Assessing environmental extrapolation

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Here we show how to assess extrapolation (in environmental space), using the the continuous Shape metric (Velazco et al. 2024).

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Load required packages

```
# remotes::install_github("sjevelazco/flexsdm")

library(tidyverse)
packages <- c("amt", "sf", "terra", "tictoc", "beepr", "flexsdm", "tmap", "patchwork", "ggsp
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 dttm
(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$time, "tzone") <- "Australia/Queensland"
buffalo_clean$sex <- "f"
buffalo_clean$life_stage <- "adult"
head(buffalo_clean)
```

```
# A tibble: 6 x 6
  id    time                 lon   lat sex   life_stage
  <chr> <dttm>             <dbl> <dbl> <chr> <chr>
1 2005  2018-07-25 10:04:02  134. -12.3 f     adult
2 2005  2018-07-25 11:04:23  134. -12.3 f     adult
3 2005  2018-07-25 12:04:39  134. -12.3 f     adult
4 2005  2018-07-25 13:04:17  134. -12.3 f     adult
5 2005  2018-07-25 14:04:39  134. -12.3 f     adult
6 2005  2018-07-25 15:04:27  134. -12.3 f     adult
```

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

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

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

write_csv(buffalo_clean, "data/buffalo_clean.csv")
```

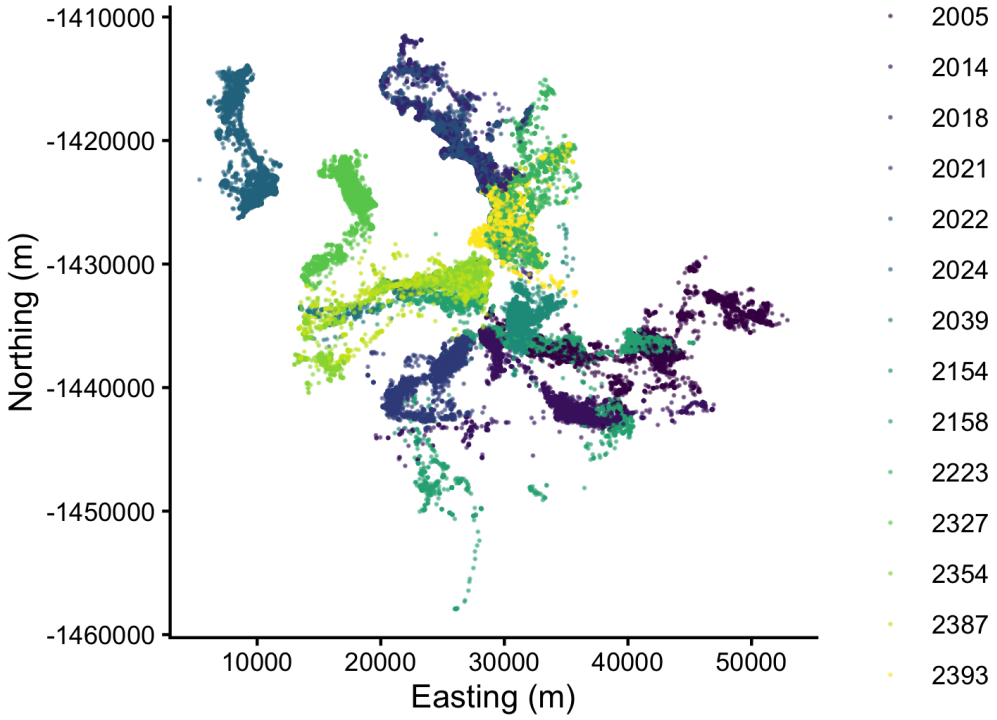
Create a step object

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)
```

Creating a step object

```
# nest the data by individual
buffalo_all_nested <- buffalo_all %>% arrange(id) %>% nest(data = -"id")
```

```
buffalo_all_nested_steps <- buffalo_all_nested %>%
  mutate(steps = map(data, function(x)
    x %>% track_resample(rate = hours(1), tolerance = minutes(10)) %>%
      steps()))
```

```
Warning: There were 14 warnings in `mutate()`.
The first warning was:
i In argument: `steps = map(...)`.
Caused by warning in `steps.track_xyt()`:
! burst's are ignored, use steps_by_burst instead.
i Run `dplyr::last_dplyr_warnings()` to see the 13 remaining warnings.
```

```
# unnest the data after creating 'steps' objects
buffalo_all_steps <- buffalo_all_nested_steps %>%
  amt::select(id, steps) %>%
  amt::unnest(cols = steps)

buffalo_all_steps <- buffalo_all_steps %>%
  mutate(t2_rounded = round_date(t2_, "hour"), # round the time to the nearest hour
         hour_t2 = ifelse(hour(t2_rounded) == 0, 24, hour(t2_rounded))) # change the 0 hour

head(buffalo_all_steps, 10)
```

```
# A tibble: 10 x 13
   id       x1_    x2_       y1_       y2_    sl_ direction_p     ta_
 * <chr>  <dbl>  <dbl>     <dbl>     <dbl>  <dbl>       <dbl>   <dbl>
 1 2005  41941. 41969. -1435875. -1435671. 206.         1.43  NA
 2 2005  41969. 41922. -1435671. -1435654.  50.7        2.80   1.37
 3 2005  41922. 41779. -1435654. -1435601. 152.         2.78  -0.0214
 4 2005  41779. 41841. -1435601. -1435635.  70.7       -0.507  2.99
 5 2005  41841. 41655. -1435635. -1435604. 188.         2.98  -2.80
 6 2005  41655. 41619. -1435604. -1435608.  37.1       -3.02   0.285
 7 2005  41619. 41688. -1435608. -1436126. 522.        -1.44   1.58
 8 2005  41688. 41684. -1436126. -1436119.   8.13       2.10  -2.75
 9 2005  41684. 41675. -1436119. -1436119.   9.75      -3.13   1.05
10 2005  41675. 41425. -1436119. -1435938. 308.         2.52  -0.635
# i 5 more variables: t1_ <dttm>, t2_ <dttm>, dt_ <drtn>, t2_rounded <dttm>,
#   hour_t2 <dbl>
```

Fitting step length and turning angle distributions

Fitting exponential and von Mises distributions to the steps of ALL individuals (only one Gamma and one von Mises distribution for the whole population). This should be done

when fitting a hierarchical model to update the 'population' parameters, but also makes it straightforward to update after model fitting to each individual separately.

```
# fitting step length and turning angle distributions to all locations
gamma_dist <- fit_distr(buffalo_all_steps$sl_, "gamma")
vonmises_dist <- fit_distr(buffalo_all_steps$ta_, "vonmises")

# checking parameters - which can then be saved to update movement parameters
# after fitting the step selection model
gamma_dist$params$shape
```

```
[1] 0.4266711
```

```
gamma_dist$params$scale
```

```
[1] 664.0039
```

```
vonmises_dist$params$kappa
```

```
[1] 0.1990268
```

```
vonmises_dist$params$mu
```

```
Circular Data:
Type = angles
Units = radians
Template = none
Modulo = asis
Zero = 0
Rotation = counter
[1] 0
```

For some reason, the `random_steps` function does not work when using the `bursted_steps_xyt` class. I'm not sure why (the error is `Error in bursts[[i]] : subscript out of bounds`), but it works when that class label is removed, and appears to sample random steps correctly. For taxa that have irregular fixes and many bursts, this may be worth exploring in more detail.

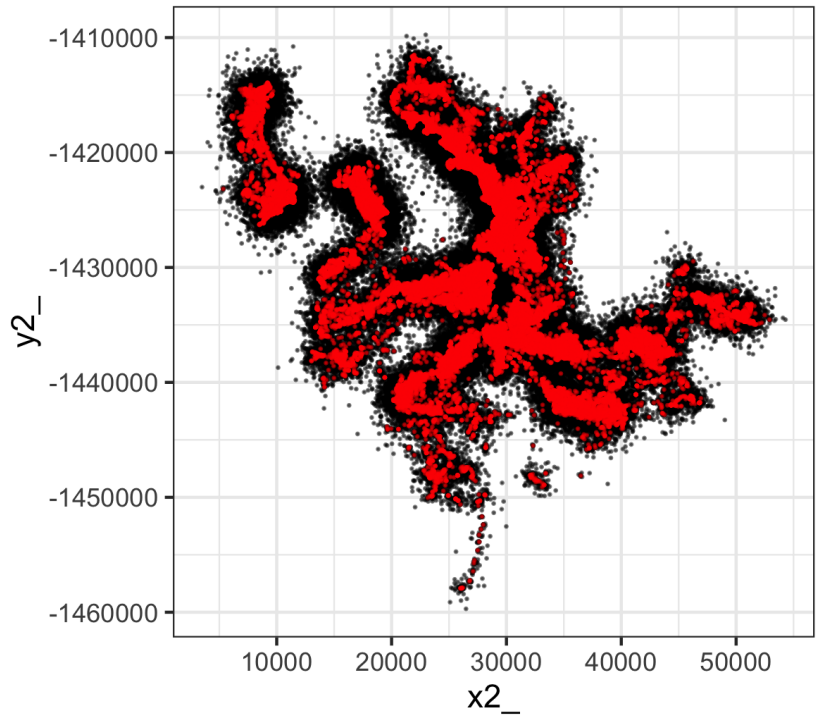
```
tic()

buffalo_parametric_popn_GvM <- buffalo_all_steps %>%
  random_steps(n_control = 10,
               sl_distr = gamma_dist,
               ta_distr = vonmises_dist) %>%
  mutate(y = as.numeric(case_))

toc()
```

```
14.242 sec elapsed
```

Plotting the random step distributions

Spatially plot the used and random steps, with the used steps in red.

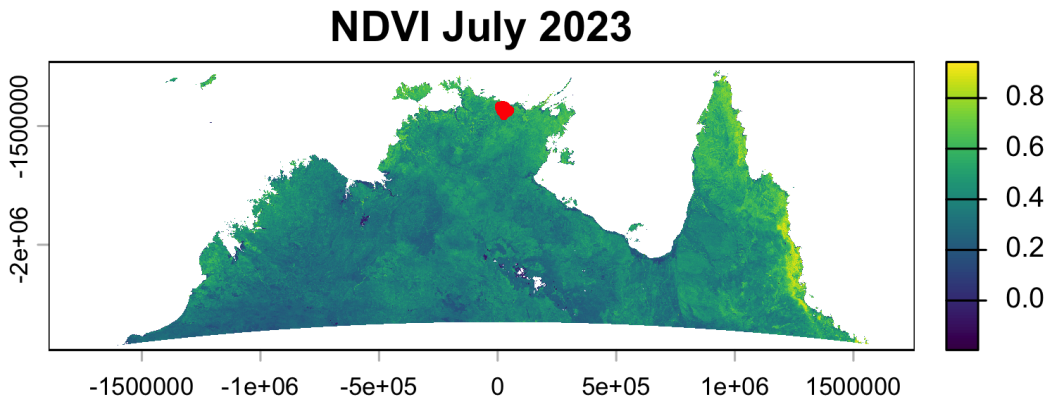
```
buffalo_parametric_popn_GvM %>% ggplot() +
  geom_point(data = . %>% filter(y == 0), aes(x = x2_, y = y2_),
             colour = "black", size = 0.1, alpha = 0.5) +
  geom_point(data = . %>% filter(y == 1), aes(x = x2_, y = y2_),
             colour = "red", size = 0.1, alpha = 0.5) +
  coord_equal() +
  theme_bw()
```



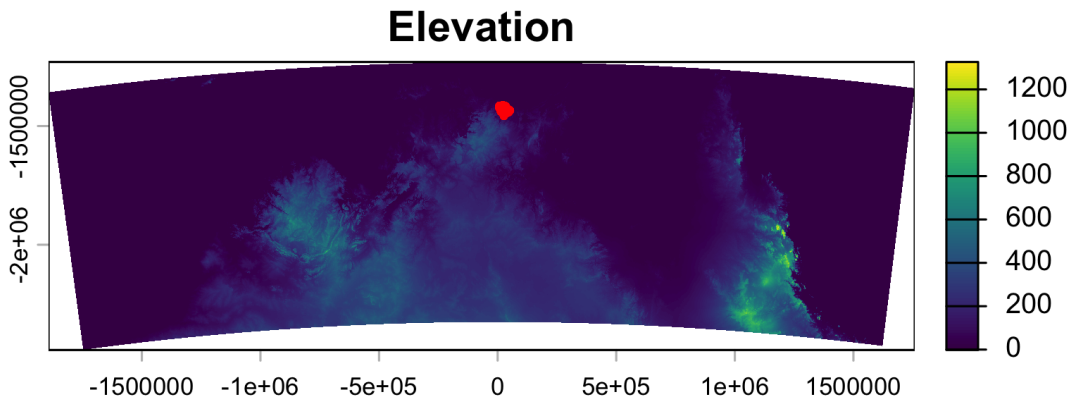
Import spatial covariates

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

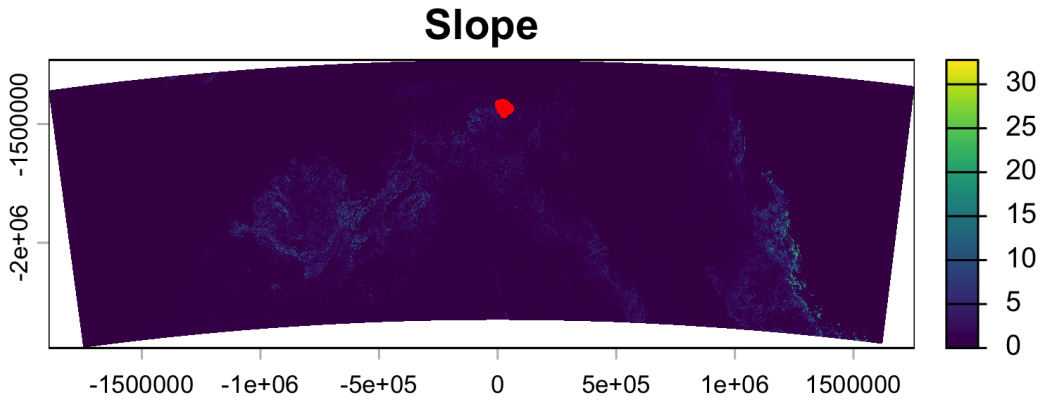
```
# NDVI
# ndvi <- terra::rast("mapping/large_files/NDVI_2023_250m.tif")
# ndvi <- terra::project(ndvi, "EPSG:3112")
# writeRaster(ndvi, "mapping/large_files/NDVI_2023_250m_projected3112.tif", overwrite = TRUE

ndvi <- terra::rast("mapping/large_files/NDVI_2023_250m_projected3112.tif")
plot(ndvi, main = "NDVI July 2023")
points(buffalo_all$x_, buffalo_all$y_, col = "red", pch = 16, cex = 0.5)
```




```
# elevation
# elev <- terra::rast("mapping/large_files/DEM_SRTM_250m.tif")
# elev <- terra::project(elev, "EPSG:3112")
# writeRaster(elev, "mapping/large_files/DEM_SRTM_250m_projected3112.tif", overwrite = TRUE)

elev <- terra::rast("mapping/large_files/DEM_SRTM_250m_projected3112.tif")
plot(elev, main = "Elevation")
points(buffalo_all$x_, buffalo_all$y_, col = "red", pch = 16, cex = 0.5)
```




```
# create slope layer
slope <- terra::terrain(elev, v = "slope", neighbors = 8)
plot(slope, main = "Slope")
points(buffalo_all$x_, buffalo_all$y_, col = "red", pch = 16, cex = 0.5)
```



Sample values of the environmental covariates at the end of the steps.

```
buffalo_parametric_popn_covs <- buffalo_parametric_popn_GvM %>%

  extract_covariates(ndvi,
                     where = "end") %>%
  extract_covariates(elev,
                     where = "end") %>%
  extract_covariates(slope,
                     where = "end") %>%

  mutate(y = as.numeric(case_),
         cos_ta_ = cos(ta_),
         log_sl_ = log(sl_))
```

Assess extrapolation

```
# uncomment to run the code - takes a while
# tic()
```

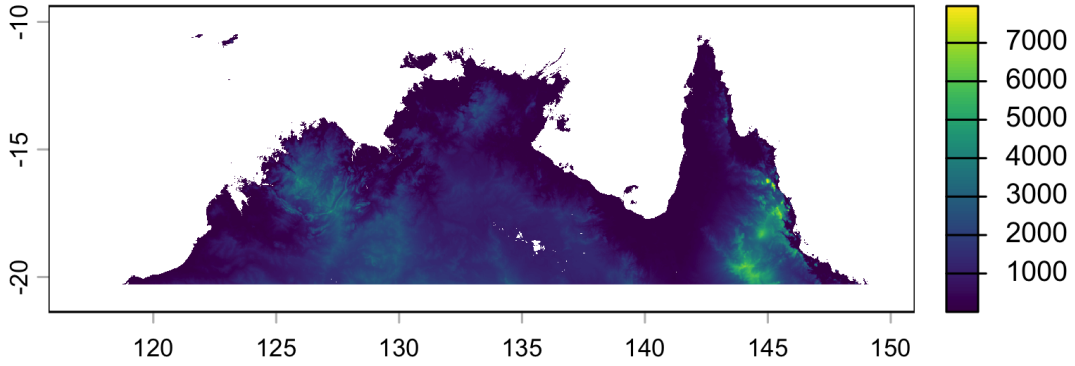
```
#
# extrapolation_raster <- extra_eval(
#   training_data = buffalo_parametric_popn_covs,
#   pr_ab = "y",
#   projection_data = c(ndvi, elev, slope),
#   metric = "mahalanobis",
#   univar_comb = FALSE,
#   aggreg_factor = 10
# )
#
# beep(sound = 2)
#
# toc()
```

Write the raster

```
# terra::writeRaster(extrapolation_raster, "outputs/extrapolation_raster.tif", overwrite = T
extrapolation_raster <- terra::rast("outputs/extrapolation_raster.tif")
```

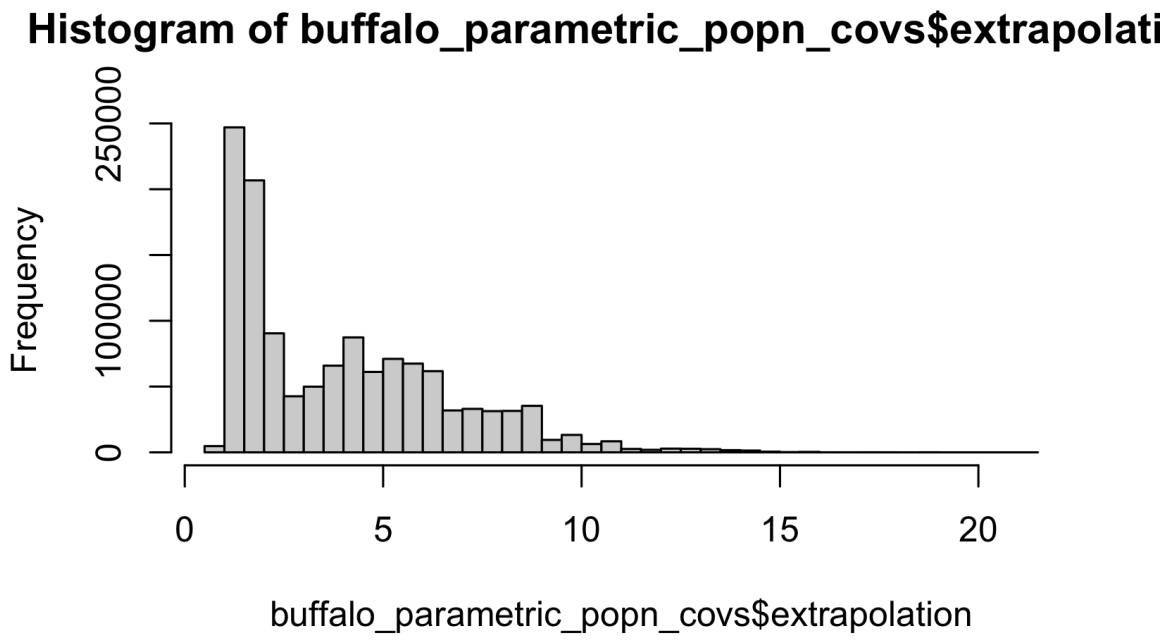
Mask out NAs and plot

```
extrapolation_raster <- terra::mask(extrapolation_raster, ndvi)
extrapolation_raster_wgs84 <- terra::project(extrapolation_raster, "EPSG:4326")
plot(extrapolation_raster_wgs84)
```



Add Shape values back to the training dataframe

```
buffalo_parametric_popn_covs <- buffalo_parametric_popn_covs %>%
  extract_covariates(extrapolation_raster,
                     where = "end")

hist(buffalo_parametric_popn_covs$extrapolation, breaks = 30)
```




```
# what is the 99th percentile of the Shape values in the training data?
threshold_q99 <- quantile(buffalo_parametric_popn_covs$extrapolation, 0.99, na.rm = TRUE)
paste0("The 99th percentile of the Shape values in the training data is ", threshold_q99)
```

```
[1] "The 99th percentile of the Shape values in the training data is 11.8537864685059"
```

```
# what is the maximum Shape value in the training data?
threshold_max <- max(buffalo_parametric_popn_covs$extrapolation, na.rm = TRUE)
paste0("The maximum Shape value in the training data is ", threshold_max)
```

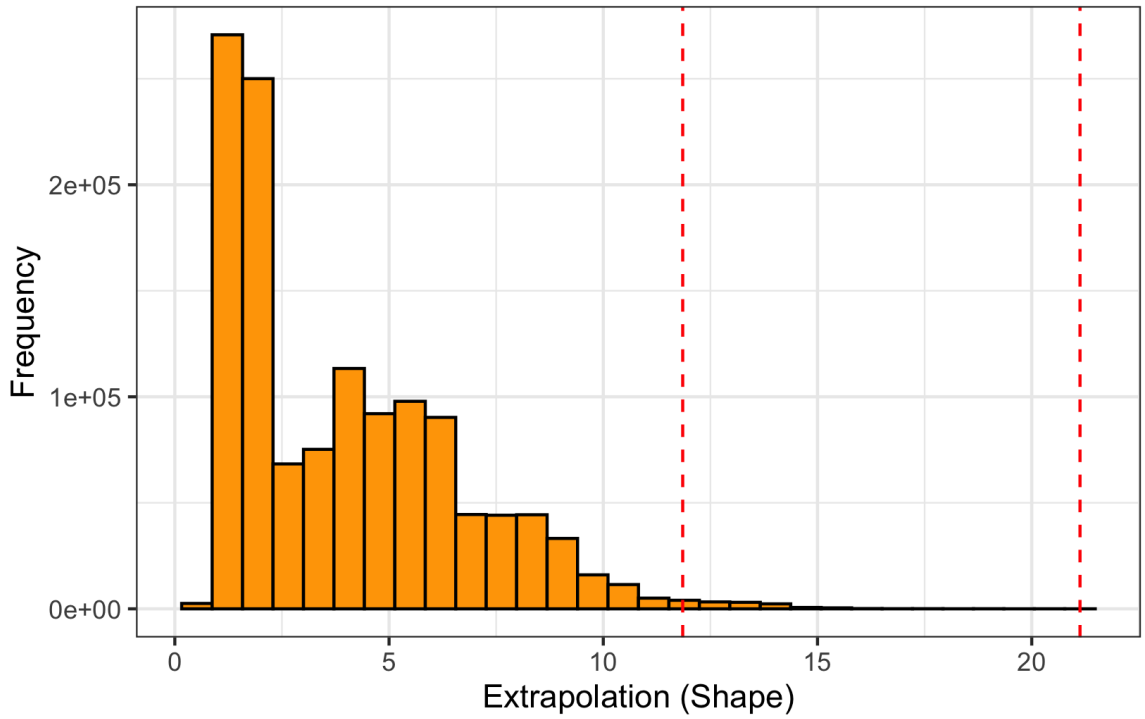
```
[1] "The maximum Shape value in the training data is 21.1267185211182"
```

Plot histogram of Shape values in the training data with the 99th percentile and maximum values indicated

```
ggplot() +
  geom_histogram(data = buffalo_parametric_popn_covs, aes(x = extrapolation),
                 fill = "orange", colour = "black", bins = 30) +
  geom_vline(xintercept = threshold_q99, color = "red", linetype = "dashed") +
  geom_vline(xintercept = threshold_max, color = "red", linetype = "dashed") +
```

```
  labs(x = "Extrapolation (Shape)", y = "Frequency") +
  theme_bw()
```

```
Warning: Removed 52 rows containing non-finite outside the scale range
(`stat_bin()`).
```



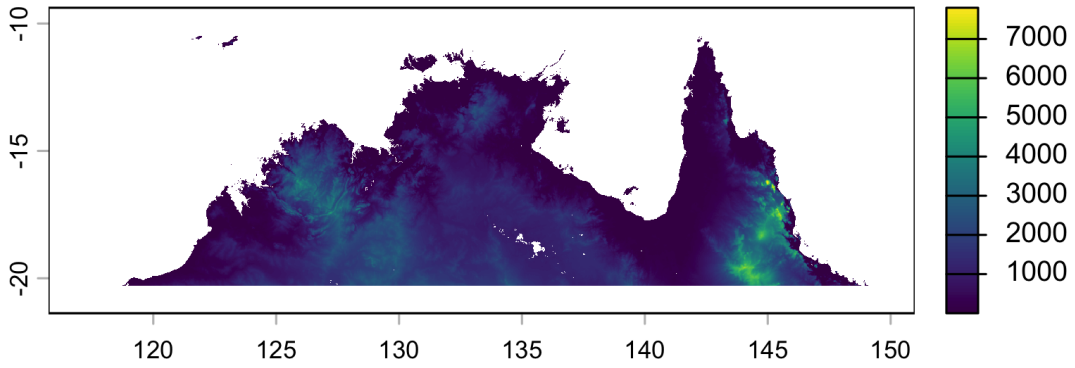
Plot the extrapolation

Create dataframe

```
# prevent scientific notation in the legend
options(scipen=999)

extrapolation_raster_wgs84_agg <- terra::aggregate(extrapolation_raster_wgs84, fact = 4, fun
```

```
|---------|---------|---------|---------|
=========================================
```

```r
plot(extrapolation_raster_wgs84_agg)
```




```r
extrapolation_raster_wgs84_agg_df <- as.data.frame(extrapolation_raster_wgs84_agg, xy = TRUE
```

Thin the training data

```r
buffalo_parametric_popn_covs_thin <- buffalo_parametric_popn_covs %>% dplyr::slice_sample(pr

# project to WGS84 for plotting with ggplot
xy_wgs84 <- buffalo_parametric_popn_covs_thin %>%
  st_as_sf(coords = c("x1_", "y1_"), crs = 3112) %>%
  st_transform(crs = 4326) %>%
  st_coordinates() %>%
  as.data.frame() %>%
  rename(x1_wgs84 = X, y1_wgs84 = Y)

buffalo_parametric_popn_covs_thin <- buffalo_parametric_popn_covs_thin %>%
  bind_cols(xy_wgs84)
```

Plot with ggplot

```
raster_alpha <- 0.5
training_points_alpha <- 0.1

extrapolation_aus_plot <- ggplot(data = extrapolation_raster_wgs84_agg_df, aes(x = x, y = y,

  geom_raster() +
    scale_fill_viridis_c(
    na.value = "transparent",
    transform = "log1p",
    breaks = c(1, 10, 100, 1000, 5000)
  ) +

  geom_contour(aes(z = extrapolation),
               breaks = c(threshold_max), color = "orange", linewidth = 0.2) +

  geom_point(data = buffalo_parametric_popn_covs_thin,
             aes(x = x1_wgs84, y = y1_wgs84),
             colour = "red", alpha = training_points_alpha, size = 0.01) +

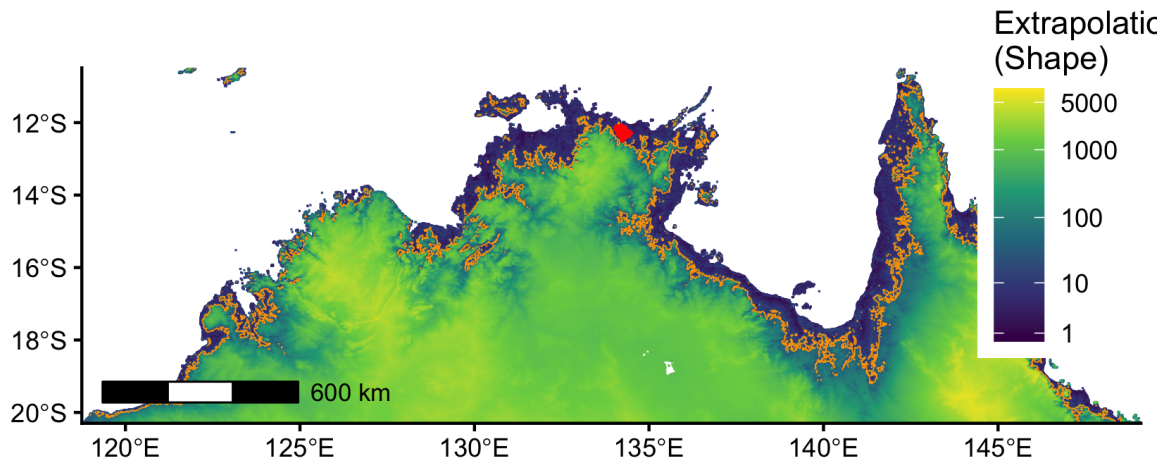
  annotation_scale(location = "bl", width_hint = 0.2) +
  coord_sf(crs = 4326, default_crs = 4326, expand = FALSE) +
  labs(x = NULL, y = NULL, fill = "Extrapolation\n(Shape)") +
  theme_classic() +
  theme(
    legend.position = "inside",
    legend.position.inside = c(0.95, 0.7)
    )

extrapolation_aus_plot
```

```
Warning: The following aesthetics were dropped during statistical transformation: fill.
i This can happen when ggplot fails to infer the correct grouping structure in
  the data.
i Did you forget to specify a `group` aesthetic or to convert a numerical
  variable into a factor?
```

```
Warning: Raster pixels are placed at uneven horizontal intervals and will be shifted
i Consider using `geom_tile()` instead.
```

```
`geom_raster()` only works with linear coordinate systems, not `coord_sf()`.
i Falling back to drawing as `geom_rect()`.
```




```
ggsave("outputs/extrapolation_raster_ggplot.png",
       width = 180, height = 60, units = "mm", scale = 1.5, dpi = 1000)
```

```
Warning: The following aesthetics were dropped during statistical transformation: fill.
i This can happen when ggplot fails to infer the correct grouping structure in
  the data.
i Did you forget to specify a `group` aesthetic or to convert a numerical
  variable into a factor?
Raster pixels are placed at uneven horizontal intervals and will be shifted
i Consider using `geom_tile()` instead.

`geom_raster()` only works with linear coordinate systems, not `coord_sf()`.
i Falling back to drawing as `geom_rect()`.
```

Check distributions of covariates against Shape values

```
cov_extrap_stack <- c(ndvi, elev, slope, extrapolation_raster)
cov_extrap_stack_df <- as.data.frame(cov_extrap_stack, xy = TRUE) %>% drop_na()

# thin to reduce computation and make plot look less messy
cov_extrap_stack_df_thin <- cov_extrap_stack_df %>% dplyr::slice_sample(prop = 0.001)
```

Plot NDVI and elevation with Shape values

```
ndvi_elev_plot <- ggplot() +

  geom_point(data = cov_extrap_stack_df_thin,
             aes(x = NDVI, y = elevation, colour = extrapolation), alpha = raster_alpha) +

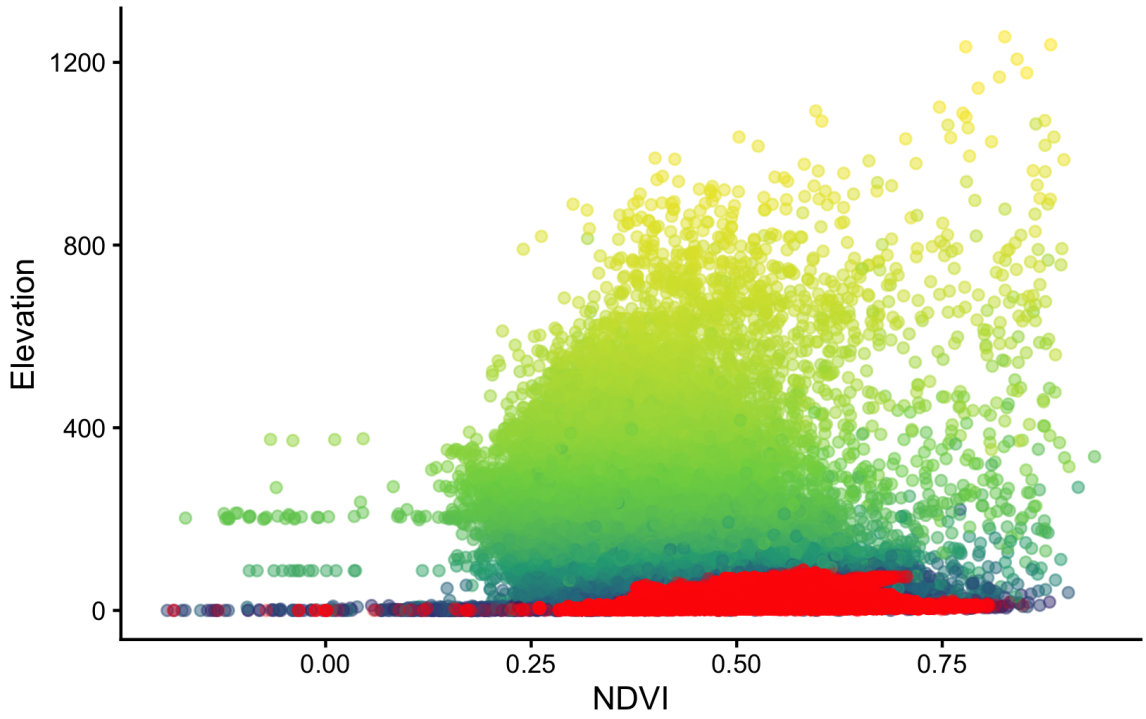
  geom_point(data = buffalo_parametric_popn_covs_thin,
             aes(x = NDVI, y = elevation),
             colour = "red", alpha = training_points_alpha) +

  scale_colour_viridis_c(
    transform = "log1p",
    breaks = c(1, 10, 100, 1000, 5000)
    ) +

  labs(x = "NDVI", y = "Elevation", colour = "Extrapolation\n(Shape)")  +
  theme_classic() +
  theme(legend.position = "none")

ndvi_elev_plot
```

```
Warning: Removed 52 rows containing missing values or values outside the scale range
(`geom_point()`).
```



Plot NDVI and slope with Shape values

```
ndvi_slope_plot <- ggplot() +

  geom_point(data = cov_extrap_stack_df_thin,
             aes(x = NDVI, y = slope, colour = extrapolation), alpha = raster_alpha) +

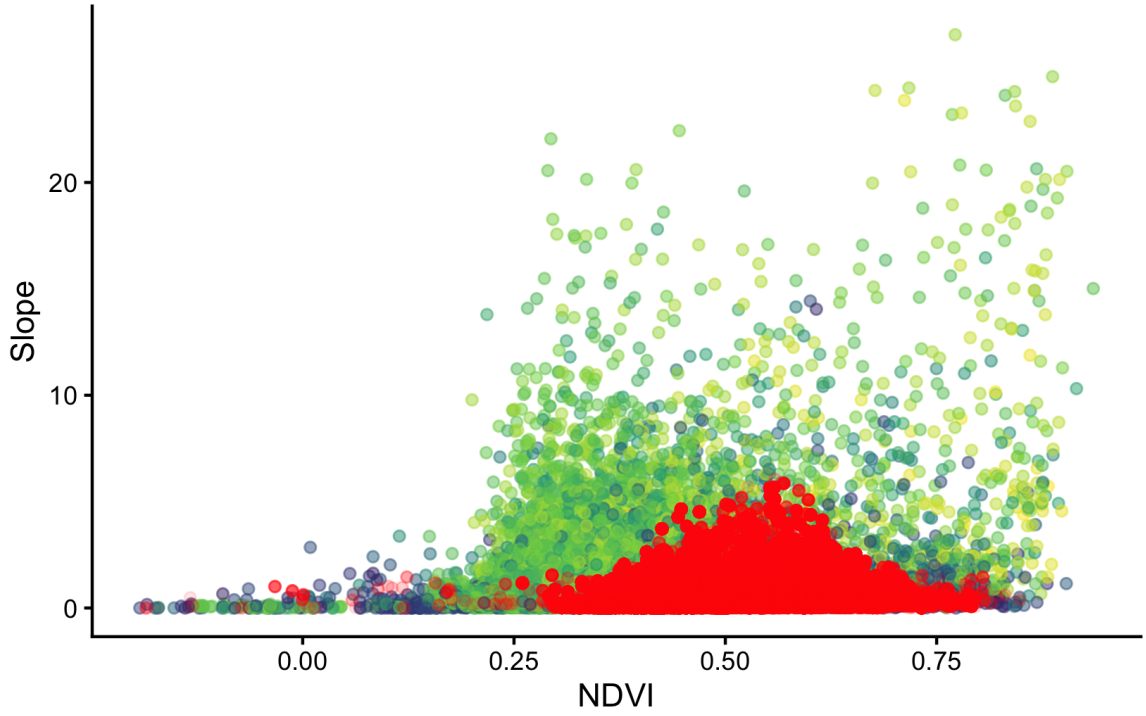
  geom_point(data = buffalo_parametric_popn_covs_thin,
             aes(x = NDVI, y = slope),
             colour = "red", alpha = training_points_alpha) +

  scale_colour_viridis_c(
    transform = "log1p",
    breaks = c(1, 10, 100, 1000, 5000)
    ) +

  labs(x = "NDVI", y = "Slope", colour = "Extrapolation\n(Shape)") +
  theme_classic() +
  theme(legend.position = "none")

ndvi_slope_plot
```

```
Warning: Removed 52 rows containing missing values or values outside the scale range
(`geom_point()`).
```



Plot elevation and slope with Shape values

```
elev_slope_plot <- ggplot() +

  geom_point(data = cov_extrap_stack_df_thin,
             aes(x = elevation, y = slope, colour = extrapolation), alpha = raster_alpha) +

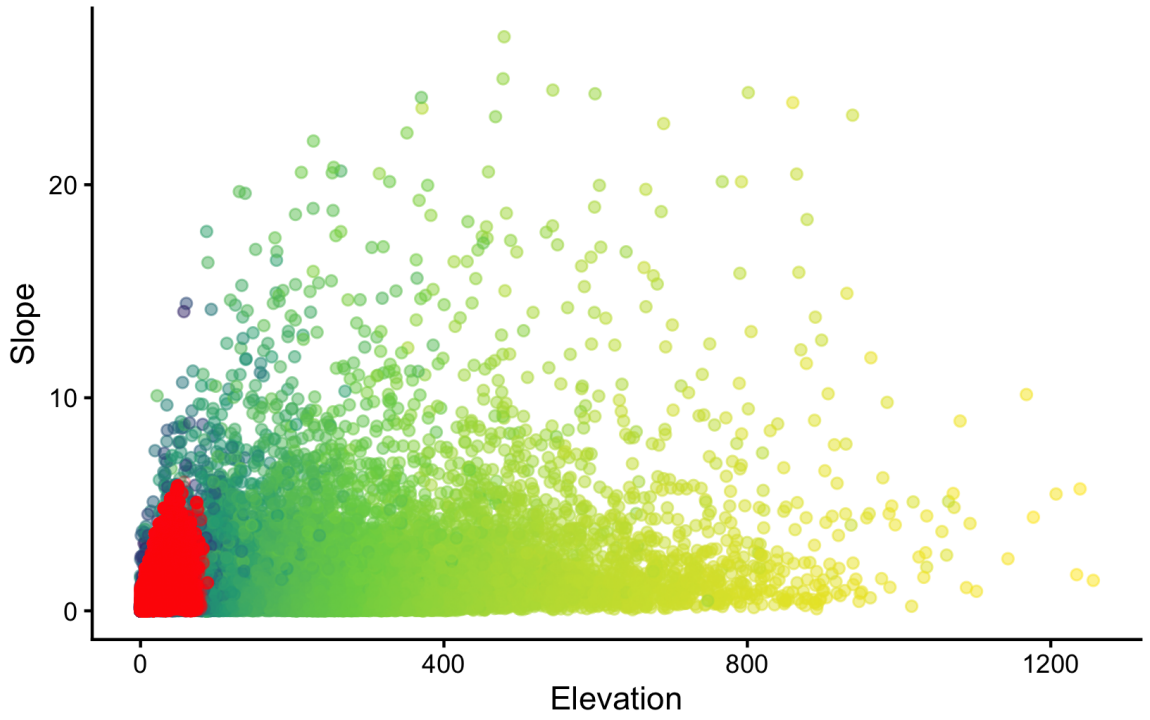
  geom_point(data = buffalo_parametric_popn_covs_thin,
             aes(x = elevation, y = slope),
             colour = "red", alpha = training_points_alpha) +

  scale_colour_viridis_c(
    transform = "log1p",
    breaks = c(1, 10, 100, 1000, 5000)
    ) +

  labs(x = "Elevation", y = "Slope", colour = "Extrapolation\n(Shape)") +
  theme_classic() +
```

```
  theme(legend.position = "none")

elev_slope_plot
```



Combine the plots

```
extrapolation_aus_plot /
  (ndvi_elev_plot | ndvi_slope_plot | elev_slope_plot) +
  plot_layout(heights = c(2, 1)) #+
```

```
Warning: The following aesthetics were dropped during statistical transformation: fill.
i This can happen when ggplot fails to infer the correct grouping structure in
  the data.
i Did you forget to specify a `group` aesthetic or to convert a numerical
  variable into a factor?

Warning: Raster pixels are placed at uneven horizontal intervals and will be shifted
i Consider using `geom_tile()` instead.

`geom_raster()` only works with linear coordinate systems, not `coord_sf()`.
i Falling back to drawing as `geom_rect()`.
```

```
Warning: Removed 52 rows containing missing values or values outside the scale range
(`geom_point()`).

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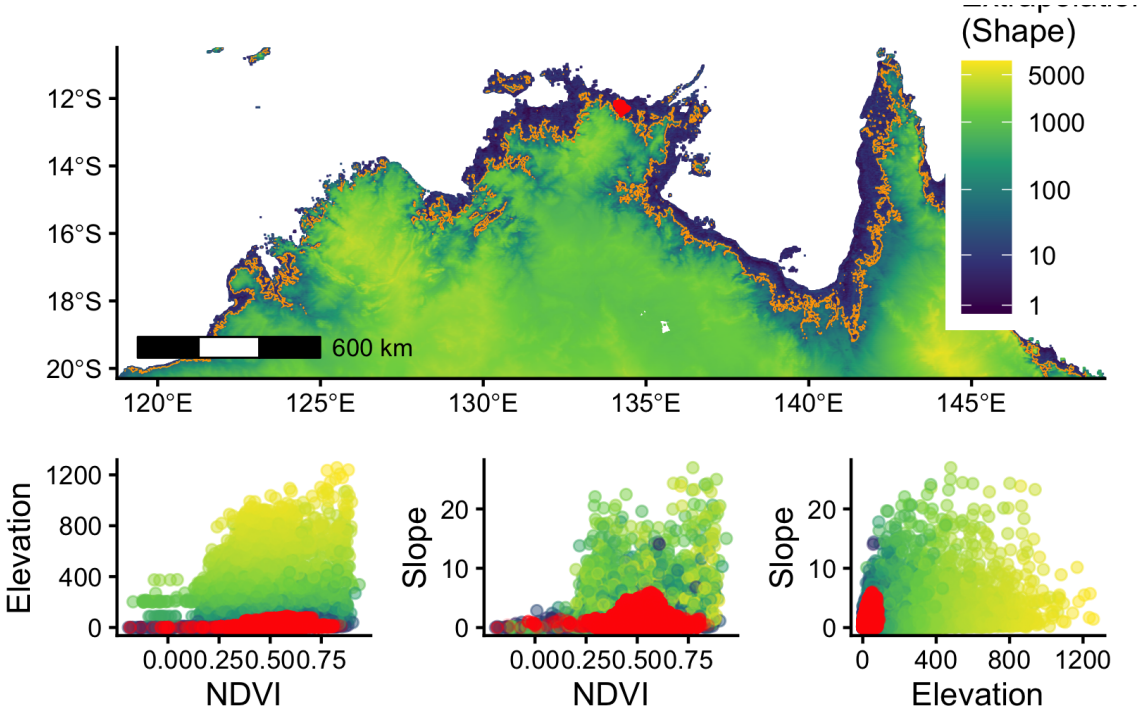
(`geom_point()`).
```




```
  # plot_annotation(tag_levels = "A")

ggsave("outputs/extrapolation_aus_covs.png",
       width = 180, height = 110, units = "mm", scale = 1.5, dpi = 600)
```

```
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  variable into a factor?

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```
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(`geom_point()`).
```

Create zoomed plot for earlier figure

Crop spatial covariates

```
# set the extent
zoom_extent_min_x <- min(buffalo_parametric_popn_covs_thin$x1_) - 20000
zoom_extent_max_x <- max(buffalo_parametric_popn_covs_thin$x1_) + 120000
zoom_extent_min_y <- min(buffalo_parametric_popn_covs_thin$y1_) - 50000
zoom_extent_max_y <- max(buffalo_parametric_popn_covs_thin$y1_) + 20000

# create extent
crop_extent <- terra::ext(
  zoom_extent_min_x,
  zoom_extent_max_x,
  zoom_extent_min_y,
  zoom_extent_max_y
)

ndvi_crop <- terra::crop(ndvi, crop_extent)
elev_crop <- terra::crop(elev, crop_extent)
slope_crop <- terra::crop(slope, crop_extent)
```

Assess extrapolation

```
# commented out here as it takes about 45 minutes to run
# tic()
#
# extrapolation_raster_crop <- extra_eval(
#   training_data = buffalo_parametric_popn_covs,
#   pr_ab = "y",
#   projection_data = c(ndvi_crop, elev_crop, slope_crop),
#   metric = "mahalanobis",
#   univar_comb = FALSE,
#   aggreg_factor = 1
```

```
# )
#
# beep(sound = 2)
#
# toc()

# terra::writeRaster(extrapolation_raster_crop, "outputs/extrapolation_raster_crop.tif", ove
extrapolation_raster_crop <- terra::rast("outputs/extrapolation_raster_crop.tif")
```

```
# mask and create dataframe for plotting
extrapolation_raster_crop <- terra::mask(extrapolation_raster_crop, ndvi_crop)
extrapolation_raster_cropped_df <- as.data.frame(extrapolation_raster_crop, xy = TRUE)

# plot with ggplot
ggplot(data = extrapolation_raster_cropped_df, aes(x = x, y = y, fill = extrapolation)) +

  geom_raster() +

  scale_fill_viridis_c(
    na.value = "transparent",
    transform = "log1p",
    breaks = c(1, 10, 100, 500)
  ) +

  geom_contour(aes(z = extrapolation),
               breaks = c(threshold_max), color = "orange", linewidth = 0.3) +

  # geom_point(data = buffalo_parametric_popn_covs %>% filter(y == 0),
  #            aes(x = x2_, y = y2_),
  #            colour = "black", alpha = 0.25, size = 0.01) +

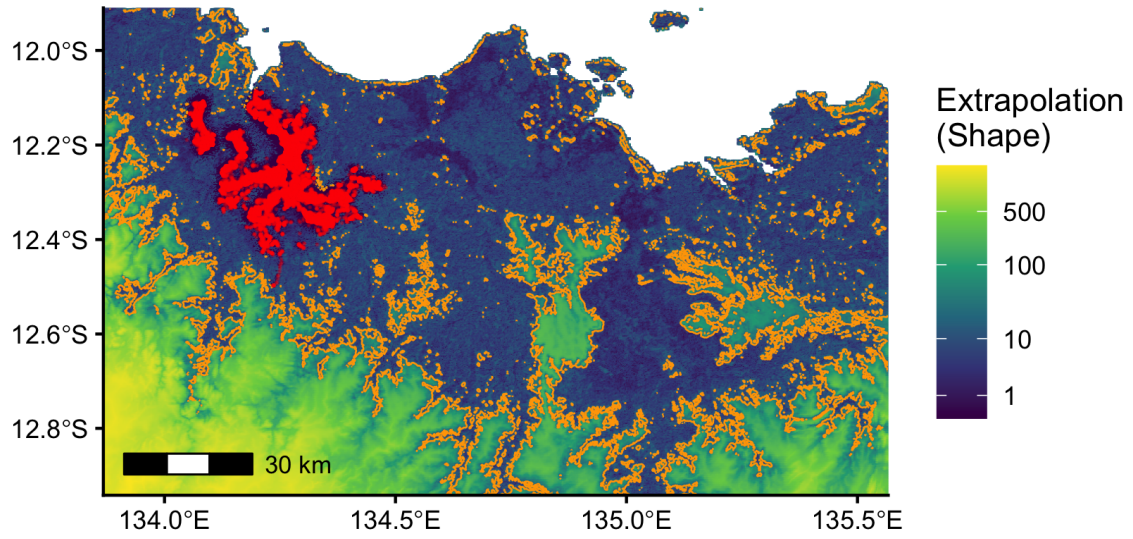
  geom_point(data = buffalo_parametric_popn_covs %>% filter(y == 1),
             aes(x = x1_, y = y1_),
             colour = "red", alpha = 0.25, size = 0.01) +

  annotation_scale(location = "bl", width_hint = 0.2) +
  coord_sf(crs = 3112, default_crs = 3112, expand = FALSE) +
  labs(x = NULL, y = NULL, fill = "Extrapolation\n(Shape)") +
  theme_classic() +
  theme(
    legend.position = "right"
    )
```

```
Warning: The following aesthetics were dropped during statistical transformation: fill.
```

```
i This can happen when ggplot fails to infer the correct grouping structure in
  the data.
i Did you forget to specify a `group` aesthetic or to convert a numerical
  variable into a factor?

`geom_raster()` only works with linear coordinate systems, not `coord_sf()`.
i Falling back to drawing as `geom_rect()`.
```




```
ggsave("outputs/extrapolation_raster_cropped_ggplot.png",
       width = 180, height = 90, units = "mm", scale = 1.5, dpi = 600)
```

```
Warning: The following aesthetics were dropped during statistical transformation: fill.
i This can happen when ggplot fails to infer the correct grouping structure in
  the data.
i Did you forget to specify a `group` aesthetic or to convert a numerical
  variable into a factor?

`geom_raster()` only works with linear coordinate systems, not `coord_sf()`.
i Falling back to drawing as `geom_rect()`.
```

References

Velazco, Santiago José Elías, Miranda Brooke Rose, Paulo De Marco Jr, Helen M Regan, and Janet Franklin. 2024. "How far can I extrapolate my species distribution model? Exploring shape, a novel method." *Ecography* 2024 (March). https://doi.org/10.1111/ecog.06992.