

Continuous-Time Markov Chains

Transition rate matrix

From probabilities to rates

Transition probabilities

- λ_i = inverse of the mean sojourn time in i
- $p_{i,j}$ = proba. to jump from i to j

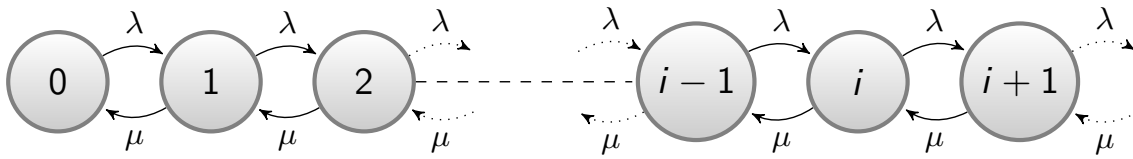
Transition rates

- $q_{i,i} = -\lambda_i$ unit = s^{-1}
- $q_{i,j} = \lambda_i \times p_{i,j}$ unit = s^{-1}
- Remark : $\sum_j q_{i,j} = 0$

We saw that a continuous-time Markov chain is characterized by two sets of parameters. First, the λ_i , which are the inverse of the mean sojourn time in state i . And second, the $p_{i,j}$, which are the probabilities that at a given jump time, the process goes from state i to state j . Unfortunately, these two parameters which have an intuitive meaning are not the best for the mathematical analysis of continuous-time Markov chains.

We need to construct some particular quantities, which we will call the transition rates. $q_{i,i}$ is by definition the opposite of λ_i and $q_{i,j}$ is defined as $\lambda_i \times p_{i,j}$. It is interesting to note that they are both homogeneous to the inverse of a time, meaning that their unit is the inverse of seconds (or the time unit used). $q_{i,j}$ can be interpreted as the average number of transitions from i to j per unit of time when in state i (for $j \neq i$). Something interesting to take note of is that the sum of the $q_{i,j}$ is zero because the $p_{i,j}$ sum to one when j varies over all its possible values except i .

M/M/1 revisited



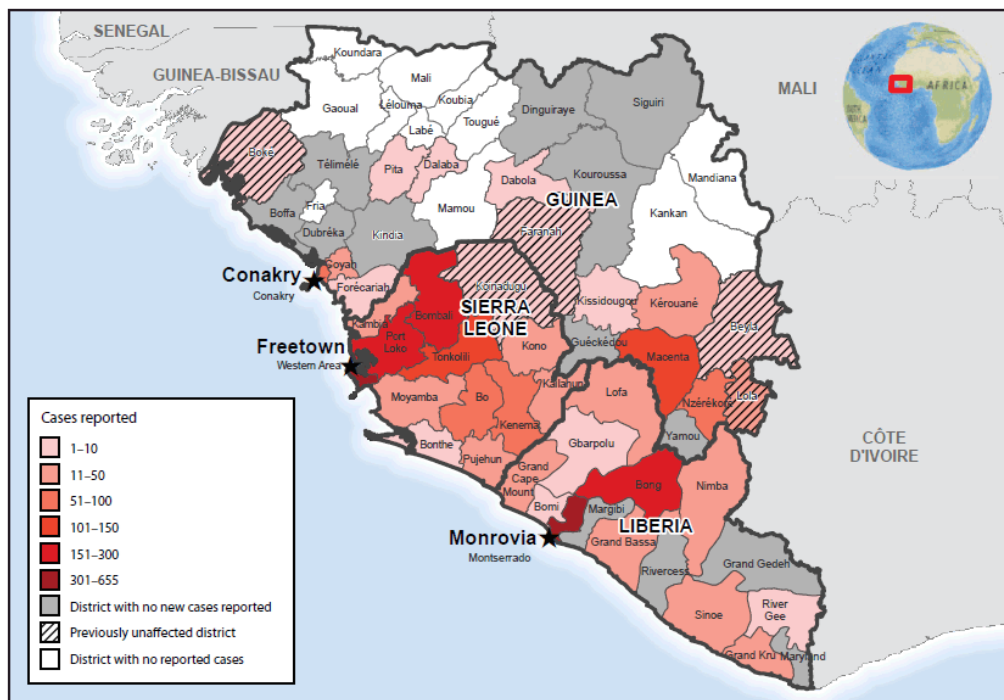
$$Q = \begin{matrix} & \begin{matrix} 0 & 1 & 2 & 3 & \dots \end{matrix} \\ \begin{matrix} 0 \\ 1 \\ 2 \\ \vdots \end{matrix} & \begin{pmatrix} -\lambda & \lambda & & & \\ \mu & -(\lambda + \mu) & \lambda & & \\ & \mu & -(\lambda + \mu) & \lambda & \\ & & \ddots & \ddots & \ddots \end{pmatrix} \end{matrix}$$

Q : transition rate matrix

Let's come back to our M/M/1 queue example. We can represent a continuous time Markov chain with a diagram like we did for discrete time Markov chains. The main difference is that instead of having probabilities of the edges between states, we now have transition rates. For the M/M/1 queue, we know that the time between two arrivals is an exponential of parameter λ , whatever the state of the process is. This means that the transition rate from i to $i + 1$ is always λ . Now, as for departures, they also happen at a constant rate which is μ if there is at least one client in the system.

We can also consider the matrix form like we did for discrete-time Markov chains. The matrix Q that characterizes a continuous-time Markov Chain is called the transition rate matrix. We can construct this matrix as follows. In the line corresponding to state i , we put in column j the transition rate from i to j , $q_{i,j}$. The diagonal term is the opposite of the parameter of the sojourn time in state i , so, $-\lambda_i$. This is for example the transition rate matrix Q that characterizes the M/M/1 queue.

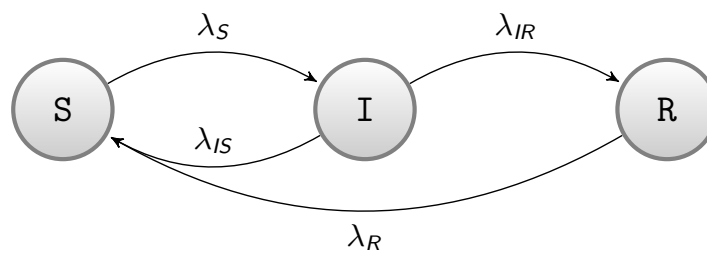
Epidemiology: Ebola outbreak 2015



Continuous-time Markov chains are very common tools for modeling very different phenomena from various fields. They are not confined to queuing analysis. Let's have a look at an epidemiology example. The Susceptible, Infected, Recovered model, or SIR model, is a very popular one, as it captures the evolution of most diseases. This is a key model in public health policy and it was used during the last outbreak of the Ebola virus in Africa to determine the human and financial commitments of the World Health Organisation.

Epidemiology: SIR model

- An individual may be Susceptible (S), Infected (I), Recovered (R)
- When in state (S), he can only become (I) after $\text{Exp}(\lambda_S)$
- When in state (I), the individual can either spontaneously return to (S) or after a treatment go to (R)
- When in (R), the individual may not be infected for a while, say $\text{Exp}(\lambda_R)$, after which he becomes susceptible again



In this model, an individual can be in three states: Susceptible, which means not yet infected but with potential for becoming infected; Infected; and Recovered, meaning that you're no longer infected and can't be infected again for a while because you're protected by your antibodies. When you're in state S, you will eventually become infected in an exponential time of parameter λ_S . Of course in real life, you may not be infected by the flu or any other disease, but it is just a matter of time scale: if the epidemic lasts forever, you will be infected. What saves you is that generally, an epidemic has an end, relatively quick compared to the rate of contamination. When you're infected, you can either cure spontaneously and thus be susceptible again, or you can recover after treatment. The transition rate from I to S is $\lambda_{I,S}$. And the transition rate from I to R is $\lambda_{I,R}$. Another way to put it is to say that you're infected during an exponential time of parameter $\lambda_I = \lambda_{I,S} + \lambda_{I,R}$ and that you switch from I to R with probability $\lambda_{I,R}/\lambda_I$. When the antibodies are no longer efficient, you become susceptible again at rate λ_R . The most difficult part is to estimate the different values of the parameters. The organization of the population (rural, urban, with high or low mobility, etc.) and the contagiousness of the virus determine the value of λ_S . The efficiency of the treatment impacts $\lambda_{I,R}$. The two parameters $\lambda_{I,S}$ and λ_R depend on the virus and can't be influenced by human actions. The most efficient procedure to prevent an epidemic is to put in quarantine all infected people so that λ_S is kept low. If you have a good vaccine then λ_R becomes low.