

Package ‘couplr’

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Title Optimal Pairing and Matching via Linear Assignment

Version 1.0.10

Description Solves optimal pairing and matching problems using linear assignment algorithms. Provides implementations of the Hungarian method (Kuhn 1955) <[doi:10.1002/nav.3800020109](https://doi.org/10.1002/nav.3800020109)>, Jonker-Volgenant shortest path algorithm (Jonker and Volgenant 1987) <[doi:10.1007/BF02278710](https://doi.org/10.1007/BF02278710)>, Auction algorithm (Bertsekas 1988) <[doi:10.1007/BF02186476](https://doi.org/10.1007/BF02186476)>, cost-scaling (Goldberg and Kennedy 1995) <[doi:10.1007/BF01585996](https://doi.org/10.1007/BF01585996)>, scaling algorithms (Gabow and Tarjan 1989) <[doi:10.1137/0218069](https://doi.org/10.1137/0218069)>, push-relabel (Goldberg and Tarjan 1988) <[doi:10.1145/48014.61051](https://doi.org/10.1145/48014.61051)>, and Sinkhorn entropy-regularized transport (Cuturi 2013) <[doi:10.48550/arxiv.1306.0895](https://doi.org/10.48550/arxiv.1306.0895)>. Designed for matching plots, sites, samples, or any pairwise optimization problem. Supports rectangular matrices, forbidden assignments, data frame inputs, batch solving, k-best solutions, and pixel-level image morphing for visualization. Includes automatic preprocessing with variable health checks, multiple scaling methods (standardized, range, robust), greedy matching algorithms, and comprehensive balance diagnostics for assessing match quality using standardized differences and distribution comparisons.

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assignment	<i>Linear assignment solver</i>
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Description

Solve the linear assignment problem (minimum- or maximum-cost matching) using several algorithms. Forbidden edges can be marked as NA or Inf.

Usage

```
assignment(
  cost,
  maximize = FALSE,
  method = c("auto", "jv", "hungarian", "auction", "auction_gs", "auction_scaled", "sap",
            "ssp", "csflow", "hk01", "bruteforce", "ssap_bucket", "cycle_cancel", "gabow_tarjan",
            "lapmod", "csa", "ramshaw_tarjan", "push_relabel", "orlin", "network_simplex"),
  auction_eps = NULL,
  eps = NULL
)
```

Arguments

cost	Numeric matrix; rows = tasks, columns = agents. NA or Inf entries are treated as forbidden assignments.
maximize	Logical; if TRUE, maximizes the total cost instead of minimizing.
method	Character string indicating the algorithm to use. Options: General-purpose solvers:

- "auto" — Automatic selection based on problem characteristics (default)
- "jv" — 'Jonker-Volgenant', fast general-purpose $O(n^3)$
- "hungarian" — Classic 'Hungarian' algorithm $O(n^3)$

Auction-based solvers:

- "auction" — 'Bertsekas' auction with adaptive epsilon
- "auction_gs" — 'Gauss-Seidel' variant, good for spatial structure
- "auction_scaled" — 'Epsilon-scaling', fastest for large dense problems

Specialized solvers:

- "sap" / "ssp" — Shortest augmenting path, handles sparsity well
- "lapmod" — Sparse JV variant, faster when $>50\backslash$
- "hk01" — 'Hopcroft-Karp' for binary (0/1) costs only
- "ssap_bucket" — 'Dial' algorithm for integer costs
- "line_metric" — $O(n \log n)$ for 1D assignment problems
- "bruteforce" — Exact enumeration for tiny problems ($n \leq 8$)

Advanced solvers:

- "csa" — 'Goldberg-Kennedy' cost-scaling, often fastest for medium-large
- "gabow_tarjan" — 'Gabow-Tarjan' bit-scaling with complementary slackness $O(n^3 \log C)$
- "cycle_cancel" — Cycle-canceling with 'Karp' algorithm
- "csflow" — Cost-scaling network flow
- "network_simplex" — 'Network simplex' with spanning tree representation
- "orlin" — 'Orlin-Ahuja' scaling $O(\sqrt{n} * m * \log(nC))$
- "push_relabel" — 'Push-relabel' max-flow based solver
- "ramshaw_tarjan" — 'Ramshaw-Tarjan', optimized for rectangular matrices ($n \neq m$)

auction_eps	Optional numeric epsilon for the 'Auction'/'Auction-GS' methods. If NULL, an internal default (e.g., 1e-9) is used.
eps	Deprecated. Use auction_eps. If provided and auction_eps is NULL, its value is used for auction_eps.

Details

method = "auto" selects an algorithm based on problem size/shape and data characteristics:

- Very small ($n \leq 8$): "bruteforce" — exact enumeration
- Binary/constant costs: "hk01" — specialized for 0/1 costs
- Large sparse ($n > 100, > 50\backslash$)
- Sparse or very rectangular: "sap" — handles sparsity well
- Small-medium ($8 < n \leq 50$): "hungarian" — provides exact dual solutions
- Medium ($50 < n \leq 75$): "jv" — fast general-purpose solver
- Large ($n > 75$): "auction_scaled" — fastest for large dense problems

Benchmarks show 'Auction-scaled' and 'JV' are 100-1500x faster than 'Hungarian' at $n=500$.

Value

An object of class `lap_solve_result`, a list with elements:

- `match` — integer vector of length `min(nrow(cost), ncol(cost))` giving the assigned column for each row (0 if unassigned).
- `total_cost` — numeric scalar, the objective value.
- `status` — character scalar, e.g. "optimal".
- `method_used` — character scalar, the algorithm actually used.

See Also

- [lap_solve\(\)](#) — Tidy interface returning tibbles
- [lap_solve_kbest\(\)](#) — Find k-best assignments ('Murty' algorithm)
- [assignment_duals\(\)](#) — Extract dual variables for sensitivity analysis
- [bottleneck_assignment\(\)](#) — Minimize maximum edge cost (minimax)
- [sinkhorn\(\)](#) — Entropy-regularized optimal transport

Examples

```
cost <- matrix(c(4,2,5, 3,3,6, 7,5,4), nrow = 3, byrow = TRUE)
res <- assignment(cost)
res$match; res$total_cost
```

assignment_duals

*Solve assignment problem and return dual variables***Description**

Solves the linear assignment problem and returns dual potentials (u , v) in addition to the optimal matching. The dual variables provide an optimality certificate and enable sensitivity analysis.

Usage

```
assignment_duals(cost, maximize = FALSE)
```

Arguments

- | | |
|-----------------------|---|
| <code>cost</code> | Numeric matrix; rows = tasks, columns = agents. NA or Inf entries are treated as forbidden assignments. |
| <code>maximize</code> | Logical; if TRUE, maximizes the total cost instead of minimizing. |

Details

The dual variables satisfy the complementary slackness conditions:

- For minimization: $u[i] + v[j] \leq cost[i, j]$ for all (i, j)
- For any assigned pair (i, j) : $u[i] + v[j] = cost[i, j]$

This implies that $\sum(u) + \sum(v) = total_cost$ (strong duality).

Applications of dual variables:

- **Optimality verification:** Check that duals satisfy constraints
- **Sensitivity analysis:** Reduced cost $c[i, j] - u[i] - v[j]$ shows how much an edge cost must decrease before it enters the solution
- **Pricing in column generation:** Use duals to price new columns
- **Warm starting:** Reuse duals when costs change slightly

Value

A list with class "assignment_duals_result" containing:

- **match** - integer vector of column assignments (1-based)
- **total_cost** - optimal objective value
- **u** - numeric vector of row dual variables (length n)
- **v** - numeric vector of column dual variables (length m)
- **status** - character, e.g. "optimal"

See Also

[assignment\(\)](#) for standard assignment without duals

Examples

```
cost <- matrix(c(4, 2, 5, 3, 3, 6, 7, 5, 4), nrow = 3, byrow = TRUE)
result <- assignment_duals(cost)

# Check optimality: u + v should equal cost for assigned pairs
for (i in 1:3) {
  j <- result$match[i]
  cat(sprintf("Row %d -> Col %d: u + v = %.2f, cost = %.2f\n",
             i, j, result$u[i] + result$v[j], cost[i, j]))
}

# Verify strong duality
cat("sum(u) + sum(v) =", sum(result$u) + sum(result$v), "\n")
cat("total_cost =", result$total_cost, "\n")

# Reduced costs (how much must cost decrease to enter solution)
reduced <- outer(result$u, result$v, "+")
reduced_cost <- cost - reduced
print(round(reduced_cost, 2))
```

as_assignment_matrix *Convert assignment result to a binary matrix*

Description

Turns a tidy assignment result back into a 0/1 assignment matrix.

Usage

```
as_assignment_matrix(x, n_sources = NULL, n_targets = NULL)
```

Arguments

x	An assignment result object of class <code>lap_solve_result</code>
n_sources	Number of source nodes, optional
n_targets	Number of target nodes, optional

Value

Integer matrix with 0 and 1 entries

augment *Generic Augment Function*

Description

S3 generic for augmenting model results with original data.

Usage

```
augment(x, ...)
```

Arguments

x	An object to augment
...	Additional arguments passed to methods

Value

Augmented data (depends on method)

augment.matching_result*Augment Matching Results with Original Data (broom-style)***Description**

S3 method for augmenting matching results following the broom package conventions. This is a thin wrapper around `join_matched()` with sensible defaults for quick exploration.

Usage

```
## S3 method for class 'matching_result'
augment(x, left, right, ...)
```

Arguments

<code>x</code>	A <code>matching_result</code> object
<code>left</code>	The original left dataset
<code>right</code>	The original right dataset
<code>...</code>	Additional arguments passed to <code>join_matched()</code>

Details

This method follows the `augment()` convention from the broom package, making it easy to integrate couplr into tidymodels workflows. It's equivalent to calling `join_matched()` with default parameters.

If the broom package is not loaded, you can use `couplr::augment()` to access this function.

Value

A tibble with matched pairs and original data (see `join_matched()`)

Examples

```
left <- data.frame(
  id = 1:5,
  treatment = 1,
  age = c(25, 30, 35, 40, 45)
)

right <- data.frame(
  id = 6:10,
  treatment = 0,
  age = c(24, 29, 36, 41, 44)
)

result <- match_couples(left, right, vars = "age")
```

```
couplr::augment(result, left, right)
```

balance_diagnostics *Balance Diagnostics for Matched Pairs*

Description

Computes comprehensive balance statistics comparing the distribution of matching variables between left and right units in the matched sample.

Usage

```
balance_diagnostics(  
  result,  
  left,  
  right,  
  vars = NULL,  
  left_id = "id",  
  right_id = "id"  
)
```

Arguments

result	A matching result object from <code>match_couples()</code> or <code>greedy_couples()</code>
left	Data frame of left units
right	Data frame of right units
vars	Character vector of variable names to check balance for. Defaults to the variables used in matching (if available in result).
left_id	Character, name of ID column in left data (default: "id")
right_id	Character, name of ID column in right data (default: "id")

Details

This function computes several balance metrics:

Standardized Difference: The difference in means divided by the pooled standard deviation. Values less than 0.1 indicate excellent balance, 0.1-0.25 good balance.

Variance Ratio: The ratio of standard deviations (left/right). Values close to 1 are ideal.

KS Statistic: Kolmogorov-Smirnov test statistic comparing distributions. Lower values indicate more similar distributions.

Overall Metrics include mean absolute standardized difference across all variables, proportion of variables with large imbalance (`lstd diff > 0.25`), and maximum standardized difference.

Value

An S3 object of class `balance_diagnostics` containing:

var_stats Tibble with per-variable balance statistics
overall List with overall balance metrics
pairs Tibble of matched pairs with variables
n_matched Number of matched pairs
n_unmatched_left Number of unmatched left units
n_unmatched_right Number of unmatched right units
method Matching method used
has_blocks Whether blocking was used
block_stats Per-block statistics (if blocking used)

Examples

```
# Create sample data
set.seed(123)
left <- data.frame(
  id = 1:10,
  age = rnorm(10, 45, 10),
  income = rnorm(10, 50000, 15000)
)
right <- data.frame(
  id = 11:30,
  age = rnorm(20, 47, 10),
  income = rnorm(20, 52000, 15000)
)

# Match
result <- match_couples(left, right, vars = c("age", "income"))

# Get balance diagnostics
balance <- balance_diagnostics(result, left, right, vars = c("age", "income"))
print(balance)

# Get balance table
balance_table(balance)
```

Description

Formats balance diagnostics into a clean table for display or export.

Usage

```
balance_table(balance, digits = 3)
```

Arguments

balance	A balance_diagnostics object from balance_diagnostics()
digits	Number of decimal places for rounding (default: 3)

Value

A tibble with formatted balance statistics

bottleneck_assignment *Solve the Bottleneck Assignment Problem*

Description

Finds an assignment that minimizes (or maximizes) the maximum edge cost in a perfect matching. Unlike standard LAP which minimizes the sum of costs, BAP minimizes the maximum (bottleneck) cost.

Usage

```
bottleneck_assignment(cost, maximize = FALSE)
```

Arguments

cost	Numeric matrix; rows = tasks, columns = agents. NA or Inf entries are treated as forbidden assignments.
maximize	Logical; if TRUE, maximizes the minimum edge cost instead of minimizing the maximum (maximin objective). Default is FALSE (minimax).

Details

The Bottleneck Assignment Problem (BAP) is a variant of the Linear Assignment Problem where instead of minimizing the sum of assignment costs, we minimize the maximum cost among all assignments (minimax objective).

Algorithm: Uses binary search on the sorted unique costs combined with 'Hopcroft-Karp' bipartite matching to find the minimum threshold that allows a perfect matching.

Complexity: $O(E * \sqrt{V} * \log(\text{unique costs}))$ where E = edges, V = vertices.

Applications:

- Task scheduling with deadline constraints (minimize latest completion)
- Resource allocation (minimize maximum load/distance)
- Network routing (minimize maximum link utilization)
- Fair division problems (minimize maximum disparity)

Value

A list with class "bottleneck_result" containing:

- `match` - integer vector of length `nrow(cost)` giving the assigned column for each row (1-based indexing)
- `bottleneck` - numeric scalar, the bottleneck (max/min edge) value
- `status` - character scalar, e.g. "optimal"

See Also

[assignment\(\)](#) for standard LAP (sum objective), [lap_solve\(\)](#) for tidy LAP interface

Examples

```
# Simple example: minimize max cost
cost <- matrix(c(1, 5, 3,
                 2, 4, 6,
                 7, 1, 2), nrow = 3, byrow = TRUE)
result <- bottleneck_assignment(cost)
result$bottleneck # Maximum edge cost in optimal assignment

# Maximize minimum (fair allocation)
profits <- matrix(c(10, 5, 8,
                     6, 12, 4,
                     3, 7, 11), nrow = 3, byrow = TRUE)
result <- bottleneck_assignment(profits, maximize = TRUE)
result$bottleneck # Minimum profit among all assignments

# With forbidden assignments
cost <- matrix(c(1, NA, 3,
                 2, 4, Inf,
                 5, 1, 2), nrow = 3, byrow = TRUE)
result <- bottleneck_assignment(cost)
```

Description

Precomputes a distance matrix between left and right datasets, allowing it to be reused across multiple matching operations with different constraints. This is particularly useful when exploring different matching parameters (`max_distance`, `calipers`, `methods`) without recomputing distances.

Usage

```
compute_distances(
  left,
  right,
  vars,
  distance = "euclidean",
  weights = NULL,
  scale = FALSE,
  auto_scale = FALSE,
  left_id = "id",
  right_id = "id",
  block_id = NULL
)
```

Arguments

<code>left</code>	Left dataset (data frame)
<code>right</code>	Right dataset (data frame)
<code>vars</code>	Character vector of variable names to use for distance computation
<code>distance</code>	Distance metric (default: "euclidean")
<code>weights</code>	Optional numeric vector of variable weights
<code>scale</code>	Scaling method: FALSE, "standardize", "range", or "robust"
<code>auto_scale</code>	Apply automatic preprocessing (default: FALSE)
<code>left_id</code>	Name of ID column in left (default: "id")
<code>right_id</code>	Name of ID column in right (default: "id")
<code>block_id</code>	Optional block ID column name for blocked matching

Details

This function computes distances once and stores them in a reusable object. The resulting `distance_object` can be passed to `match_couples()` or `greedy_couples()` instead of providing datasets and variables.

Benefits:

- **Performance:** Avoid recomputing distances when trying different constraints
- **Exploration:** Quickly test `max_distance`, calipers, or methods
- **Consistency:** Ensures same distances used across comparisons
- **Memory efficient:** Can use sparse matrices when many pairs are forbidden

The `distance_object` stores the original datasets, allowing downstream functions like `join_matched()` to work seamlessly.

Value

An S3 object of class "distance_object" containing:

- **cost_matrix**: Numeric matrix of distances
- **left_ids**: Character vector of left IDs
- **right_ids**: Character vector of right IDs
- **block_id**: Block ID column name (if specified)
- **metadata**: List with computation details (vars, distance, scale, etc.)
- **original_left**: Original left dataset (for later joining)
- **original_right**: Original right dataset (for later joining)

Examples

```
# Compute distances once
left <- data.frame(id = 1:5, age = c(25, 30, 35, 40, 45), income = c(45, 52, 48, 61, 55) * 1000)
right <- data.frame(id = 6:10, age = c(24, 29, 36, 41, 44), income = c(46, 51, 47, 60, 54) * 1000)

dist_obj <- compute_distances(
  left, right,
  vars = c("age", "income"),
  scale = "standardize"
)

# Reuse for different matching strategies
result1 <- match_couples(dist_obj, max_distance = 0.5)
result2 <- match_couples(dist_obj, max_distance = 1.0)
result3 <- greedy_couples(dist_obj, strategy = "sorted")

# All use the same precomputed distances
```

diagnose_distance_matrix

Diagnose distance matrix and suggest fixes

Description

Comprehensive diagnostics for a distance matrix with actionable suggestions.

Usage

```
diagnose_distance_matrix(
  cost_matrix,
  left = NULL,
  right = NULL,
  vars = NULL,
  warn = TRUE
)
```

Arguments

<code>cost_matrix</code>	Numeric matrix of distances
<code>left</code>	Left dataset (for variable checking)
<code>right</code>	Right dataset (for variable checking)
<code>vars</code>	Variables used for matching
<code>warn</code>	If TRUE, issue warnings

Value

List with diagnostic results and suggestions

`example_costs`

Example cost matrices for assignment problems

Description

Small example datasets for demonstrating couplr functionality across different assignment problem types: square, rectangular, sparse, and binary.

Usage

`example_costs`

Format

A list containing four example cost matrices:

simple_3x3 A 3x3 cost matrix with costs ranging from 2-7. Optimal assignment: row 1 -> col 2 (cost 2), row 2 -> col 1 (cost 3), row 3 -> col 3 (cost 4). Total optimal cost: 9.

rectangular_3x5 A 3x5 rectangular cost matrix demonstrating assignment when rows < columns. Each of 3 rows is assigned to one of 5 columns; 2 columns remain unassigned. Costs range 1-6.

sparse_with_na A 3x3 matrix with NA values indicating forbidden assignments. Use this to test algorithms' handling of constraints. Position (1,3), (2,2), and (3,1) are forbidden.

binary_costs A 3x3 matrix with binary (0/1) costs, suitable for testing the HK01 algorithm. Diagonal entries are 0 (preferred), off-diagonal entries are 1 (penalty).

Details

These matrices are designed to test different aspects of LAP solvers:

simple_3x3: Basic functionality test. Any correct solver should find total cost = 9.

rectangular_3x5: Tests handling of non-square problems. The optimal solution assigns all 3 rows with minimum total cost.

sparse_with_na: Tests constraint handling. Algorithms must avoid NA positions while finding an optimal assignment among valid entries.

binary_costs: Tests specialized binary cost algorithms. The optimal assignment uses all diagonal entries (total cost = 0).

See Also

[lap_solve](#), [example_df](#)

Examples

```
# Simple 3x3 assignment
result <- lap_solve(example_costs$simple_3x3)
print(result)
# Optimal: sources 1,2,3 -> targets 2,1,3 with cost 9

# Rectangular problem (3 sources, 5 targets)
result <- lap_solve(example_costs$rectangular_3x5)
print(result)
# All 3 sources assigned; 2 targets unassigned

# Sparse problem with forbidden assignments
result <- lap_solve(example_costs$sparse_with_na)
print(result)
# Avoids NA positions

# Binary costs - test HK01 algorithm
result <- lap_solve(example_costs$binary_costs, method = "hk01")
print(result)
# Finds diagonal assignment (cost = 0)
```

example_df

Example assignment problem data frame

Description

A tidy data frame representation of assignment problems, suitable for use with grouped workflows and batch solving. Contains two independent 3x3 assignment problems in long format.

Usage

`example_df`

Format

A tibble with 18 rows and 4 columns:

- sim** Simulation/problem identifier. Integer with values 1 or 2, distinguishing two independent assignment problems. Use with `group_by(sim)` for grouped solving.
- source** Source node index. Integer 1-3 representing the row (source) in each 3x3 cost matrix.
- target** Target node index. Integer 1-3 representing the column (target) in each 3x3 cost matrix.
- cost** Cost of assigning source to target. Numeric values ranging from 1-7. Each source-target pair has exactly one cost entry.

Details

This dataset demonstrates couplr's data frame interface for LAP solving. The long format (one row per source-target pair) is converted internally to a cost matrix for solving.

Simulation 1: Costs from `example_costs$simple_3x3`

- Optimal assignment: (1->2, 2->1, 3->3)
- Total cost: 9

Simulation 2: Different cost structure

- Optimal assignment: (1->1, 2->3, 3->3) or equivalent
- Total cost: 4

See Also

[lap_solve](#), [lap_solve_batch](#), [example_costs](#)

Examples

```
library(dplyr)

# Solve both problems with grouped workflow
example_df |>
  group_by(sim) |>
  lap_solve(source, target, cost)

# Batch solving for efficiency
example_df |>
  group_by(sim) |>
  lap_solve_batch(source, target, cost)

# Inspect the data structure
example_df |>
  group_by(sim) |>
  summarise(
    n_pairs = n(),
    min_cost = min(cost),
    max_cost = max(cost)
  )
```

`get_method_used`

Extract method used from assignment result

Description

Extract method used from assignment result

Usage

```
get_method_used(x)
```

Arguments

x An assignment result object

Value

Character string indicating method used

get_total_cost *Extract total cost from assignment result*

Description

Extract total cost from assignment result

Usage

```
get_total_cost(x)
```

Arguments

x An assignment result object

Value

Numeric total cost

greedy_couples *Fast approximate matching using greedy algorithm*

Description

Performs fast one-to-one matching using greedy strategies. Does not guarantee optimal total distance but is much faster than [match_couples\(\)](#) for large datasets. Supports blocking, distance constraints, and various distance metrics.

Usage

```
greedy_couples(
  left,
  right = NULL,
  vars = NULL,
  distance = "euclidean",
  weights = NULL,
  scale = FALSE,
  auto_scale = FALSE,
  max_distance = Inf,
  calipers = NULL,
  block_id = NULL,
  ignore_blocks = FALSE,
  require_full_matching = FALSE,
  strategy = c("row_best", "sorted", "pq"),
  return_unmatched = TRUE,
  return_diagnostics = FALSE,
  parallel = FALSE,
  check_costs = TRUE
)
```

Arguments

<code>left</code>	Data frame of "left" units (e.g., treated, cases)
<code>right</code>	Data frame of "right" units (e.g., control, controls)
<code>vars</code>	Variable names to use for distance computation
<code>distance</code>	Distance metric: "euclidean", "manhattan", "mahalanobis", or a custom function
<code>weights</code>	Optional named vector of variable weights
<code>scale</code>	Scaling method: FALSE (none), "standardize", "range", or "robust"
<code>auto_scale</code>	If TRUE, automatically check variable health and select scaling method (default: FALSE)
<code>max_distance</code>	Maximum allowed distance (pairs exceeding this are forbidden)
<code>calipers</code>	Named list of per-variable maximum absolute differences
<code>block_id</code>	Column name containing block IDs (for stratified matching)
<code>ignore_blocks</code>	If TRUE, ignore block_id even if present
<code>require_full_matching</code>	If TRUE, error if any units remain unmatched
<code>strategy</code>	Greedy strategy: <ul style="list-style-type: none"> • "row_best": For each row, find best available column (default) • "sorted": Sort all pairs by distance, greedily assign • "pq": Use priority queue (good for very large problems)
<code>return_unmatched</code>	Include unmatched units in output

<code>return_diagnostics</code>	Include detailed diagnostics in output
<code>parallel</code>	Enable parallel processing for blocked matching. Requires 'future' and 'future.apply' packages. Can be:
	<ul style="list-style-type: none"> • FALSE: Sequential processing (default) • TRUE: Auto-configure parallel backend • Character: Specify future plan (e.g., "multisession", "multicore")
<code>check_costs</code>	If TRUE, check distance distribution for potential problems and provide helpful warnings before matching (default: TRUE)

Details

Greedy strategies do not guarantee optimal total distance but are much faster:

- "row_best": $O(n*m)$ time, simple and often produces good results
- "sorted": $O(nm\log(n*m))$ time, better quality but slower
- "pq": $O(nm\log(n*m))$ time, memory-efficient for large problems

Use `greedy_couples` when:

- Dataset is very large ($> 10,000 \times 10,000$)
- Approximate solution is acceptable
- Speed is more important than optimality

Value

A list with class "matching_result" (same structure as `match_couples`)

Examples

```
# Basic greedy matching
left <- data.frame(id = 1:100, x = rnorm(100))
right <- data.frame(id = 101:200, x = rnorm(100))
result <- greedy_couples(left, right, vars = "x")

# Compare to optimal
result_opt <- match_couples(left, right, vars = "x")
result_greedy <- greedy_couples(left, right, vars = "x")
result_greedy$info$total_distance / result_opt$info$total_distance # Quality ratio
```

hospital_staff *Hospital staff scheduling example dataset*

Description

A comprehensive example dataset for demonstrating couplr functionality across vignettes. Contains hospital staff scheduling data with nurses, shifts, costs, and preference scores suitable for assignment problems, as well as nurse characteristics for matching workflows.

Usage

```
hospital_staff
```

Format

A list containing eight related datasets:

basic_costs A 10x10 numeric cost matrix for assigning 10 nurses to 10 shifts. Values range from approximately 1-15, where lower values indicate better fit (less overtime, matches skills, respects preferences). Use with `lap_solve()` for basic assignment.

preferences A 10x10 numeric preference matrix on a 0-10 scale, where higher values indicate stronger nurse preference for a shift. Use with `lap_solve(..., maximize = TRUE)` to optimize preferences rather than minimize costs.

schedule_df A tibble with 100 rows (10 nurses x 10 shifts) in long format for data frame workflows:

nurse_id Integer 1-10. Unique identifier for each nurse.

shift_id Integer 1-10. Unique identifier for each shift.

cost Numeric. Assignment cost (same values as `basic_costs`).

preference Numeric 0-10. Nurse preference score.

skill_match Integer 0/1. Binary indicator: 1 if nurse skills match shift requirements, 0 otherwise.

nurses A tibble with 10 rows describing nurse characteristics:

nurse_id Integer 1-10. Links to `schedule_df` and `basic_costs` rows.

experience_years Numeric 1-20. Years of nursing experience.

department Character. Primary department: "ICU", "ER", "General", or "Pediatrics".

shift_preference Character. Preferred shift type: "day", "evening", or "night".

certification_level Integer 1-3. Certification level where 3 is highest (e.g., 1=RN, 2=BSN, 3=MSN).

shifts A tibble with 10 rows describing shift requirements:

shift_id Integer 1-10. Links to `schedule_df` and `basic_costs` cols.

department Character. Department needing coverage.

shift_type Character. Shift type: "day", "evening", or "night".

min_experience Numeric. Minimum years of experience required.

min_certification Integer 1-3. Minimum certification level.

weekly_df A tibble for batch solving with 500 rows (5 days x 10 nurses x 10 shifts):

day Character. Day of week: "Mon", "Tue", "Wed", "Thu", "Fri".

nurse_id Integer 1-10. Nurse identifier.

shift_id Integer 1-10. Shift identifier.

cost Numeric. Daily assignment cost (varies by day).

preference Numeric 0-10. Daily preference score.

Use with `group_by(day)` for solving each day's schedule.

nurses_extended A tibble with 200 nurses for matching examples, representing a treatment group (e.g., full-time nurses):

nurse_id Integer 1-200. Unique identifier.

age Numeric 22-65. Nurse age in years.

experience_years Numeric 0-40. Years of nursing experience.

hourly_rate Numeric 25-75. Hourly wage in dollars.

department Character. Primary department assignment.

certification_level Integer 1-3. Certification level.

is_fulltime Logical. TRUE for full-time status.

controls_extended A tibble with 300 potential control nurses (e.g., part-time or registry nurses) for matching. Same structure as `nurses_extended`. Designed to have systematic differences from `nurses_extended` (older, less experience on average) to demonstrate matching's ability to create comparable groups.

Details

This dataset is used throughout the couplr documentation to provide a consistent, realistic example that evolves in complexity. It supports three use cases: (1) basic LAP solving with cost matrices, (2) batch solving across multiple days, and (3) matching workflows comparing nurse groups.

The dataset is designed to demonstrate progressively complex scenarios:

Basic LAP (`vignette("getting-started")`):

- `basic_costs`: Simple 10x10 assignment
- `preferences`: Maximization problem
- `schedule_df`: Data frame input, grouped workflows
- `weekly_df`: Batch solving across days

Algorithm comparison (`vignette("algorithms")`):

- Use `basic_costs` to compare algorithm behavior
- Modify with NA values for sparse scenarios

Matching workflows (`vignette("matching-workflows")`):

- `nurses_extended`: Treatment group (full-time nurses)
- `controls_extended`: Control pool (part-time/registry nurses)
- Match on age, experience, department for causal analysis

See Also

[lap_solve](#) for basic assignment solving, [lap_solve_batch](#) for batch solving, [match_couples](#) for matching workflows, vignette("getting-started") for introductory tutorial

Examples

```
# Basic assignment: assign nurses to shifts minimizing cost
lap_solve(hospital_staff$basic_costs)

# Maximize preferences instead
lap_solve(hospital_staff$preferences, maximize = TRUE)

# Data frame workflow
library(dplyr)
hospital_staff$schedule_df |>
  lap_solve(nurse_id, shift_id, cost)

# Batch solve weekly schedule
hospital_staff$weekly_df |>
  group_by(day) |>
  lap_solve(nurse_id, shift_id, cost)

# Matching workflow: match full-time to part-time nurses
match_couples(
  left = hospital_staff$nurses_extended,
  right = hospital_staff$controls_extended,
  vars = c("age", "experience_years", "certification_level"),
  auto_scale = TRUE
)
```

`is_distance_object` *Check if Object is a Distance Object*

Description

Check if Object is a Distance Object

Usage

```
is_distance_object(x)
```

Arguments

x	Object to check
---	-----------------

Value

Logical: TRUE if x is a distance_object

Examples

```
left <- data.frame(id = 1:3, x = c(1, 2, 3))
right <- data.frame(id = 4:6, x = c(1.1, 2.1, 3.1))
dist_obj <- compute_distances(left, right, vars = "x")
is_distance_object(dist_obj) # TRUE
is_distance_object(list()) # FALSE
```

is_lap_solve_batch_result

Check if object is a batch assignment result

Description

Check if object is a batch assignment result

Usage

```
is_lap_solve_batch_result(x)
```

Arguments

x	Object to test
---	----------------

Value

Logical indicating if x is a batch assignment result

is_lap_solve_kbest_result

Check if object is a k-best assignment result

Description

Check if object is a k-best assignment result

Usage

```
is_lap_solve_kbest_result(x)
```

Arguments

x	Object to test
---	----------------

Value

Logical indicating if x is a k-best assignment result

is_lap_solve_result *Check if object is an assignment result*

Description

Check if object is an assignment result

Usage

```
is_lap_solve_result(x)
```

Arguments

x Object to test

Value

Logical indicating if x is an assignment result

join_matched *Join Matched Pairs with Original Data*

Description

Creates an analysis-ready dataset by joining matched pairs with variables from the original left and right datasets. This eliminates the need for manual joins and provides a convenient format for downstream analysis.

Usage

```
join_matched(  
  result,  
  left,  
  right,  
  left_vars = NULL,  
  right_vars = NULL,  
  left_id = "id",  
  right_id = "id",  
  suffix = c("_left", "_right"),  
  include_distance = TRUE,  
  include_pair_id = TRUE,  
  include_block_id = TRUE  
)
```

Arguments

<code>result</code>	A matching_result object from <code>match_couples()</code> or <code>greedy_couples()</code>
<code>left</code>	The original left dataset
<code>right</code>	The original right dataset
<code>left_vars</code>	Character vector of variable names to include from left. If NULL (default), includes all variables except the ID column.
<code>right_vars</code>	Character vector of variable names to include from right. If NULL (default), includes all variables except the ID column.
<code>left_id</code>	Name of the ID column in left dataset (default: "id")
<code>right_id</code>	Name of the ID column in right dataset (default: "id")
<code>suffix</code>	Character vector of length 2 specifying suffixes for left and right variables (default: <code>c("_left", "_right")</code>)
<code>include_distance</code>	Include the matching distance in output (default: TRUE)
<code>include_pair_id</code>	Include pair_id column (default: TRUE)
<code>include_block_id</code>	Include block_id if blocking was used (default: TRUE)

Details

This function simplifies the common workflow of joining matched pairs with original data. Instead of manually merging `result$pairs` with left and right datasets, `join_matched()` handles the joins automatically and applies consistent naming conventions.

When variables appear in both left and right datasets, suffixes are appended to distinguish them (e.g., "age_left" and "age_right"). This makes it easy to compute differences or use both values in models.

Value

A tibble with one row per matched pair, containing:

- `pair_id`: Sequential pair identifier (if `include_pair_id` = TRUE)
- `left_id`: ID from left dataset
- `right_id`: ID from right dataset
- `distance`: Matching distance (if `include_distance` = TRUE)
- `block_id`: Block identifier (if blocking used and `include_block_id` = TRUE)
- Variables from left dataset (with left suffix)
- Variables from right dataset (with right suffix)

Examples

```

# Basic usage
left <- data.frame(
  id = 1:5,
  treatment = 1,
  age = c(25, 30, 35, 40, 45),
  income = c(45000, 52000, 48000, 61000, 55000)
)

right <- data.frame(
  id = 6:10,
  treatment = 0,
  age = c(24, 29, 36, 41, 44),
  income = c(46000, 51500, 47500, 60000, 54000)
)

result <- match_couples(left, right, vars = c("age", "income"))
matched_data <- join_matched(result, left, right)
head(matched_data)

# Specify which variables to include
matched_data <- join_matched(
  result, left, right,
  left_vars = c("treatment", "age", "income"),
  right_vars = c("age", "income"),
  suffix = c("_treated", "_control")
)

# Without distance or pair_id
matched_data <- join_matched(
  result, left, right,
  include_distance = FALSE,
  include_pair_id = FALSE
)

```

Description

Provides a tidy interface for solving the linear assignment problem using 'Hungarian' or 'Jonker-Volgenant' algorithms. Supports rectangular matrices, NA/Inf masking, and data frame inputs.

Usage

```
lap_solve(
  x,
  source = NULL,
```

```

    target = NULL,
    cost = NULL,
    maximize = FALSE,
    method = "auto",
    forbidden = NA
)

```

Arguments

<code>x</code>	Cost matrix, data frame, or tibble. If a data frame/tibble, must include columns specified by <code>source</code> , <code>target</code> , and <code>cost</code> .
<code>source</code>	Column name for source/row indices (if <code>x</code> is a data frame)
<code>target</code>	Column name for target/column indices (if <code>x</code> is a data frame)
<code>cost</code>	Column name for costs (if <code>x</code> is a data frame)
<code>maximize</code>	Logical; if TRUE, maximizes total cost instead of minimizing (default: FALSE)
<code>method</code>	Algorithm to use. One of: <ul style="list-style-type: none"> • "auto" (default): automatically selects best algorithm • "jv": 'Jonker-Volgenant' algorithm (general purpose, fast) • "hungarian": Classic 'Hungarian' algorithm • "auction": 'Bertsekas' auction algorithm (good for large dense problems) • "sap": Sparse assignment (good for sparse/rectangular problems) • "hk01": 'Hopcroft-Karp' for binary/uniform costs
<code>forbidden</code>	Value to mark forbidden assignments (default: NA). Can also use Inf.

Value

A tibble with columns:

- `source`: row/source indices
- `target`: column/target indices
- `cost`: cost of each assignment
- `total_cost`: total cost (attribute)

Examples

```

# Matrix input
cost <- matrix(c(4, 2, 5, 3, 3, 6, 7, 5, 4), nrow = 3)
lap_solve(cost)

# Data frame input
library(dplyr)
df <- tibble(
  source = rep(1:3, each = 3),
  target = rep(1:3, times = 3),
  cost = c(4, 2, 5, 3, 3, 6, 7, 5, 4)
)
lap_solve(df, source, target, cost)

```

```

# With NA masking (forbidden assignments)
cost[1, 3] <- NA
lap_solve(cost)

# Grouped data frames
df <- tibble(
  sim = rep(1:2, each = 9),
  source = rep(1:3, times = 6),
  target = rep(1:3, each = 3, times = 2),
  cost = runif(18, 1, 10)
)
df |> group_by(sim) |> lap_solve(source, target, cost)

```

lap_solve_batch*Solve multiple assignment problems efficiently***Description**

Solve many independent assignment problems at once. Supports lists of matrices, 3D arrays, or grouped data frames. Optional parallel execution via `n_threads`.

Usage

```
lap_solve_batch(
  x,
  source = NULL,
  target = NULL,
  cost = NULL,
  maximize = FALSE,
  method = "auto",
  n_threads = 1,
  forbidden = NA
)
```

Arguments

<code>x</code>	One of: List of cost matrices, 3D array, or grouped data frame
<code>source</code>	Column name for source indices (if <code>x</code> is a grouped data frame)
<code>target</code>	Column name for target indices (if <code>x</code> is a grouped data frame)
<code>cost</code>	Column name for costs (if <code>x</code> is a grouped data frame)
<code>maximize</code>	Logical; if TRUE, maximizes total cost (default: FALSE)
<code>method</code>	Algorithm to use (default: "auto"). See <code>lap_solve</code> for options.
<code>n_threads</code>	Number of threads for parallel execution (default: 1). Set to NULL to use all available cores.
<code>forbidden</code>	Value to mark forbidden assignments (default: NA)

Value

A tibble with columns:

- `problem_id`: identifier for each problem
- `source`: source indices for assignments
- `target`: target indices for assignments
- `cost`: cost of each assignment
- `total_cost`: total cost for each problem
- `method_used`: algorithm used for each problem

Examples

```
# List of matrices
costs <- list(
  matrix(c(1, 2, 3, 4), 2, 2),
  matrix(c(5, 6, 7, 8), 2, 2)
)
lap_solve_batch(costs)

# 3D array
arr <- array(runif(2 * 2 * 10), dim = c(2, 2, 10))
lap_solve_batch(arr)

# Grouped data frame
library(dplyr)
df <- tibble(
  sim = rep(1:5, each = 9),
  source = rep(1:3, times = 15),
  target = rep(1:3, each = 3, times = 5),
  cost = runif(45, 1, 10)
)
df |> group_by(sim) |> lap_solve_batch(source, target, cost)

# Parallel execution (requires n_threads > 1)
lap_solve_batch(costs, n_threads = 2)
```

Description

Returns the top k optimal (or near-optimal) assignments using 'Murty' algorithm. Useful for exploring alternative optimal solutions or finding robust assignments.

Usage

```
lap_solve_kbest(
  x,
  k = 3,
  source = NULL,
  target = NULL,
  cost = NULL,
  maximize = FALSE,
  method = "murty",
  single_method = "jv",
  forbidden = NA
)
```

Arguments

x	Cost matrix, data frame, or tibble. If a data frame/tibble, must include columns specified by <code>source</code> , <code>target</code> , and <code>cost</code> .
k	Number of best solutions to return (default: 3)
source	Column name for source/row indices (if x is a data frame)
target	Column name for target/column indices (if x is a data frame)
cost	Column name for costs (if x is a data frame)
maximize	Logical; if TRUE, finds k-best maximizing assignments (default: FALSE)
method	Algorithm for each sub-problem (default: "murty"). Future versions may support additional methods.
single_method	Algorithm used for solving each node in the search tree (default: "jv")
forbidden	Value to mark forbidden assignments (default: NA)

Value

A tibble with columns:

- `rank`: ranking of solutions (1 = best, 2 = second best, etc.)
- `solution_id`: unique identifier for each solution
- `source`: source indices
- `target`: target indices
- `cost`: cost of each edge in the assignment
- `total_cost`: total cost of the complete solution

Examples

```
# Matrix input - find 5 best solutions
cost <- matrix(c(4, 2, 5, 3, 3, 6, 7, 5, 4), nrow = 3)
lap_solve_kbest(cost, k = 5)

# Data frame input
```

```

library(dplyr)
df <- tibble(
  source = rep(1:3, each = 3),
  target = rep(1:3, times = 3),
  cost = c(4, 2, 5, 3, 3, 6, 7, 5, 4)
)
lap_solve_kbest(df, k = 3, source, target, cost)

# With maximization
lap_solve_kbest(cost, k = 3, maximize = TRUE)

```

lap_solve_line_metric *Solve 1-D Line Assignment Problem*

Description

Solves the linear assignment problem when both sources and targets are ordered points on a line. Uses efficient O(n*m) dynamic programming for rectangular problems and O(n) sorting for square problems.

Usage

```
lap_solve_line_metric(x, y, cost = "L1", maximize = FALSE)
```

Arguments

x	Numeric vector of source positions (will be sorted internally)
y	Numeric vector of target positions (will be sorted internally)
cost	Cost function for distance. Either: <ul style="list-style-type: none"> • "L1" (default): absolute distance ('Manhattan' distance) • "L2": squared distance (squared 'Euclidean' distance) Can also use aliases: "abs", "manhattan" for L1; "sq", "squared", "quadratic" for L2
maximize	Logical; if TRUE, maximizes total cost instead of minimizing (default: FALSE)

Details

This is a specialized solver that exploits the structure of 1-dimensional assignment problems where costs depend only on the distance between points on a line. It is much faster than general LAP solvers for this special case.

The algorithm works as follows:

Square case ($n == m$): Both vectors are sorted and matched in order: $x[1] \rightarrow y[1]$, $x[2] \rightarrow y[2]$, etc. This is optimal for any metric cost function on a line.

Rectangular case ($n < m$): Uses dynamic programming to find the optimal assignment that matches all n sources to a subset of the m targets, minimizing total distance. The DP recurrence is:

```
dp[i][j] = min(dp[i][j-1], dp[i-1][j-1] + cost(x[i], y[j]))
```

This finds the minimum cost to match the first i sources to the first j targets.

Complexity:

- Time: $O(n*m)$ for rectangular, $O(n \log n)$ for square
- Space: $O(n*m)$ for DP table

Value

A list with components:

- **match**: Integer vector of length n with 1-based column indices
- **total_cost**: Total cost of the assignment

Examples

```
# Square case: equal number of sources and targets
x <- c(1.5, 3.2, 5.1)
y <- c(2.0, 3.0, 5.5)
result <- lap_solve_line_metric(x, y, cost = "L1")
print(result)

# Rectangular case: more targets than sources
x <- c(1.0, 3.0, 5.0)
y <- c(0.5, 2.0, 3.5, 4.5, 6.0)
result <- lap_solve_line_metric(x, y, cost = "L2")
print(result)

# With unsorted inputs (will be sorted internally)
x <- c(5.0, 1.0, 3.0)
y <- c(4.5, 0.5, 6.0, 2.0, 3.5)
result <- lap_solve_line_metric(x, y, cost = "L1")
print(result)
```

Description

Constructs blocks (strata) for matching, using either grouping variables or clustering algorithms. Returns the input data frames with block IDs assigned, along with block summary statistics.

Usage

```
matchmaker(
  left,
  right,
  block_type = c("none", "group", "cluster"),
  block_by = NULL,
  block_vars = NULL,
  block_method = "kmeans",
  n_blocks = NULL,
  min_left = 1,
  min_right = 1,
  drop_imbalanced = FALSE,
  imbalance_threshold = Inf,
  return_dropped = TRUE,
  ...
)
```

Arguments

<code>left</code>	Data frame of "left" units (e.g., treated, cases)
<code>right</code>	Data frame of "right" units (e.g., control, controls)
<code>block_type</code>	Type of blocking to use: <ul style="list-style-type: none"> • "none": No blocking (default) • "group": Block by existing categorical variable(s) • "cluster": Block using clustering algorithm
<code>block_by</code>	Variable name(s) for grouping (if <code>block_type = "group"</code>)
<code>block_vars</code>	Variable names for clustering (if <code>block_type = "cluster"</code>)
<code>block_method</code>	Clustering method (if <code>block_type = "cluster"</code>): <ul style="list-style-type: none"> • "kmeans": K-means clustering • "hclust": Hierarchical clustering
<code>n_blocks</code>	Target number of blocks (for clustering)
<code>min_left</code>	Minimum number of left units per block
<code>min_right</code>	Minimum number of right units per block
<code>drop_imbalanced</code>	Drop blocks with extreme imbalance
<code>imbalance_threshold</code>	Maximum allowed $ n_{left} - n_{right} / \max(n_{left}, n_{right})$
<code>return_dropped</code>	Include dropped blocks in output
<code>...</code>	Additional arguments passed to clustering function

Details

This function does NOT perform matching - it only creates the block structure. Use [match_couples\(\)](#) or [greedy_couples\(\)](#) to perform matching within blocks.

Value

A list with class "matchmaker_result" containing:

- `left`: Left data frame with `block_id` column added
- `right`: Right data frame with `block_id` column added
- `block_summary`: Summary statistics for each block
- `dropped`: Information about dropped blocks (if any)
- `info`: Metadata about blocking process

Examples

```
# Group blocking
left <- data.frame(id = 1:10, region = rep(c("A", "B"), each = 5), x = rnorm(10))
right <- data.frame(id = 11:20, region = rep(c("A", "B"), each = 5), x = rnorm(10))
blocks <- matchmaker(left, right, block_type = "group", block_by = "region")
print(blocks$block_summary)

# Clustering
blocks <- matchmaker(left, right, block_type = "cluster",
                      block_vars = "x", n_blocks = 3)
```

match_couples

*Optimal matching using linear assignment***Description**

Performs optimal one-to-one matching between two datasets using linear assignment problem (LAP) solvers. Supports blocking, distance constraints, and various distance metrics.

Usage

```
match_couples(
  left,
  right = NULL,
  vars = NULL,
  distance = "euclidean",
  weights = NULL,
  scale = FALSE,
  auto_scale = FALSE,
  max_distance = Inf,
  calipers = NULL,
  block_id = NULL,
  ignore_blocks = FALSE,
  require_full_matching = FALSE,
  method = "auto",
```

```

    return_unmatched = TRUE,
    return_diagnostics = FALSE,
    parallel = FALSE,
    check_costs = TRUE
)

```

Arguments

<code>left</code>	Data frame of "left" units (e.g., treated, cases)
<code>right</code>	Data frame of "right" units (e.g., control, controls)
<code>vars</code>	Variable names to use for distance computation
<code>distance</code>	Distance metric: "euclidean", "manhattan", "mahalanobis", or a custom function
<code>weights</code>	Optional named vector of variable weights
<code>scale</code>	Scaling method: FALSE (none), "standardize", "range", or "robust"
<code>auto_scale</code>	If TRUE, automatically check variable health and select scaling method (default: FALSE)
<code>max_distance</code>	Maximum allowed distance (pairs exceeding this are forbidden)
<code>calipers</code>	Named list of per-variable maximum absolute differences
<code>block_id</code>	Column name containing block IDs (for stratified matching)
<code>ignore_blocks</code>	If TRUE, ignore block_id even if present
<code>require_full_matching</code>	If TRUE, error if any units remain unmatched
<code>method</code>	LAP solver: "auto", "hungarian", "jv", "gabow_tarjan", etc.
<code>return_unmatched</code>	Include unmatched units in output
<code>return_diagnostics</code>	Include detailed diagnostics in output
<code>parallel</code>	Enable parallel processing for blocked matching. Requires 'future' and 'future.apply' packages. Can be: <ul style="list-style-type: none"> • FALSE: Sequential processing (default) • TRUE: Auto-configure parallel backend • Character: Specify future plan (e.g., "multisession", "multicore")
<code>check_costs</code>	If TRUE, check distance distribution for potential problems and provide helpful warnings before matching (default: TRUE)

Details

This function finds the matching that minimizes total distance among all feasible matchings, subject to constraints. Use [greedy_couples\(\)](#) for faster approximate matching on large datasets.

Value

A list with class "matching_result" containing:

- `pairs`: Tibble of matched pairs with distances
- `unmatched`: List of unmatched left and right IDs
- `info`: Matching diagnostics and metadata

Examples

```
# Basic matching
left <- data.frame(id = 1:5, x = c(1, 2, 3, 4, 5), y = c(2, 4, 6, 8, 10))
right <- data.frame(id = 6:10, x = c(1.1, 2.2, 3.1, 4.2, 5.1), y = c(2.1, 4.1, 6.2, 8.1, 10.1))
result <- match_couples(left, right, vars = c("x", "y"))
print(result$pairs)

# With constraints
result <- match_couples(left, right, vars = c("x", "y"),
                        max_distance = 1,
                        calipers = list(x = 0.5))

# With blocking
left$region <- c("A", "A", "B", "B", "B")
right$region <- c("A", "A", "B", "B", "B")
blocks <- matchmaker(left, right, block_type = "group", block_by = "region")
result <- match_couples(blocks$left, blocks$right, vars = c("x", "y"))
```

pixel_morph

Pixel-level image morphing (final frame only)

Description

Computes optimal pixel assignment from A to B and returns the final transported frame (without intermediate animation frames).

Usage

```
pixel_morph(
  imgA,
  imgB,
  n_frames = 16L,
  mode = c("color_walk", "exact", "recursive"),
  lap_method = "jv",
  maximize = FALSE,
  quantize_bits = 5L,
  downscale_steps = 0L,
  alpha = 1,
  beta = 0,
  patch_size = 1L,
  upscale = 1,
  show = interactive()
)
```

Arguments

<code>imgA</code>	Source image (file path or magick image object)
<code>imgB</code>	Target image (file path or magick image object)
<code>n_frames</code>	Internal parameter for rendering (default: 16)
<code>mode</code>	Assignment algorithm: "color_walk" (default), "exact", or "recursive"
<code>lap_method</code>	LAP solver method (default: "jv")
<code>maximize</code>	Logical, maximize instead of minimize cost (default: FALSE)
<code>quantize_bits</code>	Color quantization for "color_walk" mode (default: 5)
<code>downscale_steps</code>	Number of 2x reductions before computing assignment (default: 0)
<code>alpha</code>	Weight for color distance in cost function (default: 1)
<code>beta</code>	Weight for spatial distance in cost function (default: 0)
<code>patch_size</code>	Tile size for tiled modes (default: 1)
<code>upscale</code>	Post-rendering upscaling factor (default: 1)
<code>show</code>	Logical, display result in viewer (default: <code>interactive()</code>)

Details

Transport-Only Semantics:

This function returns a SHARP, pixel-perfect transport of A's pixels to positions determined by the assignment to B.

Key Points:

- Assignment computed using: $\text{cost} = \text{alpha} * \text{color_dist} + \text{beta} * \text{spatial_dist}$
- B's COLORS influence assignment but DO NOT appear in output
- Result has A's colors arranged to match B's layout
- No motion blur (unlike intermediate frames in animation)

See [pixel_morph_animate](#) for detailed explanation of assignment vs rendering semantics.

Permutation Warnings:

Assignment is guaranteed to be a bijection (permutation) ONLY when:

- `downscale_steps = 0` (no resolution changes)
- `mode = "exact"` with `patch_size = 1`

With downscaling or tiled modes, assignment may have:

- **Overlaps:** Multiple source pixels map to same destination (last write wins)
- **Holes:** Some destinations never filled (remain transparent)

If assignment is not a bijection (due to downscaling or tiling), a warning will be issued. The result may contain:

- Overlapped pixels (multiple sources \rightarrow one destination)
- Transparent holes (some destinations unfilled)

For guaranteed pixel-perfect results, use:

```
pixel_morph(A, B, mode = "exact", downscale_steps = 0)
```

Value

magick image object of the final transported frame

See Also

[pixel_morph_animate](#) for animated version

Examples

```
if (requireNamespace("magick", quietly = TRUE)) {  
  imgA <- system.file("extdata/icons/circleA_40.png", package = "couplr")  
  imgB <- system.file("extdata/icons/circleB_40.png", package = "couplr")  
  if (nzchar(imgA) && nzchar(imgB)) {  
    result <- pixel_morph(imgA, imgB, n_frames = 4, show = FALSE)  
  }  
}
```

pixel_morph_animate *Pixel-level image morphing (animation)*

Description

Creates an animated morph by computing optimal pixel assignment from image A to image B, then rendering intermediate frames showing the transport.

Usage

```
pixel_morph_animate(  
  imgA,  
  imgB,  
  n_frames = 16L,  
  fps = 10L,  
  format = c("gif", "webp", "mp4"),  
  outfile = NULL,  
  show = interactive(),  
  mode = c("color_walk", "exact", "recursive"),  
  lap_method = "jv",  
  maximize = FALSE,  
  quantize_bits = 5L,  
  downscale_steps = 0L,  
  alpha = 1,  
  beta = 0,  
  patch_size = 1L,  
  upscale = 1  
)
```

Arguments

<code>imgA</code>	Source image (file path or magick image object)
<code>imgB</code>	Target image (file path or magick image object)
<code>n_frames</code>	Integer number of animation frames (default: 16)
<code>fps</code>	Frames per second for playback (default: 10)
<code>format</code>	Output format: "gif", "webp", or "mp4"
<code>outfile</code>	Optional output file path
<code>show</code>	Logical, display animation in viewer (default: <code>interactive()</code>)
<code>mode</code>	Assignment algorithm: "color_walk" (default), "exact", or "recursive"
<code>lap_method</code>	LAP solver method (default: "jv")
<code>maximize</code>	Logical, maximize instead of minimize cost (default: FALSE)
<code>quantize_bits</code>	Color quantization for "color_walk" mode (default: 5)
<code>downscale_steps</code>	Number of 2x reductions before computing assignment (default: 0)
<code>alpha</code>	Weight for color distance in cost function (default: 1)
<code>beta</code>	Weight for spatial distance in cost function (default: 0)
<code>patch_size</code>	Tile size for tiled modes (default: 1)
<code>upscale</code>	Post-rendering upscaling factor (default: 1)

Details

Assignment vs Rendering Semantics:

CRITICAL: This function has two separate phases with different semantics:

Phase 1 - Assignment Computation:

The assignment is computed by minimizing:

$$\text{cost}(i, j) = \text{alpha} * \text{color_distance}(A[i], B[j]) + \\ \text{beta} * \text{spatial_distance}(\text{pos}_i, \text{pos}_j)$$

This means B's COLORS influence which pixels from A map to which positions.

Phase 2 - Rendering (Transport-Only):

The renderer uses ONLY A's colors:

- Intermediate frames: A's pixels move along paths with motion blur
- Final frame: A's pixels at their assigned positions (sharp, no blur)
- B's colors NEVER appear in the output

Result: You get A's colors rearranged to match B's geometry/layout.

What This Means:

- B influences WHERE pixels go (via similarity in cost function)
- B does NOT determine WHAT COLORS appear in output
- Final image has A's palette arranged to mimic B's structure

Parameter Guidance:**For pure spatial rearrangement (ignore B's colors in assignment):**

```
pixel_morph_animate(A, B, alpha = 0, beta = 1)
```

For color-similarity matching (default):

```
pixel_morph_animate(A, B, alpha = 1, beta = 0)
```

For hybrid (color + spatial):

```
pixel_morph_animate(A, B, alpha = 1, beta = 0.2)
```

Permutation Guarantees:

Assignment is guaranteed to be a bijection (permutation) ONLY when:

- `downscale_steps = 0` (no resolution changes)
- `mode = "exact"` with `patch_size = 1`

With downscaling or tiled modes, assignment may have:

- **Overlaps:** Multiple source pixels map to same destination (last write wins)
- **Holes:** Some destinations never filled (remain transparent)

A warning is issued if overlaps/holes are detected in the final frame.

Value

Invisibly returns a list with animation object and metadata:

<code>animation</code>	magick animation object
<code>width</code>	Image width in pixels
<code>height</code>	Image height in pixels
<code>assignment</code>	Integer vector of 1-based assignment indices (R convention)
<code>n_pixels</code>	Total number of pixels
<code>mode</code>	Mode used for matching
<code>upscale</code>	Upscaling factor applied

Examples

```
if (requireNamespace("magick", quietly = TRUE)) {
  imgA <- system.file("extdata/icons/circleA_40.png", package = "couplr")
  imgB <- system.file("extdata/icons/circleB_40.png", package = "couplr")
  if (nzchar(imgA) && nzchar(imgB)) {
    outfile <- tempfile(fileext = ".gif")
    pixel_morph_animate(imgA, imgB, outfile = outfile, n_frames = 4, show = FALSE)
  }
}
```

plot.balance_diagnostics*Plot method for balance diagnostics***Description**

Produces a Love plot (dot plot) of standardized differences.

Usage

```
## S3 method for class 'balance_diagnostics'
plot(x, type = c("love", "histogram", "variance"), threshold = 0.1, ...)
```

Arguments

- | | |
|------------------------|--|
| <code>x</code> | A <code>balance_diagnostics</code> object |
| <code>type</code> | Type of plot: "love" (default), "histogram", or "variance" |
| <code>threshold</code> | Threshold line for standardized differences (default: 0.1) |
| <code>...</code> | Additional arguments passed to plotting functions |

Value

The `balance_diagnostics` object (invisibly)

plot.matching_result *Plot method for matching results***Description**

Produces a histogram of pairwise distances from a matching result.

Usage

```
## S3 method for class 'matching_result'
plot(x, type = c("histogram", "density", "ecdf"), ...)
```

Arguments

- | | |
|-------------------|---|
| <code>x</code> | A <code>matching_result</code> object |
| <code>type</code> | Type of plot: "histogram" (default), "density", or "ecdf" |
| <code>...</code> | Additional arguments passed to plotting functions |

Value

The `matching_result` object (invisibly)

preprocess_matching_vars

Preprocess matching variables with automatic checks and scaling

Description

Main preprocessing function that orchestrates variable health checks, categorical encoding, and automatic scaling selection.

Usage

```
preprocess_matching_vars(  
  left,  
  right,  
  vars,  
  auto_scale = TRUE,  
  scale_method = "auto",  
  check_health = TRUE,  
  remove_problematic = TRUE,  
  verbose = TRUE  
)
```

Arguments

<code>left</code>	Data frame of left units
<code>right</code>	Data frame of right units
<code>vars</code>	Character vector of variable names
<code>auto_scale</code>	Logical, whether to perform automatic preprocessing (default: TRUE)
<code>scale_method</code>	Scaling method: "auto", "standardize", "range", "robust", or FALSE
<code>check_health</code>	Logical, whether to check variable health (default: TRUE)
<code>remove_problematic</code>	Logical, automatically exclude constant/all-NA variables (default: TRUE)
<code>verbose</code>	Logical, whether to print warnings (default: TRUE)

Value

A list with class "preprocessing_result" containing:

- `left`: Preprocessed left data frame
- `right`: Preprocessed right data frame
- `vars`: Final variable names (after exclusions)
- `health`: Variable health diagnostics
- `scaling_method`: Selected scaling method
- `excluded_vars`: Variables that were excluded
- `warnings`: List of warnings issued

```
print.balance_diagnostics
```

Print Method for Balance Diagnostics

Description

Print Method for Balance Diagnostics

Usage

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

Arguments

x	A balance_diagnostics object
...	Additional arguments (ignored)

Value

Invisibly returns the input object x.

```
print.distance_object  Print Method for Distance Objects
```

Description

Print Method for Distance Objects

Usage

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

Arguments

x	A distance_object
...	Additional arguments (ignored)

Value

Invisibly returns the input object x.

```
print.lap_solve_batch_result
    Print method for batch assignment results
```

Description

Prints a summary and the table of results for a batch of assignment problems solved with `lap_solve_batch()`.

Usage

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

Arguments

x	A <code>lap_solve_batch_result</code> object.
...	Additional arguments passed to <code>print()</code> . Currently ignored.

Value

Invisibly returns the input object `x`.

```
print.lap_solve_kbest_result
    Print method for k-best assignment results
```

Description

Print method for k-best assignment results

Usage

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

Arguments

x	A <code>lap_solve_kbest_result</code> .
...	Additional arguments passed to <code>print()</code> . Ignored.

Value

Invisibly returns the input object `x`.

```
print.lap_solve_result
```

Print method for assignment results

Description

Nicely prints a `lap_solve_result` object, including the assignments, total cost, and method used.

Usage

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

Arguments

<code>x</code>	A <code>lap_solve_result</code> object.
<code>...</code>	Additional arguments passed to <code>print()</code> . Currently ignored.

Value

Invisibly returns the input object `x`.

```
print.matching_result  Print method for matching results
```

Description

Print method for matching results

Usage

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

Arguments

<code>x</code>	A <code>matching_result</code> object
<code>...</code>	Additional arguments (ignored)

Value

Invisibly returns the input object `x`.

```
print.matchmaker_result
```

Print method for matchmaker results

Description

Print method for matchmaker results

Usage

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

Arguments

x	A matchmaker_result object
...	Additional arguments (ignored)

Value

Invisibly returns the input object x.

```
print.preprocessing_result
```

Print method for preprocessing result

Description

Print method for preprocessing result

Usage

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

Arguments

x	A preprocessing_result object
...	Additional arguments (ignored)

Value

Invisibly returns the input object x.

`print.variable_health` *Print method for variable health*

Description

Print method for variable health

Usage

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

Arguments

<code>x</code>	A variable_health object
<code>...</code>	Additional arguments (ignored)

Value

Invisibly returns the input object `x`.

<code>sinkhorn</code>	<i>'Sinkhorn-Knopp' optimal transport solver</i>
-----------------------	--

Description

Compute an entropy-regularized optimal transport plan using the 'Sinkhorn-Knopp' algorithm. Unlike other LAP solvers that return a hard 1-to-1 assignment, this returns a soft assignment (doubly stochastic matrix).

Usage

```
sinkhorn(
  cost,
  lambda = 10,
  tol = 1e-09,
  max_iter = 1000,
  r_weights = NULL,
  c_weights = NULL
)
```

Arguments

<code>cost</code>	Numeric matrix of transport costs. NA or Inf entries are treated as very high cost (effectively forbidden).
<code>lambda</code>	Regularization parameter (default 10). Higher values produce sharper (more deterministic) transport plans; lower values produce smoother distributions. Typical range: 1-100.
<code>tol</code>	Convergence tolerance (default 1e-9).
<code>max_iter</code>	Maximum iterations (default 1000).
<code>r_weights</code>	Optional numeric vector of row marginals (source distribution). Default is uniform. Will be normalized to sum to 1.
<code>c_weights</code>	Optional numeric vector of column marginals (target distribution). Default is uniform. Will be normalized to sum to 1.

Details

The 'Sinkhorn-Knopp' algorithm solves the entropy-regularized optimal transport problem:

$$P^* = \arg \min_P \langle C, P \rangle - \frac{1}{\lambda} H(P)$$

subject to row sums = `r_weights` and column sums = `c_weights`.

The entropy term $H(P)$ encourages spread in the transport plan. As `lambda` \rightarrow Inf, the solution approaches the standard (unregularized) optimal transport.

Key differences from standard LAP solvers:

- Returns a soft assignment (probabilities) not a hard 1-to-1 matching
- Supports unequal marginals (weighted distributions)
- Differentiable, making it useful in ML pipelines
- Very fast: $O(n^2)$ per iteration with typically $O(1/tol^2)$ iterations

Use `sinkhorn_to_assignment()` to round the soft assignment to a hard matching.

Value

A list with elements:

- `transport_plan` — numeric matrix, the optimal transport plan P . Row sums approximate `r_weights`, column sums approximate `c_weights`.
- `cost` — the transport cost $\langle C, P \rangle$ (without entropy term).
- `u, v` — scaling vectors ($P = \text{diag}(u) * K * \text{diag}(v)$ where $K = \exp(-\lambda * C)$).
- `converged` — logical, whether the algorithm converged.
- `iterations` — number of iterations used.
- `lambda` — the regularization parameter used.

References

Cuturi, M. (2013). 'Sinkhorn Distances': Lightspeed Computation of Optimal Transport. *Advances in Neural Information Processing Systems*, 26.

See Also

[assignment\(\)](#) for hard 1-to-1 matching, [sinkhorn_to_assignment\(\)](#) to round soft assignments.

Examples

```
cost <- matrix(c(1, 2, 3, 4, 5, 6, 7, 8, 9), nrow = 3, byrow = TRUE)

# Soft assignment with default parameters
result <- sinkhorn(cost)
print(round(result$transport_plan, 3))

# Sharper assignment (higher lambda)
result_sharp <- sinkhorn(cost, lambda = 50)
print(round(result_sharp$transport_plan, 3))

# With custom marginals (more mass from row 1)
result_weighted <- sinkhorn(cost, r_weights = c(0.5, 0.25, 0.25))
print(round(result_weighted$transport_plan, 3))

# Round to hard assignment
hard_match <- sinkhorn_to_assignment(result)
print(hard_match)
```

`sinkhorn_to_assignment`

Round 'Sinkhorn' transport plan to hard assignment

Description

Convert a soft transport plan from [sinkhorn\(\)](#) to a hard 1-to-1 assignment using greedy rounding.

Usage

```
sinkhorn_to_assignment(result)
```

Arguments

result	Either a result from sinkhorn() or a transport plan matrix.
--------	---

Details

Greedy rounding iteratively assigns each row to its most probable column, ensuring no column is assigned twice. This may not give the globally optimal hard assignment; for that, use the transport plan as a cost matrix with [assignment\(\)](#).

Value

Integer vector of column assignments (1-based), same format as [assignment\(\)](#).

See Also

[sinkhorn\(\)](#)

Examples

```
cost <- matrix(c(1, 2, 3, 4, 5, 6, 7, 8, 9), nrow = 3, byrow = TRUE)
result <- sinkhorn(cost, lambda = 20)
hard_match <- sinkhorn_to_assignment(result)
print(hard_match)
```

summary.balance_diagnostics

Summary method for balance diagnostics

Description

Summary method for balance diagnostics

Usage

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

Arguments

object	A <code>balance_diagnostics</code> object
...	Additional arguments (ignored)

Value

A list containing summary statistics (invisibly)

```
summary.distance_object
```

Summary Method for Distance Objects

Description

Summary Method for Distance Objects

Usage

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

Arguments

object	A distance_object
...	Additional arguments (ignored)

Value

Invisibly returns the input object.

```
summary.lap_solve_kbest_result
```

Get summary of k-best results

Description

Extract summary information from k-best assignment results.

Usage

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

Arguments

object	An object of class lap_solve_kbest_result.
...	Additional arguments (unused).

Value

A tibble with one row per solution containing:

- `rank`: solution rank
- `solution_id`: solution identifier
- `total_cost`: total cost of the solution
- `n_assignments`: number of assignments in the solution

`summary.matching_result`

Summary method for matching results

Description

Summary method for matching results

Usage

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

Arguments

<code>object</code>	A <code>matching_result</code> object
<code>...</code>	Additional arguments (ignored)

Value

A list containing summary statistics (invisibly)

`update_constraints`

Update Constraints on Distance Object

Description

Apply new constraints to a precomputed distance object without recomputing the underlying distances. This is useful for exploring different constraint scenarios quickly.

Usage

```
update_constraints(dist_obj, max_distance = Inf, calipers = NULL)
```

Arguments

<code>dist_obj</code>	A distance_object from <code>compute_distances()</code>
<code>max_distance</code>	Maximum allowed distance (pairs with distance > max_distance become Inf)
<code>calipers</code>	Named list of per-variable calipers

Details

This function creates a new distance_object with modified constraints applied to the cost matrix. The original distance_object is not modified.

Constraints:

- `max_distance`: Sets cost to Inf for pairs exceeding this threshold
- `calipers`: Per-variable restrictions (e.g., `calipers = list(age = 5)`)

The function returns a new object rather than modifying in place, following R's copy-on-modify semantics.

Value

A new distance_object with updated cost_matrix

Examples

```
left <- data.frame(id = 1:5, age = c(25, 30, 35, 40, 45))
right <- data.frame(id = 6:10, age = c(24, 29, 36, 41, 44))
dist_obj <- compute_distances(left, right, vars = "age")

# Apply constraints
constrained <- update_constraints(dist_obj, max_distance = 2)
result <- match_couples(constrained)
```

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