

Exploration of temporal dynamics

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In this script we demonstrate different approaches to including covariates in an SSF model.

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Load required packages

```
library(tidyverse)
packages <- c("amt", "sf", "terra", "RColorBrewer", "leaflet")
walk(packages, require, character.only = T)
```

Import data and clean

```
buffalo_data <- read_csv("data/buffalo.csv")
```

New names:

Rows: 133161 Columns: 11

-- Column specification

```
----- Delimiter: "," chr
(2): node, dates dbl (7): ...1, lat, lon, height, accuracy, heading, speed dtm
(2): timestamp, DateTime
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.
* `` -> `...1`
```

```
# remove individuals that have poor data quality or less than about 3 months of data.
# The "2014.GPS_COMPACT copy.csv" string is a duplicate of ID 2024, so we exclude it
buffalo_data <- buffalo_data %>% filter(!node %in% c("2014.GPS_COMPACT copy.csv",
                                                    2029, 2043, 2265, 2284, 2346))
```

```
buffalo_data <- buffalo_data %>%
  group_by(node) %>%
  arrange(DateTime, .by_group = T) %>%
  distinct(DateTime, .keep_all = T) %>%
  arrange(node) %>%
  mutate(ID = node)
```

```
buffalo_clean <- buffalo_data[, c(12, 2, 4, 3)]
colnames(buffalo_clean) <- c("id", "time", "lon", "lat")
attr(buffalo_clean$time, "tzone") <- "Australia/Queensland"
head(buffalo_clean)
```

A tibble: 6 x 4

id	time	lon	lat
<chr>	<dtm>	<dbl>	<dbl>

```

1 2005 2018-07-25 10:04:02 134. -12.3
2 2005 2018-07-25 11:04:23 134. -12.3
3 2005 2018-07-25 12:04:39 134. -12.3
4 2005 2018-07-25 13:04:17 134. -12.3
5 2005 2018-07-25 14:04:39 134. -12.3
6 2005 2018-07-25 15:04:27 134. -12.3

```

```
tz(buffalo_clean$time)
```

```
[1] "Australia/Queensland"
```

```
buffalo_ids <- unique(buffalo_clean$id)
```

Create a step object

Use the `amt` package to create a trajectory object from the cleaned data.

```

buffalo_all <- buffalo_clean %>% mk_track(id = id,
                                          lon,
                                          lat,
                                          time,
                                          all_cols = T,
                                          crs = 4326) %>%
  transform_coords(crs_to = 3112, crs_from = 4326) # Transformation to GDA94 /
# Geoscience Australia Lambert (https://epsg.io/3112)

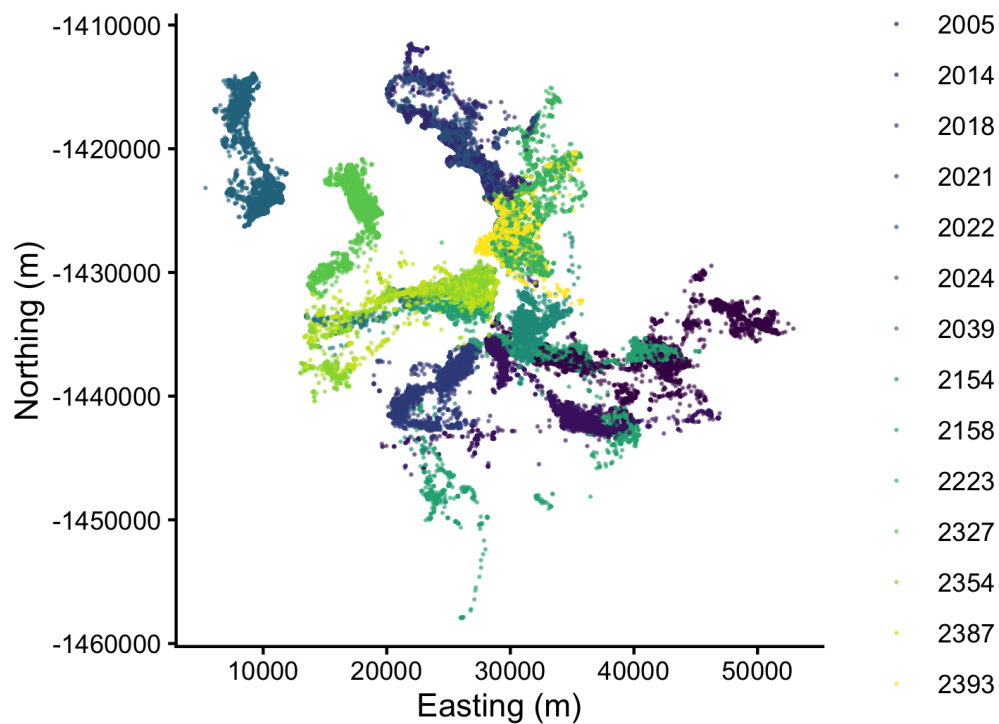
```

Plot the data spatially

```

buffalo_all %>%
  ggplot(aes(x = x_, y = y_, colour = id)) +
  geom_point(alpha = 0.5, size = 0.1) +
  coord_fixed() +
  scale_x_continuous("Easting (m)") +
  scale_y_continuous("Northing (m)") +
  scale_colour_viridis_d() +
  theme_classic() +
  theme(legend.position = "right")

```

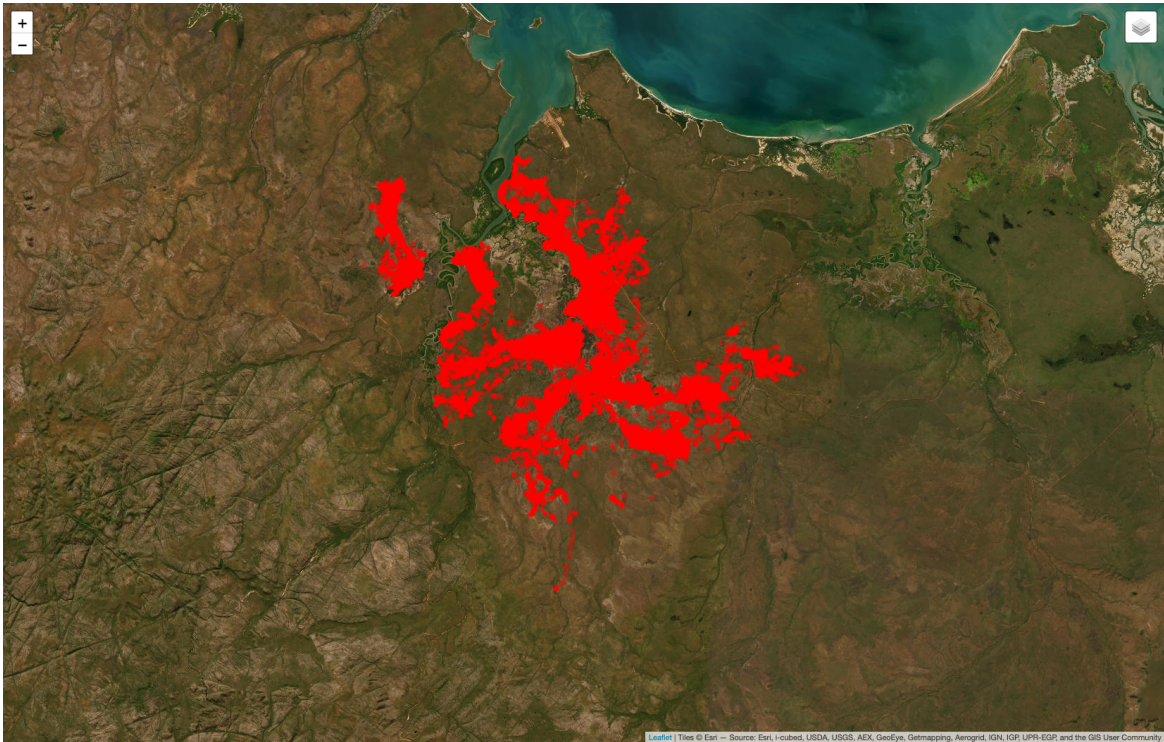


```
# ggsave("outputs/data_prep/buffalo_djelk_map.png",
#         width = 150, height = 150, units = "mm", dpi = 600)
```

Show data on a satellite basemap

If viewing as a PDF this will be an automated screenshot. It viewing the HTML file this should be interactive.

```
# Use the original longitude/latitude data for mapping
leaflet(data = buffalo_clean) %>%
  addProviderTiles(providers$Esri.WorldImagery) %>%
  addCircleMarkers(
    lng = ~lon, lat = ~lat,
    color = "red", radius = 0.5, opacity = 0.5,
    popup = ~paste("ID:", id, "<br>", "Time:", time)
  ) %>%
  addLayersControl(
    baseGroups = c("Satellite"),
    options = layersControlOptions(collapsed = TRUE)
  )
```

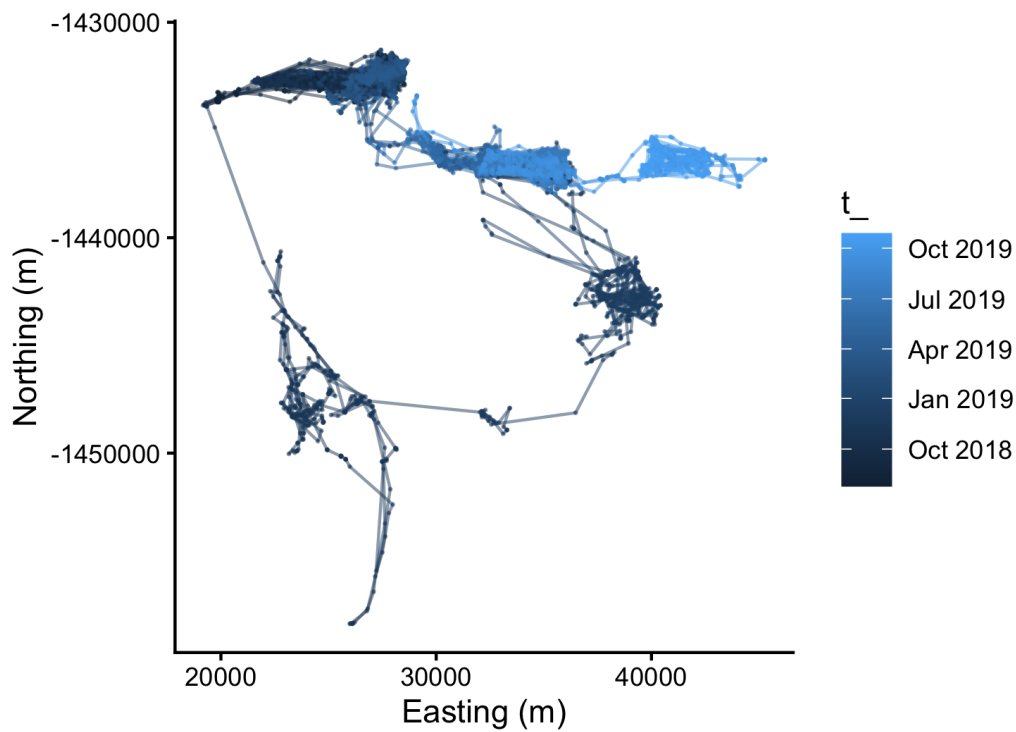


Pick out a single individual

```
which_buffalo <- "2158" # select a single buffalo ID

buffalo_id <- buffalo_all %>% filter(id == which_buffalo)

buffalo_id %>%
  ggplot(aes(x = x_, y = y_, colour = t_)) +
  geom_path(alpha = 0.5) +
  geom_point(alpha = 0.5, size = 0.1) +
  coord_fixed() +
  scale_x_continuous("Easting (m)") +
  scale_y_continuous("Northing (m)") +
  theme_classic()
```



Create steps

We will just use a steps object here for now

```
buffalo_id_steps <- buffalo_id %>%
  steps()

head(buffalo_id_steps)
```

```
# A tibble: 6 x 10
   x1_    x2_    y1_    y2_    sl_ direction_p  ta_ t1_
* <dbl> <dbl>   <dbl>   <dbl> <dbl>   <dbl> <dbl> <dtm>
1 26818. 26607. -1432572. -1433023. 498.    -2.01    NA   2018-07-
25 10:41:00
2 26607. 26610. -1433023. -1433023.  3.76   -0.0922  1.92 2018-07-
25 11:40:34
3 26610. 26610. -1433023. -1433024.  1.05   -2.06   -1.97 2018-07-
25 12:40:32
4 26610. 26252. -1433024. -1432758. 446.    2.50   -1.72 2018-07-
25 13:40:32
5 26252. 26251. -1432758. -1432762.  3.89   -1.71    2.07 2018-07-
25 16:40:44
```

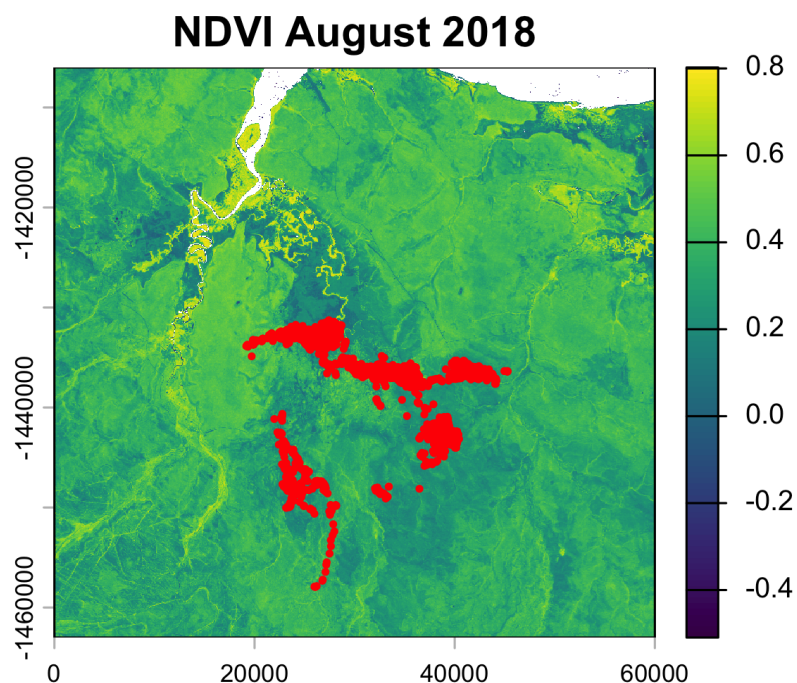
```
6 26251. 26247. -1432762. -1432764. 5.33 -2.75 -1.04 2018-07-
25 17:40:32
# i 2 more variables: t2_ <dtm>, dt_ <drtn>
```

Import spatial covariates

NDVI

Although NDVI changes over time, and we have access to monthly layers, we will just select a single month here.

```
ndvi <- rast("mapping/ndvi_aug_2018.tif")
plot(ndvi, main = "NDVI August 2018")
points(buffalo_id$x_, buffalo_id$y_, col = "red", pch = 16, cex = 0.5)
```



```
ndvi
```

```
class      : SpatRaster
size       : 2280, 2400, 1 (nrow, ncol, nlyr)
resolution : 25, 25 (x, y)
extent     : 0, 60000, -1463000, -1406000 (xmin, xmax, ymin, ymax)
```

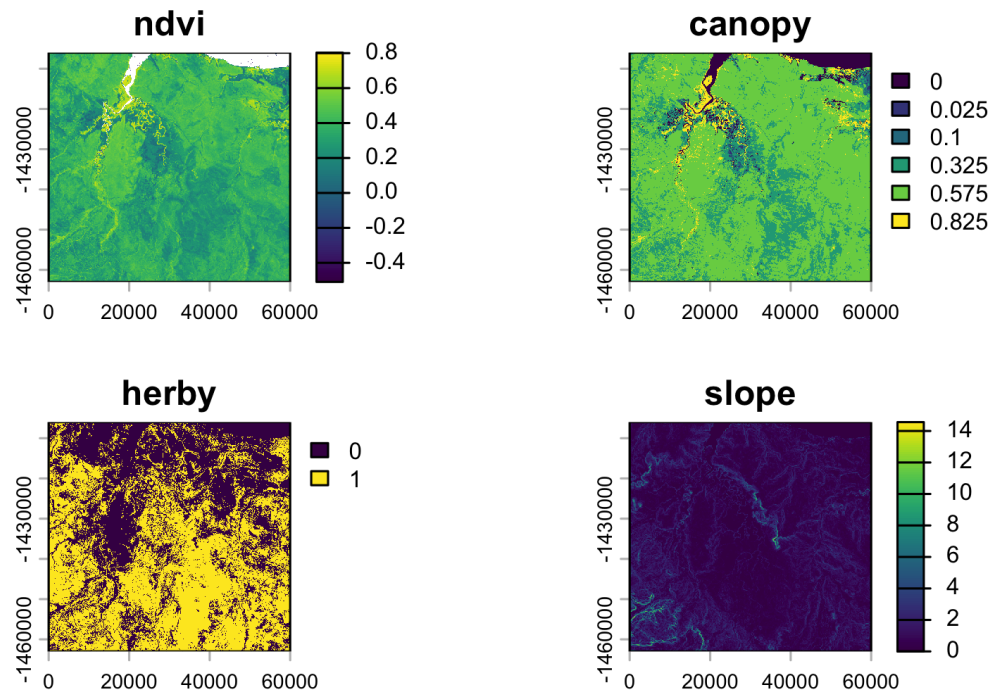


```
coord. ref. : GDA94 / Geoscience Australia Lambert (EPSG:3112)
source      : ndvi_aug_2018.tif
name        : ndvi
min value   : -0.544105
max value   : 0.808655
```

Other covariates

```
canopy <- rast("mapping/canopy_cover.tif")/100
herby <- rast("mapping/veg_herby.tif")
slope <- rast("mapping/slope_raster.tif")

spatial_covs <- c(ndvi, canopy, herby, slope)
names(spatial_covs) <- c("ndvi", "canopy", "herby", "slope")
plot(spatial_covs)
```



Crop covariates to the range of data to determine the background values

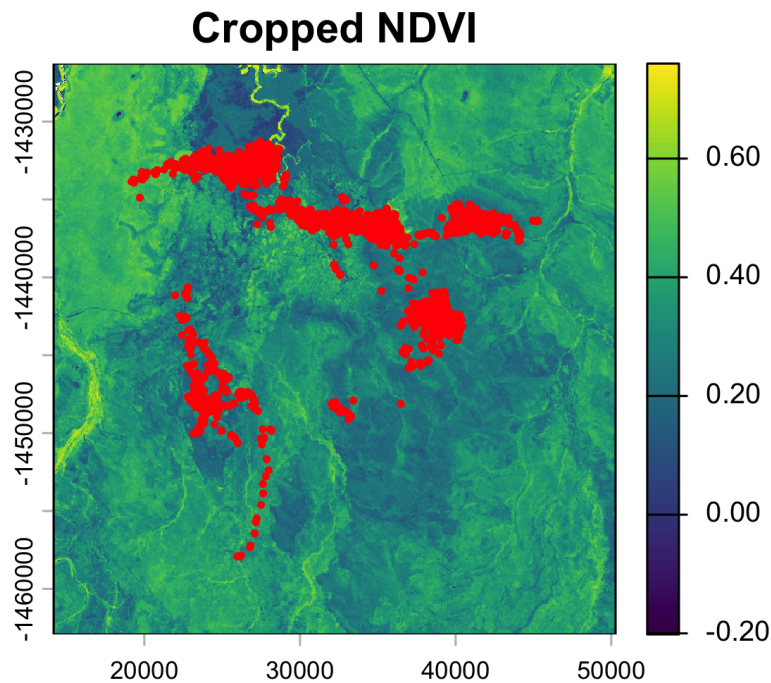

```

study_area <- st_as_sf(buffalo_id, coords = c("x_", "y_"), crs = 3112) %>%
  st_buffer(5000) # buffer to ensure we capture the background values]

spatial_covs_cropped <- spatial_covs %>%
  terra::crop(terra::ext(study_area))

plot(spatial_covs_cropped$ndvi, main = "Cropped NDVI")
points(buffalo_id$x_, buffalo_id$y_, col = "red", pch = 16, cex = 0.5)

```



Create dataframes of the covariate values

```

spatial_covs_cropped_df <- as.data.frame(spatial_covs_cropped, xy = T)

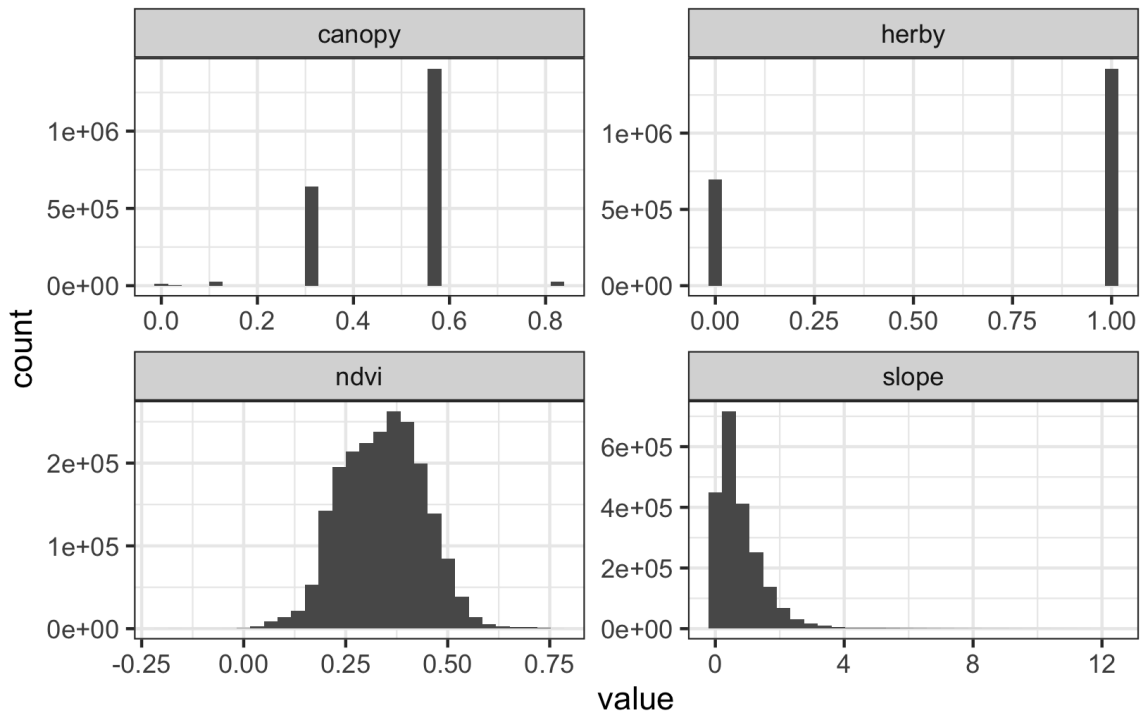
spatial_covs_cropped_df_long <- spatial_covs_cropped_df %>%
  pivot_longer(cols = -c(x, y), names_to = "covariate", values_to = "value")

spatial_covs_cropped_df_long %>%
  ggplot(aes(x = value)) +
  geom_histogram() +
  facet_wrap(~covariate, scales = "free") +
  theme_bw()

```

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

Warning: Removed 271 rows containing non-finite outside the scale range (``stat_bin()``).



```
spatial_covs_summary <- spatial_covs_cropped_df_long %>% drop_na() %>%  
  group_by(covariate) %>%  
  summarise(n = n(),  
            mean = mean(value),  
            q025 = quantile(value, 0.025),  
            q25 = quantile(value, 0.25),  
            median = quantile(value, 0.5),  
            q75 = quantile(value, 0.75),  
            q975 = quantile(value, 0.975)  
  )
```

Extract covariate values at the end of each step

```
buffalo_id_steps <- buffalo_id_steps %>%  
  extract_covariates(covariates = spatial_covs_cropped, where = "end")
```

```
head(buffalo_id_steps)
```

```
# A tibble: 6 x 14
   x1_    x2_    y1_    y2_    sl_ direction_p    ta_ t1_
* <dbl> <dbl>    <dbl>    <dbl> <dbl>    <dbl> <dbl> <dtm>
1 26818. 26607. -1432572. -1433023. 498.      -2.01    NA  2018-07-
25 10:41:00
2 26607. 26610. -1433023. -1433023.  3.76     -0.0922  1.92 2018-07-
25 11:40:34
3 26610. 26610. -1433023. -1433024.  1.05     -2.06    -1.97 2018-07-
25 12:40:32
4 26610. 26252. -1433024. -1432758. 446.       2.50    -1.72 2018-07-
25 13:40:32
5 26252. 26251. -1432758. -1432762.  3.89     -1.71     2.07 2018-07-
25 16:40:44
6 26251. 26247. -1432762. -1432764.  5.33     -2.75    -1.04 2018-07-
25 17:40:32
# i 6 more variables: t2_ <dtm>, dt_ <drtn>, ndvi <dbl>, canopy <dbl>,
#   herby <dbl>, slope <dbl>
```

Prepare data for extracting covariate information

```
buffalo_id_steps <- buffalo_id_steps %>%
  mutate(t1_ = lubridate::with_tz(buffalo_id_steps$t1_, tzone = "Australia/Darwin"),
         t2_ = lubridate::with_tz(buffalo_id_steps$t2_, tzone = "Australia/Darwin"))

buffalo_id_steps <- buffalo_id_steps %>%
  mutate(x1 = x1_, x2 = x2_,
         y1 = y1_, y2 = y2_,
         t1 = t1_,
         t1_rounded = round_date(t1_, "hour"),
         hour_t1 = hour(t1_rounded),
         t2 = t2_,
         t2_rounded = round_date(t2_, "hour"),
         hour_t2 = hour(t2_rounded),
         hour_t2 = ifelse(hour_t2 == 0, 24, hour_t2),
         yday = yday(t1_),
         year = year(t1_),
         month = month(t1_),
         sl = sl_,
         log_sl = log(sl_),
         ta = ta_,
```

```

cos_ta = cos(ta_)

head(buffalo_id_steps)

```

```

# A tibble: 6 x 31
  x1_    x2_    y1_    y2_    sl_ direction_p  ta_ t1_
*   <dbl> <dbl>   <dbl>   <dbl> <dbl>   <dbl> <dbl> <dtm>
1 26818. 26607. -1432572. -1433023. 498.    -2.01  NA    2018-07-
25 10:11:00
2 26607. 26610. -1433023. -1433023.  3.76   -0.0922  1.92 2018-07-
25 11:10:34
3 26610. 26610. -1433023. -1433024.  1.05    -2.06  -1.97 2018-07-
25 12:10:32
4 26610. 26252. -1433024. -1432758. 446.     2.50  -1.72 2018-07-
25 13:10:32
5 26252. 26251. -1432758. -1432762.  3.89    -1.71   2.07 2018-07-
25 16:10:44
6 26251. 26247. -1432762. -1432764.  5.33    -2.75  -1.04 2018-07-
25 17:10:32
# i 23 more variables: t2_ <dtm>, dt_ <drtn>, ndvi <dbl>, canopy <dbl>,
#   herby <dbl>, slope <dbl>, x1 <dbl>, x2 <dbl>, y1 <dbl>, y2 <dbl>,
#   t1 <dtm>, t1_rouned <dtm>, hour_t1 <int>, t2 <dtm>, t2_rouned <dtm>,
#   hour_t2 <dbl>, yday <dbl>, year <dbl>, month <dbl>, sl <dbl>, log_sl <dbl>,
#   ta <dbl>, cos_ta <dbl>

```

Hourly movement behaviour and selection of covariates

Here we bin the trajectories into the hours of the day, and calculate the mean, and quantiles for the step lengths and four habitat covariates. This is a similar approach to in Forrest et al. (2025) and Forrest et al. (2026), where we used this approach to assess temporal dynamics as an exploratory step, but also as a validation step by assessing whether the simulated trajectories had also learned the temporally dynamic behaviour.

Observed buffalo data

```

buffalo_hourly_habitat <-
  buffalo_id_steps %>% dplyr::group_by(hour_t2) %>%
  summarise(n = n(),

            # step lengths
            step_length_mean = mean(sl_),

```

```

step_length_q025 = quantile(sl_, 0.025),
step_length_q25 = quantile(sl_, 0.25),
step_length_median = quantile(sl_, 0.5),
step_length_q75 = quantile(sl_, 0.75),
step_length_q975 = quantile(sl_, 0.975),

# ndvi
ndvi_mean = mean(ndvi),
ndvi_q025 = quantile(ndvi, 0.025),
ndvi_q25 = quantile(ndvi, 0.25),
ndvi_median = median(ndvi),
ndvi_q75 = quantile(ndvi, 0.75),
ndvi_q975 = quantile(ndvi, 0.975),

# herby
herby_mean = mean(herby),
herby_q025 = quantile(herby, 0.025),
herby_q25 = quantile(herby, 0.25),
herby_median = median(herby),
herby_q75 = quantile(herby, 0.75),
herby_q975 = quantile(herby, 0.975),

# canopy cover
canopy_mean = mean(canopy),
canopy_q025 = quantile(canopy, 0.025),
canopy_q25 = quantile(canopy, 0.25),
canopy_median = median(canopy),
canopy_q75 = quantile(canopy, 0.75),
canopy_q975 = quantile(canopy, 0.975),

# slope
slope_mean = mean(slope),
slope_q025 = quantile(slope, 0.025),
slope_q25 = quantile(slope, 0.25),
slope_median = median(slope),
slope_q75 = quantile(slope, 0.75),
slope_q975 = quantile(slope, 0.975)

) %>% ungroup()

```

```
head(buffalo_hourly_habitat)
```

```
# A tibble: 6 x 32
```

```
hour_t2      n step_length_mean step_length_q025 step_length_q25
```

```

      <dbl> <int>          <dbl>          <dbl>          <dbl>
1         1    441          166.           1.81           11.4
2         2    436          147.           1.66           12.7
3         3    438          131.           1.04           6.46
4         4    438          123.           1.41           5.35
5         5    438          113.           1.04           4.65
6         6    405          190.           1.25           5.61
# i 27 more variables: step_length_median <dbl>, step_length_q75 <dbl>,
#   step_length_q975 <dbl>, ndvi_mean <dbl>, ndvi_q025 <dbl>, ndvi_q25 <dbl>,
#   ndvi_median <dbl>, ndvi_q75 <dbl>, ndvi_q975 <dbl>, herby_mean <dbl>,
#   herby_q025 <dbl>, herby_q25 <dbl>, herby_median <dbl>, herby_q75 <dbl>,
#   herby_q975 <dbl>, canopy_mean <dbl>, canopy_q025 <dbl>, canopy_q25 <dbl>,
#   canopy_median <dbl>, canopy_q75 <dbl>, canopy_q975 <dbl>, slope_mean <dbl>,
#   slope_q025 <dbl>, slope_q25 <dbl>, slope_median <dbl>, slope_q75 <dbl>, ...

```

Lengthen the dataframe

```

buffalo_hourly_habitat_long <- buffalo_hourly_habitat %>%
  pivot_longer(cols = !c(hour_t2), names_to = "variable", values_to = "value") %>%
  filter(!variable == "n")

head(buffalo_hourly_habitat_long)

```

```

# A tibble: 6 x 3
  hour_t2 variable      value
  <dbl> <chr>         <dbl>
1     1 1 step_length_mean 166.
2     1 1 step_length_q025  1.81
3     1 1 step_length_q25 11.4
4     1 1 step_length_median 73.7
5     1 1 step_length_q75 215.
6     1 1 step_length_q975 789.

```

Set plotting parameters

```

# set plotting parameters here that will change in each plot

# path
path_linewidth <- 0.5
path_alpha <- 0.1
path_95_alpha <- 1

```

```
# ribbon
ribbon_95_alpha <- 0.25
ribbon_50_alpha <- 0.5
```

Loop over each variable to create a plot

As we have some categorical (canopy cover) and binary variables (herbaceous vegetation), we use the **mean** for the line, rather than the median. Having categorical and binary variables also explains why some of the ribbons look weird, as the quantile doesn't change across the day, or jump to a different level (as in the observed ribbon for canopy cover).

In these plots, the grey ribbon represents the 50% quantiles of the covariate values across the landscape (i.e., the background availability), and the dashed line represents the mean value across the landscape. The black line represents the mean value of the covariate at the end of each step, binned by hour of the day, with the orange ribbon representing the 50% quantiles of the covariate values at the end of each step at each hour.

```
# variables <- unique(buffalo_hourly_habitat_long$variable)

# variables to loop over
variables <- c("step_length", "ndvi", "herby", "canopy", "slope")

for(i in 1:length(variables)){

  # Filter data for the current variable
  var_data <- buffalo_hourly_habitat_long %>%
    filter(str_detect(variable, variables[i]))

  # Extract specific quantiles for ribbons
  var_summary <- buffalo_hourly_habitat %>%
    select(hour_t2,
           mean = !!paste0(variables[i], "_mean"),
           q025 = !!paste0(variables[i], "_q025"),
           q25 = !!paste0(variables[i], "_q25"),
           median = !!paste0(variables[i], "_median"),
           q75 = !!paste0(variables[i], "_q75"),
           q975 = !!paste0(variables[i], "_q975"))

  spatial_covs_summary_cov <- spatial_covs_summary %>% filter(covariate == variables[i])

  plot <- ggplot(data = var_summary) +

    # background
```



```

geom_rect(xmin = -Inf, xmax = Inf,
          ymin = spatial_covs_summary_cov$q25, ymax = spatial_covs_summary_cov$q75,
          fill = "grey", alpha = 0.05) +
geom_hline(yintercept = spatial_covs_summary_cov$mean, linetype = "dashed", colour = "black")

# ribbons
# 95% ribbon
# geom_ribbon(aes(x = hour_t2,
#                 ymin = q025,
#                 ymax = q975),
#             alpha = ribbon_95_alpha, fill = "orange") +

# 50% ribbon
geom_ribbon(aes(x = hour_t2,
               ymin = q25,
               ymax = q75),
           alpha = ribbon_50_alpha, fill = "orange") +

# lines
geom_line(aes(x = hour_t2, y = mean), colour = "black", size = 1) +
geom_point(aes(x = hour_t2, y = mean), colour = "black", size = 1) +

scale_x_continuous(breaks = seq(0, 24, by = 2)) +
coord_cartesian(expand = TRUE) +
labs(x = "Hour of the day",
     y = variables[i],
     title = paste0("Hourly ", variables[i], " - 50% quantiles")) +
theme_bw()

print(plot)

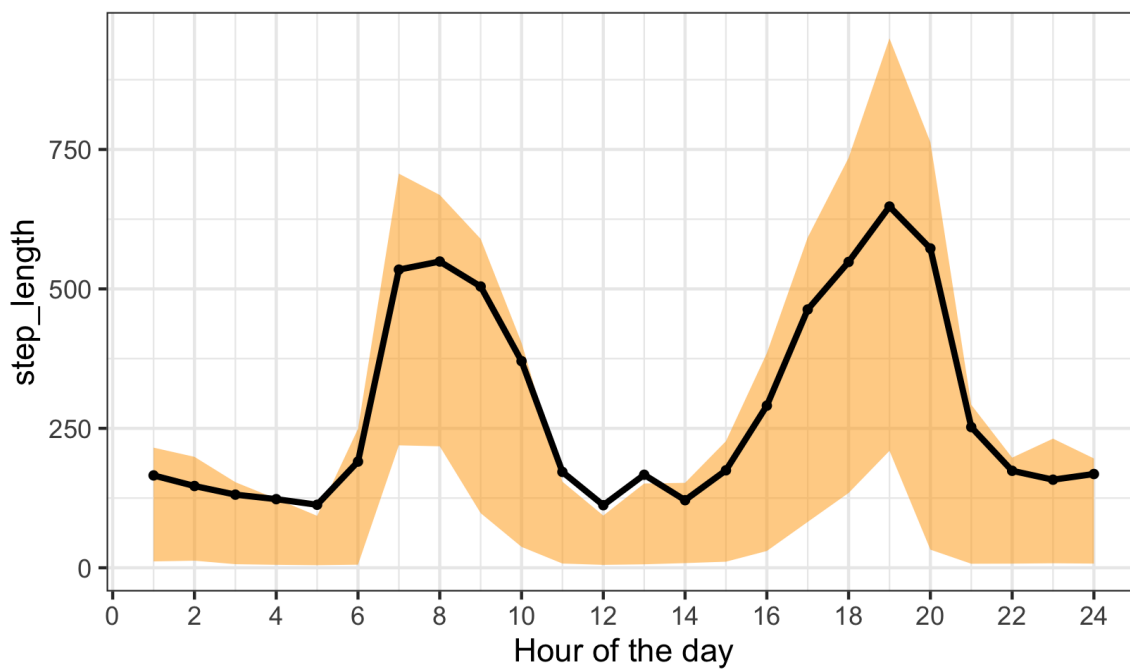
ggsave(paste0("outputs/exploratory_temporal_dynamics/buffalo_hourly_", variables[i], ".png"),
       plot = plot,
       width = 150, height = 100, units = "mm", dpi = 600)
}

```

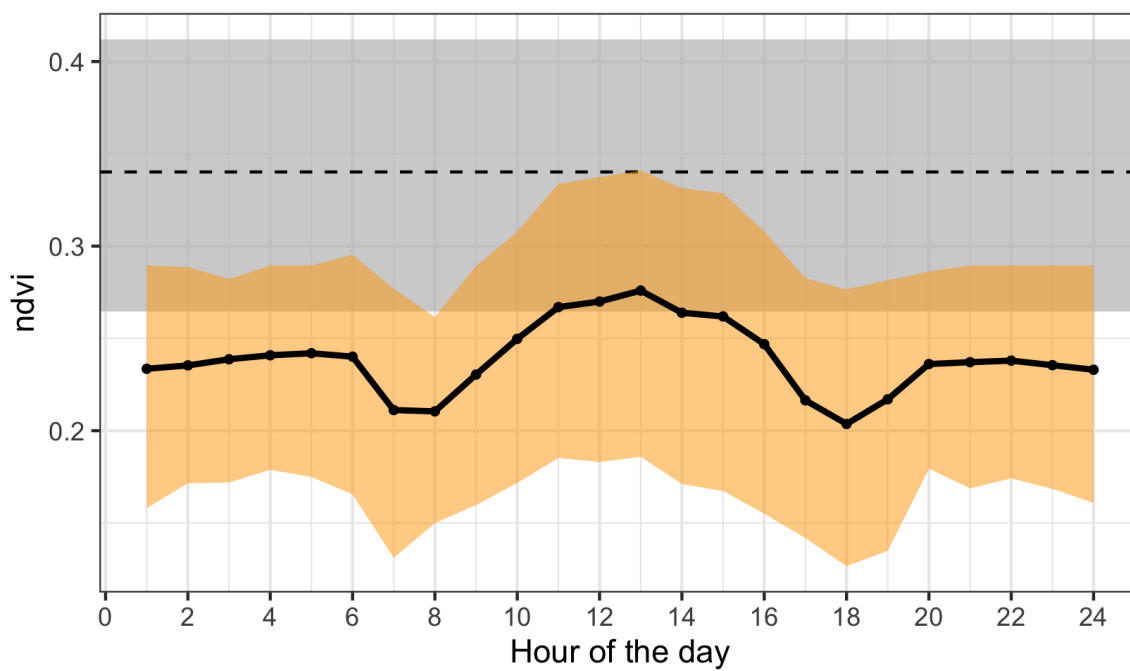
Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
 i Please use `linewidth` instead.

Warning in geom_rect(xmin = -Inf, xmax = Inf, ymin = spatial_covs_summary_cov\$q25, : Ignoring empty aesthetics: `ymin` and `ymax`.

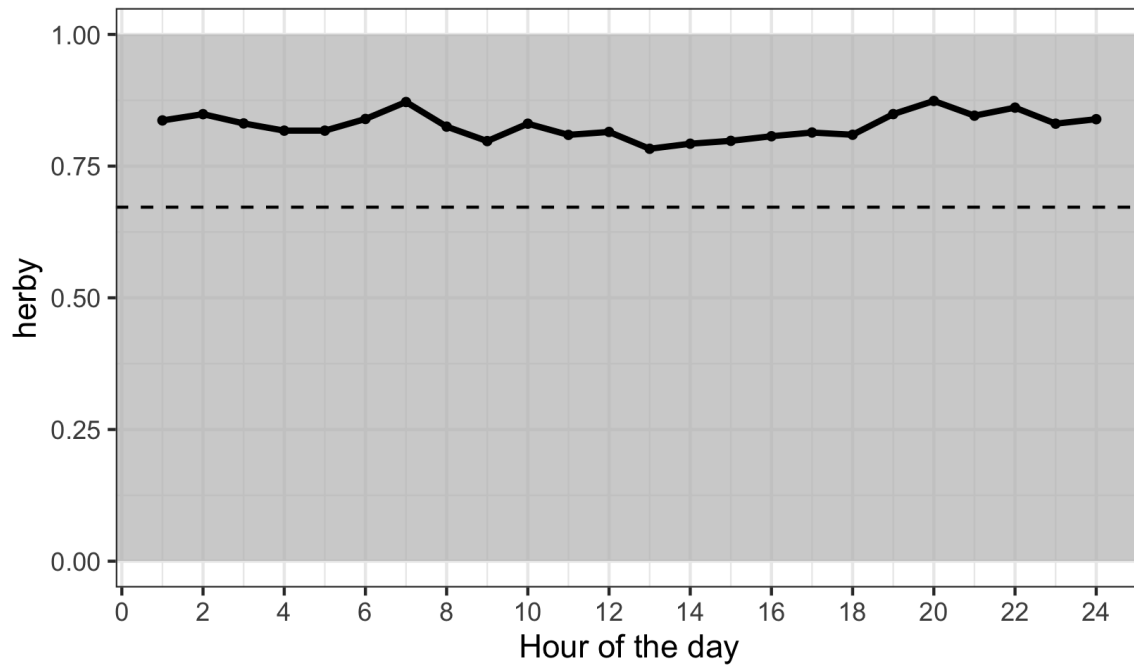
Hourly step_length - 50% quantiles



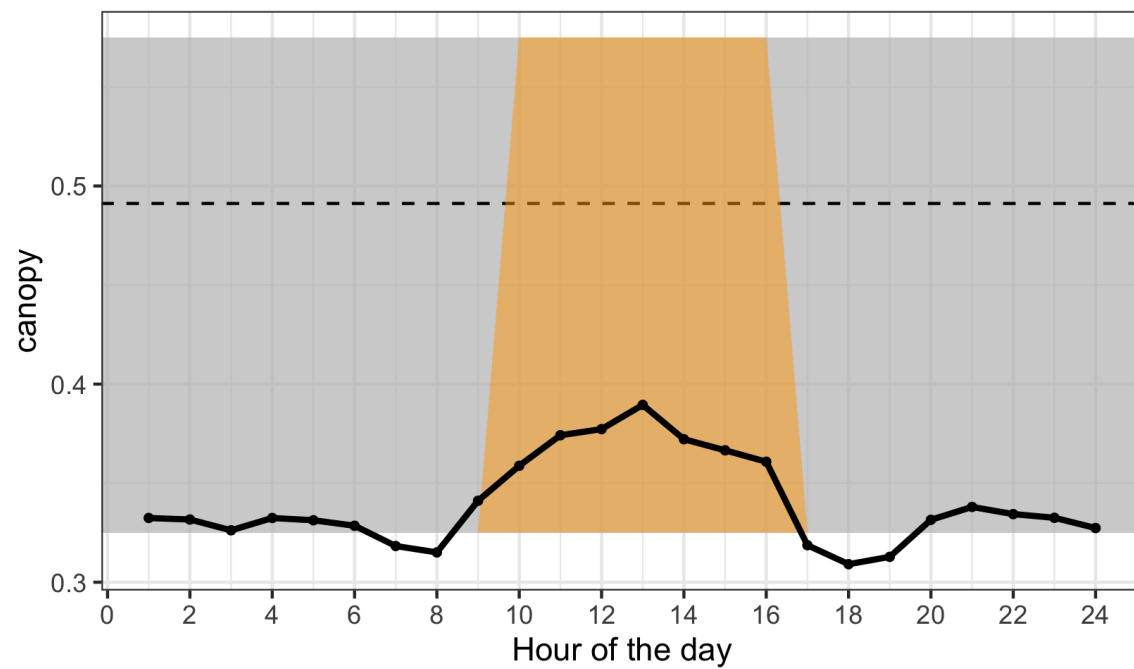
Hourly ndvi - 50% quantiles



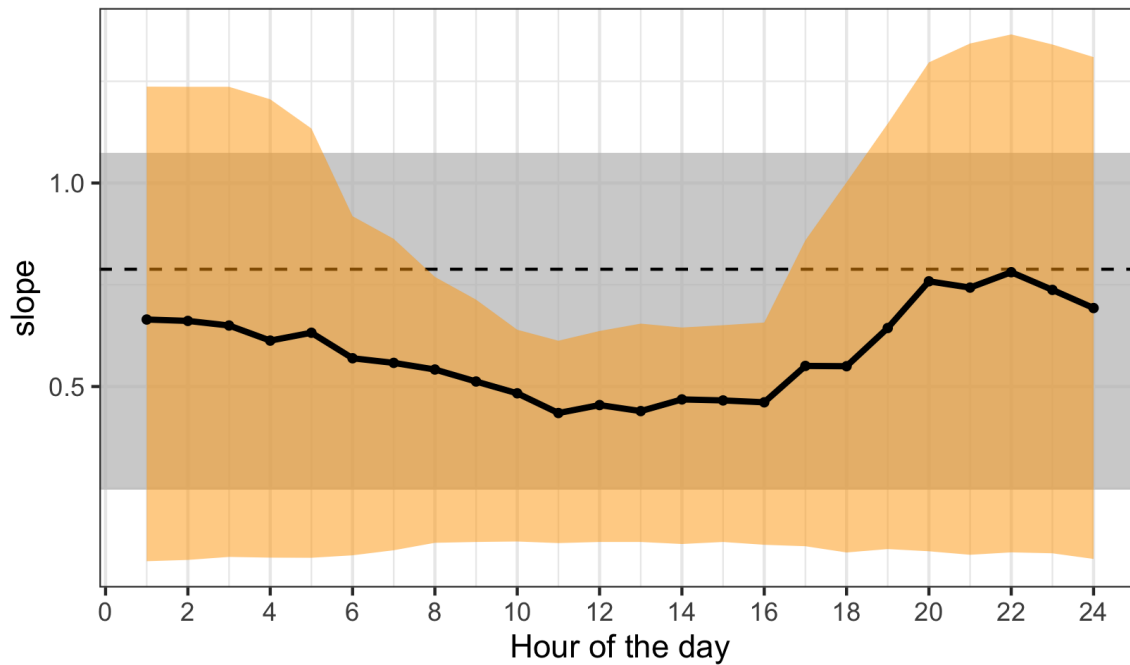
Hourly herby - 50% quantiles



Hourly canopy - 50% quantiles



Hourly slope - 50% quantiles



References

- Forrest, Scott W, Dan Pagendam, Michael Bode, et al. 2025. "Predicting fine-scale distributions and emergent spatiotemporal patterns from temporally dynamic step selection simulations." *Ecography* 2025 (February). <https://doi.org/10.1111/ecog.07421>.
- Forrest, Scott W, Dan Pagendam, Conor Hassan, et al. 2026. "Predicting animal movement with deepSSF : A deep learning step selection framework." *Methods in Ecology and Evolution* 17 (February): 371–91. <https://doi.org/10.1111/2041-210x.70136>.