

Week 13 Assignment

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2025-11-18

```
## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
## v dplyr     1.1.4     v readr     2.1.5
## vforcats   1.0.0     v stringr   1.5.2
## v ggplot2   4.0.0     v tibble    3.3.0
## v lubridate 1.9.4     v tidyv     1.3.1
## v purrr    1.1.0
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()   masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

1. For Loop Basics (30 pts)

1a.

```
## [1] 3
## [1] 6
## [1] 9
## [1] 12
## [1] 15
```

1b.

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

1c.

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

1d.

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

1e.

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

2. Size Estimates by Name (30 pts)

```
## Rows: 500 Columns: 2
## -- Column specification -----
## Delimiter: ","
```

```

## chr (1): species
## dbl (1): lengths
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.

2a.

## [1] 24341.68 27017.90 67453.38 22114.19 53884.76 52026.34

2b.

## # A tibble: 6 x 3
##   species      lengths   masses
##   <chr>        <dbl>    <dbl>
## 1 Stegosauria     18.5  24342.
## 2 Ankylosauria    16.4  27018.
## 3 Ankylosauria    23.7  67453.
## 4 Sauropoda       23.9  22114.
## 5 Ankylosauria    21.7  53885.
## 6 Ankylosauria    21.4  52026.

2c.

## # A tibble: 4 x 2
##   species      avg_mass
##   <chr>        <dbl>
## 1 Ankylosauria  46819.
## 2 Sauropoda     16104.
## 3 Stegosauria   31924.
## 4 Theropoda     45572.

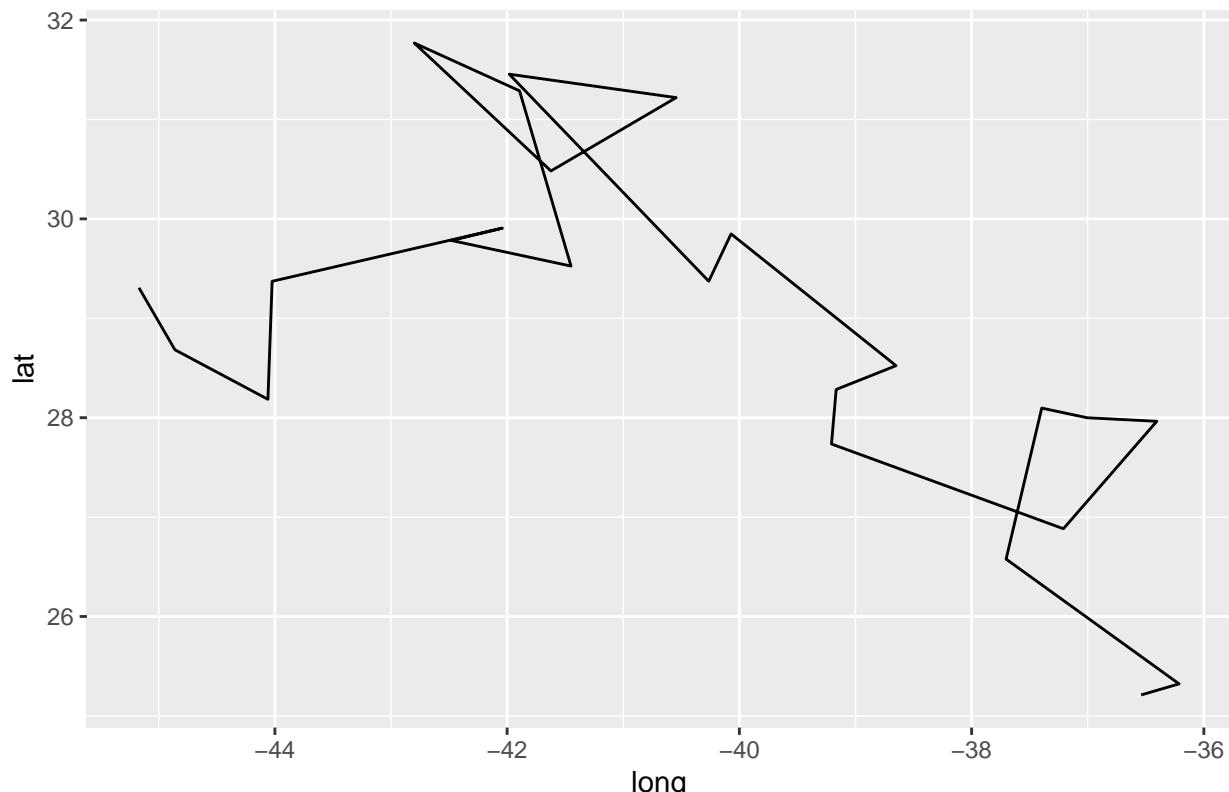
```

3. Multi-file Analysis (40 pts)

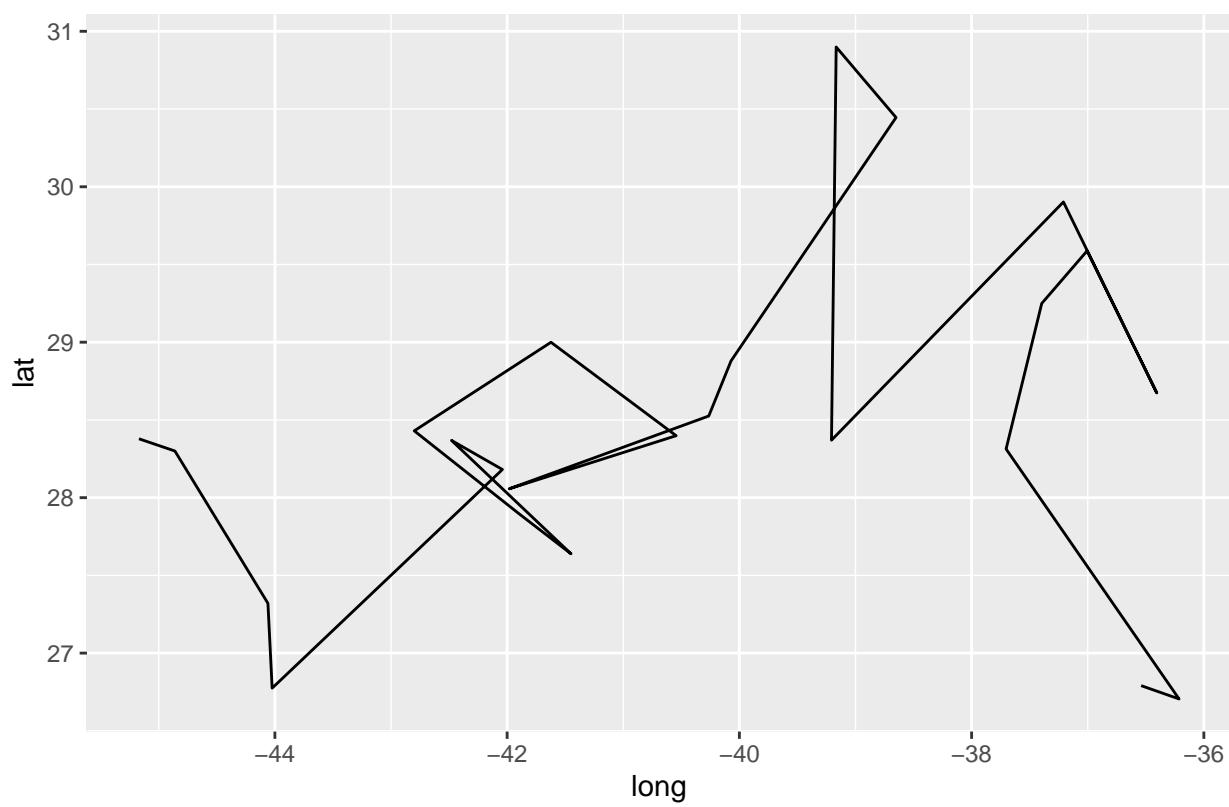
3a.

```
## [1] "3a"
```

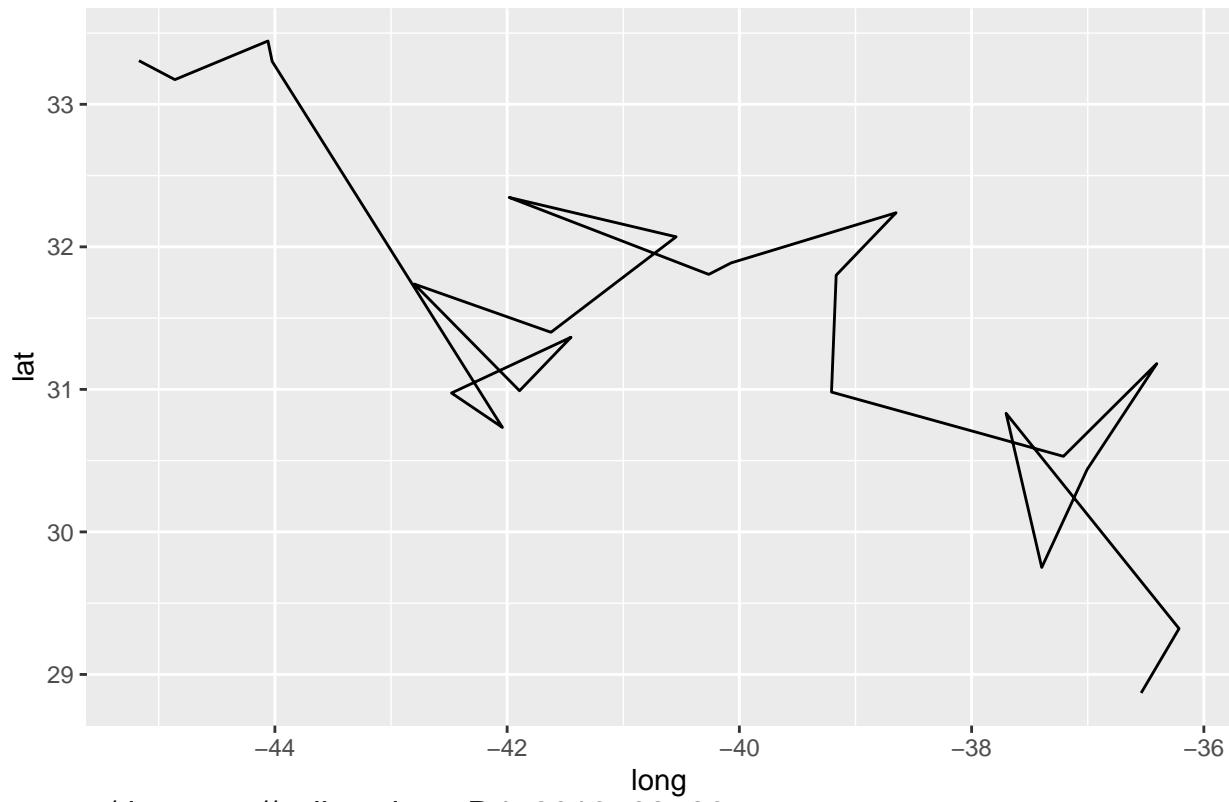
..../data_raw//collar-data-A1-2016-02-26.txt



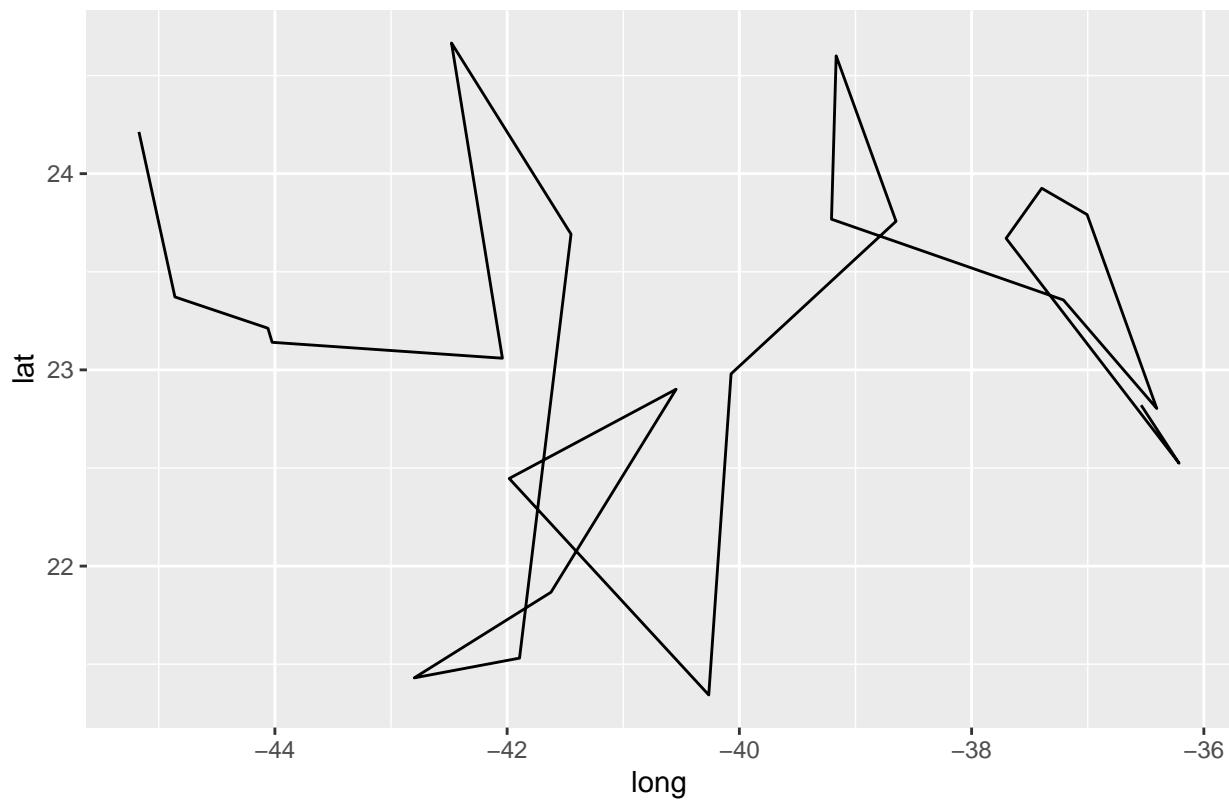
..../data_raw//collar-data-B2-2016-02-26.txt



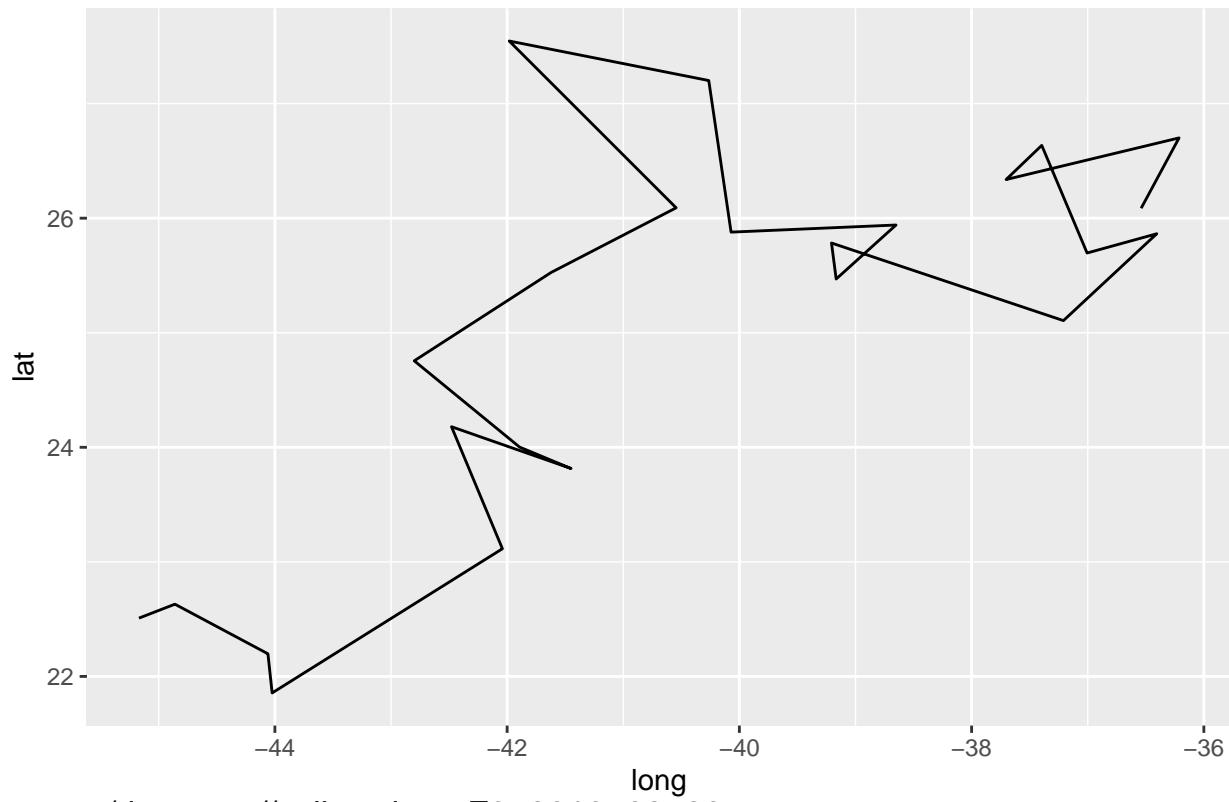
..../data_raw//collar-data-C3-2016-02-26.txt



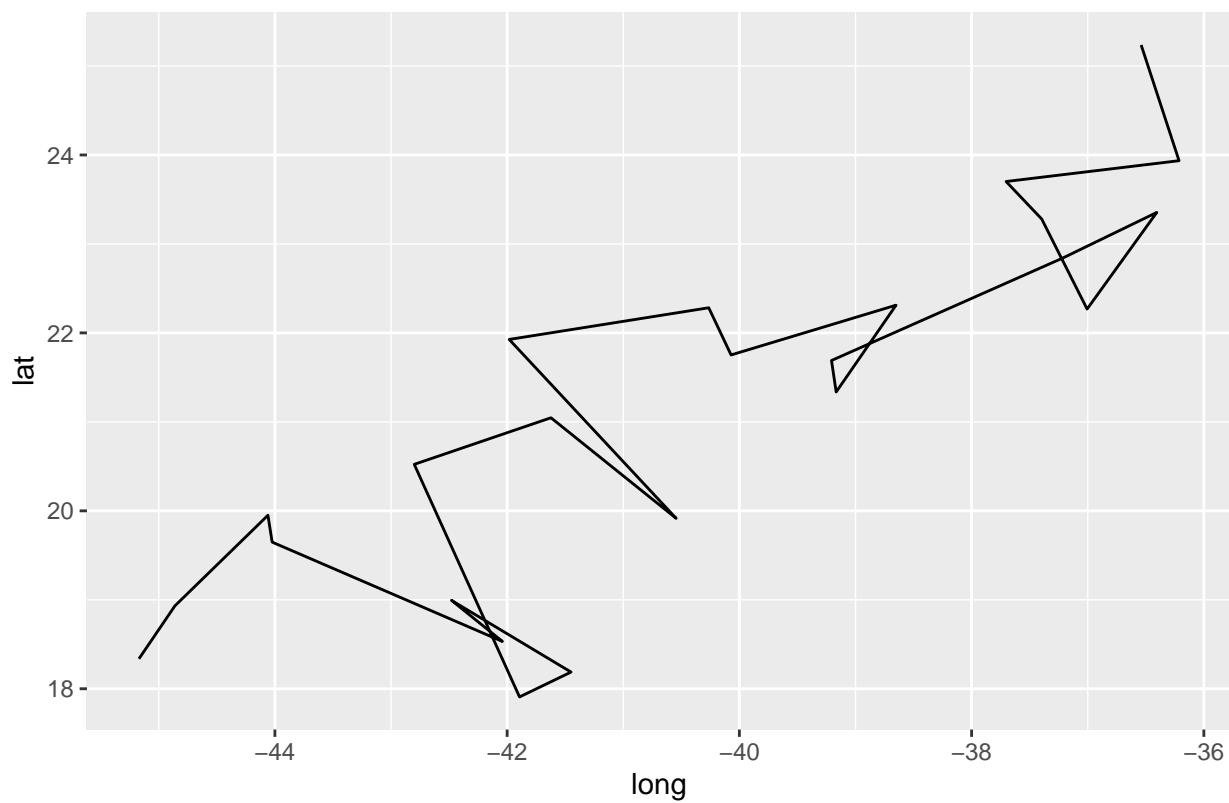
..../data_raw//collar-data-D4-2016-02-26.txt



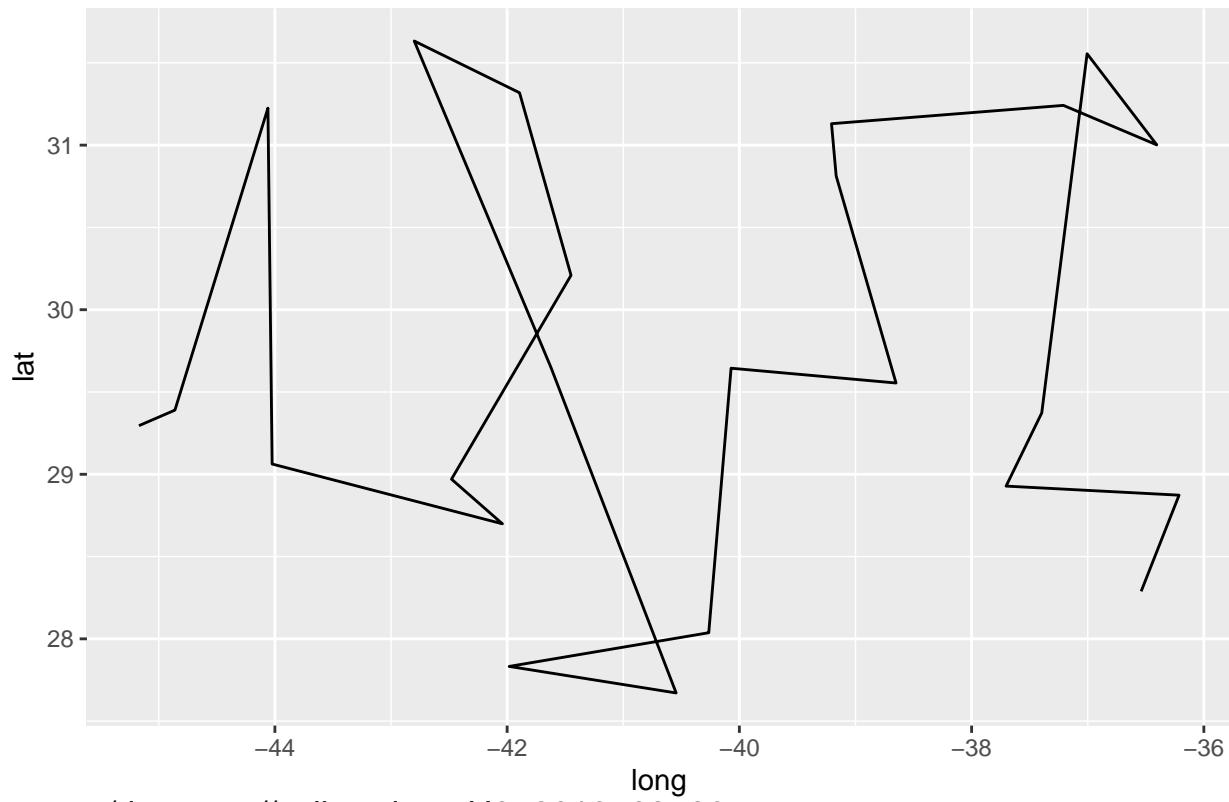
..../data_raw//collar-data-E5-2016-02-26.txt



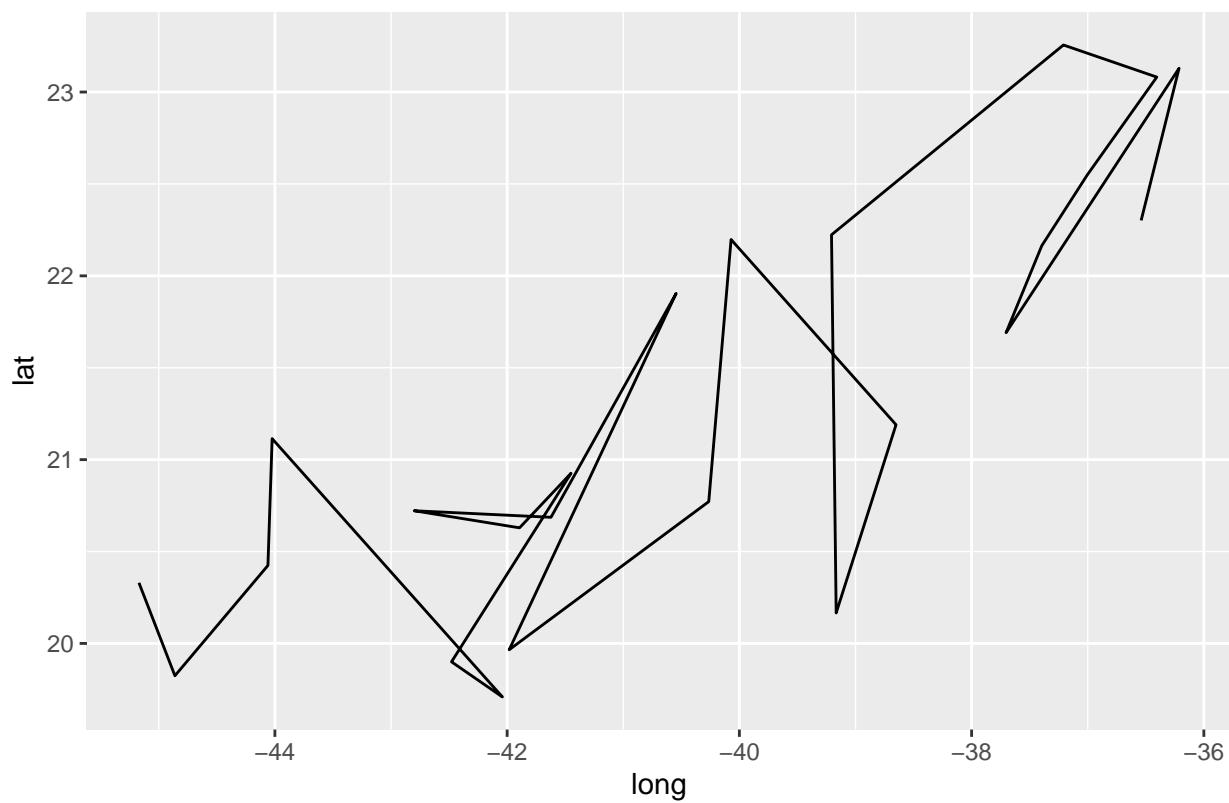
..../data_raw//collar-data-F6-2016-02-26.txt



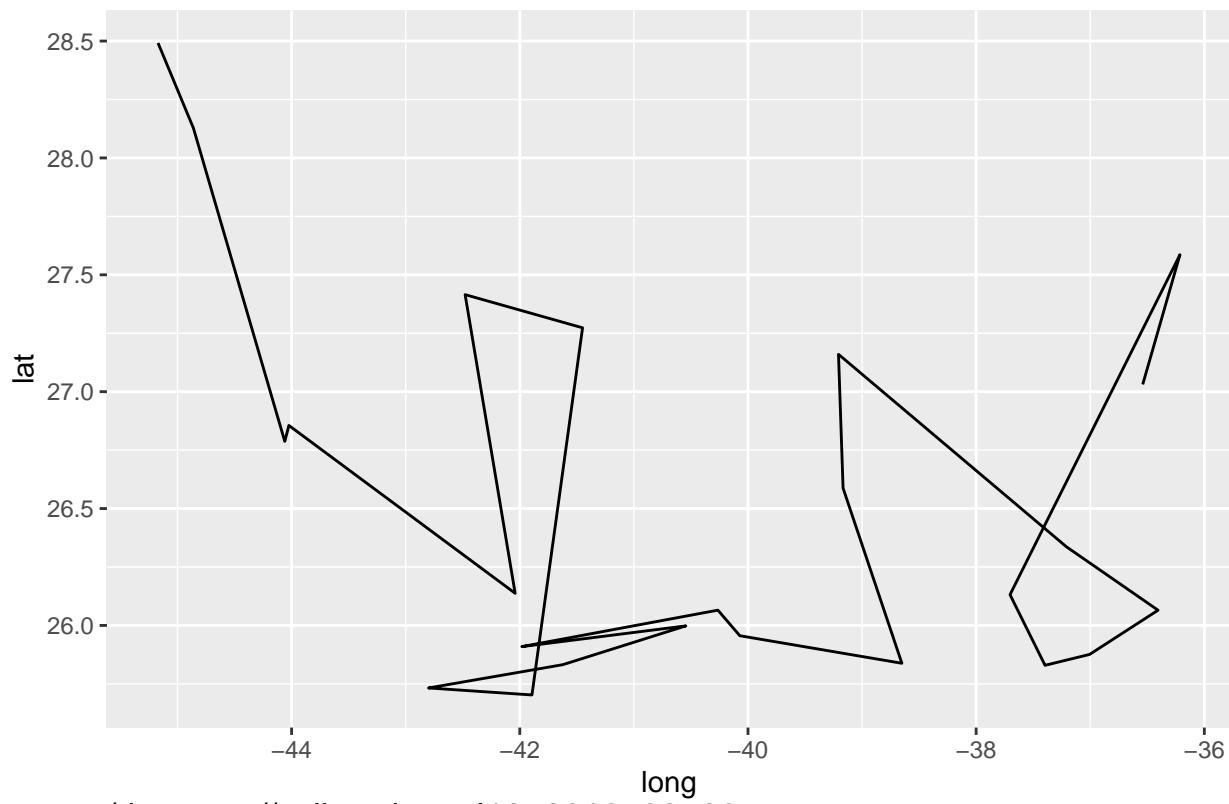
..../data_raw//collar-data-G7-2016-02-26.txt



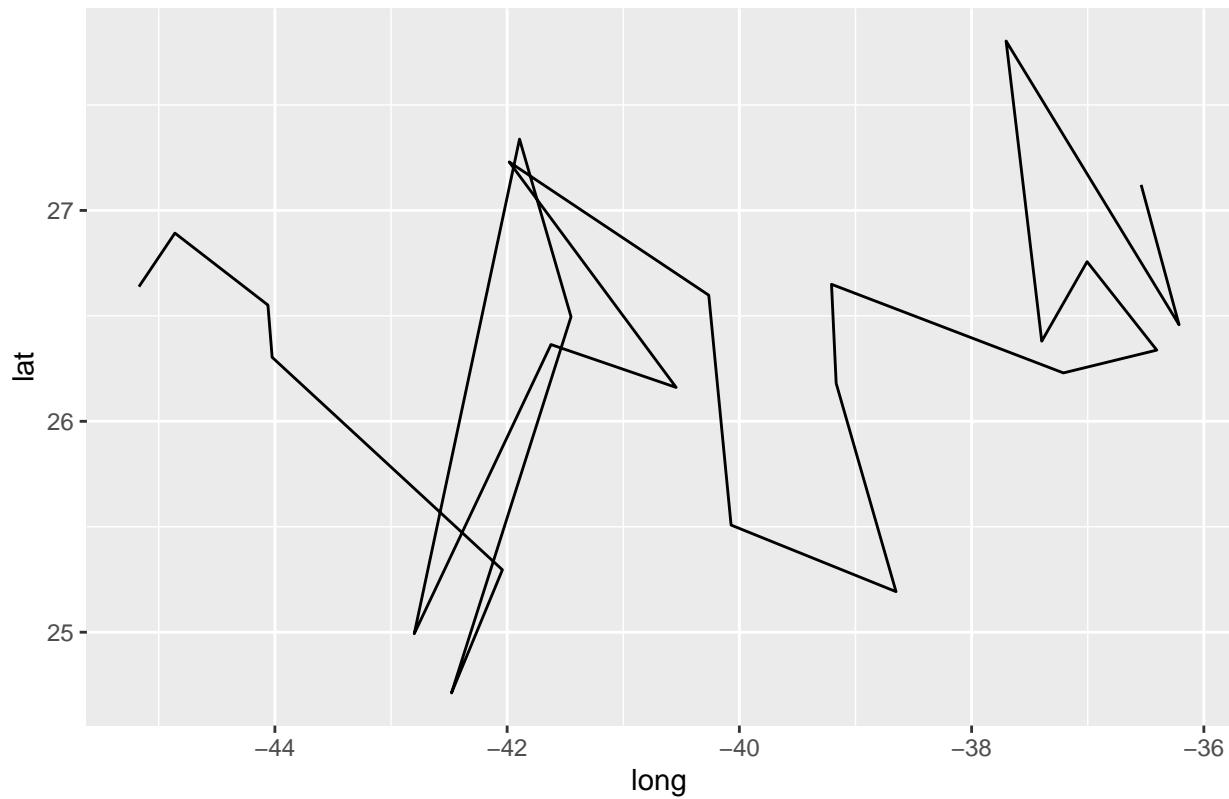
..../data_raw//collar-data-H8-2016-02-26.txt

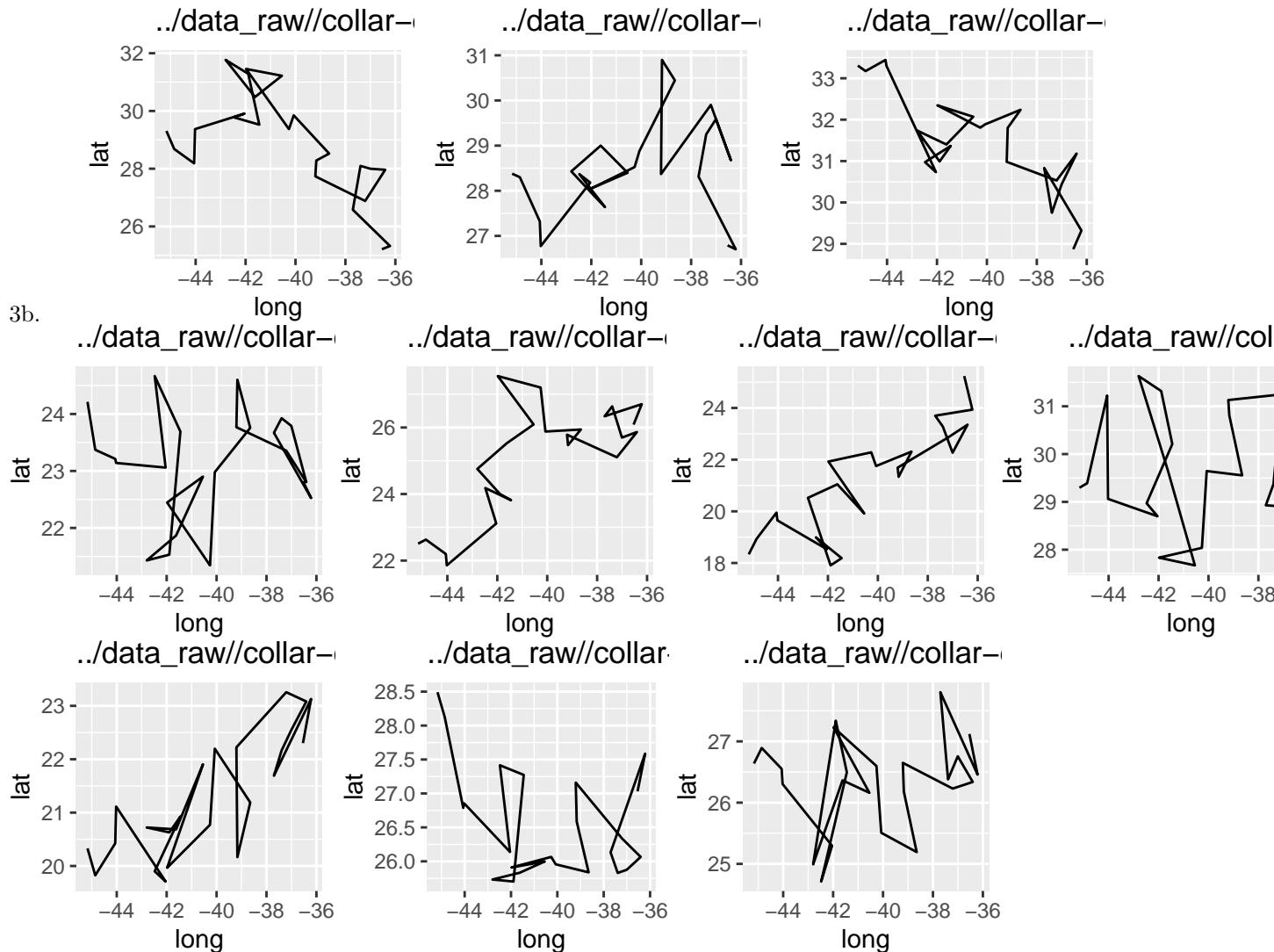


./data_raw//collar-data-I9-2016-02-26.txt



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





```
##                                     file_name max_lat min_lat observations
## 1  ./data_raw//collar-data-A1-2016-02-26.txt 31.76912 25.21080      24
## 2  ./data_raw//collar-data-B2-2016-02-26.txt 30.89907 26.70509      24
## 3  ./data_raw//collar-data-C3-2016-02-26.txt 33.44421 28.86998      24
## 4  ./data_raw//collar-data-D4-2016-02-26.txt 24.66598 21.34315      24
## 5  ./data_raw//collar-data-E5-2016-02-26.txt 27.54663 21.85565      24
## 6  ./data_raw//collar-data-F6-2016-02-26.txt 25.23623 17.90788      24
## 7  ./data_raw//collar-data-G7-2016-02-26.txt 31.63272 27.67120      24
## 8  ./data_raw//collar-data-H8-2016-02-26.txt 23.25601 19.70875      24
## 9  ./data_raw//collar-data-I9-2016-02-26.txt 28.49172 25.70252      24
## 10 ./data_raw//collar-data-J10-2016-02-26.txt 27.80325 24.71200      24
```

4. DNA or RNA (20 points)

4a.

```
## [1] "DNA"
## [1] "RNA"
## [1] "UNKNOWN"
```

4b.

```
## [1] "DNA"  
## [1] "RNA"  
## [1] "UNKNOWN"  
## [1] "RNA"  
## [1] "RNA"
```

4c.

```
##      type  
## 1    DNA  
## 2    RNA  
## 3 UNKNOWN  
## 4    RNA  
## 5    RNA  
  
##                                         sequence  
## 1 ttgaatgccttacaactgatcattacacaggcgcatgaagaaaaataactgtgaaccaatgcaggcg  
## 2 gauuuauuccccacaaaggagugggauuaggagcugcaucauuacaagagcagaauguuucaaaugcau  
## 3 gaaagcaagaaaaggcaggcgaggagggaaagaaggggggaaacc  
## 4 guuuuccuacaguauuuugaugagaaugagagcaccugaucagguggauaaggaagaugaagacu  
## 5 gauaaggaagaugaagacuuucagggaaucuaauaaaaugcacuccaugaauggauucauguauuggaaucagccggguc
```

4d.

```
##      type  
## 1    DNA  
## 2    RNA  
## 3 UNKNOWN  
## 4    RNA  
## 5    RNA  
  
##                                         sequence  
## 1 ttgaatgccttacaactgatcattacacaggcgcatgaagaaaaataactgtgaaccaatgcaggcg  
## 2 gauuuauuccccacaaaggagugggauuaggagcugcaucauuacaagagcagaauguuucaaaugcau  
## 3 gaaagcaagaaaaggcaggcgaggagggaaagaaggggggaaacc  
## 4 guuuuccuacaguauuuugaugagaaugagagcaccugaucagguggauaaggaagaugaagacu  
## 5 gauaaggaagaugaagacuuucagggaaucuaauaaaaugcacuccaugaauggauucauguauuggaaucagccggguc
```

4e. OPTIONAL

```
## ttgaatgccttacaactgatcattacacaggcgcatgaagaaaaataactgtgaaccaatgcaggcg  
## "DNA"  
## gauuuauuccccacaaaggagugggauuaggagcugcaucauuacaagagcagaauguuucaaaugcau  
## "RNA"  
## gaaagcaagaaaaggcaggcgaggagggaaagaaggggggaaacc  
## "UNKNOWN"  
## guuuuccuacaguauuuugaugagaaugagagcaccugaucagguggauaaggaagaugaagacu  
## "RNA"  
## gauaaggaagaugaagacuuucagggaaucuaauaaaaugcacuccaugaauggauucauguauuggaaucagccggguc  
## "RNA"
```

4f. OPTIONAL

```
## # A tibble: 5 x 2  
## # Rowwise:  
##   type    sequences  
##   <chr>   <chr>  
## 1 DNA     ttgaatgccttacaactgatcattacacaggcgcatgaagaaaaataactgtgaaccaatgcaggcg
```

```
## 2 RNA      gauuaauuccccacaaaggagugggauuaggagcugcaucauuacaagagcagaauguuucaaugcau  
## 3 UNKNOWN  gaaaggcaaaaaggcaggcgaggaagggaagaagggggggaaacc  
## 4 RNA      guuuccuacaguauuugaugagaaugagagcaccugaucagguggauaaggaaagaugacu  
## 5 RNA      gauaagggaagagacuuucaggaauaaaaugcacuccauggauucauguaugggaa~
```