Package 'eam'

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Title Evidence Accumulation Models

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Suggests testthat (>= 3.0.0), pbapply, abc

Description Simulation-based evidence accumulation models for analyzing responses and reaction times in single- and multi-response tasks. The package includes simulation engines for five representative models: the Diffusion Decision Model (DDM), Leaky Competing Accumulator (LCA), Linear Ballistic Accumulator (LBA), Racing Diffusion Model (RDM), and Levy Flight Model (LFM), and extends these frameworks to multi-response settings. The package supports user-defined functions for item-level parameterization and the incorporation of covariates, enabling flexible customization and the development of new model variants based on existing architectures. Inference is performed using simulation-based methods, including Approximate Bayesian Computation (ABC) and Amortized Bayesian Inference (ABI), which allow parameter estimation without requiring tractable likelihood functions. In addition to core inference tools, the package provides modules for parameter recovery, posterior predictive checks, and model comparison, facilitating the study of a wide range of cognitive processes in tasks involving perceptual decision making, memory retrieval, and value-based decision making. Key methods implemented in the package are described in Ratcliff (1978) <doi:10.1037/0033-295X.85.2.59>, Usher and McClelland (2001) <doi:10.1037/0033-295X.108.3.550>, Brown and Heathcote (2008) <doi:10.1016/j.cogpsych.2007.12.002>, Tillman, Van Zandt and Logan (2020) <doi:10.3758/s13423-020-01719-6>, Wieschen, Voss and Radev (2020) <doi:10.20982/tqmp.16.2.p120>, Csilléry, François and Blum (2012) <doi:10.1111/j.2041-210X.2011.00179.x>, Beaumont (2019) <doi:10.1146/annurev-statistics-030718-105212>, and Sainsbury-Dale, Zammit-Mangion and Huser (2024) <doi:10.1080/00031305.2023.2249522>.

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Contents

`+.eam_summarise_by_spec` *Add two summarise_by specs together*

Description

S3 method for the + operator to combine two ‘eam_summarise_by_spec‘ objects into a single spec that will apply both operations.

Usage

```
## S3 method for class 'eam_summarise_by_spec'
e1 + e2
```

Arguments

`e1`	First eam_summarise_by_spec or eam_summarise_by_tbl object
`e2`	Second eam_summarise_by_spec or eam_summarise_by_tbl object

Value

A combined eam_summarise_by_spec object

`+.eam_summarise_by_tbl` *Join two eam_summarise_by_tbl objects*

Description

S3 method for the + operator to join two summary tables created by `summarise_by`. Tables must have identical .wider_by attributes to be joined.

Usage

```
## S3 method for class 'eam_summarise_by_tbl'
e1 + e2
```

Arguments

`e1`	First eam_summarise_by_tbl object
`e2`	Second eam_summarise_by_tbl object

Value

A joined data frame with class "eam_summarise_by_tbl", preserving the .wider_by attribute from the input tables

abc_posterior_bootstrap *Bootstrap resample ABC posterior samples*

Description

Bootstrap resample ABC posterior samples

Usage

```
abc_posterior_bootstrap(abc_result, n_samples, replace = TRUE)
```

Arguments

abc_result	An abc object from abc
n_samples	Number of bootstrap samples to draw (default 1000)
replace	Logical, whether to sample with replacement (default TRUE)

Value

Data frame of bootstrapped parameter values

Examples

```
# Load an example abc output, you should generate it by applying ABC to your data
# check abc::abc for details on fitting ABC models
rdm_minimal_example <- system.file("extdata", "rdm_minimal", package = "eam")
abc_model <- readRDS(file.path(rdm_minimal_example, "abc", "abc_neuralnet_model.rds"))

# Bootstrap resample posterior parameters
posterior_params <- abc_posterior_bootstrap(
  abc_model,
  n_samples = 100
)

# View the first few rows of the bootstrapped posterior parameters
head(posterior_params)
```

abc_postpr *ABC model comparison wrapper*

Description

Wrapper function for postpr to facilitate model comparison. This function simplifies the process of comparing multiple models using ABC by automatically stacking summary statistics and creating model indices.

Usage

```
abc_postpr(sumstats = list(), target, ...)
```

Arguments

sumstats	A named list of summary statistics matrices from different models. Each element should be a matrix or data frame with the same columns.
target	Target summary statistics from observed data (vector or matrix)
...	Additional arguments passed to postpr

Value

An object of class "postpr" from postpr

Examples

```
# Load pre-computed ABC input for model comparison
# This example compares the same model to itself for demonstration
rdm_minimal_example <- system.file("extdata", "rdm_minimal", package = "eam")
abc_input <- readRDS(file.path(rdm_minimal_example, "abc", "abc_input.rds"))

# Compare two models using their summary statistics
# In practice, create different abc_input objects for different models:
# abc_input_1 <- build_abc_input(..., simulation_summary = sim_summary_1, ...)
# abc_input_2 <- build_abc_input(..., simulation_summary = sim_summary_2, ...)
postpr_result <- abc_postpr(
  sumstats = list(model1 = abc_input$sumstat, model2 = abc_input$sumstat),
  target = abc_input$target,
  tol = 0.5,
  method = "rejection"
)

# View model comparison results
summary(postpr_result)
```

abc_resample *ABC with resampling*

Description

Performs ABC inference with resampling to assess stability and uncertainty. Each iteration draws a random sample from the simulation pool and runs ABC, producing multiple posterior estimates for comparison.

Usage

```
abc_resample(
  target,
  param,
  sumstat,
  n_iterations,
  n_samples,
  replace = FALSE,
  ...
)
```

Arguments

target	Target summary statistics from observed data
param	Parameter values matrix or data frame
sumstat	Summary statistics matrix or data frame
n_iterations	Number of resample iterations
n_samples	Number of samples to draw in each iteration
replace	Logical, whether to sample with replacement (default FALSE)
...	Additional arguments passed to abc::abc

Value

A list of length n_iterations, where each element is an object of class abc returned by abc. Each list element contains the ABC posterior for one bootstrap iteration, allowing assessment of stability and uncertainty in parameter estimates.

Examples

```
# Load ABC input data from example simulation
abc_input <- readRDS(
  system.file("extdata", "rdm_minimal", "abc", "abc_input.rds", package = "eam")
)

# Perform ABC resampling
results <- abc_resample(
```

```
  target = abc_input$target,
  param = abc_input$param,
  sumstat = abc_input$sumstat,
  n_iterations = 2,
  n_samples = 2,
  tol = 0.5,
  method = "rejection"
)

# check the abc results
str(results)
```

`build_abc_input` *Build input for Approximate Bayesian Computation (ABC)*

Description

Prepares simulation output, summary statistics, and target data for ABC analysis using the abc package. Extracts parameters and summary statistics from simulation results and formats them into matrices suitable for ABC parameter estimation.

Usage

```
build_abc_input(simulation_output, simulation_summary, target_summary, param)
```

Arguments

`simulation_output`	A eam_simulation_output object containing that is from `run_simulation` or `load_simulation_output`.
`simulation_summary`	A data frame containing summary statistics for each simulated condition. Should have a 'condition_idx' column and be created by `summarise_by`.
`target_summary`	A data frame containing target summary statistics to match against simulation results. Should have the same summary statistic columns as simulation_summary (excluding 'wider_by' columns).
`param`	Character vector of parameter names to extract from simulation_output. These parameters will be used as the parameter space for ABC estimation.

Details

This function provides a streamlined workflow for preparing ABC inputs, but it requires that all components be constructed using this package's functions. Specifically, `simulation_output` must be created by `run_simulation` or `load_simulation_output`, and both `simulation_summary` and `target_summary` must be generated using `summarise_by`. If your data originates from external sources or custom pipelines, you should manually construct the ABC input list instead, ensuring proper matrix formatting and column alignment as expected by `abc::abc`.

Value

A list with components suitable for abc::abc

Required format for summary statistics

Both simulation_summary and target_summary must be created using summarise_by. This ensures consistent column naming and data structure required for ABC analysis. See summarise_by for details on generating properly formatted summaries, and map_by_condition for typical workflow examples. If you want more flexibility in summary statistic calculation, you can manually construct the ABC input list. It is not necessary to use this function if you are familiar with the abc package.

Examples

```
# Load the example dataset
rdm_minimal_example <- system.file("extdata", "rdm_minimal", package = "eam")
sim_output <- load_simulation_output(file.path(rdm_minimal_example, "simulation"))
obs_df <- read.csv(file.path(rdm_minimal_example, "observation", "observation_data.csv"))

# Define summary statistics pipeline
summary_pipe <- summarise_by(
  .by = c("condition_idx"),
  rt_mean = mean(rt)
)

# Calculate summary statistics for simulation and observation
sim_summary <- map_by_condition(
  sim_output,
  .progress = FALSE,
  .parallel = FALSE,
  function(cond_df) {
    summary_pipe(cond_df)
  }
)
obs_summary <- summary_pipe(obs_df)

# Build ABC input
abc_input <- build_abc_input(
  simulation_output = sim_output,
  simulation_summary = sim_summary,
  target_summary = obs_summary,
  param = c("V_beta_1", "V_beta_group")
)

# Perform ABC parameter estimation using rejection method
abc_rejection_model <- abc::abc(
  target = abc_input$target,
  param = abc_input$param,
  sumstat = abc_input$sumstat,
  tol = 0.5,
  method = "rejection"
```

```
)
```

---

load_simulation_output *Rebuild eam_simulation_output from an existing output directory*

Description

This function reconstructs a eam_simulation_output object from a previously saved simulation output directory.

Usage

```
load_simulation_output(output_dir)
```

Arguments

output_dir	The directory containing the simulation results and config

Value

A eam_simulation_output object

Examples

```
# Load simulation output from package data
sim_output_path <- system.file(
  "extdata", "rdm_minimal", "simulation",
  package = "eam"
)
sim_output <- load_simulation_output(sim_output_path)

# Access the configuration
sim_output$simulation_config

# Access the dataset (check arrow documentation for working with the dataset)
dataset <- sim_output$open_dataset()
```

`map_by_condition` *Map a function by condition across simulation output chunks*

Description

This function processes simulation output by gathering all chunks, iterating through them one by one, filtering and collecting data by chunk, then applying a user-defined function by condition within each chunk.

Usage

```
map_by_condition(
  simulation_output,
  .f,
  ...,
  .combine = dplyr::bind_rows,
  .parallel = NULL,
  .n_cores = NULL,
  .progress = FALSE
)
```

Arguments

`simulation_output`	A eam_simulation_output object containing the dataset and configuration
`.f`	A function to apply to each condition's data. The function should accept a data frame representing one condition's results
`...`	Additional arguments passed to the function .f
`.combine`	Function to combine results (default: dplyr::bind_rows)
`.parallel`	Logical or NULL.
`.n_cores`	Integer. Number of CPU cores to use for parallel processing. If NULL, uses `detectCores() - 1`. Only used when `.parallel = TRUE`.
`.progress`	Logical, whether to show a progress bar (default: FALSE)

Details

This function handles out-of-core computation automatically using Apache Arrow, so you don't need to understand Arrow internals. It loads data chunk by chunk to avoid memory issues with large simulations.

If you prefer to manually work with the raw Arrow dataset, you can access it via `simulation_output$open_dataset()`, which returns an Arrow Dataset object. You can then use `dplyr` verbs to filter and query before calling `dplyr::collect()` to load data into memory.

Value

A list containing the results of applying .f to each condition, with names corresponding to condition indices

Examples

```
# Load simulation output
sim_output_path <- system.file(
  "extdata", "rdm_minimal", "simulation",
  package = "eam"
)
sim_output <- load_simulation_output(sim_output_path)

# Define a summary pipeline
summary_pipe <- summarise_by(
  .by = c("condition_idx"),
  rt_mean = mean(rt),
  rt_quantiles = quantile(rt, probs = c(0.1, 0.5, 0.9))
)

# Apply function to each condition
sim_sumstat <- map_by_condition(
  sim_output,
  .progress = FALSE,
  .parallel = FALSE,
  function(cond_df) {
    summary_pipe(cond_df)
  }
)
```

---

new_simulation_config *Create a new simulation configuration*

Description

This function creates a new eam simulation configuration object that contains all parameters needed to run a simulation.

Usage

```
new_simulation_config(
  prior_params = list(),
  prior_formulas = list(),
  between_trial_formulas = list(),
  item_formulas = list(),
  n_conditions_per_chunk = NULL,
  n_conditions,
  n_trials_per_condition,
```

```
  n_items,
  max_reached = n_items,
  max_t,
  dt = 0.001,
  noise_mechanism = "add",
  noise_factory = NULL,
  model = "ddm",
  parallel = FALSE,
  n_cores = NULL,
  rand_seed = NULL
)
```

Arguments

prior_params	A list or data frame of initial values for prior
prior_formulas	A list of formulas defining prior distributions for condition-level parameters
between_trial_formulas	A list of formulas defining between-trial parameters
item_formulas	A list of formulas defining item-level parameters
n_conditions_per_chunk	Number of conditions to process per chunk (optional, typically does not need to be set. It determine the storage and in-memory size of each chunk, if you find memory issues, try reducing this number)
n_conditions	Total number of conditions to simulate
n_trials_per_condition	Number of trials per condition
n_items	Number of items per trial
max_reached	Maximum number of items that can be recalled (default: n_items)
max_t	Maximum simulation time
dt	Time step size (default: 0.001)
noise_mechanism	Noise mechanism ("add", "mult_evidence", or "mult_t", default: "add")
noise_factory	Function that creates noise functions.
model	Model name or backend names (e.g., "ddm", "rdm", "lca")
parallel	Whether to run in parallel (default: FALSE)
n_cores	Number of cores for parallel processing (default: NULL, auto-detect)
rand_seed	Random seed for parallel processing (default: NULL)

Details

This function only creates the configuration object and does not run the simulation. To actually execute the simulation, you must pass the returned configuration object to run_simulation.

Supported Models:

This package supports three evidence accumulation models. The appropriate backend is automatically selected based on the model parameter and the parameters defined in your formulas.

DDM (Drift Diffusion Model) Models evidence accumulation towards a single upper threshold. Items either reach the threshold and are recalled, or time out.

Required parameters (must appear in `prior_formulas`, `between_trial_formulas`, or `item_formulas`):

- `A` - Upper decision boundary/threshold
- `V` - Drift rate (evidence accumulation rate)
- `Z` - Starting point of evidence
- `ndt` - Non-decision time

Set `model = "ddm"`

RDM (Racing Diffusion Model) Models multiple racing evidence accumulators, each with upper and lower thresholds for binary decisions (correct/incorrect).

Required parameters:

- `A_upper` - Upper decision boundary (correct response)
- `A_lower` - Lower decision boundary (incorrect response)
- `V` - Drift rate
- `Z` - Starting point of evidence
- `ndt` - Non-decision time

Set `model = "rdm"`. Note: If you set `model = "ddm"` but define `A_upper` instead of `A`, the model will automatically switch to RDM.

LCA (Leaky Competing Accumulator) Models competitive evidence accumulation with leakage and mutual inhibition between accumulators.

Required parameters:

- `A` - Decision threshold
- `V` - Input strength/drift rate
- `Z` - Starting point of evidence
- `ndt` - Non-decision time
- `beta` - Self-excitation/leak parameter
- `k` - Lateral inhibition strength

Set `model = "lca"`

LFM (Lévy Flight Model) Uses the same parameters as `DDM`. See `DDM` above.

Set `model = "lfm"`

LBA (Linear Ballistic Accumulator) Uses the same parameters as `RDM`. See `RDM` above.

Set `model = "lba"`

Note: All required parameters must be defined at least once across `prior_params`, `prior_formulas`, `between_trial_formulas`, and `item_formulas`.

Parameter Hierarchy and Formula Evaluation:

The simulation uses a hierarchical parameter system with sequential formula evaluation, allowing later formulas to reference earlier ones:

1. **prior_params** - Initial constant values available to all formulas
2. **prior_formulas** - Evaluated once per condition, can reference `prior_params`. Use for condition-level parameters that vary across conditions.

3. **between_trial_formulas** - Evaluated once per trial within each condition. Can reference both `prior_params` and variables from `prior_formulas`. Use for trial-level variability.
4. **item_formulas** - Evaluated once per item within each trial. Can reference all previous parameters. Use for item-specific parameters.

Using Distributions:

You can use the `distributional` package to define random parameters. For example:

- `A ~ distributional::dist_uniform(0.5, 2.0)` - Uniform distribution
- `V_condition ~ distributional::dist_normal(1.0, 0.2)` - Normal distribution
- `sigma ~ 0.5` - Constant value
- `V ~ distributional::dist_normal(V_condition, sigma)` - Reference earlier parameters

Each formula is evaluated sequentially, so you can build complex parameter dependencies. For instance, you might define a base drift rate `V` in `prior_formulas`, then add trial-level noise in `between_trial_formulas`, and finally scale by item position in `item_formulas`.

Value

An S3 object of class `eam_simulation_config` containing validated simulation parameters. This object should be passed to `run_simulation` to execute the simulation.

Examples

```
# Define formulas for the simulation
prior_formulas <- list(
  V ~ distributional::dist_uniform(0.1, 1.0),
  ndt ~ 0.3,
  noise_coef ~ 1
)

between_trial_formulas <- list()

item_formulas <- list(
  A_upper ~ 1,
  A_lower ~ -1,
  V ~ V
)

# Define noise factory
noise_factory <- function(context) {
  noise_coef <- context$noise_coef
  function(n, dt) {
    noise_coef * rnorm(n, mean = 0, sd = sqrt(dt))
  }
}

# Create configuration
config <- new_simulation_config(
  prior_formulas = prior_formulas,
  between_trial_formulas = between_trial_formulas,
```

```
  item_formulas = item_formulas,
  n_conditions = 10,
  n_trials_per_condition = 10,
  n_items = 5,
  max_reached = 5,
  max_t = 10,
  dt = 0.01,
  noise_mechanism = "add",
  noise_factory = noise_factory,
  model = "ddm",
  parallel = FALSE
)

# print the config
config

# Run simulation
sim_output <- run_simulation(config)
sim_output
```

`plot_accuracy` *Plot accuracy comparison between posterior and observed data*

Description

Visualizes accuracy metrics comparing posterior simulation results with observed data. Creates side-by-side bar plots for easy comparison across conditions.

Usage

```
plot_accuracy(
  simulated_output,
  observed_df,
  x = "item_idx",
  facet_x = c(),
  facet_y = c()
)
```

Arguments

`simulated_output`	Posterior simulation output from run_simulation()
`observed_df`	Observed data frame
`x`	Variable for x-axis (default: "item_idx")
`facet_x`	Variables for faceting columns
`facet_y`	Variables for faceting rows

Value

A ggplot2 object

Examples

```
# Load posterior simulation output and observed data
base_dir <- system.file("extdata", "rdm_minimal", package = "eam")
post_output <- load_simulation_output(file.path(base_dir, "abc", "posterior", "neuralnet"))
obs_df <- read.csv(file.path(base_dir, "observation", "observation_data.csv"))

# Plot accuracy comparison between posterior and observed data
# The plot shows side-by-side bars comparing hit rates or accuracy
plot_accuracy(
  post_output,
  obs_df,
  facet_x = c("group")
)
```

`plot_cv_pair_correlation` *Plot CV parameter pair correlations*

Description

Create a matrix of pairwise plots for cross-validation parameter estimates, including scatter plots with fitted trends, rank correlations, and marginal distributions.

Usage

```
plot_cv_pair_correlation(data, ...)

## S3 method for class 'cv4abc'
plot_cv_pair_correlation(data, ...)
```

Arguments

`data`	A `cv4abc` object containing true parameters and cross-validated estimates.
`...`	Additional arguments:
	interactive Logical; whether to pause between tolerance levels and wait for input

Value

Invisibly returns ‘NULL‘. Called for its side effect of producing plots.

See Also

`plot_cv_pair_correlation.cv4abc`

Examples

```
# Load CV output from saved file
cv_file <- system.file(
  "extdata", "rdm_minimal", "abc", "cv", "neuralnet.rds",
  package = "eam"
)
abc_neuralnet_cv <- readRDS(cv_file)

# Plot parameter pair correlations
plot_cv_pair_correlation(abc_neuralnet_cv)
```

`plot_cv_recovery` *Plot CV parameter recovery*

Description

Visualize parameter recovery from cross-validation results, showing estimated vs. true parameter values and residual distributions for each parameter.

Usage

```
plot_cv_recovery(data, ...)

## S3 method for class 'cv4abc'
plot_cv_recovery(data, ...)
```

Arguments

`data`	A `cv4abc` object containing true parameters and cross-validated estimates.
`...`	Additional arguments:
	n_rows Integer; number of rows in the plot grid (default: 3)
	n_cols Integer; number of columns in the plot grid, multiplied by 2 for paired plots (default: 1)
	method Character; smoothing method for `geom_smooth` (default: "lm")
	formula Formula; used in `geom_smooth` (default: y ~ x)
	resid_tol Numeric; quantile threshold for filtering residuals by absolute value. If specified, only observations with residuals below this quantile are plotted (default: NULL, no filtering)
	interactive Logical; whether to pause between pages and wait for user input (default: FALSE)

Value

Invisibly returns ‘NULL‘. Called for its side effect of producing plots.

See Also

plot_cv_recovery.cv4abc

Examples

```
# Load CV output from saved file
cv_file <- system.file(
  "extdata", "rdm_minimal", "abc", "cv", "neuralnet.rds",
  package = "eam"
)
abc_neuralnet_cv <- readRDS(cv_file)

# Plot parameter recovery
plot_cv_recovery(
  abc_neuralnet_cv,
  n_rows = 2,
  n_cols = 1,
  resid_tol = 0.99
)
```

---

plot_posterior_parameters

Plot parameter posterior distributions

Description

Plotting posterior distributions (and optionally prior distributions) from ABC results.

Usage

```
plot_posterior_parameters(data, ...)

## S3 method for class 'abc'
plot_posterior_parameters(data, abc_input = NULL, ...)
```

Arguments

data	An abc object containing posterior samples in adj.values or unadj.values.
...	Additional arguments: **n_rows** Integer; number of rows in the plot grid (default: 2) **n_cols** Integer; number of columns in the plot grid (default: 2) **interactive** Logical; whether to pause between pages and wait for input
abc_input	Optional abc_input object containing prior samples for comparison.

Value

Invisibly returns 'NULL'. Called for its side effect of producing plots.

See Also

plot_posterior_parameters.abc

Examples

```
# Load ABC output from saved file
abc_file <- system.file(
  "extdata", "rdm_minimal", "abc", "abc_rejection_model.rds",
  package = "eam"
)
abc_rejection_model <- readRDS(abc_file)

# Load ABC input for prior comparison
abc_input_file <- system.file(
  "extdata", "rdm_minimal", "abc", "abc_input.rds",
  package = "eam"
)
abc_input <- readRDS(abc_input_file)

# Plot posterior distributions with prior comparison
plot_posterior_parameters(abc_rejection_model, abc_input)
```

---

plot_resample_forest *Plot resample forest plots*

Description

Create forest plots showing parameter ranges across resample iterations. Each iteration is displayed as a horizontal line with quantile intervals.

Usage

```
plot_resample_forest(
  data,
  n_rows = 2,
  n_cols = 2,
  interactive = FALSE,
  ci_level = 0.95
)
```

Arguments

data	List of abc results from abc_resample
n_rows	Number of rows in plot grid (default 2)
n_cols	Number of columns in plot grid (default 2)
interactive	Whether to pause between pages (default FALSE)
ci_level	quantile intervals (default 0.95 for 95% interval)

Value

No return value, called for side effects (plotting). Creates forest plots displayed in the graphics device.

Examples

```
# Load ABC input data from example simulation
abc_input <- readRDS(
  system.file("extdata", "rdm_minimal", "abc", "abc_input.rds", package = "eam")
)

# Perform ABC resampling
results <- abc_resample(
  target = abc_input$target,
  param = abc_input$param,
  sumstat = abc_input$sumstat,
  n_iterations = 100,
  n_samples = 100,
  tol = 0.5,
  method = "rejection"
)

# plot forest plots showing parameter ranges
plot_resample_forest(results, ci_level = 0.95)
```

---

plot_resample_medians *Plot resample median distributions*

Description

Plot density distributions of parameter medians across resample iterations.

Usage

```
plot_resample_medians(data, n_rows = 2, n_cols = 2, interactive = FALSE)
```

Arguments

data	List of abc results from abc_resample
n_rows	Number of rows in plot grid (default 2)
n_cols	Number of columns in plot grid (default 2)
interactive	Whether to pause between pages (default FALSE)

Value

No return value, called for side effects (plotting). Creates density plots displayed in the graphics device.

Examples

```
# Load ABC input data from example simulation
abc_input <- readRDS(
  system.file("extdata", "rdm_minimal", "abc", "abc_input.rds", package = "eam")
)

# Perform ABC resampling
results <- abc_resample(
  target = abc_input$target,
  param = abc_input$param,
  sumstat = abc_input$sumstat,
  n_iterations = 100,
  n_samples = 100,
  tol = 0.5,
  method = "rejection"
)

# plot the resample medians for each parameter
plot_resample_medians(results)
```

---

plot_rt *Plot reaction time distributions*

Description

Visualize reaction time distributions from your model predictions. Overlay observed experimental data for reference.

Usage

```
plot_rt(simulated_output, observed_df, facet_x = c("item_idx"), facet_y = c())
```

Arguments

simulated_output	Output from run_simulation containing posterior predictions
observed_df	Your observed data as a data frame
facet_x	Variables to split plots horizontally. Default is "item_idx" to show separate plots for each item
facet_y	Variables to split plots vertically. Default is none (c())

Value

A plot showing predicted RT distributions (blue), with observed data (red) if provided

Examples

```
# Load example posterior simulation output
post_output_path <- system.file(
  "extdata", "rdm_minimal", "abc", "posterior", "neuralnet",
  package = "eam"
)
post_output <- load_simulation_output(post_output_path)

# Load example observed data
obs_file <- system.file(
  "extdata", "rdm_minimal", "observation", "observation_data.csv",
  package = "eam"
)
obs_df <- read.csv(obs_file)

# Plot RT distributions by item
plot_rt(post_output, obs_df, facet_x = c("item_idx"))

# Plot RT distributions by item and group
plot_rt(
  post_output,
  obs_df,
  facet_x = c("item_idx"),
  facet_y = c("group")
)
```

---

print.eam_simulation_config

Print method for eam simulation configuration

Description

Print method for eam simulation configuration

Usage

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

Arguments

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

Value

Invisibly returns the input object

run_simulation *Run a simulation with specified configuration*

Description

This function runs a complete simulation based on the provided eam_simulation_config object, which is generated by the new_simulation_config function.

Usage

```
run_simulation(config, output_dir = NULL)
```

Arguments

config	A eam_simulation_config object containing all simulation parameters, you should use new_simulation_config to create one.
output_dir	The directory to save out-of-core results (optional, will use temp directory if not provided)

Details

This function uses an out-of-core approach to handle potentially large simulation results. Instead of returning a data frame directly, it persists the data to disk and returns an eam_simulation_output object that contains metadata and file system paths.

To access the simulation data, use the following methods on the returned object:

- open_dataset() - Returns an Arrow Dataset containing the simulation results, e.g. sim_output$open_dataset()
- open_evaluated_conditions() - Returns an Arrow Dataset containing the evaluated condition parameters, e.g. sim_output$open_evaluated_conditions()

Both methods return Arrow Dataset objects rather than data frames, allowing for efficient querying and filtering before loading data into memory. To convert to a data frame, use dplyr::collect() or as.data.frame().

Throughout this package, the eam_simulation_output object is used as the standard parameter for downstream analysis functions, rather than passing Arrow objects or data frames directly.

For multi-item backends, at each discrete time point, only one item can reach the threshold. The precision of this detection depends on the dt parameter. This design choice was made for performance considerations. For almost all experimental scenarios, it is negligible. But users should be aware of this limitation, if it is critical, try to increase the temporal resolution by reducing dt. For implementation details, refer to the backend source code (accumulate_evidence_* functions).

Value

A S3 object of class eam_simulation_output containing the output information

Examples

```
# Define formulas for the simulation
prior_formulas <- list(
  V ~ distributional::dist_uniform(0.1, 1.0),
  ndt ~ 0.3,
  noise_coef ~ 1
)

between_trial_formulas <- list()

item_formulas <- list(
  A_upper ~ 1,
  A_lower ~ -1,
  V ~ V
)

# Define noise factory
noise_factory <- function(context) {
  noise_coef <- context$noise_coef
  function(n, dt) {
    noise_coef * rnorm(n, mean = 0, sd = sqrt(dt))
  }
}

# Create configuration
config <- new_simulation_config(
  prior_formulas = prior_formulas,
  between_trial_formulas = between_trial_formulas,
  item_formulas = item_formulas,
  n_conditions = 10,
  n_trials_per_condition = 10,
  n_items = 5,
  max_reached = 5,
  max_t = 10,
  dt = 0.01,
  noise_mechanism = "add",
  noise_factory = noise_factory,
  model = "ddm",
  parallel = FALSE
)

# Run simulation
sim_output <- run_simulation(config)

# Access results
dataset <- sim_output$open_dataset()
dataset # an arrow dataset object

# if you want to load it into memory, you can use:
df <- as.data.frame(dataset)
head(df)
```

```
# Access evaluated condition parameters
cond_dataset <- sim_output$open_evaluated_conditions()
df_cond <- as.data.frame(cond_dataset)
head(df_cond)
```

---

summarise_by *Summarise data by groups with optional pivoting*

Description

This function provides a flexible way to group data, compute summary statistics, and reshape results. It works similar to ‘dplyr::summarise()‘ but with added capabilities for pivoting results wider.

Usage

```
summarise_by(
  .data = NULL,
  ...,
  .by = c("condition_idx"),
  .wider_by = c("condition_idx")
)
```

Arguments

.data	A data frame to summarise, or NULL to create a reusable summary function
...	Summary expressions using dplyr-style syntax. Named arguments become column names in the output (e.g., ‘mean_rt = mean(rt)‘).
.by	Character vector of grouping column names. Default is "condition_idx".
.wider_by	Character vector of columns to keep as identifiers when pivoting. Default is "condition_idx". Must be a subset of ‘.by‘. When ‘.wider_by‘ differs from ‘.by‘, the extra columns in ‘.by‘ will be spread across as column suffixes.

Details

You can use ‘summarise_by()‘ in two ways: 1. **Direct use**: Pass your data directly and get results immediately 2. **Build-then-apply**: Create reusable summary functions, combine them with ‘+‘, then apply to your data later

The build-then-apply approach is useful when you want to compute different types of summaries (e.g., RT statistics and accuracy statistics) and automatically join them together.

Value

- If ‘.data‘ is provided: A data frame with summarised results - If ‘.data‘ is NULL: A function that can be applied to data later

Usage with ABC workflows

If you plan to use build_abc_input for ABC analysis, you must use summarise_by() to generate summary statistics (or manually handle the arrow output format). This function typically works together with map_by_condition to process simulation results. See map_by_condition for workflow examples.

Examples

```
# Example 1: Direct use - pass data and get results immediately
trial_data <- data.frame(
  condition_idx = rep(1:2, each = 4),
  item_idx = rep(1:2, 4),
  rt = c(0.5, 0.6, 0.7, 0.8, 0.55, 0.65, 0.75, 0.85),
  accuracy = c(1, 1, 0, 1, 1, 0, 1, 1)
)

# Compute mean RT and accuracy by condition and item
result <- summarise_by(
  trial_data,
  mean_rt = mean(rt),
  mean_acc = mean(accuracy),
  .by = c("condition_idx", "item_idx"),
  .wider_by = "condition_idx"
)
# Result has columns: condition_idx, mean_rt_item_idx_1, mean_rt_item_idx_2, etc.
result

# Example 2: Build-then-apply - create reusable summary functions
# Build separate summary functions for different statistics
rt_summary_pipe <- summarise_by(
  mean_rt = mean(rt),
  sd_rt = stats::sd(rt),
  .by = c("condition_idx", "item_idx"),
  .wider_by = "condition_idx"
)

acc_summary_pipe <- summarise_by(
  mean_acc = mean(accuracy),
  n_trials = length(accuracy),
  .by = c("condition_idx", "item_idx"),
  .wider_by = "condition_idx"
)

# Combine with + and apply to data
combined_summary_pipe <- rt_summary_pipe + acc_summary_pipe
result <- combined_summary_pipe(trial_data)
# Result has all summaries joined by condition_idx
result
```

summarise_posterior_parameters *Summarise posterior parameter distributions*

Description

Compute summary statistics (mean, median, confidence intervals) for posterior parameters from ABC results.

Usage

```
summarise_posterior_parameters(data, ...)

## S3 method for class 'abc'
summarise_posterior_parameters(data, ..., ci_level = 0.95)
```

Arguments

data	An abc object containing posterior samples in adj.values or unadj.values.
...	Additional arguments for custom summary functions. Functions passed as named arguments will be applied to each parameter's posterior samples.
ci_level	Numeric; confidence interval level (default: 0.95).

Value

A data frame with summary statistics for each parameter.

See Also

summarise_posterior_parameters.abc

Examples

```
# Load ABC output from saved file
abc_file <- system.file(
  "extdata", "rdm_minimal", "abc", "abc_rejection_model.rds",
  package = "eam"
)
abc_rejection_model <- readRDS(abc_file)

# Summarise posterior distributions
summarise_posterior_parameters(abc_rejection_model)

# Custom confidence interval level
summarise_posterior_parameters(abc_rejection_model, ci_level = 0.90)
```

summarise_resample_medians *Summarise resample medians*

Description

Calculate summary statistics for parameter medians across resample iterations. Returns mean, median, and confidence intervals of the median distributions.

Usage

```
summarise_resample_medians(data, ..., ci_level = 0.95)
```

Arguments

data	List of abc results from abc_resample
...	Additional custom summary functions (named functions)
ci_level	Confidence level for intervals (default 0.95)

Value

Data frame with summary statistics for each parameter

Examples

```
# Load ABC input data from example simulation
abc_input <- readRDS(
  system.file("extdata", "rdm_minimal", "abc", "abc_input.rds", package = "eam")
)

# Perform ABC resampling
results <- abc_resample(
  target = abc_input$target,
  param = abc_input$param,
  sumstat = abc_input$sumstat,
  n_iterations = 100,
  n_samples = 100,
  tol = 0.5,
  method = "rejection"
)

# summarise the resample medians
summary_stats <- summarise_resample_medians(results, ci_level = 0.95)
print(summary_stats)
```

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