

Package: pfwim (via r-universe)

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Title Food Web Construction for Paleo Communities

Version 1.0.2

Description R tools for reconstructing paleo food webs from species traits and size rules.

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 feeding_rules

 Example feeding rules for traits

Description

A mock trait dataset using four trait classes specified in traits to infer feeding interactions

A mock trait dataset using four trait classes specified in traits to infer feeding interactions

Usage

```
feeding_rules
```

```
feeding_rules
```

Format

```
feeding_rules:
```

A data frame with 7,240 rows and 60 columns:

trait_type_resource broader resource trait class - i.e. column name in traits

trait_resource specific resource trait class - i.e. row entry in trait column

trait_type_consumer broader consumer trait class - i.e. column name in traits

trait_consumer specific consumer trait class - i.e. row entry in trait column ...

```
feeding_rules:
```

A data frame with 7,240 rows and 60 columns:

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trait_resource specific resource trait class - i.e. row entry in trait column

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trait_consumer specific consumer trait class - i.e. row entry in trait column ...

Source

NA

NA

infer_edgelist	<i>Infer trophic interactions using PFWIM trait rules</i>
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Description

Infers a consumer–resource edgelist using categorical trait matching rules based on the PFWIM (Paleo Food Web Inference Model) described in Shaw (2024). Interactions are inferred by comparing resource and consumer trait combinations against a set of allowed trait rules.

Usage

```
infer_edgelist(
  data,
  cat_combo_list,
  col_taxon = "taxon",
  col_num_size = NULL,
  cat_trait_types = NULL,
  num_size_rule = NULL,
  certainty_req = "all",
  allow_self = TRUE,
  return_full_matrix = FALSE,
  print_dropped_taxa = FALSE,
  hide_printout = FALSE,
  ...
)
```

Arguments

data	A data.frame containing taxa and associated trait values. Each row represents a taxon and each column represents a trait.
cat_combo_list	A data.frame defining allowed consumer–resource trait combinations. Must contain columns: <ul style="list-style-type: none"> trait_type_resource Resource trait category trait_resource Resource trait value trait_type_consumer Consumer trait category trait_consumer Consumer trait value
col_taxon	Character string indicating the column containing taxon names in data. Default "taxon".
col_num_size	Optional column name containing numerical size values for taxa. Used when applying a numeric predator–prey size rule.
cat_trait_types	Optional character vector specifying a subset of categorical trait columns to use. If NULL, all traits appearing in cat_combo_list are used.

num_size_rule	Optional function defining the predator–prey size feasibility rule. The function must accept two numeric vectors: (resource_size, consumer_size) and return 1 for feasible interactions and 0 otherwise. Example: function(res_size, con_size) { ifelse(res_size <= con_size, 1, 0) }
certainty_req	Defines how many trait rules must be satisfied for an interaction to be considered feasible. "all" All trait types must match numeric Minimum number of matching trait types required
allow_self	Logical. If TRUE, allows interactions where the resource and consumer are the same taxon (self-loops). Default is FALSE.
return_full_matrix	Logical. If TRUE, returns the full matrix of taxon pairs and the number of matching trait rules. If FALSE, returns only inferred interactions as an edgelist.
print_dropped_taxa	Logical. If TRUE, prints taxa that were removed from the inferred food web because they have no feasible interactions.
hide_printout	Logical. If TRUE, suppresses progress messages.
...	Additional arguments reserved for future extensions.

Details

Trait matching is performed across all trait types present in `cat_combo_list`. For each potential taxon pair, the number of satisfied trait rules is calculated. An interaction is inferred when the number of satisfied rules meets the required threshold defined by `certainty_req`.

Optionally, a numerical predator–prey size rule can also be applied using `num_size_rule`.

The function evaluates all possible consumer–resource taxon pairs and determines interaction feasibility using categorical trait rules and, optionally, a numerical size constraint. The final edgelist includes only interactions meeting the certainty requirement.

Value

If `return_full_matrix = FALSE`:

A two-column matrix containing:

taxon_resource Resource taxon

taxon_consumer Consumer taxon

If `return_full_matrix = TRUE`:

A matrix containing all taxon pairs and the number of trait rules satisfied.

References

Shaw, J. (2024). PFWIM: Paleo Food web Inference Model. *Preprint*.

Examples

```
infer_edgelist(
  data = traits,
  cat_combo_list = feeding_rules,
  col_taxon = "species",
  certainty_req = "all"
)
```

powerlaw_pre	<i>Generate hypothetical realised webs using a power-law link distribution</i>
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Description

PFWIM generates a series of replicate hypothetical realised food webs by reducing the feasible links for each consumer to match a target link distribution. The default distribution is a mixed exponential–power law in-degree distribution as described in Shaw (2024) and Roopnarine (2006).

Usage

```
powerlaw_pre(
  e1,
  n_samp = 50,
  y = 2.5,
  func = function(r, M, y) exp(-r/(exp((y - 1) * (log(M)/y))))
)
```

Arguments

e1	Data frame or matrix containing a feasible consumer–resource edgelist. Column 1 = resource, Column 2 = consumer.
n_samp	Integer. Number of replicate realised webs to generate. Default = 50.
y	Numeric. Parameter controlling the shape of the power-law distribution. Default = 2.5.
func	Function. Probability function of the in-degree r , total prey richness M , and parameter y . Must return a numeric value > 0 . Default: $\text{function}(r, M, y) \exp(-r / (\exp((y - 1) * (\log(M) / y))))$.

Details

For each consumer in `e1`, the number of prey links in a realised web is sampled according to the distribution defined by `func`. The sampled prey are drawn randomly without exceeding the maximum feasible prey for that consumer.

Value

A list of length `n_samp`. Each element is a data frame representing a realised food web edgelist with two columns:

resource Resource species

consumer Consumer species

References

Shaw, J. (2024). PFWIM: Paleo Food-web Inference Model. *Preprint*.
 Roopnarine, P. (2006). *Palaeoecology and food-web structure in fossil communities*.

Examples

```
# Infer a minimal edgelist
edgelist <- infer_edgelist(
  data = data.frame(
    species = c("plankton", "plant_1", "plant_2", "cod", "rat", "deer"),
    feeding = c("primary", "primary", "primary", "secondary", "secondary", "secondary")
  ),
  cat_combo_list = data.frame(
    trait_type_resource = c("feeding", "feeding", "feeding"),
    trait_resource = c("primary", "primary", "primary"),
    trait_type_consumer = c("feeding", "feeding", "feeding"),
    trait_consumer = c("secondary", "secondary", "secondary")
  ),
  col_taxon = "species",
  certainty_req = "all"
)

# Generate realized webs
webs <- powerlaw_preymodel(edgelist, n_samp = 3, y = 2.5)
```

 traits

Example species traits data to infer feeding rules

Description

A mock trait dataset using four trait classes to determine interactions as specified in `feeding_rules`

Usage

```
traits
```

Format

traits:

A data frame with 7,240 rows and 60 columns:

species species name

motility motility class of species

habitat habitat species found in

feeding trophic level of species

size categorical size classes ...

Source

NA

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