

Lecture notes, Part 1: Population Dynamics

The class is divided in two parts. The first part of the class deals with models for population dynamics. We are going to explore:

- Models for a single population
- Models for two populations
- Models for disease dynamics
- Models for many populations (if time allows)

Computing

The [GitHub repository](#) associated with the lecture notes contains the code used to generate the lecture notes, including all the figures and simulations. Crucially, the code depends on the following R packages:

```
library(tidyverse) # plotting, data organization
library(deSolve) # integrate differential equations
```

Notation

- We write $x(t)$ for the **density** of population x at time t . In many cases, we will write simply x , as the dependency on time is always assumed. For discrete-time models, we write x_t instead. Typically, $x(t)$ is measured in either [mass]/[area/volume] or [number of individuals]/[area/volume]
- The density of a population typically changes in time, and the change is modulated by several parameters. Unless specified, we use **Greek letters for scalars**, **lower-case Latin letters for vectors**, and **upper-case Latin letters for matrices**.
- Other useful notation:
 - i is the imaginary unit, such that $i^2 = -1$
 - 0_n is a vector of zeros of length n
 - 1_n is a vector of ones of length n
 - I is the identity matrix (i.e., a matrix with 1_n on the diagonal, and zeros elsewhere)
 - $D(a)$ is a diagonal matrix with vector a on the diagonal
 - $\frac{dx(t)}{dt}$ is sometimes written as $\frac{dx}{dt}$ or \dot{x}