

loops

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2022-11-17

```
sum (1, 2, 3, 4, 5)
```

```
## [1] 15
```

```
numbers <- c(1, 2, 3, 4, 5)
numbers <- 1:5
numbers <- seq(1,5,0.3)

for (number in numbers){
  print(number)
}
```

```
## [1] 1
## [1] 1.3
## [1] 1.6
## [1] 1.9
## [1] 2.2
## [1] 2.5
## [1] 2.8
## [1] 3.1
## [1] 3.4
## [1] 3.7
## [1] 4
## [1] 4.3
## [1] 4.6
## [1] 4.9
```

```
mass_lbs <- c(2.2, 3.5, 9.6, 1.2)
for(numbers in mass_lbs){
  mass_kg = 2.2 * numbers
  print(mass_kg)
}
```

```
## [1] 4.84
## [1] 7.7
## [1] 21.12
## [1] 2.64
```

```
our_names <- c("Azul", "jai", "marcos", "luna")
for (names in our_names) {
  print(names)
}
```

```
## [1] "Azul"
## [1] "jai"
## [1] "marcos"
## [1] "luna"
```

```
birds <- c('robin', 'woodpecker', 'blue jay', 'sparrow')
for (i in 1:length(birds)){
  print(birds[i])
}
```

```
## [1] "robin"
## [1] "woodpecker"
## [1] "blue jay"
## [1] "sparrow"
```

```
radius <- c(1.3, 2.1, 3.5)
areas <- vector(mode = "numeric", length = length(radius))
for ( i in 1:length(radius)){
  areas[i] <- pi * radius[i] ^ 2
}
areas
```

```
## [1] 5.309292 13.854424 38.484510
```

```
lengths = c(1.1, 2.2, 1.6)
widths = c(3.5, 2.4, 2.8)
areas <- vector(length = length(lengths), mode = "numeric")
for (i in 1:length(areas)) {
  areas[i] <- lengths[i] * widths[i]
}
areas
```

```
## [1] 3.85 5.28 4.48
```

#Size Estimates By Name Loop

```
dinosaur_lengths <- read.csv("../raw-data/dinosaur_lengths.csv")
head(dinosaur_lengths)
```

```
##      species lengths
## 1 Stegosauria 18.52588
## 2 Ankylosauria 16.43598
## 3 Ankylosauria 23.73421
## 4 Sauropoda 23.93411
## 5 Ankylosauria 21.68718
## 6 Ankylosauria 21.38363
```

```

mass_from_length <- function(lengths, species){
  mass <- a * length^b
  if (name == "Stegosauria") {
    a <- 10.95
    b <- 2.64
  } else if (name == "Theropoda") {
    a <- 0.73
    b <- 3.63
  } else if (name == "Sauropoda") {
    a <- 214.44
    b <- 1.46
  } else {
    a <- 25.37
    b <- 2.49
  }
  return(mass)
}

```

```

library(dplyr)

dinosaur_lengths <- read.csv("../raw-data/dinosaur_lengths.csv")
head(dinosaur_lengths)
dinosaur_lengths %>%
  rowwise() %>%
  mutate(masses = mass_from_length(lengths, species))

mass_from_length <- function(lengths, species){
  if (species == "Stegosauria") {
    a <- 10.95
    b <- 2.64
  } else if (species == "Theropoda") {
    a <- 0.73
    b <- 3.63
  } else if (species == "Sauropoda") {
    a <- 214.44
    b <- 1.46
  } else {
    a <- 25.37
    b <- 2.49
  }
  mass <- a * length ^ b
  return(mass)
}

library(dplyr)

lengths <- dinosaur_lengths$lengths
lengths
species <- dinosaur_lengths$species
species

```

```
dino_masses <- vector(length = length(lengths), mode = "numeric")

for (i in 1:length(species)){
  dino_masses[i] <- mass_from_length(lengths[i], species[i])
}
```

```
library(dplyr)
```

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

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

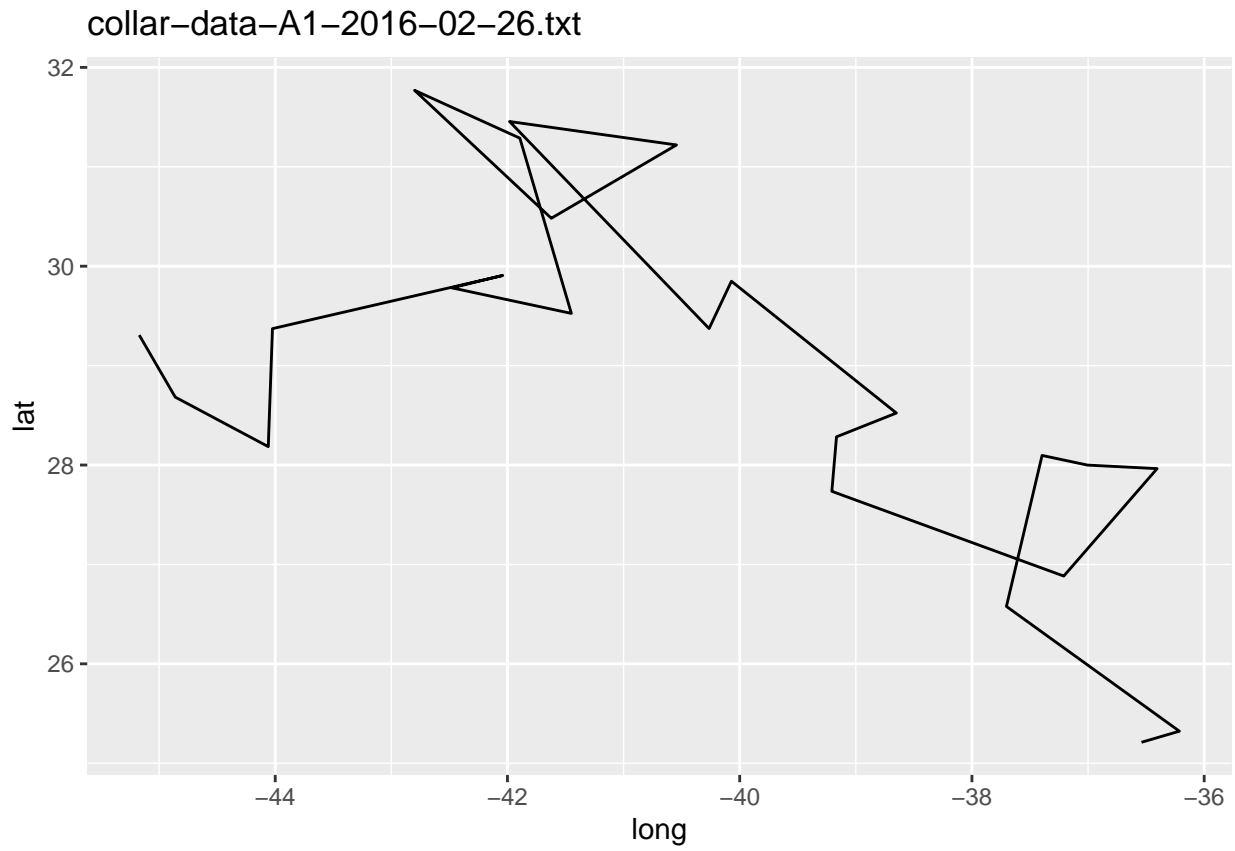
## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union
```

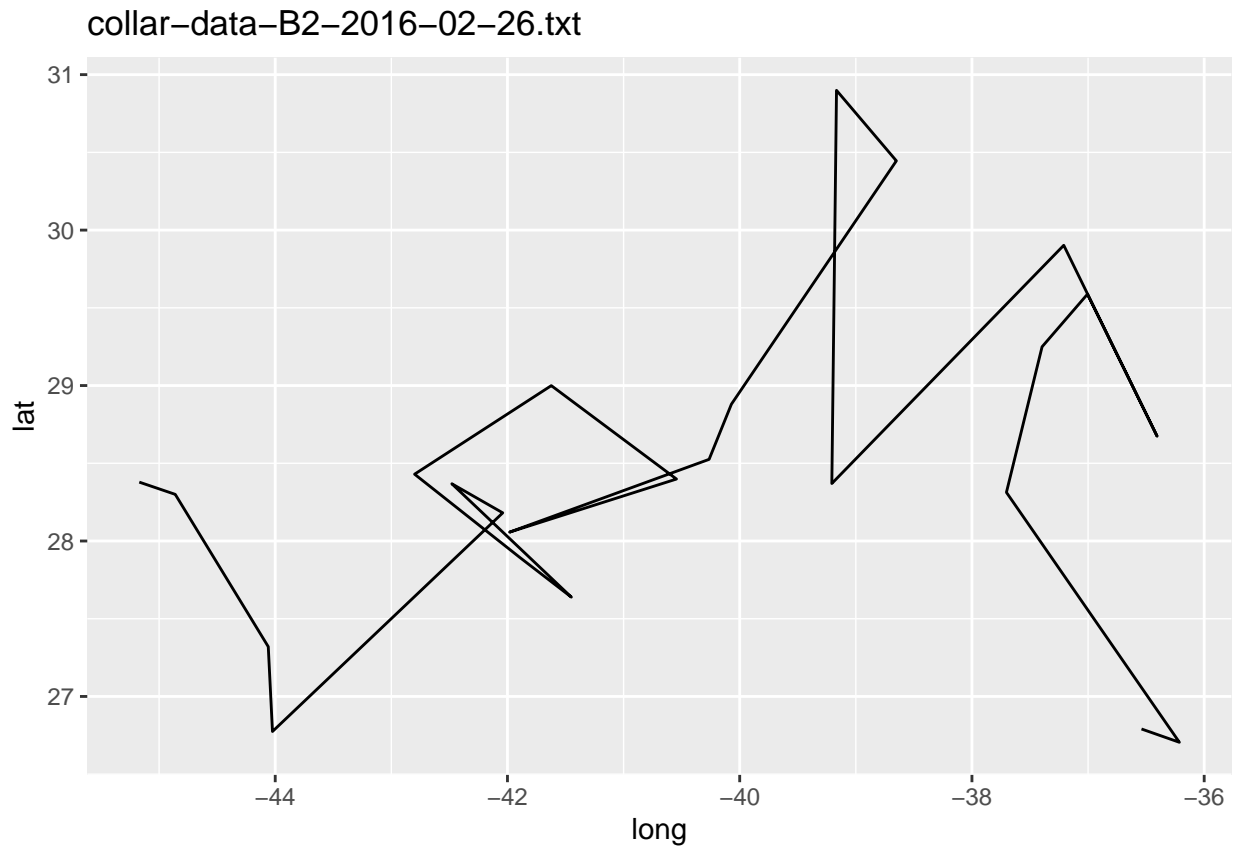
```
library(ggplot2)
download.file("http://www.datacarpentry.org/semester-biology/data/individual_collar_data.zip", "collar.zip")
unzip("collar.zip")
collar_data_files <- list.files(pattern = "collar-")
collar_data_files
```

```
## [1] "collar-data-A1-2016-02-26.txt" "collar-data-B2-2016-02-26.txt"
## [3] "collar-data-C3-2016-02-26.txt" "collar-data-D4-2016-02-26.txt"
## [5] "collar-data-E5-2016-02-26.txt" "collar-data-F6-2016-02-26.txt"
## [7] "collar-data-G7-2016-02-26.txt" "collar-data-H8-2016-02-26.txt"
## [9] "collar-data-I9-2016-02-26.txt" "collar-data-J10-2016-02-26.txt"
```

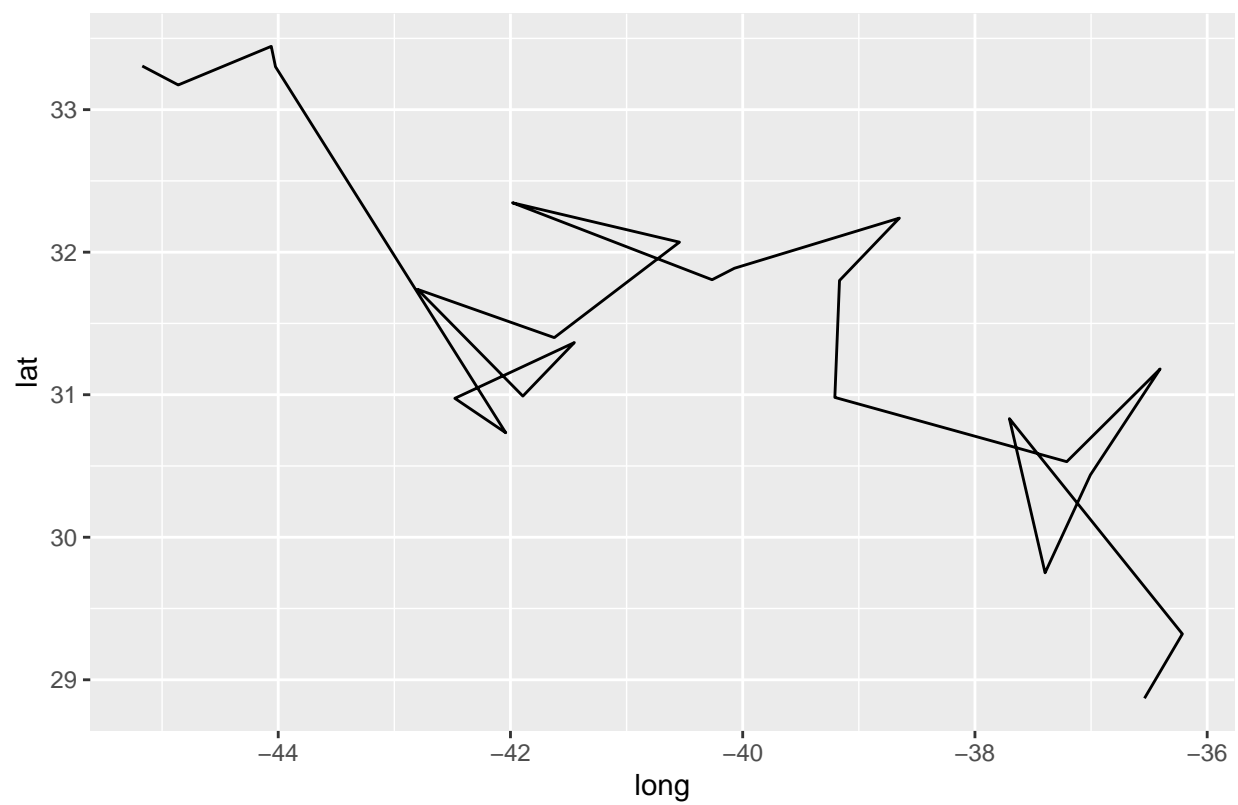
```
min_results <- vector(mode = "integer", length(collar_data_files))
max_results <- vector(mode = "integer", length(collar_data_files))
```

```
for(i in 1:length(collar_data_files)){
  filename <- collar_data_files[i]
  data <- read.csv(filename)
  data %>%
    ggplot(aes(x = long, y = lat )) +
    labs(title = filename) +
  geom_path() -> plots
  print(plots)
  min_results[i] <- min(data$lat)
  max_results[i] <- max(data$lat)
}
```

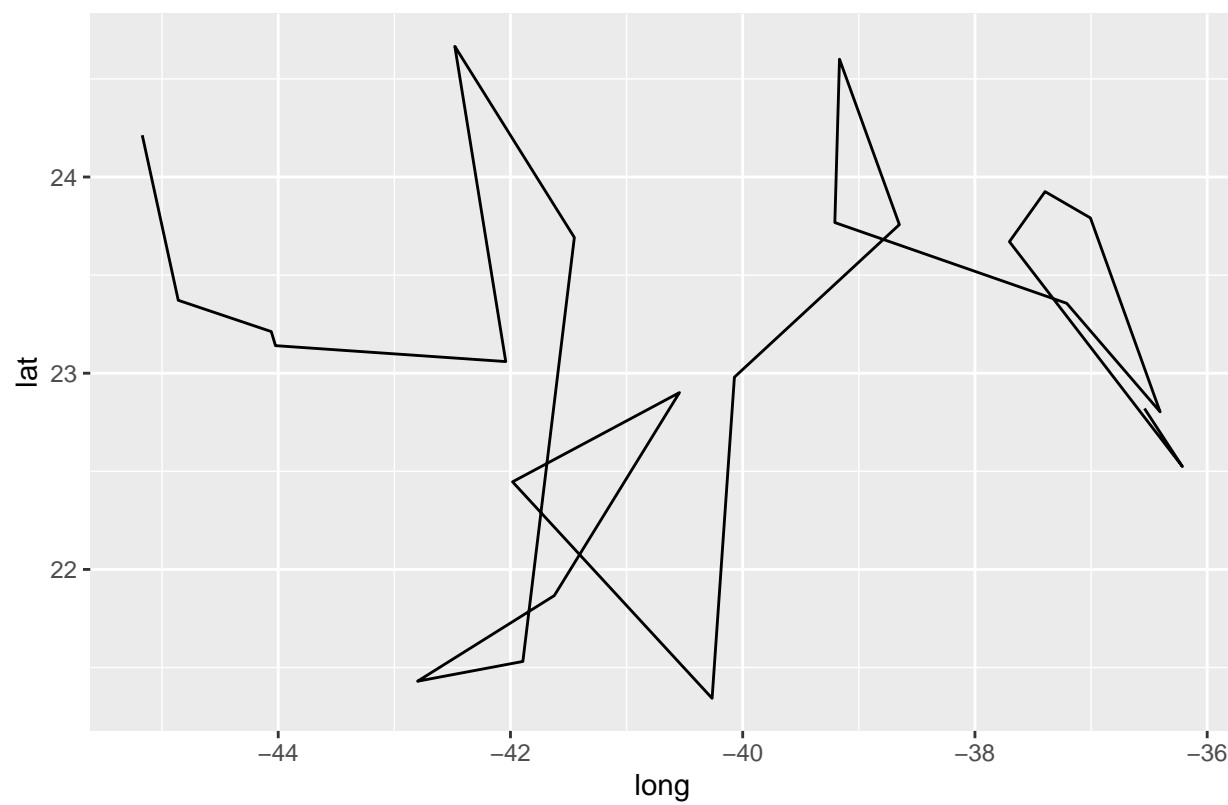




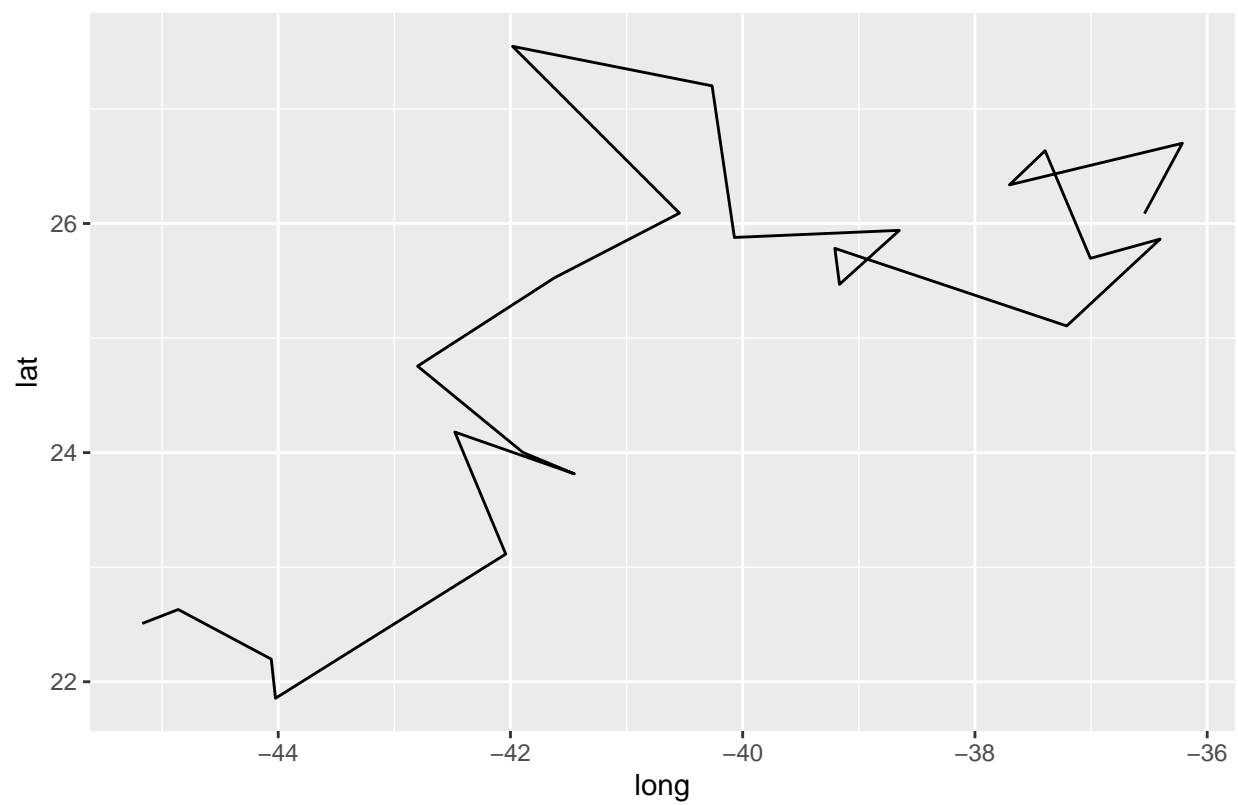
collar-data-C3-2016-02-26.txt



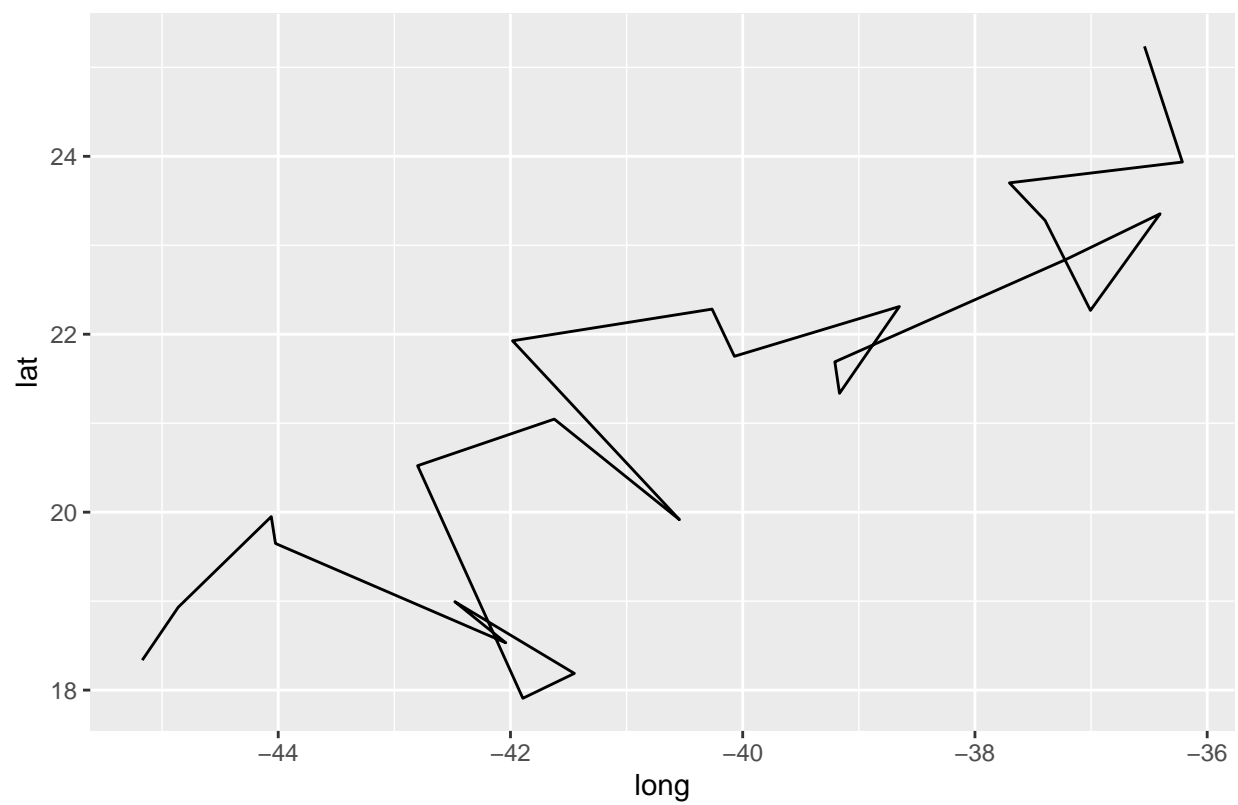
collar-data-D4-2016-02-26.txt



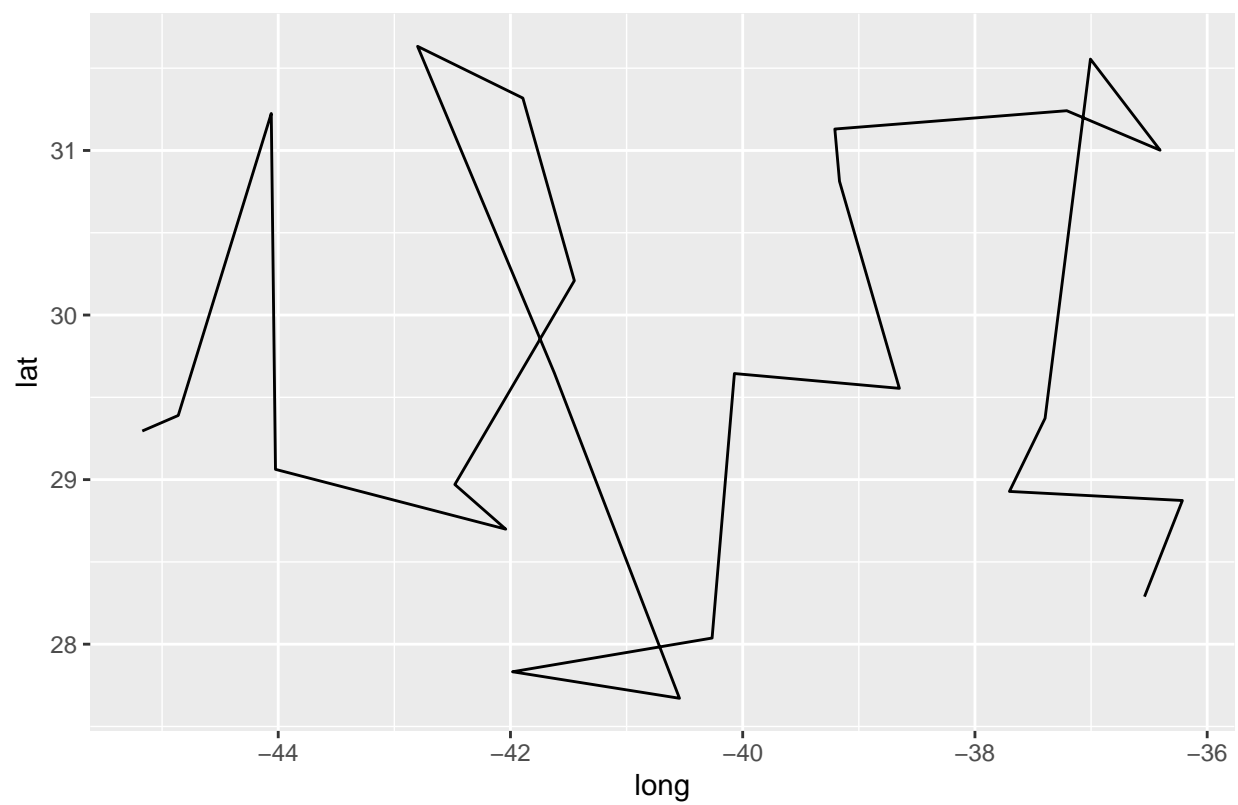
collar-data-E5-2016-02-26.txt



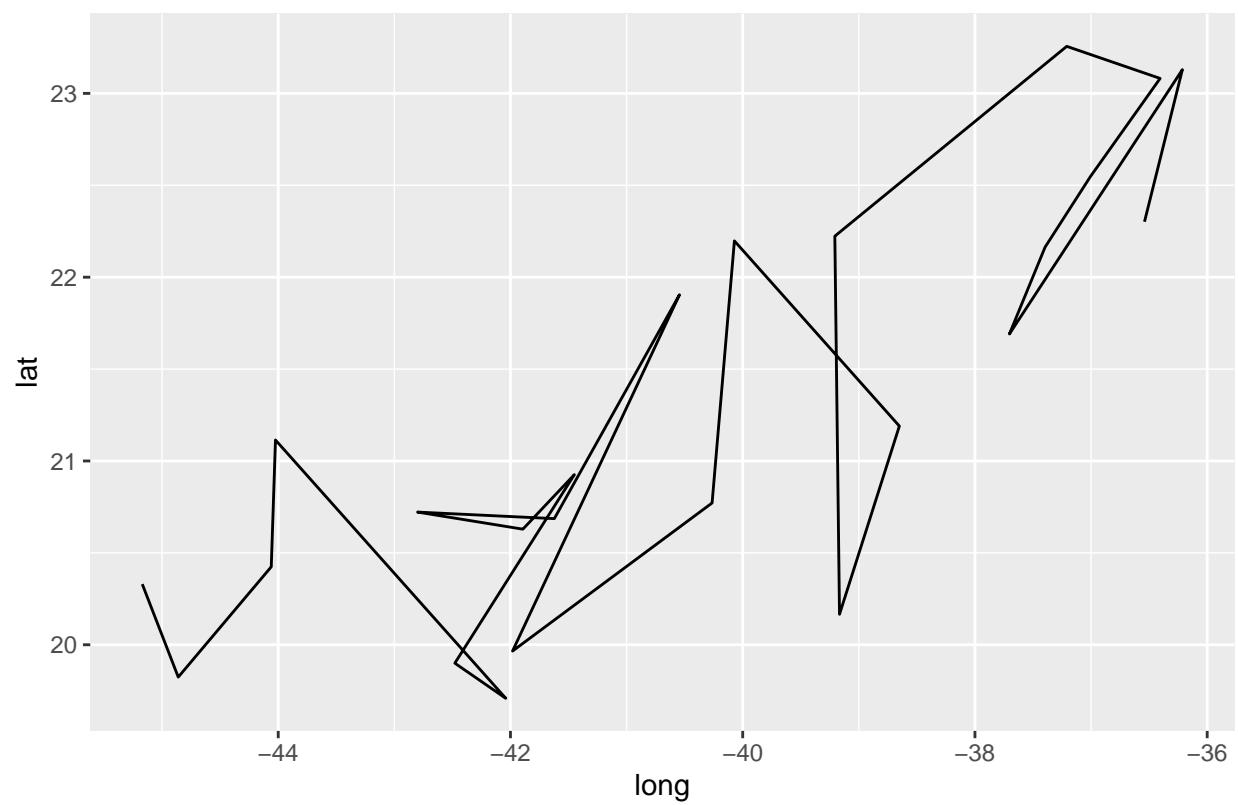
collar-data-F6-2016-02-26.txt

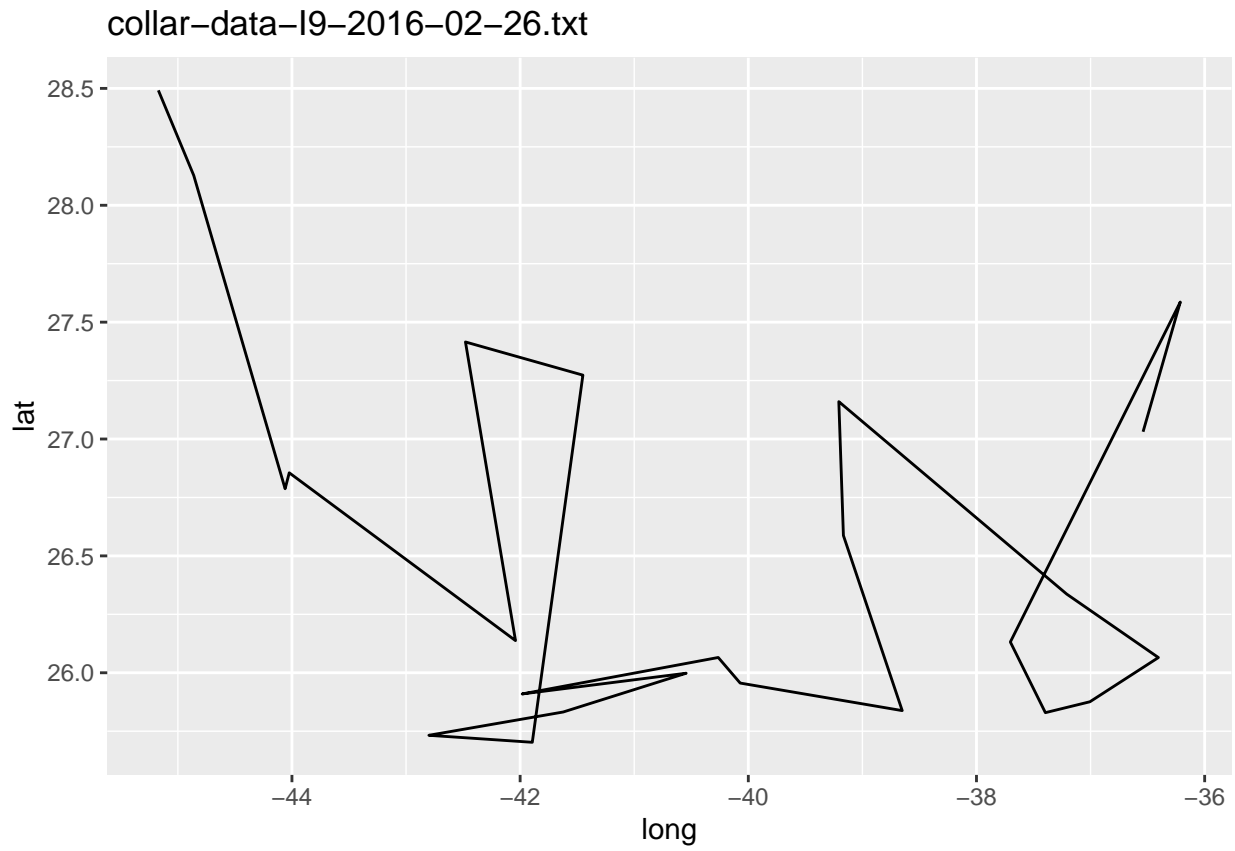


collar-data-G7-2016-02-26.txt

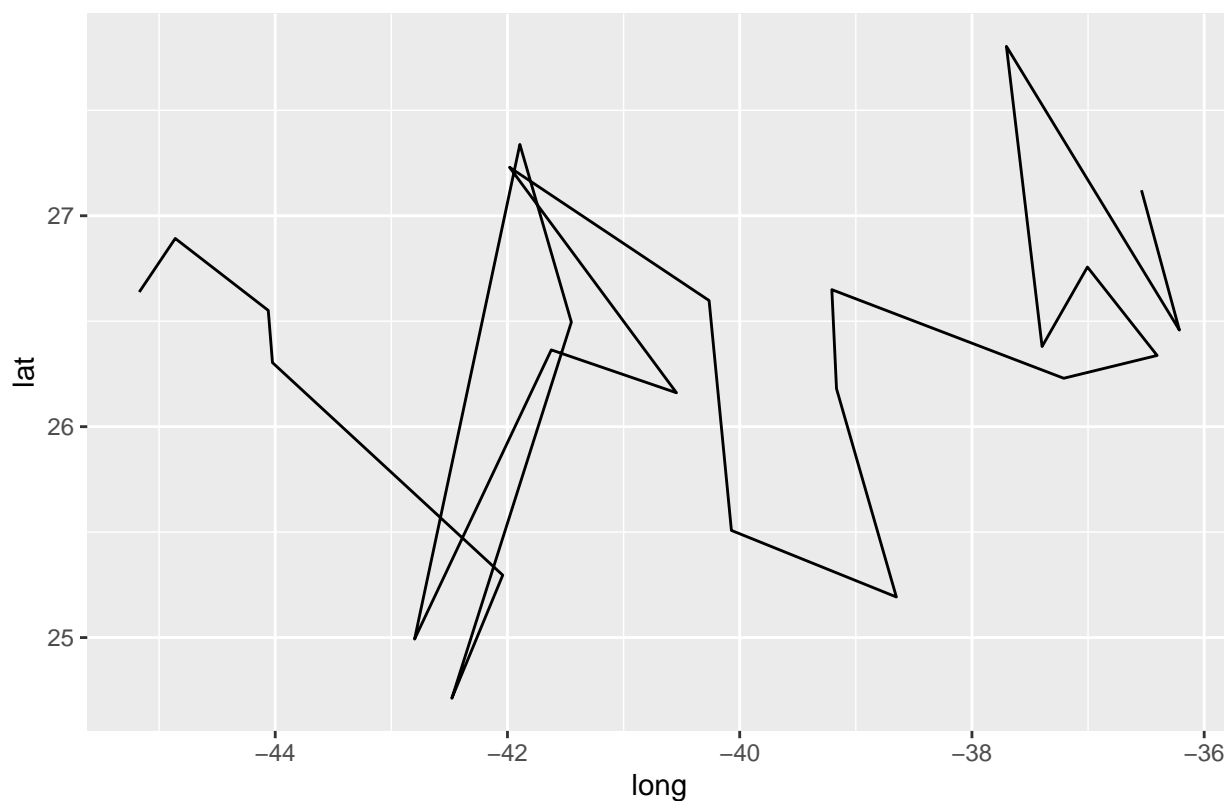


collar-data-H8-2016-02-26.txt





collar-data-J10-2016-02-26.txt



```
min_max_data <- data.frame(collar_data_files, min_results, max_results)
```

```
min_max_data
```

##	collar_data_files	min_results	max_results
## 1	collar-data-A1-2016-02-26.txt	25.21080	31.76912
## 2	collar-data-B2-2016-02-26.txt	26.70509	30.89907
## 3	collar-data-C3-2016-02-26.txt	28.86998	33.44421
## 4	collar-data-D4-2016-02-26.txt	21.34315	24.66598
## 5	collar-data-E5-2016-02-26.txt	21.85565	27.54663
## 6	collar-data-F6-2016-02-26.txt	17.90788	25.23623
## 7	collar-data-G7-2016-02-26.txt	27.67120	31.63272
## 8	collar-data-H8-2016-02-26.txt	19.70875	23.25601
## 9	collar-data-I9-2016-02-26.txt	25.70252	28.49172
## 10	collar-data-J10-2016-02-26.txt	24.71200	27.80325