

BIOM4051 R Practical 4. Back to the birds



Figure 1: Common Guillemot (left) and Razorbill (right)

Introduction

In this practical we are going to go back to the first maps you produced in QGIS Practical 1 and attempt to replicate them using R! As before, our goal in this practical is to produce a map showing the distribution of major colonies of Common Guillemot and Razorbill along the Cornish Coastline, using data from the JNCC Seabird Monitoring Programme.

Datasets

In the Practical 4 data folder you will find the following datasets:

1. *SMP.gpkg* A geopackage containing seabird counts from 194 SMP monitoring sites in Cornwall from the [JNCC Seabird Monitoring Programme data portal](#).
2. *cornwall.gpkg* and *gb.gpkg* Administrative units of Cornwall and Great Britain obtained from the [Office for National Statistics \(ONS\) geportal](#).
3. *cornwall_6NM_gebco_bathy.tif* A bathymetric raster downloaded from the [General Bathymetric Chart of the Oceans \(GEBCO\)](#) and cropped to the Cornish 6 nm inshore fishing limit
4. *cornwall_towns.gpkg* Locations of towns and cities from [Open Street Map](#)

Task

We are going to have a go at styling and laying out a publication ready map like the one below showing the distribution of all colonies with > 50 breeding pairs. The map should include all the usual elements, including legend, overview map, labelling, north arrow and scalebar.

```
library(sf)
library(terra)
library(tidyverse)
library(tidyterra)
library(colorspace)
library(ggnewscale)
library(patchwork)
library(ggspatial)

gb = st_read('data/gb.gpkg')
cornwall = st_read('data/cornwall.gpkg')
bathy = rast('data/cornwall_6NM_gebco_bathy.tif')
limit = st_read('data/6nm_limit.shp')

birds = st_read('data/SMP.gpkg') %>%
  subset(Count>=50)

towns = st_read('data/cornwall_towns.gpkg') %>%
  subset(name %in% c('Truro', 'Penzance', 'Newquay', 'Padstow'))

bird_map =
  ggplot() +
    geom_spatraster(data = bathy) +
    scale_fill_hypso_c(palette = 'wiki-2.0_bathy', limits = c(-85,0),
                      guide = guide_colourbar(title = 'Bathymetry (m)',
                                              frame.colour = 'black',
                                              ticks.colour = 'black',
                                              barheight = unit(0.3, 'cm'))
    ) +
    geom_sf(data = cornwall, fill = 'grey80') +
    geom_sf(data = limit, linetype = 'dashed', linewidth = 0.2) +
    new_scale_fill() +
    geom_sf(data = birds, aes(fill = Species, size = Count), shape=21) +
    scale_fill_manual(values = c('#bb86e0', '#90b444')) +
    scale_size_continuous(breaks = c(50,200,500,1000)) +
    guides(fill = 'none', size = guide_legend(title = 'Breeding Pairs:')) +
    geom_sf(data = towns, colour = 'white', fill='grey20', shape=21, size=1) +
    geom_sf_text(data = towns, aes(label = name), size=2, nudge_x = 8000, nudge_y = -3000) +
    facet_wrap(~Species) +
    theme_bw() +
    annotation_north_arrow(location = 'tl', width = unit(0.5, 'cm'), height = unit(0.8, 'cm')) +
    annotation_scale(height = unit(0.2, 'cm'), location = 'br') +
    theme(legend.position = 'bottom',
          strip.background = element_blank(),
          panel.grid = element_line(linetype = 'dashed', linewidth = 0.2),
          panel.spacing.x = unit(0.6, 'cm'),
          axis.title = element_blank())
```

```
inset = ggplot() +
  geom_sf(data = gb, fill = 'grey60', colour = 'transparent') +
  geom_sf(data = cornwall, fill = 'red', colour = 'transparent') +
  theme_void()

final = bird_map + inset + plot_layout(ncol=2, widths = c(0.8,0.2))

ggsave('seabird_colonies.jpg',final,width = 8, height = 4)
```

