Seascape Ecology

Lab 05 - Analysing Animal Movement Data

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Introduction

This week we'll be trying our hand at some basic analyses of animal tracking data.

There are numerous methods for analysing animal movement data, and many R packages too. Joo et al. (2019) provide a recent overview: https://besjournals.onlinelibrary.wiley.com/doi/10.1111/1365-2656.13116#:~:text=https%3A//doi.org/10.1111/1365%2D2656.13116. You'll see in Table 1 of Joo et al. that for a given task several packages could be used. So, tools I've used in this tutorial are usually only one of the options.

We'll be using GPS tracking data for two species of giant petrel: the northern giant petrel (*Macronectes halli*) and the southern giant petrel (*Macronectes giganteus*). The data come from a paper where my colleagues and I looked at niche segregation in these sibling species - how do the two species (as well as males and females) avoid competing for the same resources?

All the scripts and data for the analyses in that paper are stored on a Github repository https://github.com/ryanreisinger/giantPetrels. We'll use some of the data from there.

Let's load the packages we'll be using.

```
library(dplyr) # for working with data
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(rnaturalearth)
library(rnaturalearthdata) # for map data
library(ggplot2) # for plotting
library(sf) # for working with spatial vector data
```

```
## Linking to GEOS 3.10.2, GDAL 3.4.2, PROJ 8.2.1; sf_use_s2() is TRUE
```

```
library(geosphere) # distance calculations
library(adehabitatHR)
```

```
## Loading required package: sp
```

```
## Loading required package: deldir
```

```
## deldir 1.0-6      Nickname: "Mendacious Cosmonaut"
```

```
##
##      The syntax of deldir() has had an important change.
##      The arguments have been re-ordered (the first three
##      are now "x, y, z") and some arguments have been
##      eliminated.  The handling of the z ("tags")
##      argument has been improved.
##
##      The "dummy points" facility has been removed.
##      This facility was a historical artefact, was really
##      of no use to anyone, and had hung around much too
##      long.  Since there are no longer any "dummy points",
##      the structure of the value returned by deldir() has
##      changed slightly.  The arguments of plot.deldir()
##      have been adjusted accordingly; e.g. the character
##      string "wpoints" ("which points") has been
##      replaced by the logical scalar "showpoints".
##      The user should consult the help files.

## Loading required package: ade4

## Loading required package: adehabitatMA

## Registered S3 methods overwritten by 'adehabitatMA':
##   method                      from
##   print.SpatialPixelsDataFrame sp
##   print.SpatialPixels          sp

## Loading required package: adehabitatLT

## Loading required package: CircStats

## Loading required package: MASS

##
## Attaching package: 'MASS'

## The following object is masked from 'package:dplyr':
##
##     select

## Loading required package: boot

##
## Attaching package: 'adehabitatLT'

## The following object is masked from 'package:dplyr':
##
##     id
library(terra) # for working with rasters

## terra 1.6.7

##
## Attaching package: 'terra'

## The following object is masked from 'package:MASS':
##
##     area

## The following object is masked from 'package:adehabitatMA':
##
```

```
##     buffer
```

```
library(tidyterra) # for plotting terra rasters in ggplot
```

```
##
## Attaching package: 'tidyterra'
```

```
## The following object is masked from 'package:MASS':
##
##     select
```

```
## The following object is masked from 'package:stats':
##
##     filter
```

```
library(EMbC)
library(marmap)
```

```
##
## Attaching package: 'marmap'
```

```
## The following object is masked from 'package:terra':
##
##     as.raster
```

```
## The following object is masked from 'package:grDevices':
##
##     as.raster
```

First, let's read in the tracking data directly from a URL.

```
# We can pass a URL directly to read.csv()
tracks <- read.csv("https://github.com/ryanreisinger/giantPetrels/raw/master/Data/GP_tracks_2019-07-01.
```

Let's take a peak at the top of the file.

```
# The head() function shows us the first 6 rows of a dataframe.
head(tracks)
```

```
##   sp_code       scientific_name     individual_id Culmen_length Culmen_depth
## 1      NG Northern Giant Petrel NGP01_KD_SEP_2015         100.1         40.4
## 2      NG Northern Giant Petrel NGP01_KD_SEP_2015         100.1         40.4
## 3      NG Northern Giant Petrel NGP01_KD_SEP_2015         100.1         40.4
## 4      NG Northern Giant Petrel NGP01_KD_SEP_2015         100.1         40.4
## 5      NG Northern Giant Petrel NGP01_KD_SEP_2015         100.1         40.4
## 6      NG Northern Giant Petrel NGP01_KD_SEP_2015         100.1         40.4
##   breeding_stage deployment_site deployment_decimal_latitude
## 1     Incubation       Kildalkey                   37.8553287
## 2     Incubation       Kildalkey                   37.8553287
## 3     Incubation       Kildalkey                   37.8553287
## 4     Incubation       Kildalkey                   37.8553287
## 5     Incubation       Kildalkey                   37.8553287
## 6     Incubation       Kildalkey                   37.8553287
##   deployment_decimal_longitude device_type device_id       date      time
## 1                    -46.95416         GPS      5084 2015/09/15  13:55:14
## 2                    -46.95416         GPS      5084 2015/09/15  13:55:15
## 3                    -46.95416         GPS      5084 2015/09/15  13:55:16
## 4                    -46.95416         GPS      5084 2015/09/15  13:55:17
## 5                    -46.95416         GPS      5084 2015/09/15  13:55:18
```

```
## 6                    -46.95416         GPS      5084 2015/09/15  13:55:19
##   decimal_latitude decimal_longitude location_quality
## 1        -46.95463          37.85330               NA
## 2        -46.95462          37.85330               NA
## 3        -46.95462          37.85330               NA
## 4        -46.95461          37.85329               NA
## 5        -46.95461          37.85329               NA
## 6        -46.95460          37.85329               NA
##   latitude_uncertainty_metres longitude_uncertainty_metres          track_id
## 1                          NA                            NA NGP01_KD_SEP_2015
## 2                          NA                            NA NGP01_KD_SEP_2015
## 3                          NA                            NA NGP01_KD_SEP_2015
## 4                          NA                            NA NGP01_KD_SEP_2015
## 5                          NA                            NA NGP01_KD_SEP_2015
## 6                          NA                            NA NGP01_KD_SEP_2015
##     datetime trip
## 1 1442318114    0
## 2 1442318115    0
## 3 1442318116    0
## 4 1442318117    0
## 5 1442318118    0
## 6 1442318119    0
```

The date and time are in separate columns and they are also character vectors. So, let's first join those and convert the new column to a column with class `POSIXlt`, used for dates and times.

```
# 'date' and 'time' are currently character vectors
class(tracks$date)
```

```
## [1] "character"
```

```
class(tracks$time)
```

```
## [1] "character"
```

```
# Join them in a new column
tracks$date_time <- paste(tracks$date, tracks$time, sep = " ")

# And convert to a date using the 'strptime' function
tracks$date_time <- strptime(tracks$date_time, format = "%Y/%m/%d %H:%M:%S", tz = "UTC")

# Look at the class
class(tracks$date_time)
```

```
## [1] "POSIXlt" "POSIXt"
```

For this analysis, we're only interested in a few of the columns, so let's select those.

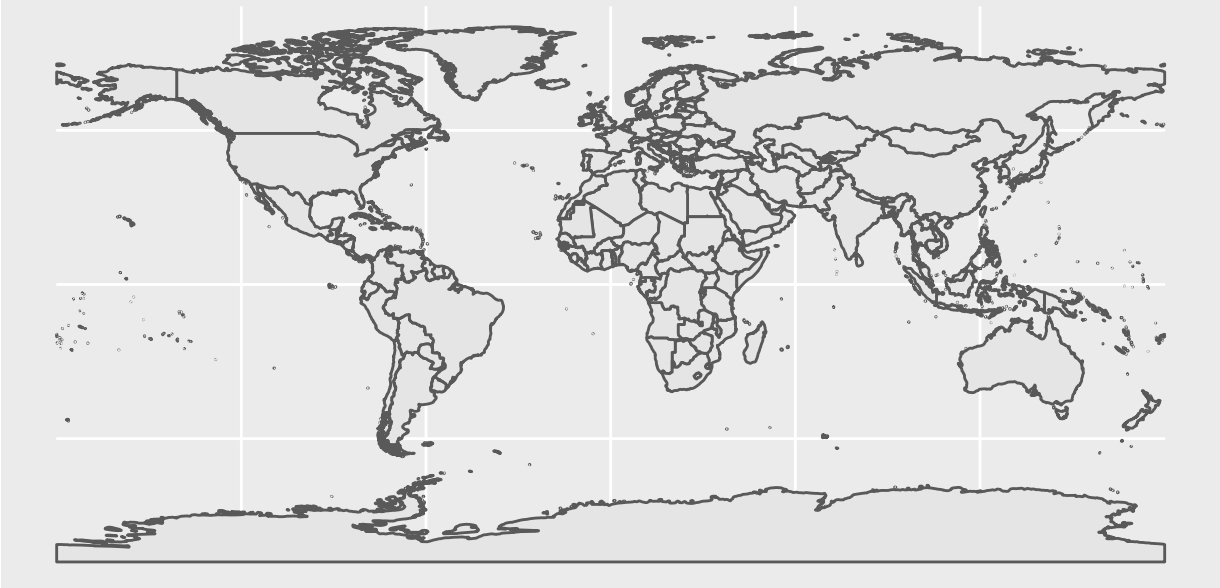
`track_id` is the unique id of each track, `date_time` is the date and time, UTC, in POSXIct format, and `decimal_longitude` and `decimal_latitude` are the longitude and latitude, respectively, in the WGS 1984 coordinate reference system that GPSs use.

```
# Note that I've used dplyr::select() to force R to use the 'select' function from the 'dplyr' package.
tracks <- dplyr::select(tracks,
                  scientific_name,
                  individual_id,
                  date_time,
                  decimal_longitude,
```

```
                  decimal_latitude)
```

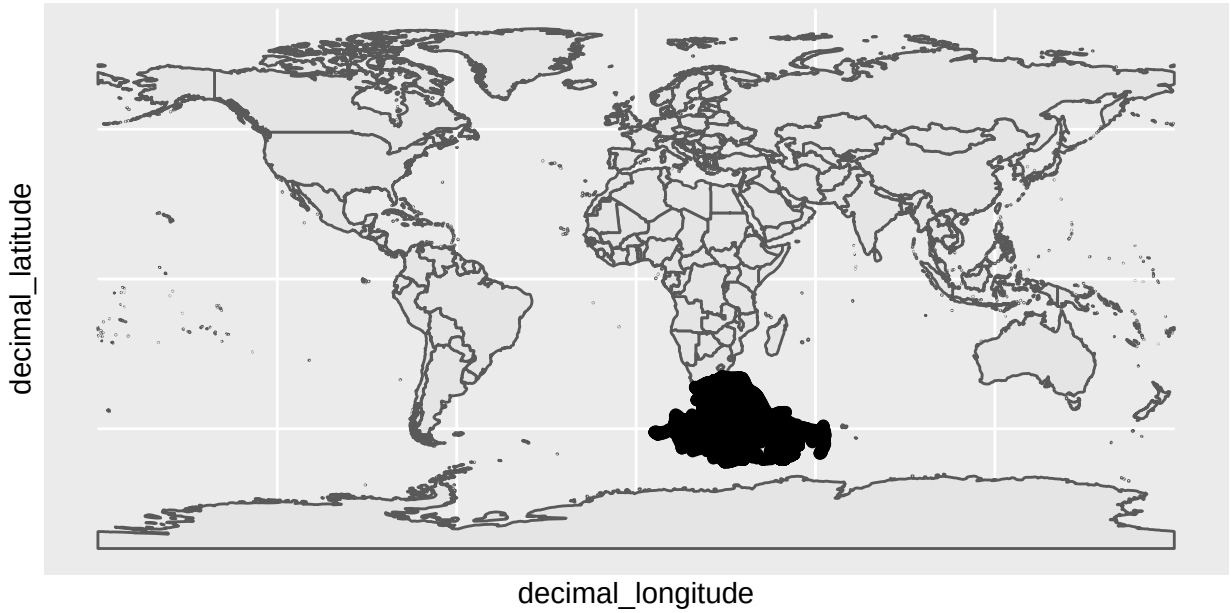
We can make a quick map of all the tracks.

```
# First let's get some map data from the 'rnaturalearth' package.
# Note that we ask the function to return the data in 'sf' class.
world <- ne_countries(scale = "medium", returnclass = "sf")

# Map
ggplot(data = world) +
    geom_sf()
```



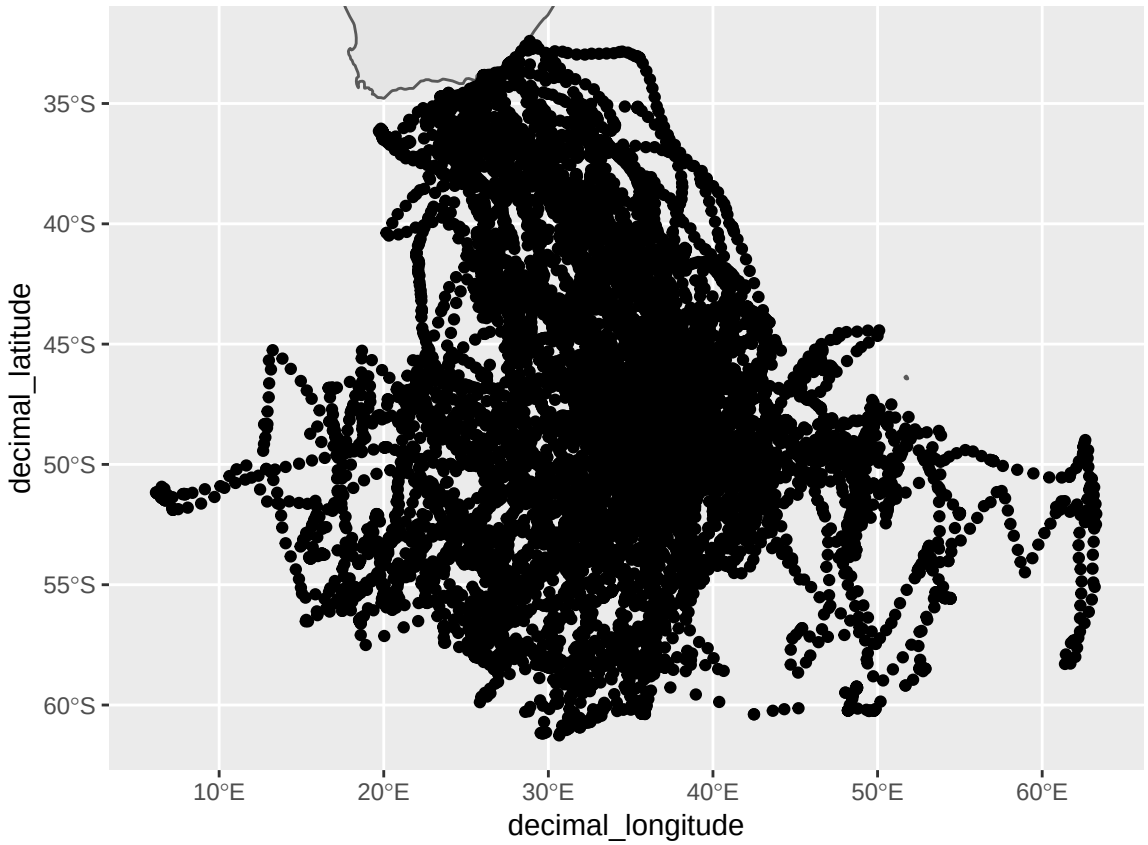
```
# And let's add our tracks on top
ggplot(data = world) +
    geom_sf() +
  geom_point(data = tracks, aes(x = decimal_longitude,
                                y = decimal_latitude))
```

```
## Warning: Removed 53 rows containing missing values (geom_point).
```




```
# Let's 'zoom in' on the tracks by limiting the spatial extent of the map
# according to the tracking data
min_x <- min(tracks$decimal_longitude, na.rm = T)
max_x <- max(tracks$decimal_longitude, na.rm = T)
min_y <- min(tracks$decimal_latitude, na.rm = T)
max_y <- max(tracks$decimal_latitude, na.rm = T)

# We add this spatial extent using the 'coord_sf' function
ggplot(data = world) +
    geom_sf() +
  geom_point(data = tracks, aes(x = decimal_longitude,
                                y = decimal_latitude)) +
  coord_sf(xlim = c(min_x, max_x),
           ylim = c(min_y, max_y))
```

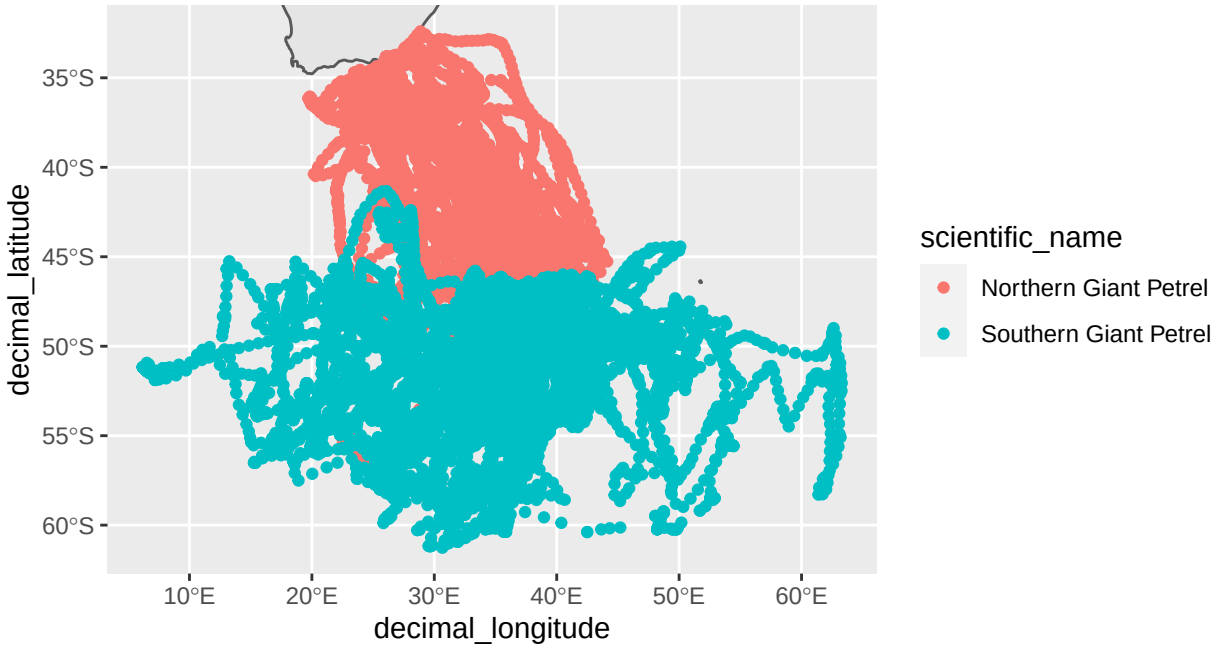
```
## Warning: Removed 53 rows containing missing values (geom_point).
```



You can look through this tutorial for more ways to improve and customise your maps. But for the moment, let's customise one more thing: we'll specify the tracks to be coloured according to the species, using arguments in the `aes()` function in ggplot. Notice how different the movements of northern and southern giant petrels are.

```
ggplot(data = world) +
    geom_sf() +
  geom_point(data = tracks, aes(x = decimal_longitude,
                                y = decimal_latitude,
                                colour = scientific_name)) +
  coord_sf(xlim = c(min_x, max_x),
           ylim = c(min_y, max_y))
```

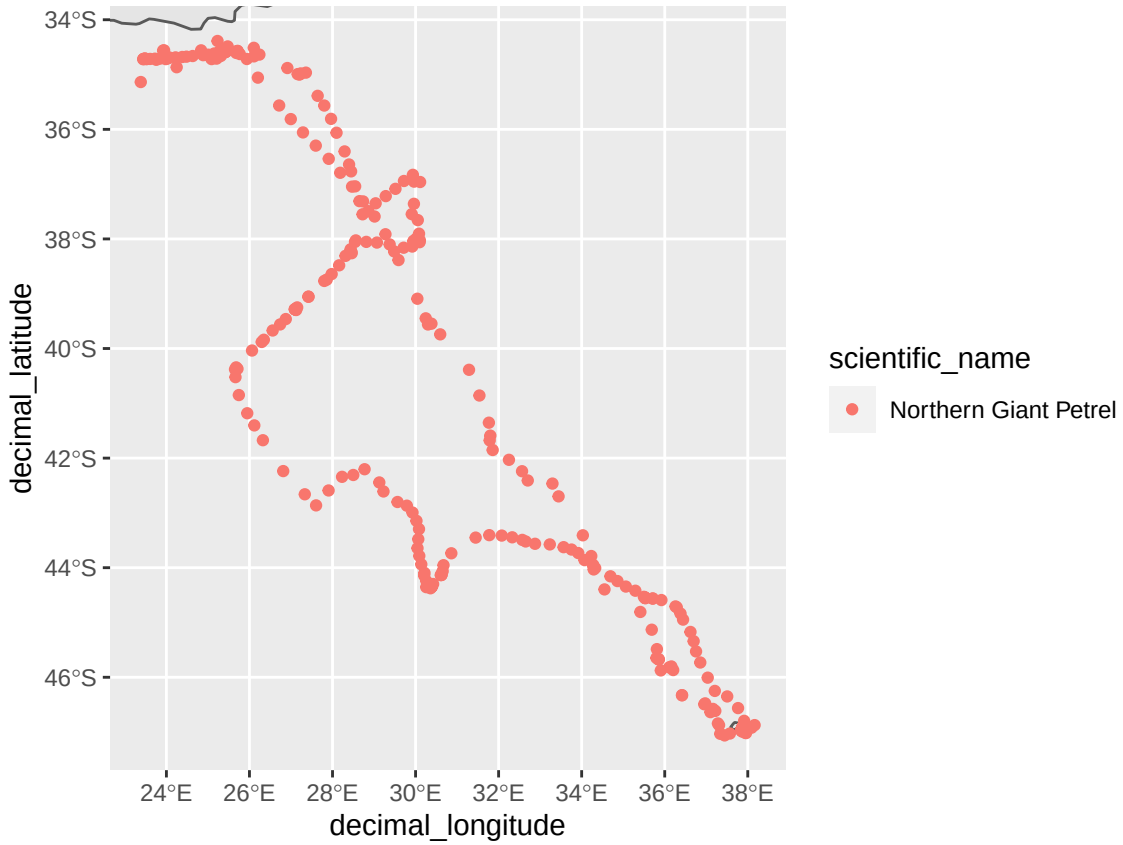
```
## Warning: Removed 53 rows containing missing values (geom_point).
```



Basic analyses

For the following analyses, we'll select one individual to work with. Let's use one of the northern giant petrels, track id `NGP03_KD_SEP_2015`.

```
ngp <- dplyr::filter(tracks, individual_id == "NGP06_KD_SEP_2015")

# Instead of recalculating the x and y limits manually, we'll calculate
# them 'on the fly' inside the ggplot call.

ggplot(data = world) +
    geom_sf() +
  geom_point(data = ngp, aes(x = decimal_longitude,
                             y = decimal_latitude,
                             colour = scientific_name)) +
  coord_sf(xlim = c(min(ngp$decimal_longitude, na.rm = T),
                    max(ngp$decimal_longitude, na.rm = T)),
           ylim = c(min(ngp$decimal_latitude, na.rm = T),
                    max(ngp$decimal_latitude, na.rm = T)))
```



We can calculate some basic parameters from the track, starting with the duration (or spatial extent).

```
start_date <- min(ngp$date_time)
end_date <- max(ngp$date_time)
track_duration <- end_date - start_date
track_duration
```

```
## Time difference of 15.65057 days
```

```
# Note that track_duration is an object of class 'difftime'
class(track_duration)
```

```
## [1] "difftime"
```

```
# We could also do the following, if we want to control the units
track_duration <- difftime(time1 = end_date,
                           time2 = start_date,
                           units = "hours")

track_duration
```

```
## Time difference of 375.6136 hours
```

```
track_duration <- difftime(time1 = end_date,
                           time2 = start_date,
                           units = "days")

track_duration
```

```
## Time difference of 15.65057 days
```

Let's look at distance travelled, each step and in total. For this, we use the `geosphere` package.

```
ngp$distance <- distGeo(p1 = ngp[,c("decimal_longitude", "decimal_latitude")])

# Divide by 1000 to get distance in km
ngp$distance <- ngp$distance/1000

# Total distance travelled in km
sum(ngp$distance, na.rm = T) # We need na.rm = TRUE to remove NAs - the last value is NA
```

```
## [1] 5570.265
```

Now let's look at the time steps, whereafter we can calculate speed (because we have just calculated distance).

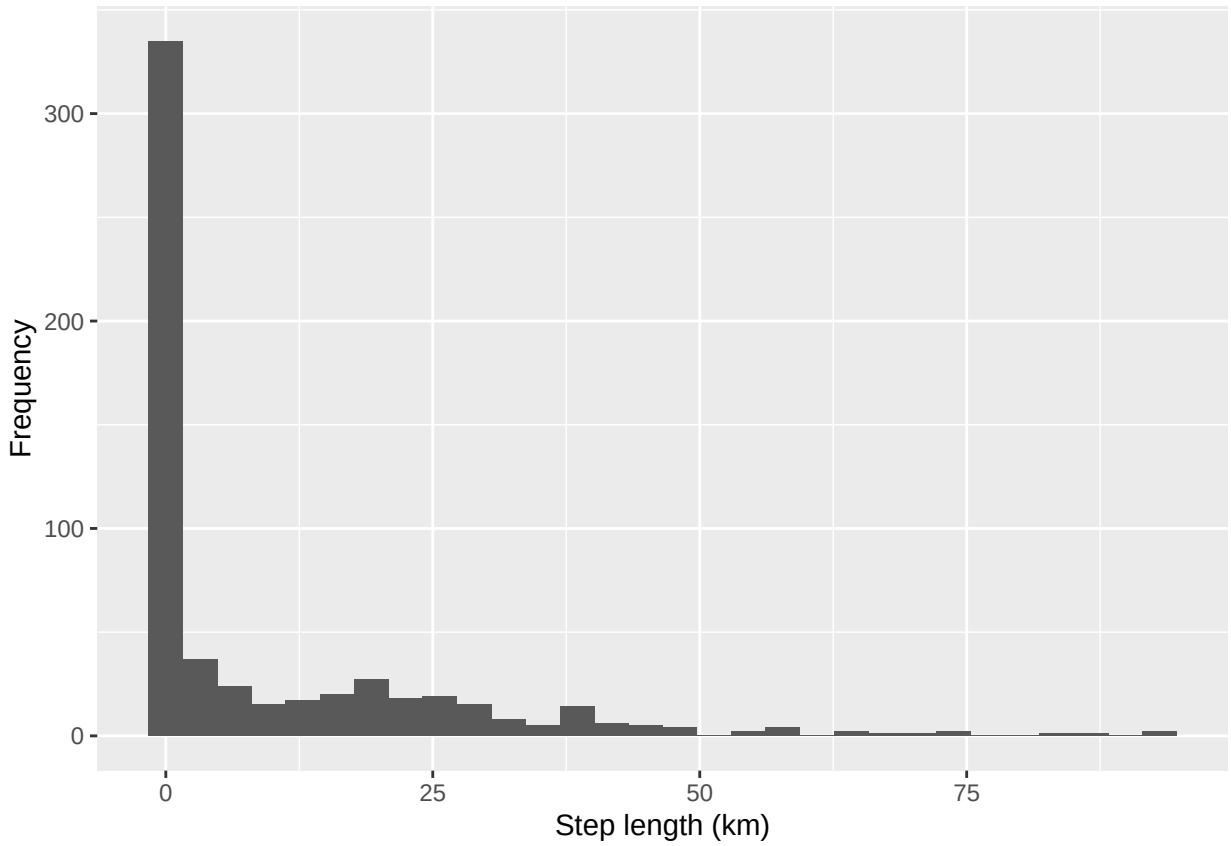
```
timediff <- diff(ngp$date_time)
units(timediff) <- "hours"
timediff <- as.numeric(timediff)
timediff <- c(timediff, NA)
ngp$timestep <- timediff

# We needed to do a few things here
# 1) Change the output from the 'diff' function into hours (it was in seconds)
# 2) Coerce the result into a nummeric
# 3) to add an NA at the end, since diff is not as clever as distGeo
```

Let's plot the frequency distributions of step lengths and step durations.

```
ggplot(data = ngp,
       aes(x = distance)) +
         geom_histogram() +
  labs(main = "Step length distribution",
       x = "Step length (km)",
       y = "Frequency")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

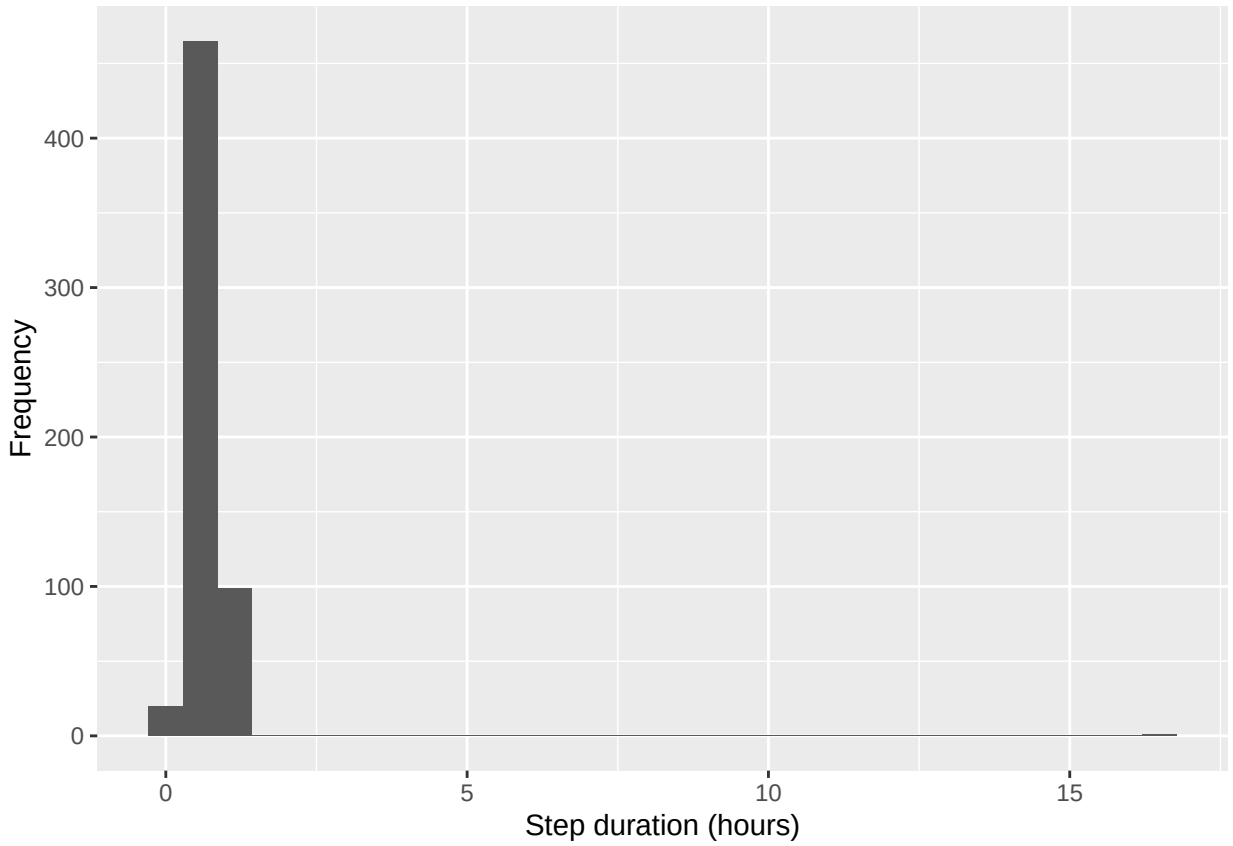
```
## Warning: Removed 1 rows containing non-finite values (stat_bin).
```




```
ggplot(data = ngp,
       aes(x = timestep)) +
         geom_histogram() +
  labs(main = "Step duration distribution",
       x = "Step duration (hours)",
       y = "Frequency")
```

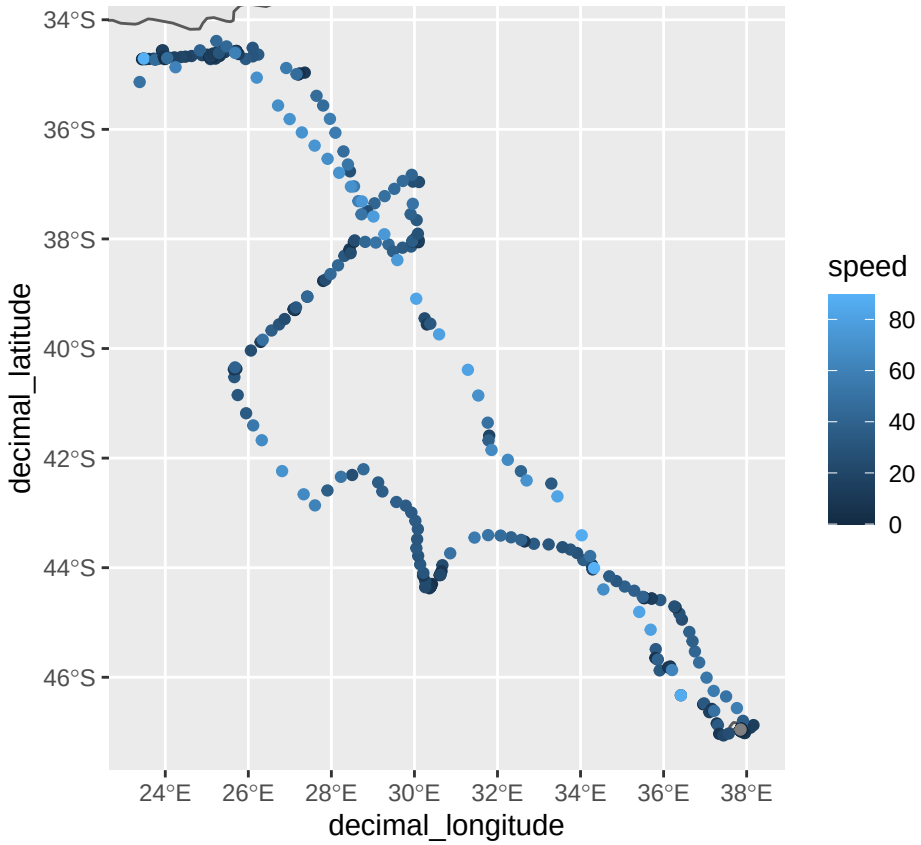
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

```
## Warning: Removed 1 rows containing non-finite values (stat_bin).
```



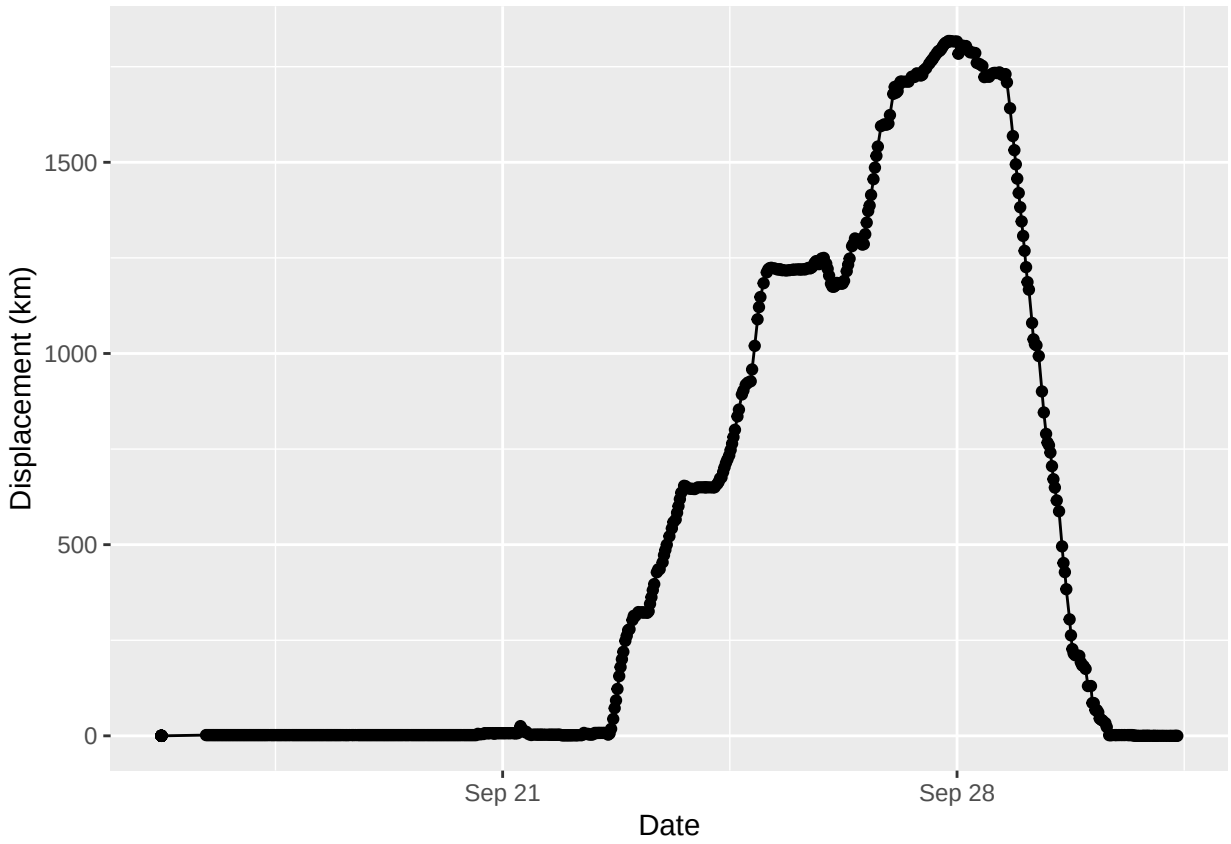
Since we calculated step length and duration, we can work out speed in km/h, and map that. Note that in the call to ggplot, we replace the aesthetic (`aes`), `scientific_name` with `speed`.

```
ngp$speed <- ngp$distance / ngp$timestep

ggplot(data = world) +
    geom_sf() +
  geom_point(data = ngp, aes(x = decimal_longitude,
                             y = decimal_latitude,
                             colour = speed)) +
  coord_sf(xlim = c(min(ngp$decimal_longitude, na.rm = T),
                    max(ngp$decimal_longitude, na.rm = T)),
           ylim = c(min(ngp$decimal_latitude, na.rm = T),
                    max(ngp$decimal_latitude, na.rm = T)))
```



Related to the step length (distance), but related, is calculating the displacement. This is, at each location, the distance of that point from the track's origin. Again, we use the `distGeo` function, but this time we calculate the distance to a pair of 'home' coordinates (the start of the track).

```
# First we define 'home' as the coordinates at the start of the track
home <- ngp[1, c("decimal_longitude", "decimal_latitude")] # Select row 1

# Now we use the distGeo function again
ngp$displacement <- distGeo(p1 = ngp[,c("decimal_longitude", "decimal_latitude")],
                            p2 = home)

# Remember to divide by 1000 to convert from distance in m to km
ngp$displacement <- ngp$displacement/1000

# And we can plot this over time to get a displacement plot
ggplot(data = ngp,
       aes(x = as.POSIXct(date_time), y = displacement)) +
       geom_path() +
         geom_point() +
  labs(main = "Displacement plot",
       x = "Date",
       y = "Displacement (km)")
```



In the plot we can also see that lots of the first locations are likely to be while the bird was still sitting on its nest, after the tag was deployed on it. In a thorough analysis we would trim the track, manually or programatically. Techniques called 'net squared displacement' and 'mean squared displacement' are sometime used to determine the kind of migratory behavior that animals are displaying, from these plots. See Singh et al. (2016) for more details.

Calculating utilization distributions

We'll use the `adehabitathr` package (https://cran.r-project.org/web/packages/adehabitatHR/index.html) to calculate utilisation distribuitons for our single track. There are three 'sibling' adehabitat packages for different analyses (Calenge 2006). Unfortunately, they all still rely on the `sp` package, which you will recall is the older version of `sf`. Nonetheless, they remain a useful and comprehensive set of tools.

Minimum Convex Polygons

Minimum convex polygons (MCPs) are one of the simplest estimators of spatial utilisation. MCPs are 'the smallest polygon around points with all interior angles less than 180 degrees. MCPs are common estimators of home range, but can potentially include area not used by the animal and overestimate the home range' (from https://jamesepaterson.github.io/jamespatersonblog/03_trackingworkshop_homeranges).

Calculating utilsiation distributions with adehabitat takes a litle bit of preparation. Let's calculate MCPs...

```
# First, we need to create an object of class 'spatial points' (a vector format) to use in the mcp func

# Load the sp library
library(sp)

# Make a copy of our tracks
```

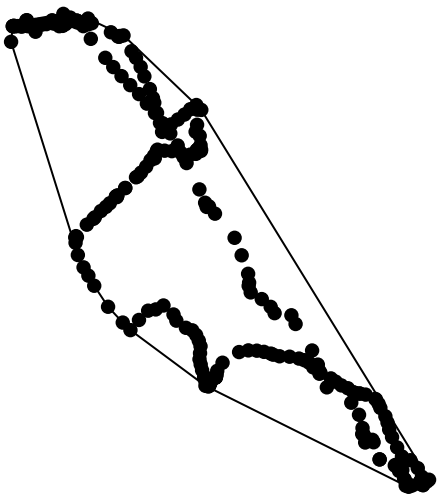
```r
ngp_sp <- ngp

# The mcp function only allows one extra column, the animal id, so
ngp_sp <- dplyr::select(ngp_sp,
                        decimal_longitude,
                        decimal_latitude,
                        individual_id)

# Tell R the object has spatial coordinates
coordinates(ngp_sp) <- c("decimal_longitude", "decimal_latitude")

# And what the coordinate reference system is
proj4string(ngp_sp) <- CRS("EPSG:4326")

# Now we see the object has a new class: spatial points data frame
class(ngp_sp)
```

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

```r
# We can use this object as input for the MCP function
ngp_mcp <- mcp(ngp_sp, percent = 100)
```

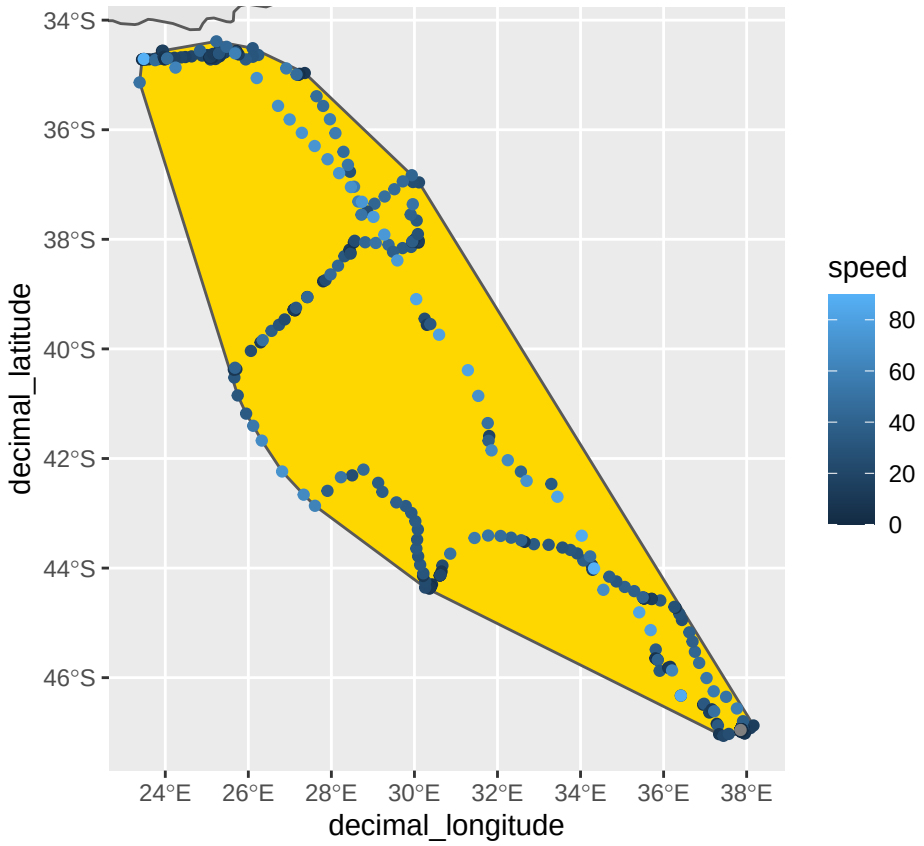
```
## Warning in proj4string(xy): CRS object has comment, which is lost in output; in tests, see
## https://cran.r-project.org/web/packages/sp/vignettes/CRS_warnings.html
```

```r
# And we can plot the result, with the locations on top
plot(ngp_mcp)
plot(ngp_sp, add = TRUE, pch = 16)
```



```r
# If we want to plot the mcp with ggplot, we need to convert it to sf
ngp_mcp_sf <- st_as_sf(ngp_mcp)

# And we plot it by adding a geom_sf layer to our plot
ggplot(data = world) +
    geom_sf() +
  geom_sf(data = ngp_mcp_sf, fill = "gold") +
    geom_point(data = ngp, aes(x = decimal_longitude,
```

```
                                y = decimal_latitude,
                                colour = speed)) +
  coord_sf(xlim = c(min(ngp$decimal_longitude, na.rm = T),
                    max(ngp$decimal_longitude, na.rm = T)),
           ylim = c(min(ngp$decimal_latitude, na.rm = T),
                    max(ngp$decimal_latitude, na.rm = T)))
```



Kernel density estimates

Next, we can calculate the kernel density estimate (kde).

Calenge (2015) writes:

> The MCP has met a large success in the ecological literature. However, many authors have stressed that the definition of the home range which is commonly used in the literature was rather imprecise: "that area traversed by the animal during its normal activities of food gathering, mating and caring for young" (Burt, 1943). Although this definition corresponds well to the feeling of many ecologists concerning what is the home range, it lacks formalism: what is an area traversed? what is a normal activity? Several authors have therefore proposed to replace this definition by a more formal model: the utilization distribution (UD, van Winkle, 1975). Under this model, we consider that the animals use of space can be described by a bivariate probability density function, the UD, which gives the probability density to relocate the animal at any place according to the coordinates (x, y) of this place. The study of the space use by an animal could consist in the study of the properties of the utilization distribution. The issue is therefore to estimate the utilization distribution from the relocation data. The seminal paper of Worton (1989) proposed the use of the kernel method (Silverman, 1986; Wand and Jones, 1995) to estimate the UD using the relocation data. The kernel method was probably the most frequently used function in the package adehabitat.

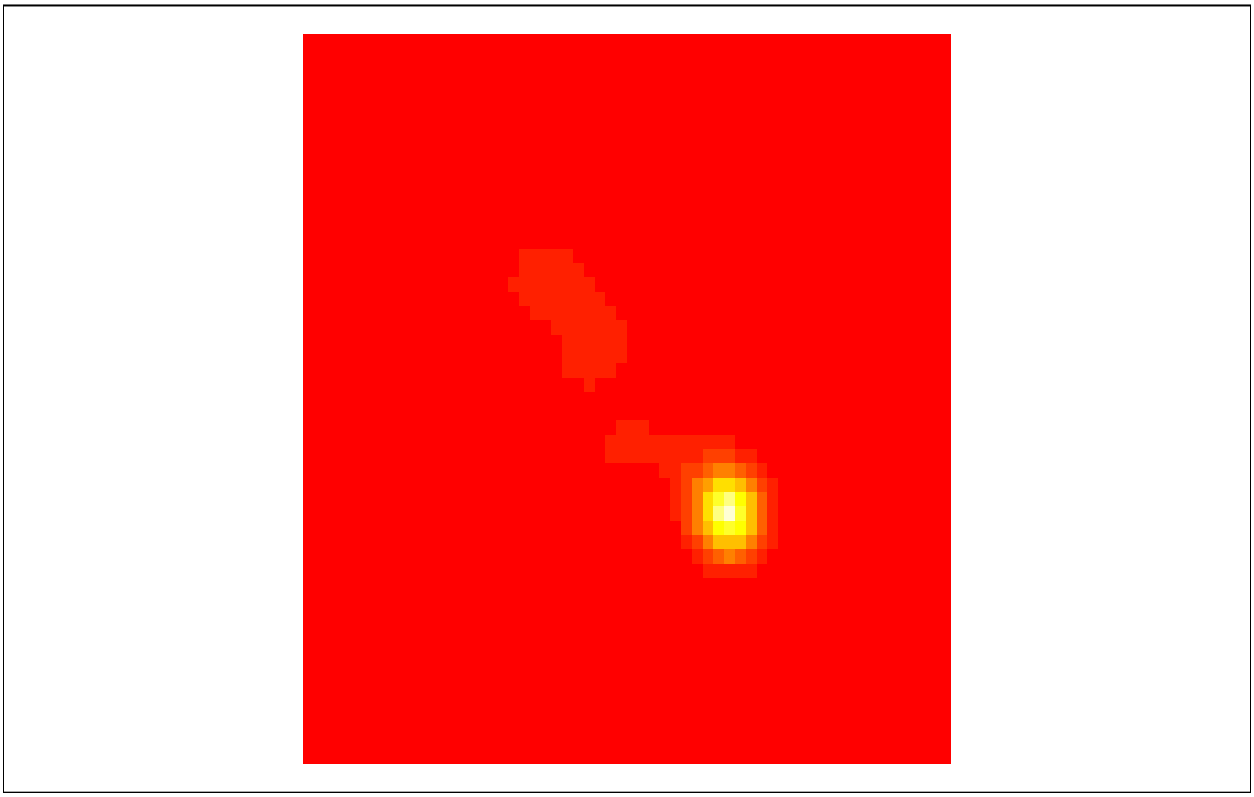
Let's go...

```
# We can calculate the kde using the same input we used for the mcp
ngp_kde <- kernelUD(ngp_sp, h = "href")
```

```
## Warning in proj4string(xy): CRS object has comment, which is lost in output; in tests, see
## https://cran.r-project.org/web/packages/sp/vignettes/CRS_warnings.html
```

```
## Warning in proj4string(xy): CRS object has comment, which is lost in output; in tests, see
## https://cran.r-project.org/web/packages/sp/vignettes/CRS_warnings.html
```

```
# The output has its own bespoke class, but we can plot it with
image(ngp_kde)
```




```
# We can create a raster-package raster with
ngp_vud <- getvolumeUD(ngp_kde)
```

```
## Warning in proj4string(x): CRS object has comment, which is lost in output; in tests, see
## https://cran.r-project.org/web/packages/sp/vignettes/CRS_warnings.html
```

```
ngp_kde_raster <- rast(as(ngp_vud$NGP06_KD_SEP_2015,"SpatialPixelsDataFrame"))

# Remember that the 95% kde is often designated the home range and the 50% kde the core range. To get a
ngp_kde_95 <- getverticeshr(ngp_kde, percent = 95)
```

```
## Warning in proj4string(x): CRS object has comment, which is lost in output; in tests, see
## https://cran.r-project.org/web/packages/sp/vignettes/CRS_warnings.html
```

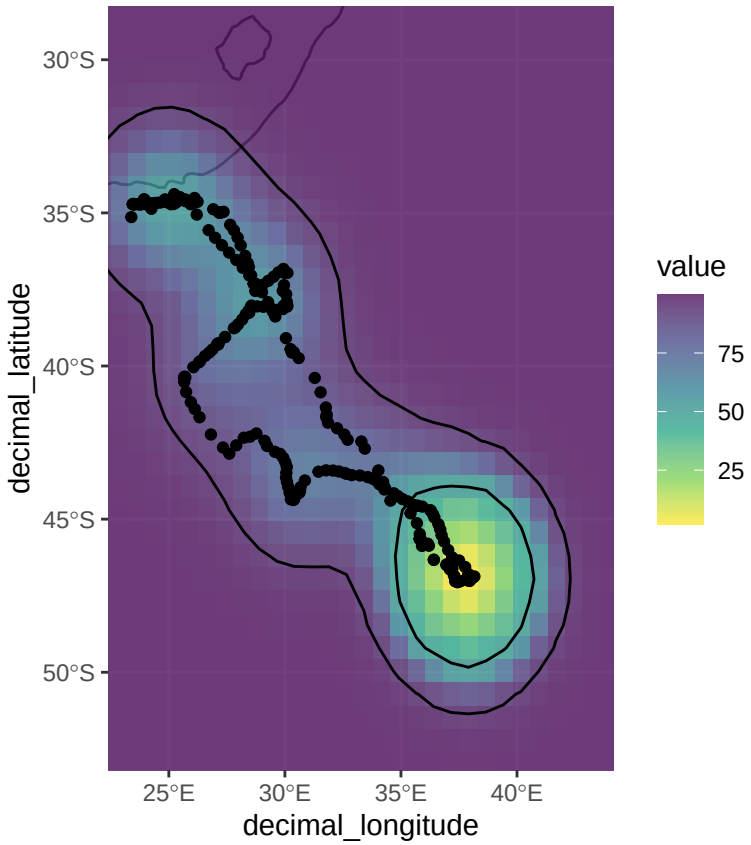
```
## Warning in proj4string(x): CRS object has comment, which is lost in output; in tests, see
## https://cran.r-project.org/web/packages/sp/vignettes/CRS_warnings.html
```

```
ngp_kde_50 <- getverticeshr(ngp_kde, percent = 50)
```

```
## Warning in proj4string(x): CRS object has comment, which is lost in output; in tests, see
## https://cran.r-project.org/web/packages/sp/vignettes/CRS_warnings.html
```

```
## Warning in proj4string(x): CRS object has comment, which is lost in output; in tests, see
## https://cran.r-project.org/web/packages/sp/vignettes/CRS_warnings.html
```

```
# And we can convert these to sf objects for plotting
ngp_kde_95 <- st_as_sf(ngp_kde_95)
ngp_kde_50 <- st_as_sf(ngp_kde_50)

# Let's plot the kde and its contours in ggplot
# to plot the terra raster in ggplot we use the tidyterra package
# see https://www.r-bloggers.com/2022/05/introducing-tidyterra/ for more
ggplot(data = world) +
    geom_sf() +
  # first, the raster
  geom_spatraster(data = ngp_kde_raster) +
  scale_fill_viridis_c(direction = -1, alpha = 0.75) +
  # then, the kernel contours
  geom_sf(data = ngp_kde_50, colour = "black", fill = NA) +
    geom_sf(data = ngp_kde_95, colour = "black", fill = NA) +
  # then, the tracking data
    geom_point(data = ngp, aes(x = decimal_longitude,
                               y = decimal_latitude)) +
  # and then we 'zoom' the map -- note I expanded the area by 5 degrees
    coord_sf(xlim = c(min(ngp$decimal_longitude, na.rm = T)-5,
                      max(ngp$decimal_longitude, na.rm = T))+5,
             ylim = c(min(ngp$decimal_latitude, na.rm = T)-5,
                       max(ngp$decimal_latitude, na.rm = T)+5))
```



Remember that the **low kde value represents high density**. Notice how the kde overestimates the area (the mcp too), and how it ignores hard barriers like land (South Africa in the north-east of the plot). As I mentioned in lecture, and as stated in Pittman chapter 7, LoCoH (Getz et al. 2007) is an alternative to mcp, and movement-based kernel density estimation, or biased random bridge, (Benhamou & Cornelis 2010) is an alternative to kde. We won't use these two methods in this tutorial, but you can calculate them in adehabitat. See `?LoCoH()` and `?BRB()` in adehabitatHR.

Behavioural classification

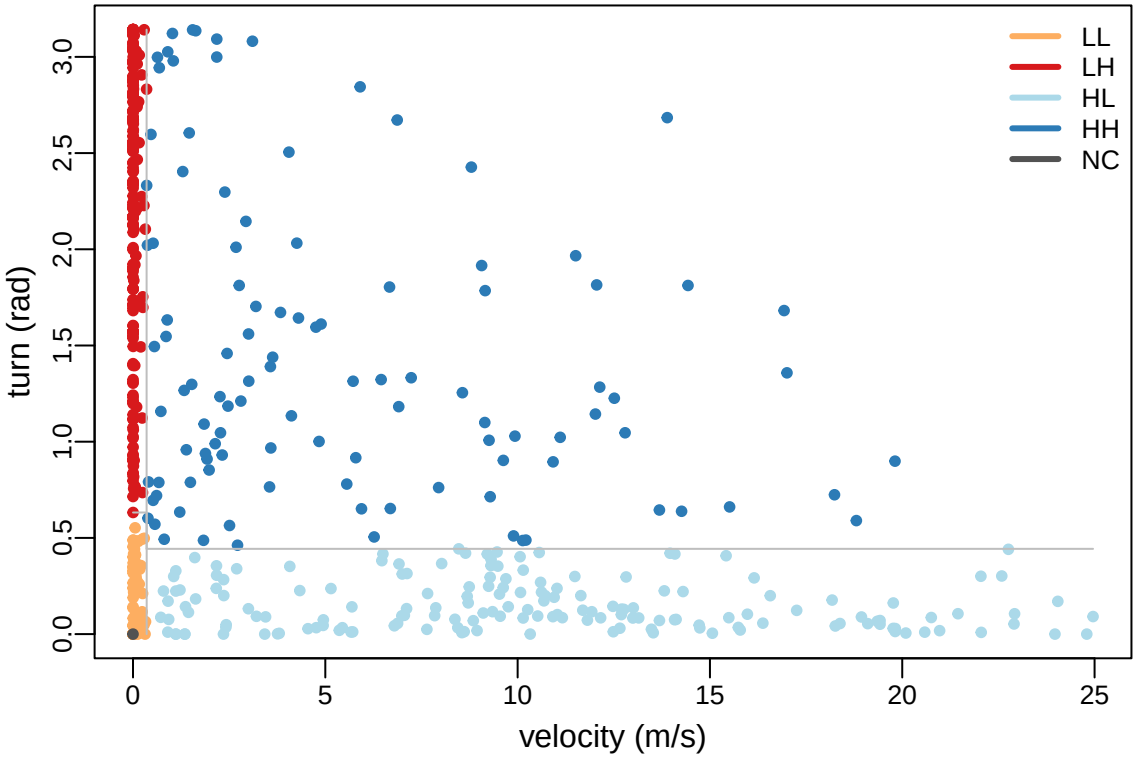
There are many ways of estimating behaviour from movement data. Table X in Pittman lists several. We'll look at a method called Expectation Maximisation Binary Clustering (EMbC) (Garriga).

A quick start guide is at https://rdrr.io/cran/EMbC/f/vignettes/EMbC_qckref.Rmd

```
# EBbC expects the data in a specif format
# Look at the 'obj' argument in the help file ?stbc()
ngp_embc_data <- dplyr::select(ngp,
                               date_time,
                               decimal_longitude,
                               decimal_latitude)

# Run the function
mybcp <- stbc(ngp_embc_data, info=-1)
```

```
## [1]   0  -0.0000e+00       4       586
## [1] ... Stable clustering
```

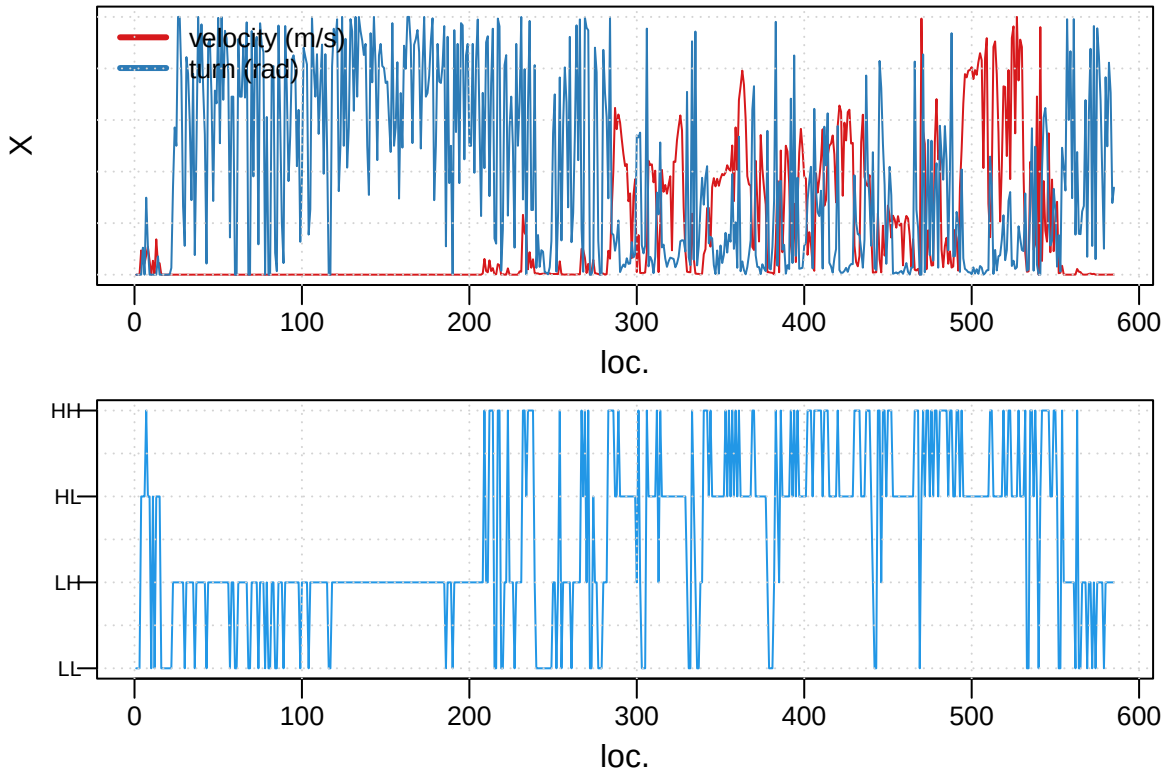
```
# Inspect the clustering results
sctr(mybcp)
```



This plot shows us the each tracking location according to the turning angle (vertical axis) and velocity (horizontal axis) of the preceding step. The algorithm then performs bivariate (two variable - speed and angle) clustering, and clusters the locations into four categories according to low and high speed and turning angle.

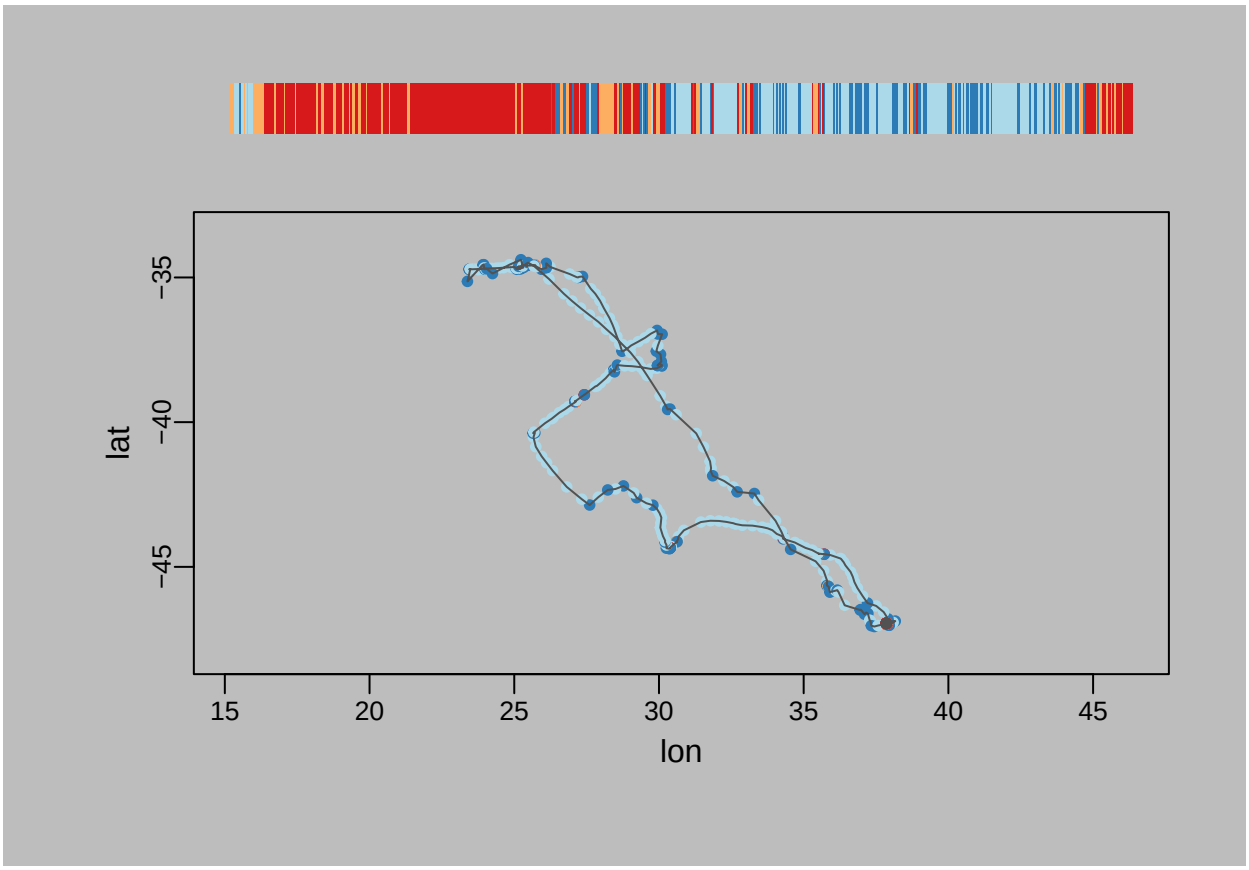
We can look at the labelled (annotated) trajectory over time.

```
lblp(mybcp)
```



Or map the labelled trajectory:

```
view(mybcp)
```

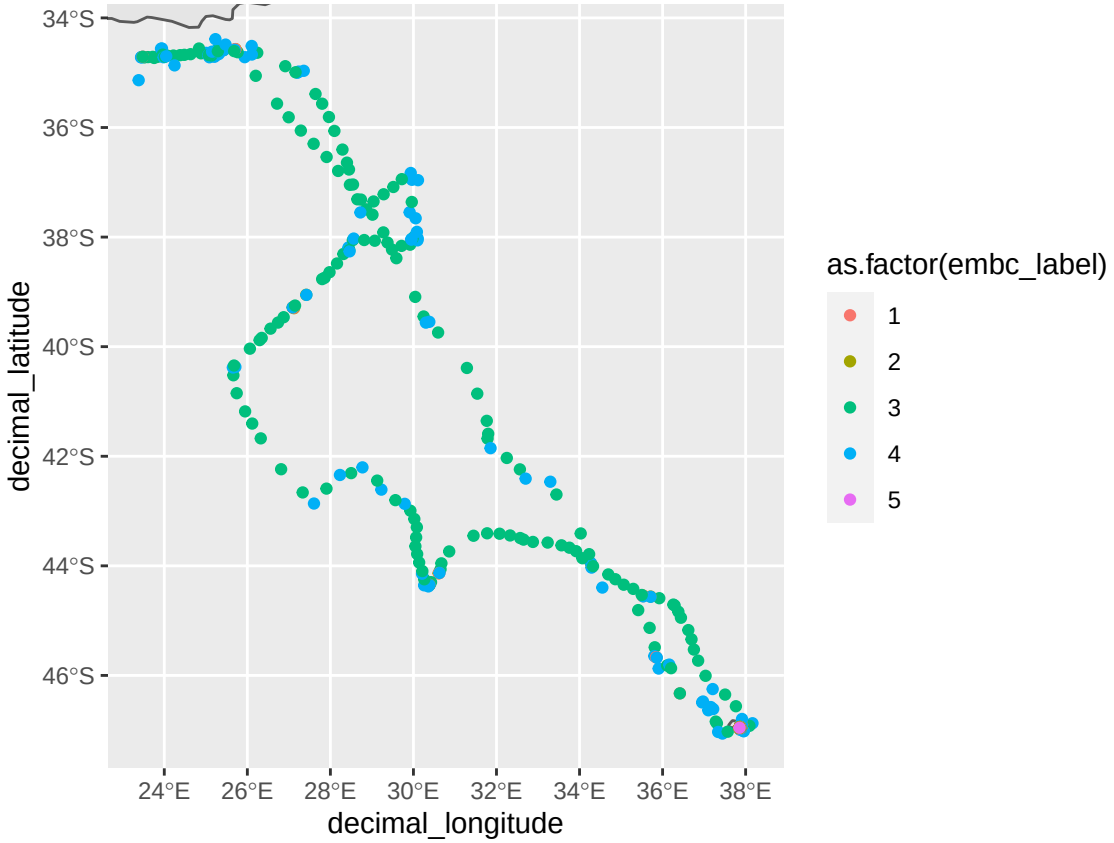


We can get these outputs from the EMbC object, and add them to our data.

```
# We can look at the cutoff values with
mybcp@R
```

```
##         X1.min    X2.min     X1.max    X2.max
## 1.LL 0.0000000 0.0000000  0.3558894 0.6321050
## 2.LH 0.0000000 0.6321050  0.3536850 3.1415927
## 3.HL 0.3558894 0.0000000 24.9606512 0.4431287
## 4.HH 0.3536850 0.4431287 24.9606512 3.1415927
```

```
# We can write the outputs to the data frame
ngp_embc_data$embc_velocity <- mybcp@X[,1]
ngp_embc_data$embc_turnrad <- mybcp@X[,2]
ngp_embc_data$embc_label <- mybcp@A # These are the EMbC labels

# Let's map the labels
# Notice that I put as.factor() around the embc_label
# That's because embc returns the label as a numeric, but we want to treat it as a categorical factor.
ggplot(data = world) +
    geom_sf() +
  geom_point(data = ngp_embc_data, aes(x = decimal_longitude,
                                       y = decimal_latitude,
                                       colour = as.factor(embc_label))) +
  coord_sf(xlim = c(min(ngp_embc_data$decimal_longitude, na.rm = T),
                    max(ngp_embc_data$decimal_longitude, na.rm = T)),
           ylim = c(min(ngp_embc_data$decimal_latitude, na.rm = T),
                    max(ngp_embc_data$decimal_latitude, na.rm = T)))
```



Notice that there are five classes. The fifth class corresponds with locations that were not classified (NC in the first EMbC plot). Most location are in class 3 and 4. Class 4 seems to be associated with slower, more tortuous movements than class 3.

Environmental relationships

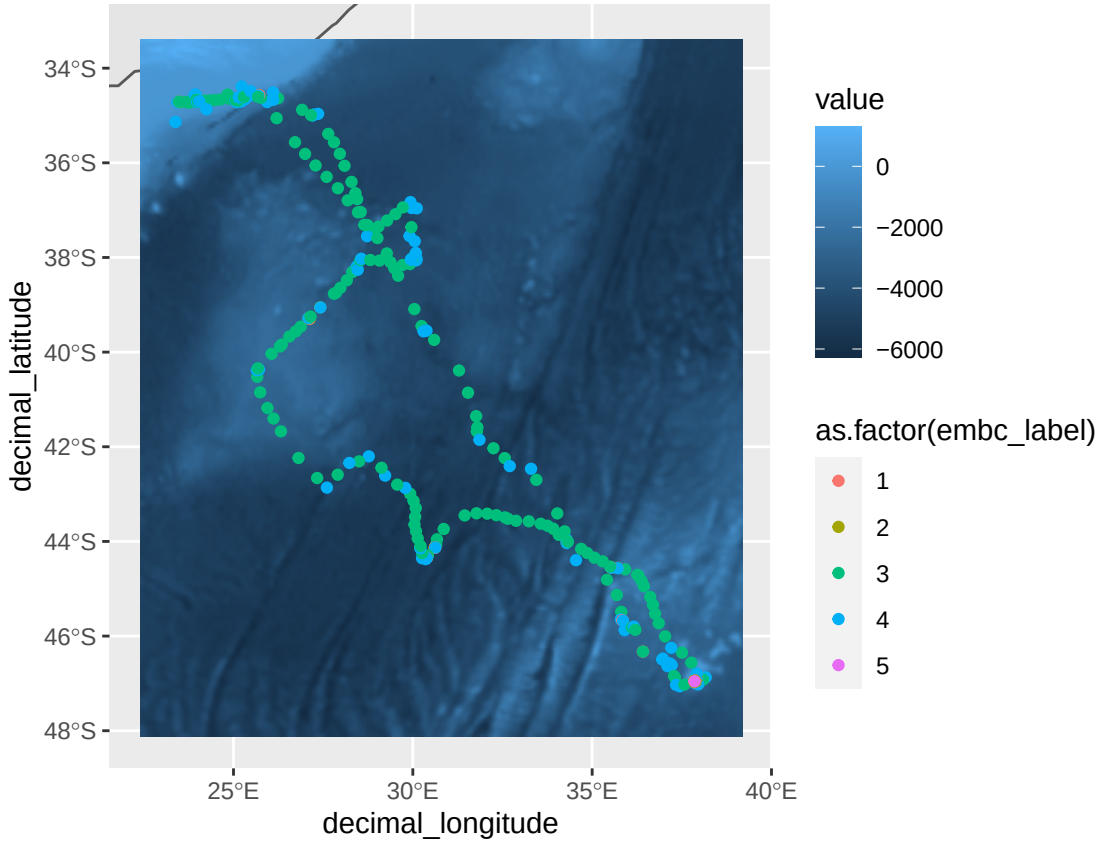
We can examine the relationship between animals' space use or movement behavior, and the environment. Again, there are many ways to do this, and many environmental variables we could look at, but let's use a very simple example, making use of what we have here, and what we did in previous weeks. We'll download some bathymetry data like we did in Lab 4, and look at how bathymetry corresponds with the EMbC labels.

Let's get the bathymetry data using `marmap`.

```
# First, we define the spatial extent, similar to what we did for the first plot
min_x <- min(ngp_embc_data$decimal_longitude, na.rm = T) - 1
max_x <- max(ngp_embc_data$decimal_longitude, na.rm = T) + 1
min_y <- min(ngp_embc_data$decimal_latitude, na.rm = T) - 1
max_y <- max(ngp_embc_data$decimal_latitude, na.rm = T) + 1

bathy <- getNOAA.bathy(lon1=min_x,lon2=max_x, lat1=min_y,lat2=max_y,resolution=4)
```

```
## Querying NOAA database ...

## This may take seconds to minutes, depending on grid size

## Building bathy matrix ...
```

```
# Convert it to a raster, than a terra raster
bathy <- marmap::as.raster(bathy)
bathy <- terra::rast(bathy)

# Plot to check
ggplot(data = world) +
    geom_sf() +
  # first, the raster
  geom_spatraster(data = bathy) +
  # then, the tracking data
    geom_point(data = ngp_embc_data, aes(x = decimal_longitude,
                                         y = decimal_latitude,
                                         colour = as.factor(embc_label))) +
  # and then we 'zoom' the map -- note I euse the limits we just calculated
    coord_sf(xlim = c(min_x, max_x),
             ylim = c(min_y, max_y))
```



We can now use a handy feature to 'extract' the values from the bathymetry raster at each tracking location.

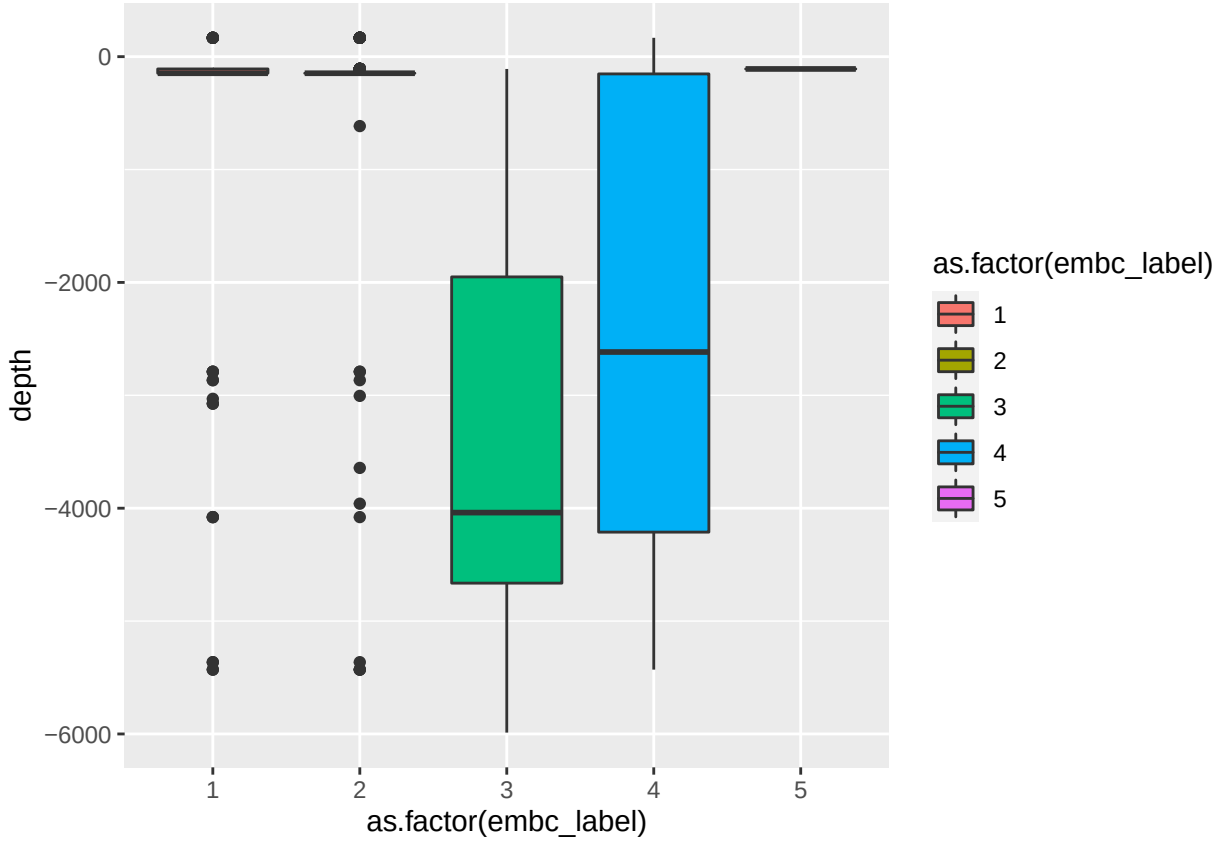
```
ngp_embc_data$depth <- terra::extract(bathy, ngp_embc_data[,c("decimal_longitude", "decimal_latitude")])

# If we look at the first few rows now, we see depth is added as a column
head(ngp_embc_data)
```

```
##             date_time decimal_longitude decimal_latitude embc_velocity
## 1 2015-09-15 17:49:44          37.85326        -46.95477      0.000000
## 2 2015-09-15 17:49:45          37.85326        -46.95477      0.000000
## 3 2015-09-15 17:49:46          37.85326        -46.95477      0.000000
```

```
## 4 2015-09-15 17:49:47          37.85326        -46.95477      2.352481
## 5 2015-09-15 17:49:48          37.85327        -46.95475      1.113195
## 6 2015-09-15 17:49:49          37.85327        -46.95474      1.113195
##   embc_turnrad embc_label depth
## 1    0.0000000          1  -109
## 2    0.0000000          1  -109
## 3    0.0000000          1  -109
## 4    0.0000000          3  -109
## 5    0.3288924          3  -109
## 6    0.0000000          3  -109
```

We can then look at the depth values corresponding with each label class.

```
ggplot(data = ngp_embc_data, aes(x = as.factor(embc_label),
                                 y = depth,
                                 fill = as.factor(embc_label))) +
  geom_boxplot()
```



So, we see that class 5 indeed corresponds with NC (not classified) and classes 1 and 2 seem to be mainly on or near land locations (but not only). Remember: for this analysis we did not trim out the initial locations when the bird was probably still on its nest.

We see that the boxes for class 3 and 4 overlap a great deal, but there is some difference. Class 4 is associated with shallower water. Let's focus on those two classes and see if there is a significance difference according to a t-test. Note, in a thorough analysis you would probably not use a t-test, because these data violate the assumption of independence – they are auto-correlated because they are measured one after the other in a temporal sequence. They are also unlike to be normally distributed. But that's a discussion for another time!

```
class_3 <- dplyr::filter(ngp_embc_data, embc_label == 3)
class_4 <- dplyr::filter(ngp_embc_data, embc_label == 4)
t.test(class_3$depth, class_4$depth)
```

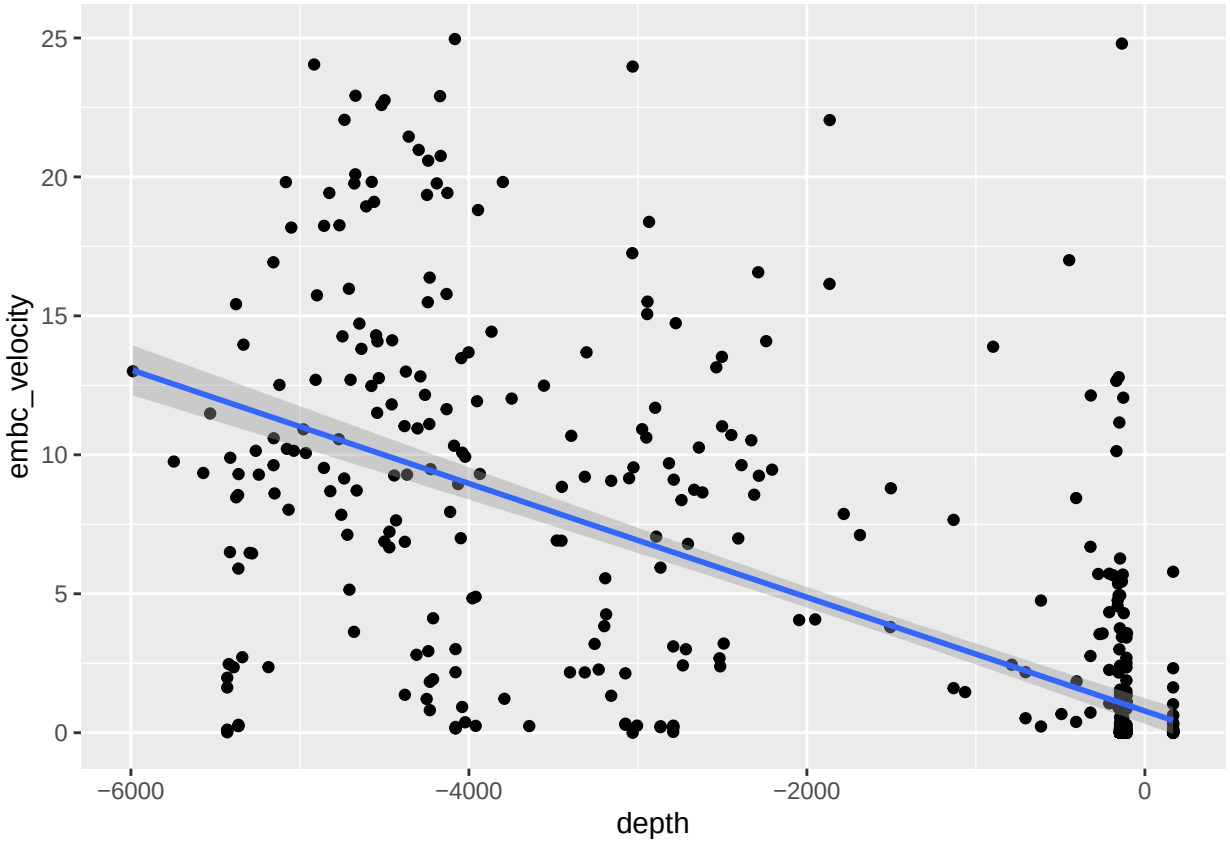
```
##
##  Welch Two Sample t-test
##
## data:  class_3$depth and class_4$depth
## t = -3.8398, df = 216.61, p-value = 0.0001617
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -1386.2563  -445.8309
## sample estimates:
## mean of x mean of y
## -3190.479 -2274.435
```

There is a significant difference, but as I say, we are violating some assumptions...

Looks look at the case where we have a continuous-value response variable, like velocity. We can plot the relationship and fit a linear model.

```
ggplot(data = ngp_embc_data, aes(x = depth,
                                 y = embc_velocity)) +
  geom_point() +
  geom_smooth(method = "lm")
```

```
## `geom_smooth()` using formula 'y ~ x'
```



```
# Correlation
cor(ngp_embc_data$embc_velocity, ngp_embc_data$depth)
```

```
## [1] -0.6675504
```

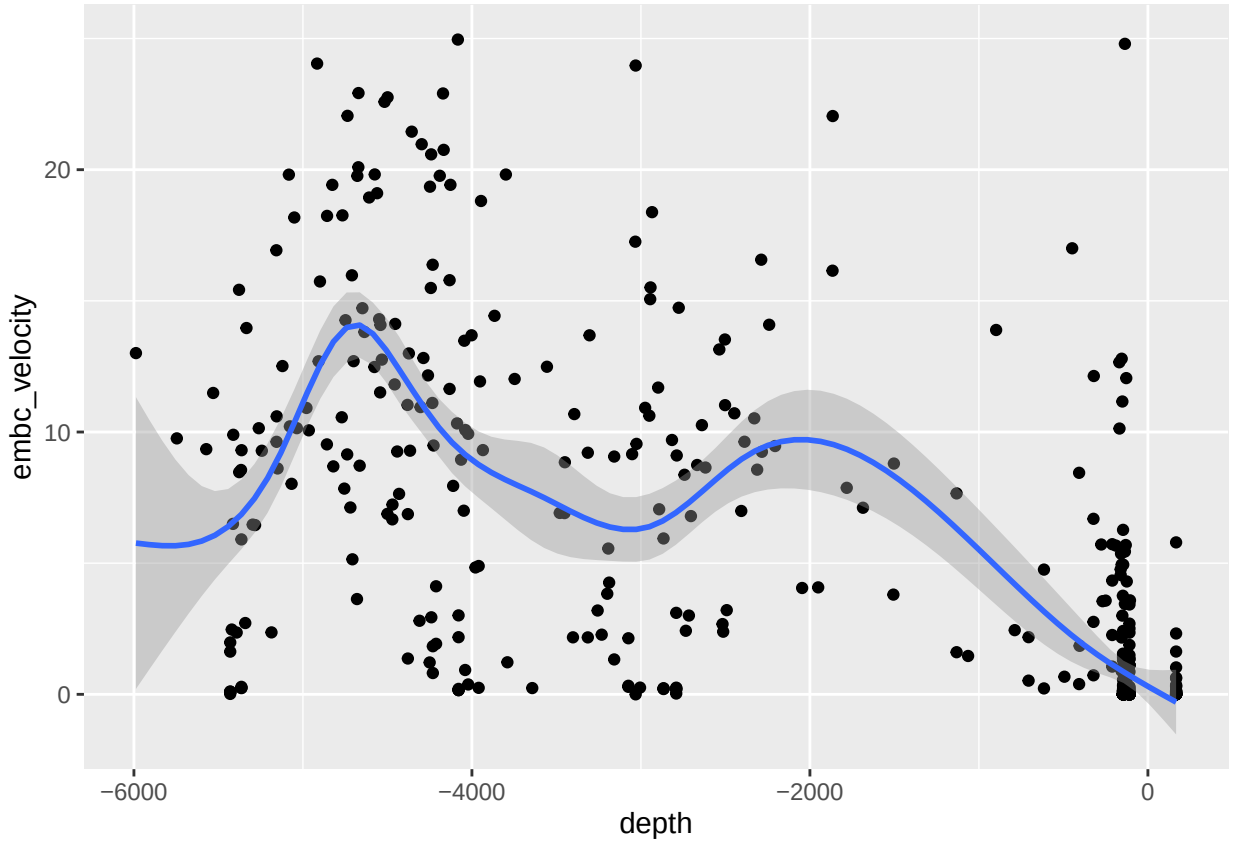
```
# Linear model
lm(ngp_embc_data$embc_velocity ~ ngp_embc_data$depth)
```

```
##
## Call:
## lm(formula = ngp_embc_data$embc_velocity ~ ngp_embc_data$depth)
##
## Coefficients:
##         (Intercept)  ngp_embc_data$depth
##            0.782845            -0.002046
```

We fitted a linear regression, and find a strong correlation, although these kinds of relationships are very unlikely to be linear, so we more often fitting a smooth of some kind, for example using a generalized additive model (GAM).

```
ggplot(data = ngp_embc_data, aes(x = depth,
                                 y = embc_velocity)) +
  geom_point() +
  geom_smooth(method = "gam")
```

```
## `geom_smooth()` using formula 'y ~ s(x, bs = "cs")'
```



So, you've conducted your first movement analyses! There's a massive variety of other things you could analyse, and ways to do that, but this is a basic tutorial to get you started. Come and chat to me if you're

interested in anything specific.