Continuous time Markov models (CTMC) may have discrete states, but instead of \( x_1, x_2, x_3, \ldots \) we have \( x(t) \) which expresses the state at any value for \( t > 0 \).

If the rates of transition only depend on the current state, then it is still a Markov process. So, if we had 3 discrete states

\[
P(t) = \begin{bmatrix}
P(X(t) = 1 | x_0 = 1) & P(X(t) = 2 | x_0 = 1) & P(X(t) = 3 | x_0 = 1) \\
P(X(t) = 1 | x_0 = 2) & P(X(t) = 2 | x_0 = 2) & P(X(t) = 3 | x_0 = 2) \\
P(X(t) = 1 | x_0 = 3) & P(X(t) = 2 | x_0 = 3) & P(X(t) = 3 | x_0 = 3)
\end{bmatrix}
\]  

Or more generally each element is \( P(X(t) = j | x_0 = i) \).

How can we calculate \( P(t) \)? It is the solution to a series of differential equations.

\[
P(t) = e^{tQ}
\]  

where \( Q \) is a matrix of the instantaneous rates of change from each state to each other state.

e.g. for the chromosome example from last lecture

\[
Q = \begin{bmatrix}
q_{AA \rightarrow AA} & q_{AB \rightarrow AA} & q_{BB \rightarrow AA} \\
q_{AA \rightarrow AB} & q_{AB \rightarrow AB} & q_{BB \rightarrow AB} \\
q_{AA \rightarrow BB} & q_{AB \rightarrow BB} & q_{BB \rightarrow BB}
\end{bmatrix}
\]

\[
= \begin{bmatrix}
-2r & r & 0 \\
2r & -2r & 2r \\
0 & r & -2r
\end{bmatrix}
\]

To solve for the stationary distribution:

\[
Q \pi = 0
\]

\[
\begin{bmatrix}
0 \\
0 \\
0
\end{bmatrix}
= \begin{bmatrix}
-2r & r & 0 \\
2r & -2r & 2r \\
0 & r & -2r
\end{bmatrix}
\begin{bmatrix}
\pi_{AA} \\
\pi_{AB} \\
\pi_{BB}
\end{bmatrix}
\]

\[
-2r \pi_{AA} + r \pi_{AB} + 0 \pi_{BB} = 0
\]

\[
\pi_{AB} = 2 \pi_{AA}
\]

If your data is in terms of waiting times until the next change of state, then we can model this as an exponential distribution with a hazard parameter that is the diagonal of the \( Q \) matrix.