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 lenght n
  - 1_n is a vector of ones of lenght 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
  - $\dfrac{dx(t)}{dt}$ is sometimes written as $\dfrac{dx}{dt}$ or $\dot{x}$