Chapter 2: Continuous-time Models

When may a continuous-time model be relevant?

- Processes where instantaneous change is relevant
- Duality: Large number of individuals.

The basic dynamical assumption is the Law of mass action. The amount of events scale with system size (a more precise formulation will follow later).


General shape: $\dot{x} = f(x)$. Examples:

$\dot{x} = kx \rightarrow x(t) = e^{kt}x(0)$.

$\dot{x} = kx(1 - x) \rightarrow x(t) = \frac{e^{kt}x(0)}{1 - x(0) + e^{kt}x(0)}$.

**Theorem 2.1 (Picard-Lindelöf):** If $f(x)$ is Lipschitz (i.e., $|f(x) - f(y)| \leq K|x - y|$ in some open domain, with $K > 0$ finite) then there exists a unique solution $x(t)$ given an initial condition $x(0)$ for a sufficiently small time-interval around $t = 0$. The solution is differentiable and depends continuously on the initial condition (if $f \in C^1$ the dependence with the initial condition is also $C^1$).

The Concepts of Dynamical Systems Theory.

- Vector field
- Phase Space
- Orbits (solutions)
- Fixed points
- Linear (local) stability analysis
- Limit cycle (periodic orbit)
- Chaos and Strange attractors

**Theorem 2.2:** Let $\lambda$ be an eigenvalue of the Jacobi matrix $Jac = \frac{df}{dx}(x^*)$ at a fixed point, i.e., a solution of $f(x^*) = 0$. Then, for initial conditions near $x^*$ the local behaviour is governed by the eigenvalues of $Jac$. If the eigenvalues satisfy: $Re(\lambda) \begin{cases} < 0 & x^* \text{ stable} \\ > 0 & x^* \text{ unstable} \\ = 0 & x^* \text{ neutral} \end{cases}$

Real, nonzero eigenvalues: Exponential behaviour (node).

Complex, non-imaginary eigenvalues: Exponential spiraling behaviour (focus). Neutral case undecidable without nonlinear terms.

A more precise theorem (Hartman-Grobman Theorem) states that if $Re(\lambda) \neq 0$ then the whole dynamical flow in a small neighbourhood of the fixed point can be mapped onto the flow of the linearisation through a coordinate transformation.

**Example 1: Competition, Cooperation, etc**

As in Exercise 3 of the previous chapter, we can consider a continuous-time version of predator–prey, cooperation and competition toy-models:

\[
\begin{cases}
\dot{x} = ax + \beta xy \\
\dot{y} = \gamma xy + \delta y
\end{cases}
\]
Exercise 1: For the previous model, discuss the ranges of the real-valued constants $\alpha$, $\beta$, $\gamma$ and $\delta$ leading to models mimicking competition, cooperation and predator–prey situations.

Meta-modeling Question 1: What is the basic flaw so far? We did not start from the problem, but from the method.

Example 2 and Exercise 2 (Logistic Growth and Competition):

\[
\begin{align*}
\dot{x} &= kx(1-x) - \beta xy \\
\dot{y} &= -\beta xy + ry(1-y)
\end{align*}
\]

One parameter may be eliminated by rescaling time. Find fixed point(s) and stability as much as it goes.

Linear 2-d Systems: $\dot{x} = Ax; \quad x(t) = e^{tA}x(0)$.

Diagonalisable Case: $\lambda_{1,2}$: eigenvalues. $S_{1,2}$: (linearly independent) eigenvectors, $S = (S_1, S_2)$ eigenvector matrix. Then $x(t) = S \left( e^{\lambda_1 t} \begin{pmatrix} 0 \\ e^{\lambda_2 t} \end{pmatrix} \right) S^{-1}x(0)$. Alternatively, $x(t) = c_1 e^{\lambda_1 t}S_1 + c_2 e^{\lambda_2 t}S_2$ for appropriate constants $c_1, c_2$.

Non-diagonalisable Case: Without loss of generality we may demand $a_{12} \neq 0$ (otherwise, exchange rows in $x$ since $a_{12}$ and $a_{21}$ cannot be both zero). Let $r = \frac{a_{22} - a_{11}}{2}$. For a matrix to be non-diagonalisable, the following two conditions must also be fulfilled: $r^2 = -a_{12}a_{21}$ and $a_{21} \neq a_{12}$. The (double) eigenvalue of $A$ is $\lambda = \frac{a_{22} + a_{11}}{2}$, the associated eigenvector is $S_1 = \begin{pmatrix} a_{12} \\ r \end{pmatrix}$, and the matrix $S = \begin{pmatrix} a_{12} & r \\ r & -a_{12} \end{pmatrix}$ is invertible. Letting $\beta = -a_{12}(1 + \frac{r^2 + a_{21}^2}{r^2 + a_{12}^2})$ we have: $x(t) = e^{\lambda t}S \begin{pmatrix} 1 & t\beta \\ 0 & 1 \end{pmatrix} S^{-1}x(0)$.

Exercise 3: Illustrate the different phase-space diagrams arising in linear 2-d systems according to Theorem 2.2, diagonalisable and non-diagonalisable cases.

Epidemic Models

- Population is assumed to be homogeneous with respect to the infection.
- When necessary, immigration, birth, emigration and mortality (global or infection-originated) rates are incorporated into the problem.
- Population is classified in susceptible, infected and recovered (the latter are temporarily or permanently immune to the infection). Thereof the general name for these models is SIR or SIRS.

Example 3: Constant population, i.e., $S(t) + I(t) + R(t) = S(0) + I(0) = N$.

\[
\begin{align*}
\dot{S} &= -\beta SI \\
\dot{I} &= \beta SI - rI
\end{align*}
\]

$\beta$: infection rate (note the assumptions about the infection process)

$r$: recovery rate
Example 4: McKendrick and Kermack (1927):

\[
\begin{align*}
\dot{S} &= -\beta SI + \gamma R \\
\dot{I} &= \beta SI - rI \\
\dot{R} &= rI - \gamma R
\end{align*}
\]

\(\gamma \neq 0\): recovered individuals lose immunity and become susceptible to infections again.

Comments

Why are these models called "toy-models"?

- Terms in the equations are chosen to be the simplest possible achieving a given qualitative behaviour. No falsifiable hypothesis supporting the choices are (usually) given.
- In particular, the assumption of a totally homogeneous population (in space, time, infective potential, recovery potential, etc) is highly unlikely.
- No ecological model motivating the values of parameters is given.
- The environment and the nature of the infecting agent are largely absent.
- Parameters may be estimated \textit{a posteriori} (i.e., when epidemic has started and a large number of people is already infected or dead).
- No expectations of quantitative accuracy nor of predictive power, rendering falsification (validation) practically impossible.

Example 5: Some computations.

\[
\begin{align*}
\dot{S} &= -\beta SI \\
\dot{I} &= \beta SI - \alpha I \\
\end{align*}
\]

Let \(t = \tau/\beta\) and \(r = \alpha/\beta\). Then,

\[
\begin{align*}
\dot{S} &= -SI \\
\dot{I} &= SI - rI
\end{align*}
\]

A fixed point at the origin. A whole invariant line of fixed points at \(I = 0\). Stability matrix for \((S, I) = (s, 0)\): \(Jac = \begin{pmatrix} 0 & -s \\ 0 & s-r \end{pmatrix}\), having a zero eigenvalue (corresponding to the neutral invariant direction) and \(\lambda_2 = s - r\). Eliminating \(t\) we obtain the orbital equation

\[
\frac{dI}{dS} = -1 + \frac{r}{S}
\]

Hence, \(I(S) + S - r \ln(S) = \text{const}\). From the equation for \(\dot{I}\) we note that since \(I > 0\), then

- \(\dot{I} < 0\) if \(S(t) < r\) (the system evolves towards cure) and
- \(\dot{I} > 0\) if \(S(t) > r\) (the system evolves towards epidemics).

**Main qualitative result:** \(S(0) > r\) implies epidemics.

Epidemiological Indicators

There is no clear-cut definition of "epidemic outbreak". All existing definitions are "operational", in the sense that they are tools suggested by each model that more or less vaguely indicate that something is going on.

In the previous example, it is clear that \(S(t) > 0\), so we have constant population \(N\) and \textit{some} individuals will never be infected. If \(\dot{I} < 0\) the number of infected people decreases
monotonically. We can hardly speak of epidemic in such a situation when the number of infected people decreases. Moreover, $S(t)$ decreases monotonically, and hence it is never larger than $S(0)$. The suggested definition is:

**Definition 1**: The system above has an epidemic outbreak whenever $R = \frac{\beta S(0)}{\alpha} > 1$.

If we can trust the model, the definition makes sense: It says that things will get worse in the near future.

The quantity $R$ or its equivalent appears quite often and has gotten a name, the **basic reproduction number**. It has also a nice interpretation as the quotient between the number of secondary infections per unit time ($\beta S(0)$), times the average infective period ($1/\alpha$). In other words, it gauges how many infections are generated by each infected. This wording of the definition will inspire future analysis.

For the case $R > 1$ we can compute the maximum number of infective individuals given by the epidemic, i.e., the maximum value of $I$, namely $I(r) = N - r + r \log(r/S(0))$.

See page 29 in Bauer’s book: Parameters are estimated *a posteriori*.

**Exercise 4 (Population dependent contact rates)**: Analyse the model in pp. 32-36 of Bauer’s book. Check in particular how $R$ is defined and how it works.

**Exercise 5 (Harvesting)**: $\dot{u} = ru(1-u)-cu$. Which $c$ allows for a persistent population?

**Exercise 6 (Fishing models)**:

\[
\begin{align*}
\dot{x} &= rx(1-x) - H_1 \\
\dot{x} &= rx(1-x) - H_2 x \\
\dot{x} &= rx(1-x) - H_3 \frac{x}{A+x}
\end{align*}
\]

Give some interpretation for the “fishing term” $H$. Criticise and choose the "best" model.

**Demographic effects.**

Long-lived diseases require some analysis of population change (birth, immigration, death, etc).

**Example 6 (Another SIR)**:

\[
\begin{align*}
\dot{S} &= \Lambda(N) - \beta(N)SI - \mu S \quad \Lambda(N): \text{Birth rate (pop dependent). Individuals born} \\
\dot{I} &= \beta(N)SI - \alpha I - \mu I \quad \text{without disease}, \\
\dot{N} &= \Lambda(N) - (1-f)\alpha I - \mu N \quad N = S + I + R. \mu: \text{death rate (without disease)}.
\end{align*}
\]

$f\alpha$ indicates the amount of infected that recover while $(1-f)\alpha$ describes those who die by the disease ($0 \leq f \leq 1$). For $f = 1$ it is easily solved, since the equation for $N$ is decoupled, hence the population approaches the limit value $K$ such that $\Lambda(K) = \mu K$. If $R = \frac{\beta(K)}{\mu + \alpha} > 1$, there is a stable endemic equilibrium at $S = \frac{\mu + \alpha}{\beta(K)}$, $I = \frac{\mu K}{\mu + \alpha} - \frac{\mu}{\beta(K)}$. Under the condition $\Lambda'(K) < \mu$ and $R < 1$, the disease-free equilibrium $I = 0$ is stable.

**Exercise 7**: Find the conditions for a stable endemic equilibrium when $f = 1 - f$, $\beta = \beta_0$, and $\Lambda = \mu(1+N(1-\frac{2}{K}))$ (Hint: The idea is to compute the equilibrium point and to verify that the eigenvalues of the linearisation matrix have negative real parts. This may get very involved, try for $K$ arbitrarily large).