

# Package ‘ECDFniche’

December 19, 2025

**Type** Package

**Title** Empirical Cumulative Distribution Function Niche Modeling Tools

**Version** 0.1.0

**Description** Simulate ecological niche models using Mahalanobis distance, transform distances to suitability with 1 - empirical cumulative distribution function and 1 - chi-squared, and generate comparison figures.

**License** MIT + file LICENSE

**Encoding** UTF-8

**RoxygenNote** 7.3.3

**Depends** R (>= 4.0.0)

**Imports** ggplot2, lemon, MASS, stats

**Suggests** knitr, rmarkdown, roxyglobals, tictoc

**VignetteBuilder** knitr

**Config/roxyglobals/filename** globals.R

**Config/roxyglobals/unique** FALSE

**NeedsCompilation** no

**Author** Dayani Bailly [aut] (ORCID: <<https://orcid.org/0000-0002-6954-9902>>),  
Marcos R. Lima [aut] (ORCID: <<https://orcid.org/0000-0002-5901-0911>>),  
Reginaldo Ré [aut] (ORCID: <<https://orcid.org/0000-0001-6452-3466>>),  
Luíz Fernando Esser [aut, cre, cph] (ORCID:  
<<https://orcid.org/0000-0003-2982-7223>>)

**Maintainer** Luíz Fernando Esser <luizesser@gmail.com>

**Repository** CRAN

**Date/Publication** 2025-12-19 20:20:22 UTC

## Contents

create_distance_suitability_plot . . . . .	2
ecdf_niche . . . . .	2
run_ecdf_mahal_analysis . . . . .	3

## Index

5

---

```
create_distance_suitability_plot
    Create distance-suitability plot
```

---

**Description**

Create distance–suitability plot

**Usage**

```
create_distance_suitability_plot(analysis_results)
```

**Arguments**

analysis\_results  
List returned by `ecdf_niche()`.

**Value**

A ggplot object.

**Examples**

```
# Create ECDF-niche based on personalized options:
ecdf_niche <- ecdf_niche(n = 3,
                           n_population = 20000,
                           sample_sizes = seq(50, 1000, 50),
                           seed = 123)

# Plot analysis results
create_distance_suitability_plot(ecdf_niche)
```

---

**Description**

Simulate niche suitability from Mahalanobis distance using both chi-squared and empirical CDF transformations, for a given number of predictor variables.

**Usage**

```
ecdf_niche(
  n,
  n_population = 10000L,
  sample_sizes = seq(20L, 500L, 20L),
  seed = NULL
)
```

**Arguments**

n	Integer; number of predictor variables (dimensions).
n_population	Integer; size of simulated environmental population.
sample_sizes	Integer vector of sample sizes to evaluate.
seed	Optional integer seed for reproducibility.

**Value**

A list with:

- corplot: ggplot object with correlation vs sample size.
- sample\_data: matrix of simulated sample points.
- sample\_niche: numeric vector of “true” niche suitability.
- chisq\_suits: numeric vector,  $1 - \text{pchisq}(\text{Mahalanobis})$ .
- ecdf\_suits: numeric vector,  $1 - \text{ECDF}(\text{Mahalanobis})$ .
- mahal\_dists: numeric vector of Mahalanobis distances.

**Examples**

```
# Create ECDF-niche based on personalized options:
ecdf_niche <- ecdf_niche(n = 3,
                           n_population = 20000,
                           sample_sizes = seq(50, 1000, 50),
                           seed = 123)
```

run\_ecdf\_mahal\_analysis

*Run full ECDF–Mahalanobis analysis*

**Description**

Convenience function that reproduces the three figures from the original manuscript for 1–5 dimensions.

**Usage**

```
run_ecdf_mahal_analysis(dims = 1:5, seed = 3L)
```

**Arguments**

dims	Integer vector of dimensions (default 1:5).
seed	Optional seed for reproducibility.

**Value**

A list containing:

- analyses: list of `ecdf_niche()` outputs.
- figure1, figure2, figure3: grobs with arranged plots.

**Examples**

```
# Recreate original manuscript output:  
set.seed(3)  
full_res <- run_ecdf_mahal_analysis(dims = 1:5)
```

# Index

`create_distance_suitability_plot`, [2](#)

`ecdf_niche`, [2](#)

`run_ecdf_mahal_analysis`, [3](#)