

# Week 13 Assignment

Ellen Bledsoe

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```
## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
## v dplyr      1.1.4      v readr      2.1.5
## v forcats    1.0.0      v stringr   1.5.1
## v ggplot2    3.5.2      v tibble    3.2.1
## v lubridate  1.9.4      v tidyr     1.3.1
## v purrr      1.0.4
## -- 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.

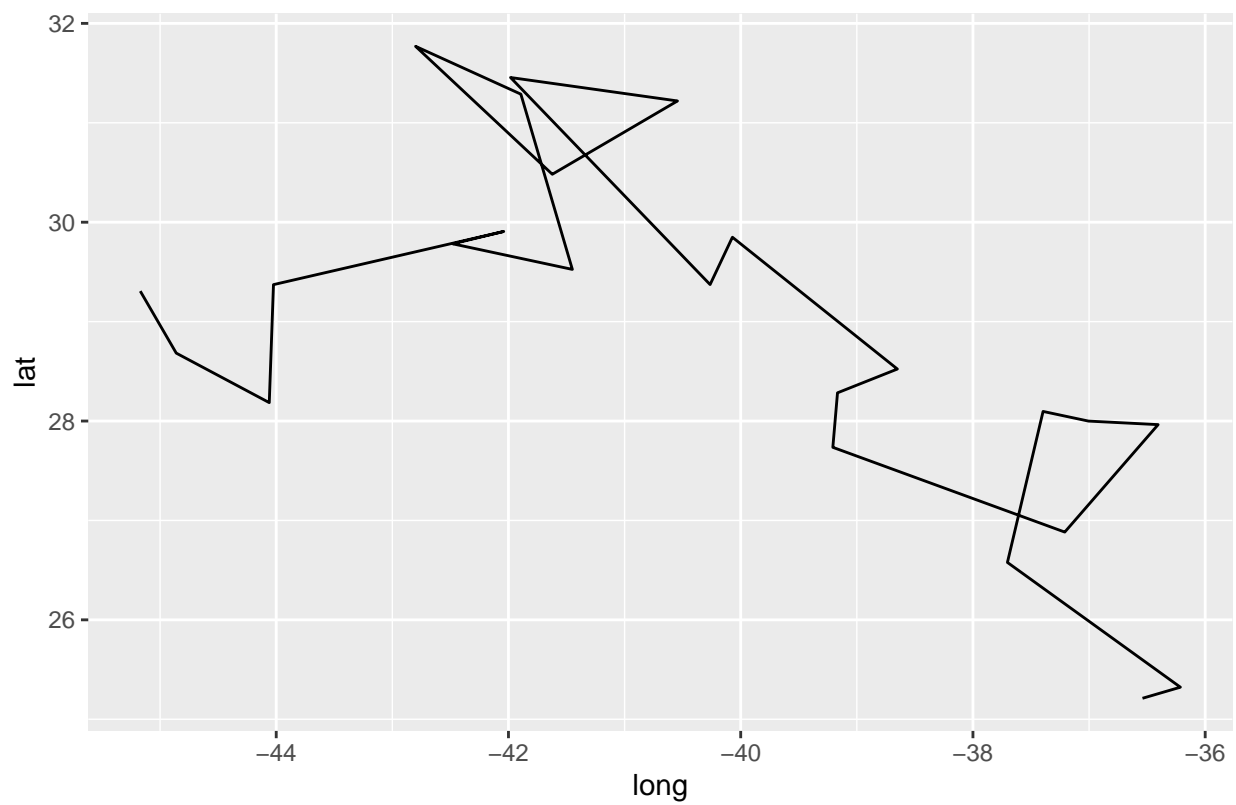
```
## # A tibble: 4 x 2
##   species      avg_mass
##   <chr>         <dbl>
## 1 Ankylosauria  46819.
## 2 Sauropoda    16104.
## 3 Stegosauria  31924.
## 4 Theropoda    45572.
```

### 3. Multi-file Analysis (40 pts)

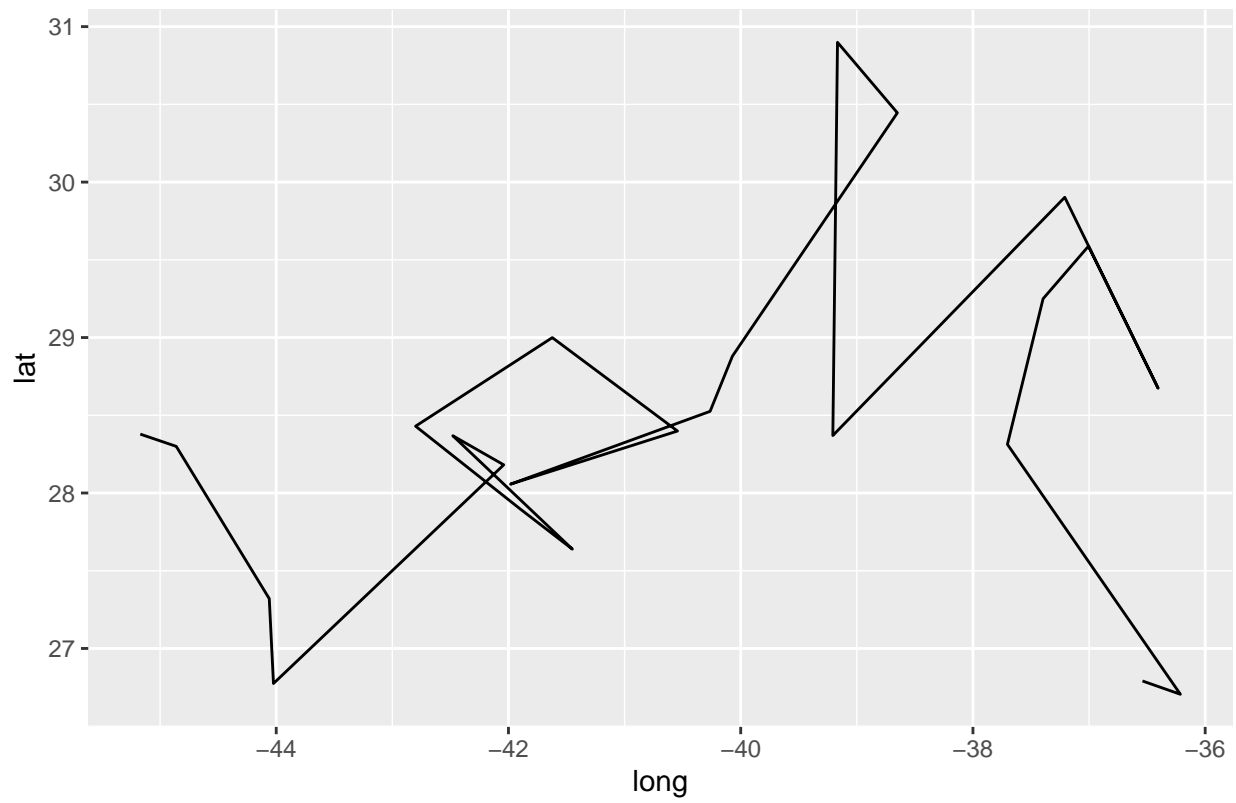
3a.

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

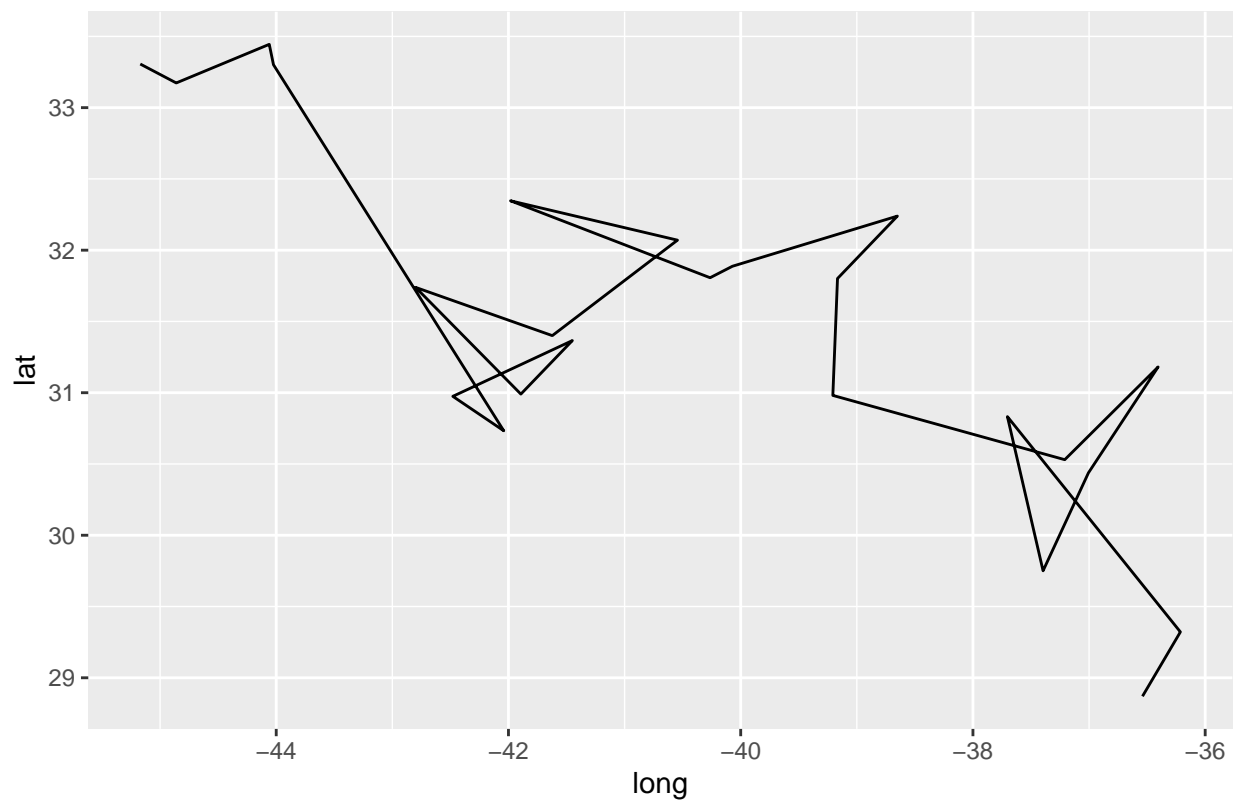
../data\_raw//collar-data-A1-2016-02-26.txt



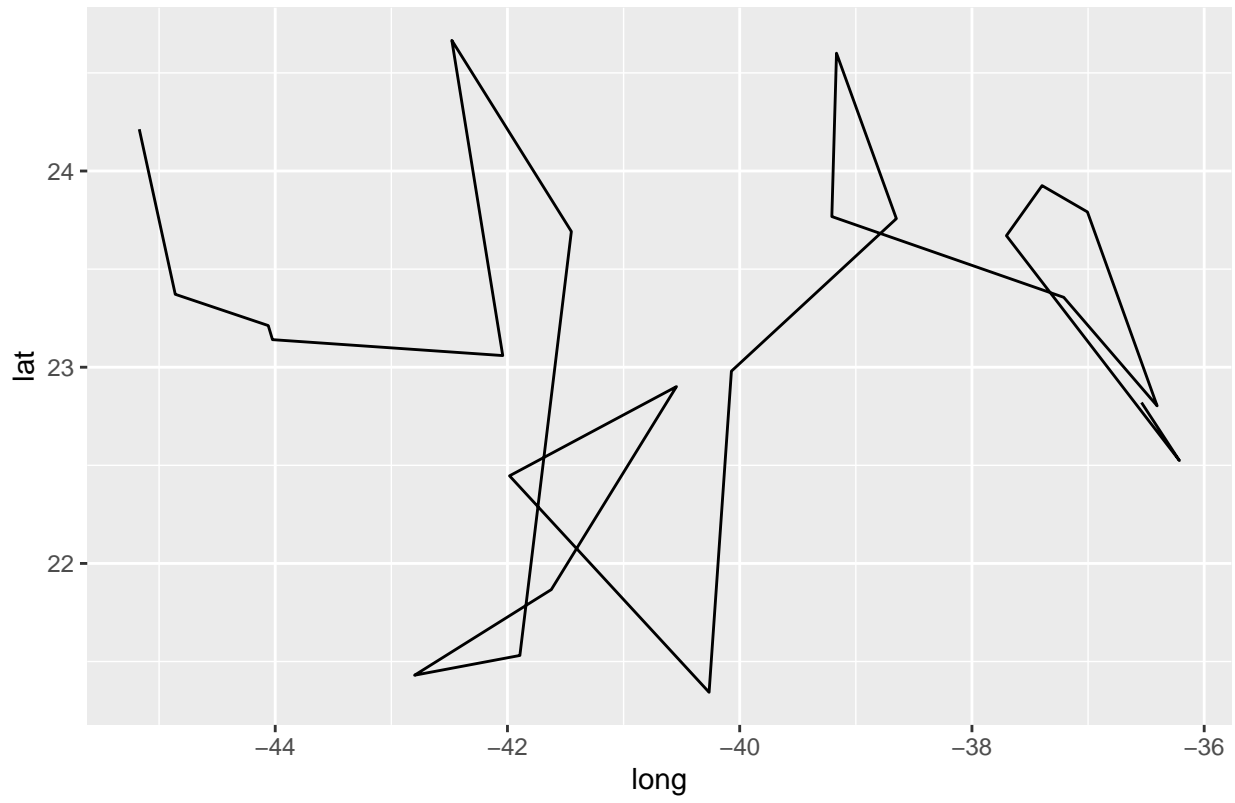
../data\_raw//collar-data-B2-2016-02-26.txt



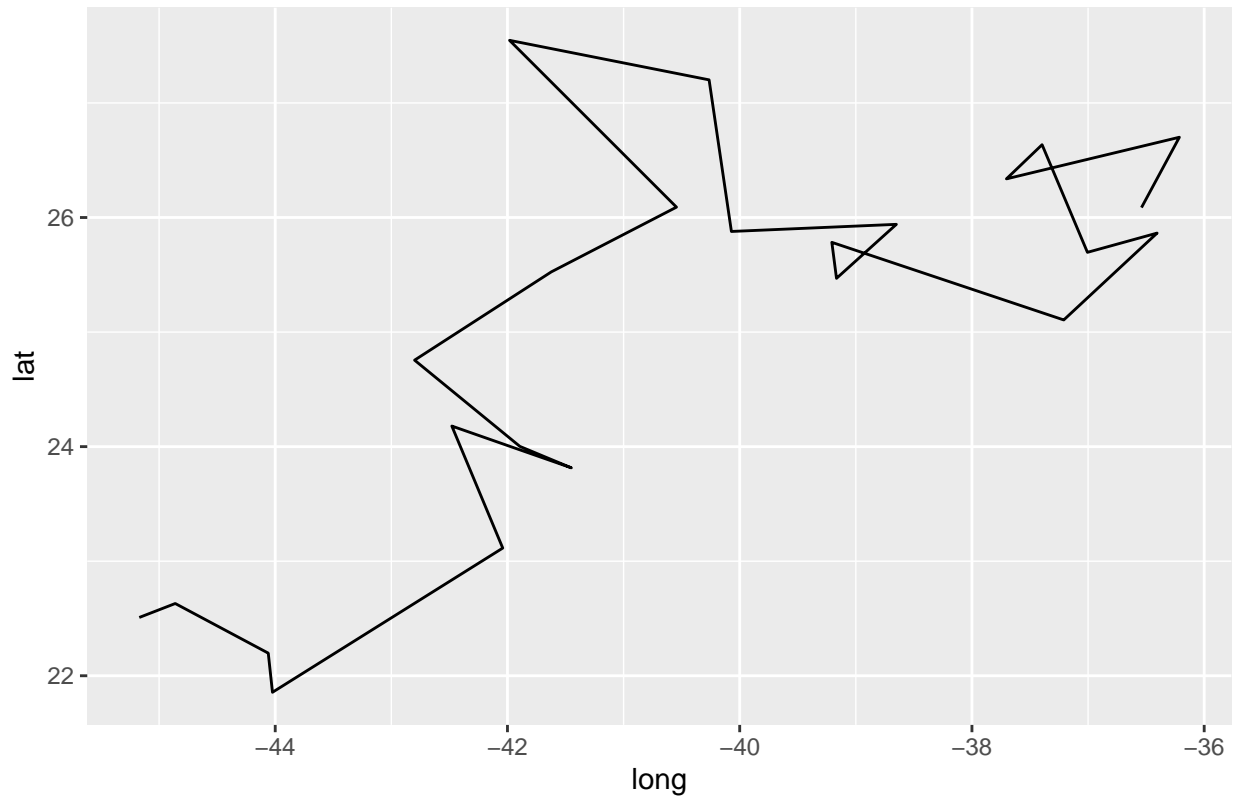
../data\_raw//collar-data-C3-2016-02-26.txt



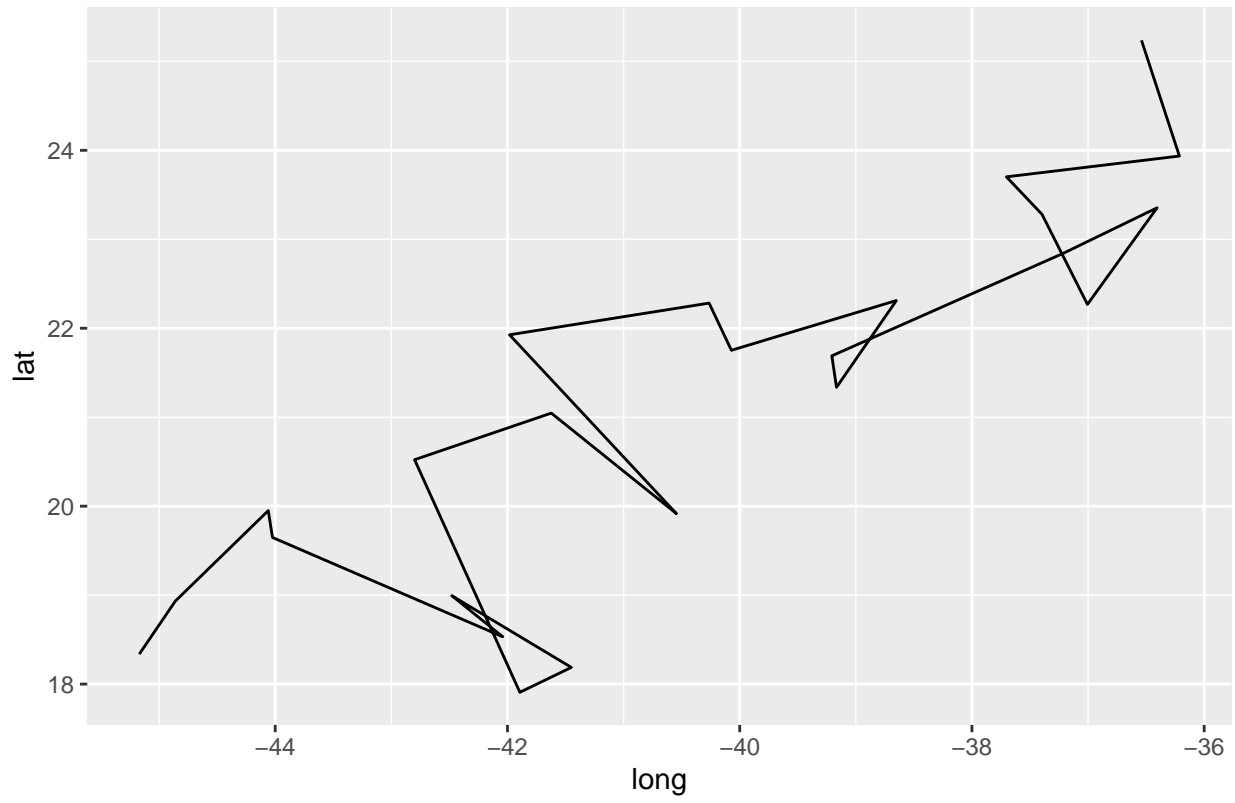
../data\_raw//collar-data-D4-2016-02-26.txt



../data\_raw//collar-data-E5-2016-02-26.txt

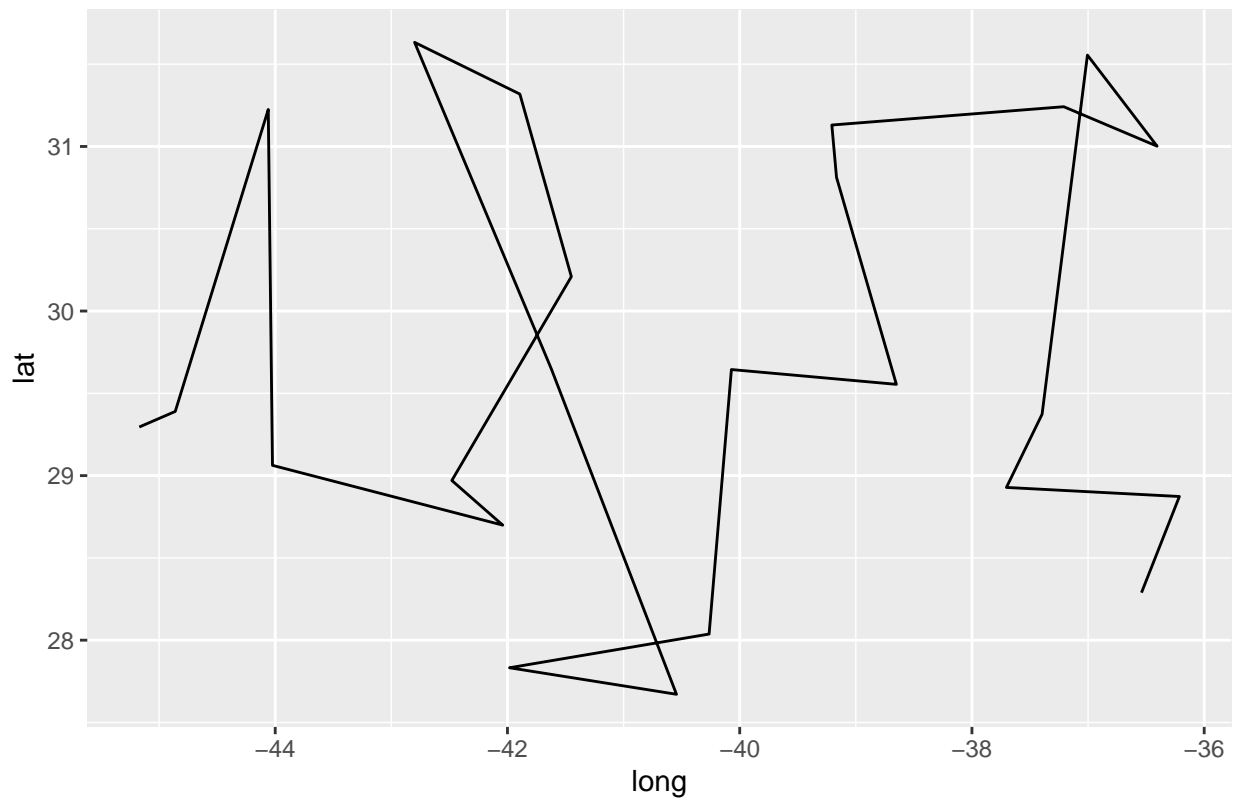


../data\_raw//collar-data-F6-2016-02-26.txt

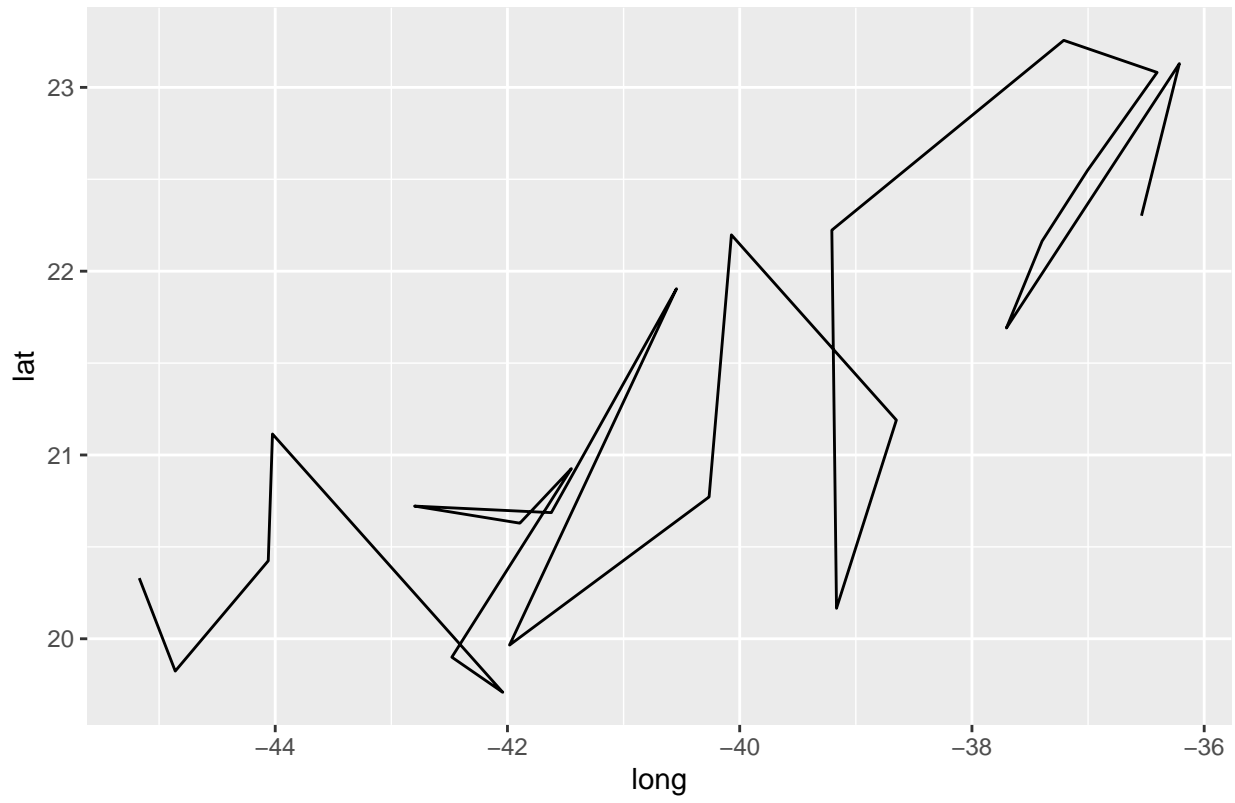




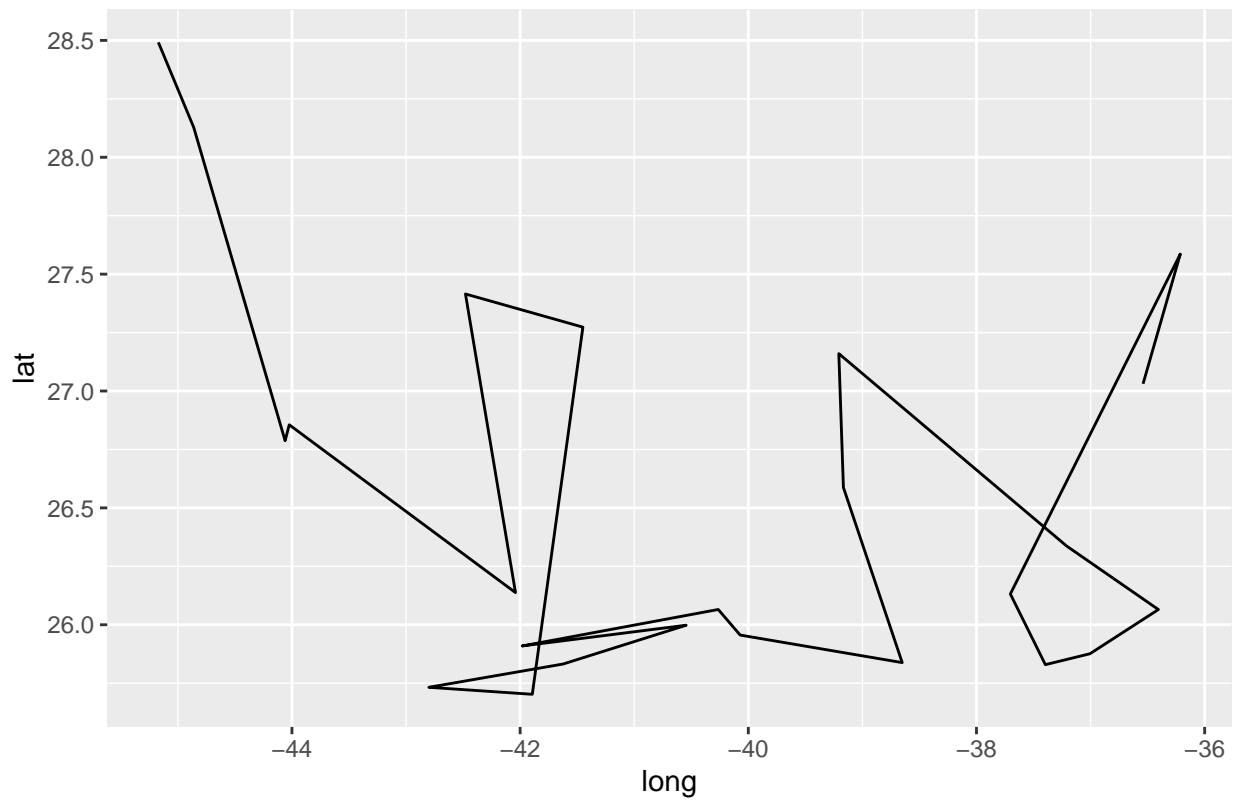
../data\_raw//collar-data-G7-2016-02-26.txt



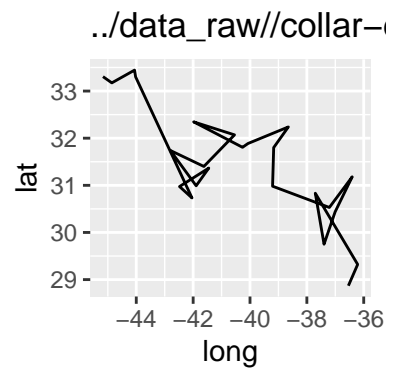
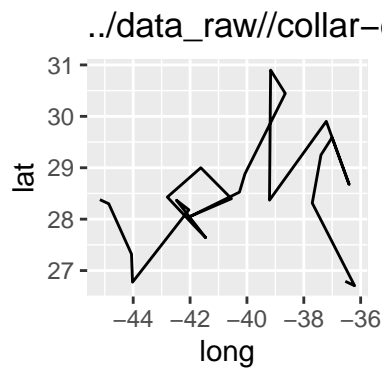
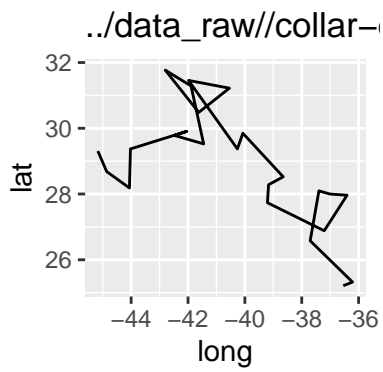
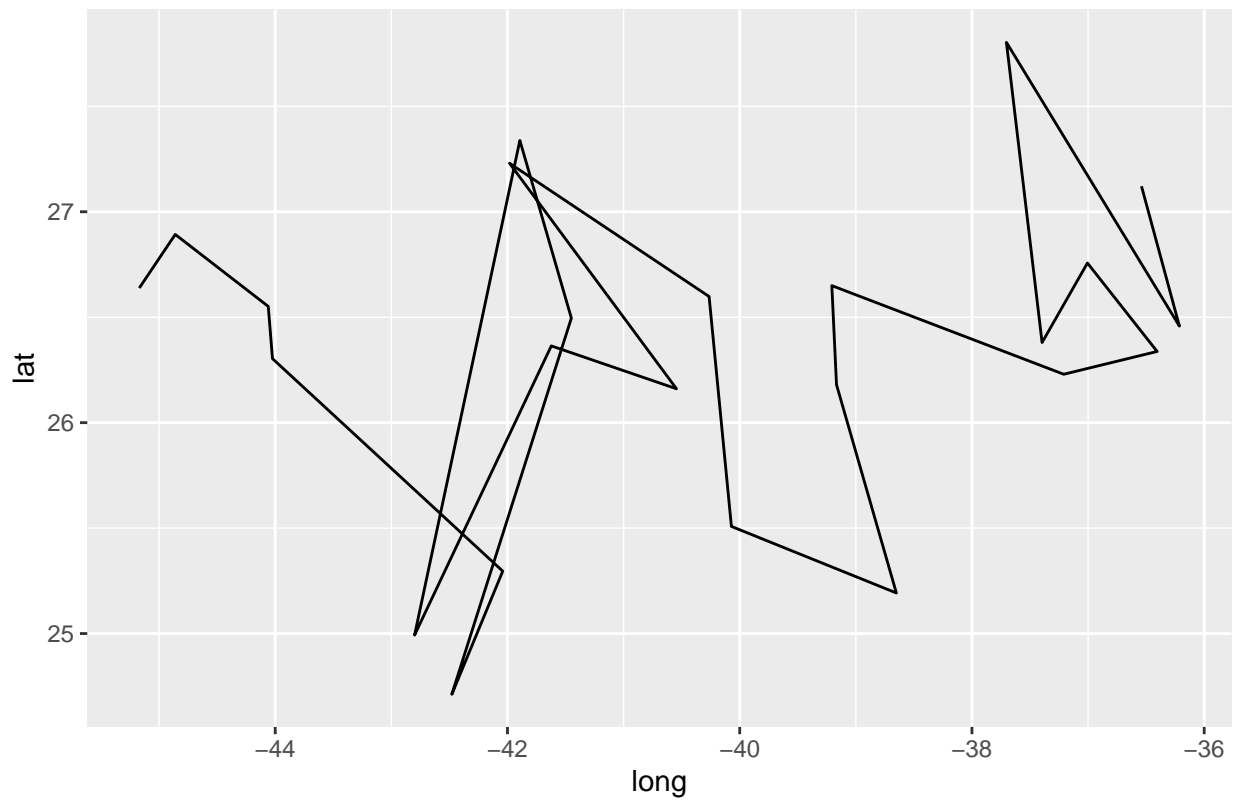
../data\_raw//collar-data-H8-2016-02-26.txt



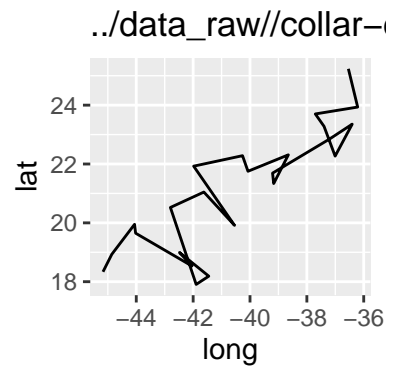
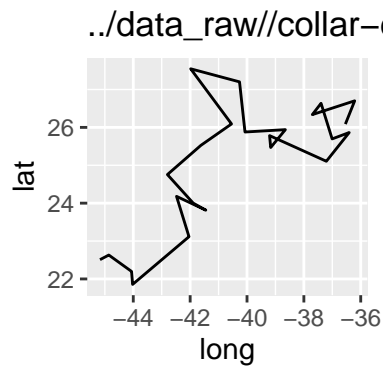
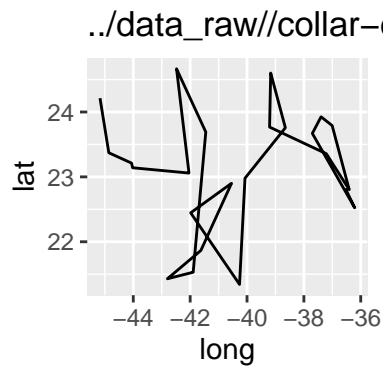
../data\_raw//collar-data-l9-2016-02-26.txt

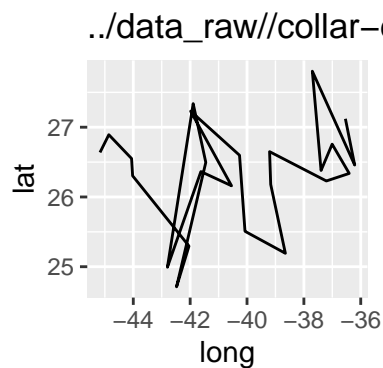
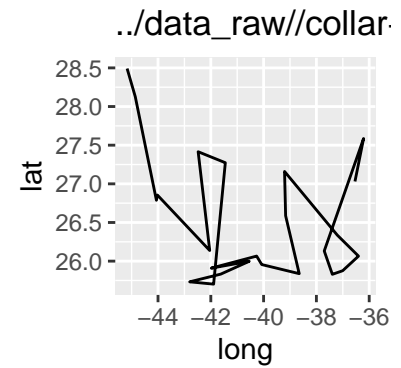
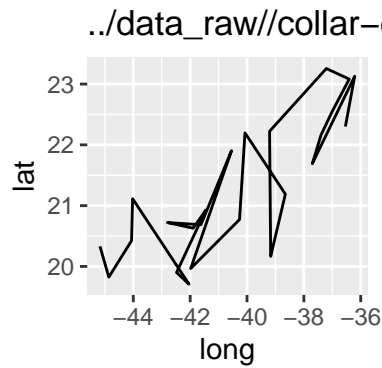
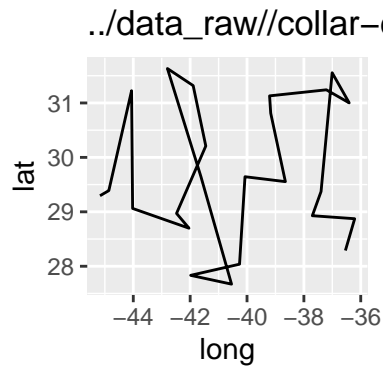


../data\_raw//collar-data-J10-2016-02-26.txt



3b.





##	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)

4b.

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

4c.

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

4d.

```
## Warning: `as.tibble()` was deprecated in tibble 2.0.0.
```

```
## i Please use `as_tibble()` instead.
## i The signature and semantics have changed, see `?as_tibble`.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.

## # A tibble: 5 x 2
##   type      sequence
##   <chr>    <chr>
## 1 DNA      ttgaatgccttacaactgatcattacacaggcggcatgaagcaaaaatatactgtgaaccaatgcaggcg
## 2 RNA      gauuauuccccacaaaggagugggauuaggagcugcaucauuuacaagagcagaauuucaaaugcau
## 3 UNKNOWN  gaaagcaagaaaaggcaggcgaggaagggaagaaggggggaaacc
## 4 RNA      guuuccuacaguauuugaugagagaauagagauuuacuccuggaagauaaauuagaauuuuacaacugc~
## 5 RNA      gaaaggaagaagaagacuucaggaaucaauaaaaugcacuccaagaauaggauucauguaugggaau~
```

#### 4e. OPTIONAL

```
##                                     ttgaatgccttacaactgatcattacacaggcggcatgaagcaaaaatatactgtgaaccaatgcaggcg
##                                     "DNA
##                                     gauuauuccccacaaaggagugggauuaggagcugcaucauuuacaagagcagaauuucaaaugcau
##                                     "RNA
##                                     gaaagcaagaaaaggcaggcgaggaagggaagaaggggggaaacc
##                                     "UNKNOWN
## guuuccuacaguauuugaugagagaauagagauuuacuccuggaagauaaauuagaauuuuacaacugcaccugaucagguggauaaggaagaagaagac
##                                     "RNA
##                                     gaaaggaagaagaagacuucaggaaucaauaaaaugcacuccaagaauaggauucauguaugggaaucaagccgggu
##                                     "RNA
```

#### 4f. OPTIONAL

```
## # A tibble: 5 x 2
## # Rowwise:
##   type      sequences
##   <chr>    <chr>
## 1 DNA      ttgaatgccttacaactgatcattacacaggcggcatgaagcaaaaatatactgtgaaccaatgcaggcg
## 2 RNA      gauuauuccccacaaaggagugggauuaggagcugcaucauuuacaagagcagaauuucaaaugcau
## 3 UNKNOWN  gaaagcaagaaaaggcaggcgaggaagggaagaaggggggaaacc
## 4 RNA      guuuccuacaguauuugaugagagaauagagauuuacuccuggaagauaaauuagaauuuuacaacugc~
## 5 RNA      gaaaggaagaagaagacuucaggaaucaauaaaaugcacuccaagaauaggauucauguaugggaau~
```