

Central-place foraging red-footed boobies, *Sula sula*

ExMove

Raw tracking data

GV37501_201606_DG_RFB.csv
GV37503_201606_DG_RFB.csv
GV37734_201807_NI_RFB.csv

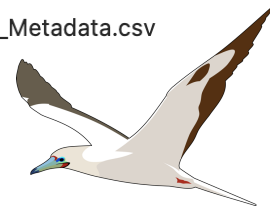
1
df_raw

Import, combine tracking files, parse dates

2
df_metadataslim

Metadata

RFB_Metadata.csv



3
Merge tracking & metadata

```
df_metamerged <- df_raw %>%  
  left_join(., df_metadataslim, by=ID_type)
```

4

Clean = remove NAs & keep deployment times

```
df_clean <- df_metamerged %>%  
  drop_na(all_of(na_cols)) %>%  
  filter(case_when(!is.na(Retrievedatetime) ~  
    Deploydatetime < DateTime &  
    DateTime < Retrievedatetime,  
    .default = Deploydatetime < DateTime))
```

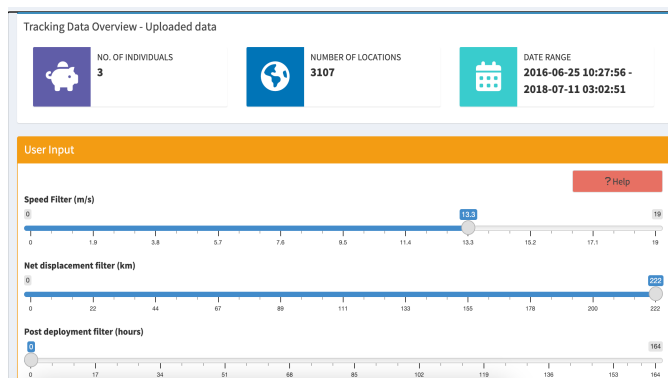
5

Process spatial & temporal metrics

df_diagnostic

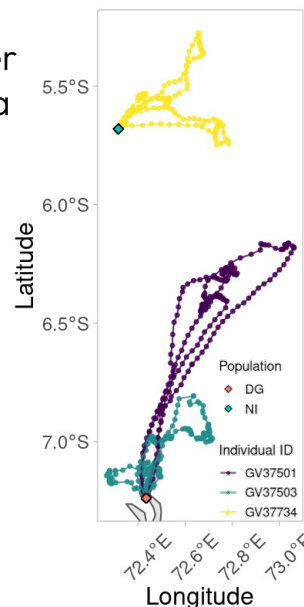
ID	Y	X	DateTime	Year	Species	Population	Age	BreedStage	dist	difftime	netdisp	speed	turnangle
GV37501	-7.24	72.43	2016-06-28 20:24:59	2016	RFB	DG	Adult	Chick rearing	16.56	425	70.41	0.04	38.42
GV37501	-6.44	72.68	2016-06-28 06:12:56	2016	RFB	DG	Adult	Chick rearing	114.48	309	93972.36	0.37	323.38
GV37503	-7.24	72.43	2016-06-29 01:28:16	2016	RFB	DG	Adult	Chick rearing	17.90	300	51.23	0.06	115.45
GV37503	-7.24	72.43	2016-06-30 14:15:32	2016	RFB	DG	Adult	Chick rearing	2306.19	339	54.25	6.80	124.72
GV37734	-5.68	72.32	2018-07-09 02:21:33	2018	RFB	NI	Adult	Chick rearing	2.21	308	101.29	0.01	49.09
GV37734	-5.68	72.32	2018-07-09 15:29:39	2018	RFB	NI	Adult	Chick rearing	4.56	301	103.07	0.02	348.69

Shiny app: determine filter parameters



6

Filter data

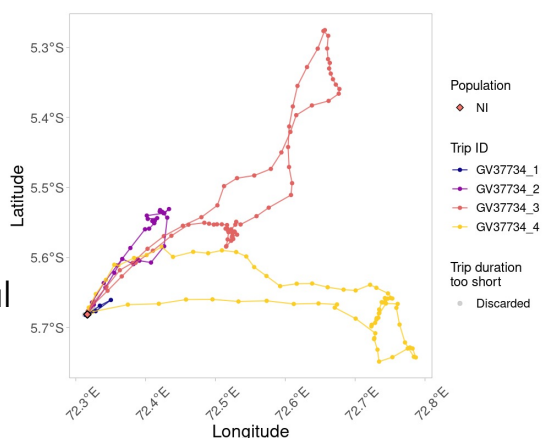


1

Define central place location & trip thresholds

2

Define individual trips



3

Summarise trip metrics

Species	Population	N_Trips	Duration	Total_dist	Max_dist
RFB	DG	7	483.56 ± 2.49	148.34 ± 6.43	55.41 ± 4.63
RFB	NI	1	4240.67 ± NA	360.05 ± NA	172.34 ± NA

df_tripmetrics_summary_pop

How to report: Tracking data were processed following the ExMove toolkit and Shiny app (Langley et al. 2023) to standardise data, using a speed filter of 20 m/s and a net displacement filter of 300 km, and define central place foraging trips, using a colony radius buffer of 1km, and a minimum trip duration of 15mins

Standardised processing pipeline: Workflow.R

Define central place trips using optional script