

Package: adlaplace (via r-universe)

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Type Package

Title Laplace Approximations Using Automatic Differentiation

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Maintainer Patrick Brown <patrick.borgnine@gmail.com>

Description Computes Laplace-approximate maximum likelihood for hierarchical and latent Gaussian models. A formula interface specifies observation densities (e.g. Gaussian, negative Binomial), fixed effects, and random terms (independent effects, smoothing terms). Customized response distributions and models for random effects can be specified through a low-level interface or by writing interoperable packages. Derivatives are computed using automatic differentiation with 'CppAD', and used in trust region optimization to find modes of random effects. Derivatives of the Laplace approximation of the log-likelihood are computed using third order contractions and is compatible with custom atomics. The approach follows Kristensen, Nielsen, Berg, Skaug, and Bell (2016) <doi:10.18637/jss.v070.i05>.

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 'log_lik.R' 'fit.R' 'grad_obs_units.R' 'amip.R' 'deriv_scan.R'
 'dirichlet_multinom.R' 'effects.R' 'families.R' 'sim_fit.R'
 'fit_methods.R' 'fixed_terms.R' 'format_parameters.R'
 'germany-data.R' 'hessian_map.R' 'iid.R' 'iwp.R'
 'london-data.R' 'mvn_utils.R' 'prepare_model_rows.R' 'prior.R'
 'replace_vars.R' 'rpoly.R' 'sim_iid.R' 'takahashi_davis.R'
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<code>.model_role_levels</code>	<i>Valid model type factor levels</i>
---------------------------------	---------------------------------------

Description

Character vector of allowed levels for the `model_role` slot on `model_term` objects.

Usage

```
.model_role_levels
```

Value

A character vector of length 3, with elements "fixed", "random", and "response" in that order. These are the allowed levels of the `model_role` factor on `model_term` objects, indicating a fixed effect, a random effect, or the response.

<code>ad_pack</code>	<i>Build AD function with Hessian templates</i>
----------------------	---

Description

Build AD function with Hessian templates

Usage

```
ad_pack(
  x,
  config = NULL,
  num_threads = 1L,
  reorder_shards = c("none", "gradient", "hessian", "third"),
  templates = NULL,
  ...
)

## S4 method for signature 'ad_pack_ptr'
ad_pack(
  x,
  config = NULL,
  num_threads = 1L,
  reorder_shards = c("none", "gradient", "hessian", "third"),
  templates = NULL,
  ...
)
```

```

## S4 method for signature 'density_data'
ad_pack(
  x,
  config = NULL,
  num_threads = 1L,
  reorder_shards = c("none", "gradient", "hessian", "third"),
  templates = NULL,
  ...
)

## S4 method for signature 'list'
ad_pack(
  x,
  config = NULL,
  num_threads = 1L,
  reorder_shards = c("none", "gradient", "hessian", "third"),
  templates = NULL,
  ...
)

```

Arguments

x	One of: an <code>ad_pack_ptr</code> , an <code>density_data</code> shard with <code>ad_kind/ad_pack</code> set, or a <code>model_data()</code> bundle (list with observations, random, parameters).
config	Model configuration list. Required for <code>density_data</code> and <code>model_data</code> ; unused for <code>ad_pack_ptr</code> . For <code>model_data</code> , <code>beta</code> , <code>gamma</code> , and <code>theta</code> are filled from <code>x\$term_data\$info</code> when omitted (only shards, <code>transform_theta</code> , etc. are needed). When <code>config\$num_threads</code> is set, it overrides the <code>num_threads</code> argument for <code>density_data</code> and <code>model_data</code> methods. When <code>config\$reorder_shards</code> is set, it overrides <code>reorder_shards</code> . <code>config\$hessian_sparsity</code> (default <code>TRUE</code>) controls whether observation / parameter / random tapes discover and calibrate Hessian sparsity. Set <code>FALSE</code> for grad-only packs (usable with grad , not with inner_opt LDL / Hessian paths); see grad_obs_units . <code>config\$obs_hessian</code> is "analytic" (default) or "discover". Analytic builds the observation Hessian pattern from design co-occurrence (and ELGM strata for Dirichlet-multinomial) instead of CppAD for_hes_sparsity. Use "discover" as an escape hatch. When <code>config\$obs_groups</code> is missing and <code>config\$obs_units</code> is set (0-based unit indices), observation shards are built via obs_groups_units (see also ad_pack_drop).
num_threads	Positive integer; OpenMP thread count for <code>inner_opt</code> and parallel <code>trace_hinv_t</code> . Default 1L (serial).
reorder_shards	Character; how to assign OpenMP owner threads when <code>num_threads > 1</code> and there are multiple shards: "none" (default) uses <code>owner_thread = shard_index % num_threads</code> ; "gradient" times each shard's outer grad (..., inner = FALSE) (mean of 2; no warmup), then longest-processing-time (LPT) assignment; "hessian" times each shard's outer hessian (..., inner = FALSE) (1 warmup + mean of 2), then LPT; "third" times a Reverse3 sweep with dummy directions matching the symbolic <code>half_H_inv / trace_columns</code> sparsity (no numeric Cholesky), then LPT. Physical shard order is unchanged; only <code>owner_thread</code> is rewritten.

templates	Optional existing ad_pack whose Hessian templates (and group sparsity) are reused when the new pack has identical beta/gamma/theta sizes and the same number of shards. Useful when rebuilding packs for modular inference over exposure samples.
...	For ad_pack_ptr input, optional additional ad_pack_ptr shards to combine before attaching templates.

Value

Object of class ad_pack.

ad_pack-class	<i>AD function with Hessian templates attached</i>
---------------	--

Description

AD function with Hessian templates attached

Slots

ptr Raw combined handle (ad_pack_ptr).

group_sparsity Per-group inner gradient sparsity patterns.

outer Outer Hessian template (dgCMatrix).

inner Inner-gamma Hessian template (dgCMatrix).

map_outer Outer Hessian shard map.

map_inner Inner Hessian shard map.

parallel_map Thread-affinity map (ngCMatrix); rows are shards, columns are threads, with one nonzero per shard row.

chol_inner Symbolic LDL factor or empty sparse matrix.

chol_inner_list Numeric LDL list for C++ (L1, Linv, perm, perm_inv, half_H_inv, H_inv), plus trace_columns (per-shard column indices for trace_hinv_t) and hinv_q_index (per-shard slots of Q into H_inv, when a shard defines [hinv_trace_index](#)).

sizes Named numeric vector beta/gamma/theta.

info List of parameter metadata (beta, gamma, theta, parameters); populated from model_data()\$term_data\$info when the handle is built from a model-data bundle, otherwise empty.

ad_pack_drop	<i>Retape an AD pack after dropping observation units</i>
--------------	---

Description

Builds a new [ad_pack](#) on `fit$model_data` with observation shards filtered to the remaining units (same coarse sharding as `fit$config$obs_groups` when present). Random and parameter shards are retaped; reuse of the merged fit pack is not attempted.

Usage

```
ad_pack_drop(fit, drop, num_threads = NULL, verbose = FALSE)
```

Arguments

<code>fit</code>	An "adlaplace_fit" from adlaplace .
<code>drop</code>	Integer vector of **1-based** unit indices to remove.
<code>num_threads</code>	OpenMP thread count; default from <code>fit\$config</code> .
<code>verbose</code>	Logical; forwarded into the retape config.

Value

An `ad_pack` usable with [inner_opt](#) at the original outer MLE.

See Also

[obs_groups_units](#), [influence_scores](#), [amip_set](#)

ad_pack_ptr	<i>Build raw AD handle for one density shard</i>
-------------	--

Description

Constructs CppAD tapes for a single shard. The density kind and name come from `data@ad_kind` and `data@density`. For `ad_kind = "random"`, `data@precision` is passed straight to the backend. For `random_diagonal` it must be a numeric vector of diagonal precision weights with `length == ncol(gamma_map)`. For `random_mult` it must be `list(Q, log_det, rank)` where `Q` is a square `dsCMatrix` with `uplo = "U"` (upper triangle only); use `adlaplace:::as_dsC_upper(Q)` to coerce a `dgCMatrix`. Missing precision means the shard is not built (e.g. diffuse `rpoly` with `sd = Inf` via `model_data()`); calling `ad_pack_ptr()` without it is an error.

Usage

```
ad_pack_ptr(data, config = NULL, info = NULL)
```

Arguments

data	An density_data object with ad_kind and ad_pack slots set.
config	Model configuration list (beta, theta, etc.). gamma is optional; when missing, zeros of length nrow(gamma_map) are used as AD tape seeds. config\$num_threads does not assign OpenMP threads; use num_threads on ad_pack after merging shards. When info is supplied, missing beta / theta / gamma / transform_theta are filled from it; explicit config entries win. Missing gamma becomes zeros of length nrow(info\$gamma).
info	Optional model_data()\$term_data\$info list. When provided, tape seeds use info\$beta\$init and info\$theta\$init (the latter on the log scale where info\$theta\$log is TRUE); gamma defaults to zeros (info\$gamma has no init column).

Details

Merge handles for multiple shards with `c()` before calling [ad_pack](#).

Value

External pointer of class `ad_pack_ptr`.

ad_pack_ptr-class	<i>Raw AD handle (external pointer)</i>
-------------------	---

Description

S4 class for a C++ AD backend handle. Objects are created by [ad_pack_ptr](#), combined with [c.ad_pack_ptr](#), and typically passed to [ad_pack](#) to attach Hessian templates.

See Also

[ad_pack_ptr](#), [ad_pack](#), [clone_ad_pack_ptr](#)

ad_pack_set_X	<i>Rebuild an ad_pack for a new model-data design</i>
---------------	---

Description

Covariate values in observation X_{Tp} are baked into CppAD tapes at build time, so they cannot be mutated in place. This helper retapes a new model_data bundle and reuses Hessian templates from ad_pack whenever sizes and shard counts match (identical sparsity across exposure samples). Prefer building a list of packs once for modular inference rather than calling this inside every likelihood evaluation.

Usage

```
ad_pack_set_X(
  ad_pack,
  model_data,
  config = list(),
  num_threads = 1L,
  reorder_shards = c("none", "gradient", "hessian", "third")
)
```

Arguments

ad_pack	Existing ad_pack whose templates may be reused.
model_data	A model_data() bundle with the same random-effect structure and (typically) a different fixed-effect design matrix.
config	Configuration list passed to ad_pack .
num_threads, reorder_shards	Forwarded to ad_pack .

Value

A new ad_pack.

See Also

[ad_pack](#), [replace_vars](#)

adlaplace	<i>Fit a hierarchical model by Laplace-approximate maximum likelihood</i>
-----------	---

Description

One-call interface to the **adlaplace** pipeline: parse the formula with [model_data\(\)](#), partition observations into AD shards with [obs_groups\(\)](#), build the AD handle with [ad_pack\(\)](#), maximize the Laplace-approximate marginal likelihood with [optim\(\)](#) using the exact profile gradient ([outer_fn](#) / [outer_gr](#)), and return a fitted-model object with standard accessor methods.

Usage

```
adlaplace(
  formula,
  data,
  config = list(),
  control = list(),
  control_inner = list(maxit = 100L, report.level = 0, report.freq = 0),
  method = "L-BFGS-B",
  hessian = NULL,
```

```

    start = NULL,
    verbose = FALSE,
    na_omit = TRUE
  )

```

Arguments

formula	Model formula built from model terms, e.g. <code>nbinom(y) ~ x + iid(g)</code> , a list of term objects from <code>collect_terms</code> , or a precomputed <code>model_data</code> result (in which case data is ignored).
data	Data frame containing the variables referenced in formula. Not needed when formula is already a <code>model_data</code> result.
config	List of backend options merged over the defaults <code>list(transform_theta = TRUE, verbose = verbose, num_threads = 1L, num_shards = 100L)</code> . When <code>config\$obs_groups</code> is missing it is filled by <code>obs_groups(A, num_shards = config\$num_shards)</code> , or with <code>elgm_matrix</code> when the model data includes one (e.g. case-crossover). <code>config\$num_threads</code> is the OpenMP thread count for the AD handle; <code>config\$num_shards</code> is the target number of observation shards for <code>obs_groups()</code> .
control	List of <code>optim</code> control options, merged over the defaults <code>list(maxit = 200L, parscale = <from terms>)</code> .
control_inner	List of control options for the inner (random effects) trust-region optimizer.
method	<code>optim</code> method; bounds are used for "L-BFGS-B" and "Brent" only.
hessian	Logical. When NULL (default), set to TRUE if there are at most five outer parameters and FALSE otherwise. When TRUE, <code>optimHess</code> numerically differentiates the exact AD profile gradient at the optimum, giving the observed information used by <code>vcov.adlaplace_fit</code> , <code>summary.adlaplace_fit</code> , and <code>confint.adlaplace_fit</code> .
start	Optional numeric vector of outer starting values <code>c(beta, theta)</code> on the <i>internal</i> (log-theta) scale, length <code>nrow(par_info)</code> . When NULL (default), term init values are used.
verbose	Logical, print progress.
na_omit	Passed to <code>model_data()</code> .

Value

An object of class "adlaplace_fit": a list with components

call, formula The matched call and model formula.

par_info Parameter table with `mle`, `se`, `mle_internal`, `se_internal`, `bounds`, and `log`.

gamma Named random-effect modes at the optimum.

nobs Number of observations.

details Laplace evaluation at the optimum, including `outer_opt`, `inner_opt`, `vcov`, `log_lik`, `gradient`, and `hessian`.

model_data, ad_pack, config, cache Objects needed by the accessor methods and for warm restarts.

If `optim` throws (for example L-BFGS-B when `fn` is not finite), the same class is returned with `par_info` estimates set to NA, `details$outer_opt` = NULL, and `details$error` set to the condition message. `ad_pack` and `cache` are still present so the Laplace objective can be inspected or re-run without rebuilding tapes:

```
stats::optim(
  fit$cache$last_par_fn,
  fn = adlaplace::outer_fn, gr = adlaplace::outer_gr,
  method = fit$method, control = fit$control,
  lower = fit$par_info$lower, upper = fit$par_info$upper,
  config = fit$config, ad_pack = fit$ad_pack,
  cache = fit$cache, control_inner = fit$control_inner
)
```

See Also

[summary.adlaplace_fit](#), [predict.adlaplace_fit](#), [log_lik_laplace](#), [model_data](#), [fit_outer](#)

Examples

```
set.seed(1)
n <- 80
g <- factor(sample(4, n, replace = TRUE))
x <- rbinom(n, 1, 0.5)
eta <- 0.5 + 0.4 * x + rnorm(4, sd = 0.3)[g]
nb_sd <- 0.3
z <- rgamma(n, nb_sd^(-2), nb_sd^(-2))
dat <- data.frame(y = rpois(n, exp(eta) * z), x = x, g = g)
md <- model_data(
  nbinom(y, lower = 1e-9, init = 0.15) ~ x + iid(g, init = 0.3),
  data = dat
)
config <- list(
  transform_theta = TRUE,
  obs_groups = obs_groups(md$term_data$A, num_shards = 5),
  verbose = FALSE
)
ap <- ad_pack(md, config)
cache <- new.env(parent = emptyenv())
x0 <- md$term_data$info$parameters$init
outer_fn(x = x0, config = config, cache = cache, ad_pack = ap)
outer_gr(x = x0, config = config, cache = cache, ad_pack = ap)

fit <- adlaplace(md, config = list(num_shards = 5L, verbose = FALSE))
summary(fit)
confint(fit)
```

adlaplace_cpp	C++ backend entry points
---------------	--------------------------

Description

Low-level entry points exposed to R. Accept an `ad_pack` S4 object (via `@ptr`) or a raw `ad_pack_ptr`.

Usage

```
joint_log_dens(ad_pack, x, ad_shards = NULL, negative = TRUE)

grad(ad_pack, x, ad_shards = NULL, inner = FALSE, negative = TRUE)

hessian(
  ad_pack,
  x,
  ad_shards = NULL,
  inner = FALSE,
  verbose = FALSE,
  negative = TRUE
)

trace_hinv_t(ad_pack, x, LinvPt, LinvPtColumns, verbose = FALSE, H_inv = NULL)

fun_obj_fdfh(ad_pack, parameters, gamma, inner = TRUE, verbose = FALSE)
```

Arguments

<code>ad_pack</code>	An <code>ad_pack</code> S4 object or <code>ad_pack_ptr</code> handle.
<code>x</code>	Numeric parameter vector of length <code>Nparams</code> .
<code>ad_shards</code>	Optional integer vector of 0-based shard indices; <code>NULL</code> or <code>integer(0)</code> evaluates all shards.
<code>negative</code>	Logical (default <code>TRUE</code>). If <code>TRUE</code> , return the **negative** log density $-\ell(x)$ and its derivatives (minimization / trustOptim sign, consistent with <code>inner_opt()</code>). If <code>FALSE</code> , return $\ell(x)$, $\nabla\ell$, and $\nabla^2\ell$.
<code>inner</code>	Logical; if <code>TRUE</code> , evaluate inner- γ derivatives; if <code>FALSE</code> , evaluate outer derivatives at the full parameter vector.
<code>verbose</code>	Logical; if <code>TRUE</code> , print threads, shards, and CppAD session phases.
<code>LinvPt, LinvPtColumns</code>	Sparse factors for <code>trace_hinv_t()</code> .
<code>H_inv</code>	Optional numeric values of the joint inverse Hessian, in the nonzero order of <code>chol_inner_list\$H_inv</code> . A sparse matrix contributes its <code>@x</code> slot. <code>NULL</code> keeps every shard on the column walk.
<code>parameters</code>	Numeric vector of length <code>Nbeta + Ntheta</code> .
<code>gamma</code>	Numeric vector of length <code>Ngamma</code> .

Value

See individual functions.

Sign convention

With default `negative = TRUE`, `joint_log_dens()`, `grad()`, and `hessian()` match `inner_opt()` (negative log-density). Set `negative = FALSE` for the joint log density and its derivatives at the same `x`.

Thread affinity

These are **serial debug** APIs. They error if the handle was built with `ad_pack(..., num_threads > 1)`. Use a plain `ad_pack_ptr` (or `ad_pack(..., num_threads = 1)`), or `clone_ad_pack_ptr()` before assigning multi-thread affinity. Parallel evaluation uses `fun_obj_fdfh/inner_opt/log_lik_laplace` on the affined handle.

adlaplace_fit-methods *Methods for fitted adlaplace models*

Description

Standard accessor methods for objects of class "adlaplace_fit" returned by `adlaplace()`. Estimates are stored on the optimization scale (log scale for parameters with `par_info$log = TRUE`, e.g. standard deviations); methods with a `transform` argument report the natural scale by exponentiating and, for standard errors, applying the delta method.

Usage

```
## S3 method for class 'adlaplace_fit'
coef(object, transform = TRUE, ...)

## S3 method for class 'adlaplace_fit'
vcov(object, transform = FALSE, ...)

## S3 method for class 'adlaplace_fit'
logLik(object, ...)

## S3 method for class 'adlaplace_fit'
nobs(object, ...)

## S3 method for class 'adlaplace_fit'
confint(object, parm, level = 0.95, transform = TRUE, ...)

## S3 method for class 'adlaplace_fit'
fitted(object, ...)
```

```
## S3 method for class 'adlaplace_fit'
```

```

predict(object, newdata, n = 500L, ...)

## S3 method for class 'adlaplace_fit'
print(x, digits = max(3L, getOption("digits") - 3L), ...)

## S3 method for class 'adlaplace_fit'
summary(object, level = 0.95, ...)

## S3 method for class 'summary.adlaplace_fit'
print(x, digits = max(3L, getOption("digits") - 3L), ...)

## S3 method for class 'adlaplace_fit'
plot(x, k = 200L, draws = 100L, ...)

```

Arguments

<code>object, x</code>	An <code>adlaplace_fit</code> object.
<code>transform</code>	Logical; report transformed (natural-scale) values.
<code>...</code>	Passed to downstream methods.
<code>parm</code>	Optional subset of parameter labels or indices.
<code>level</code>	Confidence level.
<code>newdata</code>	Data frame of prediction covariates.
<code>n</code>	Number of random-effect draws for predict.
<code>digits</code>	Number of significant digits to print.
<code>k</code>	Number of evaluation points per smooth term in plot.
<code>draws</code>	Number of simulation draws per smooth term in plot.

Details

`predict` draws random effects from the Laplace (Gaussian) approximation at the mode via `sim_fit` and returns the linear predictor on `newdata`: a `nrow(newdata)` by `n` matrix of simulated values (plus fixed-effect contributions from terms whose variables appear in `newdata`). Without `newdata` it returns `fitted(object)`.

`plot` draws each smooth term (terms with more than one knot) on a grid spanning its knots, showing simulated curves from the Laplace approximation with the pointwise mean in red. With no smooth terms it plots the random-effect modes.

Value

`coef` Named numeric vector of outer parameter estimates. With `transform = TRUE` (the default), parameters stored on the log scale (for example standard deviations) are exponentiated to the natural scale.

`vcov` Variance-covariance matrix of the outer parameters on the optimization scale. With `transform = TRUE`, rows and columns for log-scale parameters are mapped to the natural scale by the delta method.

logLik An object of class "logLik": the Laplace-approximate marginal log-likelihood, with attributes `df` (number of outer parameters) and `nobs`.

nobs Integer number of observations.

confint Numeric matrix of Wald intervals, one row per outer parameter. With `transform = TRUE`, endpoints for log-scale parameters are exponentiated to the natural scale.

fitted Numeric vector of length `nobs`: the linear predictor at the joint mode of the fixed effects and random effects.

predict Without `newdata`, the same vector as `fitted`. With `newdata`, a matrix with `nrow(newdata)` rows and `n` columns of linear predictors drawn from the Laplace approximation to the random effects.

summary A list of class "summary.adlaplace_fit" with the coefficient table (natural-scale estimates, standard errors, and interval endpoints), the log-likelihood, degrees of freedom, the number of observations and random effects, the outer optimizer convergence code, and the maximum absolute profile gradient.

print, print.summary, plot No return value used by the caller. They print or draw and return the input object invisibly. `plot` draws each smooth term as curves simulated from the Laplace approximation, with the pointwise mean highlighted, or the random-effect modes when the model has no smooth term.

aghq_ff

*Build **aghq** objective list from an adlaplace fit*

Description

Returns `list(fn, gr, he)` suitable for [aghq](#), closing over the fitted AD handle and cache. The wrappers return the *negated* Laplace-approximate log posterior (same convention as [outer_fn](#) / [outer_gr](#)), so call `aghq::default_control(negate = TRUE)`.

Usage

```
aghq_ff(fit, control_inner = NULL)
```

Arguments

fit An "adlaplace_fit" from [adlaplace](#).

control_inner Inner trust-region control list; defaults to `fit$control_inner` when present, otherwise a quiet short run.

Value

A list with `fn`, `gr`, and `he`. The Hessian is a numerical Jacobian of `gr` (no AD outer Hessian is available).

See Also

[outer_fn](#), [outer_gr](#), [adlaplace](#)

amip_set

*Approximate most influential removal set (AMIP)***Description**

Greedy rule: drop units with the largest scores of the same sign as ϕ until $\sum_{u \in S} \psi_u$ matches the sign of ϕ and $|\sum| \geq |\phi|$. Leaving out S changes ϕ by approximately $-\sum \psi_S$.

Usage

```
amip_set(psi, phi)
```

Arguments

psi Numeric vector of per-unit scores (e.g. from [influence_scores](#)).
phi Scalar quantity of interest at the full-data mode.

Value

A list with `idx` (1-based indices to drop), `alpha` (fraction of units), and `approx_change`. If the linear approximation cannot flip the sign, `idx` is empty and `alpha` is NA.

See Also

[influence_scores](#), [ad_pack_drop](#)

apply_theta_log

*Apply log transform to selected theta columns***Description**

When `active` is TRUE, logs values in `cols` for rows where `theta_info$log` is TRUE. Missing or NA log entries default to TRUE.

Usage

```
apply_theta_log(theta_info, cols = "init", active = TRUE)
```

Arguments

theta_info Data frame from `info$theta` (see [term_data_setup](#)).
cols Character vector of column names to transform (e.g. "init").
active Logical; when FALSE, returns `theta_info` unchanged.

Value

A copy of `theta_info` with selected entries logged.

binomial-class	<i>Binomial observation term</i>
----------------	----------------------------------

Description

Model term for the observation-level binomial log density with a logit link, registered as `binomial_obs`. For each observation with linear predictor $\eta = X\beta + A\gamma$, trial count N , and success count y , the log density contribution is $y * \eta - N * \log(1 + \exp(\eta))$ (up to a data-only constant). When `size` is omitted, $N = 1$ (Bernoulli). There are no observation-level hyperparameters.

Creates a response term wired to the `binomial_obs` AD shard. A Bernoulli likelihood (`size` omitted) has no observation-level hyperparameters. With `size`, trial counts are read from that column of data and stored as observation weights.

Usage

```
binom(x, size = NULL)
```

Arguments

<code>x</code>	Outcome variable name (counts of successes; 0/1 when Bernoulli).
<code>size</code>	Optional column name for the number of trials per observation.

Details

Binomial observation model term

Value

A binomial object.

Slots (inherited from model)

<code>ad_pack</code>	Character scalar "binomial_obs".
<code>ad_kind</code>	Character scalar "observations".

Slots

<code>size</code>	Optional column name for per-observation trial counts.
-------------------	--

by_group	<i>By-Group Classes and Functions</i>
----------	---------------------------------------

Description

Functions for creating and managing by_group objects for hierarchical model grouping information.

Usage

```
by_group(term, data = NULL, levels = NULL)
```

Arguments

term	Character, the grouping variable name
data	A data frame. If provided and levels is missing, unique values are extracted from data[[term]]
levels	Character vector of unique levels for the grouping variable. If missing and data is provided, unique values are extracted from data[[term]]

Value

A by_group object

Examples

```
# Create with explicit levels
bg <- by_group(term = "group", levels = c("A", "B", "C"))

# Create from data
dat <- data.frame(group = c("A", "B", "A", "C"))
bg <- by_group(term = "group", data = dat)
```

by_group-class	<i>By-Group Class</i>
----------------	-----------------------

Description

A class for grouping information in hierarchical model terms. Contains the grouping variable name and its levels/labels.

Slots

term	Character vector of length 1, the grouping variable name
levels	Character vector of unique levels for the grouping variable
labels	Character vector of formatted labels for the levels

c.ad_pack_ptr	<i>Combine ad_pack_ptr handles</i>
---------------	------------------------------------

Description

Moves AD shards from one or more `ad_pack_ptr` objects into a single handle. Inputs are cleared after the merge (ownership moves).

Usage

```
## S3 method for class 'ad_pack_ptr'
c(x, ...)
```

Arguments

x	An <code>ad_pack_ptr</code> .
...	Additional <code>ad_pack_ptr</code> objects.

Value

A combined `ad_pack_ptr`.

See Also

[clone_ad_pack_ptr](#), [ad_pack](#)

clone_ad_pack_ptr	<i>Deep copy of an ad_pack_ptr handle</i>
-------------------	---

Description

Returns a new `ad_pack_ptr` with independent C++ state (CppAD tapes and sparsity patterns). Hessian templates are not copied; call [ad_pack](#) on the clone to attach maps. The source handle is left unchanged, unlike [c.ad_pack_ptr](#) which moves shards and clears the inputs. OpenMP thread affinity from a prior `ad_pack(..., num_threads > 1)` is cleared on the clone so [joint_log_dens](#) / [grad](#) / [hessian](#) remain available as serial debug APIs.

Usage

```
clone_ad_pack_ptr(x)
```

Arguments

x	An <code>ad_pack_ptr</code> object.
---	-------------------------------------

Value

A new `ad_pack_ptr`.

collect_terms	<i>Parse Model Terms from Formula</i>
---------------	---------------------------------------

Description

Parses a formula and creates model terms by evaluating constructor calls in the formula environment (so `pkg::term(...)` and terms from attached packages on the search path work). Falls back to the **adlplace** namespace for built-in constructors.

Usage

```
collect_terms(formula, verbose = FALSE)
```

Arguments

formula	Model formula with constructor terms (e.g. <code>iwp(x, ...)</code> , <code>iid(fac)</code> , <code>nbinom(y, ...)</code> on the LHS). Bare symbols such as <code>x</code> are coerced to <code>linear(x)</code> . Unnamed first positional symbols are treated as column names in data; named arguments (e.g. <code>x = sites</code> for spatial terms) are evaluated as objects in the formula environment. The named argument <code>size</code> is also treated as a column name when passed as a symbol (<code>binom(y, size = N)</code>).
verbose	print extra information

Value

List of model term objects

density_data-class	<i>Per-shard layout for AD density evaluation</i>
--------------------	---

Description

Per-shard layout for AD density evaluation

Usage

```
density_data(
  y = missing(),
  A = NULL,
  X = NULL,
  beta_map = NULL,
  gamma_map = NULL,
  theta_map = NULL,
  elgm_matrix = NULL,
  density = NA_character_,
```

```

    ad_kind = NA_character_,
    package = NA_character_,
    precision = NULL,
    weights = numeric(0)
  )

```

Arguments

<code>y</code>	Response vector (default empty), or an existing <code>density_data</code> object to recast as another shard.
<code>A</code>	Random-effects design matrix (<code>nrow(A) = length(y)</code> ; any <code>Matrix</code> class).
<code>X</code>	Fixed-effects design matrix (<code>nrow(X) = length(y)</code> ; any <code>Matrix</code> class).
<code>beta_map</code>	Beta parameter map (any <code>Matrix</code> ; coerced to <code>ngCMatrix</code>), or a shorthand: <code>length-1</code> integer <code>n</code> gives <code>Matrix::Matrix(nrow = n, ncol = 0)</code> ; <code>length-2</code> <code>c(row, n)</code> gives one column with a structural 1 at row <code>row</code> (1-based); and <code>list(indices, n)</code> gives one column per entry in <code>indices</code> with structural 1s at those rows. <code>nrow</code> is the global beta block size; column <code>j</code> maps local <code>X</code> column <code>j</code> to a global beta row. When <code>ncol(X) > 0</code> , <code>ncol(beta_map)</code> must equal <code>ncol(X)</code> with exactly one nonzero per column. If <code>NULL</code> , defaults to <code>Matrix::Diagonal(ncol(X))</code> when <code>ncol(X) > 0</code> , otherwise an empty matrix.
<code>gamma_map</code>	Gamma parameter map (any <code>Matrix</code> ; coerced to <code>ngCMatrix</code> ; at most one nonzero per row and column), or the same shorthand forms as <code>beta_map</code> . Column <code>j</code> maps local <code>A</code> column <code>j</code> into the global gamma block. When <code>ncol(A) > 0</code> , <code>ncol(gamma_map)</code> must equal <code>ncol(A)</code> with exactly one nonzero per column. If <code>NULL</code> , defaults to <code>Matrix::Diagonal(ncol(A))</code> when <code>ncol(A) > 0</code> , otherwise an empty matrix.
<code>theta_map</code>	Theta parameter map (any <code>Matrix</code> ; coerced to <code>ngCMatrix</code>), or the same shorthand forms as <code>beta_map</code> . Column <code>j</code> selects global theta row for component <code>j</code> . If <code>NULL</code> , defaults to an empty matrix.
<code>elgm_matrix</code>	Optional ELGM map (any <code>Matrix</code> ; coerced to <code>ngCMatrix</code>). If <code>NULL</code> , defaults to <code>Matrix::Matrix(nrow = length(y), ncol = 0)</code> .
<code>density</code>	Registered AD density name for this shard (optional).
<code>ad_kind</code>	Shard kind ("observations", "parameters", "random"; optional).
<code>package</code>	Package recording AD tapes for this shard (optional).
<code>precision</code>	Optional precision payload (any R object). For <code>density = "random_mult"</code> , a list with <code>Q</code> as <code>dsCMatrix(uplo = "U")</code> ; <code>dgCMatrix</code> is coerced via <code>as_dsC_upper()</code> .
<code>weights</code>	Optional per-observation weights (e.g. binomial trial counts). Empty means all ones.

Value

An S4 object of class "density_data": one automatic-differentiation shard. Slots hold the response, the transposed fixed- and random-effect design blocks, the maps from local design columns into the global parameter vectors, the registered density name, and the shard kind ("observations", "parameters", or "random").

Functions

- `density_data()`: Construct a `density_data` object

Slots

`y` Response vector.

`ATp` Transpose of random-effects design matrix.

`XTp` Transpose of fixed-effects design matrix.

`beta_map` Beta parameter map (`ngCMatrix`). `nrow` is the global beta block size; column `j` has one structural nonzero at row `r` meaning local design column `j` of `X` uses global beta `r`. When `ncol(X) > 0`, require `ncol(beta_map) == ncol(X)`.

`gamma_map` Gamma parameter map (`ngCMatrix`); at most one structural nonzero per row and column. Same column convention as `beta_map` for local A columns into the global gamma block.

`theta_map` Theta parameter map (`ngCMatrix`). Column `j` selects global theta row `r` for this shard's theta component `j`.

`elgm_matrix` Optional exposure-lag map (`ngCMatrix`; empty by default).

`density` Registered AD density name for this shard.

`ad_kind` Shard kind ("observations", "parameters", "random").

`package` Package name whose shared library records tapes for this shard (defaults to "adlaplace" when missing).

`precision` Optional precision payload (any R object).

`weights` Optional per-observation weights (e.g. binomial trial counts). Empty means all ones.

`deriv_scan_joint`

Scan joint log-density AD derivatives vs finite differences

Description

Evaluates the joint log density and its AD gradient/Hessian while varying one coordinate of the full parameter vector (`beta`, `gamma`, `theta`). Returns plain matrices shaped for `matplot()`/`matlines()`.

Usage

```
deriv_scan_joint(
  ad_pack,
  x,
  index,
  width = 0.1,
  n = 11L,
  ad_shards = NULL,
  negative = FALSE
)
```

Arguments

ad_pack	An ad_pack object (typically with num_threads = 1).
x	Numeric full parameter vector.
index	Integer (1-based) coordinate of x to vary.
width	Half-width of the scan interval around x[index].
n	Integer number of grid points (default 11).
ad_shards	Optional 0-based shard indices passed to joint_log_dens / grad / hessian .
negative	Logical; passed through to the joint-density evaluators.

Value

A list with:

grid	Coordinate values (length n).
mid	Midpoints for finite differences (length n - 1).
value	Joint density along the grid.
fd_value	Midpoint differences of value.
grad	n x length(x) matrix of AD gradients (rows = grid).
fd_grad	(n-1) x length(x) midpoint slopes of grad.
hess_row	n x length(x) AD Hessian rows for index.

deriv_scan_laplace	<i>Scan Laplace profile AD derivatives vs finite differences</i>
--------------------	--

Description

Evaluates [log_lik_laplace](#)(deriv = TRUE) while varying one coordinate of the outer parameter vector (beta, theta only; gammas are profiled out). Returns plain matrices shaped for [matplot\(\)](#)/[matlines\(\)](#).

Usage

```
deriv_scan_laplace(
  ad_pack,
  x,
  index,
  width = 0.5,
  n = 7L,
  config = list(),
  gamma = NULL,
  control = list(maxit = 100L, report.level = 0, report.freq = 0)
)
```

Arguments

ad_pack	An ad_pack object.
x	Numeric outer parameter vector (length beta + theta).
index	Integer (1-based) coordinate of x to vary.
width	Half-width of the scan interval around x[index].
n	Integer number of grid points (default 7).
config	Config list passed to log_lik_laplace.
gamma	Optional gamma start for the inner optimization.
control	Inner-optimization control list.

Value

A list with:

grid	Coordinate values (length n).
mid	Midpoints for finite differences.
value	Negative log likelihood along the grid.
fd_value	Midpoint differences of value.
grad	n x length(x) AD profile gradients.
fd_grad	Midpoint slopes of grad.
half_log_det	Half log-determinant along the grid.
d_det	AD derivative of the half log-determinant wrt outer params.
fd_det	Midpoint differences of half_log_det.
u_hat	n x n_gamma inner modes.
dU_index	n x n_gamma AD dU slices for index.
fd_u	Midpoint slopes of u_hat.
mid_result	Full log_lik_laplace result at the middle grid point.

dirichlet_multinom	<i>Dirichlet-multinomial case-crossover response term</i>
--------------------	---

Description

Dirichlet-multinomial case-crossover response term

Usage

```
dirichlet_multinom(
  x,
  by,
  init = 0.001,
  lower = 0,
  upper = Inf,
  parscale = 1,
  log = TRUE
)
```

Arguments

x	Outcome variable name.
by	Character vector of stratification variables (e.g. c("year", "month", "dow")).
init	Initial value for overdispersion sd.
lower	Lower bound for sd.
upper	Upper bound for sd.
parscale	Parameter scale for optimization.
log	Whether theta is optimized on the log scale.

Value

A dirichlet_multinom object.

dirichlet_multinom-class

Dirichlet-multinomial response term

Description

Model term for the case-crossover Dirichlet-multinomial log density registered as dirichlet_multinomial.

Usage

```
## S4 method for signature 'dirichlet_multinom'
elgm_matrix(term, data)
```

```
## S4 method for signature 'dirichlet_multinom'
design(term, data)
```

```
## S4 method for signature 'dirichlet_multinom'
precision(term, data)
```

```
## S4 method for signature 'dirichlet_multinom'
```

```

theta_info(term)

## S4 method for signature 'dirichlet_multinom'
beta_info(term, data)

## S4 method for signature 'dirichlet_multinom'
random_info(term, data)

```

Arguments

<code>term</code>	A <code>dirichlet_multinom</code> term object.
<code>data</code>	Analysis-ready data frame.

Details

Dirichlet-multinomial case-crossover response term

Value

Sparse `ngCMatrix` mapping observations to strata columns.

Functions

- `elgm_matrix(dirichlet_multinom)`: Case-crossover stratum map for AD shards.
- `design(dirichlet_multinom)`: Design method (not used).
- `precision(dirichlet_multinom)`: Precision method (not used).
- `theta_info(dirichlet_multinom)`: Theta info for overdispersion sd.
- `beta_info(dirichlet_multinom)`: Beta info method (not used).
- `random_info(dirichlet_multinom)`: Random info method (not used).

Slots

`by` Character vector of stratification variables for the case-crossover design.

Slots (inherited from `model`)

`ad_pack` Character scalar "dirichlet_multinomial".
`ad_kind` Character scalar "observations".
`package` Character scalar "adlplace".

fit_outer

*Outer optimization scaffolding for Laplace profile likelihoods***Description**

Runs [optim](#) on a user-supplied outer objective / gradient (typically [outer_fn](#) / [outer_gr](#), or a modular average of several packs) and returns the standard `par_info` / `vcov` / `opt` structure used by [adlaplace](#).

Usage

```
fit_outer(
  fn,
  gr,
  par_meta,
  method = "L-BFGS-B",
  control = list(),
  hessian = FALSE,
  start = NULL,
  ...
)
```

Arguments

<code>fn, gr</code>	Objective and gradient functions with signature <code>function(par, ...)</code> .
<code>par_meta</code>	Data frame of outer-parameter metadata with columns <code>label</code> , <code>init</code> , <code>lower</code> , <code>upper</code> , <code>parscale</code> , <code>log</code> (as produced by <code>model_data()</code> \$ <code>term_data</code> \$ <code>info</code> \$ <code>parameters</code>).
<code>method</code>	optim method.
<code>control</code>	Control list for <code>optim</code> .
<code>hessian</code>	Logical; compute a numerical outer Hessian via optimHess when TRUE.
<code>start</code>	Optional starting values on the internal scale; defaults to <code>par_meta\$init</code> .
<code>...</code>	Extra arguments forwarded to <code>fn</code> / <code>gr</code> / <code>optimHess</code> (e.g. <code>config</code> , <code>ad_pack</code> , <code>cache</code> , <code>control_inner</code>).

Value

A list with components `opt`, `par_info`, `vcov`, and `error` (character message when `optim` fails, otherwise NULL).

See Also

[adlaplace](#), [outer_fn](#)

format_parameters	<i>Format Laplace estimates using parameter metadata</i>
-------------------	--

Description

Maps flat Laplace parameter vectors onto labeled tables from info (as stored on ad_pack@info or model_data()\$term_data\$info).

Usage

```
format_parameters(
  info,
  full_parameters = NULL,
  parameters = NULL,
  gamma = NULL
)
```

Arguments

info	List with beta, gamma, theta, and parameters data frames.
full_parameters	Numeric vector c(beta, gamma, theta). When supplied, parameters and gamma are ignored.
parameters	Numeric outer vector c(beta, theta); used when full_parameters is NULL.
gamma	Numeric inner vector; used when full_parameters is NULL.

Value

A list with data frames parameters and gamma, or list() when info is missing or incomplete.

fpoly-class	<i>Fixed Polynomial Model Term</i>
-------------	------------------------------------

Description

Creates and manages fixed polynomial model terms.

Usage

```
fpoly(
  x,
  p = 2,
  ref_value = 0,
  init = .my_beta_init,
  lower = .my_beta_lower,
```

```

    upper = .my_beta_upper,
    parscale = .my_beta_parscale,
    basis_scale = 1
)

## S4 method for signature 'fpoly'
design(term, data)

## S4 method for signature 'fpoly'
beta_info(term, data)

```

Arguments

x	Variable name.
p	Polynomial degree (default: 2).
ref_value	Reference value for the polynomial.
init	Initial values for beta parameters.
lower	Lower bounds for beta parameters.
upper	Upper bounds for beta parameters.
parscale	Parameter scales for optimization.
basis_scale	Positive scale for the covariate. Column k of the raw polynomial is divided by basis_scale^k . <code>iw</code> passes the mean knot spacing when the polynomial is the fixed part of an IWP.
term	A 'fpoly' term object.
data	A data frame containing the variables used in the term.

Value

A 'fpoly' term object.

A design matrix for the fixed polynomial term, or NULL if p.order is 0.

A data frame containing beta parameter information for the fixed polynomial term.

Functions

- `design(fpoly)`: Design method for fpoly objects
- `beta_info(fpoly)`: Beta info method for fpoly objects

Methods

The following methods are available for 'fpoly' objects:

```

design(term, data)  Creates design matrix for fpoly term
precision(term, data)  Creates precision matrix for fpoly term
theta_info(term)  Extracts theta parameter information
beta_info(term, data)  Extracts beta parameter information
random_info(term, data)  Extracts random effects information

```

Examples

```
# Create a fixed polynomial term
fpoly_term <- fpoly(x = "temp", p = 3, ref_value = 15)
```

gamm	<i>Example GAMM simulation data</i>
------	-------------------------------------

Description

Simulation data for the GAMM vignette example.

Format

A data frame `dat` with 500 rows and columns from `mgcv::gamSim(6, n = 500)`, plus simulated negative-binomial responses used in the GAMM vignette (`y`, `f2`, `mu`, `Z`, etc.).

Source

Generated with `mgcv::gamSim()` and a custom negative-binomial response; see the regeneration comments in `vignettes/gamm.Rmd`.

Examples

```
data("gamm", package = "adlplace")
exists("dat")
nrow(dat)
```

gaussian-class	<i>Gaussian observation term</i>
----------------	----------------------------------

Description

Model term for the observation-level Gaussian log density registered as `gaussian_obs`. This is the default observation term: a bare response symbol on the left-hand side of a formula (e.g. `y ~ x`) is coerced to `normal(y)` by `collect_terms`.

Creates a response term wired to the `gaussian_obs` AD shard, with a single residual standard deviation parameter (log scale during optimization).

Usage

```
normal(
  x,
  init = 1,
  lower = .my_theta_lower,
  upper = .my_theta_upper,
  parscale = .my_theta_parscale,
  log = TRUE
)

## S4 method for signature 'gaussian'
theta_info(term)
```

Arguments

x	Outcome variable name.
init	Initial value for the residual standard deviation.
lower	Lower bound for the residual standard deviation.
upper	Upper bound for the residual standard deviation.
parscale	Parameter scale for optimization.
log	Whether theta is optimized on the log scale.
term	A model term object (S4 methods).

Details

Gaussian observation model term

Value

A gaussian object.

Functions

- `theta_info(gaussian)`: Theta info for the residual standard deviation.

Slots (inherited from model)

`ad_pack` Character scalar "gaussian_obs".
`ad_kind` Character scalar "observations".

germany

*Germany oral cavity cancer (Besag-York-Mollie example)***Description**

Disease-mapping data distributed with **INLA** (Besag, York, and Mollie 1991). Counts y_i in 544 districts follow $y_i \sim \text{Poisson}(E_i e^{\eta_i})$ with a BYM spatial random effect. The bundled ICAR precision `Q_scaled` is the INLA `scale.model` version with sum-to-zero constraint; `prec` is the `random_mult` precision payload (`Q`, `log_det`, `rank`).

Usage

```
germany
```

Format

A list with:

Y Observed case counts (length 544).

E Expected counts (length 544).

region District index (length 544).

adj District adjacency matrix (`dgCMatrix`, 544 x 544).

Q_scaled Scaled ICAR precision (`dsCMatrix`, `uplo = "U"`).

prec List passed to `density = "random_mult"`: `Q` (`dsCMatrix`, `uplo = "U"`), `log_det`, and `rank`.

Details

District boundaries are not stored in this object (to avoid a hard dependency on **terra**). They ship as `system.file("extdata", "germany_map.gpkg", package = "adlaplace")` and can be loaded with `terra::vect(...)` when **terra** is installed.

Source

INLA Germany data and `germany.graph`.

References

- Besag, J., York, J., and Mollie, A. (1991). Bayesian image restoration, with two applications in spatial statistics. *Annals of the Institute of Statistical Mathematics*, 43(1), 1–20.
- Rue, H., Martino, S., and Chopin, N. (2009). Approximate Bayesian inference for latent Gaussian models by using integrated nested Laplace approximations. *Journal of the Royal Statistical Society: Series B*, 71(2), 319–392.

grad_obs_units	<i>Per-unit observation gradients (streaming, grad-only tapes)</i>
----------------	--

Description

Computes sparse gradients of each observation **unit** contribution at a fixed full parameter vector x , without re-running `inner_opt`. Each unit is taped temporarily with `config$hessian_sparsity = FALSE` (sparse Jac only), reverse-mode differentiated, then discarded.

Usage

```
grad_obs_units(
  data,
  x,
  config = list(),
  units = NULL,
  batch_size = 32L,
  inner = TRUE,
  negative = TRUE
)
```

Arguments

<code>data</code>	An observation density_data (e.g. <code>fit\$model_data\$observations[[1]]</code>), or a <code>model_data()</code> bundle (uses the first observation shard).
<code>x</code>	Numeric full parameter vector $c(\beta, \gamma, \theta)$ at the evaluation point (typically <code>inner_opt()</code> \$full_parameters).
<code>config</code>	Config list passed to the observation tape builder. Always forced to <code>hessian_sparsity = FALSE</code> ; <code>compact_tape</code> defaults to <code>TRUE</code> and <code>transform_theta</code> defaults to <code>TRUE</code> when omitted (same as adlaplace / ad_pack). Supply $\beta/\gamma/\theta$ seeds if needed for recording (taken from x when omitted). Prefer passing <code>fit\$config</code> (or at least its <code>transform_theta</code>) when evaluating at an MLE from adlaplace .
<code>units</code>	Optional integer vector of 0-based unit indices; default all units.
<code>batch_size</code>	Positive integer; how many one-unit tapes to hold at once.
<code>inner</code>	Logical; if <code>TRUE</code> (default), return only the γ block (rows = <code>n_gamma</code>).
<code>negative</code>	Logical; if <code>TRUE</code> (default), return the negative log density gradient (same sign as grad / inner_opt).

Details

Units are ELGM stratum columns when `data@elgm_matrix` has columns; otherwise units are rows of the observation vector y .

Value

A dgCMatrix of size n_gamma x length(units) when inner = TRUE, or n_full x length(units) when inner = FALSE. Column j is the gradient for units[j].

Config note

hessian_sparsity = FALSE yields packs usable for `grad(..., inner = TRUE)` but not for Hessian / `inner_opt` LDL paths.

See Also

`grad`, `inner_opt`, `ad_pack`

has_openmp	<i>Whether this build was compiled with OpenMP support.</i>
------------	---

Description

Whether this build was compiled with OpenMP support.

Usage

`has_openmp()`

Value

TRUE if OpenMP was enabled at compile time, otherwise FALSE.

hinv_trace_index	<i>Positions of a shard's quadratic form inside the joint inverse Hessian</i>
------------------	---

Description

Called from `ad_pack()` after the symbolic `H_inv` pattern exists. The default method returns `NULL`, which leaves that shard on the `trace_hinv_t` column walk. A backend method may return an integer vector of 0-based slots into `H_inv@x`, one per stored entry of the shard's precision, with `-1L` where the pair is absent from the pattern.

Usage

```
hinv_trace_index(shard, H_inv)

## S4 method for signature 'density_data'
hinv_trace_index(shard, H_inv)
```

Arguments

shard	A density_data shard.
H_inv	Symbolic upper triangle of the joint inverse Hessian.

Value

An integer vector, or NULL.

iid-class	<i>IID Random Effects Term</i>
-----------	--------------------------------

Description

Creates and manages IID (independent and identically distributed) random effects terms.

Usage

```
iid(
  x,
  init = .my_theta_init,
  lower = .my_theta_lower,
  upper = .my_theta_upper,
  parscale = .my_theta_parscale,
  log = TRUE
)

## S4 method for signature 'iid'
design(term, data)

## S4 method for signature 'iid'
precision(term, data)

## S4 method for signature 'iid'
random_info(term, data)

## S4 method for signature 'iid'
theta_info(term)
```

Arguments

x	Variable name (typically a factor).
init	Initial value for theta parameter.
lower	Lower bound for theta parameter.
upper	Upper bound for theta parameter.
parscale	Parameter scale for optimization.

log	Whether theta is optimized on the log scale.
term	An iid term object
data	A data frame containing the term variable

Value

An ‘iid’ term object (in a named list).

Functions

- `design(iid)`: Creates design matrix for iid term
- `precision(iid)`: Creates precision matrix for iid term
- `random_info(iid)`: Extracts random effects information for iid term
- `theta_info(iid)`: Extracts theta parameter information for iid term

influence_scores	<i>Per-unit influence scores for an inner linear functional</i>
------------------	---

Description

Freezes outer parameters at the MLE, re-optimizes γ , forms $v = H^{-1}a$ from the fit-pack inner Hessian, and streams one-unit observation gradients via `grad_obs_units` (temporary tapes). Scores are $\psi_u = -v^\top g_u$.

Usage

```
influence_scores(
  fit,
  a,
  batch_size = 32L,
  control = list(report.level = 0, report.freq = 0),
  verbose = FALSE
)
```

Arguments

fit	An "adlaplace_fit" from adlaplace .
a	Named or positional numeric vector of length n_gamma (e.g. from phi_gamma).
batch_size	Passed to grad_obs_units .
control	Control list for inner_opt .
verbose	Logical; forwarded to inner_opt .

Value

A list with phi, gamma_hat, H, v, G, psi, x_full, and n_units.

See Also

[phi_gamma](#), [amip_set](#), [grad_obs_units](#), [ad_pack_drop](#)

inner_opt

Inner optimization over gamma using trust-region CG (sparse)

Description

Runs the inner optimization over γ using the **trustOptim** sparse trust-region CG solver on a pre-built [ad_pack](#) handle.

Usage

```
inner_opt(
  parameters,
  gamma,
  ad_pack,
  control = NULL,
  deriv = FALSE,
  verbose = FALSE,
  return_hessians = TRUE
)
```

Arguments

parameters	Numeric vector of fixed outer parameters (beta, theta; length Nbeta+Ntheta).
gamma	Numeric vector of starting values for inner parameters (gamma; length Ngamma).
ad_pack	ad_pack S4 object from ad_pack .
control	List of trust-region control parameters (see trustOptim).
deriv	Logical; if TRUE, also return outer gradient/Hessian pieces, Cholesky-based quantities, and the profile gradient at the inner mode.
verbose	Logical; if TRUE, print thread/shard diagnostics.
return_hessians	Logical; if FALSE and deriv=TRUE, skip converting sparse Hessians / inverses to R Matrix objects and return only the scalar objective, inner_opt\$solution, and deriv\$d_neg_log_lik (optimizer hot path).

Details

Negates tape log-density values in C++ for minimization via **trustOptim**.

Value

A list with log_lik, neg_log_lik, parameters, full_parameters, inner_opt, gradient (list inner/outer), and hessian (list inner/outer/chol_inner/half_log_det; with deriv=TRUE and return_hessians=TRUE also half_H_inv, H_inv, trace3). With deriv=TRUE, also deriv (profile pieces including d_neg_log_lik) and dU. Objective and derivatives use the negative log-density convention.

intercept-class	<i>intercept Model Term</i>
-----------------	-----------------------------

Description

Creates and manages intercept model terms for fixed effects. With a finite sd, the intercept is treated as a random effect with a known-SD Gaussian prior ($N(0, sd^2)$), using random_diagonal without a theta parameter.

Usage

```
intercept(
  init = .my_beta_init,
  lower = .my_beta_lower,
  upper = .my_beta_upper,
  parscale = .my_beta_parscale,
  sd = Inf
)

## S4 method for signature 'intercept'
design(term, data)

## S4 method for signature 'intercept'
beta_info(term, data)

## S4 method for signature 'intercept'
precision(term, data)

## S4 method for signature 'intercept'
random_info(term, data)
```

Arguments

init	Initial value for beta parameter (default: 0)
lower	Lower bound for beta parameter (default: -Inf)
upper	Upper bound for beta parameter (default: Inf)
parscale	Parameter scale for optimization (default: 1)

sd	Prior standard deviation. Inf (default) keeps a fixed effect; a finite positive value places a known-SD Gaussian prior and moves the intercept into the random-effect block.
term	A intercept term object
data	A data frame containing the term variable

Details

intercept Model Term

Value

A intercept term object

Functions

- `design(intercept)`: Creates design matrix for intercept term
- `beta_info(intercept)`: Extracts beta parameter information for intercept term
- `precision(intercept)`: Precision for known-SD intercept prior
- `random_info(intercept)`: Random info for known-SD intercept prior

Methods

The following methods are available for ‘intercept’ objects:

`design(term, data)` Creates design matrix for intercept term

`precision(term, data)` Creates precision matrix for intercept term

`theta_info(term)` Extracts theta parameter information

`beta_info(term, data)` Extracts beta parameter information

`random_info(term, data)` Extracts random effects information

Examples

```
# Create a intercept term
intercept_term <- intercept(init=2)
```

iwp

*Integrated Wiener Process Term Constructor***Description**

Creates an integrated Wiener process (IWP) model term. The basis is divided by the mean knot spacing to the power p , and the penalty weights are the knot spacings divided by that mean spacing. Design entries and the standard-deviation parameter are then unchanged if x and the knots are rescaled by the same factor.

Usage

```
iwp(
  x,
  p = 2,
  ref_value = 0,
  knots,
  range = NULL,
  init = .my_theta_init,
  lower = .my_theta_lower,
  upper = .my_theta_upper,
  parscale = .my_theta_parscale,
  log = TRUE,
  boundary_is_random = TRUE,
  include_poly = TRUE
)
```

Arguments

<code>x</code>	Variable name.
<code>p</code>	Order of the integrated Wiener process (default: 2).
<code>ref_value</code>	Reference value for the basis.
<code>knots</code>	Vector of knot locations.
<code>range</code>	Range of the data (optional).
<code>init</code>	Initial values for theta parameters.
<code>lower</code>	Lower bounds for theta parameters.
<code>upper</code>	Upper bounds for theta parameters.
<code>parscale</code>	Parameter scales for optimization.
<code>log</code>	Whether theta is optimized on the log scale.
<code>boundary_is_random</code>	Whether boundary should be treated as random.
<code>include_poly</code>	Whether to include polynomial terms.

Value

A list containing the 'iwp' term object and optionally polynomial terms.

Examples

```
knots <- seq(0, 1, length.out = 5)
iwp_term <- iwp(x = "age", knots = knots)
iwp_term
```

iwp-class

Integrated Wiener Process Term

Description

Creates and manages integrated Wiener process (IWP) model terms.

Usage

```
## S4 method for signature 'iwp'
design(term, data)

## S4 method for signature 'iwp'
precision(term, data)

## S4 method for signature 'iwp'
theta_info(term)

## S4 method for signature 'iwp'
random_info(term, data)
```

Arguments

term	An iwp term object
data	A data frame containing the term variable

Value

design Numeric design matrix for the integrated Wiener process basis, with one column per basis function and one row per observation. Entries are the basis evaluated at data.

precision Sparse precision matrix for those basis coefficients. The penalty is the integrated Wiener process prior.

theta_info One-row data frame describing the standard-deviation parameter: label, initial value, bounds, parameter scale, and whether optimization is on the log scale.

random_info Data frame with one row per random coefficient, including `gamma_label`, the name of that coefficient in a fitted model.

Functions

- `design(iwp)`: Creates design matrix for IWP term
- `precision(iwp)`: Creates precision matrix for IWP term
- `theta_info(iwp)`: Extracts theta parameter information for IWP term
- `random_info(iwp)`: Extracts random effects information for IWP term

Methods

The following methods are available for ‘iwp’ objects:

`design(term, data)` Creates design matrix for IWP term

`precision(term, data)` Creates precision matrix for IWP term

`theta_info(term)` Extracts theta parameter information

`beta_info(term, data)` Extracts beta parameter information

`random_info(term, data)` Extracts random effects information

<code>laplace_half_H_inv</code>	<i>Extract inner inverse Cholesky factor from Laplace output</i>
---------------------------------	--

Description

Returns $H^{-1/2}$ for the inner (random-effect) Hessian from the output of `log_lik_laplace`. Accepts the flat `half_H_inv` matrix when `deriv = TRUE`, or reconstructs it from `hessian$chol_inner`.

Usage

```
laplace_half_H_inv(laplace)
```

Arguments

<code>laplace</code>	Output of <code>log_lik_laplace(..., deriv = TRUE)</code> (or <code>inner_opt(..., deriv = TRUE)</code> with the same hessian layout).
----------------------	--

Value

A sparse or dense matrix $H^{-1/2}$ with `nrow = Ngamma`.

See Also

[log_lik_laplace](#), [rmvnldl](#)

laplace_loglik	<i>Laplace-approximate log-likelihood (positive convention)</i>
----------------	---

Description

Thin wrapper around [log_lik_laplace](#) that returns the *positive* profile log-likelihood and its gradient with respect to the outer parameters $c(\text{beta}, \text{theta})$. Prefer this over reading `inner_opt(...)$deriv$d_neg_log_lik` when building custom outer objectives (e.g. modular / multi-pack likelihoods).

Usage

```
laplace_loglik(
  ad_pack,
  par,
  gamma,
  config = list(),
  control_inner = list(),
  deriv = TRUE
)
```

Arguments

<code>ad_pack</code>	An <code>ad_pack</code> object.
<code>par</code>	Numeric outer parameter vector $c(\text{beta}, \text{theta})$ on the internal (log-theta) scale.
<code>gamma</code>	Numeric vector of random-effect modes used as the inner start.
<code>config</code>	Configuration list (may be empty).
<code>control_inner</code>	Control list for the inner trust-region solve.
<code>deriv</code>	Logical; if TRUE (default), return the profile gradient.

Value

A list with components

log_lik Scalar Laplace-approximate marginal log-likelihood.

gradient Numeric vector $\nabla_{\psi} \ell$, or NULL when `deriv = FALSE`.

gamma Inner modes at the optimum.

See Also

[log_lik_laplace](#), [inner_opt](#), [outer_fn](#)

linear-class

*Linear Model Term***Description**

Creates and manages linear model terms for fixed effects. With a finite `sd`, coefficients are random effects with a known-SD Gaussian prior ($N(0, sd^2)$).

Usage

```
linear(
  x,
  init = .my_beta_init,
  lower = .my_beta_lower,
  upper = .my_beta_upper,
  parscale = .my_beta_parscale,
  sd = Inf
)

## S4 method for signature 'linear'
design(term, data)

## S4 method for signature 'linear'
beta_info(term, data)

## S4 method for signature 'linear'
precision(term, data)

## S4 method for signature 'linear'
random_info(term, data)
```

Arguments

<code>x</code>	Variable name (character) or symbol in a formula (e.g. <code>linear(x)</code> in <code>model_data()</code>).
<code>init</code>	Initial value for beta parameter (default: 0)
<code>lower</code>	Lower bound for beta parameter (default: -Inf)
<code>upper</code>	Upper bound for beta parameter (default: Inf)
<code>parscale</code>	Parameter scale for optimization (default: 1)
<code>sd</code>	Prior standard deviation. Inf (default) keeps a fixed effect; a finite positive value places a known-SD Gaussian prior and moves the coefficients into the random-effect block.
<code>term</code>	A linear term object
<code>data</code>	A data frame containing the term variable

Details

Linear Model Term

Value

A linear term object

Functions

- `design(linear)`: Creates design matrix for linear term
- `beta_info(linear)`: Extracts beta parameter information for linear term
- `precision(linear)`: Precision for known-SD linear prior
- `random_info(linear)`: Random info for known-SD linear prior

Methods

The following methods are available for ‘linear’ objects:

`design(term, data)` Creates design matrix for linear term
`precision(term, data)` Creates precision matrix for linear term
`theta_info(term)` Extracts theta parameter information
`beta_info(term, data)` Extracts beta parameter information
`random_info(term, data)` Extracts random effects information

Examples

```
# Create a linear term
linear_term <- linear(x = "temperature")
```

log_lik_laplace

Log-likelihood with inner Laplace optimization

Description

Evaluates the (profiled) log-likelihood for a hierarchical model by solving an inner optimization problem for the latent vector γ (e.g. random effects) given outer parameters x (typically β and θ). The function delegates the inner optimization to `inner_opt()` from the selected back-end package (by default **adlaplace**).

Usage

```
log_lik_laplace(
  x,
  config = list(),
  gamma,
  control = list(report.level = 4, report.freq = 1),
  ad_pack,
  data,
  package = c(config[["package"]], "adlaplace")[1L],
  deriv = FALSE,
  return_hessians = TRUE
)
```

Arguments

<code>x</code>	Numeric vector of outer parameters (beta, then theta). Length must equal <code>num_beta + num_theta</code> from <code>ad_pack@sizes</code> .
<code>config</code>	A list of backend options (verbose, package, etc.). When <code>ad_pack</code> is missing, must also include beta, gamma, and theta so <code>ad_pack()</code> can be built from data.
<code>gamma</code>	Optional numeric vector of starting values for the inner parameter gamma. If missing, uses <code>config\$gamma</code> when present, otherwise a zero vector of length <code>ad_pack@sizes["gamma"]</code> .
<code>control</code>	List of control parameters passed <i>as-is</i> to the backend inner optimizer (e.g., <code>report.level</code> , <code>report.freq</code>). See backend documentation (e.g., trustOptim) for supported options.
<code>ad_pack</code>	Optional <code>ad_pack</code> object from ad_pack . This is a single backend handle (no separate inner/outer handles). If missing, it will be constructed automatically using data.
<code>data</code>	Optional data list used to build <code>ad_pack</code> when <code>ad_pack</code> is not supplied.
<code>package</code>	Character scalar naming the backend package to use for <code>ad_pack()</code> and <code>inner_opt()</code> . Defaults to "adlaplace". Other backends must export a compatible <code>ad_pack()</code> builder and <code>inner_opt()</code> .
<code>deriv</code>	Logical scalar. If TRUE, include derivative quantities in the output (gradient, intermediate derivatives).
<code>return_hessians</code>	Logical. Forwarded to inner_opt . When FALSE with <code>deriv=TRUE</code> , skip Matrix Hessian objects (optimizer path). Default TRUE for diagnostic / post-fit evaluations.

Details

The default **adlaplace** backend uses a single AD handle. This function passes that handle to `inner_opt(..., ad_pack = ad_pack)`. Parameter block sizes are read from `ad_pack@sizes`; `config` is not required to contain beta, gamma, or theta when `ad_pack` is supplied.

When `deriv=FALSE`, the return value mirrors [inner_opt\(\)](#) with `inner_opt`, top-level gradient, and hessian. When `deriv=TRUE`, the profile gradient is assembled in C++ inside `inner_opt`; the same list is augmented with `deriv` and profile-derivative pieces in `gradient$outer`.

Value

A list. With `deriv=FALSE`, same structure as `inner_opt` (without parameters). With `deriv=TRUE`, additionally:

- deriv** Data frame of profile derivative pieces.
- gradient\$outer\$dU, gradient\$outer\$trace3** Intermediate profile objects.

Note

The Laplace approximation assumes the inner Hessian is positive definite at the optimum. If `inner_opt` fails to converge or returns a non-invertible Hessian, `log_lik_laplace()` issues a warning or error.

See Also

`ad_pack`, `inner_opt`

london	<i>London daily mortality and PM10 (case-crossover example)</i>
--------	---

Description

Daily all-cause mortality and air-quality covariates for London, 2002–2006, from the case-crossover example of Tobias et al. (2024).

Usage

`london`

Format

- A data frame with 1826 rows and columns:
- city** City label ("London").
 - date** Calendar date.
 - year, month, day** Integer calendar components.
 - dow** Day of week (integer encoding from the source file).
 - all** Daily all-cause death count.
 - tmean** Mean temperature (degrees Celsius).
 - rh** Relative humidity (percent).
 - pm10** PM10 concentration.

Source

<https://github.com/aureliotobias/casecrossover>

References

Tobias, A., et al. (2024). Case-crossover designs for air pollution epidemiology (example data).

Examples

```
data("london", package = "adlaplace")
head(london)
```

mean_mvquad	<i>Posterior mean of random effects via multivariate quadrature</i>
-------------	---

Description

Approximates $E[\gamma \mid y]$ by importance-weighted quadrature over γ , using a Gaussian proposal $N(\hat{\gamma}, H^{-1})$ (Laplace covariance) and correcting with [joint_log_dens](#).

Usage

```
mean_mvquad(
  parameters,
  mode,
  cov,
  ad_pack,
  n = 3L,
  type = "nHN",
  ndConstruction = "sparse",
  dec.type = 2L
)
```

Arguments

parameters	Outer (β, θ) at the Laplace fit.
mode	Inner mode $\hat{\gamma}$ (e.g. <code>laplace\$inner_opt\$solution</code>).
cov	H^{-1} for the inner block (e.g. <code>laplace\$hessian\$H_inv</code>).
ad_pack	ad_pack object for <code>joint_log_dens</code> .
n	Quadrature level passed to mvQuad <code>createNIGrid</code> .
type	mvQuad rule (default "nHN").
ndConstruction	mvQuad grid construction (default "sparse").
dec.type	Cholesky decomposition flag for mvQuad: :rescale.

Details

Builds a sparse nHN grid with **mvQuad**, rescales to the Laplace proposal, then forms $\sum_i w_i \gamma_i \exp(\ell(\gamma_i) - \log q(\gamma_i)) / \sum_i w_i \exp(\ell(\gamma_i) - \log q(\gamma_i))$ with log-sum-exp stabilization.

Value

Numeric vector of length `n_gamma`.

See Also

[log_lik_laplace](#), [inner_opt](#), [joint_log_dens](#), [rmvnl](#)

model-generics	<i>Model Term Generics</i>
----------------	----------------------------

Description

Generic functions for extracting model matrices and parameter information from model terms.

When non-NULL, `model_data` emits an extra `ad_kind = "parameters"` shard (e.g. FEM log-determinant) alongside the random shard. Default is NULL (no companion).

Usage

```
design(term, data)

precision(term, data)

theta_info(term)

beta_info(term, data)

random_info(term, data)

elgm_matrix(term, data)

## S4 method for signature 'model_term'
design(term, data)

## S4 method for signature 'model_term'
precision(term, data)

## S4 method for signature 'model_term'
theta_info(term)

## S4 method for signature 'model_term'
beta_info(term, data)

## S4 method for signature 'model_term'
random_info(term, data)

extra_density(term)
```

```
## S4 method for signature 'model_term'
extra_density(term)
```

Arguments

term	A model term object.
data	A data frame containing the variables.

Value

Method-specific return values.
Character density name, or NULL.

model_data	<i>Assemble model terms and per-shard density_data objects</i>
------------	--

Description

Parses a formula, builds design matrices, and returns formula terms plus density_data shards for the observation density, parameter densities, and each random-effect term.

Usage

```
model_data(formula, data, verbose = FALSE, na_omit = TRUE)
```

Arguments

formula	Model formula with constructor terms (e.g. <code>iwp()</code> , <code>iid()</code>).
data	Data frame containing variables referenced in formula.
verbose	Print extra information while parsing terms.
na_omit	When TRUE (default), drop rows with NA in covariates, outcome, stratification (by), or random-slope mult variables; impute remaining outcome NAs as zero; and sort by observation-term by columns when present.

Value

A list with:

terms	Named list of term objects from collect_terms .
data	Output of term_data_setup , including <code>elgm_matrix</code> when an observation term defines an <code>elgm_matrix</code> method.
observations	Named list of observation density_data shards.
parameters	Named list of parameter density_data shards.
random	Named list of random-effect density_data shards.

Examples

```

set.seed(1)
dat <- data.frame(
  y = rpois(30, 2),
  x1 = rnorm(30),
  x2 = runif(30)
)
md <- model_data(
  y ~ x1 + iwp(x2, p = 2, knots = seq(0, 1, length.out = 5)),
  data = dat
)
names(md$terms)

```

model_term-class	<i>Base Model Class</i>
------------------	-------------------------

Description

The base S4 class that all specific model term classes inherit from. Subclasses that need hierarchical grouping should include a by slot (either character or by_group type) and optionally by_levels and by_labels slots.

Slots

name Character vector of length 1, the term name

label Character scalar term label reused across metadata builders.

formula Formula object for the term

knots Numeric vector of knot locations (for spline terms)

ref_value Numeric reference value for centering

p.order Integer polynomial order

init Numeric vector of initial values

lower Numeric vector of lower bounds

upper Numeric vector of upper bounds

parscale Numeric vector of parameter scales for optimization

log Logical; optimize/tape each theta on the log scale (recycled to the number of thetas for multi-parameter terms).

model_role Factor indicating term role ("fixed", "random", or "response")

density Registered AD density name for ad_pack_ptr(), or NA when the term does not map to a density shard.

ad_kind Shard kind passed to ad_pack_ptr() ("observations", "parameters", "random", or NA).

package Package whose .so records AD tapes for this term (default "adlaplace" for built-in densities).

n_groups	<i>Number of AD shards in an ad_pack_ptr handle</i>
----------	---

Description

Number of AD shards in an ad_pack_ptr handle

Usage

n_groups(handle)

Arguments

handle External pointer of class ad_pack_ptr.

Value

Integer count of groups (shards).

n_obs_units	<i>Number of removable observation units</i>
-------------	--

Description

Units are ELGM stratum columns when elgm_matrix has columns; otherwise rows of the observation vector y. Same domain as [grad_obs_units](#).

Usage

n_obs_units(data)

Arguments

data An observation density_data, a model_data() bundle, or an "adlaplace_fit".

Value

Integer length-1 count of units.

nbinom-class

Negative binomial observation term

Description

Model term for the observation-level negative binomial log density registered as nbinom_obs.

Creates a response term wired to the nbinom_obs AD shard.

Usage

```
nbinom(
  x,
  init = .my_theta_init,
  lower = .my_theta_lower,
  upper = .my_theta_upper,
  parscale = .my_theta_parscale,
  log = TRUE
)

## S4 method for signature 'nbinom'
theta_info(term)
```

Arguments

x	Outcome variable name.
init	Initial value for the overdispersion parameter (log-SD scale).
lower	Lower bound for the overdispersion parameter.
upper	Upper bound for the overdispersion parameter.
parscale	Parameter scale for optimization.
log	Whether theta is optimized on the log scale.
term	A model term object (S4 methods).

Details

Negative binomial observation model term

Value

A nbinom object.

Functions

- `theta_info(nbinom)`: Theta info for the overdispersion parameter.

Slots (inherited from model)

ad_pack Character scalar "nbinom_obs".
 ad_kind Character scalar "observations".

obs_groups	<i>Partition observations into AD shards by sparsity pattern</i>
------------	--

Description

The function partitions columns into num_shards shards using quantiles of the first right singular vector, optionally using **RSpectra** for efficiency when available.

Usage

```
obs_groups(A, elgm_matrix, num_shards, min_shards = 0)
```

Arguments

A	Random-effects design matrix (nrow(A) = number of observations).
elgm_matrix	A numeric matrix (or matrix-like object) for extended latent gaussian models.
num_shards	Integer giving the maximum number of shards to construct. The actual number of shards may be smaller if fewer distinct loadings are present.
min_shards	Integer giving the minimum number of shards. When there are fewer distinct singular-vector loadings than min_shards, only the largest exact-loading group is split until min_shards is reached (or that group cannot be split further).

Details

The resulting grouping is returned as a pattern sparse matrix whose columns correspond to shards and whose nonzeros mark membership. Loadings are used only to form the partition. Shards are ordered from most heterogeneous to most homogeneous.

If the **RSpectra** package is available, the leading singular vector is computed using `RSpectra::svds`; otherwise, a full singular value decomposition via `svd` is used.

Shard boundaries are defined by empirical quantiles of the loadings. Shards are subsequently re-ordered so that shards with larger within-shard variability appear first.

Value

A sparse matrix of class "ngcMatrix" (from **Matrix**), with one column per shard and one row per observation (or ELGM stratum). Nonzero entries mark shard membership; there is no @x slot.

Examples

```
set.seed(1)
A <- matrix(rnorm(100), 20, 5)
G <- obs_groups(A, num_shards = 3)
G
```

obs_groups_units	<i>Build obs_groups for a subset of observation units</i>
------------------	---

Description

Restricts which observation units are recorded on observation tapes. Domain indices are ****0-based**** (ELGM stratum columns, or rows of y).

Usage

```
obs_groups_units(
  n_domain,
  units = NULL,
  grouping = c("identity", "together", "filter"),
  obs_groups = NULL
)
```

Arguments

n_domain	Number of units in the full domain.
units	Integer vector of 0-based unit indices to keep. Default all.
grouping	One of: "identity" One shard column per selected unit (scores). "together" One shard containing all selected units. "filter" Start from obs_groups, drop unselected rows, drop empty columns (keeps coarse fit sharding).
obs_groups	Existing shard map; required when grouping = "filter".

Value

A ngCMatrix suitable for config\$obs_groups.

See Also

[n_obs_units](#), [grad_obs_units](#), [ad_pack_drop](#)

outer_optim_wrappers *Outer objective and gradient wrappers*

Description

Convenience wrappers around [log_lik_laplace](#) for use with outer optimizers that expect `fn / gr` callbacks. Both functions solve (or warm-start) the inner problem over `gamma` via [log_lik_laplace](#) and update a mutable cache environment with the latest inner solution.

Usage

```
outer_fn(x, config, cache, ad_pack, control_inner = list(), ...)
```

```
outer_gr(x, config, cache, ad_pack, control_inner = list(), ...)
```

Arguments

<code>x</code>	Numeric outer parameter vector <code>c(beta, theta)</code> .
<code>config</code>	Configuration list passed to log_lik_laplace .
<code>cache</code>	An environment used to warm-start and store the inner <code>gamma</code> solution. If <code>cache\$gamma</code> is missing or the wrong length, it is initialized from <code>config\$gamma</code> (if present) or zeros of length <code>ad_pack@sizes["gamma"]</code> . Both functions update <code>cache\$gamma</code> after each evaluation, and share <code>cache\$fg_x / cache\$neg_log_lik / cache\$d_neg_log_lik</code> for the latest combined objective/gradient evaluation. For multi-pack / modular objectives, use one cache environment per <code>ad_pack</code> ; <code>cache\$gamma</code> is that pack's inner warm start.
<code>ad_pack</code>	<code>ad_pack</code> object from ad_pack .
<code>control_inner</code>	A list of control options forwarded to the <code>control</code> argument of log_lik_laplace for the inner optimization.
<code>...</code>	Additional arguments forwarded to log_lik_laplace (for example <code>data</code> or <code>package</code>).

Details

L-BFGS-B requests `fn` then `gr` at the same parameter vector. Both wrappers share one `inner_opt(..., deriv = TRUE, return_hessians = FALSE)` evaluation at that point: the objective is free once the profile gradient has been computed. Cached numerics are stored in `cache$fg_x`, `cache$neg_log_lik`, and `cache$d_neg_log_lik` and reused until `x` changes.

`outer_fn()` Returns the scalar objective negative log likelihood.

`outer_gr()` Returns the gradient.

Value

- `outer_fn`: a numeric scalar `neg_log_lik`.
- `outer_gr`: gradient of `neg_log_lik` (same sign as `outer_fn`).

See Also[log_lik_laplace](#)**Examples**

```

set.seed(1)
n <- 80
g <- factor(sample(4, n, replace = TRUE))
x <- rbinom(n, 1, 0.5)
eta <- 0.5 + 0.4 * x + rnorm(4, sd = 0.3)[g]
nb_sd <- 0.3
z <- rgamma(n, nb_sd^(-2), nb_sd^(-2))
dat <- data.frame(y = rpois(n, exp(eta) * z), x = x, g = g)
md <- model_data(
  nbinom(y, lower = 1e-9, init = 0.15) ~ x + iid(g, init = 0.3),
  data = dat
)
config <- list(
  transform_theta = TRUE,
  obs_groups = obs_groups(md$term_data$A, num_shards = 5),
  verbose = FALSE
)
ap <- ad_pack(md, config)
cache <- new.env(parent = emptyenv())
x0 <- md$term_data$info$parameters$init
outer_fn(x = x0, config = config, cache = cache, ad_pack = ap)
outer_gr(x = x0, config = config, cache = cache, ad_pack = ap)

```

phi_gamma

Linear functional of the inner field γ **Description**

Builds a named numeric vector a aligned to `fit$model_data$term_data$info$gamma$gamma_label` so that $\phi(\gamma) = a^\top \gamma$.

Usage

```
phi_gamma(fit, term = NULL, new_x = NULL, coef = NULL)
```

Arguments

<code>fit</code>	An "adlaplace_fit" from adlaplace .
<code>term</code>	Optional character name of a covariate whose **random** terms contribute via design (e.g. "pm10").
<code>new_x</code>	Data frame of prediction points for term (required when term is set). Typically one row, e.g. <code>data.frame(pm10 = 80)</code> .
<code>coef</code>	Optional gamma label (or labels) to set to 1 (unit / contrast vectors), e.g. a treatment coefficient name.

Value

Named numeric vector of length `n_gamma`.

See Also

[influence_scores](#), [amip_set](#), [design](#), [sim_random](#)

poisson-class

Poisson observation term

Description

Model term for the observation-level Poisson log density with a log link, registered as `poisson_obs`. For each observation with linear predictor $\eta = X\beta + A\gamma$ and optional offset `o` (via `config$offset`), the mean is $\exp(\eta + o)$ and the log density contribution is $y * \eta - \exp(\eta + o) + y * o - \text{lgamma}(y + 1)$. There are no observation-level hyperparameters.

Creates a response term wired to the `poisson_obs` AD shard. There are no observation-level hyperparameters. An exposure or expected-count offset is supplied through `config$offset` when building AD shards (for example $\log(E)$ in disease mapping).

Usage

```
pois(x)
```

Arguments

`x` Outcome variable name (non-negative counts).

Details

Poisson observation model term

Value

A `poisson` object.

Slots (inherited from model)

`ad_pack` Character scalar "poisson_obs".

`ad_kind` Character scalar "observations".

prior-class	<i>Hyperparameter prior term</i>
-------------	----------------------------------

Description

Places a prior on an existing theta (SD) parameter. Does not create a new theta; it emits an ad_kind = "parameters" shard that contributes to the joint log density.

Usage

```
prior(theta = 0L, dist = "exp", median = 1, rate = NULL)
```

Arguments

theta	Zero-based index into info\$theta\$id, or a character theta label (e.g. "ID_iid").
dist	Prior family. Currently only "exp" (exponential on the SD scale) is supported.
median	Prior median on the SD scale. For dist = "exp", the rate is log(2) / median.
rate	Optional exponential rate (overrides median when supplied).

Details

Hyperparameter prior term

Value

A prior term object.

replace_vars	<i>Replace data-column names in model terms</i>
--------------	---

Description

Rewrites the data-column references on model terms (and formulas / term lists) according to a named character map. Used by modular-inference workflows that share one model structure across exposure sample columns (e.g. sqrt_pm -> sqrt_pm_s3).

Usage

```
replace_vars(x, map)

## S4 method for signature 'model_term'
replace_vars(x, map)

## S4 method for signature 'dirichlet_multinom'
replace_vars(x, map)
```

```
## S4 method for signature 'formula'
replace_vars(x, map)

## S4 method for signature 'list'
replace_vars(x, map)
```

Arguments

<code>x</code>	A <code>model_term</code> , <code>dirichlet_multinom</code> , <code>formula</code> , or list of such objects.
<code>map</code>	Named character vector: names are current column names, values are replacement column names. Names absent from <code>map</code> are left unchanged.

Value

An object of the same type as `x`, with column references updated and labels / formulas regenerated where applicable.

Examples

```
terms <- collect_terms(nbinom(y) ~ fpoly(sqrt_pm, p = 1))
replace_vars(terms, c(sqrt_pm = "sqrt_pm1"))
```

<code>rmvnldl</code>	<i>Simulate from a multivariate normal using LDL of the precision matrix</i>
----------------------	--

Description

Draws n samples from $N(\mu, H^{-1})$ where H is the precision matrix, given its LDL factorization (unit lower $L1$, diagonal D , and permutation $perm$).

Usage

```
rmvnldl(n, mean = 0, chol_prec, fit)
```

Arguments

<code>n</code>	Number of samples.
<code>mean</code>	Mean vector μ (length <code>length(D)</code>). When <code>mean</code> is named, those names are attached to the draws. Ignored when <code>fit</code> is supplied.
<code>chol_prec</code>	Either a <code>CHMfactor</code> , <code>Cholesky</code> , or <code>dCHMsimpl</code> from <code>Matrix::Cholesky(..., LDL = TRUE)</code> , or a list like <code>res\$hessian\$chol_inner</code> with components <code>L1</code> , <code>D</code> , and <code>perm</code> . Ignored when <code>fit</code> is supplied.
<code>fit</code>	Optional "adlaplace_fit" object. When supplied, overrides <code>mean</code> and <code>chol_prec</code> with <code>fit\$gamma</code> and <code>fit\$details\$hessian\$chol_inner</code> .

Details

Uses $H^{-1/2} = P^T L^{-1} D^{-1/2}$ (same as `reformat_chol()` in `log_lik_deriv`), and `rnorm` only:
 $x = \mu + H^{-1/2}z, z \sim N(0, I)$.

Value

An n-by-p matrix; each row is one draw. When n = 1, a length-p vector. Column / element names come from `names(mean)` when present and of length p.

See Also

[Cholesky](#), [log_lik_laplace](#), [adlaplace](#)

rpoly-class

Random Polynomial Model Term

Description

Creates and manages random polynomial model terms.

Usage

```
rpoly(x, p = 2, ref_value = 0, sd = Inf, basis_scale = 1)
```

```
## S4 method for signature 'rpoly'
design(term, data)
```

```
## S4 method for signature 'rpoly'
precision(term, data)
```

```
## S4 method for signature 'rpoly'
random_info(term, data)
```

Arguments

x	Variable name.
p	Polynomial degree (default: 2).
ref_value	Reference value for the polynomial.
sd	Standard deviation for random effects.
basis_scale	Positive scale for the covariate. Column k of the raw polynomial is divided by basis_scale^k . The default 1 leaves the raw polynomial unchanged. iwp passes the mean knot spacing so the polynomial matches the normalized IWP basis.
term	A ‘rpoly’ term object.
data	A data frame containing the variables used in the term.

Details

Random Polynomial Model Term

Value

- A 'rpoly' term object.
- A design matrix for the random polynomial term.
- A precision matrix for the random polynomial term.
- A data frame containing random effects information for the random polynomial term.

Functions

- design(rpoly): Design method for rpoly objects
- precision(rpoly): Precision method for rpoly objects
- random_info(rpoly): Random info method for rpoly objects

Methods

- The following methods are available for 'rpoly' objects:
- design(term, data) Creates design matrix for rpoly term
 - precision(term, data) Creates precision matrix for rpoly term
 - theta_info(term) Extracts theta parameter information
 - beta_info(term, data) Extracts beta parameter information
 - random_info(term, data) Extracts random effects information

sim_fit	<i>Simulate linear predictors on a new covariate grid</i>
---------	---

Description

Draws random effects from the Laplace approximation and evaluates the linear predictor on x by summing fixed (β) and random (γ) contributions from each model term.

Usage

sim_fit(x, data, fit, n = 500L)

Arguments

- | | |
|------|--|
| x | Data frame of prediction covariates (same variables as the fitted model). Only terms whose variables appear in x contribute. |
| data | Object returned by model_data . |
| fit | Result from log_lik_laplace at the fitted outer parameters. |
| n | Number of draws for random-effect simulation. |

Value

The combined linear predictor: a `nrow(x)` by `n` matrix of simulated values (fixed-effect contributions are constant across columns).

sim_iid	<i>Simulate IID random effects with pointwise and global intervals</i>
---------	--

Description

Identifies IID components in an [adlaplace](#) fit, forms their marginal Laplace covariance (Woodbury identity when mixed with other random effects), draws samples, and summarizes pointwise quantiles. When **GET** is available, also returns a global central region across levels.

Usage

```
sim_iid(fit, n = 500L, probs = c(0.1, 0.5, 0.9), coverage = 0.8, ...)
```

Arguments

<code>fit</code>	An "adlaplace_fit" from adlaplace .
<code>n</code>	Number of draws.
<code>probs</code>	Quantile levels for pointwise intervals.
<code>coverage</code>	Coverage for central_region global envelopes (used only when GET is installed).
<code>...</code>	Currently unused.

Details

IID rows are those with `model == "iid"` in `fit$model_data$term_data$info$gamma`. The marginal covariance uses **WoodburyMatrix** when installed; otherwise the IID block of `fit$details$hessian$H_inv` (if present) or a dense partitioned solve.

Value

A named list with one element per IID term. Each element is a list with `x` (basis / factor levels), `sim` (levels-by-draws matrix), `pointwise` (quantile matrix with columns named by `probs`), and `global` (matrix with columns `lo`, `central`, `hi`, or `NULL` if **GET** is unavailable). Attributes `var_iid`, `iid_index`, and `iid_labels` store the joint marginal covariance and index metadata.

See Also

[sim_random](#), [rmvnldl](#), [iid](#)

sim_random	<i>Simulate a random-effect contribution for one covariate</i>
------------	--

Description

Builds a prediction grid for variable `x`, forms the design matrix for all random terms on that variable, and multiplies by Laplace draws of the random effects. Intended for plotting smooths (iwp / rpoly) and similar random contributions from an [adlplace](#) fit.

Usage

```
sim_random(
  x,
  fit,
  new_x,
  gamma_sims,
  num_grid = 101L,
  num_sim = 100L,
  probs = c(0.1, 0.5, 0.9),
  coverage = 0.8,
  transform = identity
)
```

Arguments

<code>x</code>	Character scalar: name of the covariate / grouping variable.
<code>fit</code>	An "adlplace_fit" from adlplace .
<code>new_x</code>	Optional one-column data frame of prediction points for <code>x</code> . When missing, a grid is built from term knots via pretty (or from unique basis levels in <code>fit\$model_data\$term_data\$info\$gamma</code> when there are no knots, e.g. IID).
<code>gamma_sims</code>	Optional matrix of random-effect draws (rows = draws, columns named by gamma labels). When missing, drawn with rmvnl (<code>n = num_sim</code> , <code>fit = fit</code>).
<code>num_grid</code>	Target length for the default pretty grid.
<code>num_sim</code>	Number of draws when <code>gamma_sims</code> is missing.
<code>probs</code>	Quantile levels for pointwise intervals.
<code>coverage</code>	Coverage for central_region global envelopes (used only when GET is installed).
<code>transform</code>	Function applied to each simulated linear predictor before summarizing intervals (and returned as <code>sim</code>); default identity. Use <code>exp</code> for relative-risk scale.

Details

Only terms with `model_role == "random"` whose `@name` equals `x` are included (so companion `rpoly` bases for an `iwp` are included, while fixed `fpoly` bases are not). Column names of the design must match columns of `gamma_sims`.

IID prediction grids use factor levels stored in the gamma info table; levels not present at fit time are not invented here.

Value

A list with `x` (numeric or character grid), `sim` (an `length(x)` by draws matrix after transform), `pointwise` (quantile matrix), and `global` (GET envelope with columns `lo`, `central`, `hi`, or `NULL` if **GET** is unavailable).

See Also

[rmvnldl](#), [sim_fit](#), [sim_iid](#), [design](#)

sizes	<i>Parameter-block row counts for an density_data</i>
-------	---

Description

Parameter-block row counts for an `density_data`

Usage

```
sizes(x, ...)  
  
## S4 method for signature 'density_data'  
sizes(x)
```

Arguments

- `x` An `density_data` object.
- `...` Unused; for S4 generic compatibility.

Value

Named list with `n_beta`, `n_gamma`, and `n_theta`.

takahashi_davis	<i>Sparse inverse subset of a symmetric positive-definite matrix</i>
-----------------	--

Description

Entries of Q^{-1} on the sparsity pattern of the Cholesky factor, in the original variable order. Positions the factor does not store are absent, not zeros of the inverse.

Usage

```
takahashi_davis(Q, chol = NULL)
```

Arguments

Q	Symmetric sparse positive-definite matrix.
chol	Optional list with ‘perm’ (0-based) and ‘L1’ (unit-lower factor). When ‘NULL’, the symbolic factor is computed from ‘Q’.

Details

C++ callers ‘LinkingTo: adlaplace’ and include ‘adlaplace/takahashi_impl.hpp’. That function is ‘adlaplace::chol::takahashi_davis’ and takes the unit-lower factor L and the LDL diagonal D . A caller that has only Q factors it with ‘chol_update_csc’ first.

Value

A ‘dgCMatrix’ of the selected inverse.

term_data_setup	<i>Build design matrices and parameter metadata from a formula</i>
-----------------	--

Description

Build design matrices and parameter metadata from a formula

Usage

```
term_data_setup(formula, data, verbose = FALSE)
```

Arguments

formula	Model formula or named list of term objects.
data	Data frame.
verbose	Print parsing messages.

Value

List with terms, y, A, X, data, info. The info\$theta data frame includes a logical log column: TRUE means the parameter is stored on the log scale when config\$transform_theta is TRUE (default for all rows unless a model term sets otherwise). info\$parameters stacks beta and theta rows with the same log column (FALSE for fixed effects); init, lower, and upper are already on the optimization (log) scale where log is TRUE.

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