Introduction to spatial data handling in R

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1 Introduction

This document (in its current draft form) provides a brief introduction to spatial data handling in R . I use the term 'handling' to refer to practical aspects of working with spatial data, such as importing data and manipulating it for analysis. I do not discuss the analysis of spatial data.

Spatial data refers to locations. In the context of this vignette these are geographical locations, that is, locations on earth, although most the concepts can be used for locations on other planets, or other regions such as the surface of your skin.

Before getting to spatial data I briefly review, in Chapter 2, basic data types and structures in R . Chapter 3 discusses some general properties of spatial data. Chapter 4 shows how you can represent spatial data with the basic data types and chapter 5 introduces the main spatial data types that area available in R and that make spatial data handling an easy task.

Carefully read through the example code. Copy and paste the code to R and run it yourself. Make changes to the code and predict the result before running it to test your understanding.

2 Basic data types in R

This section describes, very briefly, some of the basic data types in R . Experienced R users need not read it. It is meant as a reminder to those who have not used R much, or not recently. If the material in this section is not immediately obvious to you, you should probably consult a text book that introduces R . For example Adler's "R in a nutshell" or Zuur et al's "Introduction to R for ecologists".

2.1 Vectors

The most basic data type in R is the 'vector', a one-dimensional array of textitn values of a certain type (numeric, integer, character, logical, or factor). Even a single number is a vector (of length 1). These vectors can easily be created and manipulated:

Let's create variable v0 that holds one number, and variables v1 and v2 holding three numbers. For v1 we use the c (short for combine) function; for v2 we use : to create a regular sequence.

```
> v0 <- 7
> v0

[1] 7

> v1 <- c(1.25, 2.9, 3.0)
> v1

[1] 1.25 2.90 3.00

> # going from 5 to 7
> v2 <- 5:7
> v2

[1] 5 6 7
```

Note that when R prints the value of texttttv0 it shows [1] 7 because 7 is the first element in vector v0. That is, even a single number is a vector (of length 1). Also note that I use - for assingment (assigning a value to a variable name) because it is the original R idiom and I think it is clearer than using texttt= which is now also allowed as that might be easily confused with testing for equality (==, see below).

Now let's create variable x holding a character vector of five elements

```
> x <- c('a', 'bc', 'def', 'gh', 'i')
> x

[1] "a"   "bc"  "def" "gh"  "i"

> class(x)

[1] "character"

> length(x)

[1] 5
```

Remember to use quotes for character values (because character strings without quotes represent variable names), and hence to not use quotes for variables (x does not have quotes) because they would be interpreted as a character value.

```
> x <- c(a, bc, def)
Error:  object ’a’ not found
> ’x’
[1] "x"
```

Also remember that the character value `'a'` is not equal to `'A'` (double-quoted `"a"` is the same as single-quoted `'a'`, but you cannot mix the two: `"a'` is invalid) and that **variable** `x` is not the same as `X`. Not noting the difference between upper and lower case characters is one of the main sources of frustration for beginners with R .

A **factor** is a nominal (categorical) variable with a set of known possible values. They can be created using the `as.factor` function. In R you typically need to convert a character variable to a factor to use it in statistical modeling.

```
> f1 <- as.factor(x)
> f1

[1] a   bc  def gh  i
Levels: a bc def gh i

> f2 <- as.factor(5:7)
> f2[1]

[1] 5
Levels: 5 6 7

> as.integer(f2)

[1] 1 2 3
```

The result of as.integer(f2) may have been surprising. But it should not be, as there is no direct link between a category with label "5" and the number 5. In this case "5" is simply the first category and hence it gets converted to the integer 1. If you wanted the original numbers, you should do:

```
> fc2 <- as.character(f2)
> as.integer(fc2)

[1] 5 6 7
```

Elements of vectors can be obtained by indexing. Remember that brackets `[ ]` are used for indexing, whereas parenthesis `( )` are used to call a function.

```
> # first element
> v2[1]

[1] 5

> # elements 2 to 3
> v2[2:3]

[1] 6 7

> # all elements but the first two
> v2[-c(1:2)]
```

```
[1] 7
```

Vectors can be used to compute new vectors with simple algebraic expressions.

```
> # are the elements of v1 2?
> v1 == 2

[1] FALSE FALSE FALSE

> # are the elements of v1 larger than 2?
> f <- v1 > 2
> f

[1] FALSE  TRUE  TRUE

> # element wise multiplication
> v3 <- v1 * v2
> v3

[1]  6.25 17.40 21.00

> # add all elements
> sum(v3)

[1] 44.65
```

In the examples above the computations used either vectors of the same length, or one of the vectors had lenght 1. But be careful, you can compute with vectors of different lengths, as the shorter ones will be recycled. R only issues a warning if the length of longer vector is not a multiple of the length of the shorter object. Because of this feature, you may overlook that your data are not what you think they are.

```
> 1:6 * 1:2

[1]  1  4  3  8  5 12
```

The examples above illustrate a special feature of R not found in most other programming languages. This is that you do not need to 'loop' over elements in an array (vector in this case) to compute new values. It is important to use this feature as much as possible. In other programming languages you would need to do something like the 'for-loop' below to achieve the above. This is illustrated below. Note that the braces   are used to open and close a "block" of code.

```
> # initialization of output variables
> v3 <- vector(length=length(v1))
> s <- 0
> # i goes from 1 to 3 (the length of v1)
> for (i in 1:length(v1)) {
+         v3[i] <- v1[i] * v2[i]
+         s <- s + v3[i]
+ }
> v3

[1]  6.25 17.40 21.00

> s

[1] 44.65

> # another example, with an if/else branch:
>
> f <- vector(length=length(v1))
> # i goes from 1 to 3 (the length of v1)
> for (i in 1:length(v1)) {
+         if (v1[i] > 2) {
+                 f[i] <- TRUE
+         } else {
+                 f[i] <- FALSE
+         }
+ }
> f

[1] FALSE  TRUE  TRUE
```

In R we avoid loops wherever we can, as they tend to be much slower than 'vectorized' computation, and because they are less concise. At first code using for-loops may seem easier to read, but after using R for a while, the reverse is true is most cases.

Things are not always what they seem. (This is a little more advanced topic that is useful to know about (but you do not need to worry about much if it you do not get it). Some R functions require numbers to be integers and you need to explicitly coerce a number to become an integer. Also, by default R only prints up to 6 decimals, ommitting trailing zeros. On the other hand, in comparison for numerical equality integer '2' is equavalent to numeric '2.0'.

```
> a <- 1
> b <- 1.00000000000001
> # a and b look the same
> a

[1] 1

> b

[1] 1
```

```
> # but they are not
> a == b

[1] FALSE

> # but they are "near equal"
> all.equal(a,b)

[1] TRUE

> # inspect for small decimals
> print(b, digits=15)

[1] 1.00000000000001

> is.integer(a)

[1] FALSE

> aa <- as.integer(a)
> aa

[1] 1

> is.integer(aa)

[1] TRUE

> bb <- round(b)
> aa == bb

[1] TRUE

> is.integer(bb)

[1] FALSE
```

2.2 Matrices

A two-dimensional array can be represented with a matrix. Here is how you can create a matrix with missing NA values:

```
> matrix(ncol=3, nrow=3)

     [,1] [,2] [,3]
[1,]   NA   NA   NA
[2,]   NA   NA   NA
[3,]   NA   NA   NA
```

A matrix with values 1 to 9 (note that by default the values are distributed column-wise

```
> matrix(1:6, ncol=3, nrow=2)

     [,1] [,2] [,3]
[1,]    1    3    5
[2,]    2    4    6

> matrix(1:6, ncol=3, nrow=2, byrow=TRUE)

     [,1] [,2] [,3]
[1,]    1    2    3
[2,]    4    5    6

> # the above can also be achieved using the transpose function
> # (note the reversal of ncol and nrow valus)
> t(matrix(1:6, ncol=2, nrow=3))

     [,1] [,2] [,3]
[1,]    1    2    3
[2,]    4    5    6
```

You can also create a matrix by column-binding and/or row-binding vectors:

```
> v1 <- c(1,2,3)
> v2 <- 5:7
> # column bind
> m1 <- cbind(v1, v2)
> m1

     v1 v2
[1,]  1  5
[2,]  2  6
[3,]  3  7

> # row bind
> m2 <- rbind(v1, v2, v1*v2)
> m2

   [,1] [,2] [,3]
v1    1    2    3
v2    5    6    7
      5   12   21

> m3 <- cbind(m1, m2)
> # get the column names
> colnames(m3)

[1] "v1" "v2" ""   ""   ""
```

```
> # set the column names
> colnames(m3) <- c('ID', 'V2', 'X', 'Y', 'Z')
> m3

   ID V2 X  Y  Z
v1  1  5 1  2  3
v2  2  6 5  6  7
    3  7 5 12 21

> # dimensions of m3 (nrow, ncol))
> dim(m3)

[1] 3 5
```

Like vectors, values of matrices can be accessed through indexing. You can use a single number, in which case the cells are numbered column-wise (i.e. first the rows in the first column, then the second column, etc.), but it is often easier to use two numbers in a double index, the first for the row number(s) and the second for the column number(s).

```
> # one value
> m3[2,2]

[1] 6

> # equivalent to
> m3[5]

[1] 6

> # 2 columns and rows
> m3[1:2,1:2]

   ID V2
v1  1  5
v2  2  6

> # entire row
> m3[2, ]

ID V2  X  Y  Z
 2  6  5  6  7

> # entire column
> m3[ ,2]

v1 v2
 5  6  7
```

```
> # you can also use column- or rownames for subsetting
> m3[c('v1', 'v2') , c('ID', 'X')]

   ID X
v1  1 1
v2  2 5
```

Computation with matrices is also 'vectorized'. For example you can do `m3 * 5` to multiply all values of m3 with 5 or do `m3`$\hat{2}$ or `m3 * m3` to square the values of m3. But often we need to compute values for the margins of a matrix, that is, a single value for each row or column. The 'apply' function can be used for that:

```
> # sum values in each row
> apply(m3, 1, sum)

v1 v2
12 26 48

> # get mean for each column
> apply(m3, 2, mean)

       ID        V2         X         Y         Z
 2.000000  6.000000  3.666667  6.666667 10.333333
```

Note that the apply uses at least three arguments: a matrix, a 1 or 2 indicating whether the computation is for rows or for columns, and a function that computes a new value (or values) for each row or column. You can read more about this in the help file of the function (type `?apply`). In most cases you will also add the argument `na.rm=TRUE` to remove `NA` (missing) values as any computation that includes an `NA` value will return `NA`. In this case we used existing basic functions `mean` and `sum` but we could write our own function. As a toy example, we'll write a function that returns the minimum value, except when it is higher than 1, in wich case it returns `NA`.

```
> myFun <- function(x, na.rm=FALSE) {
+         v <- min(x, na.rm=na.rm)
+         v[v > 1] <- NA
+         return(v)
+ }
> # our function
> apply(m3, 1, myFun)

v1 v2
 1 NA NA

> # compare with 'min'
> apply(m3, 1, min)
```

```
v1 v2
 1  2  3
```

Note that `apply` (and related functions such as `tapply` and `sapply` are ways to avoid writing a loop. In the `apply` examples above you could have written a loop to do the computations row by row (or column by column) but using `apply` is more compact and efficient.

2.3 data.frame

In R , matrices can only contain one data type (e.g. numeric or character). In contrast, a `data.frame` can have columns (variables) of different types (each variable has to be of a single type though). A `data.frame` is what you get when you read spread-sheet like data into R with functions like `read.table` or `read.csv`. We can also create a `data.frame` with some code, for example like this:

```
> d <- data.frame(ID=as.integer(1:4), name=c('Ana', 'Rob', 'Liu', 'Veronica'),
+      sex=as.factor(c('F','M','M', 'F')), score=c(10.2, 9, 13.5, 18),
+          stringsAsFactors=FALSE)
> d

  ID     name sex score
1  1      Ana   F  10.2
2  2      Rob   M   9.0
3  3      Liu   M  13.5
4  4 Veronica   F  18.0

> class(d)

[1] "data.frame"

> class(d$name)

[1] "character"

> sapply(d, class)

         ID        name         sex       score
  "integer" "character"    "factor"   "numeric"
```

Indexing data.frames can be done as for matrices, but variables can also be accessed using the `$` sign:

```
> d$name

[1] "Ana"      "Rob"      "Liu"      "Veronica"

> d[, 'name']
```

```
[1] "Ana"      "Rob"      "Liu"      "Veronica"

> d[,2]

[1] "Ana"      "Rob"      "Liu"      "Veronica"
```

You can summarize values in a `data.frame` with functions `table`, `tapply` or `aggregate`. Have a look at the help for these functions if you are not familiar with them.

```
> # tabulate single variable
> table(d$sex)

F M
2 2

> # contingency table
> table(d[ c('name', 'sex')])

          sex
name       F M
  Ana      1 0
  Liu      0 1
  Rob      0 1
  Veronica 1 0

> # mean score by sex
> tapply(d$score, d$sex, mean)

    F     M
14.10 11.25

> aggregate(d[, 'score', drop=F], d[, 'sex', drop=FALSE], mean)

  sex score
1   F 14.10
2   M 11.25
```

2.4 Lists

Lists are the most flexible container to store data (a `data.frame` is in fact a special type of list). Each element of a list can contain any type of R object, e.g. a vector, matrix, data.frame, another list, or more complex data types such as the spatial data types described in the next chapters. Indexing can be a bit confusing as you can both refer to the elements of the list, or the elements of the data (perhaps a matrix) in one of the list elements (note the difference that double brackets make; or ignore this if it is over your head).

```
> e <- list(d , m3, 'abc')
> e

[[1]]
  ID     name sex score
1  1      Ana   F  10.2
2  2      Rob   M   9.0
3  3      Liu   M  13.5
4  4 Veronica   F  18.0

[[2]]
   ID V2 X  Y  Z
v1  1  5 1  2  3
v2  2  6 5  6  7
    3  7 5 12 21

[[3]]
[1] "abc"

> e[2][1]

[[1]]
   ID V2 X  Y  Z
v1  1  5 1  2  3
v2  2  6 5  6  7
    3  7 5 12 21

> e[[2]][1]

[1] 1
```

To iterate over a list, we can use `lapply` or `sapply`. The difference is that `lapply` always returns a list while `sapply` tries to simplify the result to a vector or matrix.

```
> lapply(e, NROW)

[[1]]
[1] 4

[[2]]
[1] 3

[[3]]
[1] 1

> sapply(e, length)

[1]  4 15  1
```

Note that the length of a matrix is defined as the number of cells, while the length of a data.frame is defined as the number of variables!

2.5 functions

We now have used many functions that come with R . But it is often important to write your own functions. Functions allow you to more clearly describe a particular task and to reuse code. Rather than repeating the same steps several times (e.g. for each of 200 species you are analysing), you write a function that gets called several times. This should lead to faster development of scripts and to fewer mistakes. Writing your own functions is easy. For exammple this function squares the sum of two numbers.

```
> sumsquare <- function(a, b) {
+         d <- a + b
+         dd <- d * d
+         return(dd)
+ }
```

We can now use the function:

```
> sumsquare(1,2)

[1] 9

> x <- 1:3
> y <- 3:5
> sumsquare(x,y)

[1] 16 36 64
```

Here is a function to compute the number of unique values in a vector:

```
> nun <- function(x)length(unique(x))
> data <- c('a', 'b', 'a', 'c', 'b')
> nun(data)

[1] 3
```

3 Spatial data

Spatial data always refers to a location, and it normally also includes information about these locations. For example, a spatial data set may describe the borders of the countries of the world, and also store the names of the countries and the size of their population in 2010. The location data can be referred to as the 'geometry' and the associated information can be referred to as the 'attributes' (or simply 'variables').

One important distinction is between the 'object' and 'field' view of spatial phenomena. In the object view space is divided into discrete spatial entities. In the field view, space consists of continuously varying quantities without obvious boundaries. The object representation is mostly implemented using 'vector' data, that is, by points, lines, or polygons (note that both the terms object and vector can lead to confusion because in R , almost everything (data, function) can be referred to as an object, and a vector is used for a simple one-dimensional data structure that can hold a set of values).

In spatial data terminology, vector data is commonly used to represent entities with well defined boundaries, like country boundaries, roads, or the location of weather stations. The geometry of such data structures is represented by one or multiple coordinate pairs. The simplest type is points. Points each have one coordinate pair, and 0 to n associated attributes. For example, a point might represent a place where a rat was trapped, and the attributes could include the date it was captured, the person who captured it, the species size and sex, and information about the habitat. Several points can be combined into a multi-point object, i.e. a combination of multiple spatial features with a single attribute record (this is common in point pattern analysis).

Lines and polygons are more complex. Note that the literature on spatial data analysis, and on geographic information systems, the terms 'line' and 'polygon' are used rather loosely. In this context, a 'line' in fact refers to a set of 1 or more polylines (connected series of line segments); a polygon refers to a set of closed polylines (the last coordinates coincide with the first ones). For example the US state of Hawaii consists of several islands. Each can be represented by a single polygon, and together then can be represent a single (multi-) polygon.

Other related vector type object data types are networks (graphs) and triangulated irregular networks (TINs); these are not discussed here.

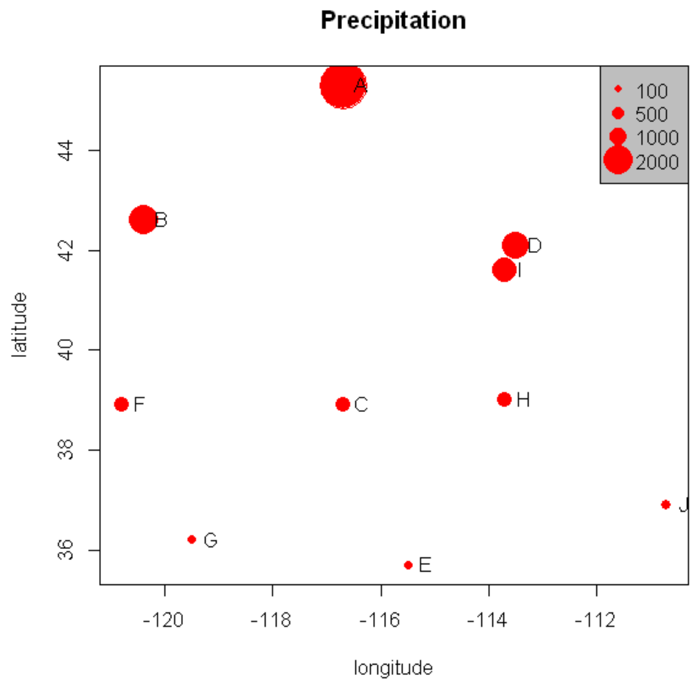
Fields are commonly represented using raster data. A raster divides the world into a grid of equally sized rectangles (referred to as cells or, in the context of air photos and satellite images, pixels) that all have values (or missing values) for the variables. In contrast to vector data, in raster data the geometry is not explicitly stored as coordinates. It is implicitly set by knowing the spatial extent and number or rows and columns (defining the spatial resolution (size of the raster cells)). Note, however, that while fields can also be represented by vedsctor data, this is in most cases inefficient and inpractical.

4 Simple representation of spatial data

We have already discussed that the basic data types in R are numbers, characters, logical (TRUE or FALSE) and factor values. Values of a single type can be combined in vectors and matrices, and variables of multiple types can be combined into a `data.frame`. This allows us to represent some basic types of spatial data. Let's say we have the location (represented by longitude and latitude) of ten weather stations (named A to J) and their annual precipitation.

In the example below we use some fake data to make a very simple map. (Note that a map is a plot of spatial data that also has labels and other graphical objects such as a scale bar or legend; the spatial data itself should not be referred to as a map).

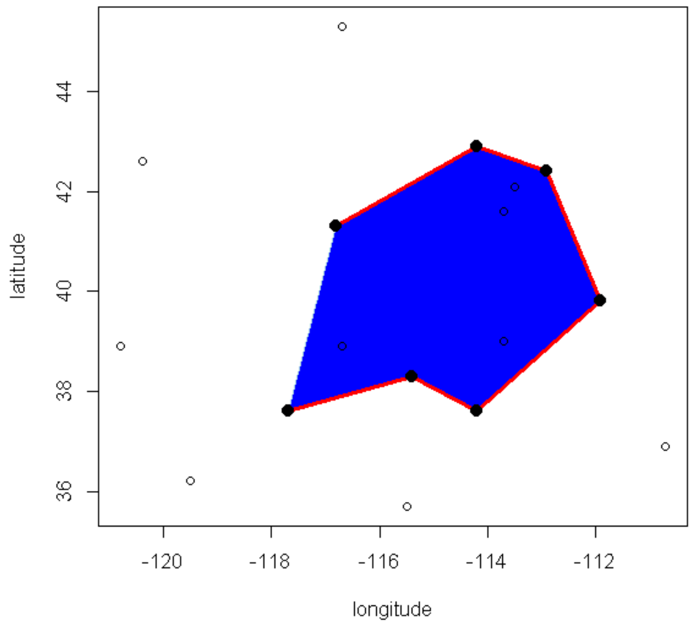
```
> name <- toupper(letters[1:10])
> longitude <- c(-116.7, -120.4, -116.7, -113.5, -115.5,
+                -120.8, -119.5, -113.7, -113.7, -110.7)
> latitude <- c(45.3, 42.6, 38.9, 42.1, 35.7, 38.9,
+               36.2, 39, 41.6, 36.9)
> precip <- (latitude-30)^3
> stations <- cbind(longitude, latitude)
> # plot locations, with size (cex) proportional to precip
> plot(stations, cex=1+precip/500, pch=20, col='red', main='Precipitation')
> text(stations, name, pos=4)
> # add a legend
> breaks <- c(100, 500, 1000, 2000)
> legend("topright", legend=breaks, pch=20, pt.cex=1+breaks/500, col='red', bg='gray')
```



The map shows the location of the weather stations and the size of the dots is indicative of the amount of precipitation. Note that the data are represented by "longitude, latitude", in that order, do not use "latitude, longitude" because on most maps latitude (North/South) is used for the vertical axis and longitude (East/West) for the horizontal axis. This is important to keep in mind, as it is a very common source of mistakes as most people organize their data as "latitude, longitude".

We can add mulitple sets of points to the plot, and even draw lines and polygons:

```
> lon <- c(-116.8, -114.2, -112.9, -111.9, -114.2, -115.4, -117.7)
> lat <- c(41.3, 42.9, 42.4, 39.8, 37.6, 38.3, 37.6)
> x <- cbind(lon, lat)
> plot(stations)
> polygon(x, col='blue', border='light blue')
> lines(x, lwd=3, col='red')
> points(x, cex=2, pch=20)
> points(stations)
```



The above illustrates how numeric vectors representing locations can be used to draw simple maps. It also shows how points can (and typically are) represented by pairs of numbers, and a line and a polygons by a number of these points. An additional criterion for polygons is that they are "closed", i.e. the first point coincides with the last point, but 'plot' takes care of that in this case.

There are cases where a simple approach like this may suffice and you may come across this in older R code or packages. Particularly when only dealing with point data such an approach may work. For example, a spatial data set representing points and attributes could be made by combining geometry and attributes in a single `data.frame`.

```
> wst <- data.frame(longitude, latitude, name, precip)
> wst

   longitude latitude name   precip
1     -116.7     45.3    A 3581.577
```

```
2     -120.4     42.6    B 2000.376
3     -116.7     38.9    C  704.969
4     -113.5     42.1    D 1771.561
5     -115.5     35.7    E  185.193
6     -120.8     38.9    F  704.969
7     -119.5     36.2    G  238.328
8     -113.7     39.0    H  729.000
9     -113.7     41.6    I 1560.896
10    -110.7     36.9    J  328.509
```

However, `wst` is a data.frame and R does not automatically understand the special meaning of the first two columns, or to what coordinate reference system it refers (longitude/latitude, or perhaps UTM zone 17S, or ....?). Moreover, it is non-trivial to do some basic spatial operations. For example, the blue polygon drawn might represent a state, and a next question might be which of the 10 stations fall within that polygon. And how about any other operation on spatial data, including reading from and writing data to files? To facilitate such operation a number of R packages have been developed that are discussed in the next chapter.

5 Spatial packages

5.1 packages

The success of R is to a large extent due to the ease of contributing new and often specialized functionality through plug-ins called "packages" or "libraries". A package is a collection of functions and/or some other R objects such as data sets, and help files. To create a package you do not need to be involved in the development of the core R software; and there is an easily accessible central repository from where these packages can be downloaded and installed. This means that there is relatively little need for oversight, a contributed package cannot break the code in already existing packages, and hence that the barrier to contributing code is very low. Thanks to this there are hundreds of active developers contributing to R . The downside is that R can be somewhat chaotic. For example, the same functionality may be implemented in slightly different ways (or not) in functions in different packages; packages doing similar things may use very different data structures and can thus be hard to use together; if newer packages improve upon older packages, the older packages still linger on, and the unsuspecting user may not be aware that and waste time learning to use obsolete software.

Despite all these issues, R has become the leading platform for data analysis. While R is particularly strong for particular domains of data analysis (e.g. molecular biology, ecology, spatial, finance, machine learning, time series), it is perhaps more important to note that it is `the` tool for interdisciplinary and creative data analysis, as one can integrate analytical methods and data types form virtually any domain; and it is very easy to build on existing functionality to create your own analytical methods.

To use a package, it must be downloaded to your computer. You need to do that each time you update the R software (which you should do at least once a year). Depending on how you use R you may be able to install packages via a menu, but it easiest to use the `install.packages` function. For example to install packages `raster` and `rgdal` you do (note the quotes):

```
> install.packages(c('raster', 'rgdal'))
```

You should only install a package every couple of months or so (to get updates, e.g. by running `update.packages()`), but on a day-to-day basis you should not re-install a package every time you use it. However, you must the `library` function to **load** a package to make its functions and data available for use in a R session. Do not install a package each time you need it. For example, to use the raster package in a script, it needs to have this line (no quotes required) before the functions can be used:

```
> library(raster)
```

5.2 Package sp

Package `sp` is the main package supporting spatial data analysis in R . It does not provide very many functions to modify or analyze spatial data. Rather it defines a set of "classes" to represent spatial data. A class defines a particular data structure such that functions (also known as 'methods') can be written for them (they know what to expect in terms of the data structure, not the values). A `data.frame` is an example of a class. Any particular `data.frame` is an 'instantiation' of the class, or an 'object'. Package `sp` introduces a number of classes with names that start with `Spatial`. The basic types are the `SpatialPoints`, `SpatialLines`, `SpatialPolygons`, `SpatialGrid` (raster) and `SpatialPixels` (sparse raster). These classes only represent geometries. To also store attributes, classes are available with these names plus `DataFrame`, e.g., `SpatialPolygonsDataFrame`.

In most cases you will not create such data types with R code. Rather you will read them from a file or database, for example from a shapefile (and it is important to recognise the difference between such a file and the object created in R to represent the data in the file). Shapefiles can be read with function `readOGR` in the `rgdal` package and with the (easier to use) function texttttshapefile in the `raster` package. Other functions exist (e.g. `readShapePoly` in `maptools` but these should not be used.

Let's do an example anyway, using the same data as in the previous chapter. A `SpatialPoints` and a `SpatialPointsDataFrame` object:

```
> longitude <- c(-116.7, -120.4, -116.7, -113.5, -115.5,
+                -120.8, -119.5, -113.7, -113.7, -110.7)
> latitude <- c(45.3, 42.6, 38.9, 42.1, 35.7, 38.9,
+               36.2, 39, 41.6, 36.9)
> library(sp)
> st1 <- SpatialPoints(cbind(longitude, latitude))
> df <- data.frame(precip=(latitude-30)^3)
> st2 <- SpatialPointsDataFrame(st1, data=df)
> class(st1)

[1] "SpatialPoints"
attr(,"package")
[1] "sp"

> class(st2)

[1] "SpatialPointsDataFrame"
attr(,"package")
[1] "sp"

> st2

      coordinates   precip
1  (-116.7, 45.3) 3581.577
2  (-120.4, 42.6) 2000.376
3  (-116.7, 38.9)  704.969
4  (-113.5, 42.1) 1771.561
5  (-115.5, 35.7)  185.193
6  (-120.8, 38.9)  704.969
7  (-119.5, 36.2)  238.328
8    (-113.7, 39)  729.000
9  (-113.7, 41.6) 1560.896
10 (-110.7, 36.9)  328.509
```

And a `SpatialPolygons` object:

```
> lon <- c(-116.8, -114.2, -112.9, -111.9, -114.2, -115.4, -117.7)
> lat <- c(41.3, 42.9, 42.4, 39.8, 37.6, 38.3, 37.6)
> x <- cbind(lon, lat)
> # close the ring of the polygon
> x <- rbind(x, x[1,])
> pols <- SpatialPolygons( list(  Polygons(list(Polygon(x)), 1)))
> str(pols)

Formal class 'SpatialPolygons' [package "sp"] with 4 slots
  ..@ polygons   :List of 1
  .. ..$ :Formal class 'Polygons' [package "sp"] with 5 slots
  .. .. .. ..@ Polygons :List of 1
  .. .. .. .. ..$ :Formal class 'Polygon' [package "sp"] with 5 slots
  .. .. .. .. .. .. ..@ labpt  : num [1:2] -114.7 40.1
  .. .. .. .. .. .. ..@ area   : num 19.7
  .. .. .. .. .. .. ..@ hole   : logi FALSE
  .. .. .. .. .. .. ..@ ringDir: int 1
  .. .. .. .. .. .. ..@ coords : num [1:8, 1:2] -117 -114 -113 -112 -114 ...
  .. .. .. .. .. .. .. ..- attr(*, "dimnames")=List of 2
  .. .. .. .. .. .. .. .. ..$ : NULL
  .. .. .. .. .. .. .. .. ..$ : chr [1:2] "lon" "lat"
  .. .. .. ..@ plotOrder: int 1
  .. .. .. ..@ labpt    : num [1:2] -114.7 40.1
  .. .. .. ..@ ID       : chr "1"
  .. .. .. ..@ area     : num 19.7
  ..@ plotOrder  : int 1
  ..@ bbox       : num [1:2, 1:2] -117.7 37.6 -111.9 42.9
  .. ..- attr(*, "dimnames")=List of 2
  .. .. ..$ : chr [1:2] "x" "y"
  .. .. ..$ : chr [1:2] "min" "max"
  ..@ proj4string:Formal class 'CRS' [package "sp"] with 1 slots
  .. .. ..@ projargs: chr NA
```

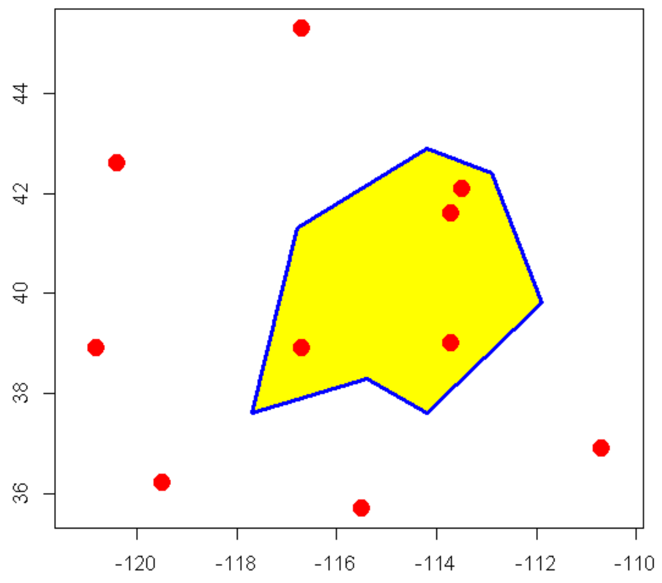
```
> class(pols)
```

```
[1] "SpatialPolygons"
attr(,"package")
[1] "sp"
```

The structure of the SpatialPolygons class is somewhat complex as it needs to accomodate the possibility of multiple polygons, each consisting of multiple sub-polygons, some of which may be ”holes”.

As these Spatial* objects are now known entities we can use generic functions like plot to make a map:

```
> plot(st2, axes=TRUE)
> plot(pols, border='blue', col='yellow', lwd=3, add=TRUE)
> points(st2, col='red', pch=20, cex=3)
```



For much more information and examples see `vignette('intro_sp')`

5.3 Package raster

The raster package is built around a number of classes of which the `RasterLayer`, `RasterBrick`, and `RasterStack` classes are the most important. See Chambers (2009) for a detailed discussion of the use of classes in R . When discussing methods that can operate on all three of these objects, they are referred to as 'Raster*' objects.

A `RasterLayer` object represents single-layer (variable) raster data. A `RasterLayer` object always stores a number of fundamental parameters that describe it. These include the number of columns and rows, the coordinates of its spatial extent ('bounding box'), and the coordinate reference system (the 'map projection'). In addition, a `RasterLayer` can store information about the file in which the raster cell values are stored (if there is such a file). A `RasterLayer` can also hold the raster cell values in memory.

Multiple layers can be represented by a `RasterStack` and by a `RasterBrick`. These are very similar objects. The main differnce is that a `RasterStack` is loose collection of `RasterLayer` objects that can refer to different files (but must all have the same extent and resolution), whereas a `RasterBrick` can only point to a single file.

Here I create a RasterLayer from scratch. But note that in most cases these objects are created from a file.

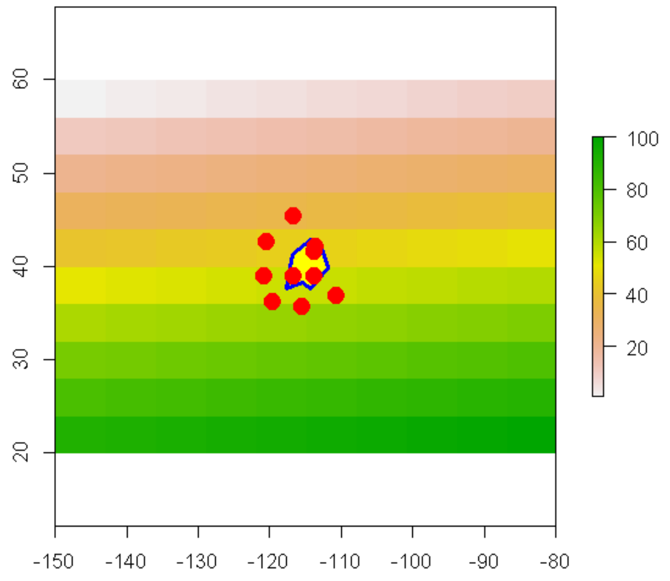
```
> library(raster)
> # create empty RasterLayer
> r <- raster(ncol=10, nrow=10, xmx=-80, xmn=-150, ymn=20, ymx=60)
> r

class       : RasterLayer
dimensions  : 10, 10, 100  (nrow, ncol, ncell)
resolution  : 7, 4  (x, y)
extent      : -150, -80, 20, 60  (xmin, xmax, ymin, ymax)
coord. ref. : +proj=longlat +datum=WGS84

> # assign values
> r[] <- 1:ncell(r)
> r

class       : RasterLayer
dimensions  : 10, 10, 100  (nrow, ncol, ncell)
resolution  : 7, 4  (x, y)
extent      : -150, -80, 20, 60  (xmin, xmax, ymin, ymax)
coord. ref. : +proj=longlat +datum=WGS84
data source : in memory
names       : layer
values      : 1, 100  (min, max)

> # plot
> plot(r)
> # add polygon and points
> plot(pols, border='blue', col='yellow', lwd=3, add=TRUE)
> points(st2, col='red', pch=20, cex=3)
```

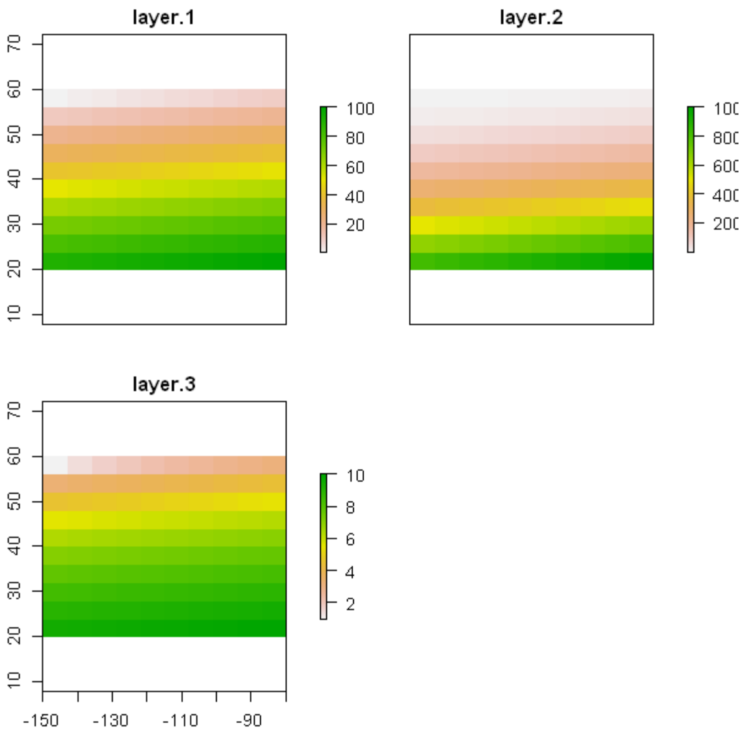


Make a RasterStack from mulitple layers:

```
> r2 <- r * r
> r3  <- sqrt(r)
> s <- stack(r, r2, r3)
> s

class       : RasterStack
dimensions  : 10, 10, 100, 3  (nrow, ncol, ncell, nlayers)
resolution  : 7, 4  (x, y)
extent      : -150, -80, 20, 60  (xmin, xmax, ymin, ymax)
coord. ref. : +proj=longlat +datum=WGS84
names       : layer.1, layer.2, layer.3
min values  :       1,       1,       1
max values  :     100,   10000,      10

> plot(s)
```



See `vignette('raster')` for more info about these objects and how they can be manipulated.

5.4 Other packages

Other important packages (to be discussed in more detail in the future):

`rgdal` – reading and writing spatial data (GIS data)

`rgeos` – geometric operations on vector (notably polygon) data, e.g. intersecting and merging of polygons

`dismo` – species distribution modelling

`vegan` – spatial ecology, biodiversity indices

`gdistance` – compute ecological distances (such as resistance distance or cost distance)

`spatstat` – point pattern analysis

`gstat` – geostatistics: kriging

`spdep` – inference with spatial data (detecting and correcting for spatial autocorrelation)

Most of the these packages have vignettes that illustrate their use. For example, the `dismo` package has a vignette called 'sdm' that illustrates the basic steps in species distribtion modeling. You can use Bivand et al, 20087 or Plant 2012 for a more general introduction to spatial statistics.

6 References

Adler, J. R in a nutshell. O'Reilly.

Bivand, R.S., E.J. Pebesma and V. Gomez-Rubio, 2008. Applied spatial data analysis with R . Springer. 378p.

Chambers, J.M., 2009. Software for data analysis: programming with R . Springer. 498p.

Plant, R., 2012. Spatial data analysis in ecology and agriculture using R . CRC Press 648p.

Zuur, Ieno and Meesters, 2009. A beginner's guide to R . Springer