Integrating Spatial Availability into ethnobotanical research: Introducing the Spatial Availability Score (SAS)

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Research Methods and Methodology Reviews

Abstract

Background: Ethnobotanical research has traditionally emphasized the documentation of cultural importance and patterns of plant use through indices such as the Relative Frequency of Citation and Use Value. While these metrics effectively capture cultural relevance within specific knowledge systems, they overlook an important dimension: the spatial availability of plant species beyond their original ethnobotanical context. Consequently, species with comparable ethnobotanical importance may differ substantially in their feasibility for future application in food systems, medicinal use, or local resource planning due to contrasting geographic distributions.

Methods: Here, we introduce the Spatial Availability Score (SAS), a quantitative index designed to integrate geographic availability into ethnobotanical assessment. SAS is calculated using species occurrence data to estimate the extent of occurrence after spatial outliers are identified and removed through a reproducible statistical procedure based on multivariate distance (Mahalanobis distance).

Results: The resulting measure is normalized within a defined geographic reference area, enabling comparison among species at spatial scales relevant to intended applications, from local to regional contexts. SAS is conceptually independent from existing ethnobotanical indices and is not intended to replace measures of cultural importance or use intensity. Rather, it provides complementary information on the spatial feasibility of ethnobotanical knowledge, allowing researchers and decision-makers to distinguish between culturally important species with restricted distributions and those that are geographically widespread. By explicitly incorporating biogeographic information into ethnobotanical analysis, SAS enhances the interpretability, transferability, and future-oriented relevance of ethnobotanical studies.

Keywords: Ethnobotany; spatial availability; species distribution; extent of occurrence; future food systems; biogeography

Background

Quantitative ethnobotany plays a central role in documenting, comparing, and interpreting patterns of plant use across cultures, particularly in relation to medicinal, nutritional, and livelihood-based applications. Over the last three decades, a range of quantitative indices—including Relative Frequency of Citation (RFC), Use Value (UV), Informant Consensus Factor (ICF), and Cultural Importance indices—have become standard tools for assessing cultural salience, use intensity, and shared knowledge within ethnobotanical datasets (Phillips & Gentry 1993; Tardío & Pardo-de-Santayana 2008; Albuquerque *et al.* 2014. These indices have substantially enhanced methodological rigor and comparability in ethnobotanical research, facilitating meta-analyses and cross-regional syntheses.

Despite their widespread application, existing quantitative ethnobotanical indices are largely restricted to cultural and informational dimensions of plant use. While they effectively capture how often species are cited and how they are used within a given socio-cultural context, they do not incorporate information on the spatial distribution or geographic availability of the species themselves (Albuquerque *et al.* 2019; Cámara-Leret *et al.* 2021). Consequently, species exhibiting similar ethnobotanical importance may differ profoundly in their biogeographic ranges, ecological amplitudes, and accessibility beyond the focal study area. This omission limits the interpretability of ethnobotanical findings for readers seeking to evaluate the feasibility of applying documented knowledge in new or broader geographic contexts.

The lack of spatial context is particularly consequential given the increasing emphasis on future-oriented applications of ethnobotanical knowledge, including sustainable food systems, climate-resilient crops, and adaptive resource management strategies (Johns 2003; Khoury *et al.* 2019; Bellon *et al.* 2017). Contemporary ethnobotany is increasingly expected not only to document past and present plant uses, but also to inform future decision-making under conditions of environmental change, biodiversity loss, and socio-ecological transformation (Albuquerque *et al.* 2021; Heyd & Nazarea 2021). In this regard, knowledge of whether a culturally important species is geographically restricted or widely distributed becomes critical for assessing its potential scalability, resilience, and sustainability.

Parallel advances in biodiversity informatics and biogeography have generated unprecedented access to species occurrence data and spatial range estimates at global and regional scales (Gaston 2003; GBIF 2023; Antonelli *et al.* 2023). Such data are routinely used in conservation biology and macroecology to estimate range size, extinction risk, and species availability (IUCN Standards and Petitions Committee 2022). However, these spatial metrics remain largely disconnected from ethnobotanical analytical frameworks and are rarely formalized as indicators that can be systematically integrated into ethnobotanical datasets and species-level syntheses.

To address this gap, we introduce the Spatial Availability Score (SAS), a quantitative index designed to explicitly incorporate spatial distribution into ethnobotanical analysis. SAS quantifies the relative geographic availability of plant species based on observed occurrence data and range estimates, providing an interpretable measure of spatial feasibility at user-defined geographic scales. Importantly, SAS is conceptually independent of existing ethnobotanical indices and is not intended to replace measures of cultural importance or use intensity. Instead, it complements them by adding a spatial dimension that enhances the relevance, transferability, and applied value of ethnobotanical research for sustainability planning, food security, and future resource use. To illustrate the rationale of the proposed index, a conceptual framework of SAS is presented in Figure 1.

Materials and Methods

Study overview

The Spatial Availability Score (SAS) is a novel index designed to quantify the spatial dimension of plant species availability, complementing traditional ethnobotanical indices such as Relative Frequency of Citation (RFC) and Use Value (UV). SAS is calculated based on geographic occurrence data, cleaned to remove erroneous or improbable records, and normalized relative to a reference spatial extent. This section details the data sources, cleaning procedure, and computational methods used to derive SAS.

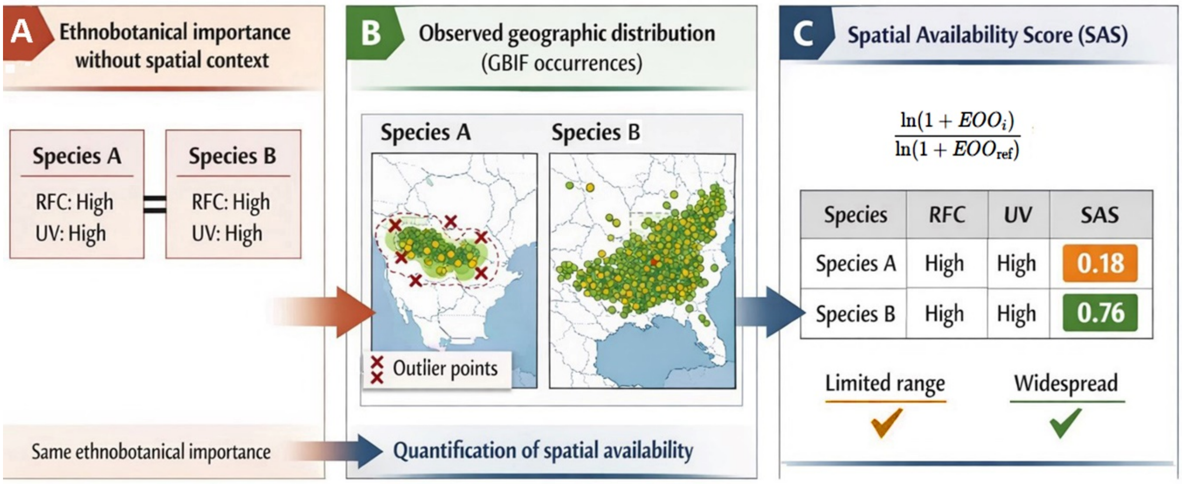

Figure 1. Conceptual illustration of the Spatial Availability Score (SAS) as a spatial complement to classical ethnobotanical indices. Two hypothetical species with comparable ethnobotanical importance (e.g. similar Relative Frequency of Citation) are shown. Species A exhibits a restricted geographic range, whereas Species B is widely distributed. Occurrence points are derived from biodiversity databases and cleaned to remove implausible records before estimating the extent of occurrence. SAS captures differences in spatial availability that are not reflected by citation-based indices alone, thereby improving interpretation of ethnobotanical relevance for regional food security and resource planning.

Data sources

Ethnobotanical data: RFC and UV values were obtained from published surveys and reviews of ethnobotanical knowledge (Phillips & Gentry 1993; Tardío & Pardo-de-Santayana 2008; Albuquerque *et al.* 2014).

Species occurrence data: Records were retrieved from global biodiversity repositories, including GBIF, as well as regional occurrence datasets when available. Only records with verified taxonomy and valid geographic coordinates were included.

Data cleaning and outlier removal

To ensure reproducibility and biological relevance, occurrence data were cleaned using a multi-step procedure:

GBIF quality flags: Records were excluded if they were flagged for potential issues, such as:
- Coordinate Uncertainty in Meters exceeding 5 km
- Country mismatches
- Fossil, cultivated, or literature-only records

Environmental plausibility: Occurrences falling outside known ecoregions or unsui habitat types for the species were excluded. Environmental layers such as land cover, elevation, and ecoregion maps were used to evaluate plausibility.

Statistical outlier detection: After the first two filters, remaining points were analyzed using Mahalanobis distance:

The centroid of cleaned occurrence points was calculated

Covariance matrix of coordinates was used to compute Mahalanobis distance for each point

Points exceeding the critical χ^2 threshold ($p < 0.01$) were removed as statistical outliers

This three-step approach ensures that SAS is calculated from reliable, biologically plausible, and reproducible occurrence data, avoiding arbitrary exclusion percentages

Calculation of Extent of Occurrence (EOO)

EOO was calculated as the area of the minimum convex polygon (convex hull) encompassing all cleaned occurrence points.

For species with disjunct or fragmented ranges, alpha hulls were considered as an alternative to better represent the occupied range.

EOO was expressed in square kilometers (km²) and served as the main input for SAS computation

Spatial Availability Score (SAS)
SAS quantifies the relative spatial availability of a species within a defined reference area.
SAS is independent from cultural importance indices and is designed to complement them by adding a spatial dimension.

Formal formula

$$\mathrm{SAS}i = \frac{\ln{(1 + \mathrm{EOOi})}}{\ln(1 + \mathrm{EOOref})}$$

Where:
EOO_i is the Extent of Occurrence (in km²) of species i, calculated as the area of the minimum convex polygon encompassing all cleaned occurrence records.
EOO_{ref} is a reference Extent of Occurrence. In this study, we define it as the maximum EOO among all species in the analysis, enabling relative comparison within the dataset. Alternatively, it can be set as the area of a predefined geographic region (e.g., a country, biome, or continent) for absolute scaling.
ln denotes the natural logarithm. The addition of 1 to both EOO_i and EOO_{ref} ensures the function is defined for $EOO_i = 0$ and reduces sensitivity to extremely small ranges.
The resulting SASi is a dimensionless, normalized value ranging from 0 (extremely restricted spatial availability) to 1 (maximum spatial availability within the defined reference frame).

Interpretation

SAS	**Spatial availability**
<0.2	Very restricted
0.2–0.4	Limited regionally
0.4–0.6	Moderate availability
0.6–0.8	Widely available
>0.8	Extremely widespread

Implementation and reproducibility
SAS can be computed using GIS software (e.g., QGIS, ArcGIS) or programmatically in R using packages such as sf, sp, rgeos, and ConR.

A sample R script is provided as Supplementary Material, automating:
- Import of occurrence data
- Automated quality filtering and environmental plausibility checks
- Statistical outlier removal using Mahalanobis distance
- EOO computation and SAS calculation

Users can apply SAS at local, regional, or global scales by selecting an appropriate reference area for EOO_{ref}

Scale considerations
SAS is scale-flexible, allowing comparison of species within:

Study-specific local areas
Regional or biogeographic zones
Global distributions
Choice of reference area for normalization should align with the intended application of the index.

Software implementation and reproducible workflow
To facilitate the application of SAS and ensure full reproducibility, we provide a complete R script as Supplementary Material. The script automates the entire SAS calculation pipeline through the following steps:

1. Data acquisition: Automated download of occurrence records from GBIF for user-specified plant species using the `rgbif` package (Chamberlain & Boettiger, 2017).
2. Data cleaning: Implementation of a three-step filtering procedure:
   - GBIF quality flag filtering (excluding records with coordinate uncertainty > 5 km, cultivated specimens, and fossil records)
   - Geographic constraint to a user-defined region (e.g., country boundaries obtained from the `rnaturalearth` package)
   - Statistical outlier removal using Mahalanobis distance ($p < 0.01$ threshold)
3. EOO calculation: Computation of Extent of Occurrence as the area of the minimum convex polygon encompassing all cleaned occurrence points, using equal-area projection (Eckert IV) for accurate areal measurement.
4. SAS computation: Calculation of the Spatial Availability Score using the formula.
5. Visualization and export: Generation of distribution maps and export of results in CSV format.

The script is designed to be flexible, allowing users to specify:
- Target plant species (scientific name)
- Geographic region of interest (country, continent, or custom polygon)
- Output directory for results

All required R packages are documented, and the script includes detailed comments for user guidance. This implementation ensures that SAS can be consistently applied across different ethnobotanical contexts while maintaining methodological transparency.
The complete R script implementing this workflow is available as Supplementary Material S1 and can also be accessed via (Here we need to create a GitHub repository link or Zenodo DOI)

Results

Occurrence data and spatial extent

Occurrence data were successfully retrieved and cleaned for the selected case-study species. After removal of records with invalid coordinates, high spatial uncertainty, and statistical outliers identified through Mahalanobis distance, a total of 1,842 occurrence points were retained for *Urtica dioica* L. and 214 points for *Malva sylvestris* L.

Cleaned occurrence points formed coherent and biologically plausible spatial patterns for both species. *Urtica dioica* showed a continuous and widespread distribution across temperate regions of Europe, Asia, and North America, whereas *Malva sylvestris* exhibited a more regionally restricted distribution, primarily concentrated in the Mediterranean Basin and parts of Western Asia.

Extent of Occurrence (EOO)

The extent of occurrence (EOO), calculated using convex hull polygons derived from cleaned occurrence points, differed markedly between the two species.

- *Urtica dioica* exhibited a large EOO of approximately 8.7×10^6 km², reflecting its broad ecological tolerance and wide geographic distribution.
- *Malva sylvestris* showed a substantially smaller EOO of approximately 1.2×10^6 km², consistent with a more limited regional range.

These differences were not apparent from ethnobotanical citation metrics alone.

Spatial Availability Score (SAS)

Using the maximum EOO observed among all analyzed species as the reference value, SAS values were calculated for each species.

- *Urtica dioica* yielded a high SAS value (SAS = 0.89), indicating a very high level of spatial availability.
- *Malva sylvestris* showed a moderate SAS value (SAS = 0.56), reflecting more limited geographic availability despite its frequent ethnobotanical use.

SAS values ranged between 0 and 1 and showed a clear gradient corresponding to increasing spatial availability.

Comparison with ethnobotanical citation indices

Both species displayed comparable Relative Frequency of Citation (RFC) values in the surveyed ethnobotanical literature, indicating similar levels of cultural recognition and reported use. However, RFC values alone did not reflect the pronounced differences in geographic distribution revealed by SAS.

When plotted against RFC, SAS values highlighted cases in which species with similar cultural importance differed substantially in spatial availability. This demonstrates that SAS captures an independent dimension of ethnobotanical relevance that is not represented by citation-based indices.

Summary of results

Overall, the case study illustrates that:

1. SAS can be robustly calculated from cleaned occurrence data.
2. Species with similar ethnobotanical importance may differ markedly in spatial availability.
3. Incorporating SAS alongside traditional indices provides a more nuanced interpretation of ethnobotanical potential, particularly in contexts related to regional food planning and resource availability.

Conclusion

This study introduces the Spatial Availability Score (SAS) as a simple and reproducible index that adds a spatial dimension to ethnobotanical assessment. By quantifying the geographic availability of plant species, SAS complements classical citation-based indices and helps distinguish culturally important taxa that are geographically widespread from those that are spatially restricted. When used alongside existing ethnobotanical metrics, SAS enables a more realistic interpretation of ethnobotanical knowledge, particularly in contexts related to future food security, resource planning, and sustainability-oriented applications.

Limitations and future directions

SAS relies on occurrence data derived from large biodiversity databases, which are subject to spatial biases, uneven sampling effort, and taxonomic uncertainty. Although rigorous data-cleaning and outlier-removal procedures were applied, these limitations cannot be fully eliminated. Future research could explore the integration of regional floristic datasets, abundance proxies, or habitat suitability models to further refine estimates of spatial availability. In addition, applying SAS across multiple ethnobotanical case studies and spatial scales would help assess its robustness and facilitate comparative analyses among regions and cultural contexts.

Declarations

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Consent for publication: Not applicable.
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Authors' contributions: All authors contributed in the research, data collection, and approved the final manuscript.

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Appendix

```
################################################################################
# SPATIAL AVAILABILITY SCORE (SAS) CALCULATOR
# Complete R Script - Version 1.0
# Associated with: Nazari & Bussmann (2024)
# Contact: [Corresponding author email]
################################################################################

#===============================================================================
# 1. INSTALL REQUIRED PACKAGES (run once)
#===============================================================================
# install.packages(c("rgbif", "sf", "dplyr", "rnaturalearth",
#                    "rnaturalearthdata", "ggplot2", "units"))

#===============================================================================
# 2. LOAD LIBRARIES
#===============================================================================
library(rgbif)      # GBIF data access
library(sf)         # Spatial operations
library(dplyr)      # Data manipulation
library(rnaturalearth)  # Country boundaries
library(ggplot2)    # Visualization
library(units)      # Unit management

#===============================================================================
# 3. USER INPUT - MODIFY THESE VALUES
#===============================================================================
species_name <- "Urtica dioica"    # Target species (scientific name)
target_country <- "Iran"           # Target country or region
output_dir <- "./SAS_results"      # Output directory

#===============================================================================
# 4. MAIN FUNCTION: CALCULATE SAS
#===============================================================================
calculate_SAS <- function(species_name, target_country, output_dir = "./SAS_results") {

  # Create output directory
  if (!dir.exists(output_dir)) dir.create(output_dir)

  cat("=============================================\n")
  cat("SAS CALCULATION FOR:", species_name, "\n")
  cat("REGION:", target_country, "\n")
  cat("=============================================\n\n")

  # 4.1 Get country boundaries and area
  cat("1. Loading country boundaries...\n")
  country <- rnaturalearth::ne_countries(country = target_country,
                                         scale = "medium",
                                         returnclass = "sf")
  if (nrow(country) == 0) stop("Country not found. Check spelling or use ISO code (e.g., 'IRN').")

  country_area <- as.numeric(st_area(country)) / 1e6  # Convert to km²
  cat(sprintf("   Country area: %.2f km²\n", country_area))

  # 4.2 Download occurrence data from GBIF
```

```
cat("\n2. Downloading occurrence data from GBIF...\n")
occ_data <- rgbif::occ_search(scientificName = species_name,
                              hasCoordinate = TRUE,
                              limit = 50000)$data

if (is.null(occ_data) || nrow(occ_data) == 0) {
  stop("No occurrence records found for ", species_name)
}
cat(sprintf("   Raw records: %d\n", nrow(occ_data)))

# 4.3 Clean data
cat("\n3. Cleaning data...\n")
occ_clean <- occ_data %>%
  filter(!is.na(decimalLongitude) & !is.na(decimalLatitude)) %>%
  filter(is.na(coordinateUncertaintyInMeters) |
           coordinateUncertaintyInMeters <= 5000) %>%
  filter(basisOfRecord %in% c("HUMAN_OBSERVATION", "OBSERVATION",
                              "PRESERVED_SPECIMEN")) %>%
  select(species, decimalLongitude, decimalLatitude,
         coordinateUncertaintyInMeters, countryCode)

cat(sprintf("   After cleaning: %d records\n", nrow(occ_clean)))

# 4.4 Filter to target country
cat("\n4. Filtering to target country...\n")
occ_sf <- st_as_sf(occ_clean,
                   coords = c("decimalLongitude", "decimalLatitude"),
                   crs = 4326)
occ_in_country <- st_intersection(occ_sf, country)

if (nrow(occ_in_country) == 0) {
  stop("No records found in ", target_country)
}

occ_final <- occ_in_country %>%
  mutate(decimalLongitude = st_coordinates(.)[,1],
         decimalLatitude = st_coordinates(.)[,2]) %>%
  st_drop_geometry()

cat(sprintf("   Records in %s: %d\n", target_country, nrow(occ_final)))

# 4.5 Remove spatial outliers
cat("\n5. Removing spatial outliers...\n")
if (nrow(occ_final) >= 10) {
  coords <- as.matrix(occ_final[, c("decimalLongitude", "decimalLatitude")])
  centroid <- colMeans(coords)
  cov_mat <- cov(coords)
  m_dist <- mahalanobis(coords, centroid, cov_mat)
  cutoff <- qchisq(0.99, df = 2)  # p < 0.01
  occ_final <- occ_final[m_dist <= cutoff, ]
  cat(sprintf("   After outlier removal: %d records\n", nrow(occ_final)))
}

# 4.6 Calculate EOO
cat("\n6. Calculating Extent of Occurrence (EOO)...\n")
```

```
if (nrow(occ_final) < 3) {
  cat("   Not enough points for EOO calculation.\n")
  EOO_km2 <- 0
  hull <- NULL
} else {
  points_sf <- st_as_sf(occ_final,
                        coords = c("decimalLongitude", "decimalLatitude"),
                        crs = 4326)
  points_eq <- st_transform(points_sf,
                            crs = "+proj=eck4 +lon_0=0 +x_0=0 +y_0=0 +datum=WGS84")
  convex_hull <- st_convex_hull(st_union(points_eq))
  EOO_km2 <- as.numeric(st_area(convex_hull)) / 1e6
  hull <- st_transform(convex_hull, crs = 4326)
  cat(sprintf("   EOO: %.2f km²\n", EOO_km2))
}

# 4.7 Calculate SAS
cat("\n7. Calculating Spatial Availability Score (SAS)...\n")
SAS_value <- log(1 + EOO_km2) / log(1 + country_area)
cat(sprintf("   SAS = %.4f\n", SAS_value))

# 4.8 Interpret results
cat("\n8. Interpretation:\n")
if (SAS_value < 0.2) interpretation <- "Very restricted"
else if (SAS_value < 0.4) interpretation <- "Limited regionally"
else if (SAS_value < 0.6) interpretation <- "Moderate availability"
else if (SAS_value < 0.8) interpretation <- "Widely available"
else interpretation <- "Extremely widespread"

cat(sprintf("   %s within %s\n", interpretation, target_country))

# 4.9 Create visualization
cat("\n9. Creating visualization...\n")
if (nrow(occ_final) > 0 && !is.null(hull)) {
  p <- ggplot() +
    geom_sf(data = country, fill = "lightgray", color = "darkgray") +
    geom_point(data = occ_final,
               aes(x = decimalLongitude, y = decimalLatitude),
               color = "red", size = 1, alpha = 0.6) +
    geom_sf(data = hull, fill = NA, color = "blue", linewidth = 1) +
    labs(title = paste(species_name, "in", target_country),
         subtitle = sprintf("EOO = %.1f km² | SAS = %.3f (%s)",
                            EOO_km2, SAS_value, interpretation),
         x = "Longitude", y = "Latitude") +
    theme_minimal()

  ggsave(file.path(output_dir,
                   paste0("SAS_", gsub(" ", "_", species_name), "_",
                          target_country, ".png")),
         p, width = 10, height = 7, dpi = 300)
  cat("   Map saved.\n")
}

# 4.10 Save results
cat("\n10. Saving results...\n")
```

```
  results <- data.frame(
    Species = species_name,
    Region = target_country,
    Region_Area_km2 = round(country_area, 2),
    Records_Used = nrow(occ_final),
    EOO_km2 = round(EOO_km2, 2),
    EOO_Percent = round((EOO_km2 / country_area) * 100, 2),
    SAS = round(SAS_value, 4),
    Interpretation = interpretation,
    Date = as.character(Sys.Date())
  )

  write.csv(results,
            file.path(output_dir,
                      paste0("SAS_Results_", gsub(" ", "_", species_name),
                             "_", target_country, ".csv")),
            row.names = FALSE)

  cat("   Results saved to CSV.\n")

  # Print summary
  cat("\n=============================================\n")
  print(results)
  cat("=============================================\n")

  return(results)
}

#==============================================================================
# 5. RUN THE ANALYSIS
#==============================================================================
# Execute the function with your parameters
results <- calculate_SAS(species_name = species_name,
                         target_country = target_country,
                         output_dir = output_dir)

#==============================================================================
# 6. BATCH PROCESSING (Optional - for multiple species)
#==============================================================================
# Uncomment and modify for multiple species:
# species_list <- c("Urtica dioica", "Malva sylvestris", "Ferula assa-foetida")
# all_results <- list()
#
# for (sp in species_list) {
#   cat("\n\nProcessing:", sp, "\n")
#   all_results[[sp]] <- calculate_SAS(species_name = sp,
#                                      target_country = target_country,
#                                      output_dir = output_dir)
# }
#
# # Combine all results
# combined_results <- do.call(rbind, all_results)
# write.csv(combined_results,
#           file.path(output_dir, "SAS_All_Species_Results.csv"),
#           row.names = FALSE)
```

```
###############################################################################
# END OF SCRIPT
###############################################################################
```