

# Package ‘cforward’

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**Title** Forward Selection using Concordance/C-Index

**Version** 0.2.0

**Description** Performs forward model selection, using the C-index/concordance in survival analysis models.

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.3.2

**Imports** survival, dplyr, stats, magrittr, tibble

**URL** <https://github.com/muschellij2/cforward>

**BugReports** <https://github.com/muschellij2/cforward/issues>

**Depends** R (>= 2.10)

**Suggests** testthat

**NeedsCompilation** no

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**Repository** CRAN

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`cforward`*Forward Selection Based on C-Index/Concordance*

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## Description

Forward Selection Based on C-Index/Concordance

## Usage

```
cforward(  
  data,  
  event_time = "event_time_years",  
  event_status = "mortstat",  
  weight_column = "WTMEC4YR_norm",  
  variables = NULL,  
  included_variables = NULL,  
  n_folds = 10,  
  seed = 1989,  
  max_model_size = 50,  
  c_threshold = NULL,  
  verbose = TRUE,  
  cfit_args = list(),  
  save_memory = FALSE,  
  ...  
)
```

```
cforward_one(  
  data,  
  event_time = "event_time_years",  
  event_status = "mortstat",  
  weight_column = "WTMEC4YR_norm",  
  variables,  
  included_variables = NULL,  
  verbose = TRUE,  
  cfit_args = list(),  
  save_memory = FALSE,  
  ...  
)
```

```
make_folds(data, event_status = "mortstat", n_folds = 10, verbose = TRUE)
```

## Arguments

<code>data</code>	A data set to perform model selection and cross-validation.
<code>event_time</code>	Character vector of length 1 with event times, passed to <a href="#">Surv</a>
<code>event_status</code>	Character vector of length 1 with event status, passed to <a href="#">Surv</a>

<code>weight_column</code>	Character vector of length 1 with weights for model. If no weights are available, set to NULL
<code>variables</code>	Character vector of variables to perform selection. Must be in data.
<code>included_variables</code>	Character vector of variables forced to have in the model. Must be in data
<code>n_folds</code>	Number of folds for Cross-validation. If you want to run on the full data, set to 1
<code>seed</code>	Seed set before folds are created.
<code>max_model_size</code>	maximum number of variables in the model. Selection will stop if reached. Note, this does not correspond to the number of coefficients, due to categorical variables.
<code>c_threshold</code>	threshold for concordance. If the difference in the best concordance and this one does not reach a certain threshold, break.
<code>verbose</code>	print diagnostic messages
<code>cfit_args</code>	Arguments passed to <code>concordancefit</code> . If strata is to be passed, set <code>strata_column</code> in this list.
<code>save_memory</code>	save only a minimal amount of information, discard the fitted models
<code>...</code>	Additional arguments to pass to <code>coxph</code>

### Value

A list of lists, with elements of:

**full\_concordance** Concordance when fit on the full data

**models** Cox model from full data set fit, stripped of large memory elements

**cv\_concordance** Cross-validated Concordance

**included\_variables** Variables included in the model, other than those being selection upon

### Examples

```
variables = c("gender",
             "age_years_interview", "education_adult")

res = cforward(nhanes_example,
              event_time = "event_time_years",
              event_status = "mortstat",
              weight_column = "WTMEC4YR_norm",
              variables = variables,
              included_variables = NULL,
              n_folds = 5,
              c_threshold = 0.02,
              seed = 1989,
              max_model_size = 50,
              verbose = TRUE)
conc = sapply(res, `[[`, "best_concordance")
```

```

res = cforward(nhanes_example,
               event_time = "event_time_years",
               event_status = "mortstat",
               weight_column = "WTMEC4YR_norm",
               variables = variables,
               included_variables = NULL,
               n_folds = 5,
               seed = 1989,
               max_model_size = 50,
               verbose = TRUE)
conc = sapply(res, `[`, "best_concordance")
threshold = 0.01
included_variables = names(conc)[c(1, diff(conc)) > threshold]

new_variables = c("diabetes", "stroke")
second_level = cforward(nhanes_example,
                       event_time = "event_time_years",
                       event_status = "mortstat",
                       weight_column = "WTMEC4YR_norm",
                       variables = new_variables,
                       included_variables = included_variables,
                       n_folds = 5,
                       seed = 1989,
                       max_model_size = 50,
                       verbose = TRUE)
second_conc = sapply(second_level, `[`, "best_concordance")
result = second_level[[which.max(second_conc)]]
final_model = result$models[[which.max(result$cv_concordance)]]

```

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estimate\_concordance *Estimate Out-of-Sample Concordance*

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## Description

Estimate Out-of-Sample Concordance

## Usage

```

estimate_concordance(
  train,
  test = train,
  event_time = "event_time_years",
  event_status = "mortstat",
  weight_column = "WTMEC4YR_norm",
  all_variables = NULL,
  cfit_args = list(),
  ...
)

```

**Arguments**

<code>train</code>	A data set to perform model training.
<code>test</code>	A data set to estimate concordance, from fit model with <code>train</code> . Set to <code>train</code> if estimating on the same data
<code>event_time</code>	Character vector of length 1 with event times, passed to <a href="#">Surv</a>
<code>event_status</code>	Character vector of length 1 with event status, passed to <a href="#">Surv</a>
<code>weight_column</code>	Character vector of length 1 with weights for model. If no weights are available, set to <code>NULL</code>
<code>all_variables</code>	Character vector of variables to put in the model. All must be in data.
<code>cfit_args</code>	Arguments passed to <a href="#">concordancefit</a> . If <code>strata</code> is to be passed, set <code>strata_column</code> in this list.
<code>...</code>	Additional arguments to pass to <a href="#">coxph</a>

**Value**

A list of concordance and the model fit with the training data

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<code>nhanes_example</code>	<i>Example Data from National Health and Nutrition Examination Survey ('NHANES')</i>
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**Description**

Example Data from National Health and Nutrition Examination Survey ('NHANES')

**Usage**

```
nhanes_example
```

**Format**

A data.frame with 7 columns, which are:

**SEQN** ID of participant  
**mortstat** mortality status, 1-died, 0 - censored  
**event\_time\_years** time observed  
**WTMEC4YR\_norm** weights normalized for survey  
**gender** gender  
**age\_years\_interview** age in years at interview  
**education\_adult** educational status

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