Nondimensionalization for dummies
Richard Hall CEESG presentation on 29 Feb 2012

Definition:
Nondimensionalization, or rescaling, refers to the process of transforming a series of equations (usually ODEs or PDEs) to dimensionless (i.e. unit-less) forms by rescaling the model variables.

Why do it?

- It reduces number of model parameters to a key set of aggregate parameters that govern the dynamics.

- Less likely to make mistakes when writing code or attempting algebraic manipulations with pen and paper if you're carrying around less parameters.

- It reduces computational time if you wish to perform extensive simulations to fully explore parameter space.

- Can help with model simplification: if one dimensionless parameter is small compared to others drop one or more terms in from your system of equations, to simplify the analysis or obtain approximate solutions. We can also specify exactly what we mean by a parameter being ‘small’ or ‘large’.

- Sometimes the aggregate dimensionless parameters that emerge from rescaling have useful biological interpretations. Examples include $R_0$, the basic reproductive number of a pathogen, and $Re$, the Reynolds number for describing whether fluid flow is viscous.

- Can also aid comparison between systems governed by the same mechanisms but operating on very different timescales. Large mammals’ population sizes look constant while bacterial populations increase exponentially when viewed on a timescale of days, but the population dynamics of both look surprisingly similar if viewed over timescales relating to their respective lifespans.

How to nondimensionalize

The first step is to define your original model variables as the product of a constant, called the scaling parameter, and a dimensionless variable. The scaling parameter must have the same units as the original variable.

Step two is to substitute these rescaled variables into your original model equations and cancel as many terms as possible.

Step three is to choose the your rescaling parameters. These can be chosen either entirely for convenience (i.e. to reduce the number of parameters as much as
possible), or \textit{a priori} using your knowledge of the system (e.g. the carrying capacity of a logistically-growing population is a natural choice to rescale your population size). There is no unique and correct single way to rescale a given system of equations.

Finally, combine all remaining parameters into a set of aggregate parameters to explore model behaviour, calculate steady states, and so on.

**Example: simple predator-prey model**

The simplest model of a predator-prey interaction assumes that in the absence of the predator, the prey population grows logistically; that predation can be described by a simple mass-action term, and that predators have a constant per-capita mortality rate. This is described by the following system of differential equations:

\[
\begin{align*}
\frac{dN}{dt} &= rN\left(1 - \frac{N}{K}\right) - bNP \\
\frac{dP}{dt} &= e b NP - m P
\end{align*}
\]

The original (dimensional) system has 5 model parameters:
- \( r \) – prey intrinsic growth rate
- \( K \) – prey carrying capacity
- \( b \) – predation rate
- \( e \) – conversion efficiency
- \( m \) – per capita predator mortality rate

Our model variables are the prey population density, \( N \), predator population density \( P \), and time \( t \). We rescale them as follows, denoting the respective dimensionless variables \( n \), \( p \) and \( \tau \) and corresponding rescaling variables \( \theta, \phi, \) and \( \psi \).

\[
\begin{align*}
N &= \theta n \\
N &= \phi p \\
N &= \psi \tau
\end{align*}
\]

First we substitute for \( N, P \) and \( t \) in our original equations.

\[
\begin{align*}
\frac{\theta dn}{\psi d\tau} &= r\theta n\left(1 - \frac{\theta n}{K}\right) - b\theta n\phi p \\
\frac{\phi dp}{\psi d\tau} &= e b \theta n \phi p - m \phi p
\end{align*}
\]
Next we rearrange so that we only have the derivatives of the rescaled variables on the left-hand side. In other words, we multiply each side of the first equation by $\psi/\theta$ and the second equation by $\psi/\phi$, and cancel similar terms on the right-hand side, yielding

\[
\frac{dn}{d\tau} = r \frac{\psi n}{\theta} \left(1 - \frac{\theta n}{K}\right) - b \phi \psi np
\]
\[
\frac{dp}{d\tau} = e \beta \psi np - m \psi p
\]

Our aim is to choose values of $\theta, \phi$, and $\psi$ that simplify the model structure by reducing the total number of parameters. We see that choosing $\theta = K$ will remove a parameter from the parentheses of the first equation. As already noted, the prey carrying capacity is a natural choice for rescaling prey density, and the rescaled prey density will now vary between 0 and 1. To rescale time we could choose either $\psi = 1/r$ or $\psi = 1/m$ to remove parameters from either the first term of the first equation or the last term of the second. Both are natural timescales in the system (prey response time and average predator lifespan), and the choice doesn’t really matter. They may be determined by whether you’re more interested in the dynamics of the predator or prey population. We’ll choose the latter, $\psi = 1/m$. The choice of $\phi$ isn’t immediately obvious at this stage, so let’s plug in our choices of $\theta$ and $\psi$ and worry about it later:

\[
\frac{dn}{d\tau} = \frac{r}{m} \left(1 - n\right) - b \phi \psi np
\]
\[
\frac{dp}{d\tau} = \frac{e \beta K \psi np}{m} - p
\]

Now we see that $\phi$ only appears in one term, so let’s choose $\phi = m/b$ to remove another parameter from the top equation. Our final step is to define our two aggregate parameters

\[
c_1 = \frac{r}{m}
\]
\[
c_2 = \frac{e \beta K}{m}
\]

Our dimensionless equations are now

\[
\frac{dn}{d\tau} = c_1 n \left(1 - n\right) - np
\]
\[
\frac{dp}{d\tau} = c_2 np - p
\]
and our 5-parameter system has now been reduced to a 2-parameter system. It’s now easy to solve for the coexistence equilibrium population sizes by setting each derivative to zero and rearranging:

\[
\begin{align*}
    n^* &= \frac{1}{c_2} \\
    p^* &= c_1 \left(1 - \frac{1}{c_2}\right)
\end{align*}
\]

Note that for the equilibrium predator population to exist (i.e. be greater than zero), we require that \( c_2 > 1 \). \( c_2 \) is a threshold parameter whose value determines whether one or both populations persist. \( c_2 \) also has a nice biological interpretation: it represents the number of new predators produced by a single predator over its lifetime, when introduced to a prey population at its maximum population size. It makes biological sense that if each predator leaves behind less than one offspring in this ideal situation, it won’t persist. Disease ecologists will note the obvious analogy with the basic reproductive number in a host-parasite system. Increasing \( c_2 \) decreases the equilibrium prey population and increases the predator equilibrium, and by recalling the definition of \( c_2 \) we see that doubling the predator conversion efficiency, predation rate or carrying capacity have exactly the same effect of halving the equilibrium prey population.

\( c_1 \) measures the ratio of the two natural timescales in this system: prey response time and predator lifespan. If the prey response time is short relative to the predator lifespan (\( c_1 \gg 1 \)), prey populations can quickly recover from predator attack, which in turn should allow predators to reach higher density. Indeed we see that this is the case, and the equilibrium predator density increases linearly with \( c_1 \), so that doubling the prey growth rate or halving the predator lifespan have the same effect of doubling the equilibrium predator population.

The key point here is that the complete behaviour of this predator-prey system over all possible combinations of our original 5 parameters can be understood by varying just our two aggregate parameters. This helps hone our intuition that the relative size of model parameters is often more important in determining dynamics than the absolute size of individual parameters. It is sometimes clearer to present results conceptually and graphically using this reduced parameter set. For example, a contour plot showing the equilibrium predator density as a function of prey growth rate per predator generation (\( c_1 \)) and maximum predator fecundity (\( c_2 \)) neatly summarizes all possible model outcomes while remaining biologically interpretable.