

# Package ‘ZonationR’

April 21, 2026

**Title** Interface to 'Zonation' for Reproducible Prioritization Workflows

**Version** 1.0.1

**Description** An interface to 'Zonation' software, enabling users to run spatial conservation prioritization workflows in 'R'. It streamlines input preparation, execution, and post-processing, while supporting reproducibility and lowering the entry barrier for learning, teaching, and research in conservation planning. The methods implemented in 'Zonation' are described in Moilanen et al. (2022) <[doi:10.1111/2041-210X.13819](https://doi.org/10.1111/2041-210X.13819)>.

**License** GPL (>= 3)

**Encoding** UTF-8

**RoxygenNote** 7.3.3

**Imports** dplyr, ggplot2, ggspatial, rlang, terra, tidyr, utils, viridis

**Suggests** knitr, mockery, rmarkdown, testthat (>= 3.0.0), withr

**Config/testthat/edition** 3

**URL** <https://github.com/thiago-cav/ZonationR>,  
<https://thiago-cav.github.io/ZonationR/>

**BugReports** <https://github.com/thiago-cav/ZonationR/issues>

**Config/Needs/website** rmarkdown

**Depends** R (>= 4.1.0)

**NeedsCompilation** no

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**Repository** CRAN

**Date/Publication** 2026-04-21 19:22:08 UTC

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---

check_dir_writable	<i>Check that an output directory is writable</i>
--------------------	---

---

### Description

This helper validates that a given directory exists and that the current R process has permission to create and delete a temporary file in it. It is intended for use before writing output files.

### Usage

```
check_dir_writable(out_dir)
```

### Arguments

out\_dir            character(1). Path to the directory that should be writable.

### Value

Returns TRUE invisibly when the directory exists and is writable. The function otherwise throws an error describing the problem:

- if the directory does not exist, an error stating that it does not exist;
- if the directory is not writable, an error stating that it is not writable.

### See Also

Other preflight: [check\\_raster\\_uniformity\(\)](#), [check\\_zonation\\_executable\(\)](#)

**Examples**

```
dir <- tempdir()
check_dir_writable(dir)
```

---

```
check_raster_uniformity
  Check raster uniformity
```

---

**Description**

Verifies that all raster files in a folder are compatible with Zonation. Compatibility requires that all rasters have:

- identical resolution (cell size)
- identical extent (number of rows and columns)
- identical projection (CRS)

**Usage**

```
check_raster_uniformity(spp_file_dir)
```

**Arguments**

spp\_file\_dir    Character. Path to the folder containing raster files.

**Details**

Supported raster formats: .tif, .tiff, .img, .asc.

**Value**

Prints a message confirming uniformity. Stops with an error otherwise.

**See Also**

Other preflight: [check\\_dir\\_writable\(\)](#), [check\\_zonation\\_executable\(\)](#)

**Examples**

```
withr::with_tempdir({

  r1 <- terra::rast(nrows = 5, ncols = 5)
  terra::values(r1) <- runif(terra::ncell(r1))

  r2 <- terra::rast(r1)
  terra::values(r2) <- runif(terra::ncell(r2))
```

```
terra::writeRaster(r1, "r1.tif", overwrite = TRUE)
terra::writeRaster(r2, "r2.tif", overwrite = TRUE)

check_raster_uniformity(".")
})
```

---

check\_zonation\_executable

*Check for Zonation 5 executable*

---

### Description

This function checks if the Zonation 5 executable is available on the system. It can verify a specific path provided by the user or search common installation locations. The function works on both Windows and Linux systems.

### Usage

```
check_zonation_executable(zonation_path = NULL, os = NULL)
```

### Arguments

zonation_path	Optional character string specifying the path to check. If not provided, the function will search common installation locations.
os	Operating system. If NULL (default), automatically detected from the system. Can be set to "Windows" or "Linux" manually.

### Details

For Windows, the function searches for z5.exe in:

- The provided path (if given)
- C:/Program Files (x86)/Zonation5
- C:/Program Files/Zonation5

For Linux, the function searches for zonation5 in:

- The provided path (if given)
- Common locations like ~/Applications, ~/bin, /usr/local/bin, /usr/bin
- The system PATH

**Value**

A list with the following components:

found	Logical indicating if the executable was found
path	Character string with the path where the executable was found (or NULL)
executable	Character string with the full path to the executable (or NULL)
os	Character string indicating the detected operating system
message	Character string with a descriptive message

**See Also**

Other preflight: [check\\_dir\\_writable\(\)](#), [check\\_raster\\_uniformity\(\)](#)

**Examples**

```
check_zonation_executable()
```

---

command_file	<i>Create a Zonation command file</i>
--------------	---------------------------------------

---

**Description**

This function generates a command file for running Zonation and specifies the analysis options and related parameters. The file is saved with a .cmd (Windows) or .sh (Linux) suffix.

**Usage**

```
command_file(  
  os = "os_detection",  
  zonation_path,  
  flags = "",  
  marginal_loss_mode = "CAZ2",  
  gui_activated = FALSE,  
  settings_file = "settings_file.z5",  
  output_dir = "output"  
)
```

**Arguments**

os	Operating system. By default, the system is detected automatically. Alternatively, users can explicitly specify "Windows" or "Linux".
zonation_path	The specification for the path where Zonation 5 is installed.
flags	Flags that control which analysis options are used. Used to include single letter codes that switch analysis options on. Available options are: a, w, g, h, x, X, t.

marginal_loss_mode	Character string specifying the marginal loss rule. Available options are "CAZ1", "CAZ2", "ABF", "CAZMAX", "LOAD", and "RAND". Default is "CAZ2".
gui_activated	This parameter controls whether the Zonation Graphical User Interface (GUI) is launched when running the command file. Default is FALSE.
settings_file	Character string specifying the settings file. Default is "settings_file.z5".
output_dir	A character string specifying the name of the output directory where the analysis results will be saved. Default is "output".

**Value**

A Zonation command file containing the specified analysis options.

**See Also**

Other preprocessing: [feature\\_list\(\)](#), [settings\\_file\(\)](#)

**Examples**

```
withr::with_tempdir({

  tmp_settings <- tempfile(fileext = ".z5")
  writeLines("feature list file = feature_list.txt", tmp_settings)

  command_file(
    zonation_path = "path/to/zonation",
    settings_file = tmp_settings
  )

  command_file(
    zonation_path = "path/to/zonation",
    marginal_loss_mode = "ABF",
    gui_activated = TRUE,
    settings_file = tmp_settings
  )
})
```

---

cost\_summary

*Summarize remaining cost at specified landscape proportions*

---

**Description**

Reads a Zonation `summary_curves.csv` file (space-separated), finds the row closest to each value in `landscape_prop`, and returns remaining cost and percentage of maximum cost at those proportions. Optionally writes the result to `dir/performance/cost_summary.csv`.

**Usage**

```
cost_summary(
  dir,
  output_folder_name = "output",
  landscape_prop,
  save_output = FALSE
)
```

**Arguments**

`dir` Character. Path to the directory containing the Zonation output folder.

`output_folder_name` Character. Name of the output folder inside `dir`. Default is "output".

`landscape_prop` Numeric vector. Landscape proportions (rank values) at which to report cost (e.g. `c(0.03, 0.2, 0.5)`).

`save_output` Logical. If TRUE, the result is written as a CSV to `dir/performance/cost_summary.csv`. Default FALSE.

**Value**

A data frame with columns:

- `rank` - the requested proportion
- `remaining_cost` - remaining cost at that rank
- `percentage` - remaining cost as percentage of maximum cost

**See Also**

Other postprocessing: [coverage\\_distribution\(\)](#), [feature\\_curves\(\)](#), [feature\\_representation\(\)](#), [priority\\_map\(\)](#), [rank\\_similarity\(\)](#), [summary\\_curves\(\)](#)

**Examples**

```
withr::with_tempdir({
  dir.create("output")

  # simulate Zonation-style summary_curves.csv structure
  write.table(
    data.frame(
      rank = seq(0, 1, length.out = 10),
      remaining_cost = runif(10, 50, 100),
      dummy1 = runif(10),
      dummy2 = runif(10)
    ),
    file = file.path("output", "summary_curves.csv"),
    row.names = FALSE,
    col.names = TRUE,
    sep = " "
  )
})
```

```
)  
  
cost_summary(  
  dir = ".",  
  output_folder_name = "output",  
  landscape_prop = c(0.2, 0.5, 0.8)  
)  
  
})
```

---

coverage\_distribution *Plot coverage distribution at a given rank*

---

### Description

This function reads a Zonation feature curves file and plots the distribution of feature coverage values at a specified priority rank. The output is a ggplot object, which can be further customized by the user. Optionally, the plot can be saved to disk as a high-quality figure.

### Usage

```
coverage_distribution(  
  dir,  
  output_folder_name = "output",  
  target_rank,  
  save_path = NULL,  
  dpi = 300,  
  width = 8,  
  height = 6  
)
```

### Arguments

dir	Character. Path to the directory containing the Zonation output folder.
output_folder_name	Character. Name of the Zonation output folder inside dir (default: "output").
target_rank	Numeric. The rank value at which coverage distributions should be extracted and plotted.
save_path	Character. Optional file path to save the plot. The file format is inferred from the specified extension (e.g. ".png", ".pdf", ".tiff").
dpi	Numeric. Resolution (dots per inch) for saved figures. Default is 300.
width	Numeric. Width of the saved figure in inches. Default is 8.
height	Numeric. Height of the saved figure in inches. Default is 6.

**Value**

A ggplot object showing the distribution of feature coverage values at the specified priority rank.

**See Also**

Other postprocessing: [cost\\_summary\(\)](#), [feature\\_curves\(\)](#), [feature\\_representation\(\)](#), [priority\\_map\(\)](#), [rank\\_similarity\(\)](#), [summary\\_curves\(\)](#)

**Examples**

```
withr::with_tempdir({  
  
  data_path <- system.file(  
    "extdata",  
    "feature_curves.csv",  
    package = "ZonationR"  
  )  
  
  dir.create("output")  
  
  file.copy(  
    data_path,  
    file.path("output", "feature_curves.csv"),  
    overwrite = TRUE  
  )  
  
  p <- coverage_distribution(  
    dir = ".",  
    output_folder_name = "output",  
    target_rank = 0.9  
  )  
  
  print(p)  
})
```

---

feature\_curves

*Plot feature performance curves*

---

**Description**

Reads the Zonation feature\_curves.csv and features\_info.csv files, standardizes the feature names, and plots representation vs priority rank for each feature. Supports a single color with transparency or the viridis palette.

**Usage**

```
feature_curves(
  dir,
  output_folder_name = "output",
  palette = "gray",
  alpha = 0.3,
  show_legend = FALSE,
  save_path = NULL,
  dpi = 300,
  width = 8,
  height = 6
)
```

**Arguments**

<code>dir</code>	Character. Path to the directory containing the Zonation output folder.
<code>output_folder_name</code>	Character. Name of the Zonation output folder (default: "output").
<code>palette</code>	Character. Either "gray" (default) for a single-color plot, a single color name, or "viridis" to use the viridis palette for multiple features.
<code>alpha</code>	Numeric. Transparency of lines (0 fully transparent, 1 fully opaque). Default is 0.3.
<code>show_legend</code>	Logical. If TRUE, shows legend (only applicable when palette = "viridis"). Default is FALSE.
<code>save_path</code>	Character. Optional path to save the plot as PNG. Default is NULL (does not save).
<code>dpi</code>	Numeric. Resolution (dots per inch) for saved figures. Default is 300.
<code>width</code>	Numeric. Width of the saved figure in inches. Default is 12.
<code>height</code>	Numeric. Height of the saved figure in inches. Default is 8.

**Value**

A ggplot object representing feature curves. If `save_path` is provided, also saves the plot as PNG.

**See Also**

Other postprocessing: [cost\\_summary\(\)](#), [coverage\\_distribution\(\)](#), [feature\\_representation\(\)](#), [priority\\_map\(\)](#), [rank\\_similarity\(\)](#), [summary\\_curves\(\)](#)

**Examples**

```
withr::with_tempdir({
  data_path <- system.file(
    "extdata",
    package = "ZonationR"
  )
})
```

```
dir.create("output")

file.copy(
  file.path(data_path, "feature_curves.csv"),
  "output/feature_curves.csv",
  overwrite = TRUE
)

file.copy(
  file.path(data_path, "features_info.csv"),
  "output/features_info.csv",
  overwrite = TRUE
)

p1 <- feature_curves(
  dir = ".",
  output_folder_name = "output"
)

print(p1)

# Plot using viridis palette with legend
p2 <- feature_curves(
  dir = ".",
  output_folder_name = "output",
  palette = "viridis",
  show_legend = TRUE
)

print(p2)
})
```

---

feature\_list

*Create a feature list from raster files*

---

### **Description**

This function generates a feature list from raster files in a specified directory, adding optional attributes to the list based on user-defined parameters. The resulting feature list is written to a text file. Supported raster formats include GeoTIFF (.tif, .tiff), ERDAS Imagine (.img), and ASCII Grid (.asc).

### **Usage**

```
feature_list(spp_file_dir, weight = NULL, group = NULL, threshold = NULL)
```

**Arguments**

spp_file_dir	A character string specifying the directory containing the raster files.
weight	An optional numeric vector (float) to assign weights to the features in the list.
group	An optional integer vector (int) representing the output group number for each raster.
threshold	An optional numeric vector (float) representing threshold values for each raster. If thresholding is applied, values in the input raster below the threshold are set to zero. Layers that contain only zeros after thresholding are removed from the analysis.

**Value**

A text file containing a feature list of rasters along with any additional attributes specified by the user.

**See Also**

Other preprocessing: [command\\_file\(\)](#), [settings\\_file\(\)](#)

**Examples**

```
withr::with_tempdir({  
  
  file.create("species1.tif")  
  file.create("species2.tif")  
  
  feature_list(spp_file_dir = ".")  
})
```

---

feature\_representation

*Calculate feature representation within an area*

---

**Description**

This function calculates the representation of each feature across raster cells, and can optionally summarize results within a specified area.

**Usage**

```
feature_representation(feature_layers, area_mask = NULL)
```

**Arguments**

- `feature_layers` A `terra::SpatRaster` with one or more layers representing feature distributions (e.g., species distributions, habitat suitability).
- `area_mask` Optional. A `terra::SpatRaster` or `terra::SpatVector` defining the analysis area. If a raster is provided, it should follow the Zonation analysis area mask convention, where cells with value 1 represent the area of interest and cells with value 0 or NA are excluded. If a `SpatVector` is provided, it will be rasterized to match the resolution and extent of `feature_layers`.

**Value**

A list with two elements:

**representation\_layers** A `terra::SpatRaster` where each layer contains the fractional representation of the corresponding feature across the landscape. Each cell value represents the proportion of the global total representation of that feature occurring in that cell.

**representation\_in\_area** A named numeric vector containing the representation of each feature within the specified `area_mask`. If no area is provided, this element returns `NULL`.

**See Also**

Other postprocessing: [cost\\_summary\(\)](#), [coverage\\_distribution\(\)](#), [feature\\_curves\(\)](#), [priority\\_map\(\)](#), [rank\\_similarity\(\)](#), [summary\\_curves\(\)](#)

**Examples**

```
r <- terra::rast(nrows = 10, ncols = 10)
f1 <- terra::setValues(r, runif(terra::ncell(r)))
f2 <- terra::setValues(r, runif(terra::ncell(r)))
features <- c(f1, f2)
names(features) <- c("feature_1", "feature_2")

mask <- r
terra::values(mask) <- sample(c(0,1), terra::ncell(mask), replace = TRUE)

result <- feature_representation(features, mask)
result$representation_in_area
```

---

priority\_map

*Plot priority ranking maps*

---

**Description**

`priority_map()` reads a rank map raster from a specified folder and creates a `ggplot2` map. It can plot the raster as continuous values or classify it into discrete categories with custom breaks and labels.

## Usage

```
priority_map(  
  dir,  
  output_folder_name = "output",  
  breaks = NULL,  
  labels = NULL,  
  palette = "viridis",  
  classify = FALSE,  
  show_legend = TRUE,  
  save_path = NULL,  
  dpi = 300,  
  width = 8,  
  height = 6  
)
```

## Arguments

<code>dir</code>	Character. Path to the variant folder containing the output folder.
<code>output_folder_name</code>	Character. Name of the output folder inside <code>dir</code> . Default is "output".
<code>breaks</code>	Numeric vector. Break points for reclassifying rank values. Required only if <code>classify = TRUE</code> . Must have length equal to <code>length(labels) + 1</code> .
<code>labels</code>	Character vector. Category labels for each reclassification interval. Required only if <code>classify = TRUE</code> . Length must equal <code>length(breaks) - 1</code> .
<code>palette</code>	Character or vector of colors. If "viridis", the function uses a reversed viridis palette (option "H") for classified maps. Otherwise, a vector of colors can be provided. Default is "viridis".
<code>classify</code>	Logical. If TRUE, raster values are converted into classes using breaks and labels. Default is FALSE.
<code>show_legend</code>	Logical. Whether to display the legend. Default is TRUE.
<code>save_path</code>	Character. File path to save the plot. If NULL (default), the plot is not saved.
<code>dpi</code>	Numeric. Resolution (dots per inch) for saved figures. Default is 300.
<code>width</code>	Numeric. Width of the saved figure in inches. Default is 8.
<code>height</code>	Numeric. Height of the saved figure in inches. Default is 6.

## Value

A ggplot object representing the priority map.

## See Also

Other postprocessing: [cost\\_summary\(\)](#), [coverage\\_distribution\(\)](#), [feature\\_curves\(\)](#), [feature\\_representation\(\)](#), [rank\\_similarity\(\)](#), [summary\\_curves\(\)](#)

**Examples**

```
withr::with_tempdir({

  data_path <- system.file(
    "extdata",
    package = "ZonationR"
  )

  dir.create("output")

  # copy example rankmap
  file.copy(
    file.path(data_path, "rankmap.tif"),
    "output/rankmap.tif",
    overwrite = TRUE
  )

  # ---- continuous map ----
  p1 <- priority_map(
    dir = ".",
    output_folder_name = "output",
    classify = FALSE
  )

  print(p1)

  # ---- classified map ----
  breaks <- c(0, 0.25, 0.5, 0.75, 1)
  labels <- c("Low", "Medium", "High", "Very High")

  p2 <- priority_map(
    dir = ".",
    output_folder_name = "output",
    classify = TRUE,
    breaks = breaks,
    labels = labels
  )

  print(p2)

})
```

**Description**

This function calculates similarity between two spatial rank maps using Schoener's D or the Jaccard index.

**Usage**

```
rank_similarity(
  r1 = NULL,
  r2 = NULL,
  rstack = NULL,
  method = c("schoener", "jaccard"),
  threshold = NULL
)
```

**Arguments**

r1	A SpatRaster rank map (from the terra package). Required if rstack is not provided.
r2	A SpatRaster rank map with the same dimensions as r1. Required if rstack is not provided.
rstack	A SpatRaster with multiple layers. If provided, the function calculates pairwise coefficients between all layers.
method	Character, either "schoener" (default) or "jaccard".
threshold	Numeric, required if method = "jaccard". Cells with rank greater than or equal to this threshold are considered selected.

**Value**

A numeric value between 0 and 1 if comparing two rasters, or a matrix of pairwise coefficients if using rstack.

**See Also**

Other postprocessing: [cost\\_summary\(\)](#), [coverage\\_distribution\(\)](#), [feature\\_curves\(\)](#), [feature\\_representation\(\)](#), [priority\\_map\(\)](#), [summary\\_curves\(\)](#)

**Examples**

```
# Create two example priority rank maps
r1 <- terra::rast(nrows = 5, ncols = 5)
terra::values(r1) <- runif(terra::ncell(r1))

r2 <- terra::rast(r1)
terra::values(r2) <- runif(terra::ncell(r2))

# Schoener's D
rank_similarity(r1, r2, method = "schoener")

# Jaccard index with threshold
```

```
rank_similarity(r1, r2, method = "jaccard", threshold = 0.7)
```

---

run_command_file	<i>Run a Zonation command file</i>
------------------	------------------------------------

---

### Description

This function runs a Zonation 5 analysis directly from R by executing a command file located in the specified folder. On Windows, the function looks for a single .cmd file; on Linux, it looks for a single .sh file.

### Usage

```
run_command_file(folder)
```

### Arguments

folder	A character string specifying the path to the folder containing the Zonation command file.
--------	--

### Value

Nothing is returned. The function is used to run the Zonation analysis.

### Examples

```
## Not run:  
run_command_file("C:/path/to/folder")  
  
## End(Not run)
```

---

settings_file	<i>Create a settings file for a Zonation analysis</i>
---------------	---

---

### Description

This function generates a settings file with various parameters related to the input data and analysis configuration. The resulting settings file is saved with a .z5 extension and can be used directly in the Zonation software.

**Usage**

```
settings_file(  
  feature_list_file,  
  external_solution_file = NULL,  
  analysis_area_mask_layer = NULL,  
  hierarchic_mask_layer = NULL,  
  cost_layer = NULL  
)
```

**Arguments**

`feature_list_file` A character string specifying the feature list file. This is a compulsory parameter.

`external_solution_file` A character string specifying the full path and/or name of the external solution file.

`analysis_area_mask_layer` A character string specifying the full path and/or name of the analysis area mask layer file.

`hierarchic_mask_layer` A character string specifying the full path and/or name of the hierarchic mask layer file.

`cost_layer` A character string specifying the full path and/or name of the cost layer file.

**Value**

A .z5 file containing the specified settings.

**See Also**

Other preprocessing: [command\\_file\(\)](#), [feature\\_list\(\)](#)

**Examples**

```
withr::with_tempdir({  
  
  tmp <- tempfile(fileext = ".txt")  
  writeLines("feature list file = feature_list.txt", tmp)  
  
  settings_file(feature_list_file = "feature_list.txt")  
})
```

---

`summary_curves`*Plot summary performance curves*

---

## Description

This function reads a Zonation summary curves file and plots one or more summary metrics against the priority rank. The output is a ggplot object, which can be further customized by the user. Optionally, the plot can be saved to disk as a high-quality figure.

## Usage

```
summary_curves(  
  dir,  
  output_folder_name = "output",  
  metrics,  
  facet = FALSE,  
  save_path = NULL,  
  dpi = 300,  
  width = 8,  
  height = 6  
)
```

## Arguments

<code>dir</code>	Character. Path to the variant folder containing the output folder.
<code>output_folder_name</code>	Character. Name of the output folder inside <code>dir</code> . Default is "output".
<code>metrics</code>	Character vector. Names of the summary metrics to plot. Metrics can be overlaid only if they share the same units and value range. Fraction-based metrics can be overlaid together, while <code>remaining_area</code> and <code>remaining_cost</code> cannot be overlaid with other metrics.
<code>facet</code>	Logical. If TRUE, metrics are plotted in separate panels. This should be used when plotting metrics with different units or value ranges. Default is FALSE.
<code>save_path</code>	Character. Optional file path to save the plot. The file format is inferred from the file extension (e.g. ".tiff").
<code>dpi</code>	Numeric. Resolution (dots per inch) for saved figures. Default is 300.
<code>width</code>	Numeric. Width of the saved figure in inches. Default is 8.
<code>height</code>	Numeric. Height of the saved figure in inches. Default is 6.

## Value

A ggplot object visualizing one or more Zonation summary metrics plotted against priority rank.

**See Also**

Other postprocessing: [cost\\_summary\(\)](#), [coverage\\_distribution\(\)](#), [feature\\_curves\(\)](#), [feature\\_representation\(\)](#), [priority\\_map\(\)](#), [rank\\_similarity\(\)](#)

**Examples**

```
withr::with_tempdir({

  data_path <- system.file(
    "extdata",
    package = "ZonationR"
  )

  dir.create("output")

  file.copy(
    file.path(data_path, "summary_curves.csv"),
    "output/summary_curves.csv",
    overwrite = TRUE
  )

  p1 <- summary_curves(
    dir = ".",
    output_folder_name = "output",
    metrics = c("mean", "max")
  )

  print(p1)

})
```

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