M/D/1 queue analysis experiment design

Background

Given the topology below, we are going to measure the mean queue length of M/D/1 queue. Also the scenario is given corresponding to the topology.

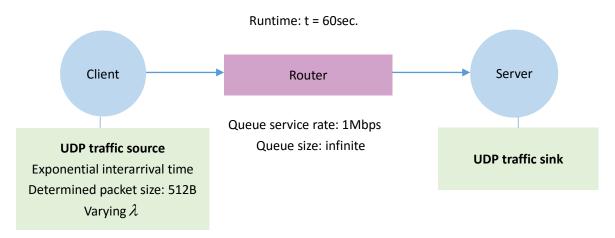


Figure 1. Topology of M/D/1 queue analysis experiment

According to Pollaczek-Khinchine formula, the mean number of packets in the system is given by:

$$E[N] = \frac{\rho}{1-\rho} [1 - \frac{\rho}{2} (1 - \mu^2 \sigma^2)]$$

It says when service time is determined, that is our case M/D/1, the variance term will go to zero and yield expected queue length:

$$E[N] = \frac{\rho}{1-\rho} (1 - \frac{\rho}{2})$$

where

$$\rho = \frac{\lambda}{u}$$

And λ , μ are the rate at which packets arrives at the queue and the rate at which packets served

by the queue. Both of two numbers are in packets/ sec. Here we predefined the interarrival time to be exponentially distributed, which means the arrival rate to be Poisson distributed with parameter λ . Also to compute the service rate, we use queue service rate together with packets

size, in this case
$$\mu = \frac{10^6}{512 \times 8} = 244.14$$
 is determined.

In this experiment we are going to monitor the average queue length.

When ρ approaching to 1, the average queue length should be approximately half of M/M/1 queue length. When ρ closes to zero, the average queue length should be like M/M/1 queue length.

Experiment design

In this experiment we going to measure the average based using both GENI testbed and ns2 simulation method. Also we going to compare the result with our analytical result depicted in background section.

GENI testbed

Set up topology as Figure 1. We use D-ITG to generate UDP traffic in client node, while on the server node check receiver log still using tool from D-ITG suite. The UDP traffic generated with determined packet size of 512Bytes. We vary the mean packets arriving rate from 225 to 125 by step 25, five replications for each packets arriving rate. Note this experiment will be as simple experiment. Each time we vary λ and set all other parameters remains the same status.

The average queue length monitoring is through using Linux Traffic Control (tc) running at router node. Note this is not the entire queue length. It is rather the queue length apart from packet in

the service. Correspondingly, we will modify the expected analytical result as $E[N] - \rho$

NS2 simulation

To run a NS2 simulation, we installed NS2 on any of three node on previous GENI testbed node. Write simulation script in tcl scripting language and run the experiment. The script will generate two output trace files. In the simulation script, we also use previous experiment design logic, which is to vary λ from 225 to 125 by step 25. Each λ 5 replications are required. This is also a simple experiment strategy.

Result

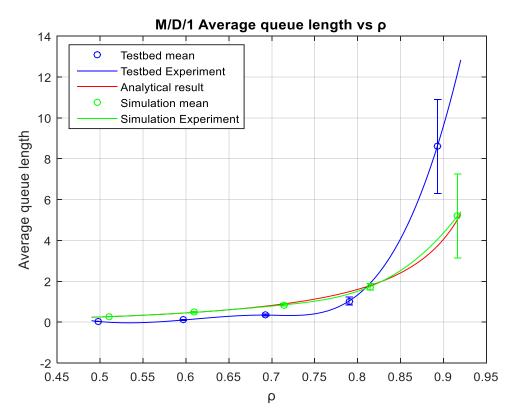


Figure 2. M/D/1 average queue length vs ho

M/D/1 queue analysis

Each experiment was repeated totally 25 times. For each of different ho , the experiment was repeated 5 times.

<u>GENI testbed</u>: when ρ started from mean 0.4976, the mean queue length is 0.0340 ± 0.0071 (90%

confidence interval), while analytical result shows exactly 0.2464. Analytical result is 624% higher than GENI testbed result, with standard deviation 0.00416. As mean of ρ grows to 0.8928 the mean queue length is 8.5984 ± 2.1889 (90% confidence interval), while analytical result shows exactly 3.718. GENI testbed is 130% higher than analytical result. It represent a scenario that GENI testbed result start at a very low number, (when utilization is low) and grows fast then exceed analytical result. This is intuitive from above figure 2.

The possible reason for this is while started at little number, our measurement could be somehow not so accurate. Although here we say a 624% higher difference, they are both very small. So a tiny difference could result in a huge higher rate.

NS2 simulation: when ρ started from mean 0.5110, the mean queue length is 0.2687 ± 0.0058

(90% confidence interval), while analytical result shows exactly 0.2464. Analytical result is 8.29% lower than NS2 simulation result, with standard deviation 0.003. As mean of ρ grows to 0.9163 the mean queue length is 5.1885 ± 1.9618 (90% confidence interval), while analytical result shows exactly 5.02. Analytical result is 3.24% lower than NS2 simulation result. It represent a scenario that NS2 simulation result always sticks with analytical result.

Also, both experiment variance grows when ρ grows to near 1.

T = 2.132 (n =4, confidence 90%)

Table 1 GENI testbed ho and confidence interval of M/D/1 queue

ho GENI testbed	0.4976	0.5967	0.6928	0.7900	0.8928			
Confidence interval	0.0071	0.0159	0.0409	0.1888	2.1889			
Table 2 ns2 simulation $ ho$ and confidence interval of M/D/1 queue								
ho ns2 simulation	0.5110	0.6090	0.7139	0.8143	0.9163			
Confidence interval	0.0058	0.0351	0.0558	0.1592	1.9618			

M/M/1 queue and M/D/1 queue

For the comparison between M/M/1 queue and M/D/1 queue, here we present only GENI testbed result and analytical result. The method used to compare NS2 simulation result is the same as compare GENI testbed.

Table 3 GENI testbed ρ and confidence interval of M/M/1 gueue

ho GENI testbed	0.4976	0.5967	0.6928	0.7900	0.8928
Confidence interval	0.0394	0.0894	0.1591	0.7436	4.4596

As a coincidence, M/M/1 queue's utilization is somehow get the same mean value of M/D/1 queue.

When ρ started from mean 0.4976, the M/M/1 mean queue length is 0.3047 ± 0.0394 (90%

confidence interval), while M/D/1 mean queue length is 0.0340 ± 0.0071 (90% confidence interval). M/M/1 result is 796.17% higher M/D/1 GENI testbed result, with standard deviation

(90% confidence interval) while M/D/1 mean queue length is 8.5984 ± 2.1889 (90% confidence interval). M/M/1 GENI testbed is 128.46% higher than M/D/1 result. At utilization rate low, also troubled by not accurately record every number, the result is far from our expectation, and however, both are very small. At high utilization, M/D/1 mean queue length is approximately grows to half of M/M/1 queue length. This is intuitive from below figure 3.

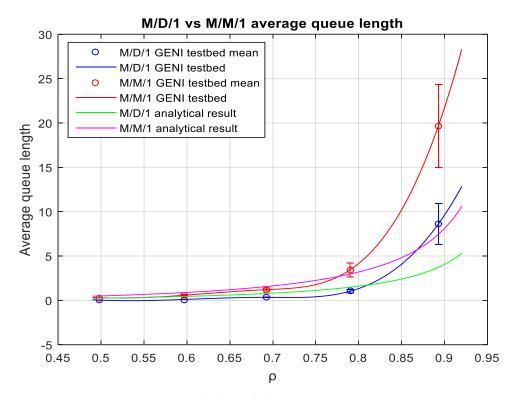


Figure 3. M/D/1 vs M/M/1 GENI testbed results