# Package: fastbackward (via r-universe)

**Type** Package

**Title** Fast Backward Elimination Based on Information Criterion

**Version** 1.0.1

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**URL** https://github.com/JacobSeedorff21/fastbackward

**BugReports** https://github.com/JacobSeedorff21/fastbackward/issues

**Description** Performs backward elimination with similar syntax to the
stepAIC() function from the 'MASS' package. A bounding
algorithm is used to avoid fitting unnecessary models, making
it much faster.

**License** Apache License (>= 2)

**Encoding** UTF-8

**Suggests** testthat (>= 3.0.0)

**Config/testthat/edition** 3

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.1

**Imports** MASS

**Repository** https://jacobseedorff21.r-universe.dev

**RemoteUrl** https://github.com/jacobseedorff21/fastbackward

**RemoteRef** HEAD

**RemoteSha** 18a1a20f3f3a00904f1dcaf11e433ba7088c32ec

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| fastbackward | *Performs Fast Backward Elimination by AIC* |
|---|---|

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### Description

Performs backward elimination by AIC, backward elimination is performed with a bounding algorithm to make it faster.

### Usage

```
fastbackward(
  object,
  scope,
  scale = 0,
  trace = 1,
  keep = NULL,
  steps = 1000,
  k = 2,
  ...
)
```

### Arguments

| | |
|---|---|
| object | an object representing a model of an appropriate class. This is used as the initial model in the stepwise search. |
| scope | defines the range of models examined in the stepwise search. This should be missing or a single formula. If a formula is included, all of the components on the right-hand-side of the formula are always included in the model. If missing, then only the intercept (if included) is always included in the model. |
| scale | used in the definition of the AIC statistic for selecting the models, currently only for lm and aov models (see extractAIC for details). |
| trace | if positive, information is printed during the running of fastbackward. Larger values may give more detailed information. If trace is greater than 1, then information about which variables at each step are not considered for removal due to the bounding algorithm are printed. |
| keep | a filter function whose input is a fitted model object and the associated AIC statistic, and whose output is arbitrary. Typically keep will select a subset of the components of the object and return them. The default is not to keep anything. |
| steps | the maximum number of steps to be considered. The default is 1000 (essentially as many as required). It is typically used to stop the process early. |
| k | the multiple of the number of degrees of freedom used for the penalty. Only k = 2 gives the genuine AIC: k = log(n) is sometimes referred to as BIC or SBC. |
| ... | any additional arguments to extractAIC. |

## Details

The bounding algorithm allows us to avoid fitting models that cannot possibly provide an improvement in AIC. At a high-level, the algorithm basically works by identifying important predictors whose removal from the current model cannot possibly improve upon the current AIC.

Test statistics, p-values, and confidence intervals from the final selected model are not reliable due to the selection process. Thus, it is not recommended to use these quantities.

See more details at MASS::stepAIC.

## Value

The stepwise-selected model is returned, with up to two additional components. There is an "anova" component corresponding to the steps taken in the search, as well as a "keep" component if the keep= argument was supplied in the call. The "Resid. Dev" column of the analysis of deviance table refers to a constant minus twice the maximized log likelihood: it will be a deviance only in cases where a saturated model is well-defined (thus excluding lm, aov and survreg fits, for example)

## See Also

MASS::stepAIC, MASS::dropterm, and extractAIC

## Examples

```
# Loading fastbackward
library(fastbackward)

# Using examples provided in MASS::stepAIC, but with fastbackward instead
## aov with quine dataset
quine.hi <- aov(log(Days + 2.5) ~ .^4, MASS::quine)
quine.nxt <- update(quine.hi, . ~ . - Eth:Sex:Age:Lrn)
quine.stp <- fastbackward(quine.nxt, trace = FALSE)
quine.stp$anova

## lm with cpus dataset
cpus1 <- MASS::cpus
for(v in names(MASS::cpus)[2:7])
 cpus1[[v]] <- cut(MASS::cpus[[v]], unique(quantile(MASS::cpus[[v]])),
                   include.lowest = TRUE)
cpus0 <- cpus1[, 2:8]  # excludes names, authors' predictions
cpus.samp <- sample(1:209, 100)
cpus.lm <- lm(log10(perf) ~ ., data = cpus1[cpus.samp,2:8])
cpus.lm2 <- fastbackward(cpus.lm, trace = FALSE)
cpus.lm2$anova

## glm with bwt dataset
example(birthwt, package = "MASS")
birthwt.glm <- glm(low ~ ., family = binomial, data = bwt)
birthwt.step <- fastbackward(birthwt.glm, trace = FALSE)
birthwt.step$anova
```

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