

Package ‘brms.mmrn’

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Title Bayesian MMRMs using 'brms'

Version 1.0.1

Description The mixed model for repeated measures (MMRM) is a popular model for longitudinal clinical trial data with continuous endpoints, and 'brms' is a powerful and versatile package for fitting Bayesian regression models. The 'brms.mmrn' R package leverages 'brms' to run MMRMs, and it supports a simplified interfaced to reduce difficulty and align with the best practices of the life sciences. References: Bürkner (2017) <[doi:10.18637/jss.v080.i01](https://doi.org/10.18637/jss.v080.i01)>, Mallinckrodt (2008) <[doi:10.1177/009286150804200402](https://doi.org/10.1177/009286150804200402)>.

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URL <https://openpharma.github.io/brms.mmrn/>,
<https://github.com/openpharma/brms.mmrn>

BugReports <https://github.com/openpharma/brms.mmrn/issues>

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brms.mmrn-package

*brms.mmrn: Bayesian MMRMs using brms***Description**

The mixed model for repeated measures (MMRM) is a popular model for longitudinal clinical trial data with continuous endpoints, and *brms* is a powerful and versatile package for fitting Bayesian regression models. The *brms.mmrn* R package leverages *brms* to run MMRMs, and it supports a simplified interface to reduce difficulty and align with the best practices of the life sciences.

References

- Bürkner, P.-C. (2017), "brms: An R package for Bayesian multilevel models using Stan," *Journal of Statistical Software*, 80, 1–28. <https://doi.org/10.18637/jss.v080.i01>.
- Holzhauer, B., and Weber, S. (2024), "Bayesian mixed effects model for repeated measures," in *Applied Modeling in Drug Development*, Novartis AG. https://opensource.nibr.com/bamdd/src/02h_mmrn.html.
- Mallinckrodt, C. H., Lane, P. W., Schnell, D., and others (2008), "Recommendations for the primary analysis of continuous endpoints in longitudinal clinical trials," *Therapeutic Innovation and Regulatory Science*, 42, 303–319. <https://doi.org/10.1177/009286150804200402>.
- Mallinckrodt, C. H., and Lipkovich, I. (2017), *Analyzing longitudinal clinical trial data: A practical guide*, CRC Press, Taylor & Francis Group.

brm_archetype_average_cells

*Cell-means-like time-averaged archetype***Description**

Create a cell-means-like informative prior archetype with a special fixed effect to represent the average across time.

Usage

```
brm_archetype_average_cells(
  data,
  covariates = TRUE,
  prefix_interest = "x_",
  prefix_nuisance = "nuisance_",
  baseline = !is.null(attr(data, "brm_baseline")),
  baseline_subgroup = !is.null(attr(data, "brm_baseline")) && !is.null(attr(data,
    "brm_subgroup")),
  baseline_subgroup_time = !is.null(attr(data, "brm_baseline")) && !is.null(attr(data,
    "brm_subgroup")),
  baseline_time = !is.null(attr(data, "brm_baseline"))
)
```

Arguments

data	A classed data frame from <code>brm_data()</code> , or an informative prior archetype from a function like <code>brm_archetype_successive_cells()</code> .
covariates	Logical of length 1. TRUE (default) to include any additive covariates declared with the <code>covariates</code> argument of <code>brm_data()</code> , FALSE to omit. For informative prior archetypes, this option is set in functions like <code>brm_archetype_successive_cells()</code> rather than in <code>brm_formula()</code> in order to make sure columns are appropriately centered and the underlying model matrix has full rank.
prefix_interest	Character string to prepend to the new columns of generated fixed effects of interest (relating to group, subgroup, and/or time). In rare cases, you may need to set a non-default prefix to prevent name conflicts with existing columns in the data, or rename the columns in your data. <code>prefix_interest</code> must not be the same value as <code>prefix_nuisance</code> .
prefix_nuisance	Same as <code>prefix_interest</code> , but relating to generated fixed effects NOT of interest (not relating to group, subgroup, or time). Must not be the same value as <code>prefix_interest</code> .
baseline	Logical of length 1. TRUE to include an additive effect for baseline response, FALSE to omit. Default is TRUE if <code>brm_data()</code> previously declared a baseline variable in the dataset. Ignored for informative prior archetypes. For informative prior archetypes, this option should be set in functions like <code>brm_archetype_successive_cells()</code> rather than in <code>brm_formula()</code> in order to make sure columns are appropriately centered and the underlying model matrix has full rank.
baseline_subgroup	Logical of length 1.
baseline_subgroup_time	Logical of length 1. TRUE to include baseline-by-subgroup-by-time interaction, FALSE to omit. Default is TRUE if <code>brm_data()</code> previously declared baseline and subgroup variables in the dataset. Ignored for informative prior archetypes. For informative prior archetypes, this option should be set in functions like <code>brm_archetype_successive_cells()</code> rather than in <code>brm_formula()</code> in order to make sure columns are appropriately centered and the underlying model matrix has full rank.
baseline_time	Logical of length 1. TRUE to include baseline-by-time interaction, FALSE to omit. Default is TRUE if <code>brm_data()</code> previously declared a baseline variable in the dataset. Ignored for informative prior archetypes. For informative prior archetypes, this option should be set in functions like <code>brm_archetype_successive_cells()</code> rather than in <code>brm_formula()</code> in order to make sure columns are appropriately centered and the underlying model matrix has full rank.

Details

This archetype has a special fixed effect for each treatment group to represent the mean response averaged across all the time points.

To illustrate, suppose the dataset has two treatment groups A and B, time points 1, 2, and 3, and no other covariates. Let μ_{gt} be the marginal mean of the response at group g time t given data

and hyperparameters. The model has fixed effect parameters $\beta_1, \beta_2, \dots, \beta_6$ which express the marginal means μ_{gt} as follows:

```
`mu_A1 = 3 * beta_1 - beta_2 - beta_3`
`mu_A2 = beta_2`
`mu_A3 = beta_3`

`mu_B1 = 3 * beta_4 - beta_5 - beta_6`
`mu_B2 = beta_5`
`mu_B3 = beta_6`
```

For group A, β_1 is the average response in group A averaged across time points. You can confirm this yourself by expressing the average across time $(\mu_{A1} + \mu_{A2} + \mu_{A3}) / 3$ in terms of the β_{*} parameters and confirming that the expression simplifies down to just β_1 . β_2 represents the mean response in group A at time 2, and β_3 represents the mean response in group A at time 3. $\beta_4, \beta_5,$ and β_6 are analogous for group B.

Value

A special classed tibble with data tailored to the cell-means-like time-averaged archetype. The dataset is augmented with extra columns with the "archetype_" prefix, as well as special attributes to tell downstream functions like `brm_formula()` what to do with the object.

Prior labeling for `brm_archetype_average_cells()`

Within each treatment group, the initial time point represents the average, and each successive time point represents the response within that actual time. To illustrate, consider the example in the Details section. In the labeling scheme for `brm_archetype_average_cells()`, you can label the prior on β_1 using `brm_prior_label(code = "normal(1.2, 5)", group = "A", time = "1")`. Similarly, you can label the prior on β_5 with `brm_prior_label(code = "normal(1.3, 7)", group = "B", time = "2")`. To confirm that you set the prior correctly, compare the brms prior with the output of `summary(your_archetype)`. See the examples for details.

Nuisance variables

In the presence of covariate adjustment, functions like `brm_archetype_successive_cells()` convert nuisance factors into binary dummy variables, then center all those dummy variables and any continuous nuisance variables at their means in the data. This ensures that the main model coefficients of interest are not implicitly conditional on a subset of the data. In other words, preprocessing nuisance variables this way preserves the interpretations of the fixed effects of interest, and it ensures informative priors can be specified correctly.

Prior labeling

Informative prior archetypes use a labeling scheme to assign priors to fixed effects. How it works:

1. First, assign the prior of each parameter a collection of labels from the data. This can be done manually or with successive calls to `[brm_prior_label()]`.

2. Supply the labeling scheme to `[brm_prior_archetype()]`.
`[brm_prior_archetype()]` uses attributes of the archetype to map labeled priors to their rightful parameters in the model.

For informative prior archetypes, this process is much more convenient and robust than manually calling `brms::set_prior()`. However, it requires an understanding of how the labels of the priors map to parameters in the model. This mapping varies from archetype to archetype, and it is documented in the help pages of archetype-specific functions such as `brm_archetype_successive_cells()`.

See Also

Other informative prior archetypes: `brm_archetype_average_effects()`, `brm_archetype_cells()`, `brm_archetype_effects()`, `brm_archetype_successive_cells()`, `brm_archetype_successive_effects()`

Examples

```
set.seed(0L)
data <- brm_simulate_outline(
  n_group = 2,
  n_patient = 100,
  n_time = 4,
  rate_dropout = 0,
  rate_lapse = 0
) |>
dplyr::mutate(response = rnorm(n = dplyr::n())) |>
brm_data_change() |>
brm_simulate_continuous(names = c("biomarker1", "biomarker2")) |>
brm_simulate_categorical(
  names = c("status1", "status2"),
  levels = c("present", "absent")
)
dplyr::select(
  data,
  group,
  time,
  patient,
  starts_with("biomarker"),
  starts_with("status")
)
archetype <- brm_archetype_average_cells(data)
archetype
summary(archetype)
formula <- brm_formula(archetype)
formula
prior <- brm_prior_label(
  code = "normal(1, 2.2)",
  group = "group_1",
  time = "time_2"
) |>
brm_prior_label("normal(1, 3.3)", group = "group_1", time = "time_3") |>
brm_prior_label("normal(1, 4.4)", group = "group_1", time = "time_4") |>
brm_prior_label("normal(2, 2.2)", group = "group_2", time = "time_2") |>
```

```

brm_prior_label("normal(2, 3.3)", group = "group_2", time = "time_3") |>
brm_prior_label("normal(2, 4.4)", group = "group_2", time = "time_4") |>
brm_prior_archetype(archetype)
prior
class(prior)
if (identical(Sys.getenv("BRM_EXAMPLES", unset = ""), "true")) {
tmp <- utils::capture.output(
  suppressMessages(
    suppressWarnings(
      model <- brm_model(
        data = archetype,
        formula = formula,
        prior = prior,
        chains = 1,
        iter = 100,
        refresh = 0
      )
    )
  )
)
suppressWarnings(print(model))
brms::prior_summary(model)
draws <- brm_marginal_draws(
  data = archetype,
  formula = formula,
  model = model
)
summaries_model <- brm_marginal_summaries(draws)
summaries_data <- brm_marginal_data(data)
brm_plot_compare(model = summaries_model, data = summaries_data)
}

```

brm_archetype_average_effects

Treatment effect time-averaged archetype

Description

Create a treatment effect informative prior archetype with a special fixed effect to represent the average across time.

Usage

```

brm_archetype_average_effects(
  data,
  covariates = TRUE,
  prefix_interest = "x_",
  prefix_nuisance = "nuisance_",
  baseline = !is.null(attr(data, "brm_baseline")),

```

```

baseline_subgroup = !is.null(attr(data, "brm_baseline")) && !is.null(attr(data,
  "brm_subgroup")),
baseline_subgroup_time = !is.null(attr(data, "brm_baseline")) && !is.null(attr(data,
  "brm_subgroup")),
baseline_time = !is.null(attr(data, "brm_baseline"))
)

```

Arguments

data	A classed data frame from <code>brm_data()</code> , or an informative prior archetype from a function like <code>brm_archetype_successive_cells()</code> .
covariates	Logical of length 1. TRUE (default) to include any additive covariates declared with the <code>covariates</code> argument of <code>brm_data()</code> , FALSE to omit. For informative prior archetypes, this option is set in functions like <code>brm_archetype_successive_cells()</code> rather than in <code>brm_formula()</code> in order to make sure columns are appropriately centered and the underlying model matrix has full rank.
prefix_interest	Character string to prepend to the new columns of generated fixed effects of interest (relating to group, subgroup, and/or time). In rare cases, you may need to set a non-default prefix to prevent name conflicts with existing columns in the data, or rename the columns in your data. <code>prefix_interest</code> must not be the same value as <code>prefix_nuisance</code> .
prefix_nuisance	Same as <code>prefix_interest</code> , but relating to generated fixed effects NOT of interest (not relating to group, subgroup, or time). Must not be the same value as <code>prefix_interest</code> .
baseline	Logical of length 1. TRUE to include an additive effect for baseline response, FALSE to omit. Default is TRUE if <code>brm_data()</code> previously declared a baseline variable in the dataset. Ignored for informative prior archetypes. For informative prior archetypes, this option should be set in functions like <code>brm_archetype_successive_cells()</code> rather than in <code>brm_formula()</code> in order to make sure columns are appropriately centered and the underlying model matrix has full rank.
baseline_subgroup	Logical of length 1.
baseline_subgroup_time	Logical of length 1. TRUE to include baseline-by-subgroup-by-time interaction, FALSE to omit. Default is TRUE if <code>brm_data()</code> previously declared baseline and subgroup variables in the dataset. Ignored for informative prior archetypes. For informative prior archetypes, this option should be set in functions like <code>brm_archetype_successive_cells()</code> rather than in <code>brm_formula()</code> in order to make sure columns are appropriately centered and the underlying model matrix has full rank.
baseline_time	Logical of length 1. TRUE to include baseline-by-time interaction, FALSE to omit. Default is TRUE if <code>brm_data()</code> previously declared a baseline variable in the dataset. Ignored for informative prior archetypes. For informative prior archetypes, this option should be set in functions like <code>brm_archetype_successive_cells()</code> rather than in <code>brm_formula()</code> in order to make sure columns are appropriately centered and the underlying model matrix has full rank.

Details

This archetype has a special fixed effect for each treatment group to represent the mean response averaged across all the time points, and treatment effects are explicitly parameterized.

To illustrate, suppose the dataset has two treatment groups A (placebo/reference group) and B (active/non-reference group), time points 1, 2, and 3, and no other covariates. Let μ_{gt} be the marginal mean of the response at group g time t given data and hyperparameters. The model has fixed effect parameters $\beta_1, \beta_2, \dots, \beta_6$ which express the marginal means μ_{gt} as follows:

```

`mu_A1 = 3 * beta_1 - beta_2 - beta_3`
`mu_A2 = beta_2`
`mu_A3 = beta_3`

`mu_B1 = 3 * beta_1 - beta_2 - beta_3 + 3 * beta_4 - beta_5 - beta_6`
`mu_B2 = beta_2 + beta_5`
`mu_B3 = beta_3 + beta_6`

```

For group A, β_1 is the average response in group A averaged across time points. You can confirm this yourself by expressing the average across time $(\mu_{A1} + \mu_{A2} + \mu_{A3}) / 3$ in terms of the β_{*} parameters and confirming that the expression simplifies down to just β_1 . β_2 represents the mean response in group A at time 2, and β_3 represents the mean response in group A at time 3. β_4 is the treatment effect of group B relative to group A, averaged across time points. β_5 is the treatment effect of B vs A at time 2, and β_6 is analogous for time 3.

Value

A special classed tibble with data tailored to the treatment effect time-averaged archetype. The dataset is augmented with extra columns with the "archetype_" prefix, as well as special attributes to tell downstream functions like `brm_formula()` what to do with the object.

Prior labeling for `brm_archetype_average_effects()`

Within each treatment group, the initial time point represents the average, and each successive time point represents the response within that actual time. To illustrate, consider the example in the Details section. In the labeling scheme for `brm_archetype_average_effects()`, you can label the prior on β_1 using `brm_prior_label(code = "normal(1.2, 5)", group = "A", time = "1")`. Similarly, you can label the prior on β_5 with `brm_prior_label(code = "normal(1.3, 7)", group = "B", time = "2")`. To confirm that you set the prior correctly, compare the brms prior with the output of `summary(your_archetype)`. See the examples for details.

Nuisance variables

In the presence of covariate adjustment, functions like `brm_archetype_successive_cells()` convert nuisance factors into binary dummy variables, then center all those dummy variables and any continuous nuisance variables at their means in the data. This ensures that the main model coefficients of interest are not implicitly conditional on a subset of the data. In other words, preprocessing nuisance variables this way preserves the interpretations of the fixed effects of interest, and it ensures informative priors can be specified correctly.

Prior labeling

Informative prior archetypes use a labeling scheme to assign priors to fixed effects. How it works:

1. First, assign the prior of each parameter a collection of labels from the data. This can be done manually or with successive calls to `[brm_prior_label()]`.
2. Supply the labeling scheme to `[brm_prior_archetype()]`. `[brm_prior_archetype()]` uses attributes of the archetype to map labeled priors to their rightful parameters in the model.

For informative prior archetypes, this process is much more convenient and robust than manually calling `brms::set_prior()`. However, it requires an understanding of how the labels of the priors map to parameters in the model. This mapping varies from archetype to archetype, and it is documented in the help pages of archetype-specific functions such as `brm_archetype_successive_cells()`.

See Also

Other informative prior archetypes: `brm_archetype_average_cells()`, `brm_archetype_cells()`, `brm_archetype_effects()`, `brm_archetype_successive_cells()`, `brm_archetype_successive_effects()`

Examples

```
set.seed(0L)
data <- brm_simulate_outline(
  n_group = 2,
  n_patient = 100,
  n_time = 4,
  rate_dropout = 0,
  rate_lapse = 0
) |>
dplyr::mutate(response = rnorm(n = dplyr::n())) |>
brm_data_change() |>
brm_simulate_continuous(names = c("biomarker1", "biomarker2")) |>
brm_simulate_categorical(
  names = c("status1", "status2"),
  levels = c("present", "absent")
)
dplyr::select(
  data,
  group,
  time,
  patient,
  starts_with("biomarker"),
  starts_with("status")
)
archetype <- brm_archetype_average_effects(data)
archetype
summary(archetype)
formula <- brm_formula(archetype)
formula
prior <- brm_prior_label(
```

```

    code = "normal(1, 2.2)",
    group = "group_1",
    time = "time_2"
  ) |>
  brm_prior_label("normal(1, 3.3)", group = "group_1", time = "time_3") |>
  brm_prior_label("normal(1, 4.4)", group = "group_1", time = "time_4") |>
  brm_prior_label("normal(2, 2.2)", group = "group_2", time = "time_2") |>
  brm_prior_label("normal(2, 3.3)", group = "group_2", time = "time_3") |>
  brm_prior_label("normal(2, 4.4)", group = "group_2", time = "time_4") |>
  brm_prior_archetype(archetype)
prior
class(prior)
if (identical(Sys.getenv("BRM_EXAMPLES", unset = ""), "true")) {
  tmp <- utils::capture.output(
    suppressMessages(
      suppressWarnings(
        model <- brm_model(
          data = archetype,
          formula = formula,
          prior = prior,
          chains = 1,
          iter = 100,
          refresh = 0
        )
      )
    )
  )
  suppressWarnings(print(model))
  brms::prior_summary(model)
  draws <- brm_marginal_draws(
    data = archetype,
    formula = formula,
    model = model
  )
  summaries_model <- brm_marginal_summaries(draws)
  summaries_data <- brm_marginal_data(data)
  brm_plot_compare(model = summaries_model, data = summaries_data)
}

```

brm_archetype_cells *Cell means archetype*

Description

Create an informative prior archetype for cell means.

Usage

```
brm_archetype_cells(
  data,
```

```

covariates = TRUE,
prefix_interest = "x_",
prefix_nuisance = "nuisance_",
baseline = !is.null(attr(data, "brm_baseline")),
baseline_subgroup = !is.null(attr(data, "brm_baseline")) && !is.null(attr(data,
  "brm_subgroup")),
baseline_subgroup_time = !is.null(attr(data, "brm_baseline")) && !is.null(attr(data,
  "brm_subgroup")),
baseline_time = !is.null(attr(data, "brm_baseline"))
)

```

Arguments

data	A classed data frame from <code>brm_data()</code> , or an informative prior archetype from a function like <code>brm_archetype_successive_cells()</code> .
covariates	Logical of length 1. TRUE (default) to include any additive covariates declared with the <code>covariates</code> argument of <code>brm_data()</code> , FALSE to omit. For informative prior archetypes, this option is set in functions like <code>brm_archetype_successive_cells()</code> rather than in <code>brm_formula()</code> in order to make sure columns are appropriately centered and the underlying model matrix has full rank.
prefix_interest	Character string to prepend to the new columns of generated fixed effects of interest (relating to group, subgroup, and/or time). In rare cases, you may need to set a non-default prefix to prevent name conflicts with existing columns in the data, or rename the columns in your data. <code>prefix_interest</code> must not be the same value as <code>prefix_nuisance</code> .
prefix_nuisance	Same as <code>prefix_interest</code> , but relating to generated fixed effects NOT of interest (not relating to group, subgroup, or time). Must not be the same value as <code>prefix_interest</code> .
baseline	Logical of length 1. TRUE to include an additive effect for baseline response, FALSE to omit. Default is TRUE if <code>brm_data()</code> previously declared a baseline variable in the dataset. Ignored for informative prior archetypes. For informative prior archetypes, this option should be set in functions like <code>brm_archetype_successive_cells()</code> rather than in <code>brm_formula()</code> in order to make sure columns are appropriately centered and the underlying model matrix has full rank.
baseline_subgroup	Logical of length 1.
baseline_subgroup_time	Logical of length 1. TRUE to include baseline-by-subgroup-by-time interaction, FALSE to omit. Default is TRUE if <code>brm_data()</code> previously declared baseline and subgroup variables in the dataset. Ignored for informative prior archetypes. For informative prior archetypes, this option should be set in functions like <code>brm_archetype_successive_cells()</code> rather than in <code>brm_formula()</code> in order to make sure columns are appropriately centered and the underlying model matrix has full rank.

`baseline_time` Logical of length 1. TRUE to include baseline-by-time interaction, FALSE to omit. Default is TRUE if `brm_data()` previously declared a baseline variable in the dataset. Ignored for informative prior archetypes. For informative prior archetypes, this option should be set in functions like `brm_archetype_successive_cells()` rather than in `brm_formula()` in order to make sure columns are appropriately centered and the underlying model matrix has full rank.

Details

In this archetype, each fixed effect is a cell mean: the group mean for a given value of treatment group and discrete time (and subgroup level, if applicable).

Value

A special classed tibble with data tailored to the successive differences archetype. The dataset is augmented with extra columns with the "archetype_" prefix, as well as special attributes to tell downstream functions like `brm_formula()` what to do with the object.

Prior labeling for `brm_archetype_cells()`

Within each treatment group, each model parameter is a cell mean, and the labeling scheme in `brm_prior_label()` and `brm_prior_archetype()` translate easily. For example, `brm_prior_label(code = "normal(1.2, 5)", group = "B", time = "VISIT2")` declares a normal(1.2, 5) prior on the cell mean of treatment group B at discrete time point VISIT2. To confirm that you set the prior correctly, compare the brms prior with the output of `summary(your_archetype)`. See the examples for details.

Nuisance variables

In the presence of covariate adjustment, functions like `brm_archetype_successive_cells()` convert nuisance factors into binary dummy variables, then center all those dummy variables and any continuous nuisance variables at their means in the data. This ensures that the main model coefficients of interest are not implicitly conditional on a subset of the data. In other words, preprocessing nuisance variables this way preserves the interpretations of the fixed effects of interest, and it ensures informative priors can be specified correctly.

Prior labeling

Informative prior archetypes use a labeling scheme to assign priors to fixed effects. How it works:

1. First, assign the prior of each parameter a collection of labels from the data. This can be done manually or with successive calls to `[brm_prior_label()]`.
2. Supply the labeling scheme to `[brm_prior_archetype()]`. `[brm_prior_archetype()]` uses attributes of the archetype to map labeled priors to their rightful parameters in the model.

For informative prior archetypes, this process is much more convenient and robust than manually calling `brms::set_prior()`. However, it requires an understanding of how the labels of the priors

map to parameters in the model. This mapping varies from archetype to archetype, and it is documented in the help pages of archetype-specific functions such as `brm_archetype_successive_cells()`.

See Also

Other informative prior archetypes: `brm_archetype_average_cells()`, `brm_archetype_average_effects()`, `brm_archetype_effects()`, `brm_archetype_successive_cells()`, `brm_archetype_successive_effects()`

Examples

```
set.seed(0L)
data <- brm_simulate_outline(
  n_group = 2,
  n_patient = 100,
  n_time = 4,
  rate_dropout = 0,
  rate_lapse = 0
) |>
dplyr::mutate(response = rnorm(n = dplyr::n())) |>
brm_data_change() |>
brm_simulate_continuous(names = c("biomarker1", "biomarker2")) |>
brm_simulate_categorical(
  names = c("status1", "status2"),
  levels = c("present", "absent")
)
dplyr::select(
  data,
  group,
  time,
  patient,
  starts_with("biomarker"),
  starts_with("status")
)
archetype <- brm_archetype_cells(data)
archetype
summary(archetype)
formula <- brm_formula(archetype)
formula
prior <- brm_prior_label(
  code = "normal(1, 2.2)",
  group = "group_1",
  time = "time_2"
) |>
brm_prior_label("normal(1, 3.3)", group = "group_1", time = "time_3") |>
brm_prior_label("normal(1, 4.4)", group = "group_1", time = "time_4") |>
brm_prior_label("normal(2, 2.2)", group = "group_2", time = "time_2") |>
brm_prior_label("normal(2, 3.3)", group = "group_2", time = "time_3") |>
brm_prior_label("normal(2, 4.4)", group = "group_2", time = "time_4") |>
brm_prior_archetype(archetype)
prior
class(prior)
if (identical(Sys.getenv("BRM_EXAMPLES", unset = ""), "true")) {
```

```

tmp <- utils::capture.output(
  suppressMessages(
    suppressWarnings(
      model <- brm_model(
        data = archetype,
        formula = formula,
        prior = prior,
        chains = 1,
        iter = 100,
        refresh = 0
      )
    )
  )
)
suppressWarnings(print(model))
brms::prior_summary(model)
draws <- brm_marginal_draws(
  data = archetype,
  formula = formula,
  model = model
)
summaries_model <- brm_marginal_summaries(draws)
summaries_data <- brm_marginal_data(data)
brm_plot_compare(model = summaries_model, data = summaries_data)
}

```

brm_archetype_effects *Treatment effect archetype*

Description

Create an informative prior archetype for a simple treatment effect parameterization.

Usage

```

brm_archetype_effects(
  data,
  covariates = TRUE,
  prefix_interest = "x_",
  prefix_nuisance = "nuisance_",
  baseline = !is.null(attr(data, "brm_baseline")),
  baseline_subgroup = !is.null(attr(data, "brm_baseline")) && !is.null(attr(data,
    "brm_subgroup")),
  baseline_subgroup_time = !is.null(attr(data, "brm_baseline")) && !is.null(attr(data,
    "brm_subgroup")),
  baseline_time = !is.null(attr(data, "brm_baseline"))
)

```

Arguments

data	A classed data frame from <code>brm_data()</code> , or an informative prior archetype from a function like <code>brm_archetype_successive_cells()</code> .
covariates	Logical of length 1. TRUE (default) to include any additive covariates declared with the <code>covariates</code> argument of <code>brm_data()</code> , FALSE to omit. For informative prior archetypes, this option is set in functions like <code>brm_archetype_successive_cells()</code> rather than in <code>brm_formula()</code> in order to make sure columns are appropriately centered and the underlying model matrix has full rank.
prefix_interest	Character string to prepend to the new columns of generated fixed effects of interest (relating to group, subgroup, and/or time). In rare cases, you may need to set a non-default prefix to prevent name conflicts with existing columns in the data, or rename the columns in your data. <code>prefix_interest</code> must not be the same value as <code>prefix_nuisance</code> .
prefix_nuisance	Same as <code>prefix_interest</code> , but relating to generated fixed effects NOT of interest (not relating to group, subgroup, or time). Must not be the same value as <code>prefix_interest</code> .
baseline	Logical of length 1. TRUE to include an additive effect for baseline response, FALSE to omit. Default is TRUE if <code>brm_data()</code> previously declared a baseline variable in the dataset. Ignored for informative prior archetypes. For informative prior archetypes, this option should be set in functions like <code>brm_archetype_successive_cells()</code> rather than in <code>brm_formula()</code> in order to make sure columns are appropriately centered and the underlying model matrix has full rank.
baseline_subgroup	Logical of length 1.
baseline_subgroup_time	Logical of length 1. TRUE to include baseline-by-subgroup-by-time interaction, FALSE to omit. Default is TRUE if <code>brm_data()</code> previously declared baseline and subgroup variables in the dataset. Ignored for informative prior archetypes. For informative prior archetypes, this option should be set in functions like <code>brm_archetype_successive_cells()</code> rather than in <code>brm_formula()</code> in order to make sure columns are appropriately centered and the underlying model matrix has full rank.
baseline_time	Logical of length 1. TRUE to include baseline-by-time interaction, FALSE to omit. Default is TRUE if <code>brm_data()</code> previously declared a baseline variable in the dataset. Ignored for informative prior archetypes. For informative prior archetypes, this option should be set in functions like <code>brm_archetype_successive_cells()</code> rather than in <code>brm_formula()</code> in order to make sure columns are appropriately centered and the underlying model matrix has full rank.

Details

In this archetype, each fixed effect is either a placebo response or a treatment effect.

To illustrate, suppose the dataset has two treatment groups A and B, time points 1, 2, and 3, and no other covariates. Assume group A is the reference group (e.g. placebo). Let μ_{gt} be the marginal

mean of the response at group g time t given data and hyperparameters. The model has fixed effect parameters $\beta_1, \beta_2, \dots, \beta_6$ which express the marginal means μ_{gt} as follows:

```

`mu_A1 = beta_1`
`mu_A2 = beta_2`
`mu_A3 = beta_3`

`mu_B1 = beta_1 + beta_4`
`mu_B2 = beta_2 + beta_5`
`mu_B3 = beta_3 + beta_6`

```

Above, β_2 is the group mean of treatment group A at time 2, and β_5 is the treatment effect of B relative to A at time 2.

Value

A special classed tibble with data tailored to the successive differences archetype. The dataset is augmented with extra columns with the "archetype_" prefix, as well as special attributes to tell downstream functions like `brm_formula()` what to do with the object.

Prior labeling for `brm_archetype_effects()`

In the reference group (e.g. placebo) each fixed effect is a cell mean at a time point. In each non-reference group, each fixed effect is the treatment effect relative to the reference (at a time point). The labeling scheme in `brm_prior_label()` and `brm_prior_archetype()` translate straightforwardly. For example, `brm_prior_label(code = "normal(1.2, 5)", group = "A", time = "2")` declares a $\text{normal}(1.2, 5)$ on β_2 (cell mean of the reference group at time 2). Similarly, `brm_prior_label(code = "normal(1.3, 6)", group = "B", time = "2")` declares a $\text{normal}(1.3, 6)$ prior on the treatment effect of group B relative to group A at discrete time point 2. To confirm that you set the prior correctly, compare the brms prior with the output of `summary(your_archetype)`. See the examples for details.

Nuisance variables

In the presence of covariate adjustment, functions like `brm_archetype_successive_cells()` convert nuisance factors into binary dummy variables, then center all those dummy variables and any continuous nuisance variables at their means in the data. This ensures that the main model coefficients of interest are not implicitly conditional on a subset of the data. In other words, preprocessing nuisance variables this way preserves the interpretations of the fixed effects of interest, and it ensures informative priors can be specified correctly.

Prior labeling

Informative prior archetypes use a labeling scheme to assign priors to fixed effects. How it works:

1. First, assign the prior of each parameter a collection of labels from the data. This can be done manually or with successive calls to `[brm_prior_label()]`.
2. Supply the labeling scheme to `[brm_prior_archetype()]`.

[`brm_prior_archetype()`] uses attributes of the archetype to map labeled priors to their rightful parameters in the model.

For informative prior archetypes, this process is much more convenient and robust than manually calling `brms::set_prior()`. However, it requires an understanding of how the labels of the priors map to parameters in the model. This mapping varies from archetype to archetype, and it is documented in the help pages of archetype-specific functions such as `brm_archetype_successive_cells()`.

See Also

Other informative prior archetypes: `brm_archetype_average_cells()`, `brm_archetype_average_effects()`, `brm_archetype_cells()`, `brm_archetype_successive_cells()`, `brm_archetype_successive_effects()`

Examples

```
set.seed(0L)
data <- brm_simulate_outline(
  n_group = 2,
  n_patient = 100,
  n_time = 4,
  rate_dropout = 0,
  rate_lapse = 0
) |>
dplyr::mutate(response = rnorm(n = dplyr::n())) |>
brm_data_change() |>
brm_simulate_continuous(names = c("biomarker1", "biomarker2")) |>
brm_simulate_categorical(
  names = c("status1", "status2"),
  levels = c("present", "absent")
)
dplyr::select(
  data,
  group,
  time,
  patient,
  starts_with("biomarker"),
  starts_with("status")
)
archetype <- brm_archetype_effects(data)
archetype
summary(archetype)
formula <- brm_formula(archetype)
formula
prior <- brm_prior_label(
  code = "normal(1, 2.2)",
  group = "group_1",
  time = "time_2"
) |>
brm_prior_label("normal(1, 3.3)", group = "group_1", time = "time_3") |>
brm_prior_label("normal(1, 4.4)", group = "group_1", time = "time_4") |>
brm_prior_label("normal(2, 2.2)", group = "group_2", time = "time_2") |>
brm_prior_label("normal(2, 3.3)", group = "group_2", time = "time_3") |>
```

```

    brm_prior_label("normal(2, 4.4)", group = "group_2", time = "time_4") |>
    brm_prior_archetype(archetype)
prior
class(prior)
if (identical(Sys.getenv("BRM_EXAMPLES", unset = ""), "true")) {
tmp <- utils::capture.output(
  suppressMessages(
    suppressWarnings(
      model <- brm_model(
        data = archetype,
        formula = formula,
        prior = prior,
        chains = 1,
        iter = 100,
        refresh = 0
      )
    )
  )
)
suppressWarnings(print(model))
brms::prior_summary(model)
draws <- brm_marginal_draws(
  data = archetype,
  formula = formula,
  model = model
)
summaries_model <- brm_marginal_summaries(draws)
summaries_data <- brm_marginal_data(data)
brm_plot_compare(model = summaries_model, data = summaries_data)
}

```

brm_archetype_successive_cells

Cell-means-like successive differences archetype

Description

Create an informative prior archetype where the fixed effects are successive differences between adjacent time points.

Usage

```

brm_archetype_successive_cells(
  data,
  covariates = TRUE,
  prefix_interest = "x_",
  prefix_nuisance = "nuisance_",
  baseline = !is.null(attr(data, "brm_baseline")),
  baseline_subgroup = !is.null(attr(data, "brm_baseline")) && !is.null(attr(data,

```

```

    "brm_subgroup")),
  baseline_subgroup_time = !is.null(attr(data, "brm_baseline")) && !is.null(attr(data,
    "brm_subgroup")),
  baseline_time = !is.null(attr(data, "brm_baseline"))
)

```

Arguments

data	A classed data frame from <code>brm_data()</code> , or an informative prior archetype from a function like <code>brm_archetype_successive_cells()</code> .
covariates	Logical of length 1. TRUE (default) to include any additive covariates declared with the <code>covariates</code> argument of <code>brm_data()</code> , FALSE to omit. For informative prior archetypes, this option is set in functions like <code>brm_archetype_successive_cells()</code> rather than in <code>brm_formula()</code> in order to make sure columns are appropriately centered and the underlying model matrix has full rank.
prefix_interest	Character string to prepend to the new columns of generated fixed effects of interest (relating to group, subgroup, and/or time). In rare cases, you may need to set a non-default prefix to prevent name conflicts with existing columns in the data, or rename the columns in your data. <code>prefix_interest</code> must not be the same value as <code>prefix_nuisance</code> .
prefix_nuisance	Same as <code>prefix_interest</code> , but relating to generated fixed effects NOT of interest (not relating to group, subgroup, or time). Must not be the same value as <code>prefix_interest</code> .
baseline	Logical of length 1. TRUE to include an additive effect for baseline response, FALSE to omit. Default is TRUE if <code>brm_data()</code> previously declared a baseline variable in the dataset. Ignored for informative prior archetypes. For informative prior archetypes, this option should be set in functions like <code>brm_archetype_successive_cells()</code> rather than in <code>brm_formula()</code> in order to make sure columns are appropriately centered and the underlying model matrix has full rank.
baseline_subgroup	Logical of length 1.
baseline_subgroup_time	Logical of length 1. TRUE to include baseline-by-subgroup-by-time interaction, FALSE to omit. Default is TRUE if <code>brm_data()</code> previously declared baseline and subgroup variables in the dataset. Ignored for informative prior archetypes. For informative prior archetypes, this option should be set in functions like <code>brm_archetype_successive_cells()</code> rather than in <code>brm_formula()</code> in order to make sure columns are appropriately centered and the underlying model matrix has full rank.
baseline_time	Logical of length 1. TRUE to include baseline-by-time interaction, FALSE to omit. Default is TRUE if <code>brm_data()</code> previously declared a baseline variable in the dataset. Ignored for informative prior archetypes. For informative prior archetypes, this option should be set in functions like <code>brm_archetype_successive_cells()</code> rather than in <code>brm_formula()</code> in order to make sure columns are appropriately centered and the underlying model matrix has full rank.

Details

In this archetype, each fixed effect is either an intercept on the first time point or the difference between two adjacent time points, and each treatment group has its own set of fixed effects independent of the other treatment groups.

To illustrate, suppose the dataset has two treatment groups A and B, time points 1, 2, and 3, and no other covariates. Let μ_{gt} be the marginal mean of the response at group g time t given data and hyperparameters. The model has fixed effect parameters $\beta_1, \beta_2, \dots, \beta_6$ which express the marginal means μ_{gt} as follows:

```

`mu_A1 = beta_1`
`mu_A2 = beta_1 + beta_2`
`mu_A3 = beta_1 + beta_2 + beta_3`

`mu_B1 = beta_4`
`mu_B2 = beta_4 + beta_5`
`mu_B3 = beta_4 + beta_5 + beta_6`

```

For group A, β_1 is the time 1 intercept, β_2 represents time 2 minus time 1, and β_3 represents time 3 minus time 2. β_4, β_5 , and β_6 represent the analogous roles.

Value

A special classed tibble with data tailored to the successive differences archetype. The dataset is augmented with extra columns with the "archetype_" prefix, as well as special attributes to tell downstream functions like `brm_formula()` what to do with the object.

Nuisance variables

In the presence of covariate adjustment, functions like `brm_archetype_successive_cells()` convert nuisance factors into binary dummy variables, then center all those dummy variables and any continuous nuisance variables at their means in the data. This ensures that the main model coefficients of interest are not implicitly conditional on a subset of the data. In other words, preprocessing nuisance variables this way preserves the interpretations of the fixed effects of interest, and it ensures informative priors can be specified correctly.

Prior labeling for `brm_archetype_successive_cells()`

Within each treatment group, each intercept is labeled by the earliest time point, and each successive difference term gets the successive time point as the label. To illustrate, consider the example in the Details section. In the labeling scheme for `brm_archetype_successive_cells()`, you can label the prior on β_1 using `brm_prior_label(code = "normal(1.2, 5)", group = "A", time = "1")`. Similarly, you can label the prior on β_5 with `brm_prior_label(code = "normal(1.3, 7)", group = "B", time = "2")`. To confirm that you set the prior correctly, compare the brms prior with the output of `summary(your_archetype)`. See the examples for details.

Prior labeling

Informative prior archetypes use a labeling scheme to assign priors to fixed effects. How it works:

1. First, assign the prior of each parameter a collection of labels from the data. This can be done manually or with successive calls to `[brm_prior_label()]`.
2. Supply the labeling scheme to `[brm_prior_archetype()]`. `[brm_prior_archetype()]` uses attributes of the archetype to map labeled priors to their rightful parameters in the model.

For informative prior archetypes, this process is much more convenient and robust than manually calling `brms::set_prior()`. However, it requires an understanding of how the labels of the priors map to parameters in the model. This mapping varies from archetype to archetype, and it is documented in the help pages of archetype-specific functions such as `brm_archetype_successive_cells()`.

See Also

Other informative prior archetypes: `brm_archetype_average_cells()`, `brm_archetype_average_effects()`, `brm_archetype_cells()`, `brm_archetype_effects()`, `brm_archetype_successive_effects()`

Examples

```
set.seed(0L)
data <- brm_simulate_outline(
  n_group = 2,
  n_patient = 100,
  n_time = 4,
  rate_dropout = 0,
  rate_lapse = 0
) |>
dplyr::mutate(response = rnorm(n = dplyr::n())) |>
brm_data_change() |>
brm_simulate_continuous(names = c("biomarker1", "biomarker2")) |>
brm_simulate_categorical(
  names = c("status1", "status2"),
  levels = c("present", "absent")
)
dplyr::select(
  data,
  group,
  time,
  patient,
  starts_with("biomarker"),
  starts_with("status")
)
archetype <- brm_archetype_successive_cells(data)
archetype
summary(archetype)
formula <- brm_formula(archetype)
formula
prior <- brm_prior_label(
  code = "normal(1, 2.2)",
  group = "group_1",
  time = "time_2"
) |>
```

```

brm_prior_label("normal(1, 3.3)", group = "group_1", time = "time_3") |>
brm_prior_label("normal(1, 4.4)", group = "group_1", time = "time_4") |>
brm_prior_label("normal(2, 2.2)", group = "group_2", time = "time_2") |>
brm_prior_label("normal(2, 3.3)", group = "group_2", time = "time_3") |>
brm_prior_label("normal(2, 4.4)", group = "group_2", time = "time_4") |>
brm_prior_archetype(archetype)
prior
class(prior)
if (identical(Sys.getenv("BRM_EXAMPLES", unset = ""), "true")) {
tmp <- utils::capture.output(
  suppressMessages(
    suppressWarnings(
      model <- brm_model(
        data = archetype,
        formula = formula,
        prior = prior,
        chains = 1,
        iter = 100,
        refresh = 0
      )
    )
  )
)
suppressWarnings(print(model))
brms::prior_summary(model)
draws <- brm_marginal_draws(
  data = archetype,
  formula = formula,
  model = model
)
summaries_model <- brm_marginal_summaries(draws)
summaries_data <- brm_marginal_data(data)
brm_plot_compare(model = summaries_model, data = summaries_data)
}

```

brm_archetype_successive_effects

Treatment-effect-like successive differences archetype

Description

Create an informative prior archetype where the fixed effects are successive differences between adjacent time points and terms in non-reference groups are treatment effects.

Usage

```

brm_archetype_successive_effects(
  data,
  covariates = TRUE,
  prefix_interest = "x_",

```

```

prefix_nuisance = "nuisance_",
baseline = !is.null(attr(data, "brm_baseline")),
baseline_subgroup = !is.null(attr(data, "brm_baseline")) && !is.null(attr(data,
  "brm_subgroup")),
baseline_subgroup_time = !is.null(attr(data, "brm_baseline")) && !is.null(attr(data,
  "brm_subgroup")),
baseline_time = !is.null(attr(data, "brm_baseline"))
)

```

Arguments

data	A classed data frame from <code>brm_data()</code> , or an informative prior archetype from a function like <code>brm_archetype_successive_cells()</code> .
covariates	Logical of length 1. TRUE (default) to include any additive covariates declared with the <code>covariates</code> argument of <code>brm_data()</code> , FALSE to omit. For informative prior archetypes, this option is set in functions like <code>brm_archetype_successive_cells()</code> rather than in <code>brm_formula()</code> in order to make sure columns are appropriately centered and the underlying model matrix has full rank.
prefix_interest	Character string to prepend to the new columns of generated fixed effects of interest (relating to group, subgroup, and/or time). In rare cases, you may need to set a non-default prefix to prevent name conflicts with existing columns in the data, or rename the columns in your data. <code>prefix_interest</code> must not be the same value as <code>prefix_nuisance</code> .
prefix_nuisance	Same as <code>prefix_interest</code> , but relating to generated fixed effects NOT of interest (not relating to group, subgroup, or time). Must not be the same value as <code>prefix_interest</code> .
baseline	Logical of length 1. TRUE to include an additive effect for baseline response, FALSE to omit. Default is TRUE if <code>brm_data()</code> previously declared a baseline variable in the dataset. Ignored for informative prior archetypes. For informative prior archetypes, this option should be set in functions like <code>brm_archetype_successive_cells()</code> rather than in <code>brm_formula()</code> in order to make sure columns are appropriately centered and the underlying model matrix has full rank.
baseline_subgroup	Logical of length 1.
baseline_subgroup_time	Logical of length 1. TRUE to include baseline-by-subgroup-by-time interaction, FALSE to omit. Default is TRUE if <code>brm_data()</code> previously declared baseline and subgroup variables in the dataset. Ignored for informative prior archetypes. For informative prior archetypes, this option should be set in functions like <code>brm_archetype_successive_cells()</code> rather than in <code>brm_formula()</code> in order to make sure columns are appropriately centered and the underlying model matrix has full rank.
baseline_time	Logical of length 1. TRUE to include baseline-by-time interaction, FALSE to omit. Default is TRUE if <code>brm_data()</code> previously declared a baseline variable in the dataset. Ignored for informative prior archetypes. For informative prior

archetypes, this option should be set in functions like `brm_archetype_successive_cells()` rather than in `brm_formula()` in order to make sure columns are appropriately centered and the underlying model matrix has full rank.

Details

Within the reference treatment group (e.g. placebo), each fixed effect is either an intercept on the first time point or the difference between two adjacent time points. In each non-reference treatment group, each model parameter is defined as an effect relative to the reference group.

To illustrate, suppose the dataset has two treatment groups A and B, time points 1, 2, and 3, and no other covariates. Say group A is the reference group (e.g. placebo). Let μ_{gt} be the marginal mean of the response at group g time t given data and hyperparameters. The model has fixed effect parameters $\beta_1, \beta_2, \dots, \beta_6$ which express the marginal means μ_{gt} as follows:

```

`mu_A1 = beta_1`
`mu_A2 = beta_1 + beta_2`
`mu_A3 = beta_1 + beta_2 + beta_3`

`mu_B1 = beta_1 + beta_4`
`mu_B2 = beta_1 + beta_2 + beta_4 + beta_5`
`mu_B3 = beta_1 + beta_2 + beta_3 + beta_4 + beta_5 + beta_6`

```

For group A, β_1 is the time 1 intercept, β_2 represents time 2 minus time 1, and β_3 represents time 3 minus time 2. β_4 is the treatment effect of group B relative to group A at time 1. β_5 is the treatment effect of the difference between times 2 and 1, relative to treatment group A. Similarly, β_6 is the treatment effect of the difference between times 3 and 2, relative to treatment group A.

Value

A special classed tibble with data tailored to the successive differences archetype. The dataset is augmented with extra columns with the "archetype_" prefix, as well as special attributes to tell downstream functions like `brm_formula()` what to do with the object.

Prior labeling for `brm_archetype_successive_effects()`

Within each treatment group, each intercept is labeled by the earliest time point, and each successive difference term gets the successive time point as the label. To illustrate, consider the example in the Details section. In the labeling scheme for `brm_archetype_successive_effects()`, you can label the prior on β_1 using `brm_prior_label(code = "normal(1.2, 5)", group = "A", time = "1")`. Similarly, you can label the prior on β_5 with `brm_prior_label(code = "normal(1.3, 7)", group = "B", time = "2")`. To confirm that you set the prior correctly, compare the brms prior with the output of `summary(your_archetype)`. See the examples for details.

Nuisance variables

In the presence of covariate adjustment, functions like `brm_archetype_successive_cells()` convert nuisance factors into binary dummy variables, then center all those dummy variables and any

continuous nuisance variables at their means in the data. This ensures that the main model coefficients of interest are not implicitly conditional on a subset of the data. In other words, preprocessing nuisance variables this way preserves the interpretations of the fixed effects of interest, and it ensures informative priors can be specified correctly.

Prior labeling

Informative prior archetypes use a labeling scheme to assign priors to fixed effects. How it works:

1. First, assign the prior of each parameter a collection of labels from the data. This can be done manually or with successive calls to `[brm_prior_label()]`.
2. Supply the labeling scheme to `[brm_prior_archetype()]`. `[brm_prior_archetype()]` uses attributes of the archetype to map labeled priors to their rightful parameters in the model.

For informative prior archetypes, this process is much more convenient and robust than manually calling `brms::set_prior()`. However, it requires an understanding of how the labels of the priors map to parameters in the model. This mapping varies from archetype to archetype, and it is documented in the help pages of archetype-specific functions such as `brm_archetype_successive_cells()`.

See Also

Other informative prior archetypes: `brm_archetype_average_cells()`, `brm_archetype_average_effects()`, `brm_archetype_cells()`, `brm_archetype_effects()`, `brm_archetype_successive_cells()`

Examples

```
set.seed(0L)
data <- brm_simulate_outline(
  n_group = 2,
  n_patient = 100,
  n_time = 4,
  rate_dropout = 0,
  rate_lapse = 0
) |>
dplyr::mutate(response = rnorm(n = dplyr::n())) |>
brm_data_change() |>
brm_simulate_continuous(names = c("biomarker1", "biomarker2")) |>
brm_simulate_categorical(
  names = c("status1", "status2"),
  levels = c("present", "absent")
)
dplyr::select(
  data,
  group,
  time,
  patient,
  starts_with("biomarker"),
  starts_with("status")
)
```

```

archetype <- brm_archetype_successive_effects(data)
archetype
summary(archetype)
formula <- brm_formula(archetype)
formula
prior <- brm_prior_label(
  code = "normal(1, 2.2)",
  group = "group_1",
  time = "time_2"
) |>
brm_prior_label("normal(1, 3.3)", group = "group_1", time = "time_3") |>
brm_prior_label("normal(1, 4.4)", group = "group_1", time = "time_4") |>
brm_prior_label("normal(2, 2.2)", group = "group_2", time = "time_2") |>
brm_prior_label("normal(2, 3.3)", group = "group_2", time = "time_3") |>
brm_prior_label("normal(2, 4.4)", group = "group_2", time = "time_4") |>
brm_prior_archetype(archetype)
prior
class(prior)
if (identical(Sys.getenv("BRM_EXAMPLES", unset = ""), "true")) {
  tmp <- utils::capture.output(
    suppressMessages(
      suppressWarnings(
        model <- brm_model(
          data = archetype,
          formula = formula,
          prior = prior,
          chains = 1,
          iter = 100,
          refresh = 0
        )
      )
    )
  )
  suppressWarnings(print(model))
  brms::prior_summary(model)
  draws <- brm_marginal_draws(
    data = archetype,
    formula = formula,
    model = model
  )
  summaries_model <- brm_marginal_summaries(draws)
  summaries_data <- brm_marginal_data(data)
  brm_plot_compare(model = summaries_model, data = summaries_data)
}

```

brm_data

Create and preprocess an MMRM dataset.

Description

Create a dataset to analyze with an MMRM.

Usage

```
brm_data(
  data,
  outcome = "CHG",
  role = "change",
  baseline = NULL,
  group = "TRT01P",
  subgroup = NULL,
  time = "AVISIT",
  patient = "USUBJID",
  covariates = character(0L),
  missing = NULL,
  reference_group = "Placebo",
  level_control = NULL,
  reference_subgroup = NULL,
  reference_time = NULL,
  level_baseline = NULL
)
```

Arguments

data	Data frame or tibble with longitudinal data.
outcome	Character of length 1, name of the outcome variable.
role	Character of length 1. Either "response" if outcome is the raw response variable (e.g. AVAL) or "change" if outcome is change from baseline (e.g. CHG).
baseline	Character of length 1, name of the baseline response variable. Only relevant if the response variable is change from baseline. Supply NULL to ignore or omit.
group	Character of length 1, name of the treatment group variable. Must point to a character vector in the data. Factors are converted to characters.
subgroup	Character of length 1, optional name of the a discrete subgroup variable. Set to NULL to omit the subgroup (default).
time	Character of length 1, name of the discrete time variable. Must point to a character vector in the data. Factors are converted to characters.
patient	Character of length 1, name of the patient ID variable.
covariates	Character vector of names of other covariates.
missing	Character of length 1, name of an optional variable in a simulated dataset to indicate which outcome values should be missing. Set to NULL to omit.
reference_group	Character of length 1, Level of the group column to indicate the control group. reference_group only applies to the post-processing that happens in functions like brm_marginal_draws() downstream of the model. It does not control the fixed effect mapping in the model matrix that brms derives from the formula from brm_formula() .
level_control	Deprecated on 2024-01-11 (version 0.2.0.9002). Use reference_group instead.

reference_subgroup	Character of length 1, level of the subgroup column to use as a reference for pairwise differences in when computing marginal means downstream of the model. It does not control the fixed effect mapping in the model matrix that brms derives from the formula from <code>brm_formula()</code> .
reference_time	Character of length 1 or NULL, level of the time column to indicate the baseline time point. This value should not be present in the data if the outcome variable is change from baseline, but it must be in the data if the outcome variable is the raw response so that <code>brms.mmrn</code> can produce model-based marginal estimates of change from baseline. In other words, set <code>reference_time</code> to NULL if role is "change", and set <code>reference_time</code> to a non-null value in <code>data[[time]]</code> if role is "response". Note: <code>reference_time</code> only applies to the post-processing that happens in functions like <code>brm_marginal_draws()</code> downstream of the model. It does not control the fixed effect mapping in the model matrix that brms derives from the formula from <code>brm_formula()</code> .
level_baseline	Deprecated on 2024-01-11 (version 0.2.0.9002). Use <code>reference_time</code> instead.

Value

A classed tibble with attributes which denote features of the data such as the treatment group and discrete time variables.

Preprocessing

The preprocessing steps in `brm_data()` are as follows:

- Perform basic assertions to make sure the data and other arguments are properly formatted.
- Convert the group and time columns to character vectors.
- Sanitize the levels of the group and time columns using `make.names(unique = FALSE, allow_ = TRUE)` to ensure agreement between the data and the output of brms.
- For each implicitly missing outcome observation, add explicit row with the outcome variable equal to `NA_real_`.
- Arrange the rows of the data by group, then patient, then discrete time.
- Select only the columns of the data relevant to an MMRM analysis.

Separation string

Post-processing in `brm_marginal_draws()` names each of the group-by-time marginal means with the delimiting character string from `Sys.getenv("BRM_SEP", unset = "|")`. Neither the column names nor element names of the group and time variables can contain this string. To set a custom string yourself, use `Sys.setenv(BRM_SEP = "YOUR_CUSTOM_STRING")`.

See Also

Other data: `brm_data_change()`

Examples

```

set.seed(0)
data <- brm_simulate_simple()$data
colnames(data) <- paste0("col_", colnames(data))
data
brm_data(
  data = data,
  outcome = "col_response",
  role = "response",
  group = "col_group",
  time = "col_time",
  patient = "col_patient",
  reference_group = "group_1",
  reference_time = "time_1"
)

```

brm_data_change	<i>Convert to change from baseline.</i>
-----------------	---

Description

Convert a dataset from raw response to change from baseline.

Usage

```
brm_data_change(data, name_change = "change", name_baseline = "baseline")
```

Arguments

data	A classed tibble (e.g. from <code>brm_data()</code>) with raw response as the outcome variable (role = "response" in <code>brm_data()</code>).
name_change	Character of length 1, name of the new outcome column for change from baseline.
name_baseline	Character of length 1, name of the new column for the original baseline response.

Value

A classed tibble with change from baseline as the outcome variable and the internal attributes modified accordingly. A special baseline column is also created, and the original raw response column is removed. The new baseline column is comprised of the elements of the response variable corresponding to the `reference_time` argument of `brm_data()`.

If there is a column to denote missing values for simulation purposes, e.g. the "missing" column generated by `brm_simulate_outline()`, then missing baseline values are propagated accordingly such that change from baseline will be missing if either the post-baseline response is missing or the baseline response is missing.

See Also

Other data: [brm_data\(\)](#)

Examples

```
set.seed(0)
data <- brm_data(
  data = dplyr::rename(brm_simulate_simple()$data, y_values = response),
  outcome = "y_values",
  role = "response",
  group = "group",
  time = "time",
  patient = "patient",
  reference_group = "group_1",
  reference_time = "time_1"
)
data
attr(,"brm_role")
attr(,"brm_outcome")
attr(,"brm_baseline")
attr(,"brm_reference_time")
changed <- brm_data_change(data = data, name_change = "delta")
changed
attr(,"brm_role")
attr(,"brm_outcome")
attr(,"brm_baseline")
attr(,"brm_reference_time")
```

brm_formula

Model formula

Description

Build a model formula for an MMRM, either for a generic [brm_data\(\)](#) dataset or an informative prior archetype.

Usage

```
brm_formula(
  data,
  check_rank = TRUE,
  sigma = brms.mmr::brm_formula_sigma(data = data, check_rank = check_rank),
  correlation = "unstructured",
  autoregressive_order = 1L,
  moving_average_order = 1L,
  residual_covariance_arma_estimation = FALSE,
  ...
)
```

```

## Default S3 method:
brm_formula(
  data,
  check_rank = TRUE,
  sigma = brms.mmrn::brm_formula_sigma(data = data, check_rank = check_rank),
  correlation = "unstructured",
  autoregressive_order = 1L,
  moving_average_order = 1L,
  residual_covariance_arma_estimation = FALSE,
  intercept = TRUE,
  baseline = !is.null(attr(data, "brm_baseline")),
  baseline_subgroup = !is.null(attr(data, "brm_baseline")) && !is.null(attr(data,
    "brm_subgroup")),
  baseline_subgroup_time = !is.null(attr(data, "brm_baseline")) && !is.null(attr(data,
    "brm_subgroup")),
  baseline_time = !is.null(attr(data, "brm_baseline")),
  covariates = TRUE,
  group = TRUE,
  group_subgroup = !is.null(attr(data, "brm_subgroup")),
  group_subgroup_time = !is.null(attr(data, "brm_subgroup")),
  group_time = TRUE,
  subgroup = !is.null(attr(data, "brm_subgroup")),
  subgroup_time = !is.null(attr(data, "brm_subgroup")),
  time = TRUE,
  ...,
  effect_baseline = NULL,
  effect_group = NULL,
  effect_time = NULL,
  interaction_baseline = NULL,
  interaction_group = NULL
)

## S3 method for class 'brms.mmrn_archetype'
brm_formula(
  data,
  check_rank = TRUE,
  sigma = brms.mmrn::brm_formula_sigma(data = data, check_rank = check_rank),
  correlation = "unstructured",
  autoregressive_order = 1L,
  moving_average_order = 1L,
  residual_covariance_arma_estimation = FALSE,
  ...
)

```

Arguments

data A classed data frame from [brm_data\(\)](#), or an informative prior archetype from a function like [brm_archetype_successive_cells\(\)](#).

check_rank	TRUE to check the rank of the model matrix and throw an error if rank deficiency is detected. FALSE to skip this check. Rank-deficient models may have non-identifiable parameters and it is recommended to choose a full-rank mapping.
sigma	A formula produced by <code>brm_formula_sigma()</code> . The formula is a base R formula with S3 class "brms_mmrn_formula_sigma", and it controls the parameterization of the residual standard deviations sigma.
correlation	Character of length 1, name of the correlation structure. The correlation matrix is a square $T \times T$ matrix, where T is the number of discrete time points in the data. This matrix describes the correlations between time points in the same patient, as modeled in the residuals. Different patients are modeled as independent. The correlation argument controls how this matrix is parameterized, and the choices given by brms are listed at https://paul-buerkner.github.io/brms/reference/autocor-terms.html , and the choice is ultimately encoded in the main body of the output formula through terms like <code>unstru()</code> and <code>arma()</code> , some of which are configurable through arguments <code>autoregressive_order</code> , <code>moving_average_order</code> , and <code>residual_covariance_arma_estimation</code> of <code>brm_formula()</code> . Choices in <code>brms.mmrn</code> : <ul style="list-style-type: none"> • "unstructured": the default/recommended option, a fully parameterized covariance matrix with a unique scalar parameter for each unique pair of discrete time points. C.f. https://paul-buerkner.github.io/brms/reference/unstr.html. • "autoregressive_moving_average": autoregressive moving average (ARMA), c.f. https://paul-buerkner.github.io/brms/reference/arma.html. • "autoregressive": autoregressive (AR), c.f. https://paul-buerkner.github.io/brms/reference/ar.html. • "moving_average": moving average (MA), c.f. https://paul-buerkner.github.io/brms/reference/ma.html. • "compound_symmetry": compound symmetry, c.f. https://paul-buerkner.github.io/brms/reference/cosy.html. • "diagonal": declare independent time points within patients.
autoregressive_order	Nonnegative integer, autoregressive order for the "autoregressive_moving_average" and "autoregressive" correlation structures.
moving_average_order	Nonnegative integer, moving average order for the "autoregressive_moving_average" and "moving_average" correlation structures.
residual_covariance_arma_estimation	TRUE or FALSE, whether to estimate ARMA effects using residual covariance matrices. Directly supplied to the <code>cov</code> argument in brms for "autoregressive_moving_average", "autoregressive", and "moving_average" correlation structures. C.f. https://paul-buerkner.github.io/brms/reference/arma.html .
...	Named arguments to specific <code>brm_formula()</code> methods.
intercept	Logical of length 1. TRUE (default) to include an intercept, FALSE to omit.
baseline	Logical of length 1. TRUE to include an additive effect for baseline response, FALSE to omit. Default is TRUE if <code>brm_data()</code> previously declared a baseline

variable in the dataset. Ignored for informative prior archetypes. For informative prior archetypes, this option should be set in functions like `brm_archetype_successive_cells()` rather than in `brm_formula()` in order to make sure columns are appropriately centered and the underlying model matrix has full rank.

<code>baseline_subgroup</code>	Logical of length 1.
<code>baseline_subgroup_time</code>	Logical of length 1. TRUE to include baseline-by-subgroup-by-time interaction, FALSE to omit. Default is TRUE if <code>brm_data()</code> previously declared baseline and subgroup variables in the dataset. Ignored for informative prior archetypes. For informative prior archetypes, this option should be set in functions like <code>brm_archetype_successive_cells()</code> rather than in <code>brm_formula()</code> in order to make sure columns are appropriately centered and the underlying model matrix has full rank.
<code>baseline_time</code>	Logical of length 1. TRUE to include baseline-by-time interaction, FALSE to omit. Default is TRUE if <code>brm_data()</code> previously declared a baseline variable in the dataset. Ignored for informative prior archetypes. For informative prior archetypes, this option should be set in functions like <code>brm_archetype_successive_cells()</code> rather than in <code>brm_formula()</code> in order to make sure columns are appropriately centered and the underlying model matrix has full rank.
<code>covariates</code>	Logical of length 1. TRUE (default) to include any additive covariates declared with the <code>covariates</code> argument of <code>brm_data()</code> , FALSE to omit. For informative prior archetypes, this option is set in functions like <code>brm_archetype_successive_cells()</code> rather than in <code>brm_formula()</code> in order to make sure columns are appropriately centered and the underlying model matrix has full rank.
<code>group</code>	Logical of length 1. TRUE (default) to include additive effects for treatment groups, FALSE to omit.
<code>group_subgroup</code>	Logical of length 1. TRUE to include group-by-subgroup interaction, FALSE to omit. Default is TRUE if <code>brm_data()</code> previously declared a subgroup variable in the dataset.
<code>group_subgroup_time</code>	Logical of length 1. TRUE to include group-by-subgroup-by-time interaction, FALSE to omit. Default is TRUE if <code>brm_data()</code> previously declared a subgroup variable in the dataset.
<code>group_time</code>	Logical of length 1. TRUE (default) to include group-by-time interaction, FALSE to omit.
<code>subgroup</code>	Logical of length 1. TRUE to include additive fixed effects for subgroup levels, FALSE to omit. Default is TRUE if <code>brm_data()</code> previously declared a subgroup variable in the dataset.
<code>subgroup_time</code>	Logical of length 1. TRUE to include subgroup-by-time interaction, FALSE to omit. Default is TRUE if <code>brm_data()</code> previously declared a subgroup variable in the dataset.
<code>time</code>	Logical of length 1. TRUE (default) to include a additive effect for discrete time, FALSE to omit.
<code>effect_baseline</code>	Deprecated on 2024-01-16 (version 0.0.2.9002). Use <code>baseline</code> instead.

effect_group	Deprecated on 2024-01-16 (version 0.0.2.9002). Use group instead.
effect_time	Deprecated on 2024-01-16 (version 0.0.2.9002). Use time instead.
interaction_baseline	Deprecated on 2024-01-16 (version 0.0.2.9002). Use baseline_time instead.
interaction_group	Deprecated on 2024-01-16 (version 0.0.2.9002). Use group_time instead.

Value

An object of class "brmsformula" returned from `brms::brmsformula()`. It contains the fixed effect mapping, correlation structure, and residual variance structure.

brm_data() formulas

For a `brm_data()` dataset, `brm_formula()` builds an R formula for an MMRM based on the details in the data and your choice of mapping. Customize your mapping by toggling on or off the various TRUE/FALSE arguments of `brm_formula()`, such as `intercept`, `baseline`, and `group_time`. All plausible additive effects, two-way interactions, and three-way interactions can be specified. The following interactions are not supported:

- Any interactions with the concomitant covariates you specified in the `covariates` argument of `brm_data()`.
- Any interactions which include baseline response and treatment group together. Rationale: in a randomized controlled experiment, baseline and treatment group assignment should be uncorrelated.

Formulas for informative prior archetypes

Functions like `brm_archetype_successive_cells()` tailor datasets to informative prior archetypes. For these specialized tailored datasets, `brm_formula()` works differently. It still applies the variance and correlation structure of your choosing, and it still lets you choose whether to adjust for nuisance covariates, but it no longer lets you toggle on/off individual terms in the model, such as `intercept`, `baseline`, or `group`. Instead, to ensure the correct interpretation of the parameters, `brm_formula()` uses the `x_*` and `nuisance_*` columns generated by `brm_archetype_successive_cells(prefix_interest = "x_", prefix_nuisance = "nuisance_")`.

Parameterization

For a formula on a `brm_data()` dataset, the formula is not the only factor that determines the fixed effect mapping. The ordering of the categorical variables in the data, as well as the `contrast` option in R, affect the construction of the model matrix. To see the model matrix that will ultimately be used in `brm_model()`, run `brms::make_standata()` and examine the `X` element of the returned list. See the examples below for a demonstration.

See Also

Other models: `brm_formula_sigma()`, `brm_model()`

Examples

```

set.seed(0)
data <- brm_data(
  data = brm_simulate_simple()$data,
  outcome = "response",
  role = "response",
  group = "group",
  time = "time",
  patient = "patient",
  reference_group = "group_1",
  reference_time = "time_1"
)
brm_formula(data)
brm_formula(data = data, intercept = FALSE, baseline = FALSE)
formula <- brm_formula(
  data = data,
  intercept = FALSE,
  baseline = FALSE,
  group = FALSE
)
formula
# Standard deviations of residuals are distributional parameters that can
# regress on variables in the data.
homogeneous <- brm_formula_sigma(data, time = FALSE)
by_group <- brm_formula_sigma(data, group = TRUE, intercept = TRUE)
homogeneous
by_group
brm_formula(data, sigma = homogeneous)
brm_formula(data, sigma = by_group)
# Optional: set the contrast option, which determines the model matrix.
options(contrasts = c(unordered = "contr.SAS", ordered = "contr.poly"))
# See the fixed effect mapping you get from the data:
head(brms::make_standata(formula = formula, data = data)$X)
# Specify a different contrast method to use an alternative
# mapping when fitting the model with brm_model():
options(
  contrasts = c(ordered = "contr.treatment", unordered = "contr.poly")
)
# different model matrix than before:
head(brms::make_standata(formula = formula, data = data)$X)
# Formula on an informative prior archetype:
data <- brm_simulate_outline(
  n_group = 2,
  n_patient = 100,
  n_time = 4,
  rate_dropout = 0,
  rate_lapse = 0
) |>
dplyr::mutate(response = rnorm(n = dplyr::n())) |>
brm_data_change() |>
brm_simulate_continuous(names = c("biomarker1", "biomarker2")) |>
brm_simulate_categorical(

```

```

    names = "biomarker3",
    levels = c("present", "absent")
  )
  archetype <- brm_archetype_successive_cells(data)
  formula <- brm_formula(data = archetype)
  formula

```

brm_formula_sigma *Formula for standard deviation parameters*

Description

Parameterize standard deviations using a formula for the `sigma` argument of `brm_formula()`.

Usage

```

brm_formula_sigma(
  data,
  check_rank = TRUE,
  intercept = FALSE,
  baseline = FALSE,
  baseline_subgroup = FALSE,
  baseline_subgroup_time = FALSE,
  baseline_time = FALSE,
  covariates = FALSE,
  group = FALSE,
  group_subgroup = FALSE,
  group_subgroup_time = FALSE,
  group_time = FALSE,
  subgroup = FALSE,
  subgroup_time = FALSE,
  time = TRUE
)

```

Arguments

<code>data</code>	A classed data frame from <code>brm_data()</code> , or an informative prior archetype from a function like <code>brm_archetype_successive_cells()</code> .
<code>check_rank</code>	TRUE to check the rank of the model matrix for <code>sigma</code> and throw an error if rank deficiency is detected. FALSE to skip this check. Rank-deficiency may cause <code>sigma</code> to be non-identifiable, may prevent the MCMC from converging.
<code>intercept</code>	Logical of length 1. TRUE (default) to include an intercept, FALSE to omit.
<code>baseline</code>	Logical of length 1. TRUE to include an additive effect for baseline response, FALSE to omit. If TRUE, then effect size will be omitted from the output of <code>brm_marginal_draws()</code> .
<code>baseline_subgroup</code>	Logical of length 1.

baseline_subgroup_time	Logical of length 1. TRUE to include baseline-by-subgroup-by-time interaction, FALSE to omit. If TRUE, then effect size will be omitted from the output of <code>brm_marginal_draws()</code> .
baseline_time	Logical of length 1. TRUE to include baseline-by-time interaction, FALSE to omit. If TRUE, then effect size will be omitted from the output of <code>brm_marginal_draws()</code> .
covariates	Logical of length 1. TRUE (default) to include any additive covariates declared with the <code>covariates</code> argument of <code>brm_data()</code> , FALSE to omit. If TRUE, then effect size will be omitted from the output of <code>brm_marginal_draws()</code> .
group	Logical of length 1. TRUE (default) to include additive effects for treatment groups, FALSE to omit.
group_subgroup	Logical of length 1. TRUE to include group-by-subgroup interaction, FALSE to omit.
group_subgroup_time	Logical of length 1. TRUE to include group-by-subgroup-by-time interaction, FALSE to omit.
group_time	Logical of length 1.
subgroup	Logical of length 1. TRUE to include additive fixed effects for subgroup levels, FALSE to omit.
subgroup_time	Logical of length 1. TRUE to include subgroup-by-time interaction, FALSE to omit.
time	Logical of length 1.

Details

In brms, the standard deviations of the residuals are modeled through a parameter vector called `sigma`. `brms.mmrn` always treats `sigma` as a distributional parameter (https://paul-buerkner.github.io/brms/articles/brms_distreg.html). `brm_formula_sigma()` lets you control the parameterization of `sigma`. The output of `brm_formula_sigma()` serves as input to the `sigma` argument of `brm_formula()`.

The default `sigma` formula is `sigma ~ 0 + time`, where `time` is the discrete time variable in the data. This is the usual heterogeneous variance structure which declares one standard deviation parameter for each time point in the data. Alternatively, you could write `brm_formula_sigma(data, intercept = TRUE, time = FALSE)`. This will produce `sigma ~ 1`, which yields a single scalar variance (a structure termed "homogeneous variance").

With arguments like `baseline` and `covariates`, you can specify extremely complicated variance structures. However, if `baseline` or `covariates` are used, then the output of `brm_marginal_draws()` omit effect size due to the statistical challenges of calculating marginal means of draws of `sigma` for this uncommon scenario.

Value

A base R formula with S3 class `"brms_mmrn_formula_sigma"`. This formula controls the parameterization of `sigma`, the linear-scale brms distributional parameters which represent standard deviations.

See Also

Other models: [brm_formula\(\)](#), [brm_model\(\)](#)

Examples

```
set.seed(0)
data <- brm_data(
  data = brm_simulate_simple()$data,
  outcome = "response",
  role = "response",
  group = "group",
  time = "time",
  patient = "patient",
  reference_group = "group_1",
  reference_time = "time_1"
)
homogeneous <- brm_formula_sigma(data, time = FALSE, intercept = TRUE)
by_group <- brm_formula_sigma(data, group = TRUE, intercept = TRUE)
homogeneous
by_group
brm_formula(data, sigma = homogeneous)
brm_formula(data, sigma = by_group)
```

`brm_marginal_data` *Marginal summaries of the data.*

Description

Marginal summaries of the data.

Usage

```
brm_marginal_data(
  data,
  level = 0.95,
  use_subgroup = !is.null(attr(data, "brm_subgroup"))
)
```

Arguments

<code>data</code>	A classed data frame from brm_data() , or an informative prior archetype from a function like brm_archetype_successive_cells() .
<code>level</code>	Numeric of length 1 from 0 to 1, level of the confidence intervals.
<code>use_subgroup</code>	Logical of length 1, whether to summarize the data by each subgroup level.

Value

A tibble with one row per summary statistic and the following columns:

- `group`: treatment group.
- `subgroup`: subgroup level. Only included if the `subgroup` argument of `brm_marginal_data()` is `TRUE`.
- `time`: discrete time point.
- `statistic`: type of summary statistic.
- `value`: numeric value of the estimate.

The `statistic` column has the following possible values:

- `mean`: observed mean response after removing missing values.
- `median`: observed median response after removing missing values.
- `sd`: observed standard deviation of the response after removing missing values.
- `lower`: lower bound of a normal equal-tailed confidence interval with confidence level determined by the `level` argument.
- `upper`: upper bound of a normal equal-tailed confidence interval with confidence level determined by the `level` argument.
- `n_observe`: number of non-missing values in the response.
- `n_total`: number of total records in the data for the given `group/time` combination, including both observed and missing values.

See Also

Other marginals: `brm_marginal_draws()`, `brm_marginal_draws_average()`, `brm_marginal_probabilities()`, `brm_marginal_summaries()`

Examples

```
set.seed(0L)
data <- brm_data(
  data = brm_simulate_simple()$data,
  outcome = "response",
  role = "response",
  group = "group",
  time = "time",
  patient = "patient",
  reference_group = "group_1",
  reference_time = "time_1"
)
brm_marginal_data(data = data)
```

brm_marginal_draws *MCMC draws from the marginal posterior of an MMRM*

Description

Get marginal posterior draws from a fitted MMRM.

Usage

```
brm_marginal_draws(
  data,
  formula,
  model,
  transform = brms.mmr::brm_transform_marginal(data, formula),
  effect_size = TRUE,
  use_subgroup = NULL,
  control = NULL,
  baseline = NULL
)
```

Arguments

data	A classed data frame from <code>brm_data()</code> , or an informative prior archetype from a function like <code>brm_archetype_successive_cells()</code> .
formula	An object of class "brmsformula" from <code>brm_formula()</code> or <code>brms::brmsformula()</code> . Should include the full mapping of the model, including fixed effects, residual correlation, and heterogeneity in the discrete-time-specific residual variance components.
model	A fitted model object from <code>brm_model()</code> .
transform	Matrix with one row per marginal mean and one column per model parameter. <code>brm_marginal_draws()</code> uses this matrix to map posterior draws of model parameters to posterior draws of marginal means using matrix multiplication. Please use <code>brm_transform_marginal()</code> to compute this matrix and then modify only if necessary. See the methods vignettes for details on this matrix, as well as how <code>brms.mmr</code> computes marginal means more generally.
effect_size	Logical, TRUE to derive posterior samples of effect size (treatment effect divided by residual standard deviation). FALSE to omit. <code>brms.mmr</code> does not support effect size when baseline or covariates are included in the <code>brm_formula_sigma()</code> formula. If <code>effect_size</code> is TRUE in this case, then <code>brm_marginal_draws()</code> will automatically omit effect size and throw an informative warning.
use_subgroup	Deprecated. No longer used. <code>brm_marginal_draws()</code> no longer marginalizes over the subgroup declared in <code>brm_data()</code> . To marginalize over the subgroup, declare that variable in covariates instead.
control	Deprecated. Set the control group level in <code>brm_data()</code> .
baseline	Deprecated. Set the control group level in <code>brm_data()</code> .

Value

A named list of tibbles of MCMC draws of the marginal posterior distribution of each treatment group and time point. These marginals are also subgroup-specific if `brm_formula()` included fixed effects that use the subgroup variable originally declared in `brm_data()`. In each tibble, there is 1 row per posterior sample and one column for each type of marginal distribution (i.e. each combination of treatment group and discrete time point. The specific tibbles in the returned list are described below:

- `response`: on the scale of the response variable.
- `difference_time`: change from baseline: the response at a particular time minus the response at baseline (`reference_time`). Only returned if the `role` argument of `brm_data()` was "response". (If `role` is "change", then `response` already represents change from baseline.)
- `difference_group`: treatment effect: the the `difference_time` at each active group minus the `difference_time` at the control group (`reference_group`). If `role` is "change", then treatment group is instead the difference between response at each active group minus the response at the control group.
- `difference_subgroup`: subgroup differences: the `difference_group` at each subgroup level minus the `difference_group` at the subgroup reference level (`reference_subgroup`).
- `effect`: effect size, defined as the treatment difference divided by the residual standard deviation. Omitted if the `effect_size` argument is FALSE or if the `brm_formula_sigma()` includes baseline or covariates.

Separation string

Post-processing in `brm_marginal_draws()` names each of the group-by-time marginal means with the delimiting character string from `Sys.getenv("BRM_SEP", unset = "|")`. Neither the column names nor element names of the group and time variables can contain this string. To set a custom string yourself, use `Sys.setenv(BRM_SEP = "YOUR_CUSTOM_STRING")`.

See Also

Other marginals: `brm_marginal_data()`, `brm_marginal_draws_average()`, `brm_marginal_probabilities()`, `brm_marginal_summaries()`

Examples

```
if (identical(Sys.getenv("BRM_EXAMPLES", unset = ""), "true")) {
  set.seed(0L)
  data <- brm_data(
    data = brm_simulate_simple()$data,
    outcome = "response",
    role = "response",
    group = "group",
    time = "time",
    patient = "patient",
    reference_group = "group_1",
    reference_time = "time_1"
  )
  formula <- brm_formula(
```

```

    data = data,
    baseline = FALSE,
    baseline_time = FALSE
  )
  tmp <- utils::capture.output(
    suppressMessages(
      suppressWarnings(
        model <- brm_model(
          data = data,
          formula = formula,
          chains = 1,
          iter = 100,
          refresh = 0
        )
      )
    )
  )
  brm_marginal_draws(data = data, formula = formula, model = model)
}

```

brm_marginal_draws_average

Average marginal MCMC draws across time points.

Description

Simple un-weighted arithmetic mean of marginal MCMC draws across time points.

Usage

```
brm_marginal_draws_average(data, draws, times = NULL, label = "average")
```

Arguments

data	A classed data frame from <code>brm_data()</code> , or an informative prior archetype from a function like <code>brm_archetype_successive_cells()</code> .
draws	List of posterior draws from <code>brm_marginal_draws()</code> .
times	Character vector of discrete time point levels over which to average the MCMC samples within treatment group levels. Set to <code>NULL</code> to average across all time points. Levels are automatically sanitized with <code>make.names(unique = FALSE, allow_ = TRUE)</code> to ensure agreement with brms variable names in downstream computations.
label	Character of length 1, time point label for the averages. Automatically sanitized with <code>make.names(unique = FALSE, allow_ = TRUE)</code> . Must not conflict with any existing time point labels in the data after the label and time points are sanitized.

Value

A named list of tibbles of MCMC draws of the marginal posterior distribution of each treatment group and time point (or group-by-subgroup-by-time, if applicable). In each tibble, there is 1 row per posterior sample and one column for each type of marginal distribution (i.e. each combination of treatment group and discrete time point). The specific tibbles in the returned list are described below:

- `response`: on the scale of the response variable.
- `difference_time`: change from baseline: the response at a particular time minus the response at baseline (`reference_time`). Only returned if the `role` argument of `brm_data()` was "response". (If `role` is "change", then `response` already represents change from baseline.)
- `difference_group`: treatment effect: the the `difference_time` at each active group minus the `difference_time` at the control group (`reference_group`). If `role` is "change", then treatment group is instead the difference between response at each active group minus the response at the control group.
- `difference_subgroup`: subgroup differences: the `difference_group` at each subgroup level minus the `difference_group` at the subgroup reference level (`reference_subgroup`).

Separation string

Post-processing in `brm_marginal_draws()` names each of the group-by-time marginal means with the delimiting character string from `Sys.getenv("BRM_SEP", unset = "|")`. Neither the column names nor element names of the group and time variables can contain this string. To set a custom string yourself, use `Sys.setenv(BRM_SEP = "YOUR_CUSTOM_STRING")`.

See Also

Other marginals: `brm_marginal_data()`, `brm_marginal_draws()`, `brm_marginal_probabilities()`, `brm_marginal_summaries()`

Examples

```
if (identical(Sys.getenv("BRM_EXAMPLES", unset = ""), "true")) {
  set.seed(0L)
  data <- brm_data(
    data = brm_simulate_simple()$data,
    outcome = "response",
    role = "response",
    group = "group",
    time = "time",
    patient = "patient",
    reference_group = "group_1",
    reference_time = "time_1"
  )
  formula <- brm_formula(
    data = data,
    baseline = FALSE,
    baseline_time = FALSE
  )
}
```

```

tmp <- utils::capture.output(
  suppressMessages(
    suppressWarnings(
      model <- brm_model(
        data = data,
        formula = formula,
        chains = 1,
        iter = 100,
        refresh = 0
      )
    )
  )
)
draws <- brm_marginal_draws(data = data, formula = formula, model = model)
brm_marginal_draws_average(draws = draws, data = data)
brm_marginal_draws_average(
  draws = draws,
  data = data,
  times = c("time_1", "time_2"),
  label = "mean"
)
}

```

brm_marginal_probabilities

Marginal probabilities on the treatment effect for an MMRM.

Description

Marginal probabilities on the treatment effect for an MMRM.

Usage

```
brm_marginal_probabilities(draws, direction = "greater", threshold = 0)
```

Arguments

draws	Posterior draws of the marginal posterior obtained from <code>brm_marginal_draws()</code> .
direction	Character vector of the same length as <code>threshold</code> . "greater" to compute the marginal posterior probability that the treatment effect is greater than the threshold, "less" to compute the marginal posterior probability that the treatment effect is less than the threshold. Each element <code>direction[i]</code> corresponds to <code>threshold[i]</code> for all <code>i</code> from 1 to <code>length(direction)</code> .
threshold	Numeric vector of the same length as <code>direction</code> , treatment effect threshold for computing posterior probabilities. Each element <code>direction[i]</code> corresponds to <code>threshold[i]</code> for all <code>i</code> from 1 to <code>length(direction)</code> .

Value

A tibble of probabilities of the form `Prob(treatment effect > threshold | data)` and/or `Prob(treatment effect < threshold | data)`. It has one row per probability and the following columns: * `group`: treatment group. * `subgroup`: subgroup level, if applicable. * `time`: discrete time point, * `direction`: direction of the comparison in the marginal probability: "greater" for `>`, "less" for `<` * `threshold`: treatment effect threshold in the probability statement. * `value`: numeric value of the estimate of the probability.

See Also

Other marginals: [brm_marginal_data\(\)](#), [brm_marginal_draws\(\)](#), [brm_marginal_draws_average\(\)](#), [brm_marginal_summaries\(\)](#)

Examples

```
if (identical(Sys.getenv("BRM_EXAMPLES", unset = ""), "true")) {
  set.seed(0L)
  data <- brm_data(
    data = brm_simulate_simple()$data,
    outcome = "response",
    role = "response",
    group = "group",
    time = "time",
    patient = "patient",
    reference_group = "group_1",
    reference_time = "time_1"
  )
  formula <- brm_formula(
    data = data,
    baseline = FALSE,
    baseline_time = FALSE
  )
  tmp <- utils::capture.output(
    suppressMessages(
      suppressWarnings(
        model <- brm_model(
          data = data,
          formula = formula,
          chains = 1,
          iter = 100,
          refresh = 0
        )
      )
    )
  )
  draws <- brm_marginal_draws(data = data, formula = formula, model = model)
  brm_marginal_probabilities(draws, direction = "greater", threshold = 0)
}
```

`brm_marginal_summaries`*Summary statistics of the marginal posterior of an MMRM.*

Description

Summary statistics of the marginal posterior of an MMRM.

Usage

```
brm_marginal_summaries(draws, level = 0.95)
```

Arguments

<code>draws</code>	Posterior draws of the marginal posterior obtained from <code>brm_marginal_draws()</code> .
<code>level</code>	Numeric of length 1 between 0 and 1, credible level for the credible intervals.

Value

A tibble with one row per summary statistic and the following columns:

- `marginal`: type of marginal distribution. If outcome was "response" in `brm_marginal_draws()`, then possible values include "response" for the response on the raw scale, "change" for change from baseline, and "difference" for treatment difference in terms of change from baseline. If outcome was "change", then possible values include "response" for the response on the change from baseline scale and "difference" for treatment difference.
- `statistic`: type of summary statistic. "lower" and "upper" are bounds of an equal-tailed quantile-based credible interval.
- `group`: treatment group.
- `subgroup`: subgroup level, if applicable.
- `time`: discrete time point.
- `value`: numeric value of the estimate.
- `mcse`: Monte Carlo standard error of the estimate. The `statistic` column has the following possible values:
 - `mean`: posterior mean.
 - `median`: posterior median.
 - `sd`: posterior standard deviation of the mean.
 - `lower`: lower bound of an equal-tailed credible interval of the mean, with credible level determined by the `level` argument.
 - `upper`: upper bound of an equal-tailed credible interval with credible level determined by the `level` argument.

See Also

Other marginals: [brm_marginal_data\(\)](#), [brm_marginal_draws\(\)](#), [brm_marginal_draws_average\(\)](#), [brm_marginal_probabilities\(\)](#)

Examples

```
if (identical(Sys.getenv("BRM_EXAMPLES", unset = ""), "true")) {
  set.seed(0L)
  data <- brm_data(
    data = brm_simulate_simple()$data,
    outcome = "response",
    role = "response",
    group = "group",
    time = "time",
    patient = "patient",
    reference_group = "group_1",
    reference_time = "time_1"
  )
  formula <- brm_formula(
    data = data,
    baseline = FALSE,
    baseline_time = FALSE
  )
  tmp <- utils::capture.output(
    suppressMessages(
      suppressWarnings(
        model <- brm_model(
          data = data,
          formula = formula,
          chains = 1,
          iter = 100,
          refresh = 0
        )
      )
    )
  )
  draws <- brm_marginal_draws(data = data, formula = formula, model = model)
  suppressWarnings(brm_marginal_summaries(draws))
}
```

brm_model

Fit an MMRM.

Description

Fit an MMRM model using brms.

Usage

```
brm_model(
  data,
  formula,
  ...,
  prior = NULL,
  family = brms::brmsfamily(family = "gaussian")
)
```

Arguments

data	A classed data frame from <code>brm_data()</code> , or an informative prior archetype from a function like <code>brm_archetype_successive_cells()</code> .
formula	An object of class "brmsformula" from <code>brm_formula()</code> or <code>brms::brmsformula()</code> . Should include the full mapping of the model, including fixed effects, residual correlation, and heterogeneity in the discrete-time-specific residual variance components.
...	Arguments to <code>brms::brm()</code> other than data, formula, and prior.
prior	Either NULL for default priors or a "brmsprior" object from <code>brms::prior()</code> .
family	A brms family object generated by <code>brms::brmsfamily()</code> . Must fit a continuous outcome variable and have the identity link.

Value

A fitted model object from brms.

Parameterization

For a formula on a `brm_data()` dataset, the formula is not the only factor that determines the fixed effect mapping. The ordering of the categorical variables in the data, as well as the contrast option in R, affect the construction of the model matrix. To see the model matrix that will ultimately be used in `brm_model()`, run `brms::make_standata()` and examine the X element of the returned list. See the examples below for a demonstration.

See Also

Other models: `brm_formula()`, `brm_formula_sigma()`

Examples

```
if (identical(Sys.getenv("BRM_EXAMPLES", unset = ""), "true")) {
  set.seed(0L)
  data <- brm_data(
    data = brm_simulate_simple()$data,
    outcome = "response",
    role = "response",
    group = "group",
    time = "time",
    patient = "patient",
```

```

    reference_group = "group_1",
    reference_time = "time_1"
  )
  formula <- brm_formula(
    data = data,
    baseline = FALSE,
    baseline_time = FALSE
  )
  # Optional: set the contrast option, which determines the model matrix.
  options(contrasts = c(unordered = "contr.SAS", ordered = "contr.poly"))
  # See the fixed effect mapping you get from the data:
  head(brms::make_standata(formula = formula, data = data)$X)
  # Specify a different contrast method to use an alternative
  # mapping when fitting the model with brm_model():
  options(
    contrasts = c(unordered = "contr.treatment", ordered = "contr.poly")
  )
  # different model matrix than before:
  head(brms::make_standata(formula = formula, data = data)$X)
  tmp <- utils::capture.output(
    suppressMessages(
      suppressWarnings(
        model <- brm_model(
          data = data,
          formula = formula,
          chains = 1,
          iter = 100,
          refresh = 0
        )
      )
    )
  )
  # The output model is a brms model fit object.
  suppressWarnings(print(model))
  # The `prior_summary()` function shows the full prior specification
  # which reflects the fully realized fixed effects mapping.
  brms::prior_summary(model)
}

```

brm_plot_compare

Visually compare the marginals of multiple models and/or datasets.

Description

Visually compare the marginals of multiple models and/or datasets.

Usage

```
brm_plot_compare(
  ...,

```

```

  marginal = "response",
  compare = "source",
  axis = "time",
  facet = c("group", "subgroup")
)

```

Arguments

...	Named tibbles of marginals posterior summaries from brm_marginal_summaries() and/or brm_marginal_data() .
marginal	Character of length 1, which kind of marginal to visualize. Must be a value in the marginal column of the supplied tibbles in the ... argument. Only applies to MCMC output, the data is always on the scale of the response variable.
compare	Character of length 1 identifying the variable to display using back-to-back interval plots of different colors. This is the primary comparison of interest. Must be one of "source" (the source of the marginal summaries, e.g. a model or dataset), "time" or "group" (in the non-subgroup case). Can also be "subgroup" if all the marginal summaries are subgroup-specific. The value must not be in axis or facet.
axis	Character of length 1 identifying the quantity to put on the horizontal axis. Must be one of "source" (the source of the marginal summaries, e.g. a model or dataset), "time", or "group" (in the non-subgroup case). If the marginals are subgroup-specific, then axis can also be "subgroup". The value must not be in compare or facet.
facet	Character vector of length 1 or 2 with quantities to generate facets. Each element must be "source" (the source of the marginal summaries, e.g. a model or dataset), "time", "group", or "subgroup", and c(axis, facet) must all have unique elements. "subgroup" is automatically removed if not all the marginal summaries have a subgroup column. If facet has length 1, then faceting is wrapped. If facet has length 2, then faceting is in a grid, and the first element is horizontal facet.

Details

By default, [brm_plot_compare\(\)](#) compares multiple models and/or datasets side-by-side. The compare argument selects the primary comparison of interest, and arguments axis and facet control the arrangement of various other components of the plot. The subgroup variable is automatically included if and only if all the supplied marginal summaries have a subgroup column.

Value

A ggplot object.

See Also

Other visualization: [brm_plot_draws\(\)](#)

Examples

```

if (identical(Sys.getenv("BRM_EXAMPLES", unset = ""), "true")) {
  set.seed(0L)
  data <- brm_data(
    data = brm_simulate_simple()$data,
    outcome = "response",
    role = "response",
    group = "group",
    time = "time",
    patient = "patient",
    reference_group = "group_1",
    reference_time = "time_1"
  )
  formula <- brm_formula(
    data = data,
    baseline = FALSE,
    baseline_time = FALSE
  )
  tmp <- utils::capture.output(
    suppressMessages(
      suppressWarnings(
        model <- brm_model(
          data = data,
          formula = formula,
          chains = 1,
          iter = 100,
          refresh = 0
        )
      )
    )
  )
  draws <- brm_marginal_draws(data = data, formula = formula, model = model)
  suppressWarnings(summaries_draws <- brm_marginal_summaries(draws))
  summaries_data <- brm_marginal_data(data)
  brm_plot_compare(
    model1 = summaries_draws,
    model2 = summaries_draws,
    data = summaries_data
  )
  brm_plot_compare(
    model1 = summaries_draws,
    model2 = summaries_draws,
    marginal = "difference"
  )
}

```

Description

Visualize posterior draws of marginals.

Usage

```
brm_plot_draws(draws, axis = "time", facet = c("group", "subgroup"))
```

Arguments

draws	A data frame of draws from an element of the output list of brm_marginal_summaries() .
axis	Character of length 1 identifying the quantity to put on the horizontal axis. Must be one of "time" or "group" if the marginal summaries are not subgroup-specific. If the marginals are subgroup-specific, then axis must be one of "time", "group", or "subgroup".
facet	Character vector of length 1 or 2 with quantities to generate facets. Each element must be "time", "group", or "subgroup", and <code>c(axis, facet)</code> must all have unique elements. "subgroup" is automatically removed if the marginals have no subgroup. If facet has length 1, then faceting is wrapped. If facet has length 2, then faceting is in a grid, and the first element is horizontal facet.

Value

A ggplot object.

See Also

Other visualization: [brm_plot_compare\(\)](#)

Examples

```
if (identical(Sys.getenv("BRM_EXAMPLES", unset = ""), "true")) {
  set.seed(0L)
  data <- brm_data(
    data = brm_simulate_simple()$data,
    outcome = "response",
    role = "response",
    group = "group",
    time = "time",
    patient = "patient",
    reference_group = "group_1",
    reference_time = "time_1"
  )
  formula <- brm_formula(
    data = data,
    baseline = FALSE,
    baseline_time = FALSE
  )
  tmp <- utils::capture.output(
    suppressMessages(
      suppressWarnings(
```

```

    model <- brm_model(
      data = data,
      formula = formula,
      chains = 1,
      iter = 100,
      refresh = 0
    )
  )
)
)
draws <- brm_marginal_draws(data = data, formula = formula, model = model)
brm_plot_draws(draws = draws$difference_time)
}

```

brm_prior_archetype *Informative priors for fixed effects in archetypes*

Description

Create a brms prior for fixed effects in an archetype.

Usage

```
brm_prior_archetype(label, archetype)
```

Arguments

label	A data frame with one row per model parameter in the archetype and columns to indicate the mapping between priors and labels. Generate using brm_prior_label() or manually. See the examples and the informative prior archetypes vignette for details.
archetype	An informative prior archetype generated by a function like brm_archetype_successive_cells() .

Value

A brms prior object that you can supply to the prior argument of [brm_model\(\)](#).

Prior labeling

Informative prior archetypes use a labeling scheme to assign priors to fixed effects. How it works:

1. First, assign the prior of each parameter a collection of labels from the data. This can be done manually or with successive calls to `[brm_prior_label()]`.
2. Supply the labeling scheme to `[brm_prior_archetype()]`. `[brm_prior_archetype()]` uses attributes of the archetype to map labeled priors to their rightful parameters in the model.

For informative prior archetypes, this process is much more convenient and robust than manually calling `brms::set_prior()`. However, it requires an understanding of how the labels of the priors map to parameters in the model. This mapping varies from archetype to archetype, and it is documented in the help pages of archetype-specific functions such as `brm_archetype_successive_cells()`.

See Also

Other priors: `brm_prior_label()`, `brm_prior_simple()`, `brm_prior_template()`

Examples

```
set.seed(0L)
data <- brm_simulate_outline(
  n_group = 2,
  n_patient = 100,
  n_time = 3,
  rate_dropout = 0,
  rate_lapse = 0
) |>
dplyr::mutate(response = rnorm(n = dplyr::n())) |>
brm_simulate_continuous(names = c("biomarker1", "biomarker2")) |>
brm_simulate_categorical(
  names = c("status1", "status2"),
  levels = c("present", "absent")
)
archetype <- brm_archetype_successive_cells(data)
dplyr::distinct(data, group, time)
prior <- NULL |>
  brm_prior_label("normal(1, 1)", group = "group_1", time = "time_1") |>
  brm_prior_label("normal(1, 2)", group = "group_1", time = "time_2") |>
  brm_prior_label("normal(1, 3)", group = "group_1", time = "time_3") |>
  brm_prior_label("normal(2, 1)", group = "group_2", time = "time_1") |>
  brm_prior_label("normal(2, 2)", group = "group_2", time = "time_2") |>
  brm_prior_label("normal(2, 3)", group = "group_2", time = "time_3") |>
  brm_prior_archetype(archetype = archetype)
prior
class(prior)
```

`brm_prior_label`

Label a prior with levels in the data.

Description

Label an informative prior for a parameter using a collection of levels in the data.

Usage

```
brm_prior_label(label = NULL, code, group, subgroup = NULL, time)
```

Arguments

label	A tibble with the prior labeling scheme so far, with one row per model parameter and columns for the Stan code, treatment group, subgroup, and discrete time point of each parameter.
code	Character of length 1, Stan code for the prior. Could be a string like "normal(1, 2.2)". The full set of priors is given in the Stan Function Reference at https://mc-stan.org/docs/functions-reference/ in the "Unbounded Continuous Distributions" section. See the documentation <code>brms::set_prior()</code> for more details.
group	Value of length 1, level of the treatment group column in the data to label the prior. The treatment group column is the one you identified with the group argument of <code>brm_data()</code> .
subgroup	Value of length 1, level of the subgroup column in the data to label the prior. The subgroup column is the one you identified with the subgroup argument of <code>brm_data()</code> , if applicable. Not every dataset has a subgroup variable. If yours does not, please either ignore this argument or set it to NULL.
time	Value of length 1, level of the discrete time column in the data to label the prior. The discrete time column is the one you identified with the time argument of <code>brm_data()</code> .

Value

A tibble with one row per model parameter and columns for the Stan code, treatment group, subgroup, and discrete time point of each parameter. You can supply this tibble to the label argument of `brm_prior_archetype()`.

Prior labeling

Informative prior archetypes use a labeling scheme to assign priors to fixed effects. How it works:

1. First, assign the prior of each parameter a collection of labels from the data. This can be done manually or with successive calls to `[brm_prior_label()]`.
2. Supply the labeling scheme to `[brm_prior_archetype()]`. `[brm_prior_archetype()]` uses attributes of the archetype to map labeled priors to their rightful parameters in the model.

For informative prior archetypes, this process is much more convenient and robust than manually calling `brms::set_prior()`. However, it requires an understanding of how the labels of the priors map to parameters in the model. This mapping varies from archetype to archetype, and it is documented in the help pages of archetype-specific functions such as `brm_archetype_successive_cells()`.

See Also

Other priors: `brm_prior_archetype()`, `brm_prior_simple()`, `brm_prior_template()`

Examples

```

set.seed(0L)
data <- brm_simulate_outline(
  n_group = 2,
  n_patient = 100,
  n_time = 3,
  rate_dropout = 0,
  rate_lapse = 0
) |>
dplyr::mutate(response = rnorm(n = dplyr::n())) |>
brm_simulate_continuous(names = c("biomarker1", "biomarker2")) |>
brm_simulate_categorical(
  names = c("status1", "status2"),
  levels = c("present", "absent")
)
archetype <- brm_archetype_successive_cells(data)
dplyr::distinct(data, group, time)
label <- NULL |>
brm_prior_label("normal(1, 1)", group = "group_1", time = "time_1") |>
brm_prior_label("normal(1, 2)", group = "group_1", time = "time_2") |>
brm_prior_label("normal(1, 3)", group = "group_1", time = "time_3") |>
brm_prior_label("normal(2, 1)", group = "group_2", time = "time_1") |>
brm_prior_label("normal(2, 2)", group = "group_2", time = "time_2") |>
brm_prior_label("normal(2, 3)", group = "group_2", time = "time_3")
label

```

brm_prior_simple

*Simple prior for a brms MMRM***Description**

Generate a simple prior for a brms MMRM.

Usage

```

brm_prior_simple(
  data,
  formula,
  intercept = "student_t(3, 0, 2.5)",
  coefficients = "student_t(3, 0, 2.5)",
  sigma = "student_t(3, 0, 2.5)",
  unstructured = "lkj(1)",
  autoregressive = "",
  moving_average = "",
  compound_symmetry = "",
  correlation = NULL
)

```

Arguments

data	A classed data frame from <code>brm_data()</code> , or an informative prior archetype from a function like <code>brm_archetype_successive_cells()</code> .
formula	An object of class "brmsformula" from <code>brm_formula()</code> or <code>brms::brmsformula()</code> . Should include the full mapping of the model, including fixed effects, residual correlation, and heterogeneity in the discrete-time-specific residual variance components.
intercept	Character of length 1, Stan code for the prior to set on the intercept parameter.
coefficients	Character of length 1, Stan code for the prior to set independently on each of the non-intercept model coefficients.
sigma	Character of length 1, Stan code for the prior to set independently on each of the log-scale standard deviation parameters. Should be a symmetric prior in most situations.
unstructured	Character of length 1, Stan code for an unstructured correlation prior. Supply the empty string "" to set a flat prior (default). Applies to the "cortime parameter class in brms priors. Used for formulas created with <code>brm_formula(correlation = "unstructured")</code> . LKJ is recommended. See also <code>brms::unstr()</code> .
autoregressive	Character of length 1, Stan code for a prior on autoregressive correlation parameters. Supply the empty string "" to set a flat prior (default). Applies to the "ar parameter class in brms priors. Used for formulas created with <code>brm_formula(correlation = "autoregressive")</code> and <code>brm_formula(correlation = "autoregressive_moving_average")</code> . See also <code>brms::ar()</code> and <code>brms::arma()</code> .
moving_average	Character of length 1, Stan code for a prior on moving average correlation parameters. Supply the empty string "" to set a flat prior (default). Applies to the "ma parameter class in brms priors. Used for formulas created with <code>brm_formula(correlation = "moving_average")</code> and <code>brm_formula(correlation = "autoregressive_moving_average")</code> . See also <code>brms::ma()</code> and <code>brms::arma()</code> .
compound_symmetry	Character of length 1, Stan code for a prior on compound symmetry correlation parameters. Supply the empty string "" to set a flat prior (default). Applies to the "cosy parameter class in brms priors. Used for formulas created with <code>brm_formula(correlation = "compound_symmetry")</code> . See also <code>brms::cosy()</code> .
correlation	Deprecated on 2024-04-22 (version 0.1.0.9004). Please use arguments like "unstructured", and/or "autoregressive" to supply correlation-specific priors.

Details

In `brm_prior_simple()`, you can separately choose priors for the intercept, model coefficients, log-scale standard deviations, and pairwise correlations between time points within patients. However, each class of parameters is set as a whole. In other words, `brm_prior_simple()` cannot assign different priors to different fixed effect parameters.

Value

A classed data frame with the brms prior.

See Also

Other priors: [brm_prior_archetype\(\)](#), [brm_prior_label\(\)](#), [brm_prior_template\(\)](#)

Examples

```
set.seed(0L)
data <- brm_simulate_outline()
data <- brm_simulate_continuous(data, names = c("age", "biomarker"))
formula <- brm_formula(
  data = data,
  baseline = FALSE,
  baseline_time = FALSE,
  check_rank = FALSE
)
brm_prior_simple(
  data = data,
  formula = formula,
  intercept = "student_t(3, 0, 2.5)",
  coefficients = "normal(0, 10)",
  sigma = "student_t(2, 0, 4)",
  unstructured = "lkj(2.5)"
)
```

`brm_prior_template` *Label template for informative prior archetypes*

Description

Template for the label argument of [brm_prior_archetype\(\)](#).

Usage

```
brm_prior_template(archetype)
```

Arguments

`archetype` An informative prior archetype generated by a function like [brm_archetype_successive_cells\(\)](#).

Details

The label argument of [brm_prior_archetype\(\)](#) is a tibble which maps Stan code for univariate priors to fixed effect parameters in the model. Usually this tibble is built gradually using multiple calls to [brm_prior_label\(\)](#), but occasionally it is more convenient to begin with a full template and manually write Stan code in the code column. [brm_prior_template\(\)](#) creates this template.

Value

A tibble with one row per fixed effect parameter and columns to map Stan code to each parameter. After manually writing Stan code in the code column of the template, you can supply the result to the label argument of [brm_prior_archetype\(\)](#) to build a brms prior for your model.

Prior labeling

Informative prior archetypes use a labeling scheme to assign priors to fixed effects. How it works:

1. First, assign the prior of each parameter a collection of labels from the data. This can be done manually or with successive calls to `[brm_prior_label()]`.
2. Supply the labeling scheme to `[brm_prior_archetype()]`. `[brm_prior_archetype()]` uses attributes of the archetype to map labeled priors to their rightful parameters in the model.

For informative prior archetypes, this process is much more convenient and robust than manually calling `brms::set_prior()`. However, it requires an understanding of how the labels of the priors map to parameters in the model. This mapping varies from archetype to archetype, and it is documented in the help pages of archetype-specific functions such as `brm_archetype_successive_cells()`.

See Also

Other priors: `brm_prior_archetype()`, `brm_prior_label()`, `brm_prior_simple()`

Examples

```
set.seed(0L)
data <- brm_simulate_outline(
  n_group = 2,
  n_patient = 100,
  n_time = 3,
  rate_dropout = 0,
  rate_lapse = 0
) |>
dplyr::mutate(response = rnorm(n = dplyr::n())) |>
brm_simulate_continuous(names = c("biomarker1", "biomarker2")) |>
brm_simulate_categorical(
  names = c("status1", "status2"),
  levels = c("present", "absent")
)
archetype <- brm_archetype_successive_cells(data)
label <- brm_prior_template(archetype)
label$code <- c(
  "normal(1, 1)",
  "normal(1, 2)",
  "normal(1, 3)",
  "normal(2, 1)",
  "normal(2, 2)",
  "normal(2, 3)"
)
brm_prior_archetype(label = label, archetype = archetype)
```

 brm_recenter_nuisance *Recenter nuisance variables*

Description

Change the center of a nuisance variable of an informative prior archetype.

Usage

```
brm_recenter_nuisance(data, nuisance, center)
```

Arguments

data	An informative prior archetype data frame output from brm_archetype_cells() or similar.
nuisance	Character of length 1, name of the nuisance column in the data to shift the center.
center	Numeric of length 1, value of the center to shift the column in nuisance. The affected column in the returned archetype data frame will look as if it were centered by this value to begin with.

Details

By "centering vector y at scalar x ", we mean taking the difference $z = y - x$. If x is the mean, then $\text{mean}(z)$ is 0. Informative prior archetypes center nuisance variables at their means so the parameters can be interpreted correctly for setting informative priors. This is appropriate most of the time, but sometimes it is better to center a column at a pre-specified scientifically meaningful fixed number. If you want a nuisance column to be centered at a fixed value other than its mean, use [brm_recenter_nuisance\(\)](#) to shift the center. This function can handle any nuisance variable

Value

An informative prior archetype data frame with one of the variables re-centered.

Examples

```
set.seed(0L)
data <- brm_simulate_outline(
  n_group = 2,
  n_patient = 100,
  n_time = 4,
  rate_dropout = 0,
  rate_lapse = 0
) |>
  dplyr::mutate(response = rnorm(n = dplyr::n())) |>
  brm_data_change() |>
  brm_simulate_continuous(names = c("biomarker1", "biomarker2")) |>
  brm_simulate_categorical(
    names = c("status1", "status2"),
```

```

    levels = c("present", "absent")
  )
  archetype <- brm_archetype_cells(data)
  mean(archetype$nuisance_biomarker1) # after original centering
  center <- mean(data$biomarker1)
  center # original center, before the centering from brm_archetype_cells()
  attr(archetype$nuisance_biomarker1, "brm_center") # original center
  max(abs((data$biomarker1 - center) - archetype$nuisance_biomarker1))
  # Re-center nuisance_biomarker1 at 0.75.
  archetype <- brm_recenter_nuisance(
    data = archetype,
    nuisance = "nuisance_biomarker1",
    center = 0.75
  )
  attr(archetype$nuisance_biomarker1, "brm_center") # new center
  mean(archetype$nuisance_biomarker1) # no longer equal to the center
  # nuisance_biomarker1 is now as though we centered it at 0.75.
  max(abs((data$biomarker1 - 0.75) - archetype$nuisance_biomarker1))

```

brm_simulate_categorical

Append simulated categorical covariates

Description

Simulate and append non-time-varying categorical covariates to an existing `brm_data()` dataset.

Usage

```
brm_simulate_categorical(data, names, levels, probabilities = NULL)
```

Arguments

<code>data</code>	Classed tibble as from <code>brm_data()</code> or <code>brm_simulate_outline()</code> .
<code>names</code>	Character vector with the names of the new covariates to simulate and append. Names must all be unique and must not already be column names of data.
<code>levels</code>	Character vector of unique levels of the simulated categorical covariates.
<code>probabilities</code>	Either NULL or a numeric vector of length <code>length(levels)</code> with levels between 0 and 1 where all elements sum to 1. If NULL, then all levels are equally likely to be drawn. If not NULL, then <code>probabilities</code> is a vector of sampling probabilities corresponding to each respective level of levels.

Details

Each covariate is a new column of the dataset with one independent random categorical draw for each patient, using a fixed set of levels (via `base::sample()` with `replace = TRUE`). All covariates simulated this way are independent of everything else in the data, including other covariates (to the extent that the random number generators in R work as intended).

Value

A classed tibble, like from `brm_data()` or `brm_simulate_outline()`, but with new categorical covariate columns and with the names of the new covariates appended to the `brm_covariates` attribute. Each new categorical covariate column is a character vector, not the factor type in base R.

See Also

Other simulation: `brm_simulate_continuous()`, `brm_simulate_outline()`, `brm_simulate_prior()`, `brm_simulate_simple()`

Examples

```
data <- brm_simulate_outline()
brm_simulate_categorical(
  data = data,
  names = c("site", "region"),
  levels = c("area1", "area2")
)
brm_simulate_categorical(
  data = data,
  names = c("site", "region"),
  levels = c("area1", "area2"),
  probabilities = c(0.1, 0.9)
)
```

```
brm_simulate_continuous
```

Append simulated continuous covariates

Description

Simulate and append non-time-varying continuous covariates to an existing `brm_data()` dataset.

Usage

```
brm_simulate_continuous(data, names, mean = 0, sd = 1)
```

Arguments

<code>data</code>	Classed tibble as from <code>brm_data()</code> or <code>brm_simulate_outline()</code> .
<code>names</code>	Character vector with the names of the new covariates to simulate and append. Names must all be unique and must not already be column names of data.
<code>mean</code>	Numeric of length 1, mean of the normal distribution for simulating each covariate.
<code>sd</code>	Positive numeric of length 1, standard deviation of the normal distribution for simulating each covariate.

Details

Each covariate is a new column of the dataset with one independent random univariate normal draw for each patient. All covariates simulated this way are independent of everything else in the data, including other covariates (to the extent that the random number generators in R work as intended).

Value

A classed tibble, like from `brm_data()` or `brm_simulate_outline()`, but with new numeric covariate columns and with the names of the new covariates appended to the `brm_covariates` attribute.

See Also

Other simulation: `brm_simulate_categorical()`, `brm_simulate_outline()`, `brm_simulate_prior()`, `brm_simulate_simple()`

Examples

```
data <- brm_simulate_outline()
brm_simulate_continuous(
  data = data,
  names = c("age", "biomarker")
)
brm_simulate_continuous(
  data = data,
  names = c("biomarker1", "biomarker2"),
  mean = 1000,
  sd = 100
)
```

`brm_simulate_outline` *Start a simulated dataset*

Description

Begin creating a simulated dataset.

Usage

```
brm_simulate_outline(
  n_group = 2L,
  n_subgroup = NULL,
  n_patient = 100L,
  n_time = 4L,
  rate_dropout = 0.1,
  rate_lapse = 0.05
)
```


Arguments

n_group	Positive integer of length 1, number of treatment groups.
n_subgroup	Positive integer of length 1, number of subgroup levels. Set to NULL to omit the subgroup entirely.
n_patient	Positive integer of length 1. If n_subgroup is NULL, then n_patient is the number of patients per treatment group. Otherwise, n_patient is the number of patients per treatment group <i>per subgroup</i> . In both cases, the total number of patients in the whole simulated dataset is usually much greater than the n_patients argument of <code>brm_simulate_outline()</code> .
n_time	Positive integer of length 1, number of discrete time points (e.g. scheduled study visits) per patient.
rate_dropout	Numeric of length 1 between 0 and 1, post-baseline dropout rate. A dropout is an intercurrent event when data collection for a patient stops permanently, causing the outcomes for that patient to be missing during and after the dropout occurred. The first time point is assumed to be baseline, so dropout is there. Dropouts are equally likely to occur at each of the post-baseline time points.
rate_lapse	Numeric of length 1, expected proportion of post-baseline outcomes that are missing. Missing outcomes of this type are independent and uniformly distributed across the data.

Value

A data frame from `brm_data()` with attributes to define roles for various columns in the dataset. The data frame has one row per patient per time point and the following columns:

- group: integer index of the treatment group.
- patient: integer index of the patient.
- time: integer index of the discrete time point.

See Also

Other simulation: `brm_simulate_categorical()`, `brm_simulate_continuous()`, `brm_simulate_prior()`, `brm_simulate_simple()`

Examples

```
brm_simulate_outline()
```

brm_simulate_prior *Prior predictive draws.*

Description

Simulate the outcome variable from the prior predictive distribution of an MMRM using brms.

Usage

```
brm_simulate_prior(
  data,
  formula,
  prior = brms.mrm::brm_prior_simple(data = data, formula = formula),
  ...
)
```

Arguments

data	A classed data frame from brm_data() , or an informative prior archetype from a function like brm_archetype_successive_cells() .
formula	An object of class "brmsformula" from brm_formula() or <code>brms::brmsformula()</code> . Should include the full mapping of the model, including fixed effects, residual correlation, and heterogeneity in the discrete-time-specific residual variance components.
prior	A valid brms prior object with proper priors for parameters b (model coefficients), b_sigma (log residual standard deviations for each time point), and cortime (residual correlations among time points within patients). See the brm_prior_simple() function for an example.
...	Arguments to <code>brms::brm()</code> other than data, formula, and prior.

Details

`brm_simulate_prior()` calls `brms::brm()` with `sample_prior = "only"`, which sets the default intercept prior using the outcome variable and requires at least some elements of the outcome variable to be non-missing in advance. So to provide feasible and consistent output, `brm_simulate_prior()` temporarily sets the outcome variable to all zeros before invoking `brms::brm()`.

Value

A list with the following elements:

- `data`: a classed tibble with the outcome variable simulated as a draw from the prior predictive distribution (the final row of outcome in the output). If you simulated a missingness pattern with [brm_simulate_outline\(\)](#), then that missingness pattern is applied so that the appropriate values of the outcome variable are set to NA.
- `model`: the brms model fit object.

- `model_matrix`: the model matrix of the fixed effects, obtained from `brms::make_standata()`.
- `outcome`: a numeric matrix with one column per row of data and one row per saved prior predictive draw.
- `parameters`: a tibble of saved parameter draws from the prior predictive distribution.

See Also

Other simulation: [brm_simulate_categorical\(\)](#), [brm_simulate_continuous\(\)](#), [brm_simulate_outline\(\)](#), [brm_simulate_simple\(\)](#)

Examples

```
if (identical(Sys.getenv("BRM_EXAMPLES", unset = ""), "true")) {
  set.seed(0L)
  data <- brm_simulate_outline()
  data <- brm_simulate_continuous(data, names = c("age", "biomarker"))
  data$response <- rnorm(nrow(data))
  formula <- brm_formula(
    data = data,
    baseline = FALSE,
    baseline_time = FALSE
  )
  tmp <- utils::capture.output(
    suppressMessages(
      suppressWarnings(
        out <- brm_simulate_prior(
          data = data,
          formula = formula
        )
      )
    )
  )
  out$data
}
```

`brm_simulate_simple` *Simple MMRM simulation.*

Description

Simple function to simulate a dataset from a simple specialized MMRM.

Usage

```
brm_simulate_simple(
  n_group = 2L,
  n_patient = 100L,
  n_time = 4L,
  hyper_beta = 1,
```

```

    hyper_tau = 0.1,
    hyper_lambda = 1
  )

```

Arguments

n_group	Positive integer of length 1, number of treatment groups.
n_patient	Positive integer of length 1, number of patients per treatment group.
n_time	Positive integer of length 1, number of discrete time points (e.g. scheduled study visits) per patient.
hyper_beta	Positive numeric of length 1, hyperparameter. Prior standard deviation of the fixed effect parameters beta.
hyper_tau	Positive numeric of length 1, hyperparameter. Prior standard deviation parameter of the residual log standard deviation parameters tau
hyper_lambda	Positive numeric of length 1, hyperparameter. Prior shape parameter of the LKJ correlation matrix of the residuals among discrete time points.

Details

Refer to the methods vignette for a full model specification. The `brm_simulate_simple()` function simulates a dataset from a simple pre-defined MMRM. It assumes a cell means structure for fixed effects, which means there is one fixed effect scalar parameter (element of vector beta) for each unique combination of levels of treatment group and discrete time point. The elements of beta have independent univariate normal priors with mean 0 and standard deviation hyper_beta. The residual log standard deviation parameters (elements of vector tau) have normal priors with mean 0 and standard deviation hyper_tau. The residual correlation matrix parameter lambda has an LKJ correlation prior with shape parameter hyper_lambda.

Value

A list of three objects:

- `data`: A tidy dataset with one row per patient per discrete time point and columns for the outcome and ID variables.
- `model_matrix`: A matrix with one row per row of data and columns that represent levels of the covariates.
- `parameters`: A named list of parameter draws sampled from the prior:
 - `beta`: numeric vector of fixed effects.
 - `tau`: numeric vector of residual log standard parameters for each time point.
 - `sigma`: numeric vector of residual standard parameters for each time point. `sigma` is equal to $\exp(\tau)$.
 - `lambda`: correlation matrix of the residuals among the time points within each patient.
 - `covariance`: covariance matrix of the residuals among the time points within each patient. `covariance` is equal to $\text{diag}(\sigma) \%*\% \lambda \%*\% \text{diag}(\sigma)$.

See Also

Other simulation: `brm_simulate_categorical()`, `brm_simulate_continuous()`, `brm_simulate_outline()`, `brm_simulate_prior()`

Examples

```
set.seed(0L)
simulation <- brm_simulate_simple()
simulation$data
```

```
brm_transform_marginal
```

Marginal mean transformation

Description

Transformation from model parameters to marginal means.

Usage

```
brm_transform_marginal(
  data,
  formula,
  average_within_subgroup = NULL,
  prefix = "b_"
)
```

Arguments

<code>data</code>	A classed data frame from <code>brm_data()</code> , or an informative prior archetype from a function like <code>brm_archetype_successive_cells()</code> .
<code>formula</code>	An object of class "brmsformula" from <code>brm_formula()</code> or <code>brms::brmsformula()</code> . Should include the full mapping of the model, including fixed effects, residual correlation, and heterogeneity in the discrete-time-specific residual variance components.
<code>average_within_subgroup</code>	TRUE to average concomitant covariates proportionally within subgroup levels, FALSE to average these covariates across the whole dataset. If <code>average_within_subgroup</code> is NULL (default), and if the model has a subgroup and nuisance variables, then <code>brm_transform_marginal()</code> prints an informative message (once per session) and sets <code>average_within_subgroup</code> to FALSE. If you see this message, please read https://openpharma.github.io/brms.mmrm/articles/inference.html , decide whether to set <code>average_within_subgroup</code> to TRUE or FALSE in <code>brm_transform_marginal()</code> , and then manually supply the output of <code>brm_transform_marginal()</code> to the <code>transform</code> argument of <code>brm_marginal_draws()</code> . To create marginal means, <code>brms.mmrm</code> conditions the nuisance covariates on their averages across the whole dataset (<code>average_within_subgroup = FALSE</code>

or NULL in `brm_transform_marginal()`). This may be reasonable in some cases, and it mitigates the kind of hidden confounding between the subgroup and other variables which may otherwise cause Simpson's paradox. However, for subgroup-specific marginal means, it may not be realistic to condition on a single point estimate for all levels of the reference grid (for example, if the subgroup is female vs male, but all marginal means condition on a single overall observed pregnancy rate of 5%). In these situations, it may be appropriate to instead condition on subgroup-specific averages of nuisance variables (`average_within_subgroup = TRUE` in `brm_transform_marginal()`). But if you do this, it is your responsibility to investigate and understand the hidden interactions and confounding in your dataset. For more information, please visit <https://openpharma.github.io/brms.mmrm/articles/inference.html> and <https://cran.r-project.org/package=emmeans/vignettes/interactions.html>.

`prefix` Character of length 1, prefix to add to the model matrix ("X") from `brms::make_standata()` in order to reconstruct the brms model parameter names. This argument should only be modified for testing purposes.

Details

The matrix from `brm_transform_marginal()` is passed to the `transform_marginal` argument of `brm_marginal_draws()`, and it transforms posterior draws of model parameters to posterior draws of marginal means. You may customize the output of `brm_transform_marginal()` before passing it to `brm_marginal_draws()`. However, please do not modify the dimensions, row names, or column names.

Value

A matrix to transform model parameters (columns) into marginal means (rows).

Examples

```
if (identical(Sys.getenv("BRM_EXAMPLES", unset = ""), "true")) {
  set.seed(0L)
  data <- brm_data(
    data = brm_simulate_simple()$data,
    outcome = "response",
    role = "response",
    group = "group",
    time = "time",
    patient = "patient",
    reference_group = "group_1",
    reference_time = "time_1"
  )
  formula <- brm_formula(
    data = data,
    baseline = FALSE,
    baseline_time = FALSE
  )
  transform <- brm_transform_marginal(data = data, formula = formula)
```

```
print(transform)  
}
```

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