## Step 1: Combined all reptile shapefiles into one shapefile.

library(sf)

library(dplyr)

library(tools) # for file\_path\_sans\_ext()

# Set input and output paths

input\_folder <- "C:/path/to/your/shapefiles"

output\_file <- " "C:/GIS\_Projects/Reptiles/combined\_reptiles.shp"

# Get list of .shp files in folder

shapefiles <- list.files(path = input\_folder, pattern = "\\.shp$", full.names = TRUE)

# Read, tag, and simplify each shapefile

gdf\_list <- lapply(shapefiles, function(shp) {

gdf <- st\_read(shp, quiet = TRUE)

# Get species name from file name

species\_name <- file\_path\_sans\_ext(basename(shp))

# Create new simplified dataframe: just Species + geometry

gdf\_out <- gdf %>%

select(geometry) %>%

mutate(Species = species\_name) %>%

select(Species, geometry) # Ensure correct column order

return(gdf\_out)

})

# Combine safely

combined <- do.call(rbind, gdf\_list)

# Write output

st\_write(combined, output\_file, delete\_dsn = TRUE)

cat("✅ Combined shapefile saved to:", output\_file, "\n")

### Step 2: Calculate area

The new shapefile (output) has 418 rows and only contains one column – Species. This is the species name and showcases the distribution range of each species.

Details. Create a new column called Area\_km2 in ArcGIS. Field type = Double.

A screenshot of a computer

AI-generated content may be incorrect.

Following error message pops up: WARNING 000635: Skipping feature 365 because of NULL or EMPTY geometry.

### Step 3: Fix Error

1. The polygon “Scelotes montispectus” has NULL area. Deleted row/polygon from shapefile.
2. **Check Geometry of** Scelotes montispectus

WARNING 000442: could not find spatial index at -1 in Scelotes montispectus

1. Right click on Scelotes montispectus and export as new shapefile
2. Dissolve new Scelotes montispectus on binomial field.
3. Merge dissolved Scelotes montispectus to combined\_reptiles.
4. Delete unnecessary fields.
5. Calculate area of Scelotes montispectus.
6. **Check Geometry of** Combined\_reptiles2.shp.

**WARNING 000442:** self intersections at 316 in Combined\_reptiles2.shp

1. Repair geometry.

### Reproject reptile dataset to match NLC

Spatial reference details

PROJCS["Albers\_Conic\_Equal\_Area",GEOGCS["GCS\_WGS\_1984",DATUM["D\_WGS\_1984",SPHEROID["WGS\_1984",6378137.0,298.257223563]],PRIMEM["Greenwich",0.0],UNIT["Degree",0.0174532925199433]],PROJECTION["Albers"],PARAMETER["false\_easting",0.0],PARAMETER["false\_northing",0.0],PARAMETER["central\_meridian",25.0],PARAMETER["standard\_parallel\_1",-24.0],PARAMETER["standard\_parallel\_2",-33.0],PARAMETER["latitude\_of\_origin",0.0],UNIT["Meter",1.0]]

### Removed transformed PA.

1. nlc2022\_7class.tif decides the South African landscape into 7 different land classes. This information was already been reclassified into “natural” and “not-natural.”

A screenshot of a computer

AI-generated content may be incorrect.

library(sf)

library(terra)

library(exactextractr)

# Load data

protected\_areas <- st\_read("C:/GIS\_Projects/ProtectionLevel/SAPA\_2017\_EffScore/PL\_2017\_Apr25\_SK\_Albers.shp")

landcover <- rast("Y:/NATIONAL\_GIS/Working2023/nlc2022\_7")

# Define land cover classes that represent natural land

# Example: 1 = Forest, 2 = Grassland, 3 = Wetland

natural\_classes <- c(1, 2, 3) # replace with your real codes

# Create a binary mask where natural land = 1, else = NA

natural\_mask <- classify(landcover,

rcl = matrix(c(-Inf, Inf, NA), ncol = 3, byrow = TRUE))

natural\_mask[landcover %in% natural\_classes] <- 1

# Calculate the proportion of each polygon that overlaps natural land

protected\_areas$prop\_natural <- exact\_extract(natural\_mask, protected\_areas, 'mean', progress = TRUE)

# Keep only polygons with any overlap with natural land

protected\_areas\_natural <- protected\_areas[protected\_areas$prop\_natural > 0, ]

# Optional: Save the filtered shapefile

st\_write(protected\_areas\_natural, "path/to/protected\_areas\_natural\_only.shp", delete\_dsn = TRUE)

cat("✅ Finished! Protected areas intersecting natural land saved.\n")

### Intersect PA with reptiles and calculate area

### 

1. Back to the summary document – step 1 – List the no intersected species - I would compare the intersected species list with the full list of reptiles, species that are in the full list and not in the intersected list, is those that didn’t intersect. Maybe you have a different way of doing it.
2. Step 2 – yes please do check and maybe indicate in a column those that are larger than 10km2. What I have done: I have just added a new column to calculated the areas post intersect  (step 9 here) to give the areas of speciesXPA intersect. I’m not sure if you will do this in GIS, but I think once this step is done the rest of the data checks and filtering can be done in Excel.
3. Username: admnasiphi
4. Password: Softwaredwonloads&2025