

# Package: FMCensSkewReg (via r-universe)

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**Title** Finite Mixture of Censored Regression Models with Skewed Distributions

**Version** 0.1.1

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**Description** Provides an implementation of finite mixture regression models for censored data under four distributional families: Normal (FM-NCR), Student t (FM-TCR), skew-Normal (FM-SNCR), and skew-t (FM-STCR). The package enables flexible modeling of skewness and heavy tails often observed in real-world data, while explicitly accounting for censoring. Functions are included for parameter estimation via the Expectation-Maximization (EM) algorithm, computation of standard errors, and model comparison criteria such as the Akaike Information Criterion (AIC), the Bayesian Information Criterion (BIC), and the Efficient Determination Criterion (EDC). The underlying methodology is described in Park et al. (2024) <doi:10.1007/s00180-024-01459-4>.

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**URL** <https://github.com/JiwonPark41/FMCensSkewReg>

**BugReports** <https://github.com/JiwonPark41/FMCensSkewReg/issues>

**Depends** R (>= 3.6.0)

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.3

**Imports** stats, mvtnorm, MomTrunc, mnormt, sn, truncdist, mixsmsn

**Suggests** testthat (>= 3.0.0), knitr, rmarkdown

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**Repository** <https://jiwonpark41.r-universe.dev>

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EM.skewCens.mixR	<i>EM Algorithm for Finite Mixture Censored Regression</i>
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## Description

Fits finite mixture censored regression models under four families: Normal ("Normal"), Student-t ("T"), Skew-Normal ("SN"), and Skew-t ("ST").

## Usage

```
EM.skewCens.mixR(
  cc,
  y,
  x,
  Abetas = NULL,
  sigma2 = NULL,
  shape = NULL,
  pii = NULL,
  nu = NULL,
  g = NULL,
  get.init = TRUE,
  criteria = TRUE,
  group = FALSE,
  family = "Normal",
  error = 1e-05,
  iter.max = 100,
  obs.prob = FALSE,
  kmeans.param = NULL,
  aitken = TRUE,
  IM = TRUE
)
```

**Arguments**

<code>cc</code>	Integer vector of length $n$ ; censoring indicator (1 = censored, 0 = observed).
<code>y</code>	Numeric response vector (univariate).
<code>x</code>	Numeric design matrix ( $n \times p$ ); include intercept column if needed.
<code>Abetas</code>	Optional initial regression coefficient matrix ( $p \times g$ ).
<code>sigma2</code>	Optional initial variance(s), length $g$ .
<code>shape</code>	Optional initial skewness parameter(s), length $g$ (used in SN/ST).
<code>pii</code>	Optional initial mixing proportions, length $g$ , must sum to 1.
<code>nu</code>	Degrees of freedom for T/ST models (scalar).
<code>g</code>	Number of mixture components ( $g \geq 1$ ). Required if <code>get.init = TRUE</code> .
<code>get.init</code>	Logical; if TRUE, k-means-based initialization is used.
<code>criteria</code>	Logical; if TRUE, returns AIC/BIC/EDC.
<code>group</code>	Logical; if TRUE, returns hard cluster labels.
<code>family</code>	One of "Normal", "T", "SN", "ST".
<code>error</code>	Convergence tolerance for EM.
<code>iter.max</code>	Maximum number of EM iterations.
<code>obs.prob</code>	Logical; if TRUE, returns posterior membership matrix.
<code>kmeans.param</code>	Optional list for kmeans init.
<code>aitken</code>	Logical; use Aitken acceleration for convergence monitoring.
<code>IM</code>	Logical; if TRUE, compute (robust) standard errors via information matrix.

**Details**

Left-censoring is indicated by `cc[i] = 1` and replacing `y[i]` by the censoring point. The routine supports Normal, t, Skew-Normal, and Skew-t families with finite mixtures.

**Value**

A list with elements:

<code>Abetas</code>	Estimated regression coefficients ( $p \times g$ ).
<code>sigma2</code>	Estimated variances (length $g$ ).
<code>shape</code>	Estimated skewness parameters (length $g$ ; SN/ST).
<code>pii</code>	Estimated mixing proportions (length $g$ ).
<code>sd</code>	Standard errors (if <code>IM=TRUE</code> ).
<code>nu</code>	Estimated/used degrees of freedom (T/ST).
<code>loglik</code>	Final log-likelihood.
<code>loglikT</code>	Log-likelihood trace over iterations.
<code>aic, bic, edc</code>	Information criteria (if <code>criteria=TRUE</code> ).
<code>iter</code>	Number of EM iterations.
<code>n</code>	Sample size.
<code>group</code>	Hard labels (if <code>group=TRUE</code> ).

**Examples**

```
set.seed(1)
n <- 150
X <- cbind(1, runif(n), rnorm(n))
pi <- c(0.6, 0.4); nu <- 4
b1 <- c(0.5, 1.0, -1.0); sigma1 <- 1; shape1 <- 2
b2 <- c(1.0,-0.5, 0.5); sigma2 <- 2; shape2 <- 3
mu1 <- drop(X %*% b1); mu2 <- drop(X %*% b2)
draw1 <- function(i){
  a1 <- list(mu=mu1[i], sigma2=sigma1, shape=shape1, nu=nu)
  a2 <- list(mu=mu2[i], sigma2=sigma2, shape=shape2, nu=nu)
  mixsmn::rmix(1, pi, "Skew.t", list(a1,a2), cluster=FALSE)
}
y0 <- vapply(seq_len(n), draw1, numeric(1))
cutoff <- unname(stats::quantile(y0, 0.20))
cc <- as.integer(y0 <= cutoff)
y <- ifelse(cc == 1, cutoff, y0)
fit <- EM.skewCens.mixR(cc, y, X, g=2, family="Normal", iter.max=50)
fit$loglik
```

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