LECTURE 2
CRITICAL LOADING (HEAVY TRAFFIC)
M/M/1 Queue
(Simulation of Dynamics)

$\lambda = 0.9524$

$\rho = \lambda = 0.9524$
M/M/1 Queue
(Simulation of Dynamics)

$\lambda$, $\mu$, $\rho = \lambda = 0.9524$
M/M/1 Queue
(Simulation of Dynamics)

\[ \lambda = \rho = \mu = 0.9524 \]
GI/GI/1 Queue (Dynamics)

\[ \lambda, \sigma_a^2 \quad \mu, \sigma_s^2 \]

\[ Q(t) = \text{queue length at time } t \]

Start system empty (for simplicity)

Theorem (A. Borovkov ‘67, Iglehart-Whitt ‘70): For \( \rho \approx 1 \),

\[ (1 - \rho)Q(\cdot/(1 - \rho)^2) \approx Q^*(\cdot) \]

where \( Q^*(\cdot) \) is a one-dimensional reflecting Brownian motion with drift \(-\mu\) and variance parameter \( \lambda^3 \sigma_a^2 + \mu^3 \sigma_s^2 \)
One-dimensional Reflecting Brownian Motion

\[ Q^*(t) = X^*(t) + Y^*(t) \]

\[ Y^*(t) = \sup \{-X^*(s) : 0 \leq s \leq t\} \]

\[ X^* = \text{Brownian motion} \]
SIMPLE BIOCHEMICAL MODEL
SIMPLE BIOCHEMICAL REACTION SYSTEM

∅ $\xrightarrow{\lambda} B$ (production)

$B \xrightarrow{\mu} \emptyset$ (degradation/dilution)
\[ Q(t) = \text{number of molecules of B present at time } t \]
\[ = Q(0) + A(t) - S(T(t)) \]

\[ T(t) = \int_{0}^{t} Q(s) \, ds \]

\( A \) – Poisson process of rate \( \lambda \)
\( S \) – Poisson process of rate \( \mu \)
FLUID MODEL

\[ \frac{dq}{dt} = \lambda - \mu q \]

\[ q(t) = \frac{1}{\mu} (\lambda + a \exp(-\mu t)) \]