Here the modelling is presented as described by Kendall. We consider a small element of time dt.

If dt is small enough, an evolution of the system by a jump larger than one is highly unlikely and can be neglected.

The following possible evolutions are of interest: $N(t + dt) = N(t) + 1$, $N(t + dt) = N(t) - 1$, and $N(t + dt) = N(t)$.

The probability for the event $N(t + dt) = N(t) + 1$ is: $\lambda \times N(t) \times \mathrm{d}t + o(dt)$

The probability for the event $N(t + dt) = N(t) - 1$ is: $\mu \times N(t) \times \mathrm{d}t + o(\mathrm{d}t)$

The probability for the event $N(t+dt) = N(t)$ is: $1 - (\mu+\lambda) \times N(t) \times \mathrm{d}t + o(\mathrm{d}t)$
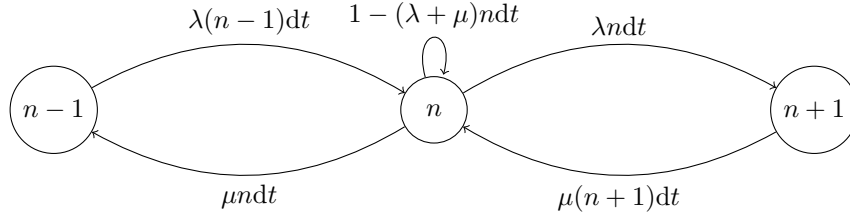

Figure 1: Time continuous Markov model; the figure represents a system that has n $(n \geq 1)$ species at time t and indicates the possible states at time $t + \mathrm{d}t$ as well as the probabilities associated with these transitions.

$P(N(t) = n)$, the probability of n species at time t, will be noted $P_n(t)$.

The following system of differential equations is deduced from these previous observations:

$$\frac{\mathrm{d}P_n(t)}{\mathrm{d}t} = P_{n-1}(t)\lambda(n-1) + P_{n+1}(t)\mu(n+1) - (\lambda+\mu)P_n(t)n \; ; \; n \geq 1$$
$$\frac{\mathrm{d}P_0(t)}{\mathrm{d}t} = \mu P_1(t)$$

An initial condition has also to be taken into account: the number of species at $t = 0$, n_0 has to be known for the system being solved. We have then $P_{n_0}(0) = 1$.

A birth rate, a death rate and an initial number of species are sufficient for describing a birth death process. Of course, in a stochastic framework the evolution of the process is not deterministic but it can be characterized by the expectation and the variance of the number of species over time. A birth death process will be noted (λ, μ, n_0).