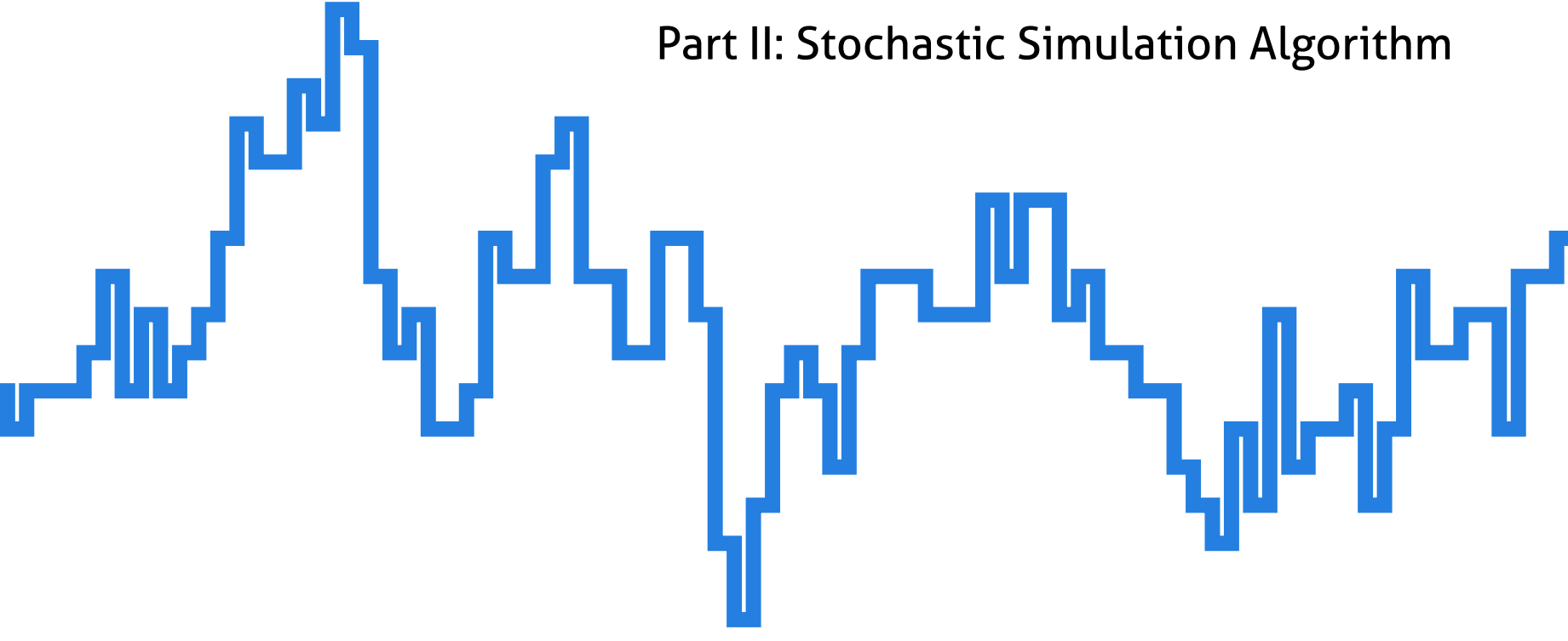
# Stochastic Modelling in Systems Biology

## Part II: Stochastic Simulation Algorithm



# Stochastic Simulation Algorithm

**We consider the simple model:**

molecule synthesis $\varnothing \xrightarrow{k_0} \mathrm{mRNA}$ (transcription)

molecule degradation $\mathrm{mRNA} \xrightarrow{k_1} \varnothing$

probability for a reaction to occur = propensity

translation propensity $a_0(m) = \Omega k_0$

degradation propensity $a_1(m) = k_1 m$

$m$ : molecule (mRNA) number

$\Omega$ : cell volume

# Stochastic Simulation Algorithm

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(3) Select reaction with smallest reaction times
and update the number of molecules accordingly.

(4) Increment time by

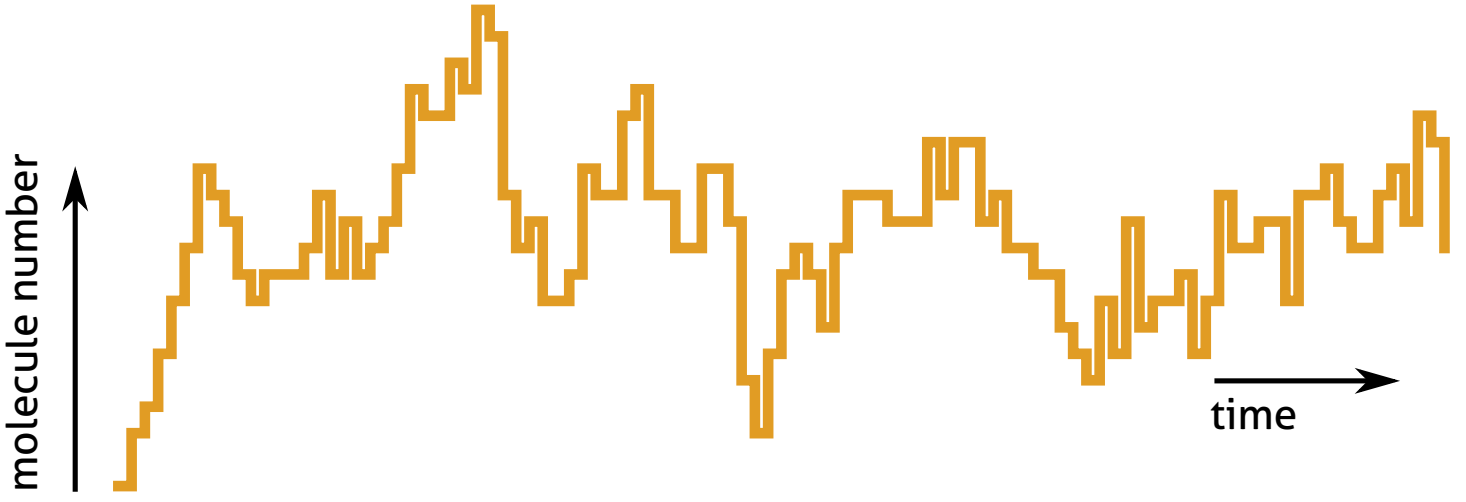
$$\Delta t = \min(\tau_1, \tau_2)$$

and repeat from (1).

**First Reaction Method.** Other more efficient formulations found in the literature.

# Stochastic Simulation Algorithm

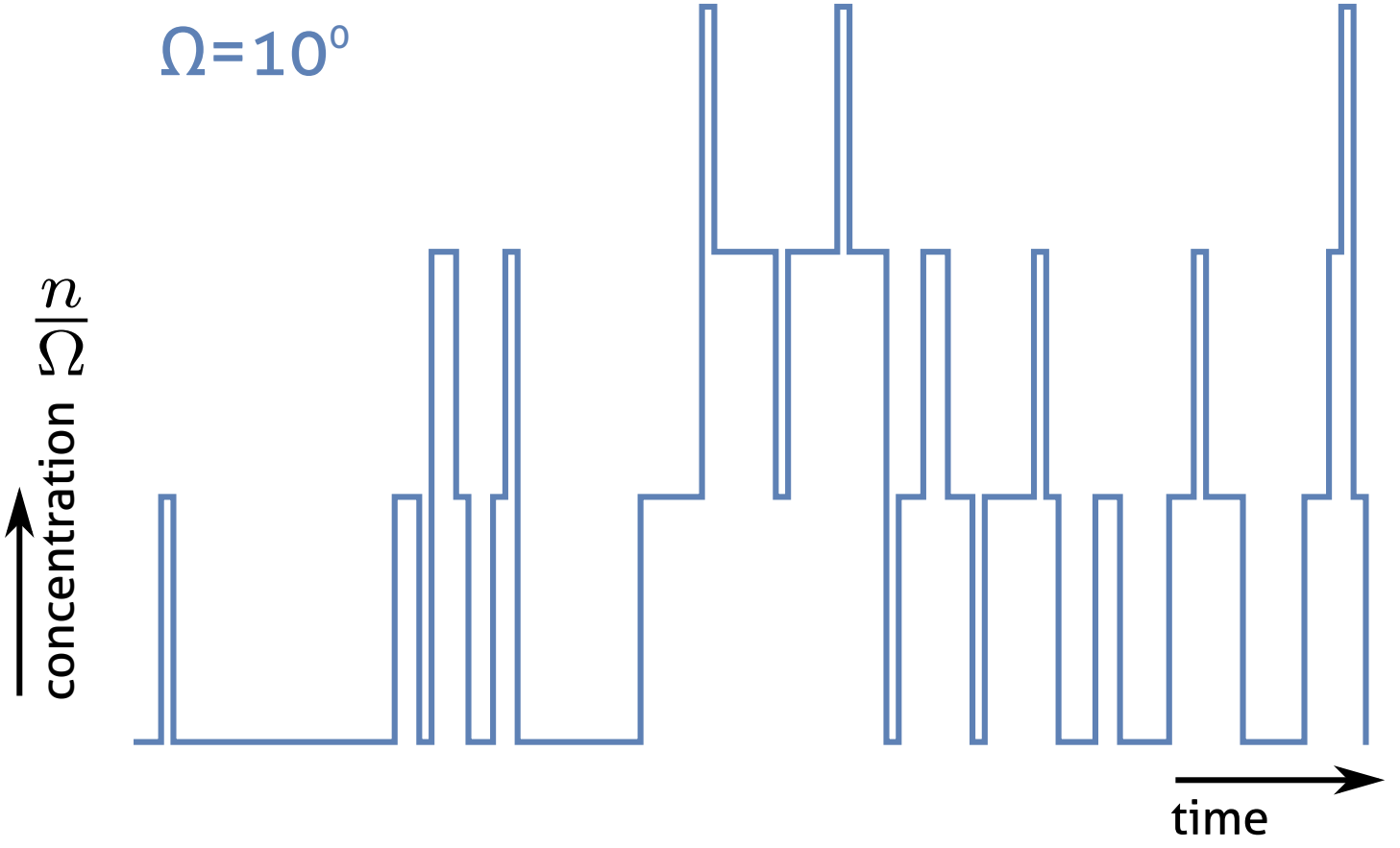
Outcome of this race: number of molecules as a function of time




**Outcome will differ every time** you repeat the algorithm because different realisations of the random numbers are used.

However, **statistics** such as probability distributions **are reproducible**. Just like for cells.

# Deterministic limit



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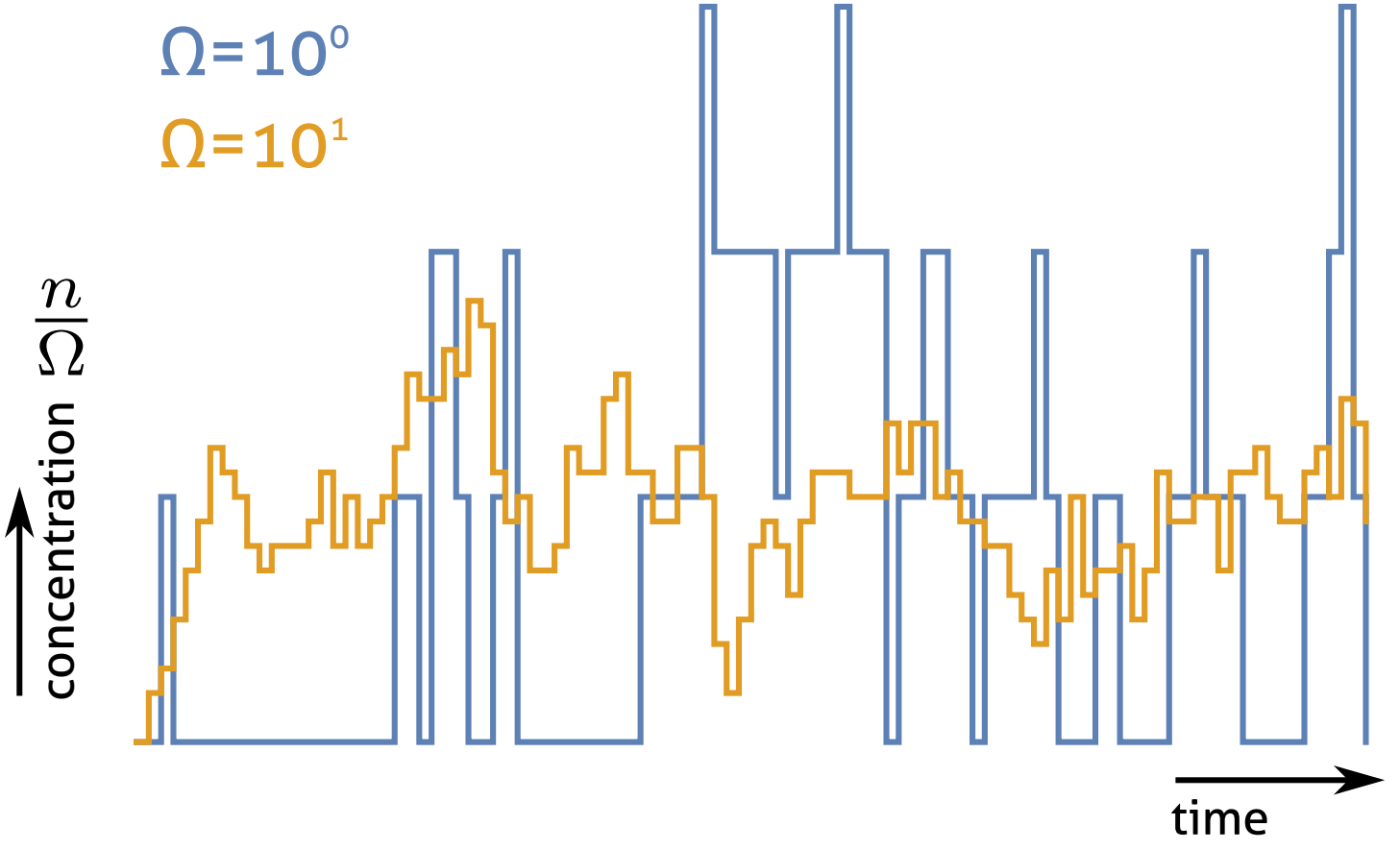

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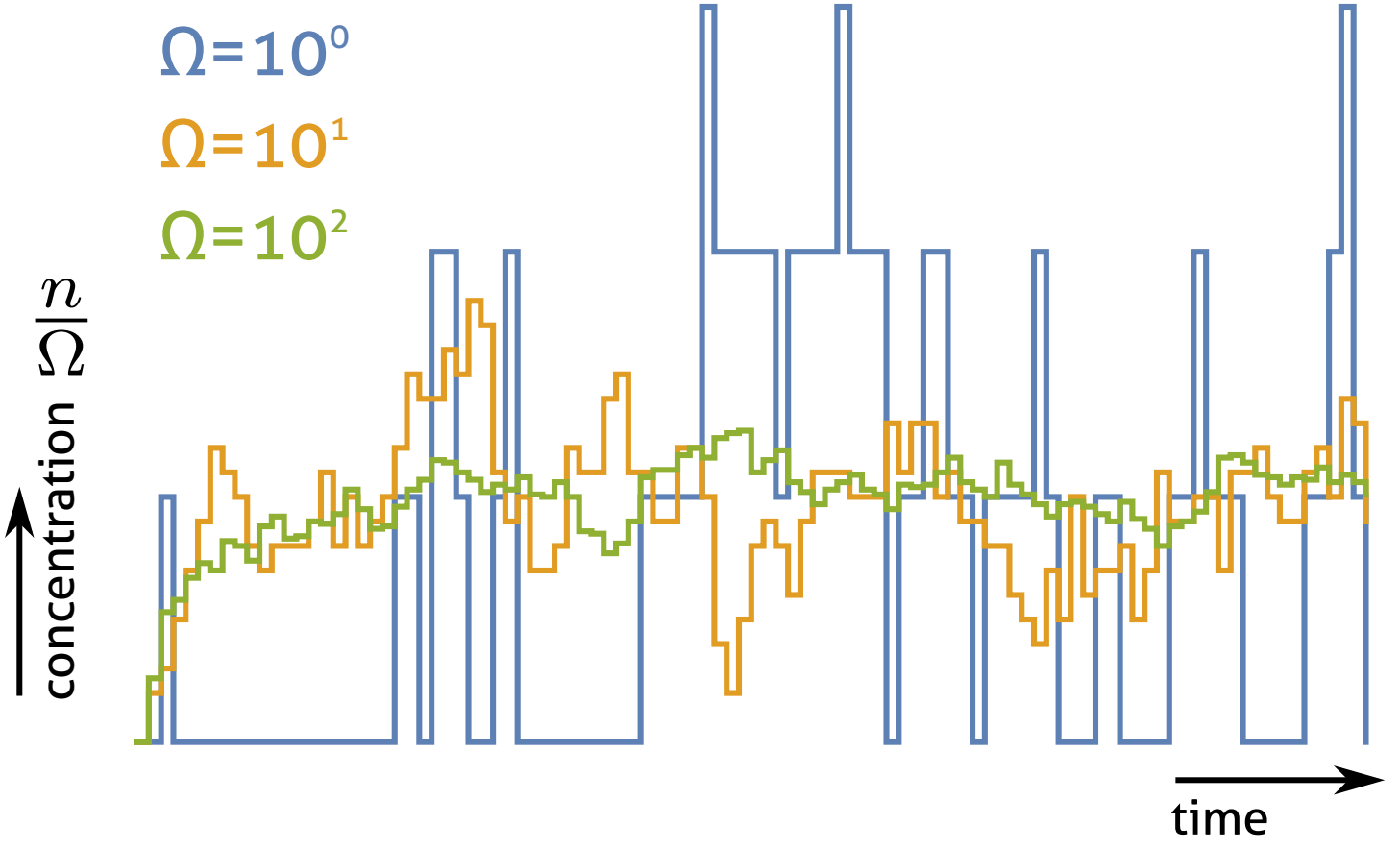
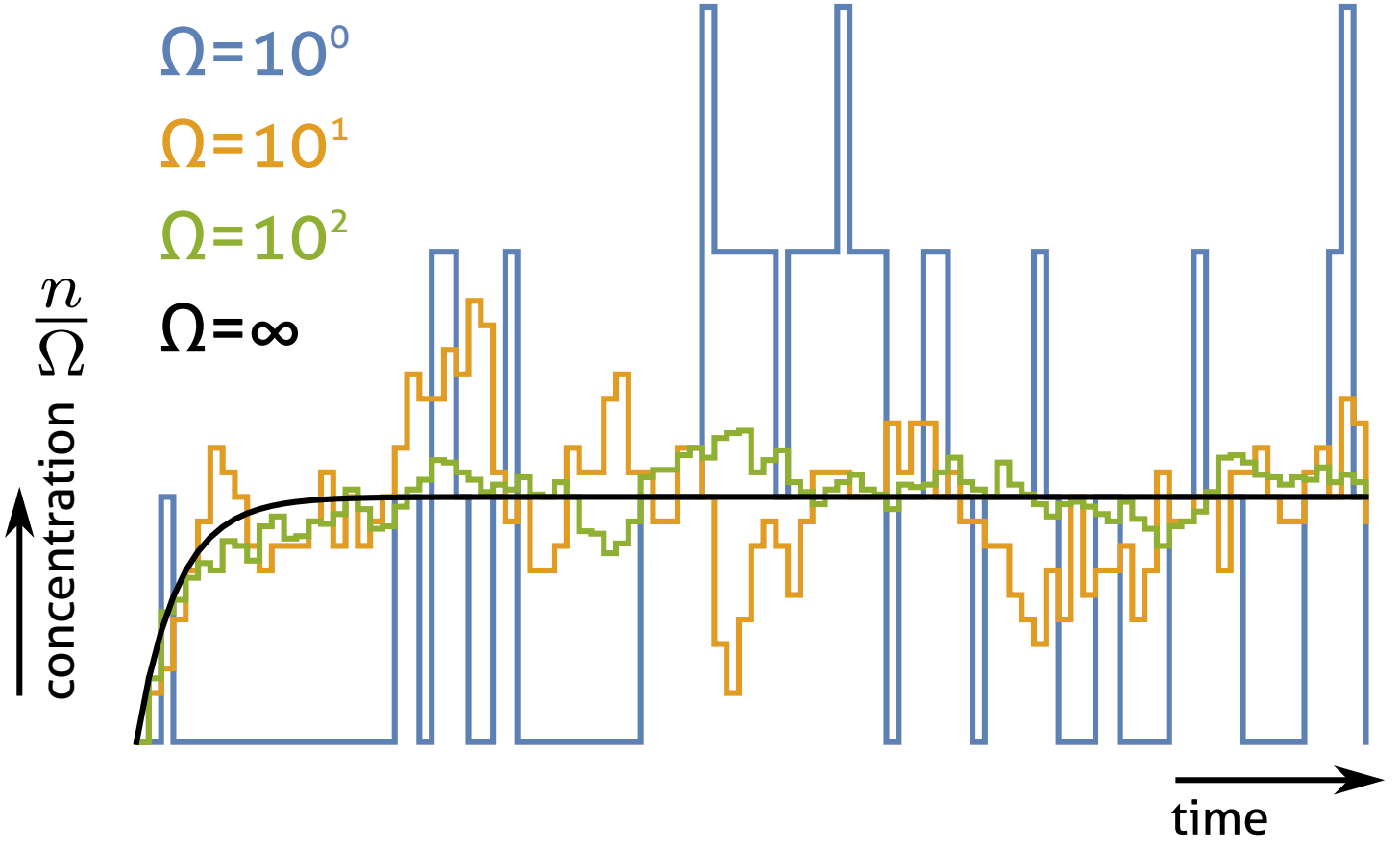



We can use cell volume **Ω** to increase molecule numbers at constant average concentration.

# Deterministic limit




Noise is most evident at low molecule numbers. **Averaging effect.**

# The determinstic limit is given by the reaction rate equations (ODEs)

The rate of change in m is

$$\frac{dm}{dt} = a_0(m) - a_1(m)$$

$$\frac{dm}{dt} = \Omega k_0 - k_1 m$$

In steady state, m does not change:

$$0 = \Omega k_0 - k_1 m$$

Which can be solved for

$$m = \Omega \frac{k_0}{k_1}$$ (absolute number) or $$\frac{m}{\Omega} = \frac{k_0}{k_1}$$ (concentration)