

Spatial Analysis Pipeline Documentation - Zonation Configuration Generator

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Overview

This R script automates the creation of species list configuration files (.spp) for Zonation conservation prioritization software. It scans directories for raster files (.tif) and generates a properly formatted configuration file that Zonation can use to run spatial prioritization analyses.

Purpose

Zonation is a spatial conservation prioritization framework that requires a species list file (.spp) to define which biodiversity features (species distributions, habitat maps, etc.) should be included in the analysis. This script eliminates the manual process of creating these configuration files.

Required R Packages

- **Base R only** - No additional packages required
- Uses built-in functions: `file.path()`, `list.files()`, `dir.exists()`, `writeLines()`

Directory Structure Requirements

The script expects the following directory structure:

```
D:/PAN - DELTA/
└── ANALISES/
    └── priorizacao/      # Main prioritization directory
        ├── *.*tif          # General raster files
        └── spp_alvo/       # Target species directory (optional)
            ├── *.*tif          # Individual species raster files
            └── 00_splist_restauracao.spp # Output file (generated)
```

Input Requirements

Raster Files

- **Format:** GeoTIFF files (`.tif` extension)
- **Location:**
 - Main directory: `ANALISES/priorizacao/`
 - Species directory: `ANALISES/priorizacao/spp_alvo/` (if exists)
- **Content:** Any biodiversity feature layers (species distributions, habitats, environmental variables)

- **Naming:** No specific requirements, but meaningful names recommended

Function Documentation

`generate_species_config(base_dir)`

Purpose

Scans specified directories for .tif files and creates a Zonation-compatible species list configuration file.

Parameters

- `base_dir`: String - Base directory path of the project (e.g., "D:/PAN - DELTA")

Process Flow

1. Constructs paths to prioritization directories
2. Lists all .tif files in the main prioritization directory
3. Checks if species subdirectory exists and lists its .tif files
4. Combines all file lists, removes duplicates, and sorts alphabetically
5. Creates configuration lines with default Zonation parameters
6. Writes the formatted .spp file

Output

- **File:** `00_splist_restauracao.spp`
- **Location:** `[base_dir]/ANALISES/priorizacao/`
- **Console feedback:**
 - Path where file was generated
 - Total number of files processed

Output File Format

The generated .spp file follows Zonation's required format:

Header Line

```
#SpeciesWeight #alfa-value #BQP #NQP #depends_of_cell_removal_rules #species_names
```

Data Lines

Each .tif file gets one line with tab-separated values:

```
0 0 1 1 1 [filename.tif]
```

Parameter Explanations

Parameter	Value	Description
SpeciesWeight	0	Species importance weight (0 = equal weight for all)
alfa-value	0	Distribution smoothing parameter (0 = no smoothing)
BQP	1	Biodiversity feature weight
NQP	1	Negative feature weight
depends_of_cell_removal_rules	1	Cell removal dependency (1 = standard)
species_names	filename	Path to the raster file

Example Output

A typical generated .spp file might look like:

```
#SpeciesWeight #alfa-value #BQP #NQP #depends_of_cell_removal_rules #species_names
0 0 1 1 1 agro.tif
0 0 1 1 1 app_antropizada.tif
0 0 1 1 1 energia.tif
0 0 1 1 1 floresta.tif
0 0 1 1 1 Alouatta_caraya.tif
0 0 1 1 1 Sapajus_cay.tif
```

Usage Instructions

1. **Ensure directory structure** matches requirements
2. **Place all .tif files** in appropriate directories
3. **Update base directory** in the script:

```
r
base_dir <- "D:/PAN - DELTA" # Change to your path
```

4. **Run the script:**

```
r
source("generate_zonation_config.R")
```

Or execute directly in R/RStudio

Integration with Zonation

After generating the .spp file:

1. **Open Zonation software**

2. **Create new project** or open existing
3. **Load the .spp file** as the species list
4. **Configure additional Zonation settings:**
 - Cell removal rule
 - Warp factor
 - Edge removal
 - Mask layers
5. **Run the prioritization**

Customization Options

To modify default parameters, edit the line generation section:

```
r  
lines <- sapply(tif_files, function(file) {  
  paste("0", "0", "1", "1", "1", file, sep = "\t")  
})
```

Change values as needed:

- First "0": Species weight (increase for higher priority species)
- Second "0": Alpha value (increase for distribution smoothing)
- First "1": BQP (biodiversity quality penalty)
- Second "1": NQP (negative quality penalty)
- Third "1": Cell removal rules dependency

Common Use Cases

1. Equal Weight Analysis

Default configuration - all features treated equally (current setup)

2. Weighted Species Priority

Modify species weights based on conservation status:

```
r  
# Example: Higher weight for endangered species  
weight <- ifelse(grepl("endangered", file), "2", "0")
```

3. Excluding Certain Files

Add filtering before creating lines:

```
r  
  
# Example: Exclude temporary files  
tif_files <- tif_files[!grepl("temp", tif_files)]
```

Troubleshooting

Issue	Solution
No files found	Check directory paths and .tif file presence
Permission denied	Ensure write permissions in output directory
Zonation won't read file	Check for proper tab separation and encoding
Missing files in Zonation	Verify relative vs absolute paths

Notes

- **File paths:** The script uses relative paths (just filenames). Ensure Zonation project is configured to find these files
- **Large datasets:** For many files (>1000), consider grouping or filtering
- **Special characters:** Avoid special characters in filenames that might cause issues
- **File order:** Files are sorted alphabetically in the output

Related Workflows

This script is typically used after:

1. Species distribution modeling
2. Raster processing and standardization
3. Environmental layer preparation

And before:

1. Zonation prioritization runs
2. Conservation planning analyses
3. Restoration priority mapping

References

For more information on Zonation parameters and configuration:

- Moilanen, A., et al. (2014). Zonation v4 User Manual

- Zonation official documentation: [https://www.syke.fi/en-US/Research_Development/Nature/Specialist work and projects/Zonation](https://www.syke.fi/en-US/Research_Development/Nature/Specialist_work_and_projects/Zonation)