

13 Spatial Poisson models applied to plant diversity

In all previous chapters we introduced theory in an applied context. In this chapter there is no new theory. Instead we present a detailed example of the analysis of a plant data set. Techniques employed are Poisson generalised linear models (GLM) without and with spatial dependency. We will include most of the R code and also discuss what to present in a paper.



Prerequisite for this chapter: You need to be familiar with all the material discussed in Chapter 12.

13.1 Introduction

The data used in this chapter were taken from Irl et al. (2015), who studied the effect of climatic and topographic variables on plant species richness and endemic richness on the oceanic island La Palma, Canary Islands, Spain. Endemic (i.e. unique to a defined geographic location) species and especially single-island endemic species are a result of isolated biological populations evolving to become distinct species. La Palma is relatively far away from the mainland and therefore species diversity is low, but it has high endemism.

Irl et al. (2015) explained that the spatial distribution of endemism within an oceanic island gives valuable information about the origin and drivers of biodiversity patterns on the landscape scale, and this has important implications for conservation. The question that we will focus on in this chapter is whether climatic and topographic variables drive single-island endemic richness.

At 890 plots on the island the absence and presence of perennial (a plant living for several years) vascular species (land plants that have lignified tissues for conducting water and minerals) was sampled. Total richness, endemic richness, single-island richness, and archipelago richness per plot were determined.

13.2 Data exploration

13.2.1 Sampling locations

We first import the data (available from Dryad; Irl et al. 2015) using the `read.table` function.

```
> LP <- read.table(file = "LaPalma.txt",
                  header = TRUE,
                  dec = ".")
```

The sampling locations in the text file are denoted by latitude and longitude, but these are in fact UTM coordinates. We can easily convert these into real latitude and longitude coordinates with some *sp* (Pebesma and Bivand 2005) magic.

```
> library(sp)
> utmcoor <- SpatialPoints(
  coords = cbind(LP$Longitude,
                 LP$Latitude),
  proj4string =
    CRS("+proj=utm +zone=28N"))
> longlat <- spTransform(utmcoor,
  CRS("+proj=longlat"))
> LP$Longitude2 <- coordinates(longlat)[,1]
> LP$Latitude2 <- coordinates(longlat)[,2]
```

We now have the real latitude and longitude coordinates of each plot, and we can use these to visualise where the plots are on La Palma; see Figure 13.1. We have a large number of plots close to one another and spatial dependency is likely to be present. We suggest that you also make a histogram of the distances between sites (see Chapter 12 for the R code and an example, and also Figure 13.6).

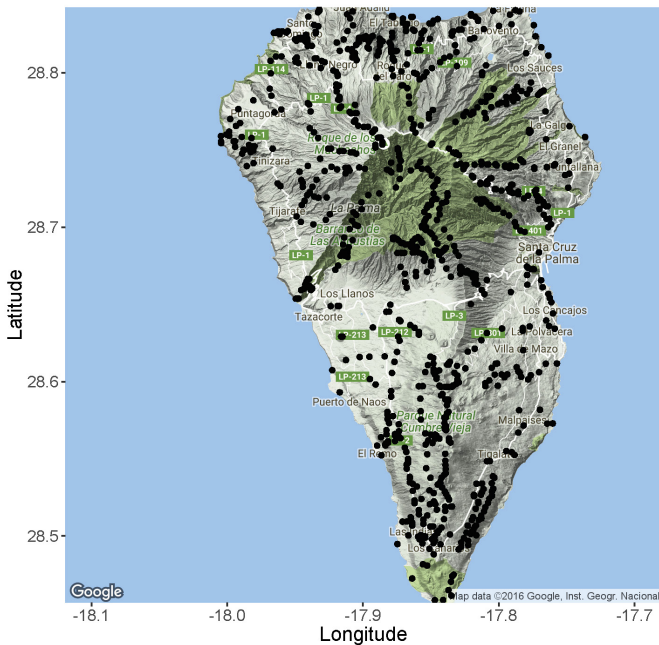


Figure 13.1. Map of La Palma (west of Morocco) and the sampling locations (dots).