# System setup for Prioritizr exercises

## We will be running our class through R, including some specific R packages. I also find it easy to run R through a GUI like RStudio.

## So please have a recent version of R and RStudio operating on your computer.

## The below code will identify the packages we will use, install them if required, and load them to make sure they are available.

## We might not have that much time to problem solve in the class on these aspects – so please try and come with functioning versions of the packages. And especially R and RStudio (which may need administrator access to install).

# specify list of what packages we want

packList <- c("raster","rgdal","sp","devtools","prioritizr")

# for each package, check if package is installed; if not, install them

for(i in 1:length(packList)){

if(!is.element(noquote(packList[i]),installed.packages()[,1])){

install.packages(packList[i],dependencies = T)

}

}

# load packages

sapply(packList, require, character.only=T)

# install and load lpsymphony (this comes from a different source)

source("https://bioconductor.org/biocLite.R")

biocLite("lpsymphony") # this may ask for updating some other packages --> "n" is ok

library(lpsymphony)