\omega)$

The corresponding value of the random variable Y , $Y(\omega)$, is the probability that the *up* state in the evolution process has been reached before the instant t_0 given that the evolution took place along the corresponding trajectory ω. $Y(\omega)$ can be computed exactly via convolutions of exponents, since the process σ_t spends an exponential time in each of the partitions along the trajectory.

The above described Monte Carlo based on evolution process with closure has several advantages. First, for each sequence of edges born there is a set of "irrelevant" edges whose future appearance would not affect the moment when the network becomes connected. These are the edges whose ends belong to one component. Thus, one sequence of born edges leading from σ_0 to σ_k represents in fact a "thick" bundle of trajectories. Secondly, it is possible to define several random variables on Ω and to obtain several valuable parameter estimates on the same sample of trajectories. This is important for calculating the $down \rightarrow up$ transition rate, as we show next.

3. **Computing the Down-Up Transition Rate** .

It is a known fact from probability theory that

$$\Phi = \Sigma_{b\in B} P(b)\mu(b), \quad (4)$$

where B is the set of all border-type down states, $p(b)$ is the stationary probability of a border state b, and $\mu(b)$ is the total transition rate from b to the *up* set. Since $\mu(b)$ remains the same for all border states belonging to the same regular partition, we can rewrite

the above formula as

$$\Phi = \Sigma_{\sigma \in Bd} P(\sigma)\mu(\sigma), \qquad (5)$$

where Bd denotes the set of all border-type partitions. For example, if "up" is the total connectivity, then Bd consists of all partitions into two components. Let us describe a Monte Carlo estimation of Φ for that case.

We already noted that the "equilibrium" for the network, is equivalent probabilistically to what happens in the evolution process at certain instant t_0. This fact allows to interpret $P(\sigma)$ as the probability that the evolution process is in a border state σ at time t_0. Suppose a trajectory ω is given. Denote by X_ω and Y_ω the random times needed for the evolution process to reach σ and the *up*-state, respectively. Then

$P(X_\omega \leq t_0) - P(Y_\omega \leq t_0) =$
$P(\sigma; |\omega)$

is the probability that, given ω, the evolution process is in σ at the instant t_0. Now it is easy to represent Φ in a form similar to (1):

$$\Phi = \Sigma_{\omega \in \Omega} p(\omega) P(\sigma; |\omega). \qquad (6)$$

4. **Simulation Results and Computational Aspects .**

We present simulation examples of several renewable networks and show that the above method provides small relative errors in parameter estimation for very moderate N values, even for highly reliable networks, see [2,3]. For example, a ladder-type renewable network with 17 edges, whose *down* state is the loss of connectivity, has $R \simeq 0.968$. Only N=100 was needed to estimate R with a 6% relative error. The value of $\Phi \simeq 0.073$, with the same accuracy.

An important definition of *computational complexity* for a Monte Carlo scheme has been suggested in [3],[4]. Suppose that we estimate the value of θ (see (1)) by the corresponding sample mean $\hat{\theta}$. Let ϵ and δ be arbitrary positive numbers, and the inequality

$$1 - \epsilon < \hat{\theta}/\theta < 1 + \epsilon \qquad (7)$$

holds with probability at least $1 - \delta$. Then $\hat{\theta}$ is called (ϵ, δ)-*polynomial* if the (ϵ, δ) -accuracy of $\hat{\theta}$ is guaranteed by a sample size N, not exceeding a polynomial of $1/\epsilon$, $1/\delta$ and the network size $n = |V|$.

It has been proved in [3] and [4] that the above described Monte Carlo based on the edge evolution process is (ϵ, δ)-polynomial with respect to the network *down* (i.e. disconnectedness) probability.

References

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