

Package ‘splinetrials’

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Type Package

Title Facilitate Clinical Trials Analysis Using Natural Cubic Splines

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Description Create mixed models with repeated measures using natural cubic splines applied to an observed continuous time variable, as described by Donohue et al. (2023) <[doi:10.1002/pst.2285](https://doi.org/10.1002/pst.2285)>. Iterate through multiple covariance structure types until one converges. Categorize observed time according to scheduled visits. Perform subgroup analyses.

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URL <https://github.com/Nikkrieger/splinetrials>,
<https://nikkrieger.github.io/splinetrials/>

BugReports <https://github.com/Nikkrieger/splinetrials/issues>

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Author Nik Krieger [aut, cre],
Daniel Sabanes Bove [ctb],
Eli Lilly and Company [cph]

Maintainer Nik Krieger <nikkrieger@gmail.com>

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bin_timepoints	<i>Categorize Observed Timepoints According to Scheduled Timepoints</i>
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Description

Create an [ordered](#) factor from a vector of observed values, associating each observed value with the [level](#) corresponding to a vector of expected/scheduled values.

Usage

```
bin_timepoints(
  observed,
  scheduled = unique(observed[!is.na(observed)]),
  breaks = c(-Inf, midpoints(scheduled), Inf),
  labels = make_visit_labels(seq_along(scheduled) - 1),
  ...
)
```

Arguments

observed	A numeric vector of values.
scheduled	A numeric vector of unique, finite values. Length must be at least 2. The default is to take the unique , finite values of observed.
breaks	A numeric vector of unique values. <code>-Inf</code> and <code>Inf</code> are valid. Passed to cut() . The default is to take the midpoints of scheduled and to put them in between <code>c(-Inf, [Inf])</code> .

labels A vector of labels for the resulting `ordered` factor. Passed to `cut()`. Must have `length()` equal to `scheduled`. Defaults to "Baseline" as the first level's label and "Visit#" for all subsequent `levels`, where # is the numeric index of the timepoint minus 1.

... Additional arguments passed to `cut()`.

Value

And [ordered] factor with the same length as observed.

Examples

```
observed_timepoints <- c(0, 1, 2, 3, 5, 8, 13, 21, 34, 55, 89)
scheduled_timepoints <- c(0, 1, 2, 3, 4, 5, 10, 15, 20, 30, 50, 75)
bin_timepoints(
  observed_timepoints,
  scheduled = scheduled_timepoints
)

bin_timepoints(
  observed_timepoints,
  scheduled = scheduled_timepoints,
  breaks = c(-Inf, 0.1, 1.5, 2.5, 3.5, 4.4, 7, 11, 15.1, 21, 31, 58, 80)
)

bin_timepoints(
  observed_timepoints,
  scheduled = scheduled_timepoints,
  labels = month.name
)

bin_timepoints(
  observed_timepoints,
  scheduled = scheduled_timepoints,
  labels = make_visit_labels(scheduled_timepoints, visit = "Week")
)

bin_timepoints(observed_timepoints)
```

change_from_baseline *Calculate the Change from Baseline or Treatment Effects from Estimated Marginal Means*

Description

Pass `emmeans::emmeans()` objects (probably obtained via `ncs_emmeans()`) to `emmeans::contrast()` using specially constructed contrast matrices so that change from baseline and treatment effects can be calculated.

- `change_from_baseline` calculate the change from baseline for each of the different study arms/subgroups.
- `treatment_effect()` calculate the treatment effect for each study arm when there is no subgroup. When there is a subgroup, calculate the treatment effect *between* subgroups (examining the differences *between* the subgroups within each study arm) or *within* subgroups (examining the differences between the study arms *within* each subgroup).

Usage

```
change_from_baseline(
  emmeans,
  time_observed_continuous = emmeans@roles$predictors[2],
  time_scheduled_baseline = 0,
  arm = emmeans@roles$predictors[1],
  subgroup = if (length(emmeans@roles$predictors) == 3) emmeans@roles$predictors[3],
  contrast_args = list(adjust = "none"),
  ...,
  as_tibble = FALSE,
  confint_args = list(level = 0.95)
)
```

```
treatment_effect(
  emmeans,
  time_observed_continuous = emmeans@roles$predictors[2],
  time_scheduled_baseline,
  arm = emmeans@roles$predictors[1],
  subgroup = if (length(emmeans@roles$predictors) == 3) emmeans@roles$predictors[3],
  ref_value,
  subgroup_type = c("between", "within"),
  contrast_args = list(adjust = "none"),
  ...,
  as_tibble = FALSE,
  confint_args = list(level = 0.95)
)
```

Arguments

`emmeans` (emmGrid)
 an object of class `emmGrid`, ideally obtained via `ncs_emmeans()`, which wraps `emmeans::emmeans()`.

`time_scheduled_baseline` (scalar numeric)
 the continuous time point when baseline was *scheduled* to occur. Defaults to 0.

`arm`, `time_observed_continuous`, `subgroup` (string)
 strings identifying the study arm variable, *observed* continuous time variable, and (optionally) subgroup variable supplied to `emmeans::emmeans()`, probably via `ncs_emmeans()`. If `ncs_emmeans()` was indeed used, these strings *should*

	be contained in the character vector <code>emmeans@roles\$predictors</code> (see the default arguments).
<code>contrast_args, ...</code>	(named list) arguments to be passed to <code>emmeans::contrast()</code> . Any arguments with the names object or method will be overwritten. Arguments in <code>contrast_args</code> override identically named arguments in ...
<code>as_tibble</code>	(flag) TRUE or FALSE indicating whether or not the results of <code>emmeans::contrast()</code> should be processed and returned as a <code>tibble</code> .
<code>confint_args</code>	(named list) arguments to be passed to <code>stats::confint()</code> when calculating confidence intervals. Ignored if <code>as_tibble = FALSE</code> . If NULL, confidence intervals will not be calculated. Defaults to <code>list(level = 0.95)</code> .
<code>ref_value</code>	(string) the value in arm (if <code>subgroup = NULL</code> or if <code>subgroup_type = "within"</code>) or the value in subgroup (if <code>subgroup</code> is not NULL and <code>subgroup_type = "between"</code>) denoting the control group.
<code>subgroup_type</code>	(string) either "between" or "within", denoting whether to calculate the treatment effect <i>between</i> subgroups (examining the differences between the subgroups within each study arm) and once <i>within</i> subgroups (examining the differences between the study arms within each subgroup).

Value

When `as_tibble = FALSE`, the value returned by `emmeans::contrast()`. If `as_tibble = TRUE`, a `tibble`:

1. `{column name will be the value of the arm argument}`: the study arm.
2. `{column name will be the value of the time_observed_continuous argument}`: the *observed* continuous time variable.
3. `{column name will be the value of the subgroup argument}`: the subgroup. **Only present if subgroup is not NULL.**
4. `estimate`: estimate for change from baseline or treatment effect.
5. `SE`: standard error of estimate.
6. `df`: degrees of freedom for calculating the confidence interval for and estimating the significance of estimate.
7. `lower.CL`: lower bound of confidence interval for estimate. **Only present if confint_args is not NULL.**
8. `upper.CL`: upper bound of confidence interval for estimate. **Only present if confint_args is not NULL.**
9. `t.ratio`: test statistic measuring the significance of estimate.
10. `p.value`: p-value for the significance of estimate.

Examples

```
# Create a usable data set out of mrmr::fev_data
fev_mod <- mrmr::fev_data
fev_mod$VISITN <- fev_mod$VISITN * 10
fev_mod$time_cont <- fev_mod$VISITN + rnorm(nrow(fev_mod))
fev_mod$obs_visit_index <- round(fev_mod$time_cont)

fit <-
  ncs_mrmr_fit(
    data = fev_mod,
    type = "subgroup_full",
    response = FEV1,
    subject = USUBJID,
    cov_structs = c("ar1", "us"),
    time_observed_continuous = time_cont,
    df = 2,
    time_observed_index = obs_visit_index,
    arm = ARMCD,
    control_group = "PBO",
    subgroup = SEX,
    subgroup_comparator = "Male",
    covariates = ~ FEV1_BL + RACE
  )

marginal_means <-
  ncs_emmeans(
    fit = fit,
    observed_time = "time_cont",
    scheduled_time = "VISITN",
    arm = "ARMCD",
    subgroup = "SEX"
  )

change_from_baseline(
  emmeans = marginal_means,
  time_observed_continuous = "time_cont",
  time_scheduled_baseline = 10,
  arm = "ARMCD",
  subgroup = "SEX"
)

# Same thing as a tibble:
change_from_baseline(
  emmeans = marginal_means,
  time_observed_continuous = "time_cont",
  time_scheduled_baseline = 10,
  arm = "ARMCD",
  subgroup = "SEX",
  as_tibble = TRUE
)

treatment_effect(
```

```
emmeans = marginal_means,  
time_observed_continuous = "time_cont",  
time_scheduled_baseline = 10,  
arm = "ARMCD",  
subgroup = "SEX",  
ref_value = "Male",  
as_tibble = TRUE  
)
```

make_visit_labels *Make Visit Labels Based on a Numeric Vector*

Description

Create a character vector of values to be used as labels for a [factor](#).

Usage

```
make_visit_labels(t, visit = "VIS", baseline = "BASELINE", pad = "0")
```

Arguments

t	A non-empty numeric vector of unique, finite elements in ascending order.
visit	A single character string specifying the prefix to add to t.
baseline	A single character string to use for the first timepoint's label. Alternatively, set to NULL so that all timepoints will have the prefix specified by visit.
pad	The character to use to pad between visit and t so that the places of t are aligned. Alternatively, set to NULL so that t is automatically converted to character without special formatting. This can result in numbers in labels not being aligned or not being in "alphabetical" order .

Details

Places visit as a prefix before the values of t. If pad is not NULL, the values of t are first formatted so that their places are aligned, and they are left-padded with zeros.

If baseline is not NULL it is used as the first label regardless of the value of t[1].

Uses [make.unique](#)(sep = "_") in case any elements are identical after [formatting](#).

Value

A [character](#) vector of length `length(t)`.

Examples

```
make_visit_labels(c(0, 5, 13, 101))
```

```
make_visit_labels(c(0, 5.23453, 13, 101.4))
```

```
make_visit_labels(c(0, 5.23453, 13, 101.4), baseline = NULL, pad = " ")
```

```
make_visit_labels(c(0, 5.23453, 13, 101.4), visit = "Week", pad = NULL)
```

midpoints

Midpoints of a Numeric Vector

Description

Returns the midpoints between the elements of a vector in the order the elements appear.

Usage

```
midpoints(x)
```

Arguments

x A numeric vector with at least 2 elements.

Details

This function does not sort.

Value

A numeric vector of [length](#) `length(x) - 1`.

Examples

```
midpoints(c(0, 1, 10, 4))
```

`ncs_analysis`*Run a Natural Cubic Spline (NCS) Analysis.*

Description

Fit and analyze an `mmrm` model wherein the continuous time variable has splines applied.

- `ncs_analysis()` fits such a model without involving subgroups.
- `ncs_analysis_subgroup()` fits a model that involves subgroups and performs additional analyses.

Usage

```
ncs_analysis(  
  data,  
  response = "response",  
  subject = "subject",  
  arm = "arm",  
  control_group,  
  time_observed_continuous = "time_observed_continuous",  
  df = 2,  
  spline_basis = NULL,  
  time_observed_index = "time_observed_index",  
  time_scheduled_continuous = "time_scheduled_continuous",  
  time_scheduled_baseline = 0,  
  time_scheduled_label = "time_scheduled_label",  
  covariates = ~1,  
  cov_structs = c("us", "toeph", "ar1h", "csh", "cs"),  
  cov_struct_group = NULL,  
  mmrm_args = list(method = "Satterthwaite"),  
  emmeans_args = list(nesting = NULL),  
  average_nuisance = TRUE,  
  conf.level = 0.95,  
  change_in_bl_contrast_args = list(adjust = "none"),  
  treatment_effect_contrast_args = list(adjust = "none"),  
  confint_args = list(level = conf.level),  
  return_models = FALSE,  
  expand_spline_terms = TRUE  
)
```

```
ncs_analysis_subgroup(  
  data,  
  response = "response",  
  subject = "subject",  
  arm = "arm",  
  control_group,  
  subgroup = "subgroup",
```

```

subgroup_comparator = "subgroup1",
time_observed_continuous = "time_observed_continuous",
df = 2,
spline_basis = NULL,
time_observed_index = "time_observed_index",
time_scheduled_continuous = "time_scheduled_continuous",
time_scheduled_baseline = 0,
time_scheduled_label = "time_scheduled_label",
covariates = ~1,
cov_structs = c("us", "toeph", "ar1h", "csh", "cs"),
cov_struct_group = NULL,
mmrm_args = list(method = "Satterthwaite"),
emmeans_args = list(nesting = NULL),
average_nuisance = TRUE,
conf.level = 0.95,
change_in_bl_contrast_args = list(adjust = "none"),
treatment_effect_contrast_args = list(adjust = "none"),
confint_args = list(level = conf.level),
subgroup_interaction_test = TRUE,
return_models = FALSE,
expand_spline_terms = TRUE
)

```

Arguments

data	(data frame) data set supplied to the data argument of <code>mmrm::mmrm()</code> when fitting models. The supplied expression is quoted and must evaluate to a data frame. See Tidy evaluation support .
response	(numeric or string) the response variable. It can be a string identifying the name of an existing variable; otherwise, the supplied expression will be quoted and added to the formula as is (see Tidy evaluation support).
subject	(atomic or string) the unique subject identifier forwarded to the subject argument of <code>mmrm::cov_struct()</code> . Ignored if <code>cov_structs</code> is a list. Can be a string identifying an existing variable; otherwise the supplied expression will be quoted and turned into a string with <code>rlang::expr_deparse()</code> (see Tidy evaluation support).
arm	(factor or string) the study arm. It must be a string or a name identifying an existing variable (i.e., it cannot be a call). If a name, it will be quoted before being added to the model formula (see Tidy evaluation support). If it does not evaluate to a factor or if <code>control_group</code> is not its first level , the data argument will be wrapped in a <code>dplyr::mutate()</code> call that forces this to be the case.
control_group	(string) the value in arm denoting the control group. If necessary, arm will be preprocessed such that it is a factor with <code>control_group</code> as its first level.

time_observed_continuous	(numeric or string) the visit's <i>observed</i> time point. It must either be a string or a name identifying an existing variable (i.e., it cannot be a call). If a name is provided, it is quoted and incorporated into the model formula as is (see Tidy evaluation support).
df	(scalar integer) number of degrees of freedom to use to create the spline basis. Passed to the df argument of time_spline_basis() . Ignored if the spline_basis argument is not NULL.
spline_basis	(basis matrix) a spline basis: probably a value returned by time_spline_basis() (which wraps splines::ns()). If NULL (the default), then the spline basis will be the result of forwarding time_observed_continuous and df to time_spline_basis() . See Providing a spline basis .
time_observed_index	(ordered or string) the visit index that the visit shall be associated with, based on the visit's <i>observed</i> time point. This will be passed as the visits argument of mmrm::cov_struct() . It can be a string identifying an existing variable; otherwise the supplied expression will be quoted and turned into a string with rlang::expr_deparse() (see Tidy evaluation support). If it does not evaluate to an ordered factor, it will be wrapped with as.ordered() . Ignored if cov_structs is a list.
time_scheduled_continuous	(numeric or string) the continuous time point when the visit was <i>scheduled</i> to occur. Its unique values will identify the time points at which the marginal means and other results will be calculated. It can be a string identifying an existing variable name; otherwise the supplied expression will be quoted before being evaluated (see Tidy evaluation support).
time_scheduled_baseline	(scalar numeric) the continuous time point when baseline was <i>scheduled</i> to occur. Defaults to 0.
time_scheduled_label	(character or string) the label associated with the scheduled visit. It can be a string identifying an existing variable name; otherwise the supplied expression will be quoted before being evaluated (see Tidy evaluation support).
covariates	(formula) formula containing additional terms that should be added to the mmrm model. Defaults to <code>~ 1</code> , in which no additional terms will be added. Must not have a left side. Cannot contain <code>..</code> To specify that the model shall not have an intercept, use include <code>+ 0</code> or <code>- 1</code> in this formula.
cov_structs	(character or list) either a list of unique cov_struct objects or a character vector of one or more of the covariance structure abbreviations as described in mmrm::cov_types() . These covariance structures will be attempted in order until one of them achieves a converging model fit. Defaults to <code>c("us", "toeph", "ar1h", "csh", "cs")</code> .

cov_struct_group	(atomic or string) optional grouping variable to be passed to the group argument of <code>mrm::cov_struct()</code> . It can be a string identifying an existing variable name; otherwise the supplied expression will be <code>quoted</code> and turned into a string with <code>rlang::expr_deparse()</code> (see Tidy evaluation support). Ignored if <code>cov_structs</code> is a list. Defaults to NULL, in which case no grouping variable will be used.
mrm_args	(named list) arguments to be passed to <code>mrm::mrm()</code> . If any elements have the names <code>formula</code> , <code>data</code> , or <code>covariance</code> they will be ignored. An element named <code>vcov</code> will also be ignored unless fitting a model with an unstructured covariance. Defaults to <code>list(method = "Satterthwaite")</code> .
emmeans_args	(named list) arguments to be passed to <code>emmeans::emmeans()</code> . If any elements have the names <code>object</code> , <code>specs</code> , or <code>at</code> they will be ignored. If <code>average_nuisance = TRUE</code> , any element named <code>nuisance</code> will be ignored. Any elements named <code>params</code> may be ignored. Defaults to <code>list(nesting = NULL)</code> .
average_nuisance	(flag) flag indicating whether the names of the terms in <code>covariates</code> should be supplied as the nuisance argument to <code>emmeans::emmeans()</code> . This results in treating all the covariates as nuisance parameters and averaging over them when calculating the reference grid to estimate marginal means. See <code>emmeans::ref_grid()</code> for details and limitations.
conf.level	(scalar numeric) confidence level for the calculation of p-values. Defaults to 0.95.
change_in_bl_contrast_args, treatment_effect_contrast_args	(named list) arguments to be passed to <code>emmeans::contrast()</code> when calculating the change from baseline and treatment effect results. If any elements have the names <code>object</code> or <code>method</code> they will be ignored. Defaults to <code>list(adjust = "none")</code> .
confint_args	(named list) arguments to be passed to <code>stats::confint()</code> when calculating confidence intervals for change in baseline and treatment effect. If any element has the name <code>object</code> it will be ignored. Defaults to <code>list(level = conf.level)</code> .
return_models	(flag) flag indicating whether or not to return the model(s) used to calculate the results. See Obtaining the models used below.
expand_spline_terms	(flag) flag indicating whether or not to separate the cubic spline matrix into separate terms (one for each degree of freedom). Defaults to TRUE. See Expanding spline terms .
subgroup	(factor or string) the subgroup. It must be a string or a <code>name</code> identifying an existing variable (i.e., it cannot be a <code>call</code>). If a name, it will be <code>quoted</code> before being added to

the model formula (see **Tidy evaluation support**). If it does not evaluate to a [factor](#) or if `subgroup_comparator` is not its first [level](#), the `data` argument will be wrapped in a `dplyr::mutate()` call that forces this to be the case.

`subgroup_comparator`

(string)

the value in `subgroup` denoting the "main" subgroup that all other subgroups should be compared to. If necessary, `subgroup` will be preprocessed such that it is a factor with `control_group` as its first level.

`subgroup_interaction_test`

(flag)

flag indicating whether or not the subgroup interaction test should be performed. If TRUE, the returned value will include an interaction element, a data frame of results. Defaults to TRUE. See **Subgroup interaction test** for details.

Value

For `ncs_analysis()`, see [splinetrials_analysis](#). For `ncs_analysis_subgroup()`, see [splinetrials_subgroup_anal](#).

Overview

These functions create an [mmrm](#) model from the user-specified arguments. They then perform a series of analyses and produce a data frame of results with a unique row for each combination of `arm`, `time_scheduled_continuous`, and `subgroup` (for `ncs_analysis_subgroup()` only). The results include:

1. Basic diagnostics on the response variable
2. Estimated marginal means
3. Change from baseline
4. Treatment effect
5. Percent slowing

Building a model

See the details of [ncs_mmrm_fit\(\)](#) for information on how the model is built.

Subgroup analysis

`ncs_analysis_subgroup()` contains more analyses and results than `ncs_analysis()`. Whereas the latter produces a data frame by default, the former produces a list of data frames.

Treatment effects:

The treatment effect is calculated twice: once *between* subgroups (examining the differences between the subgroups within each study arm) and once *within* subgroups (examining the differences between the study arms within each subgroup). The main results table is effectively returned twice as both the *between* element and the *within* element. These elements' treatment effect values differ, and only the *within* element contains the percent slowing analysis results.

Type-III ANOVA:

The subgroup analyses include a type-III analysis of variance (ANOVA) on the main analysis model's terms, using a Chi-squared test statistic. This is accomplished via the `mrm` method for `car::Anova()`. The results are included in the returned value as the `type3` element. See `vignette("hypothesis_testing", "mrm")` for details on the type-III ANOVA.

Subgroup interaction test:

When `subgroup_interaction_test = TRUE`, the function runs an ANOVA to compare a maximum-likelihood-estimated (ML) version of the original model to a reduced version. This happens as follows:

1. The original analysis model is refit with `reml = FALSE` if it was originally created with `reml = TRUE`. This may be dubbed the "full" model.
2. A reduced version of the "full" model is created, removing the second-order interaction term (see the **arm and subgroup terms** section above). This may be dubbed the "reduced" model.
3. The "full" and "reduced" models are compared using the `mrm` method of `stats::anova()`.
4. The results are processed into a table and added to the returned value as the `interaction` element.

Returning the models used

The model(s) used to conduct the analyses can be obtained by setting `return_models = TRUE`.

For `ncs_analysis()`, the analysis model will be included as the `splinetrials_analysis_model` attribute of the returned value.

For `ncs_analysis_subgroup()`, the analysis model is added to the returned value as the `analysis_model` element. Furthermore, if `subgroup_interaction_test = TRUE`, the "full" and "reduced" models will be included in the returned value as the elements `full` and `reduced` (see **Subgroup interaction test** above for details).

Examples

```
# Create a usable data set out of mrm::fev_data
fev_mod <- mrm::fev_data
fev_mod$VISITN <- fev_mod$VISITN * 10
fev_mod$time_cont <- fev_mod$VISITN + rnorm(nrow(fev_mod))
fev_mod$obs_visit_index <- round(fev_mod$time_cont)

# Without subgroup:
ncs_analysis(
  data = fev_mod,
  response = FEV1,
  subject = USBJID,
  arm = ARMCD,
  control_group = "PBO",
  time_observed_continuous = time_cont,
  df = 2,
  time_observed_index = obs_visit_index,
  time_scheduled_continuous = VISITN,
  time_scheduled_baseline = 10,
  time_scheduled_label = AVISIT,
```

```

    covariates = ~ FEV1_BL + RACE,
    cov_structs = c("ar1", "us")
  )

# With subgroup:
ncs_analysis_subgroup(
  data = fev_mod,
  response = FEV1,
  subject = USBJID,
  arm = ARMCD,
  control_group = "PBO",
  subgroup = SEX,
  subgroup_comparator = "Male",
  time_observed_continuous = time_cont,
  df = 2,
  time_observed_index = obs_visit_index,
  time_scheduled_continuous = VISITN,
  time_scheduled_baseline = 10,
  time_scheduled_label = AVISIT,
  covariates = ~ FEV1_BL + RACE,
  cov_structs = c("ar1", "us")
)

```

ncs_emmeans

Estimate Marginal Means for a Natural Cubic Splines Analysis

Description

This is wrapper around `emmeans::emmeans()` for a natural cubic splines analysis in which there is a continuous time variable, a study arm, and (optionally) a subgroup variable.

Usage

```

ncs_emmeans(
  fit,
  data = fit[["data"]],
  observed_time = NULL,
  scheduled_time = NULL,
  arm = NULL,
  subgroup = NULL,
  average_nuisance = TRUE,
  emmeans_args = list(nesting = NULL),
  ...,
  scheduled_time_spec = sort(unique(data[[scheduled_time]])),
  arm_spec = as.character(sort(unique(data[[arm]]))),
  subgroup_spec = as.character(sort(unique(data[[subgroup]]))),
  __caller_env = rlang::caller_env()
)

```

Arguments

<code>fit</code>	(mrm)	an mrm object whose terms include the variables supplied to <code>observed_time</code> , <code>scheduled_time</code> , <code>arm</code> , and (optionally) <code>subgroup</code> .
<code>data</code>	(data frame)	a data frame on which to estimate marginal means. Defaults to <code>fit[["data"]]</code> .
<code>observed_time</code>	(string)	string specifying the <i>observed</i> continuous time variable in both <code>fit</code> and in <code>data</code> .
<code>scheduled_time</code>	(string)	string specifying the <i>scheduled</i> continuous time variable in both <code>fit</code> and in <code>data</code> . Ignored if <code>scheduled_time_spec</code> is provided.
<code>arm</code>	(string)	string specifying the study arm variable in both <code>fit</code> and in <code>data</code> .
<code>subgroup</code>	(string)	string specifying the subgroup variable in both <code>fit</code> and in <code>data</code> .
<code>average_nuisance</code>	(flag)	flag indicating whether the names of the terms in <code>covariates</code> should be supplied as the nuisance argument to <code>emmeans::emmeans()</code> . This results in treating all the covariates as nuisance parameters and averaging over them when calculating the reference grid to estimate marginal means. See <code>emmeans::ref_grid()</code> for details and limitations.
<code>emmeans_args, ...</code>	(named list)	arguments to be passed to <code>emmeans::emmeans()</code> . If any elements have the names <code>object</code> , <code>specs</code> , or <code>at</code> they will be ignored. If <code>average_nuisance = TRUE</code> , any element named <code>nuisance</code> will be ignored. Any elements named <code>params</code> may be ignored. <code>emmeans_args</code> defaults to <code>list(nesting = NULL)</code> . Arguments named in <code>emmeans_args</code> supersede any named arguments in <code>...</code>
<code>scheduled_time_spec</code>	(numeric)	vector of unique, non-missing time points on which to calculate marginal means. Defaults to <code>sort(unique(data[[scheduled_time]])</code> .
<code>arm_spec</code>	(character)	vector of unique study arm values on which to calculate marginal means. Defaults to <code>as.character(sort(unique(data[[arm]]))</code> .
<code>subgroup_spec</code>		vector of unique subgroup values on which to calculate marginal means. Ignored if <code>subgroup</code> is <code>NULL</code> . Defaults to <code>as.character(sort(unique(data[[subgroup]]))</code> .
<code>._caller_env</code>	(environment)	the environment from which this function was called. Defaults to <code>rlang::caller_env()</code> .

Value

An object of class `emmGrid`: the result of `emmeans::emmeans()`. Note that for a result `result`, the elements `result@model.info$nesting` and `result@misc$display` are removed.

Examples

```
# Create a usable data set out of mrm::fev_data
fev_mod <- mrm::fev_data
fev_mod$VISITN <- fev_mod$VISITN * 10
fev_mod$time_cont <- fev_mod$VISITN + rnorm(nrow(fev_mod))
fev_mod$obs_visit_index <- round(fev_mod$time_cont)

fit <-
  ncs_mmr_fit(
    data = fev_mod,
    type = "subgroup_full",
    response = FEV1,
    subject = USUBJID,
    cov_structs = c("ar1", "us"),
    time_observed_continuous = time_cont,
    df = 2,
    time_observed_index = obs_visit_index,
    arm = ARMCD,
    control_group = "PBO",
    subgroup = SEX,
    subgroup_comparator = "Male",
    covariates = ~ FEV1_BL + RACE
  )

ncs_emmeans(
  fit = fit,
  observed_time = "time_cont",
  scheduled_time = "VISITN",
  arm = "ARMCD",
  subgroup = "SEX"
)
```

ncs_mmr_fit

Create a Mixed Model with Repeated Measures Using Natural Cubic Splines.

Description

Builds an `mmrm` model that includes a study arm, optionally a subgroup, and natural cubic splines applied to a continuous time variable. A wrapper around `mmrm::mmrm()`.

Constructs a call to `mmrm::mmrm()` for ncs analysis. Implements natural cubic splines for the continuous time variable. Attempts a sequence of covariance structures in order until one of them successfully converges. Title

Usage

```
ncs_mmr_fit(
  data,
  type = c("basic", "subgroup_full", "subgroup_reduced"),
```

```

response,
subject,
cov_structs = c("us", "toeph", "ar1h", "csh", "cs"),
cov_struct_group = NULL,
time_observed_continuous,
df = 2,
spline_basis = NULL,
time_observed_index,
arm = NULL,
control_group = "control",
subgroup = NULL,
subgroup_comparator = NULL,
covariates = ~1,
expand_spline_terms = TRUE,
mmrm_args = list(method = "Satterthwaite"),
...
)

```

Arguments

data	(data frame) data set supplied to the data argument of <code>mmrm::mmrm()</code> when fitting models. The supplied expression is quoted and must evaluate to a data frame. See Tidy evaluation support .
type	(string) one of "basic", "subgroup_full", or "subgroup_reduced".
response	(numeric or string) the response variable. It can be a string identifying the name of an existing variable; otherwise, the supplied expression will be quoted and added to the formula as is (see Tidy evaluation support).
subject	(atomic or string) the unique subject identifier forwarded to the subject argument of <code>mmrm::cov_struct()</code> . Ignored if <code>cov_structs</code> is a list. Can be a string identifying an existing variable; otherwise the supplied expression will be quoted and turned into a string with <code>rlang::expr_deparse()</code> (see Tidy evaluation support).
cov_structs	(character or list) either a list of unique <code>cov_struct</code> objects or a character vector of one or more of the covariance structure abbreviations as described in <code>mmrm::cov_types()</code> . These covariance structures will be attempted in order until one of them achieves a converging model fit. Defaults to <code>c("us", "toeph", "ar1h", "csh", "cs")</code> .
cov_struct_group	(atomic or string) optional grouping variable to be passed to the group argument of <code>mmrm::cov_struct()</code> . It can be a string identifying an existing variable name; otherwise the supplied expression will be quoted and turned into a string with <code>rlang::expr_deparse()</code> (see Tidy evaluation support). Ignored if <code>cov_structs</code> is a list. Defaults to <code>NULL</code> , in which case no grouping variable will be used.

time_observed_continuous	(numeric or string) the visit's <i>observed</i> time point. It must either be a string or a name identifying an existing variable (i.e., it cannot be a call). If a name is provided, it is quoted and incorporated into the model formula as is (see Tidy evaluation support).
df	(scalar integer) number of degrees of freedom to use to create the spline basis. Passed to the df argument of time_spline_basis() . Ignored if the spline_basis argument is not NULL.
spline_basis	(basis matrix) a spline basis: probably a value returned by time_spline_basis() (which wraps splines::ns()). If NULL (the default), then the spline basis will be the result of forwarding time_observed_continuous and df to time_spline_basis() . See Providing a spline basis .
time_observed_index	(ordered or string) the visit index that the visit shall be associated with, based on the visit's <i>observed</i> time point. This will be passed as the visits argument of mmrm::cov_struct() . It can be a string identifying an existing variable; otherwise the supplied expression will be quoted and turned into a string with rlang::expr_deparse() (see Tidy evaluation support). If it does not evaluate to an ordered factor, it will be wrapped with as.ordered() . Ignored if cov_structs is a list.
arm	(factor or string) the study arm. It must be a string or a name identifying an existing variable (i.e., it cannot be a call). If a name, it will be quoted before being added to the model formula (see Tidy evaluation support). If it does not evaluate to a factor or if control_group is not its first level , the data argument will be wrapped in a dplyr::mutate() call that forces this to be the case.
control_group	(string) the value in arm denoting the control group. If necessary, arm will be preprocessed such that it is a factor with control_group as its first level.
subgroup	(factor or string) the subgroup. It must be a string or a name identifying an existing variable (i.e., it cannot be a call). If a name, it will be quoted before being added to the model formula (see Tidy evaluation support). If it does not evaluate to a factor or if subgroup_comparator is not its first level , the data argument will be wrapped in a dplyr::mutate() call that forces this to be the case.
subgroup_comparator	(string) the value in subgroup denoting the "main" subgroup that all other subgroups should be compared to. If necessary, subgroup will be preprocessed such that it is a factor with control_group as its first level.
covariates	(formula) formula containing additional terms that should be added to the mmrm model. Defaults to <code>~ 1</code> , in which no additional terms will be added. Must not have a left side. Cannot contain <code>..</code> To specify that the model shall not have an intercept, use include <code>+ 0</code> or <code>- 1</code> in this formula.

`expand_spline_terms`
 (flag)
 flag indicating whether or not to separate the cubic spline matrix into separate terms (one for each degree of freedom). Defaults to TRUE. See **Expanding spline terms**.

`mmrm_args` (named list)
 arguments to be passed to `mmrm::mmrm()`. If any elements have the names formula, data, or covariance they will be ignored. An element named `vcov` will also be ignored unless fitting a model with an unstructured covariance. Defaults to `list(method = "Satterthwaite")`.

... additional arguments to be passed to `mmrm::mmrm()`. If any elements have the names formula, data, or covariance they will be ignored. An element named `vcov` will also be ignored unless fitting a model with an unstructured covariance. Defaults to `list(method = "Satterthwaite")`. Arguments named in `mmrm_args` supersede any named arguments in ...

Value

An `mmrm` object created by `mmrm::mmrm()`.

Providing a spline basis

This function's `spline_basis` argument was designed with `splines::ns()` in mind, which creates a matrix object with classes `basis` and `matrix` as well as multiple attributes. In theory, `spline_basis` does not have to be a matrix; however, it still must have a `stats::predict()` method wherein `stats::predict(spline_basis, data[[time_observed_continuous]])` produces an object that can serve as a term in the model.

Covariance structures

The user specifies covariance structure *candidates* via the `cov_structs` argument. These structures will be attempted in order until a model converges successfully.

When any covariance structure other than "us" (heterogeneous unstructured) is used, "Empirical-Bias-Reduced" is passed to `mmrm::mmrm()` as the `vcov` argument (see `mmrm::mmrm_control()`).

When fitting models, these analysis functions specify the covariance structure through the `covariance` argument of `mmrm::mmrm()`.

Building the model formula

These analysis functions automatically build the model formula from its arguments. The user cannot remove any of these auto-generated terms, but terms can be added via the `covariates` argument.

Time spline terms:

Natural cubic splines will be applied to the `time_observed_continuous` variable in data. These splines will be constructed according to the user-specified `spline_basis`. A custom `spline_fn()` is constructed under the hood that accepts `time_observed_continuous` and produces a spline matrix based on the `spline_basis`. Thus, the model formula includes a time spline term resembling `spline_fn(time_observed_continuous)`.

arm and subgroup terms:

All generated models include an interaction term between the time spline term and the study arm term, but arm is not included as a main effect by default. If this is desired, use the `covariates` argument (e.g., specify `covariates = ~ arm`).

Concerning `ncs_analysis_subgroup()`, the subgroup variable is included as a main effect, and its interaction with the time spline is also included. Furthermore, the second-order interaction term between the time spline, subgroup, and arm is also included for the main analysis model and the "full" model (when `subgroup_interaction_test = TRUE`; see **Subgroup interaction test** below).

Adding terms with covariates:

The user can specify additional terms through the `covariates` argument, which must be a formula.

The user cannot specify the covariance structure with this argument. See the **Covariance structures** section above.

The user can remove the intercept from the model by including \emptyset as a term in `covariates`.

Model formula templates:

The model formulas that the analysis functions construct will take the form of the formula templates below.

`ncs_analysis()` (*i.e., no subgroup*):

```
response ~
  spline_fn(time_observed_continuous) +
  spline_fn(time_observed_continuous):arm {+
  covariates}
```

`ncs_analysis_subgroup()`:

Main analysis model and "full" model:

```
response ~
  spline_fn(time_observed_continuous) +
  subgroup +
  spline_fn(time_observed_continuous):subgroup +
  spline_fn(time_observed_continuous):arm +
  spline_fn(time_observed_continuous):subgroup:arm {+
  covariates}
```

"reduced" model:

```
response ~
  spline_fn(time_observed_continuous) +
  subgroup +
  spline_fn(time_observed_continuous):subgroup +
  spline_fn(time_observed_continuous):arm {+
  covariates}
```

Expanding spline terms:

When `expand_spline_terms = TRUE` and `spline_basis` has at least two [dimensions](#) (e.g., if it is a matrix, which is typical), the spline term will be split into multiple terms: one for each of its columns.

For instance, if the user specifies a `spline_basis` with 3 degrees of freedom, the above no-subgroup model formula template would become:

```

response ~
  spline_fn(time_observed_continuous)[, 1] +
  spline_fn(time_observed_continuous)[, 2] +
  spline_fn(time_observed_continuous)[, 3] +
  spline_fn(time_observed_continuous)[, 1]:arm +
  spline_fn(time_observed_continuous)[, 2]:arm +
  spline_fn(time_observed_continuous)[, 3]:arm {+
  covariates}

```

Examples

```

# Create a usable data set out of mmrm::fev_data
fev_mod <- mmrm::fev_data
fev_mod$VISITN <- fev_mod$VISITN * 10
fev_mod$time_cont <- fev_mod$VISITN + rnorm(nrow(fev_mod))
fev_mod$obs_visit_index <- round(fev_mod$time_cont)

```

```

# Example without subgroup:
ncs_mmrn_fit(
  data = fev_mod,
  type = "basic",
  response = FEV1,
  subject = USUBJID,
  cov_structs = c("ar1", "us"),
  time_observed_continuous = time_cont,
  df = 2,
  time_observed_index = obs_visit_index,
  arm = ARMCD,
  control_group = "PBO",
  covariates = ~ FEV1_BL + RACE
)

```

```

# Example with subgroup:
ncs_mmrn_fit(
  data = fev_mod,
  type = "subgroup_full",
  response = FEV1,
  subject = USUBJID,
  cov_structs = c("ar1", "us"),
  time_observed_continuous = time_cont,
  df = 2,
  time_observed_index = obs_visit_index,
  arm = ARMCD,
  control_group = "PBO",
  subgroup = SEX,
  subgroup_comparator = "Male",
  covariates = ~ FEV1_BL + RACE
)

```

`ncs_plot_means`*Plot Actual and Predicted Response Variable Means by Study Arm.*

Description

This function accepts a data set, probably produced by `ncs_analysis()`, and it uses `ggplot2` to produce a [panel](#) of plots, one for each study arm. The time variable is along the x-axis, and the response variable is along the y-axis. The actual means of the response variable are [points](#) plotted in one color, and the modeled means are plotted in another color. Each point also has its confidence interval [plotted](#).

Usage

```
ncs_plot_means(  
  data,  
  arm = "arm",  
  time = "time",  
  est = "est",  
  lower = "lower",  
  upper = "upper",  
  model_est = "response_est",  
  model_lower = "response_lower",  
  model_upper = "response_upper"  
)
```

Arguments

<code>data</code>	(data frame) a data frame, probably produced by <code>ncs_analysis()</code> , containing the actual and predicted means. Each row should have a unique combination of arm and time.
<code>arm</code>	(string) the name of the study arm variable in data. There will be a separate plot produced for each study arm.
<code>time</code>	(string) the name of the time or visit variable in data. These values correspond to the x-axis.
<code>est, lower, upper</code>	(string) the name of the variables in data containing the actual response variable's mean and confidence interval bounds. These values correspond to the y-axis.
<code>model_est, model_lower, model_upper</code>	(string) the name of the variables in data containing the predicted response variable's mean and confidence interval bounds. These values correspond to the y-axis.

Value

An object returned by `ggplot2::ggplot()`.

Examples

```
# Create a usable data set out of mrmr::fev_data
fev_mod <- mrmr::fev_data
fev_mod$VISITN <- fev_mod$VISITN * 10
fev_mod$time_cont <- fev_mod$VISITN + rnorm(nrow(fev_mod))
fev_mod$obs_visit_index <- round(fev_mod$time_cont)

# Analysis result data set
ncs_data_results <-
  ncs_analysis(
    data = fev_mod,
    response = FEV1,
    subject = USUBJID,
    arm = ARMCD,
    control_group = "PBO",
    time_observed_continuous = time_cont,
    df = 2,
    time_observed_index = obs_visit_index,
    time_scheduled_continuous = VISITN,
    time_scheduled_baseline = 10,
    time_scheduled_label = AVISIT,
    covariates = ~ FEV1_BL + RACE,
    cov_structs = c("ar1", "us")
  )

ncs_plot_means(ncs_data_results)
```

ncs_plot_means_subgroup

Plot Actual and Predicted Response Variable Means by Study Arm and Subgroup.

Description

This function accepts a data set, probably produced by `ncs_analysis_subgroup()`, and it uses `ggplot2` to produce a `grid` of plots, one for each combination of study arm and subgroup. The time variable is along the x-axis, and the response variable is along the y-axis. The actual means of the response variable are `points` plotted in one color, and the modeled means are plotted in another color. Each point also has its confidence interval `plotted`.

Usage

```
ncs_plot_means_subgroup(
  data,
  arm = "arm",
```

```

time = "time",
subgroup = "subgroup",
est = "est",
lower = "lower",
upper = "upper",
model_est = "response_est",
model_lower = "response_lower",
model_upper = "response_upper"
)

```

Arguments

data	(data frame) a data frame, probably produced by <code>ncs_analysis()</code> , containing the actual and predicted means. Each row should have a unique combination of arm, time, and subgroup.
arm	(string) the name of the study arm variable in data. There will be a separate column of plots produced for each study arm.
time	(string) the name of the time or visit variable in data. These values correspond to the x-axis.
subgroup	(string) the name of the subgroup variable in data. There will be a separate row of plots produced for each subgroup.
est, lower, upper	(string) the name of the variables in data containing the actual response variable's mean and confidence interval bounds. These values correspond to the y-axis.
model_est, model_lower, model_upper	(string) the name of the variables in data containing the predicted response variable's mean and confidence interval bounds. These values correspond to the y-axis.

Value

An object returned by `ggplot2::ggplot()`.

Examples

```

# Create a usable data set out of mrmr::fev_data
fev_mod <- mrmr::fev_data
fev_mod$VISITN <- fev_mod$VISITN * 10
fev_mod$time_cont <- fev_mod$VISITN + rnorm(nrow(fev_mod))
fev_mod$obs_visit_index <- round(fev_mod$time_cont)

# Analysis result data set
ncs_data_results_subgroup <-
  ncs_analysis_subgroup(

```

```

data = fev_mod,
response = FEV1,
subject = USUBJID,
arm = ARMCD,
control_group = "PBO",
subgroup = RACE,
subgroup_comparator = "Asian",
time_observed_continuous = time_cont,
df = 2,
time_observed_index = obs_visit_index,
time_scheduled_continuous = VISITN,
time_scheduled_baseline = 10,
time_scheduled_label = AVISIT,
covariates = ~ FEV1_BL + RACE,
cov_structs = c("ar1", "us")
)

ncs_plot_means_subgroup(ncs_data_results_subgroup$between)

```

```
percent_slowing_using_change_from_bl
```

Calculates Percent Slowing from a Data Frame of Change-from-Baseline Data

Description

Accepts a data frame of change-from-baseline data (probably created with [change_from_baseline\(\)](#)) and returns a table of percent slowing results.

Usage

```

percent_slowing_using_change_from_bl(
  change_from_bl_tbl,
  time_observed_continuous,
  arm,
  control_group,
  subgroup = NULL,
  est = "estimate",
  se = "SE",
  conf.level = 0.95
)

```

Arguments

```
change_from_bl_tbl
```

(data frame)
a data frame of change-from-baseline data whose columns include `time_observed_continuous`, `arm`, (optionally) `subgroup`, `est`, and `se`.

time_observed_continuous, arm, subgroup, est, se
 (string)
 strings identifying the columns in change_from_bl_tbl that contain the continuous time variable, the study arm, (optionally) the subgroup, the change-from-baseline estimate, and the change-from-baseline standard error.

control_group (string)
 the value in the arm column of change_from_bl_tbl denoting the control group.

conf.level (scalar numeric)
 confidence level for the calculation of p-values. Defaults to 0.95.

Details

For each study arm that is not the control group,

$$\text{Let } \theta = \frac{\text{treatment estimate}}{\text{control estimate}}$$

$$\text{Let } \alpha = 1 - \text{conf.level}$$

$$\text{Let MOE} = 100 \times z_{1-\alpha/2} \times \frac{\sqrt{\text{treatment SE}^2 + (\theta \times \text{control SE})^2}}{|\text{control estimate}|}$$

Therefore, the percent slowing estimates and their respective confidence intervals are calculated thus:

$$\text{Percent slowing estimate} = (1 - \theta) \times 100$$

$$\text{Percent slowing CI} = \text{Percent slowing estimate} \pm \text{MOE}$$

Value

A data frame with a row for each combination of the unique values of change_from_bl_tbl[[time_observed_continuous]], change_from_bl_tbl[[arm]] (except the value denoted in control_group), and change_from_bl_tbl[[subgroup]] (if subgroup is not NULL). It will contain the following columns:

1. {column name will be the value of the arm argument}: the study arm.
2. {column name will be the value of the time_observed_continuous argument}: the *observed* continuous time variable.
3. {column name will be the value of the subgroup argument}: the subgroup. Only present if subgroup is not NULL.
4. percent_slowing_est: the percent slowing estimate
5. percent_slowing_lower: the lower bound of the confidence interval for percent_slowing_est.
6. percent_slowing_upper: the upper bound of the confidence interval for percent_slowing_est.

Examples

```
# Create a usable data set out of mrmr::fev_data
fev_mod <- mrmr::fev_data
fev_mod$VISITN <- fev_mod$VISITN * 10
fev_mod$time_cont <- fev_mod$VISITN + rnorm(nrow(fev_mod))
fev_mod$obs_visit_index <- round(fev_mod$time_cont)

fit <-
  ncs_mrmr_fit(
    data = fev_mod,
    type = "subgroup_full",
    response = FEV1,
    subject = USUBJID,
    cov_structs = c("ar1", "us"),
    time_observed_continuous = time_cont,
    df = 2,
    time_observed_index = obs_visit_index,
    arm = ARMCD,
    control_group = "PBO",
    subgroup = SEX,
    subgroup_comparator = "Male",
    covariates = ~ FEV1_BL + RACE
  )

marginal_means <-
  ncs_emmeans(
    fit = fit,
    observed_time = "time_cont",
    scheduled_time = "VISITN",
    arm = "ARMCD",
    subgroup = "SEX"
  )

change_from_bl_tbl <-
  change_from_baseline(
    emmeans = marginal_means,
    time_observed_continuous = "time_cont",
    time_scheduled_baseline = 10,
    arm = "ARMCD",
    subgroup = "SEX",
    as_tibble = TRUE
  )

percent_slowing_using_change_from_bl(
  change_from_bl_tbl = change_from_bl_tbl,
  time_observed_continuous = "time_cont",
  arm = "ARMCD",
  control_group = "PBO",
  subgroup = "SEX"
)
```

 plot_outcome_by_visit_and_group

Plot Outcome Variable by Timepoint and Study Arm

Description

Plot a continuous outcome for each combination of scheduled visit and study arm.

Usage

```
plot_outcome_by_visit_and_group(
  data,
  outcome_var,
  scheduled_timepoint_var,
  group_var,
  ...,
  geom = ggplot2::geom_boxplot,
  geom_args = list(na.rm = TRUE)
)
```

Arguments

data	(data frame) The data frame that will be supplied to <code>ggplot2::ggplot()</code> .
outcome_var	(numeric) The continuous outcome variable to supply to the y argument of <code>ggplot2::aes()</code> . Whatever is supplied will be quoted and evaluated in the context of data .
scheduled_timepoint_var	(ordered) The variable containing the scheduled timepoints to supply to the x argument of <code>ggplot2::aes()</code> . Whatever is supplied will be quoted and evaluated in the context of data .
group_var	(numeric) The grouping variable (probably the study arm) to supply to the fill argument of <code>ggplot2::aes()</code> . Whatever is supplied will be quoted and evaluated in the context of data .
...	Forwarded onto <code>ggplot2::ggplot(ggplot2::aes)</code> .
geom	(function) The ggplot2 "geom" to use. Defaults to <code>ggplot2::geom_boxplot()</code> .
geom_args	(list) A list of arguments to supply to geom. Defaults to <code>list(na.rm = TRUE)</code> .

Value

A `ggplot` object.

Examples

```
# Create a usable data set out of mrmr::fev_data
fev_mod <- mrmr::fev_data
fev_mod$VISITN <- fev_mod$VISITN * 10
fev_mod$time_cont <- fev_mod$VISITN + rnorm(nrow(fev_mod))
fev_mod$obs_visit_index <- round(fev_mod$time_cont)

plot_outcome_by_visit_and_group(
  data = fev_mod,
  outcome_var = FEV1,
  scheduled_timepoint_var = as.ordered(VISITN),
  group_var = ARMCD
)
```

splinetrials_analysis-class

splinetrials_analysis *object*

Description

`ncs_analysis()` returns an object of class `splinetrials_analysis`: a 32-column `tibble` with one row per unique combination of `data[[arm]]` and `data[[time_scheduled_label]]` (see the arguments of `ncs_analysis()`).

Columns

1. `arm`: values of `data[[arm]]`.
2. `time`: values of `data[[time_scheduled_label]]`.
3. `n`: number of times the combination appears in data.
4. `est`: [mean](#) of `data[[response]]`.
5. `sd`: [standard deviation](#) of `data[[response]]`.
6. `se`: standard error of `data[[response]]` (i.e., sd / \sqrt{n}).
7. `lower`: lower bound of confidence interval.
8. `upper`: upper bound of confidence interval.
9. `response_est`: estimated marginal mean.
10. `response_se`: standard error of `response_est`.
11. `response_df`: degrees of freedom used for calculating the confidence interval for `response_est`.
12. `response_lower`: lower bound of confidence interval for `response_est`.
13. `response_upper`: upper bound of confidence interval for `response_est`.
14. `change_est`: estimated change from baseline.
15. `change_se`: standard error of `change_est`.
16. `change_df`: degrees of freedom used for calculating the confidence interval for and testing the significance of `change_est`.

17. `change_lower`: lower bound of confidence interval for `change_est`.
18. `change_upper`: upper bound of confidence interval for `change_est`.
19. `change_test_statistic`: test statistic measuring the significance of `change_est`.
20. `change_p_value`: p-value for the significance of `change_est`.
21. `diff_est`: treatment effect.
22. `diff_se`: standard error of `diff_est`.
23. `diff_df`: degrees of freedom used for calculating the confidence interval for and testing the significance of `diff_est`.
24. `diff_lower`: lower bound of confidence interval for `diff_est`.
25. `diff_upper`: upper bound of confidence interval for `diff_est`.
26. `diff_test_statistic`: test statistic measuring the significance of `diff_est`.
27. `diff_p_value`: p-value for the significance of `diff_est`.
28. `percent_slowing_est`: estimated percent slowing.
29. `percent_slowing_lower`: lower bound of confidence interval for `percent_slowing_est`.
30. `percent_slowing_upper`: upper bound of confidence interval for `percent_slowing_est`.
31. `correlation`: the covariance structure of the analysis model. This is the same value repeated for each row.
32. `optimizer`: invariably `mrm+tmb` to indicate that `mrm::mrm()` (which uses the TMB package) was used to fit the model.

Optional `analysis_model` attribute

If `ncs_analysis()` had `return_models = TRUE`, then the analysis model, an `mrm` object, will be included as the `analysis_model` attribute.

See Also

The function `ncs_analysis()`, which produces objects of this class.

splinetrials_subgroup_analysis-class
splinetrials_subgroup_analysis *object*

Description

`ncs_analysis_subgroup()` returns an object of class `splinetrials_subgroup_analysis`: a named [list](#) with three to seven elements.

between **and** within

These are each **tibbles**, and they share many of the same columns and values but are sorted in a different order. Each contains one row per unique combination of arm, time_scheduled_label, and subgroup found in the data (see the arguments of `ncs_analysis_subgroup()`). The values in columns arm through change_p_value as well as correlation and optimizer are identical. The two tables' treatment effect analysis results columns differ in name and content, with between's columns bearing the prefix `diff_subgroup_` and within's columns bearing the prefix `diff_arm_` (see the **Treatment effects** section of `ncs_analysis_subgroup()`). Lastly, only within contains the percent slowing analysis results.

between:

A 30-column **tibble** sorted by time, then by arm, then by subgroup.

Columns:

1. arm: values of data[[arm]].
2. time: values of data[[time_scheduled_label]].
3. subgroup: values of data[[subgroup]].
4. n: number of times the combination appears in data.
5. est: **mean** of data[[response]].
6. sd: **standard deviation** of data[[response]].
7. se: standard error of data[[response]] (i.e., sd / sqrt(n)).
8. lower: lower bound of confidence interval.
9. upper: upper bound of confidence interval.
10. response_est: estimated marginal mean.
11. response_se: standard error of response_est.
12. response_df: degrees of freedom used to calculate the confidence interval for response_est.
13. response_lower: lower bound of confidence interval for response_est.
14. response_upper: upper bound of confidence interval for response_est.
15. change_est: estimated change from baseline.
16. change_se: standard error of change_est.
17. change_df: degrees of freedom used for calculating the confidence interval for and testing the significance of change_est.
18. change_lower: lower bound of confidence interval for change_est.
19. change_upper: upper bound of confidence interval for change_est.
20. change_test_statistic: test statistic measuring the significance of change_est.
21. change_p_value: p-value for the significance of change_est.
22. diff_subgroup_est: treatment effect of subgroup within arm.
23. diff_subgroup_se: standard error of diff_subgroup_est.
24. diff_subgroup_df: degrees of freedom used for calculating the confidence interval for and testing the significance of diff_subgroup_est.
25. diff_subgroup_lower: lower bound of confidence interval for diff_subgroup_est.
26. diff_subgroup_upper: upper bound of confidence interval for diff_subgroup_est.
27. diff_subgroup_test_statistic: test statistic measuring the significance of diff_subgroup_est.
28. diff_subgroup_p_value: p-value for the significance of diff_subgroup_est.

29. correlation: the covariance structure of the analysis model. This is the same value repeated for each row.
30. optimizer: invariably mrmr+tm3 to indicate that `mrmr::mrmr()` (which uses the TMB package) was used to fit the model.

within

A 33-column `tibble` sorted by subgroup, then by arm, then by time.

Columns:

1. arm: values of data[[arm]].
2. time: values of data[[time_scheduled_label]].
3. subgroup: values of data[[subgroup]].
4. n: number of times the combination appears in data.
5. est: `mean` of data[[response]].
6. sd: `standard deviation` of data[[response]].
7. se: standard error of data[[response]] (i.e., sd / \sqrt{n}).
8. lower: lower bound of confidence interval.
9. upper: upper bound of confidence interval.
10. response_est: estimated marginal mean.
11. response_se: standard error of response_est.
12. response_df: degrees of freedom used for calculating the confidence interval for response_est.
13. response_lower: lower bound of confidence interval for response_est.
14. response_upper: upper bound of confidence interval for response_est.
15. change_est: estimated change from baseline.
16. change_se: standard error of change_est.
17. change_df: degrees of freedom for calculating the confidence interval for and estimating the significance of change_est.
18. change_lower: lower bound of confidence interval for change_est.
19. change_upper: upper bound of confidence interval for change_est.
20. change_test_statistic: test statistic measuring the significance of change_est.
21. change_p_value: p-value for the significance of change_est.
22. diff_arm_est: treatment effect of arm within subgroup.
23. diff_arm_se: standard error of diff_arm_est.
24. diff_arm_df: degrees of freedom for calculating the confidence interval for and testing the significance of diff_arm_est.
25. diff_arm_lower: lower bound of confidence interval for diff_arm_est.
26. diff_arm_upper: upper bound of confidence interval for diff_arm_est.
27. diff_arm_test_statistic: test statistic measuring the significance of diff_arm_est.
28. diff_arm_p_value: p-value for the significance of diff_arm_est.

29. percent_slowing_est: estimated percent slowing.
30. percent_slowing_lower: lower bound of confidence interval for percent_slowing_est.
31. percent_slowing_upper: upper bound of confidence interval for percent_slowing_est.
32. correlation: the covariance structure of the analysis model. This is the same value repeated for each row.
33. optimizer: invariably mrm+tmb to indicate that `mrm::mrm()` (which uses the TMB package) was used to fit the model.

type3

A [tibble](#) with a row for each term in the model (not counting any intercepts). Contains the following six columns:

1. effect: the name of the model term.
2. chisquare_test_statistic: the Chi-squared test statistic measuring the significance of the model term.
3. df: the degrees of freedom used for testing the significance of the model term.
4. p_value: the p-value for the significance of the model term.
5. correlation: the covariance structure of the analysis model. This is the same value repeated for each row.
6. optimizer: invariably mrm+tmb to indicate that `mrm::mrm()` (which uses the TMB package) was used to fit the model.

interaction

This element is only present if `subgroup_interaction_test = TRUE`.

A 2 by 10 data frame with class `anova.mrm`. The first row represents the "reduced" model and the second row represents the "full" model. The columns are as follows:

1. model: `c("reduced model", "full model")`, identifying the model associated with each row.
2. aic: the [AIC](#) of the model.
3. bic: the [BIC](#) of the model.
4. loglik: the [log likelihood](#) of the model.
5. $-2 \times \log(1)$: equal to $-2 * \loglik$.
6. test_statistic: the test statistic used for testing the significance of the second-order interaction term(s) between the spline time, subgroup, and arm. This value is the second element of the column; the first element is always a missing value.
7. df: the degrees of freedom used for testing the significance of the second-order interaction term(s) between the spline term, subgroup, and arm. This value is the second element of the column; the first element is always a missing value.
8. p_value: the p-value for the significance of the second-order interaction term(s) between the spline term, subgroup, and arm. This value is the second element of the column; the first element is always a missing value.

9. correlation: the covariance structure of the analysis model. This is the same value repeated for each row.
10. optimizer: invariably `mmerm+tmb` to indicate that `mmerm::mmerm()` (which uses the TMB package) was used to fit the model.

analysis_model

This element is only present if `return_models = TRUE`.

An `mmerm` object: the fitted model used to perform analyses that produced the between, within, and type3 results.

full **and** reduced

These elements are only present if `subgroup_interaction_test = TRUE` and `return_models = TRUE`.

Both are `mmerm` objects: the two maximum-likelihood-estimated models used to perform the subgroup interaction test whose results are in the interaction element. See the **Subgroup interaction test** section of `ncs_analysis_subgroup()`.

See Also

The function `ncs_analysis_subgroup()`, which produces objects of this class.

time_spline

Create Natural Cubic Spline Approximations for Continuous Time

Description

Accepts or constructs a natural cubic spline basis for continuous time and yields a matrix of approximations for time according to that basis.

Usage

```
time_spline(
  time,
  df = NULL,
  ...,
  basis = time_spline_basis(time, df = df, ...)
)
```

Arguments

time	A numeric vector of values.
df, ...	Only used if basis is left as the default. Passed to <code>time_spline_basis()</code> (which passes all arguments to <code>splines::ns()</code>) to calculate the spline basis.
basis	Spline basis for which to create approximations of time. Defaults to <code>time_spline_basis(time, df = df, ...)</code> .

Details

time_spline() is primarily useful because it can use one step to create the spline basis from time and then re-input time into the spline basis to obtain the spline approximations. Alternatively, it can calculate predictions from a basis supplied to the basis argument.

Value

Matrix with the same dimensions as basis. Contains basis as an [attribute](#).

Examples

```
time_spline(Theoph$Time, df = 3)

# Or, compute the spline basis beforehand, and then pass it to time_spline()
basis <-
  splines::bs(Theoph$Time, df = 3, Boundary.knots = c(0, max(Theoph$Time)))

time_spline(Theoph$Time, basis = basis)
```

time_spline_basis *Natural Cubic Spline Basis Matrix for Continuous Time.*

Description

Wrapper around [splines::ns\(\)](#) with default Boundary.knots of `c(0, max(time))`.

Usage

```
time_spline_basis(time, df, Boundary.knots = c(0, max(time)), ...)
```

Arguments

time	Continuous time variable, passed directly to splines::ns() as the first argument.
df	Degrees of freedom, passed directly to the df argument of splines::ns() .
Boundary.knots	Boundary knots, passed directly to the Boundary.knots argument of splines::ns() . Defaults to <code>c(0, max(time))</code> .
...	Passed to splines::ns() .

Details

time_spline() is primarily useful because it can create the spline basis from time and then re-input time into the spline basis to obtain the predictions in one step. Or, it can calculate predictions from a basis supplied to the basis argument.

Value

A matrix of dimension `length(time) * df`. See the *Value* section of [splines::ns\(\)](#).

Examples

```
time_spline_basis(Theoph$Time, df = 3)
```

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