Package: nestedscales (via r-universe)

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Title Nested Scales and Multi-Dimensional Indexes for Modeling

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BugReports https://github.com/optimal2050/nestedscales/issues

Description Provides multi-level discrete representations of data dimensions for modeling, data processing and visualization. A nested scale records its finest units (atoms) and their membership in coarser levels (frames), including nested, cross-cutting and partially covered relationships. Recasts tabular data between levels using explicit, direction-aware rules for sums, means, standard deviations, copying and within-parent shares. Also supports labeling, subsetting, combining scales into multi-dimensional indexes, clustering units and storing data with its scale metadata. Members may carry attributes (a calorific value, an emission factor) and aliases, resolved along the hierarchy and applied row by row, and a scale is exchanged as a language-neutral definition file: a 'JSON' header with inline, 'Arrow' or 'CSV' tables ('YAML' accepted), with a catalogue of the definitions installed packages ship. Forms the dimension-agnostic core of 'timescales' <https://github.com/optimal2050/timescales> (calendars) and 'geoscales' <https://github.com/optimal2050/geoscales> (regions), designed for optimization and simulation models.

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`[.NestedScale` *Subset a NestedScale*

Description

`x[frame, unit]` is `filter_scale()`.

Usage

```
## S3 method for class 'NestedScale'
x[i, j, ...]

## S3 method for class '`nestedscales::NestedScale`'
x[i, j, ...]
```

Arguments

`x`	A `NestedScale`.
`i`	Frame name.
`j`	Unit codes to keep.
`...`	Unused.

Value

A `NestedScale`.

Examples

```
scale_example()["sector", "P"]
```

as_scale_array *Data on scales as a dense array*

Description

Reshapes a long table into an array whose dimensions are the scale's axes, in the order the product declares them, with the units as `dimnames`.

Usage

```
as_scale_array(data, x, value = NULL, frames = NULL, fill = NA, limit = 1e+07)

as_scale_table(a, x, value = "value", frames = NULL, drop_na = TRUE)
```

Arguments

`data`	A long table with one column per axis key plus the value column. Lazy inputs are materialised – an array is a dense in-memory object by definition.
`x`	A `NestedScale` or `ScaleProduct`.
`value`	Name of the value column. Defaults to the single numeric column that is not a key.
`frames`	Optional named list giving the frame each axis is keyed at; defaults to each axis's atom frame.
`fill`	Value for cells the data does not cover.
`limit`	Refuse to allocate more than this many cells.
`a`	An array produced by `as_scale_array()` (or shaped like one).
`drop_na`	Omit cells the array does not cover, rather than emitting them as rows with `NA` values.

Value

An array with one dimension per axis.

`as_scale_table()` returns a `data.frame`: one column per axis key, plus the value column.

Examples

```
p <- scale_product(a = scale_example(), b = scale_example2())
d <- merge(
  data.frame(unit = c("U1", "U2")),
  data.frame(period = c("p1", "p2"))
)
d$v <- 1:4
as_scale_array(d, p, value = "v")
as_scale_table(as_scale_array(d, p, value = "v"), p, value = "v")
```

attach_aliases_scale *Attach aliases to a scale*

Description

Appends rows to the object's alias table: alternative labels by which a member (`frame`, `unit`) is known, tagged with the `source` the spelling comes from (a palette, a model's commodity codes, a dataset). The same alias may legitimately point at several members; `scale_match()` reports that as ambiguous unless the caller names the frame.

Usage

```
attach_aliases_scale(x, aliases, source = NULL)
```

Arguments

`x`	A `NestedScale`.
`aliases`	A `data.frame` with columns `frame`, `unit`, `alias` and, unless `source` is given, `source`.
`source`	Optional single string filled into the `source` column.

Value

The scale with the rows appended.

Examples

```
s <- attach_aliases_scale(
  scale_example(),
  data.frame(frame = "sector", unit = c("P", "S"),
             alias = c("primary", "secondary")),
  source = "labels"
)
scale_match(s, c("Primary", "G1", "nope"))
```

attach_attributes_scale *Attach physical attributes to a scale*

Description

Appends rows to the object's attribute table. A row names the member it belongs to (`frame`, `unit`), the attribute (`attribute`, e.g. `"lhv"`), its `kind` (see `SCALE_ATTRIBUTE_KINDS`), its `value`, an optional `lower`/`upper` range, the physical `unit_of_measure` (`"GJ/t"`, `"kg/TJ"`), the `source` the figure was taken from and an optional `note`. Values can be attached at **any** frame: a calorific value for a whole carrier is inherited by every fuel under it that has no value of its own (see `scale_attributes()`).

Usage

```
attach_attributes_scale(x, attributes, source = NULL, kind = NULL)
```

Arguments

x	A NestedScale.
attributes	A data.frame with columns frame, unit, attribute, value, unit_of_measure, and optionally lower, upper, note; kind and source as columns or through the arguments.
source	Optional single string filled into the source column when attributes has none.
kind	Optional single string filled into the kind column when attributes has none.

Details

Existing rows are never overwritten: a row whose (frame, unit, attribute, source) already exists is an error. Attach a second source under its own source name and choose between them with source= when reading.

Value

The scale with the rows appended.

Examples

```
s <- scale_example()
s2 <- attach_attributes_scale(
  s,
  data.frame(frame = "class", unit = c("G1", "G2", "S1"),
             attribute = "density", value = c(10, 20, 5),
             unit_of_measure = "t/m3"),
  source = "survey", kind = "property"
)
scale_attributes(s2, "density", frame = "unit")
```

---

backend *Backends: the table types the verbs accept*

Description

The conversion verbs run on a data.frame, a tibble, a data.table, a dtplyr lazy table or an arrow Dataset/Table/query, and return results in the caller's type; lazy inputs stay lazy unless collected. These functions are that contract, exposed so a dimension package built on nestedscales can accept the same inputs as the core verbs.

Usage

```
backend_of(data, arg = "data")

backend_is_lazy(backend)

backend_schema(data, backend = NULL)

backend_lazy(data, backend = NULL)

backend_scan(data, backend = NULL, columns = NULL, filter = NULL)

backend_distinct(data, columns, backend = NULL)

backend_pull(table)

backend_restore(table, backend, collect = NULL)

backend_bind_rows(
  parts,
  use_dt = requireNamespace("data.table", quietly = TRUE)
)
```

Arguments

data	A data object on any supported backend.
arg	Argument name used in the error message.
backend	A backend name from `backend_of()`; `NULL` resolves it from `data`.
columns	Column names to read; `NULL` reads every column.
filter	An unevaluated dplyr filter expression (built with `rlang::expr()`), or `NULL` for every row.
table	A query or table.
collect	Force materialisation of a lazy result.
parts	List of data frames.
use_dt	Use `data.table::rbindlist()`. Defaults to whether data.table is installed; an explicit value makes both branches testable.

Details

- `backend_of()` names the backend of `data`, and errors on an unsupported input – the one place that message is written.
- `backend_is_lazy()` says whether a backend produces queries.
- `backend_schema()` describes the columns without scanning the data.
- `backend_lazy()` lifts `data` into a dplyr-compatible carrier for a pipeline (a `data.table` becomes a dtplyr step when dtplyr is installed).
- `backend_scan()` reads the needed columns and rows into memory.

- `backend_distinct()` is the distinct rows of some columns, in first-appearance order, read into memory.
- `backend_pull()` materialises a query or table as a `data.frame`.
- `backend_restore()` returns a pipeline result in the caller's type.
- `backend_bind_rows()` binds chunk results into one frame.

Value

`backend_of()` a single string naming the backend; `backend_is_lazy()` a logical; `backend_schema()` a zero-row `data.frame`; `backend_lazy()` `data`, wrapped where the backend needs it; `backend_scan()`, `backend_distinct()` and `backend_pull()` a `data.frame`; `backend_restore()` the result in the input's class; `backend_bind_rows()` one data frame, or `NULL` when every part is empty.

Examples

```
d <- data.frame(unit = c("U1", "U2", "U2"), v = 1:3)
backend_of(d)
backend_is_lazy(backend_of(d))
backend_schema(d)
backend_distinct(d, "unit")
backend_scan(d, columns = "v", filter = rlang::expr(v > 1))
```

`clear_scale_maps` *Clear the registered crosswalks*

Description

Mainly useful in tests.

Usage

```
clear_scale_maps(name = NULL)
```

Arguments

`name`	Registry keys to remove (as listed by `list_scale_maps()`); `NULL` (default) clears every registered crosswalk.

Value

Invisibly `NULL`.

Examples

```
clear_scale_maps()
```

clear_scale_rules *Clear the rule registry*

Description

Mainly useful in tests.

Usage

```
clear_scale_rules(name = NULL, scope = NULL)
```

Arguments

name	Optional character vector of parameter names to remove. NULL (default) clears everything in scope.
scope	Optional dimension namespace.

Value

Invisibly NULL.

Examples

```
register_scale_rule("tmp_param", "sum")
clear_scale_rules("tmp_param")
```

cluster_contiguous *Cluster the units of a scale under a contiguity constraint*

Description

Merges only units the constraint allows to be merged, so the resulting groups are contiguous in order (an ordered scale) or connected in space (an adjacency graph).

Usage

```
cluster_contiguous(
  data,
  x,
  k,
  frame = NULL,
  key = NULL,
  value = NULL,
  distance = "euclidean",
  scale_units = FALSE,
  adjacency = "order",
```

```
  circular = FALSE,
  linkage = "average",
  new_frame = "cluster",
  labels = "c"
)
```

Arguments

data	Long data: unit codes, one or more identifier columns saying which observation each row is, and a value column. A unit that is not observed over the same set as the others is an error rather than a hole.
x	A NestedScale.
k	Number of clusters.
frame	Frame whose units are clustered. Defaults to the atom frame.
key, value	Columns of data; inferred when unambiguous.
distance	A name from list_scale_distances().
scale_units	Standardise each unit's profile before measuring; see scale_distance().
adjacency	How units may be merged. "order" (the default) treats the units at frame as a sequence in member order and permits only neighbours – the clusters come out as consecutive blocks. Otherwise a two-column data frame or a square logical/0-1 matrix over the units, giving the pairs that may merge.
circular	For "order": treat the sequence as a loop, so the last unit neighbours the first. Right for a yearly cycle, wrong for a trajectory.
linkage	How the distance between two clusters is measured: "average", "complete" or "single".
new_frame	Name for the frame the clusters form.
labels	How to name the clusters: a prefix (the default "c" gives c01, c02, ...), or "medoid" to name each cluster after its representative unit, which keeps the codes meaningful.

Details

The constraint can make k unreachable: an adjacency graph with more connected components than k cannot be merged below that number, and the function stops with the count rather than returning something that quietly violates the constraint.

Value

As cluster_scale(): the scale with the cluster frame added, and the assignment in the "clustering" attribute.

Examples

```
s <- scale_example()
d <- data.frame(
  unit = rep(scale_units(s), each = 4),
```

```
  t = rep(sprintf("t%d", 1:4), 7), v = as.numeric(seq_len(28))
)
cl <- cluster_contiguous(d, s, k = 3)
attr(cl, "clustering")
```

`cluster_medoids` *The representative unit of each cluster*

Description

The medoid is an ACTUAL unit, not an average of units, which is what makes it usable as a representative period or a representative region: a model built on medoids is built on things that really happened.

Usage

```
cluster_medoids(x, frame = NULL)
```

Arguments

`x`	A scale returned by `cluster_scale()`.
`frame`	The cluster frame; defaults to the one the clustering added.

Value

A data frame of cluster and its representative unit.

Examples

```
s <- scale_example()
d <- data.frame(
  unit = rep(scale_units(s), each = 4),
  t = rep(sprintf("t%d", 1:4), 7), v = as.numeric(seq_len(28))
)
cluster_medoids(cluster_scale(d, s, k = 3))
```

`cluster_scale` *Cluster the units of a scale into a new frame*

Description

Groups the units at `frame` by the similarity of their profiles and returns the scale with those groups added as a new, coarser frame.

Usage

```
cluster_scale(
  data,
  x,
  k,
  frame = NULL,
  key = NULL,
  value = NULL,
  method = c("pam", "hclust", "kmeans"),
  distance = "euclidean",
  scale_units = FALSE,
  new_frame = "cluster",
  labels = "c",
  hclust_method = "ward.D2",
  seed = NULL,
  ...
)
```

Arguments

data	Long data: unit codes, one or more identifier columns saying which observation each row is, and a value column. A unit that is not observed over the same set as the others is an error rather than a hole.
x	A NestedScale.
k	Number of clusters.
frame	Frame whose units are clustered. Defaults to the atom frame.
key, value	Columns of data; inferred when unambiguous.
method	"pam" (partitioning around medoids, via the cluster package), "hclust" (stats::hclust) or "kmeans" (stats::kmeans). "pam" and "hclust" work from the distance matrix, so they honour distance=; "kmeans" works on the raw profiles and ignores it.
distance	A name from list_scale_distances().
scale_units	Standardise each unit's profile before measuring; see scale_distance().
new_frame	Name for the frame the clusters form.
labels	How to name the clusters: a prefix (the default "c" gives c01, c02, ...), or "medoid" to name each cluster after its representative unit, which keeps the codes meaningful.
hclust_method	Linkage for method = "hclust".
seed	Seed for "kmeans", which starts from a random assignment. NULL leaves the session's stream alone.
...	Passed to the underlying algorithm.

Details

The new frame goes directly above the clustered one, which is the only position that is always true: the clusters are coarser than `frame` by construction, but they need not nest inside any existing coarser frame, and `nestedscales` does not require them to. Use `scale_nests()` to ask whether a given pair happens to nest.

Value

The scale, with `new_frame` inserted directly above `frame`. The assignment is also returned as the `"clustering"` attribute: a data frame of unit, cluster and (for medoid-based methods) whether the unit is its cluster's medoid.

Examples

```
s <- scale_example()
set.seed(1)
d <- data.frame(
  unit = rep(scale_units(s), each = 4),
  t = rep(sprintf("t%d", 1:4), 7),
  v = as.numeric(seq_len(28))
)
cl <- cluster_scale(d, s, k = 3)
scale_frames(cl)
head(attr(cl, "clustering"))
```

---

cluster_sweep *Cluster quality across a range of k*

Description

Cluster quality across a range of k

Usage

```
cluster_sweep(
  data,
  x,
  ks,
  frame = NULL,
  key = NULL,
  value = NULL,
  distance = "euclidean",
  scale_units = FALSE,
  FUN = cluster_scale,
  ...
)
```

Arguments

data	Long data: unit codes, one or more identifier columns saying which observation each row is, and a value column. A unit that is not observed over the same set as the others is an error rather than a hole.
x	A NestedScale.
ks	Values of k to try.
frame	Frame whose units are clustered. Defaults to the atom frame.
key, value	Columns of data; inferred when unambiguous.
distance	A name from list_scale_distances().
scale_units	Standardise each unit's profile before measuring; see scale_distance().
FUN	The clustering function to sweep: cluster_scale() (default) or cluster_contiguous().
...	Passed to FUN.

Value

A data frame with one row per k: k, within (total within-cluster sum of distances to the cluster medoid), silhouette (average, NA at k = 1), and smallest (the size of the smallest cluster, which is often what rules a k out).

Examples

```
s <- scale_example()
d <- data.frame(
  unit = rep(scale_units(s), each = 4),
  t = rep(sprintf("t%d", 1:4), 7), v = as.numeric(seq_len(28))
)
cluster_sweep(d, s, ks = 2:4)
```

---

convert_scale *Convert unit-keyed quantities with a member attribute*

Description

Multiplies (or divides) the numeric value columns of data by the value of attribute resolved for each row's unit – a net calorific value to turn mass into energy, an emission factor to turn energy into CO2, a density to turn volume into mass. Values are resolved along the hierarchy exactly as scale_attributes() does, so a factor stored on a coarser member applies to every atom under it that has no factor of its own.

Usage

```
convert_scale(
  data,
  x,
  attribute,
  from_unit,
  to_unit,
  key = NULL,
  frame = NULL,
  values = NULL,
  source = NULL,
  na_action = c("error", "keep"),
  collect = NULL
)
```

Arguments

data	The data, in any supported backend, with a column of codes at frame.
x	A NestedScale carrying attribute.
attribute	Name of the attribute to convert with.
from_unit, to_unit	The physical units of the values before and after, matching the attribute's unit of measure.
key	Name of the code column in data; defaults to frame.
frame	Frame the codes belong to. Inferred when exactly one of the scale's frame names (or its atom level) is a column of data.
values	Value columns to convert; NULL takes every numeric column that is not the key.
source	Restrict the attribute to one source; NULL errors on a conflict between sources.
na_action	What to do with rows whose unit has no value: "error" (default) or "keep" (an NA result).
collect	For lazy inputs: materialise (TRUE) or return the query.

Details

Direction comes from the attribute's unit of measure, read as "<numerator>/<denominator>": with lhv in "GJ/t", from_unit = "t", to_unit = "GJ" multiplies, and from_unit = "GJ", to_unit = "t" divides. The inverse is allowed only when the attribute's kind is "property"; a "factor" is one-way. No unit-prefix arithmetic is done: a column in kilotonnes must be turned into tonnes before converting with a GJ/t factor.

A unit for which no value resolves is an **error** by default – a silently dropped row is a wrong total – unless na_action = "keep", which leaves NA in its rows.

Value

data with the value columns converted, plus two columns named after the attribute: <attribute> (the factor applied) and <attribute>.origin_frame (the frame the factor was taken from), in the input's class.

Examples

```
s <- attach_attributes_scale(
  scale_example(),
  data.frame(frame = c("sector", "unit"), unit = c("P", "U5"),
             attribute = "lhv", value = c(20, 30),
             unit_of_measure = "GJ/t"),
  source = "example", kind = "property"
)
mass <- data.frame(unit = c("U1", "U2", "U5"), t = c(100, 200, 50))
energy <- convert_scale(mass, s, attribute = "lhv",
                        from_unit = "t", to_unit = "GJ")
energy
# back to tonnes: a property is invertible
convert_scale(energy[c("unit", "t")], s, attribute = "lhv",
              from_unit = "GJ", to_unit = "t")
```

---

filter_product *Subset a product componentwise*

Description

Applies `filter_scale()` to one axis and returns a new product.

Usage

```
filter_product(x, axis, frame, unit, ...)
```

Arguments

`x`	A `ScaleProduct`.
`axis`	Axis to filter.
`frame, unit`	Passed to `filter_scale()`.
`...`	Passed to `filter_scale()`.

Value

A `ScaleProduct`.

Examples

```
p <- scale_product(a = scale_example(), b = scale_example2())
filter_product(p, "a", "sector", "P")
```

filter_scale *Subset a NestedScale by unit*

Description

Keeps only the atoms belonging to `unit` at `frame`, and rebuilds the member vocabularies accordingly.

Usage

```
filter_scale(x, frame, unit, drop_empty_frames = FALSE)
```

Arguments

`x`	A `NestedScale`.
`frame`	Frame that `unit` belongs to.
`unit`	Character vector of codes to keep.
`drop_empty_frames`	Drop frames left with no codes at all.

Details

A genuine subset is a SAMPLE and is book-kept as one: `meta$coverage` records, per weight column, the kept fraction of the ROOT parent's total (so filters compose against the original object), `meta$parent_totals` stores those root totals (making the coverage claim verifiable by the validator), `meta$parent_name` records the parent, and `meta$name` is mangled to `"parent[frame:codes]"` so a sample never impersonates its parent in the crosswalk registry or in `join_scale()` column names. A filter that keeps every atom is a true no-op. Read the fraction back with `scale_coverage()`.

Value

A `NestedScale`.

Examples

```
s <- scale_example()
p <- filter_scale(s, "sector", "P")
p
scale_coverage(p)
```

get_scale_rule *Look up a registered rule*

Description

A scoped lookup prefers the entry registered for that scope and falls back to an unscoped one.

Usage

```
get_scale_rule(param, scope = NULL)
```

Arguments

param	Name of the value column.
scope	Optional dimension namespace.

Value

A list with elements `rule`, `weight` and `scope`, or `NULL` if `param` has not been registered.

Examples

```
register_scale_rule("demand", "sum")
get_scale_rule("demand")
get_scale_rule("not_registered")
clear_scale_rules("demand")
```

is_valid_frame *Validate frame names*

Description

A frame name must be a non-empty, non-`NA` string that is a syntactically valid R name (so it can be used as a data.frame column without quoting).

Usage

```
is_valid_frame(x)
```

Arguments

x	Character vector of candidate frame names.

Value

A logical vector the same length as `x`.

Examples

```
is_valid_frame(c("industry", "reg32", "", "2bad"))
```

`join_product` *Attach every axis's labels to product-indexed data*

Description

`join_scale()` applied to each axis in turn, keyed by that axis's column. Because every attached column is named after its scale, the result carries all the axes' labels side by side.

Usage

```
join_product(data, x, axes = NULL, ...)
```

Arguments

`data`	The data, carrying one key column per axis.
`x`	A `ScaleProduct`.
`axes`	Axis names to attach; `NULL` (default) attaches all of them.
`...`	Passed to `join_scale()` (`attach`, `meta`, `as_factor`, ...).

Value

`data` with each axis's labels attached, in its own class.

Examples

```
p <- scale_product(a = scale_example(), b = scale_example2())
d <- data.frame(unit = c("U1", "U3"), period = c("p1", "p2"), v = 1:2)
join_product(d, p, attach = TRUE)
```

`join_scale` *Attach scale labels and memberships to a dataset*

Description

Adds a label column named after the scale, and optionally the codes of coarser frames (`"<name>.<frame>"`) and the unit's share and weight (`"<name>.share"`, `"<name>.weight"`).

Usage

```
join_scale(
  data,
  x,
  key = NULL,
  frame = NULL,
  attach = NULL,
  meta = FALSE,
  weight = NULL,
  as_factor = TRUE,
  collect = NULL,
  diagnostics = c("auto", "on", "off")
)
```

Arguments

data	The data, in any supported backend, with a column of unit codes.
x	The NestedScale to attach.
key	Name of the code column in data. Inferred from the scale's name, the keyed frame, or the scale's own key column.
frame	The frame the codes in key are at. NULL (default) is inferred as the single frame name appearing among the data's columns.
attach	Coarser frames whose codes to attach as new columns: TRUE for all of them, a character vector to choose, NULL/FALSE for none.
meta	Attach the unit's share and weight at the keyed frame.
weight	Weight column used for meta. NULL uses the default.
as_factor	Return attached membership columns as factors with the frame's full vocabulary as levels (so empty groups still plot).
collect	For lazy inputs: materialise (TRUE) or return the query.
diagnostics	Whether to run the checks that read the data (no matching codes; codes that are not units). "auto" (default) runs them on eager inputs and skips them on arrow/dtplyr, which makes this verb zero-scan there; "on"/"off" force the choice.

Details

Existing columns are never overwritten – a collision is an error.

Value

data with the attached columns, in its own class.

Examples

```
s <- scale_example()
d <- data.frame(class = c("G1", "G2", "S1"), v = 1:3)
join_scale(d, s, attach = TRUE)
join_scale(d, s, attach = "sector")
join_scale(d, s, meta = TRUE)
```

list_scale_rules *List registered rules*

Description

List registered rules

Usage

```
list_scale_rules(scope = NULL)
```

Arguments

scope	Optional dimension namespace; NULL lists every entry.

Value

A data.frame with columns param, rule, weight and scope.

Examples

```
register_scale_rule("invcost", "weighted_mean", weight = "size")
list_scale_rules()
clear_scale_rules("invcost")
```

open_scale_dataset *Open a scale-aware dataset*

Description

Open a scale-aware dataset

Usage

```
open_scale_dataset(path)

## S3 method for class 'scale_dataset'
print(x, ...)
```

Arguments

path	A folder written by write_scale_dataset().
x	A scale_dataset.
...	Ignored.

Value

A `scale_dataset`: a list with `data` (a lazily-read arrow Dataset) and `scale` (the `NestedScale` or `ScaleProduct` it is indexed by). Feed them to the verbs as `recast_scale(ds$data, ds$scale, ...)`.

Examples

```
# see write_scale_dataset()
```

`product_atoms` *Realise the atoms of a product*

Description

The cross product of the component leaftables: one row per tuple of component atoms, with each axis's key column named by `product_keys()` and its frame columns prefixed `"<axis>."`.

Usage

```
product_atoms(x, limit = 1e+06)
```

Arguments

`x`	A `ScaleProduct`.
`limit`	Maximum number of rows to build. Exceeding it is an error that reports the size, rather than a very long wait.

Details

This is guarded on purpose. An hourly calendar crossed with NUTS3 is ~12.9M rows; the whole point of a product is that its atoms exist implicitly, and conversion never needs them realised (see `recast_scale()`). Ask for them only when you actually want the grid.

Value

A `data.frame` with `product_size(x)$total` rows.

Examples

```
p <- scale_product(a = scale_example(), b = scale_example2())
head(product_atoms(p))
```

product_coverage *Coverage of each axis*

Description

Sampling is per-axis and independent, so the coverage of the product is the product of its axes' coverages – `prod(product_coverage(p))`.

Usage

```
product_coverage(x, weight = NULL)
```

Arguments

`x`	A `ScaleProduct`.
`weight`	Optional weight name, applied to every axis. `NULL` uses each axis's own default weight.

Value

A named numeric, one entry per axis.

Examples

```
p <- scale_product(a = scale_example(), b = scale_example2())
product_coverage(p)
prod(product_coverage(p))
```

product_frames *Frames of each axis*

Description

Frames of each axis

Usage

```
product_frames(x)
```

Arguments

`x`	A `ScaleProduct`.

Value

A named list of character vectors, each coarsest-first.

Examples

```
product_frames(scale_product(a = scale_example(), b = scale_example2()))
```

---

product_keys *The data key column of each axis*

Description

Data on a product carries one of these columns per axis.

Usage

```
product_keys(x)
```

Arguments

x	A ScaleProduct.

Value

A named character vector, axis -> column name.

Examples

```
product_keys(scale_product(a = scale_example(), b = scale_example2()))
```

---

product_size *Size of a product*

Description

The per-axis atom counts and their product – the number of rows a fully dense realisation would have.

Usage

```
product_size(x)
```

Arguments

x	A ScaleProduct.

Value

A list with `axes` (named integer, atoms per axis) and `total` (double, their product).

Examples

```
product_size(scale_product(a = scale_example(), b = scale_example2()))
```

product_weights *Weight columns of each axis*

Description

A product has no weights of its own: the weight of a product atom is the product of its components' weights, which is derived when needed and never stored.

Usage

```
product_weights(x)
```

Arguments

x	A ScaleProduct.

Value

A named list of character vectors.

Examples

```
product_weights(scale_product(a = scale_example(), b = scale_example2()))
```

prune_scale *Collapse a NestedScale to a coarser frame*

Description

Returns a new NestedScale whose atom layer is frame, dropping every finer frame. Weights are summed over the collapsed atoms.

Usage

```
prune_scale(x, frame)
```

Arguments

x	A NestedScale.
frame	The frame to become the new atom layer.

Details

The result is renamed "name@frame" with the parent recorded in meta$parent_name; every other meta field is preserved. Atoms with no code at frame are dropped, and that loss is reflected in meta$coverage. The concrete class is kept: a subclass comes back as itself, its attribute and alias rows at the surviving frames kept, and a positional payload merged through scale_payload_collapse().

Value

A NestedScale.

Examples

```
prune_scale(scale_example(), "class")
```

`recast` *Recast data through a scale*

Description

The bare pipeline verb, dispatching on the scale so one entry point serves a NestedScale, a ScaleProduct, and the dimension subclasses in timescales and geoscales, which register their own methods against this generic. recast_scale() and recast_product() are the explicit workers.

Usage

```
recast(x, scale, ...)
```

Arguments

x	The data to recast.
scale	The scale to recast through.
...	Passed to the dispatched method: for a NestedScale the arguments of recast_scale(), with target the target frame and source the source frame (inferred when omitted); for a ScaleProduct those of recast_product().

Details

The scale is scale; the source frame is source and the target target, as in recast_scale(), so a call reads the same through the generic and through the worker.

Value

The recast data, in the input's class.

Examples

```
s <- scale_example()
d <- data.frame(
  unit = c("U1", "U2", "U3", "U4", "U5", "U6"),
  capacity = c(1, 2, 3, 4, 5, 6)
)
recast(d, s, target = "sector", rule = "sum")
```

`recast_crosswalk` *Recast values through a given crosswalk*

Description

The engine behind `recast_scale()`, for a crosswalk built elsewhere: by a dimension package whose conversion cannot be read off one scale's leaftable, such as timescales mapping one calendar onto another through a datetime grid. The crosswalk says how much of each source code falls in each target code; the rules then aggregate exactly as in `recast_scale()`, on any supported backend.

Usage

```
recast_crosswalk(
  data,
  map,
  source,
  target,
  key = source,
  values = NULL,
  rule = NULL,
  ids = NULL,
  by = character(),
  targets = NULL,
  missing_sources = c("na", "ignore"),
  unit = "unit",
  collect = NULL
)
```

Arguments

`data`	The data, in any supported backend, with a code column and one or more numeric value columns.
`map`	The crosswalk, a `data.frame`.
`source, target`	Names of the source and target code columns of `map`.
`key`	Name of the code column of `data`. Defaults to `source`.
`values`	Value columns. Default: every numeric column that is neither `key` nor in `ids`.
`rule`	One of `SCALE_RULES` other than the share rules, for every value column, or a named vector with one entry per column. `NULL` looks each column up with `get_scale_rule()`.
`ids`	Identifier columns, preserved as groups. Default: every column that is neither `key` nor a value column. Other columns are dropped.
`by`	Columns of `map` matched against the identically named identifier columns of `data`, for a crosswalk that differs between identifier values (a calendar crosswalk per year, say).

`targets`	Optional full target vocabulary. A materialised result is completed to every target per identifier combination, in this order, with `NA` where nothing landed; an `NA` entry adds an explicit `NA` row.
`missing_sources`	`"na"` (default) or `"ignore"`; see `recast_scale()`.
`unit`	The word for a target code in error messages.
`collect`	For lazy inputs: materialise (`TRUE`) or return the query.

Details

The crosswalk is a data frame with one row per (source, target) pair:

- the source and target codes, in the columns named by `source` and `target`;
- `n_from`, the number of atoms (grid points) in the source code, and `n_overlap`, the number of them that fall in the target;
- optionally `w`, the weight of the pair for `"weighted_mean"` – by default `n_overlap`;
- optionally `w_from`, the source's total weight. With it, `"sum"` splits a source across its targets by `w / w_from`; without it, by `n_overlap / n_from`, an equal split over atoms;
- any columns named in `by`.

A target whose sources are only partly present in the data, per identifier combination, comes back `NA` unless `missing_sources = "ignore"`.

Value

The recast data in its own class, with columns `c(to, ids, values)`. Lazy in, lazy out.

Examples

```
# Two months onto one quarter, with the months' day counts as atoms
map <- data.frame(
  month = c("m01", "m02"), quarter = "Q1",
  n_from = c(31, 28), n_overlap = c(31, 28)
)
d <- data.frame(
  month = c("m01", "m02"), energy = c(310, 280),
  price = c(10, 20)
)
recast_crosswalk(d, map,
  source = "month", target = "quarter",
  rule = c(energy = "sum", price = "weighted_mean")
)
```

recast_product *Recast data indexed by a product of scales*

Description

Converts one or more axes of a product in a single call. Axes named in `target` are converted; axes left out pass through untouched.

Usage

```
recast_product(
  data,
  x,
  target,
  values = NULL,
  rules = NULL,
  weights = NULL,
  na_action = c("drop", "error", "keep"),
  collect = NULL
)
```

Arguments

`data`	The data, in any supported backend, carrying one key column per axis (see `product_keys()`) plus the value columns.
`x`	A `ScaleProduct`.
`target`	Named list or character vector, one entry per axis to convert: either a frame name of that axis's scale, or another `NestedScale` to convert into. Axes omitted pass through unchanged.
`values`	Value columns to convert. Default: all numeric columns that are not key columns. Numeric identifiers (a year) must be excluded explicitly.
`rules`	Rule per value column and axis: a scalar for everything, or a named list whose entries are scalars or vectors named by axis, e.g. `list(load = c(time = "weighted_mean", space = "sum"))`. `NULL` (default) resolves each column on each axis through that dimension's own scope in the rule registry – which is where an intensive/extensive asymmetry between dimensions belongs.
`weights`	Weight column per axis, e.g. `c(space = "pop")`; scalar applies to every axis.
`na_action`	Passed to each axis's pass.
`collect`	For lazy inputs: materialise (`TRUE`) or return the query.

Details

Execution is a sequence of ordinary single-axis `recast_scale()` calls – see the file comment in `R/product-recast.R` for why that is exactly equivalent to a joint recast for every supported rule,

and why the joint crosswalk is never built. The passes are ordered so the axis that reduces the data most runs first.

A per-axis `"sd"` is refused because it is order-dependent; a scalar `"sd"` means the pooled sd over all product atoms in a target block, which is well defined and is computed without materialising the product. `"share"` is not defined across a product, because it changes which axis the result is keyed by.

Value

The recast data in the input's class, keyed by the converted axes' target units.

Examples

```
p <- scale_product(a = scale_example(), b = scale_example2())
d <- merge(
  data.frame(unit = c("U1", "U2", "U3", "U4", "U5", "U6")),
  data.frame(period = c("p1", "p2", "p3", "p4"))
)
d$cap <- seq_len(nrow(d))

# aggregate both axes at once
recast_product(d, p, target = list(a = "sector", b = "era"), rules = "sum")

# different rules per axis
recast_product(d, p,
  target = list(a = "sector", b = "era"),
  rules = list(cap = c(a = "sum", b = "weighted_mean"))
)
```

---

recast_scale *Recast values from one resolution to another*

Description

The central conversion verb: takes a table keyed by unit code at frame `source` and returns one keyed at `target` – a frame name of the same `NestedScale`, or ANOTHER NestedScale (whose atom layer is the target, matched on shared atom keys). Handles both aggregation (fine to coarse) and disaggregation (coarse to fine) with one rule per value column; frames that cross-cut work too, because the route always goes through the atom layer. A crosswalk registered with `register_scale_map()` short-circuits the derivation.

Usage

```
recast_scale(
  data,
  x,
  source = NULL,
  target,
```

```
  key = NULL,
  values = NULL,
  rule = NULL,
  weight = NULL,
  na_action = c("drop", "error", "keep"),
  parent = NULL,
  collect = NULL,
  diagnostics = c("auto", "on", "off"),
  missing_sources = c("na", "ignore"),
  batch = NULL,
  batch_by = NULL,
  ...
)
```

Arguments

data	The data to recast, in any supported backend, with a column named by key plus one or more numeric value columns; other columns are preserved as identifiers.
x	The NestedScale the codes in data belong to.
source	Frame name the codes belong to. NULL (default) is inferred: key when it is a frame name, else the single frame name appearing among the data's columns.
target	Target frame name of x, or another (named) NestedScale – then the target is that object's atom layer, matched on shared atom keys.
key	Name of the code column in data. Defaults to source when that column exists, otherwise the scale's own key.
values	Character vector of value columns to convert. Default: all numeric columns other than the key and the scale's frame columns. Numeric identifiers (e.g. year) must be excluded explicitly.
rule	One of SCALE_RULES applied to every value column, or a named vector with one entry per column; NULL (default) looks each column up with get_scale_rule(). A column with neither an explicit rule nor a registry entry is an ERROR – there is deliberately no fallback (a silently guessed rule is a silent unit error).
weight	Weight column used by sum (splitting) and weighted_mean; scalar or named per column. NULL uses each column's registered weight, falling back to the object's default weight; when the object declares no weights at all, atoms weigh 1 (an equal split, warned about when it is material).
na_action	What to do with atoms that have no code at source or target: "drop" (default, with a warning – the affected source share is genuinely lost), "error", or "keep" (retain an explicit NA row so totals conserve).
parent	rule = "share" only: the frame defining the groups the shares are taken within. NULL (default) uses target when it differs from source, else the frame immediately above source.
collect	For lazy inputs: materialise the result (TRUE) or return the uncollected query (default).

`diagnostics` Whether to run the checks that need a scan of the data: unknown source codes, dropped shares, and source units missing from the data. `"auto"` (default) runs them on eager inputs and skips them on arrow/dtplyr, where a scan would defeat the point of returning a query; `"on"` and `"off"` force the choice. Errors that do not depend on the data – unknown frames, reserved column names, a missing rule – are raised regardless.

`missing_sources` What to do when a target unit's sources are only partially present in the data. `"na"` (default) makes the result `NA` – a partial answer is not an answer. `"ignore"` aggregates whatever is there, which is faster but silently turns incomplete data into a plausible number, so it is opt-in.

`batch`, `batch_by` Process the job in chunks of at most `batch` distinct values of the identifier column `batch_by` (default: the first identifier column), binding the pieces. Chunking by an identifier partitions the aggregation groups exactly, so the numbers are unchanged; any other column is refused. Applies only when materialising, and turns off per-chunk diagnostics, which would otherwise report sources as missing merely because they fall in another chunk.

`...` Passed to `scale_map()` (e.g. `year` for a calendar).

Details

Columns of the data that are neither the key nor a value column are treated as identifiers (panel columns – a year, a technology) and preserved as grouping columns, so panel data recasts correctly in one call. This is what makes mixed pipelines across two dimensions work: a recast in one dimension carries the other dimension's key through untouched. Columns named like the scale's own frames are treated as unit attributes and dropped.

`"sum"` splits each source value across its unit's atoms proportionally to the weight before summing up, so totals are conserved. `"weighted_mean"` weights by the atom weights; `"mean"` is the plain atom-count mean – the two differ exactly when atom weights differ. `"copy"` requires a constant value per target unit; `"sd"` is aggregation-only.

`"share"` inverts the output contract: the result stays keyed at `source`, and each value becomes that unit's share of the total over its parent group. `source` must nest within the parent. It cannot be combined with other rules in one call, and `weight=` is ignored – the observed values themselves are the weights.

Value

The recast table in the input's class, with columns `c(to, identifiers, values)`.

Backends

The data may be a `data.frame`, tibble, `data.table`, `dtplyr` lazy table, or an arrow Dataset/Table/query. The result comes back in the input's class; lazy inputs return the uncollected query unless `collect = TRUE`. Lazy results contain the observed target units only – the full-vocabulary completion (and its `NA` rows) applies when the result is materialised.

Examples

```
s <- scale_example()

# Extensive quantity, fine -> coarse: totals are preserved
d <- data.frame(
  unit = c("U1", "U2", "U3", "U4", "U5", "U6"),
  capacity = c(1, 2, 3, 4, 5, 6)
)
recast_scale(d, s, source = "unit", target = "sector", rule = "sum")

# Coarse -> fine: split proportionally to size
y <- data.frame(sector = c("P", "S"), capacity = c(10, 20))
recast_scale(y, s,
  source = "sector", target = "class",
  rule = "sum", weight = "size"
)

# Share within parent: result stays at the atoms, sums to 1 per sector
recast_scale(
  d, s,
  source = "unit", target = "sector",
  rule = "share",
  na_action = "keep"
)
```

---

recast_to_atoms *Recast unit data down to the atom layer, and back*

Description

The two public halves of the `from -> atoms -> to` route: `recast_to_atoms()` projects unit-keyed data DOWN to the atom layer (one row per atom), and `recast_from_atoms()` aggregates atom-keyed data UP into a frame's units. Their composition is `recast_scale()`, and because the atom rows are keyed by the atom IDs, `recast_from_atoms(recast_to_atoms(data, a), b, target)` recasts across two scales that share atom keys.

Usage

```
recast_to_atoms(
  data,
  x,
  source = NULL,
  key = NULL,
  values = NULL,
  rule = NULL,
  weight = NULL,
  attach_weight = TRUE,
  collect = NULL
```

```
)

recast_from_atoms(
  data,
  x,
  target,
  key = NULL,
  values = NULL,
  rule = NULL,
  weight = NULL,
  na_rm = FALSE,
  na_action = c("drop", "error", "keep"),
  collect = NULL
)
```

Arguments

data	The data: for recast_to_atoms() keyed by unit code at frame source; for recast_from_atoms() keyed by atom IDs.
x	The NestedScale the data is keyed in, or aggregated into.
source	to_atoms only: frame name the codes belong to. NULL (default) is inferred as in recast_scale().
key	The key column; defaults as in recast_scale().
values, rule	As in recast_scale().
weight	to_atoms: a declared weight column of x. from_atoms: the name of a column of data to weight by, so the weight may vary by identifier. NULL uses a weight column of the data if present, else the scale's declared weight.
attach_weight	to_atoms only: attach the weight column (default TRUE).
collect	For lazy inputs: materialise (TRUE) or return the query.
target	from_atoms only: target frame name.
na_rm	from_atoms only: read an NA value as "this member says nothing" rather than as an unknown that makes the whole group NA.
na_action	from_atoms only: what to do with atoms that have no code at target.

Details

Going down, extensive columns (rule "sum") are split across a unit's atoms proportionally to the chosen weight so totals conserve; intensive columns are repeated. A weight column is attached by default so the return trip's "weighted_mean" reproduces the source weighting exactly.

Value

recast_to_atoms(): one row per (atom x identifier combination). recast_from_atoms(): one row per (unit x identifier combination). Both in the input's class; lazy in, lazy out.

Examples

```
s <- scale_example()
d <- data.frame(sector = c("P", "S"), capacity = c(10, 20))
atoms <- recast_to_atoms(d, s,
  source = "sector", rule = "sum",
  weight = "size"
)
head(atoms)
recast_from_atoms(
  atoms, s,
  target = "class",
  rule = "sum",
  na_action = "keep"
)
```

`reconcile_scale` *Check fine data against an independent parent total*

Description

Aggregates `data` from `source` to `target` and compares the result with `totals`, the parent figure from another source. Reports the gap by default; can also close it.

Usage

```
reconcile_scale(
  data,
  x,
  source,
  target,
  totals,
  key = NULL,
  values = NULL,
  rule = "sum",
  weight = NULL,
  balance = c("none", "residual", "proportional"),
  tolerance = 1e-09
)
```

Arguments

`data`	The fine data, keyed at `source`.
`x`	A `NestedScale`.
`source, target`	Frame names: where the data is, and the coarser frame whose totals it is checked against.

totals	The independent parent figures: a table keyed at target carrying the same value columns as data, plus any identifier columns (which are matched, so a per-year total works).
key	Column of data holding the codes at source; defaults as in recast_scale().
values	Value columns to check. Default: the numeric columns common to data and totals.
rule	How the value aggregates. "sum" (default) is the question "does it add up"; an intensive quantity reconciles as "weighted_mean" instead.
weight	Weight column for rule = "weighted_mean".
balance	What to do about the gap: • "none" (default) – report it and change nothing. • "residual" – return the data with each group's gap written onto its declared residual unit at source. Needs exactly one residual per affected group, and rule = "sum". • "proportional" – return the data scaled by target / aggregated within each group, so every group hits its total.
tolerance	Relative size below which a gap counts as rounding; sets the ok column, and gaps within it are left alone when balancing.

Value

With balance = "none", a long gap table: the target column, any identifiers, value (which column), aggregated, target, gap (target - aggregated), rel_gap and ok. With a balancing method, the adjusted data keyed as the input was, carrying that same table as its "reconciliation" attribute.

Examples

```
lf <- data.frame(
  country = c("DE", "DE", "DE"),
  unit = c("DE1", "DE2", "DE_XR"),
  pop = c(40, 30, 0), stringsAsFactors = FALSE
)
s <- scale_from_leaftable(lf,
  frames = c("country", "unit"), key = "unit",
  weights = "pop", name = "geo",
  residuals = list(unit = "DE_XR")
)
fine <- data.frame(unit = c("DE1", "DE2", "DE_XR"), gdp = c(400, 300, 0))
published <- data.frame(country = "DE", gdp = 750)

reconcile_scale(fine, s, source = "unit", target = "country", published)

reconcile_scale(fine, s,
  source = "unit", target = "country", published,
  balance = "residual"
)
```

`register_scale_distance` *Register a distance*

Description

The built-ins cover level and shape; anything else – dynamic time warping, a domain-specific dissimilarity, a precomputed matrix – is registered here and then usable by name everywhere in the package.

Usage

```
register_scale_distance(name, fn)

get_scale_distance(name)

list_scale_distances()

clear_scale_distances(name = NULL)
```

Arguments

`name`	Distances to remove; `NULL` clears every registered one. Built-ins cannot be removed.
`fn`	A function of the unit-by-feature matrix returning a stats::dist object (or a square matrix) over its rows.

Value

Invisibly, `name`.

Examples

```
register_scale_distance("first_diff", function(m) {
  stats::dist(t(apply(m, 1, diff)))
})
"first_diff" %in% list_scale_distances()
clear_scale_distances("first_diff")
```

register_scale_map *Register / look up a direct crosswalk*

Description

A registered map short-circuits the atom-layer derivation in `scale_map()` or `scale_map_between()` (and thereby `recast_scale()`) for one pair of resolutions – for cases where the exact correspondence is known (hand-audited crosswalks, official concordance tables).

Usage

```
register_scale_map(x, source, target, map)

register_scale_map_between(source, target, map)

get_scale_map(x, source, target)

get_scale_map_between(source, target)

list_scale_maps()
```

Arguments

`x`	The `NestedScale` the frames belong to, or its name.
`source, target`	For the within-scale functions, frame names of `x`. For the `_between` functions, two `NestedScale` objects or their names.
`map`	A `data.frame` shaped like a `scale_map()` result: the two label columns named after the frames (or scales), plus `n_from`, `n_overlap`, `w` and `w_from`. `NULL` removes a previously registered map.

Details

`register_scale_map()` and `get_scale_map()` handle a pair of frames of one scale; the map is scoped to that scale, so the same frame pair in two different scales does not collide. `register_scale_map_between()` and `get_scale_map_between()` handle a pair of scales.

Value

Invisibly, the registry key. The `get_` functions return the registered map (or `NULL`); `list_scale_maps()` a `data.frame` of registry keys.

Examples

```
s <- scale_example()
fake <- data.frame(
  class = "G1", group = "GC", n_from = 1L,
  n_overlap = 1L, w = 1, w_from = 1
```

```
)
register_scale_map(s, "class", "group", fake)
list_scale_maps()
get_scale_map(s, "class", "group")
register_scale_map(s, "class", "group", NULL) # remove
clear_scale_maps()
```

`register_scale_rule` *Register how a parameter should be recast*

Description

Records the rule (and optionally the weight) to use for a named value column, so callers of `recast_scale()` need not repeat it. Downstream packages register their own parameter maps at load time.

Usage

```
register_scale_rule(param, rule, weight = NULL, scope = NULL)
```

Arguments

`param`	Name of the value column.
`rule`	One of `SCALE_RULES`.
`weight`	Optional weight column name used by `sum` (down) and `weighted_mean` (up). `NULL` means the scale's default weight.
`scope`	Optional dimension namespace (e.g. `"calendar"`, `"geoscale"`). `NULL` registers the rule for every dimension.

Value

Invisibly, the registered entry.

Examples

```
register_scale_rule("capacity", "sum")
register_scale_rule("eff", "weighted_mean", weight = "count")
get_scale_rule("eff")
clear_scale_rules(c("capacity", "eff"))
```

`scale_alias_property` *An alias property for a subclass*

Description

Builds a getter/setter property that reads and writes an inherited property under a different name – how timescales' `Calendar` keeps `@timeframes` and geoscales' `Geoscale` keeps `@geoframes` working over the inherited `@frames`, so no existing code has to change when they become subclasses.

Usage

```
scale_alias_property(name)
```

Arguments

`name`	Name of the inherited property to alias.

Details

The setter is a no-op on `NULL`. S7's generated constructor writes every dynamic property once with `NULL` before the real values are set, so a setter that forwards `NULL` makes the class impossible to construct.

Value

An S7 property.

Examples

```
Aliased <- S7::new_class("Aliased",
  parent = scale_class(),
  properties = list(levels = scale_alias_property("frames"))
)
a <- Aliased(
  leaftable = scale_leaftable(scale_example()),
  frames = scale_frames(scale_example()),
  members = S7::prop(scale_example(), "members")
)
a@levels
```

scale_aliases *Read the alias table*

Description

Read the alias table

Usage

```
scale_aliases(x, frame = NULL, source = NULL)
```

Arguments

x	A NestedScale.
frame	Restrict to one frame; NULL for all.
source	Restrict to one source (or several); NULL for all.

Value

A data.frame with columns frame, unit, alias, source.

Examples

```
s <- attach_aliases_scale(
  scale_example(),
  data.frame(frame = "sector", unit = "P", alias = "primary"),
  source = "labels"
)
scale_aliases(s)
scale_aliases(s, frame = "class")
```

scale_ancestry *Ancestry between all frame pairs*

Description

Every (coarser, finer) code pair that shares at least one atom, for all frame pairs.

Usage

```
scale_ancestry(x)
```

Arguments

x	A NestedScale.

Details

Computed **atom-mediated**, directly from the leaftable – deliberately not as a transitive closure of `scale_family()`. Closing a hierarchy that cross-cuts manufactures false relationships: in the example scale, group `GB` straddles both sectors, so closing `sector -> class -> group -> unit` would wrongly report sector `P` as an ancestor of unit `U5`, which lies in sector `S`.

For frames that do not nest this relation is *overlap*, not containment – test a given pair with `scale_nests()`.

Frame columns are retained because codes are not unique across frames: in the example, `"G1"` exists at both `class` and `group`, so a bare `(parent, child)` pair would read as a self-loop.

Value

A `data.frame` with columns `parent_frame`, `parent`, `child_frame`, `child`.

Examples

```
head(scale_ancestry(scale_example()))
```

---

scale_atom_level *The level at which a scale enumerates its atoms*

Description

The finest frame when one code of it sits on each leaftable row, and the key column otherwise. A `NestedScale` built from a nested hierarchy is the first kind; a timescales `Calendar` is the second, because its timeslices are combinations of its frames rather than codes of any one of them.

Usage

```
scale_atom_level(x)
```

Arguments

`x`	A `NestedScale`.

Details

Needed by the dimension packages: it is the `frame` to pass to `join_scale()` or `recast_scale()` for data keyed at the atoms.

Value

A single string – a frame name, or the key.

Examples

```
scale_atom_level(scale_example())
```

scale_atom_pairs *Atom-level correspondence between two frames*

Description

The seam a dimension package overrides when its atom layer is generated rather than enumerated. Returns one row per atom (or per atom and extra identifier, e.g. per grid instant and year).

Usage

```
scale_atom_pairs(x, ...)
```

Arguments

x	A NestedScale.
...	Method arguments: source and target (frame names of x), weight (a weight column, or NULL for the scale's default), and whatever else the dimension needs to generate its atoms – year for a calendar.

Value

A data.frame with columns source, target, w, plus any extra identifier columns the dimension carries. The extra columns must be named in the by argument of the caller.

Examples

```
head(scale_atom_pairs(scale_example(), "class", "group"))
```

SCALE_ATTRIBUTE_KINDS *Kinds of attribute*

Description

Every attribute name carries a kind, which convert_scale() consults:

Usage

```
SCALE_ATTRIBUTE_KINDS
```

Format

A character vector of length 2.

Details

`property` A physical property of the member, an invertible ratio: a calorific value in GJ/t converts tonnes to gigajoules and gigajoules back to tonnes; a density, a yield.

`factor` A one-way multiplier: an emission factor in kg/TJ turns energy into CO2, and there is no physical sense in which CO2 turns back into energy; a loss factor, a tax rate.

Value

A character vector of the two attribute kinds accepted in the `kind` column of `attach_attributes_scale()`: `"property"` and `"factor"`.

Examples

```
SCALE_ATTRIBUTE_KINDS
```

`scale_attributes` *Read attributes, resolved along the hierarchy*

Description

With `frame = NULL`, returns the stored attribute table (filtered by `attribute` and `source`). With a `frame`, returns one row per member of that frame per attribute, **resolved**: a member's own value when it has one, otherwise the value of its nearest ancestor that has one, walking coarser frames one at a time. The row reports where the value came from in `origin_frame`/`origin_unit`; a member with no value anywhere gets an `NA` row.

Usage

```
scale_attributes(
  x,
  attribute = NULL,
  frame = NULL,
  source = NULL,
  inherit = TRUE
)
```

Arguments

`x`	A `NestedScale`.
`attribute`	Character vector of attribute names; `NULL` for all.
`frame`	Frame whose members to resolve for; `NULL` returns the stored table unresolved.
`source`	Restrict to one source (or several). `NULL` uses whatever is stored and errors on a conflict.
`inherit`	Walk to coarser frames for members without a value of their own (default `TRUE`). `FALSE` reports stored values only.

Details

Two situations are errors rather than guesses:

- the walk reaches a frame where the member has **several** ancestors (the frames cross-cut) and at least one of them holds the attribute – "inheritance is ambiguous";
- several `sources` publish the attribute for the same member and `source` is `NULL` – pass `source=` to choose.

Value

A `data.frame` with the attribute columns (`frame`, `unit`, `attribute`, `kind`, `value`, `lower`, `upper`, `unit_of_measure`, `source`, `note`), plus `origin_frame` and `origin_unit` when `frame` is given.

Examples

```
s <- attach_attributes_scale(
  scale_example(),
  data.frame(frame = c("sector", "class"), unit = c("P", "S1"),
             attribute = "density", value = c(10, 5),
             unit_of_measure = "t/m3"),
  source = "survey", kind = "property"
)
scale_attributes(s)                          # stored rows
scale_attributes(s, "density", frame = "unit") # resolved per atom
```

`scale_axes` *Axes of a product*

Description

Axes of a product

Usage

```
scale_axes(x, axis = NULL)
```

Arguments

`x`	A `ScaleProduct`.
`axis`	Optional single axis name, to get just that `NestedScale`.

Value

A named list of `NestedScale` objects, or one NestedScale when `axis` is given.

Examples

```
p <- scale_product(a = scale_example(), b = scale_example2())
names(scale_axes(p))
scale_axes(p, "a")
```

scale_catalog *Shipped scale definitions*

Description

Packages ship scale definitions as files (see `write_scale()`) and register the directory holding them; `scale_catalog()` lists what every registered directory holds and `read_scale()` takes an id from it. nestedscales registers its own `inst/scales/` on load, so `read_scale("carriers")` works with nothing else attached.

Usage

```
register_scale_dir(path, package = NULL)

list_scale_dirs()

clear_scale_dirs()

scale_catalog()
```

Arguments

path	A directory of definition files or bundles.
package	The package registering it; `NULL` for a directory registered by hand (listed under `package = NA`).

Details

`register_scale_dir()` is what a dimension package calls in its `.onLoad()`: `register_scale_dir(system.file("scales`
`package = pkgname), package = pkgname)`.

Value

`scale_catalog()` a `data.frame` with one row per definition: `id`, `name`, `kind` (the class, without its package prefix), `key`, `frames` (joined by `/`), `n_atoms`, `package`, `path`. `register_scale_dir()` the registry key, invisibly; `list_scale_dirs()` a `data.frame` with `package` and `path`; `clear_scale_dirs()` `NULL`, invisibly.

Examples

```
scale_catalog()
```

scale_class *The scale classes, for subclassing and dispatch*

Description

The classes are not exported under their own names (the package's surface is its functions), so these return them. Needed to build a subclass (`S7::new_class(..., parent = scale_class())`, which is what `scale_alias_property()` is for) or to register an S7 method against one. To merely ask what an object is, use `scale_is()`.

Usage

```
scale_class()

scale_product_class()
```

Value

The S7 class object.

Examples

```
scale_class()
S7::S7_inherits(scale_example(), scale_class())
```

scale_coverage *Coverage of a sampled NestedScale*

Description

The fraction of the root parent's weight that survives in this object. A scale that was never subset covers all of itself, so every weight reports 1.

Usage

```
scale_coverage(x, weight = NULL)
```

Arguments

`x`	A `NestedScale`.
`weight`	A single weight name, or `NULL` for all declared weights.

Value

A named numeric over the declared weights, or a single unnamed numeric when `weight` is given.

Examples

```
scale_coverage(scale_example())
```

`scale_crosses` *Do two frames form a product?*

Description

`TRUE` when every unit of `a` combines with the same set of units of `b`, as the months and hours of a `MONTH x HOUR` calendar do: the frames overlay rather than nest, and the atoms are their combinations. The complement of `scale_nests()` for the other common shape; a pair can be neither.

Usage

```
scale_crosses(x, a, b)
```

Arguments

`x`	A `NestedScale`.
`a, b`	Frame names.

Value

A logical scalar. When `FALSE`, the attribute `"offenders"` names the units of `a` whose set of `b` units differs from the first one's.

Examples

```
s <- scale_example()
scale_crosses(s, "class", "group")

grid <- expand.grid(m = c("m1", "m2"), h = c("h1", "h2", "h3"),
                    stringsAsFactors = FALSE)
grid$unit <- paste(grid$m, grid$h, sep = "_")
mh <- scale_from_leaftable(grid, frames = c("m", "h"), key = "unit")
scale_crosses(mh, "m", "h")
scale_nests(mh, "m", "h")
```

scale_dataset_info *Describe a stored dataset without opening it fully*

Description

Describe a stored dataset without opening it fully

Usage

```
scale_dataset_info(path)
```

Arguments

path	A folder written by `write_scale_dataset()`.

Value

A list with `kind`, `axes`, `keys`, `files` and `bytes`.

Examples

```
# see write_scale_dataset()
```

scale_distance *Distance between the units of a scale*

Description

Reshapes long, unit-keyed data into a unit-by-observation matrix and measures the distance between its rows.

Usage

```
scale_distance(
  data,
  x,
  frame = NULL,
  key = NULL,
  value = NULL,
  method = "euclidean",
  scale_units = FALSE
)
```

Arguments

data	Long data: a column of unit codes, one or more identifier columns saying which observation each row is, and a value column.
x	A NestedScale.
frame	Frame whose units are compared. Defaults to the atom frame.
key	Column of data holding the unit codes. Defaults to frame when present, else the scale's key.
value	Value column; inferred when unambiguous.
method	A name from list_scale_distances().
scale_units	Standardise each unit's profile to mean 0, sd 1 before measuring. Turns a level distance into a shape distance; has no effect on "correlation", which already ignores level.

Value

A stats::dist object over the frame's units, in member order.

Examples

```
s <- scale_example()
d <- data.frame(
  unit = rep(scale_units(s), each = 3),
  t = rep(sprintf("t%d", 1:3), 7), v = as.numeric(seq_len(21))
)
round(scale_distance(d, s, method = "correlation"), 2)
```

SCALE_DISTANCES *Built-in distances*

Description

euclidean, manhattan, maximum Straight to stats::dist(). Compare units by the LEVEL of their profiles.

correlation 1 - cor(t(x)), Pearson. Compares SHAPE: two units that rise and fall together are close however different their magnitudes, which is what you usually want when grouping load or generation profiles.

spearman The same on ranks – shape, robust to outliers.

cosine 1 - cosine similarity. Shape again, but sensitive to sign and not centred, so a unit that is uniformly positive is close to every other such unit.

Usage

```
SCALE_DISTANCES
```

Format

A character vector.

Value

A character vector of the six built-in distance names accepted by the `method` argument of `scale_distance()`; `list_scale_distances()` adds any registered with `register_scale_distance()`.

Examples

```
SCALE_DISTANCES
```

---

scale_example *A small example NestedScale*

Description

A synthetic 3-frame hierarchy used in examples and tests. It deliberately reproduces three awkward features of real classification tables:

Usage

```
scale_example()
```

Details

- a code (`"G1"`) reused at more than one frame, so bare codes are ambiguous and every lookup must name its frame;
- a non-nesting pair of frames – group `"GB"` draws units from two different classes, so `class` and `group` do not form a tree;
- a unit (`"OTH"`) with no code at any coarser frame (partial coverage).

Value

A `NestedScale` with 7 atoms and frames `sector`/`class`/`group`/`unit`.

Examples

```
s <- scale_example()
s
scale_nests(s, "class", "group") # FALSE - they cross-cut
```

scale_example2 *A second small example NestedScale*

Description

A different dimension from `scale_example()`, for the examples that need two axes. Two frames, four atoms, its own key column (`period`) and a weight – deliberately well behaved, so the awkwardness in an example stays on the other axis.

Usage

```
scale_example2()
```

Value

A `NestedScale` with 4 atoms and frames `era`/`period`.

Examples

```
scale_example2()
scale_product(a = scale_example(), b = scale_example2())
```

scale_family *Immediate parent-child table between two frames*

Description

Immediate parent-child table between two frames

Usage

```
scale_family(x, parent = NULL, child = NULL)
```

Arguments

`x`	A `NestedScale`.
`parent`, `child`	Frame names. Defaults to every adjacent pair in `x@frames`.

Value

A `data.frame` with columns `parent_frame`, `parent`, `child_frame`, `child`. Atoms unassigned at either frame are omitted.

Examples

```
s <- scale_example()
scale_family(s, "group", "unit")
```

scale_frames *Frames of a NestedScale*

Description

The hierarchy names, ordered coarsest first. The last entry is the atom frame whenever one frame enumerates the atoms; when none does – a `Calendar`'s atoms are combinations of its frames – the key column is the atom level instead.

Usage

```
scale_frames(x, finest = FALSE)

## S3 method for class 'NestedScale'
names(x)
```

Arguments

`x`	A `NestedScale`.
`finest`	Return only the finest (atom) frame.

Value

A character vector of frame names, or a single name when `finest = TRUE`.

Examples

```
s <- scale_example()
scale_frames(s)
scale_frames(s, finest = TRUE)
```

scale_from_leaftable *Build a NestedScale from a flat table of atoms*

Description

The general constructor. Takes a wide `data.frame` with one row per atom (the finest unit) and one column per frame, and returns a `NestedScale`.

Usage

```
scale_from_leaftable(
  leaftable,
  frames,
  key = NULL,
  weights = NULL,
  default_weight = NULL,
  members = NULL,
  name = "",
  desc = "",
  attributes = NULL,
  aliases = NULL,
  ...
)
```

Arguments

leaftable	data.frame with one row per atom, one column per name in frames, and optionally numeric weight columns.
frames	Ordered character vector of frame names, **coarsest first**. Each must be a column of leaftable.
key	Name of the column holding the unique atom key. Defaults to "unit" if present, otherwise the finest frame (the last entry of frames), which is copied into a unit column.
weights	Character vector naming the weight columns. Defaults to all numeric columns that are neither frames nor reserved names.
default_weight	The weight used when a caller does not name one. Defaults to the first entry of weights.
members	Optional named list giving the ordered code vocabulary per frame. Derived from leaftable when NULL (first-appearance order).
name, desc	Short name and description.
attributes	Optional table of per-member physical attributes keyed by (frame, unit); see attach_attributes_scale() for the columns.
aliases	Optional table of alternative labels keyed by (frame, unit); see attach_aliases_scale() for the columns.
...	Further named entries merged into meta (e.g. source, labels).

Details

Blank strings ("") in frame columns are normalised to NA, meaning "this atom has no code at this frame" – partial coverage is normal in real classification tables.

Value

A NestedScale.

Examples

```
df <- data.frame(
  section = c("A", "A", "A", "B"),
  group   = c("A1", "A1", "A2", "B1"),
  unit    = c("A11", "A12", "A21", "B11"),
  gva     = c(100, 200, 300, 400)
)
scale_from_leaftable(df, frames = c("section", "group", "unit"))
```

---

scale_is *Is this a scale, or a product of scales?*

Description

The classes themselves are not exported (the package's surface is its functions), so these are how calling code asks. Build a scale with `scale_from_leaftable()` and a product with `scale_product()`.

Usage

```
scale_is(x)

scale_is_product(x)
```

Arguments

x	Any object.

Details

Named with the object prefix rather than `is_scale()`, which ggplot2 already exports.

Value

A single TRUE or FALSE. A product is NOT a scale: it holds several and materialises no atoms of its own.

Examples

```
scale_is(scale_example())
scale_is(data.frame(unit = "U1"))
scale_is_product(scale_product(a = scale_example(), b = scale_example2()))
```

scale_is_uniform *Are the units of a frame the same size?*

Description

TRUE when every unit of frame holds the same number of atoms, or the same total of a weight column: the dimension-free form of a "regular" calendar (equal durations) or an equal-area regionalisation. Atoms with no code at frame are ignored.

Usage

```
scale_is_uniform(x, frame, weight = NULL, tolerance = 1e-09)
```

Arguments

x	A NestedScale.
frame	A frame name.
weight	NULL compares atom counts; a weight column name compares its per-unit totals.
tolerance	Relative tolerance for weight totals.

Value

A logical scalar. When FALSE, the attribute "sizes" holds the per-unit counts or totals.

Examples

```
s <- scale_example()
scale_is_uniform(s, "class")                  # two atoms each
scale_is_uniform(s, "class", weight = "size") # but not the same size
```

scale_key *The atom key column name*

Description

The atom key column name

Usage

```
scale_key(x)
```

Arguments

x	A NestedScale.

Value

A single string.

Examples

```
scale_key(scale_example())
```

`scale_leaftable` *The leaftable of a NestedScale*

Description

The one-row-per-atom table the scale is built on, as a plain `data.frame` – the exported accessor to prefer over reaching for `x@leaftable`. `as.data.frame()` and `ggplot2::fortify()` on a NestedScale are equivalent, so `ggplot(s) + geom_*()` pipelines work directly.

Usage

```
scale_leaftable(x)

## S3 method for class 'NestedScale'
as.data.frame(x, row.names = NULL, optional = FALSE, ...)

## S3 method for class '`nestedscales::NestedScale`'
as.data.frame(x, row.names = NULL, optional = FALSE, ...)
```

Arguments

`x`	A `NestedScale`.
`row.names, optional`	Ignored (S3 signature compatibility).
`...`	Ignored.

Value

A `data.frame`: one row per atom, with the frame columns plus any weight columns.

Examples

```
head(scale_leaftable(scale_example()))
head(as.data.frame(scale_example()))
```

scale_map *Crosswalk between two frames of a scale*

Description

Materialises the `from -> atoms -> to` route as a table: one row per pair of overlapping units with

Usage

```
scale_map(x, source, target, weight = NULL, by = character(), ...)
```

Arguments

`x`	The `NestedScale` the frames belong to.
`source, target`	Frame names of `x`.
`weight`	Weight column for `w`. `NULL` uses the default weight; when the object declares no weights at all, every atom gets weight 1 (an equal split).
`by`	Extra identifier columns carried through from `scale_atom_pairs()` (e.g. `"year"`).
`...`	Passed to `scale_atom_pairs()`.

Details

- `n_from` – atoms in the `source` unit (its full set, before any target coverage is considered),
- `n_overlap` – atoms the pair shares,
- `w` – the weight of the overlap (summed atom weights, chosen weight column), the quantity `"weighted_mean"` aggregation uses,
- `w_from` – the full weight of the `source` unit; `w / w_from` is the split share `"sum"` disaggregation uses.

The two label columns are named by the frames; rows with an `NA` target label are atoms `target` does not cover. A crosswalk registered with `register_scale_map()` is returned as-is instead of being derived.

Value

A `data.frame` with columns `<from>`, `<to>` (`NA` = uncovered by `target`), `n_from`, `n_overlap`, `w`, `w_from`, plus any `by` columns.

See Also

`scale_map_between()` for the map between two scales.

Examples

```
s <- scale_example()
scale_map(s, "class", "group")
scale_map(s, "sector", "class", weight = "count")
```

scale_map_between *Crosswalk between two scales through their shared atoms*

Description

The counterpart of `scale_map()` for two scales: atoms are matched on their keys, so a unit of `source` overlaps a unit of `target` where they contain the same atoms. Same columns as `scale_map()`, with the two label columns named after the scales. Atoms of `source` absent from `target` get an `NA` target (with a warning). A crosswalk registered with `register_scale_map_between()` is returned as-is instead of being derived.

Usage

```
scale_map_between(source, target, weight = NULL)
```

Arguments

`source`, `target`	Two named `NestedScale` objects whose atom keys overlap.
`weight`	Weight column of `source` for `w`; `NULL` uses its default weight, or weight 1 per atom when it declares none.

Value

A `data.frame` with columns `<from name>`, `<to name>`, `n_from`, `n_overlap`, `w`, `w_from`.

Examples

```
a <- scale_example()
b <- scale_from_leaftable(
  data.frame(
    big = c("X", "X", "Y", "Y", "Y", "Y", "Z"),
    unit = c("U1", "U2", "U3", "U4", "U5", "U6", "OTH")
  ),
  frames = c("big", "unit"), name = "other"
)
scale_map_between(a, b)
```

scale_match *Match labels to members, strictly*

Description

Resolves each label to a `(frame, unit)` member in two stages, stopping at the first that hits: an **exact** member name (case-insensitive), then an **alias** (case-insensitive). A label that hits several members – the same name at two frames, or an alias shared by two members – is reported as `"ambiguous"` with the candidates, unless `frame=` narrows the search to one frame. A label that hits nothing is `"none"`. Nothing is guessed: no fuzzy matching, no substring matching.

Usage

```
scale_match(x, labels, frame = NULL, source = NULL)
```

Arguments

x	A NestedScale.
labels	Character vector of labels to resolve.
frame	Restrict matching to one frame; NULL searches all frames and the atom level.
source	Restrict the alias stage to one source (or several).

Value

A data.frame with one row per label: label, frame, unit, method ("exact", "alias", "ambiguous", "none") and candidates (the frame/unit pairs of an ambiguous hit, joined by "; ", else NA).

Examples

```
s <- scale_example()
scale_match(s, c("P", "G1", "u1", "nope"))   # G1 is a class AND a group
scale_match(s, "G1", frame = "group")
```

---

scale_navigate *Navigate a NestedScale's hierarchy*

Description

Codes related to unit at another frame, found through the atoms. scale_children()/scale_parents() step one frame down/up by default; scale_descendants()/scale_ancestors() report every finer/coarser frame as a frame-tagged table.

Usage

```
scale_children(x, frame, unit, target = NULL)

scale_parents(x, frame, unit, target = NULL)

scale_descendants(x, frame, unit, target = NULL)

scale_ancestors(x, frame, unit, target = NULL)
```

Arguments

x	A NestedScale.
frame	The frame unit belongs to.
unit	Character vector of codes.
target	Target frame. NULL uses the adjacent frame (children/parents) or every finer/coarser frame (descendants/ancestors).

Value

A character vector (children/parents) or a `data.frame` with columns `frame` and `unit` (descendants/ancestors).

Examples

```
s <- scale_example()
scale_children(s, "sector", "P")
scale_parents(s, "unit", "U5")
scale_descendants(s, "sector", "P")
scale_ancestors(s, "unit", "U5")
```

---

scale_nests *Do two frames nest?*

Description

Tests whether every code at the finer frame falls entirely within a single code at the coarser frame. Real hierarchies often fail this: a spatial code can straddle two parents, and a reporting classification can assign one detailed class to several aggregates.

Usage

```
scale_nests(x, parent, child)
```

Arguments

`x`	A `NestedScale`.
`parent`, `child`	Frame names.

Details

Nesting is *not* required by `NestedScale` – conversion routes through the atom layer and works either way. This function is a diagnostic.

Value

`TRUE` or `FALSE`. When `FALSE`, the offending child codes are attached as the `"offenders"` attribute.

Examples

```
s <- scale_example()
scale_nests(s, "class", "group") # FALSE - they cross-cut
```

scale_payload_collapse *Collapse a subclass's per-atom payload*

Description

The companion of `scale_payload_slice()` for the rebuilds that MERGE atoms rather than keep a subset of them – `prune_scale()`, which makes a coarser frame the new atom layer. Called with `map`, an integer vector with one entry per row of the OLD leaftable giving the index of the NEW row that atom was merged into, or `NA` for an atom that was dropped.

Usage

```
scale_payload_collapse(x, ...)
```

Arguments

`x`	A `NestedScale`.
`...`	Method arguments: `map`, the integer vector described above.

Details

The `NestedScale` default returns `x` unchanged, which is right for a payload keyed by member codes (the core's own attribute and alias tables are re-keyed by the engine itself). A subclass whose payload is positional – one geometry per leaftable row – must override it and merge its payload by `map`; if it does not, its own validator rejects the length mismatch, so the failure is loud rather than a silently misaligned payload.

Value

`x`, with any payload merged to the new rows.

Examples

```
identical(
  scale_payload_collapse(scale_example(), c(1L, 1L, 2L, 2L, 3L, 3L, NA)),
  scale_example()
)
```

scale_payload_io *Write and read a subclass's payload in a definition file*

Description

The seam a dimension package uses to carry what the core does not know about – geoscales' geometry – in a scale definition written by `write_scale()` and read by `read_scale()`.

Usage

```
scale_write_payload(x, ...)

scale_read_payload(x, ...)

register_scale_class(class)

list_scale_classes()
```

Arguments

x	A `NestedScale` (the subclass instance when writing; the core object when reading).
...	Method arguments: `dir`, the bundle directory or `NULL`, and `header`, the header list.
class	An S7 class that inherits from `scale_class()`.

Details

`scale_write_payload(x, dir, header)` is called after the core tables are written, with the bundle directory (`NULL` for a single-file definition, which can hold inline data only) and the header so far; it writes its files and returns the header with its entries added under `payload`. `scale_read_payload(x, dir, header)` is called with the CORE scale rebuilt from the header and returns the subclass object. The `NestedScale` defaults return the header and `x` unchanged.

`read_scale()` finds the method through the class recorded in the header, so a dimension package registers its class once, in `.onLoad()`, with `register_scale_class()`.

Value

`scale_write_payload()` the header; `scale_read_payload()` a scale; `register_scale_class()` the registry key, invisibly; `list_scale_classes()` a character vector of registered class names.

Examples

```
list_scale_classes()
```

scale_payload_slice *Subset a subclass's per-atom payload*

Description

The seam a dimension package overrides when it carries per-atom data alongside the leaftable – geoscales' `Geoscale` and its geometry. Called whenever the engine rebuilds an object from a row subset, with the kept row indices. The `NestedScale` default has no payload and returns `x` unchanged.

Usage

```
scale_payload_slice(x, ...)
```

Arguments

`x`	A `NestedScale`.
`...`	Method arguments: `i`, the integer vector of kept leaftable row indices.

Value

`x`, with any payload subset to the kept rows.

Examples

```
identical(
  scale_payload_slice(scale_example(), 1:3),
  scale_example()
)
```

scale_product *Combine scales into a product index*

Description

Combine scales into a product index

Usage

```
scale_product(..., name = "", desc = "", keys = NULL, joint_weights = NULL)
```

Arguments

...	Two or more named NestedScale objects; the argument names become the axis names.
name, desc	Short name and description of the product.
keys	Optional named character vector overriding the data key column per axis. By default each axis uses its scale's own key (scale_key()); if that would make two axes share a column name, the AXIS NAMES are used instead.
joint_weights	Reserved; see ScaleProduct.

Value

A ScaleProduct.

Examples

```
p <- scale_product(a = scale_example(), b = scale_example2())
p
product_size(p)
```

---

scale_rank *Frame rank*

Description

Position of a frame in the hierarchy: 1 is the coarsest.

Usage

```
scale_rank(x, frame)
```

Arguments

x	A NestedScale.
frame	Character vector of frame names.

Value

An integer vector of ranks; NA for names that are not frames of x.

Examples

```
s <- scale_example()
scale_rank(s, c("group", "unit"))
```

`scale_residuals` *Units that are residuals*

Description

A residual carries a real value but is not a destination for allocation: non-regionalized GDP, taxes that belong to no industry, an "n.e.c." bucket. It aggregates upward like any other unit – that is the point, it is what makes the parent total reconcile – but `recast_scale()` never splits a coarse figure INTO one.

Usage

```
scale_residuals(x, frame = NULL)
```

Arguments

`x`	A `NestedScale`.
`frame`	A single frame name for just that frame's residuals, or `NULL` for the whole named list.

Details

Declare them when building the scale, per frame, because codes are not unique across frames: `scale_from_leaftable(..., residuals = list(unit = "DE_XR"))`.

Value

A character vector of unit codes, or the named list over frames. Empty when the scale declares none.

Examples

```
s <- scale_example()
scale_residuals(s) # none declared

lf <- scale_leaftable(s)
r <- scale_from_leaftable(
  lf,
  frames = scale_frames(s), key = "unit",
  weights = scale_weights(s), name = "with_residual",
  residuals = list(unit = "OTH")
)
scale_residuals(r, "unit")
```

SCALE_RULES *Supported aggregation rules*

Description

Each rule defines behaviour in **both** directions. Direction is taken from the frame ranks, so aggregation and disaggregation are one operation:

Usage

```
SCALE_RULES
```

Format

A character vector of length 7.

Details

`sum` Up: sum. Down: split proportionally to the weight. For extensive quantities (capacity, demand, area, population).

`weighted_mean` Up: weight-weighted mean. Down: copy unchanged. For intensive quantities (efficiency, price, capacity factor).

`mean` Up: unweighted mean. Down: copy unchanged.

`copy` Up: the common value, erroring if it is not constant. Down: copy unchanged. For scale-invariant scalars.

`sd` Up: standard deviation over the atoms (aggregation only; going down it degenerates to `NA` for single-atom groups).

`share` Share within parent: each source unit's value divided by the total over its parent group. Unlike every other rule the result stays keyed at the **source** frame – the recast target (or `parent=`) names the parent – so it cannot be mixed with other rules in one call (the two share rules mix freely, being one computation). For building distribution keys and normalised profiles; requires `from` to nest within the parent.

`logshare` The same computation as `share` – the values ARE shares – but figures draw it on a fixed log10 percent scale (0.01%..100%), where `share` gets a fixed linear 0..1 scale.

Value

A character vector of the seven rule names accepted by the `rule` argument of `recast_scale()` and `register_scale_rule()`.

Examples

```
SCALE_RULES
```

scale_share *Weight shares within a frame*

Description

Normalised weights, either of the whole object or within each parent group.

Usage

```
scale_share(x, frame, weight = NULL, within = NULL)
```

Arguments

x	A NestedScale.
frame	Frame to report shares for.
weight	Weight column. NULL uses the default.
within	Optional coarser frame to normalise within. NULL normalises over the whole object.

Value

A data.frame with a code column named frame, the weight, and share. When within is given, a column of that name carries the parent code.

Examples

```
s <- scale_example()
scale_share(s, "class", weight = "size")
scale_share(s, "class", weight = "size", within = "sector")
```

scale_units *Units of a NestedScale*

Description

The code vocabulary at one frame, in canonical order.

Usage

```
scale_units(x, frame = NULL)
```

Arguments

x	A NestedScale.
frame	A single frame name; defaults to the finest frame (the atoms).

Value

A character vector of unit codes.

Examples

```
s <- scale_example()
scale_units(s)
scale_units(s, "group")
```

`scale_vocab` *The dimension vocabulary of a scale*

Description

Engine messages are written once and interpolated with the words of the dimension at hand, so a `Calendar` flowing through the shared engine still errors in the language of time ("timeframe", "timeslice") and a `Geoscale` in the language of space ("geoframe", "region"). Subclasses supply their own method; the `NestedScale` default is the neutral vocabulary.

Usage

```
scale_vocab(x, ...)
```

Arguments

`x`	A `NestedScale`.
`...`	Passed to methods.

Value

A named list with elements `object`, `frame`, `frames`, `unit`, `units`, `atoms`, and optionally `register_rule` and `register_map`: the calls that error messages suggest for registering a value column's rule or an explicit crosswalk, when the dimension package offers its own (`"register_geoscale_rule()"`).

Examples

```
scale_vocab(scale_example())
```

scale_weights *Weight columns of a NestedScale*

Description

Weight columns of a NestedScale

Usage

```
scale_weights(x)
```

Arguments

x	A NestedScale.

Value

A character vector of weight column names (possibly empty).

Examples

```
scale_weights(scale_example())
```

shipped_scales *Shipped definitions:* carriers *and the IPCC 2006 fuel defaults*

Description

nestedscales ships one scale definition, carriers, under inst/scales/, and the IPCC tables it draws on under inst/extdata/. read_scale("carriers") reads the scale; scale_catalog() lists it with every other registered definition.

carriers

A scale of 71 fuels in three nested frames, group (8) > carrier (17) > fuel (71), key fuel, taken from the carriers palette of the energypal package (its inst/extdata/palettes/carriers.yml, which cites the IPCC 2006 Guidelines and the IEA World Energy Balances for its classification). energypal remains the editable source of the names, hierarchy, labels and aliases; the definition is a snapshot built by data-raw/carriers.R, which stops when the two disagree.

The three carriers energypal declares without subtypes (Electricity, Heat, Other) become their own fuel, so every carrier is reachable from the atoms. Five names appear both as a group and as the carrier inside it (Nuclear, Electricity, Heat, Storage, Other), and Hydrogen is both a carrier (under Synthetic) and a fuel (under Storage): every lookup names its frame.

Attributes (source "IPCC2006", 26 rows): the default net calorific value lhv (kind property, GJ/t) and CO2 emission factor ef_co2 (kind factor, kg/TJ) of the IPCC 2006 Guidelines, Vol. 2 Ch. 1,

Tables 1.2 and 1.4, attached to the 13 fuels whose definition matches an IPCC fuel exactly. Fuels without a matching IPCC entry carry no value; `scale_attributes()` reports them as `NA` rather than inventing one.

Aliases (136 rows): energypal's alternative spellings (source `"energypal"`) and a set of model commodity codes such as `GAS`, `LIG`, `ELC` (source `"commodity"`). `scale_match()` resolves them.

`meta$labels` carries energypal's short and long labels per member; `meta$energypal_version` and `meta$palette_version` record the snapshot. Colours are not stored: join them from energypal by name.

IPCC 2006 default calorific values and CO2 emission factors

`system.file("extdata", "ipcc2006_fuel_defaults.csv", package = "nestedscales")` holds every row of Table 1.2 (default net calorific values, TJ/Gg, with the lower and upper limits of the 95% confidence interval) and Table 1.4 (default CO2 emission factors for combustion, kg/TJ, with the 95% interval) of the IPCC 2006 Guidelines, Vol. 2 (Energy), Chapter 1, in long form, together with how each IPCC fuel maps onto `carriers`. TJ/Gg is numerically identical to GJ/t, the unit the `lhv` attribute uses. One row per IPCC fuel and attribute:

`ipcc_fuel` The fuel's English description in the Guidelines.

`attribute` `"lhv"` (Table 1.2) or `"ef_co2"` (Table 1.4).

`kind` `"property"` or `"factor"`, see `SCALE_ATTRIBUTE_KINDS`.

`value`, `lower`, `upper` The default and its 95% interval.

`unit_of_measure` `"GJ/t"` or `"kg/TJ"`.

`table` `"1.2"` or `"1.4"`.

`source` `"IPCC2006"`.

`frame`, `unit` The `carriers` member the row maps to (`NA` when not mapped).

`mapping_status` `"mapped"` (an exact or definitional correspondence), `"review"` (a plausible correspondence awaiting a ruling; not attached) or `"unmapped"` (no counterpart).

`primary` Whether this IPCC fuel is the one `carriers` carries for that member. Only `mapped` rows with `primary = TRUE` enter the scale's attributes.

Source

energypal `carriers.yml`; IPCC (2006), *2006 IPCC Guidelines for National Greenhouse Gas Inventories*, Volume 2 (Energy), Chapter 1, Tables 1.2 and 1.4, https://www.ipcc-nggip.iges.or.jp/public/2006gl/. Transcribed in `data-raw/ipcc2006/`.

See Also

`read_scale()`, `scale_catalog()`, `convert_scale()`; `vignette("attributes")`.

Examples

```
carriers <- read_scale("carriers")
carriers
scale_units(carriers, "carrier")
scale_attributes(carriers, "lhv", frame = "fuel")
```

```
scale_match(carriers, c("GAS", "LIG", "Hydrogen"))

ipcc <- read.csv(system.file("extdata", "ipcc2006_fuel_defaults.csv",
                             package = "nestedscales"))
table(ipcc$attribute, ipcc$mapping_status)
```

`summary.NestedScale` *Summarize a NestedScale*

Description

Complements `print()` with the quantitative view: per-weight totals and coverage, and the adjacent-frame nesting table. Returns a `"summary_Scale"` object (a list) with its own print method.

Usage

```
## S3 method for class 'NestedScale'
summary(object, ...)

## S3 method for class '`nestedscales::NestedScale`'
summary(object, ...)

## S3 method for class 'summary_Scale'
print(x, ...)
```

Arguments

`object`	A `NestedScale`.
`...`	Ignored.
`x`	A `"summary_Scale"` object (the print method's argument).

Value

`summary()` returns a list of class `"summary_Scale"`: `name`, `desc`, `frames` (named member counts), `unassigned` (named NA-atom counts), `n_atoms`, `weights`, `weight_totals`, `default_weight`, `coverage` (see `scale_coverage()`), `sampled`, `parent_name`, `nesting` (adjacent-pair table with offender counts, see `scale_nests()`), `attributes` (a `data.frame` of row counts by `attribute`, `frame` and `source`), `aliases` (counts by `source`), `source`, `vocab`.

Examples

```
summary(scale_example())
```

summary.ScaleProduct *Summarize a product*

Description

Summarize a product

Usage

```
## S3 method for class 'ScaleProduct'
summary(object, ...)

## S3 method for class '`nestedscales::ScaleProduct`'
summary(object, ...)

## S3 method for class 'summary_ScaleProduct'
print(x, ...)
```

Arguments

object	A ScaleProduct.
...	Ignored.
x	A "summary_ScaleProduct" object (the print method's argument).

Value

A list of class "summary_ScaleProduct": name, desc, axes (per-axis summary rows), total, coverage, joint_coverage, joint_weights.

Examples

```
summary(scale_product(a = scale_example(), b = scale_example2()))
```

write_scale *Write a scale as a definition file, and read one back*

Description

A definition is a header (JSON, the stored form; YAML on request) plus tables. A small scale fits in **one file** with every table inline; a large one is a **bundle** directory holding scale.json and its tables as Arrow IPC files (or CSV when arrow is not installed). Either form is language-neutral: the header is plain JSON and the tables are Arrow or CSV with their column types recorded.

Usage

```
write_scale(
  x,
  path,
  format = c("json", "yaml"),
  tables = c("auto", "inline", "arrow", "csv"),
  overwrite = FALSE
)

read_scale(path, package = NULL, class = c("stored", "core"))
```

Arguments

x	A NestedScale.
path	A file (.json, .yaml, .yml) or a bundle directory; for read_scale() also a catalogue id.
format	Header format: "json" (default) or "yaml". A single-file path fixes it by its extension.
tables	Where the tables go: "auto" (inline when the tables hold at most 1000 rows in all, else "arrow" when arrow is installed, else "csv"), "inline", "arrow" or "csv". A single file can only inline.
overwrite	Replace a definition already at path.
package	For a catalogue id: the package whose definition to take when several packages ship the same id.
class	"stored" (default) returns the class recorded in the header; "core" the plain NestedScale.

Details

path ending in .json, .yaml or .yml writes a single file; any other path is a bundle directory. A bundle is only ever written into an empty directory or over a bundle written before (overwrite = TRUE); nothing else in a directory is touched.

read_scale() takes a file, a bundle directory, or the id of a shipped definition (see scale_catalog()). The scale comes back as the class it was written from when that class is registered (see register_scale_class()); class = "core" asks for the plain NestedScale instead, dropping any payload.

Value

write_scale() returns path, invisibly. read_scale() returns the scale.

Round trips

An arrow bundle reads back identical. A JSON or YAML header carries numbers at 15 significant digits, so an inline table reads back equal (all.equal()), not necessarily identical, for arbitrary doubles.

Examples

```
s <- scale_example()
f <- file.path(tempdir(), "example.json")
write_scale(s, f, overwrite = TRUE)
back <- read_scale(f)
identical(scale_frames(back), scale_frames(s))
all.equal(scale_leaftable(back), scale_leaftable(s))

# a bundle, with the tables as files
if (requireNamespace("arrow", quietly = TRUE)) {
  d <- file.path(tempdir(), "example.scale")
  write_scale(s, d, tables = "arrow", overwrite = TRUE)
  list.files(d)
  identical(scale_leaftable(read_scale(d)), scale_leaftable(s))
}
```

---

write_scale_dataset *Write data and the scales that index it to one folder*

Description

The data is written as a hive-partitioned Arrow IPC dataset and the scales travel with it, so `open_scale_dataset()` gives back both and the result can be recast without re-declaring anything. Each scale is stored as the definition `write_scale()` writes, so its attributes and aliases travel too.

Usage

```
write_scale_dataset(
  data,
  x,
  path,
  partitioning = NULL,
  compression = "zstd",
  overwrite = FALSE
)
```

Arguments

`data`	The table to write, in any supported backend.
`x`	The `NestedScale` or `ScaleProduct` the data is indexed by.
`path`	Directory to create. It must not already contain a store unless `overwrite = TRUE`.
`partitioning`	Columns to partition the data by (hive style). `NULL` (default) picks nothing; a good choice is a low-cardinality identifier such as a year, which lets a filtered read skip whole files.

compression	Codec for the IPC files, e.g. "zstd" (default), "lz4" or "uncompressed". If the codec is unavailable in the installed Arrow build, the files are written uncompressed with a warning.
overwrite	Replace an existing store at path.

Value

path, invisibly.

Examples

```
p <- scale_product(a = scale_example(), b = scale_example2())
d <- merge(
  data.frame(unit = c("U1", "U2")),
  data.frame(period = c("p1", "p2"))
)
d$v <- 1:4
dir <- file.path(tempdir(), "store")
if (requireNamespace("arrow", quietly = TRUE)) {
  write_scale_dataset(d, p, dir, overwrite = TRUE)
  ds <- open_scale_dataset(dir)
  ds
}
```

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