

Package: **hdcuremodels** (via r-universe)

August 24, 2026

Title High-Dimensional Cure Models

Version 0.0.8

Date 2026-05-17

Description Provides functions for fitting various penalized parametric and semi-parametric mixture cure models with different penalty functions, testing for a significant cure fraction, and testing for sufficient follow-up as described in Fu et al (2022)<[doi:10.1002/sim.9513](https://doi.org/10.1002/sim.9513)> and Archer et al (2024)<[doi:10.1186/s13045-024-01553-6](https://doi.org/10.1186/s13045-024-01553-6)>. False discovery rate controlled variable selection is provided using model-X knock-offs.

License MIT + file LICENSE

Encoding UTF-8

Depends R (>= 4.2.0)

Imports doParallel, flexsurv, flexsurvcure, foreach, ggplot2, ggpubr, glmnet, knockoff, mvnfast, parallel, plyr, methods, survival, withr

Config/Roxygen list(markdown = TRUE, roclets = c("` namespace", "` rd", "` srr::srr_stats_roclet"))

Config/Remotes ropensci-review-tools/srr

Suggests knitr, Rdspd, rmarkdown, roxygen2, testthat (>= 3.0.0)

VignetteBuilder knitr

LazyData true

URL <https://github.com/kelliejarcher/hdcuremodels>

BugReports <https://github.com/kelliejarcher/hdcuremodels/issues>

Config/testthat/edition 3

Config/roxygen2/version 8.0.0

Config/pak/sysreqs cmake make libicu-dev

Repository <https://ropensci.r-universe.dev>

Date/Publication 2026-08-24 15:28:53 UTC

RemoteUrl <https://github.com/kelliejarcher/hdcuremodels>
RemoteRef main
RemoteSha 768486269063f3bfe3672ea45a4a178c577be392

Contents

amltest	2
amltrain	12
auc_mcm	21
coef.mixturecure	22
concordance_mcm	24
cure_estimate	25
cureem	26
curegmifs	29
cv_cureem	32
cv_curegmifs	37
dim.mixturecure	40
family.mixturecure	41
formula.mixturecure	42
generate_cure_data	43
logLik.mixturecure	45
nobs.mixturecure	46
nonzerocure_test	47
npar_mixturecure	48
pediatric_ft3	49
plot.mixturecure	55
predict.mixturecure	56
print.mixturecure	58
sufficient_fu_test	59
summary.mixturecure	60
Index	61

amltest	<i>AML test data</i>
---------	----------------------

Description

Duration of complete response for 40 cytogenetically normal AML patients and a subset of 320 transcript expression from RNA-sequencing.

Usage

amltest

Format

A data frame with 40 rows (subjects) and 322 columns:

crry duration of complete response in years

relapse.death censoring indicator: 1 = relapsed or died; 0 = alive at last follow-up

ENSG00000001561 normalized expression for indicated transcript

ENSG00000005249 normalized expression for indicated transcript

ENSG00000006757 normalized expression for indicated transcript

ENSG00000007062 normalized expression for indicated transcript

ENSG00000007968 normalized expression for indicated transcript

ENSG00000008283 normalized expression for indicated transcript

ENSG00000008405 normalized expression for indicated transcript

ENSG00000008441 normalized expression for indicated transcript

ENSG00000010295 normalized expression for indicated transcript

ENSG00000011028 normalized expression for indicated transcript

ENSG00000011198 normalized expression for indicated transcript

ENSG00000012779 normalized expression for indicated transcript

ENSG00000012817 normalized expression for indicated transcript

ENSG00000013306 normalized expression for indicated transcript

ENSG00000013725 normalized expression for indicated transcript

ENSG00000018189 normalized expression for indicated transcript

ENSG00000022267 normalized expression for indicated transcript

ENSG00000023171 normalized expression for indicated transcript

ENSG00000023909 normalized expression for indicated transcript

ENSG00000029639 normalized expression for indicated transcript

ENSG00000047634 normalized expression for indicated transcript

ENSG00000049192 normalized expression for indicated transcript

ENSG00000053524 normalized expression for indicated transcript

ENSG00000058056 normalized expression for indicated transcript

ENSG00000060138 normalized expression for indicated transcript

ENSG00000061918 normalized expression for indicated transcript

ENSG00000065809 normalized expression for indicated transcript

ENSG00000065923 normalized expression for indicated transcript

ENSG00000068489 normalized expression for indicated transcript

ENSG00000069020 normalized expression for indicated transcript

ENSG00000070404 normalized expression for indicated transcript

ENSG00000071894 normalized expression for indicated transcript

ENSG00000072422 normalized expression for indicated transcript

ENSG00000073605 normalized expression for indicated transcript
ENSG00000076555 normalized expression for indicated transcript
ENSG00000080823 normalized expression for indicated transcript
ENSG00000089723 normalized expression for indicated transcript
ENSG00000090382 normalized expression for indicated transcript
ENSG00000090975 normalized expression for indicated transcript
ENSG00000100068 normalized expression for indicated transcript
ENSG00000100077 normalized expression for indicated transcript
ENSG00000100299 normalized expression for indicated transcript
ENSG00000100376 normalized expression for indicated transcript
ENSG00000100418 normalized expression for indicated transcript
ENSG00000100448 normalized expression for indicated transcript
ENSG00000100596 normalized expression for indicated transcript
ENSG00000100916 normalized expression for indicated transcript
ENSG00000102409 normalized expression for indicated transcript
ENSG00000102760 normalized expression for indicated transcript
ENSG00000104689 normalized expression for indicated transcript
ENSG00000104946 normalized expression for indicated transcript
ENSG00000105518 normalized expression for indicated transcript
ENSG00000105808 normalized expression for indicated transcript
ENSG00000106367 normalized expression for indicated transcript
ENSG00000106526 normalized expression for indicated transcript
ENSG00000106546 normalized expression for indicated transcript
ENSG00000106780 normalized expression for indicated transcript
ENSG00000107104 normalized expression for indicated transcript
ENSG00000107742 normalized expression for indicated transcript
ENSG00000107798 normalized expression for indicated transcript
ENSG00000107816 normalized expression for indicated transcript
ENSG00000107957 normalized expression for indicated transcript
ENSG00000109674 normalized expression for indicated transcript
ENSG00000110076 normalized expression for indicated transcript
ENSG00000110237 normalized expression for indicated transcript
ENSG00000110492 normalized expression for indicated transcript
ENSG00000110799 normalized expression for indicated transcript
ENSG00000111275 normalized expression for indicated transcript
ENSG00000112773 normalized expression for indicated transcript
ENSG00000113504 normalized expression for indicated transcript

ENSG00000114268 normalized expression for indicated transcript
ENSG00000114737 normalized expression for indicated transcript
ENSG00000115183 normalized expression for indicated transcript
ENSG00000115414 normalized expression for indicated transcript
ENSG00000115457 normalized expression for indicated transcript
ENSG00000115525 normalized expression for indicated transcript
ENSG00000116574 normalized expression for indicated transcript
ENSG00000117480 normalized expression for indicated transcript
ENSG00000119280 normalized expression for indicated transcript
ENSG00000120594 normalized expression for indicated transcript
ENSG00000120675 normalized expression for indicated transcript
ENSG00000120832 normalized expression for indicated transcript
ENSG00000120913 normalized expression for indicated transcript
ENSG00000121005 normalized expression for indicated transcript
ENSG00000121039 normalized expression for indicated transcript
ENSG00000121274 normalized expression for indicated transcript
ENSG00000123080 normalized expression for indicated transcript
ENSG00000123836 normalized expression for indicated transcript
ENSG00000124019 normalized expression for indicated transcript
ENSG00000124882 normalized expression for indicated transcript
ENSG00000126822 normalized expression for indicated transcript
ENSG00000127152 normalized expression for indicated transcript
ENSG00000129824 normalized expression for indicated transcript
ENSG00000130702 normalized expression for indicated transcript
ENSG00000131188 normalized expression for indicated transcript
ENSG00000131370 normalized expression for indicated transcript
ENSG00000132122 normalized expression for indicated transcript
ENSG00000132530 normalized expression for indicated transcript
ENSG00000132819 normalized expression for indicated transcript
ENSG00000132849 normalized expression for indicated transcript
ENSG00000133401 normalized expression for indicated transcript
ENSG00000133619 normalized expression for indicated transcript
ENSG00000134531 normalized expression for indicated transcript
ENSG00000134897 normalized expression for indicated transcript
ENSG00000135074 normalized expression for indicated transcript
ENSG00000135245 normalized expression for indicated transcript
ENSG00000135272 normalized expression for indicated transcript

ENSG00000135362 normalized expression for indicated transcript
ENSG00000135363 normalized expression for indicated transcript
ENSG00000135916 normalized expression for indicated transcript
ENSG00000136026 normalized expression for indicated transcript
ENSG00000136193 normalized expression for indicated transcript
ENSG00000136231 normalized expression for indicated transcript
ENSG00000136997 normalized expression for indicated transcript
ENSG00000137193 normalized expression for indicated transcript
ENSG00000137198 normalized expression for indicated transcript
ENSG00000138722 normalized expression for indicated transcript
ENSG00000139318 normalized expression for indicated transcript
ENSG00000140287 normalized expression for indicated transcript
ENSG00000144036 normalized expression for indicated transcript
ENSG00000144647 normalized expression for indicated transcript
ENSG00000144677 normalized expression for indicated transcript
ENSG00000145476 normalized expression for indicated transcript
ENSG00000145545 normalized expression for indicated transcript
ENSG00000146243 normalized expression for indicated transcript
ENSG00000146373 normalized expression for indicated transcript
ENSG00000147044 normalized expression for indicated transcript
ENSG00000147180 normalized expression for indicated transcript
ENSG00000148444 normalized expression for indicated transcript
ENSG00000148484 normalized expression for indicated transcript
ENSG00000149131 normalized expression for indicated transcript
ENSG00000150760 normalized expression for indicated transcript
ENSG00000150782 normalized expression for indicated transcript
ENSG00000151135 normalized expression for indicated transcript
ENSG00000151208 normalized expression for indicated transcript
ENSG00000151458 normalized expression for indicated transcript
ENSG00000152409 normalized expression for indicated transcript
ENSG00000152580 normalized expression for indicated transcript
ENSG00000152767 normalized expression for indicated transcript
ENSG00000152778 normalized expression for indicated transcript
ENSG00000153563 normalized expression for indicated transcript
ENSG00000154217 normalized expression for indicated transcript
ENSG00000154743 normalized expression for indicated transcript
ENSG00000154760 normalized expression for indicated transcript

ENSG00000154874 normalized expression for indicated transcript
ENSG00000156381 normalized expression for indicated transcript
ENSG00000157107 normalized expression for indicated transcript
ENSG00000157240 normalized expression for indicated transcript
ENSG00000157873 normalized expression for indicated transcript
ENSG00000157978 normalized expression for indicated transcript
ENSG00000158691 normalized expression for indicated transcript
ENSG00000159339 normalized expression for indicated transcript
ENSG00000159403 normalized expression for indicated transcript
ENSG00000159788 normalized expression for indicated transcript
ENSG00000160685 normalized expression for indicated transcript
ENSG00000160781 normalized expression for indicated transcript
ENSG00000161509 normalized expression for indicated transcript
ENSG00000162433 normalized expression for indicated transcript
ENSG00000162614 normalized expression for indicated transcript
ENSG00000162676 normalized expression for indicated transcript
ENSG00000163412 normalized expression for indicated transcript
ENSG00000163702 normalized expression for indicated transcript
ENSG00000163814 normalized expression for indicated transcript
ENSG00000164086 normalized expression for indicated transcript
ENSG00000164172 normalized expression for indicated transcript
ENSG00000164442 normalized expression for indicated transcript
ENSG00000165272 normalized expression for indicated transcript
ENSG00000166165 normalized expression for indicated transcript
ENSG00000166435 normalized expression for indicated transcript
ENSG00000166987 normalized expression for indicated transcript
ENSG00000167291 normalized expression for indicated transcript
ENSG00000167565 normalized expression for indicated transcript
ENSG00000167851 normalized expression for indicated transcript
ENSG00000168026 normalized expression for indicated transcript
ENSG00000168209 normalized expression for indicated transcript
ENSG00000168502 normalized expression for indicated transcript
ENSG00000168939 normalized expression for indicated transcript
ENSG00000169203 normalized expression for indicated transcript
ENSG00000169247 normalized expression for indicated transcript
ENSG00000169504 normalized expression for indicated transcript
ENSG00000169860 normalized expression for indicated transcript

ENSG00000169991 normalized expression for indicated transcript
ENSG00000170035 normalized expression for indicated transcript
ENSG00000170180 normalized expression for indicated transcript
ENSG00000170456 normalized expression for indicated transcript
ENSG00000170522 normalized expression for indicated transcript
ENSG00000170909 normalized expression for indicated transcript
ENSG00000171121 normalized expression for indicated transcript
ENSG00000171222 normalized expression for indicated transcript
ENSG00000171476 normalized expression for indicated transcript
ENSG00000171813 normalized expression for indicated transcript
ENSG00000171962 normalized expression for indicated transcript
ENSG00000172197 normalized expression for indicated transcript
ENSG00000172236 normalized expression for indicated transcript
ENSG00000173083 normalized expression for indicated transcript
ENSG00000173530 normalized expression for indicated transcript
ENSG00000173926 normalized expression for indicated transcript
ENSG00000174059 normalized expression for indicated transcript
ENSG00000174080 normalized expression for indicated transcript
ENSG00000174130 normalized expression for indicated transcript
ENSG00000174738 normalized expression for indicated transcript
ENSG00000175265 normalized expression for indicated transcript
ENSG00000175352 normalized expression for indicated transcript
ENSG00000176597 normalized expression for indicated transcript
ENSG00000179222 normalized expression for indicated transcript
ENSG00000179630 normalized expression for indicated transcript
ENSG00000179639 normalized expression for indicated transcript
ENSG00000179820 normalized expression for indicated transcript
ENSG00000180096 normalized expression for indicated transcript
ENSG00000180596 normalized expression for indicated transcript
ENSG00000180902 normalized expression for indicated transcript
ENSG00000181104 normalized expression for indicated transcript
ENSG00000182866 normalized expression for indicated transcript
ENSG00000182871 normalized expression for indicated transcript
ENSG00000183087 normalized expression for indicated transcript
ENSG00000183091 normalized expression for indicated transcript
ENSG00000184371 normalized expression for indicated transcript
ENSG00000185129 normalized expression for indicated transcript

ENSG00000185201 normalized expression for indicated transcript
ENSG00000185245 normalized expression for indicated transcript
ENSG00000185291 normalized expression for indicated transcript
ENSG00000185304 normalized expression for indicated transcript
ENSG00000185710 normalized expression for indicated transcript
ENSG00000185883 normalized expression for indicated transcript
ENSG00000185986 normalized expression for indicated transcript
ENSG00000186130 normalized expression for indicated transcript
ENSG00000186854 normalized expression for indicated transcript
ENSG00000187010 normalized expression for indicated transcript
ENSG00000187627 normalized expression for indicated transcript
ENSG00000187653 normalized expression for indicated transcript
ENSG00000187837 normalized expression for indicated transcript
ENSG00000188002 normalized expression for indicated transcript
ENSG00000188107 normalized expression for indicated transcript
ENSG00000188211 normalized expression for indicated transcript
ENSG00000188636 normalized expression for indicated transcript
ENSG00000188738 normalized expression for indicated transcript
ENSG00000188856 normalized expression for indicated transcript
ENSG00000189164 normalized expression for indicated transcript
ENSG00000189223 normalized expression for indicated transcript
ENSG00000196155 normalized expression for indicated transcript
ENSG00000196189 normalized expression for indicated transcript
ENSG00000196415 normalized expression for indicated transcript
ENSG00000196565 normalized expression for indicated transcript
ENSG00000197081 normalized expression for indicated transcript
ENSG00000197121 normalized expression for indicated transcript
ENSG00000197253 normalized expression for indicated transcript
ENSG00000197256 normalized expression for indicated transcript
ENSG00000197321 normalized expression for indicated transcript
ENSG00000197561 normalized expression for indicated transcript
ENSG00000197728 normalized expression for indicated transcript
ENSG00000197860 normalized expression for indicated transcript
ENSG00000197937 normalized expression for indicated transcript
ENSG00000197951 normalized expression for indicated transcript
ENSG00000198743 normalized expression for indicated transcript
ENSG00000198838 normalized expression for indicated transcript

ENSG00000199347 normalized expression for indicated transcript
ENSG00000200243 normalized expression for indicated transcript
ENSG00000201801 normalized expression for indicated transcript
ENSG00000203872 normalized expression for indicated transcript
ENSG00000204172 normalized expression for indicated transcript
ENSG00000205571 normalized expression for indicated transcript
ENSG00000205593 normalized expression for indicated transcript
ENSG00000208772 normalized expression for indicated transcript
ENSG00000213085 normalized expression for indicated transcript
ENSG00000213261 normalized expression for indicated transcript
ENSG00000213626 normalized expression for indicated transcript
ENSG00000213722 normalized expression for indicated transcript
ENSG00000213906 normalized expression for indicated transcript
ENSG00000213967 normalized expression for indicated transcript
ENSG00000214016 normalized expression for indicated transcript
ENSG00000214425 normalized expression for indicated transcript
ENSG00000216316 normalized expression for indicated transcript
ENSG00000220008 normalized expression for indicated transcript
ENSG00000223345 normalized expression for indicated transcript
ENSG00000224080 normalized expression for indicated transcript
ENSG00000225138 normalized expression for indicated transcript
ENSG00000226471 normalized expression for indicated transcript
ENSG00000227097 normalized expression for indicated transcript
ENSG00000227191 normalized expression for indicated transcript
ENSG00000227615 normalized expression for indicated transcript
ENSG00000228049 normalized expression for indicated transcript
ENSG00000229153 normalized expression for indicated transcript
ENSG00000230076 normalized expression for indicated transcript
ENSG00000231160 normalized expression for indicated transcript
ENSG00000231721 normalized expression for indicated transcript
ENSG00000233927 normalized expression for indicated transcript
ENSG00000233974 normalized expression for indicated transcript
ENSG00000234883 normalized expression for indicated transcript
ENSG00000236876 normalized expression for indicated transcript
ENSG00000237298 normalized expression for indicated transcript
ENSG00000237892 normalized expression for indicated transcript
ENSG00000238160 normalized expression for indicated transcript

ENSG00000239437 normalized expression for indicated transcript
ENSG00000241399 normalized expression for indicated transcript
ENSG00000241489 normalized expression for indicated transcript
ENSG00000241529 normalized expression for indicated transcript
ENSG00000244405 normalized expression for indicated transcript
ENSG00000247627 normalized expression for indicated transcript
ENSG00000249592 normalized expression for indicated transcript
ENSG00000250116 normalized expression for indicated transcript
ENSG00000250251 normalized expression for indicated transcript
ENSG00000251079 normalized expression for indicated transcript
ENSG00000253210 normalized expression for indicated transcript
ENSG00000253276 normalized expression for indicated transcript
ENSG00000254415 normalized expression for indicated transcript
ENSG00000259276 normalized expression for indicated transcript
ENSG00000260727 normalized expression for indicated transcript
ENSG00000261377 normalized expression for indicated transcript
ENSG00000264885 normalized expression for indicated transcript
ENSG00000264895 normalized expression for indicated transcript
ENSG00000267136 normalized expression for indicated transcript
ENSG00000267551 normalized expression for indicated transcript
ENSG00000267702 normalized expression for indicated transcript
ENSG00000268001 normalized expression for indicated transcript
ENSG00000268573 normalized expression for indicated transcript
ENSG00000270554 normalized expression for indicated transcript
ENSG00000270562 normalized expression for indicated transcript
ENSG00000271646 normalized expression for indicated transcript
ENSG00000273018 normalized expression for indicated transcript
ENSG00000273033 normalized expression for indicated transcript

Source

<doi:10.1186/s13045-024-01553-6>

amltrain

*AML training data***Description**

Duration of complete response for 306 cytogenetically normal AML patients and a subset of 320 transcript expression from RNA-sequencing.

Usage

amltrain

Format

A data frame with 306 rows (subjects) and 322 columns:

crryr duration of complete response in years

relapse.death censoring indicator: 1 = relapsed or died; 0 = alive at last follow-up

ENSG00000001561 normalized expression for indicated transcript

ENSG00000005249 normalized expression for indicated transcript

ENSG00000006757 normalized expression for indicated transcript

ENSG00000007062 normalized expression for indicated transcript

ENSG00000007968 normalized expression for indicated transcript

ENSG00000008283 normalized expression for indicated transcript

ENSG00000008405 normalized expression for indicated transcript

ENSG00000008441 normalized expression for indicated transcript

ENSG00000010295 normalized expression for indicated transcript

ENSG00000011028 normalized expression for indicated transcript

ENSG00000011198 normalized expression for indicated transcript

ENSG00000012779 normalized expression for indicated transcript

ENSG00000012817 normalized expression for indicated transcript

ENSG00000013306 normalized expression for indicated transcript

ENSG00000013725 normalized expression for indicated transcript

ENSG00000018189 normalized expression for indicated transcript

ENSG00000022267 normalized expression for indicated transcript

ENSG00000023171 normalized expression for indicated transcript

ENSG00000023909 normalized expression for indicated transcript

ENSG00000029639 normalized expression for indicated transcript

ENSG00000047634 normalized expression for indicated transcript

ENSG00000049192 normalized expression for indicated transcript

ENSG00000053524 normalized expression for indicated transcript
ENSG00000058056 normalized expression for indicated transcript
ENSG00000060138 normalized expression for indicated transcript
ENSG00000061918 normalized expression for indicated transcript
ENSG00000065809 normalized expression for indicated transcript
ENSG00000065923 normalized expression for indicated transcript
ENSG00000068489 normalized expression for indicated transcript
ENSG00000069020 normalized expression for indicated transcript
ENSG00000070404 normalized expression for indicated transcript
ENSG00000071894 normalized expression for indicated transcript
ENSG00000072422 normalized expression for indicated transcript
ENSG00000073605 normalized expression for indicated transcript
ENSG00000076555 normalized expression for indicated transcript
ENSG00000080823 normalized expression for indicated transcript
ENSG00000089723 normalized expression for indicated transcript
ENSG00000090382 normalized expression for indicated transcript
ENSG00000090975 normalized expression for indicated transcript
ENSG00000100068 normalized expression for indicated transcript
ENSG00000100077 normalized expression for indicated transcript
ENSG00000100299 normalized expression for indicated transcript
ENSG00000100376 normalized expression for indicated transcript
ENSG00000100418 normalized expression for indicated transcript
ENSG00000100448 normalized expression for indicated transcript
ENSG00000100596 normalized expression for indicated transcript
ENSG00000100916 normalized expression for indicated transcript
ENSG00000102409 normalized expression for indicated transcript
ENSG00000102760 normalized expression for indicated transcript
ENSG00000104689 normalized expression for indicated transcript
ENSG00000104946 normalized expression for indicated transcript
ENSG00000105518 normalized expression for indicated transcript
ENSG00000105808 normalized expression for indicated transcript
ENSG00000106367 normalized expression for indicated transcript
ENSG00000106526 normalized expression for indicated transcript
ENSG00000106546 normalized expression for indicated transcript
ENSG00000106780 normalized expression for indicated transcript
ENSG00000107104 normalized expression for indicated transcript
ENSG00000107742 normalized expression for indicated transcript

ENSG00000107798 normalized expression for indicated transcript
ENSG00000107816 normalized expression for indicated transcript
ENSG00000107957 normalized expression for indicated transcript
ENSG00000109674 normalized expression for indicated transcript
ENSG00000110076 normalized expression for indicated transcript
ENSG00000110237 normalized expression for indicated transcript
ENSG00000110492 normalized expression for indicated transcript
ENSG00000110799 normalized expression for indicated transcript
ENSG00000111275 normalized expression for indicated transcript
ENSG00000112773 normalized expression for indicated transcript
ENSG00000113504 normalized expression for indicated transcript
ENSG00000114268 normalized expression for indicated transcript
ENSG00000114737 normalized expression for indicated transcript
ENSG00000115183 normalized expression for indicated transcript
ENSG00000115414 normalized expression for indicated transcript
ENSG00000115457 normalized expression for indicated transcript
ENSG00000115525 normalized expression for indicated transcript
ENSG00000116574 normalized expression for indicated transcript
ENSG00000117480 normalized expression for indicated transcript
ENSG00000119280 normalized expression for indicated transcript
ENSG00000120594 normalized expression for indicated transcript
ENSG00000120675 normalized expression for indicated transcript
ENSG00000120832 normalized expression for indicated transcript
ENSG00000120913 normalized expression for indicated transcript
ENSG00000121005 normalized expression for indicated transcript
ENSG00000121039 normalized expression for indicated transcript
ENSG00000121274 normalized expression for indicated transcript
ENSG00000123080 normalized expression for indicated transcript
ENSG00000123836 normalized expression for indicated transcript
ENSG00000124019 normalized expression for indicated transcript
ENSG00000124882 normalized expression for indicated transcript
ENSG00000126822 normalized expression for indicated transcript
ENSG00000127152 normalized expression for indicated transcript
ENSG00000129824 normalized expression for indicated transcript
ENSG00000130702 normalized expression for indicated transcript
ENSG00000131188 normalized expression for indicated transcript
ENSG00000131370 normalized expression for indicated transcript

ENSG00000132122 normalized expression for indicated transcript
ENSG00000132530 normalized expression for indicated transcript
ENSG00000132819 normalized expression for indicated transcript
ENSG00000132849 normalized expression for indicated transcript
ENSG00000133401 normalized expression for indicated transcript
ENSG00000133619 normalized expression for indicated transcript
ENSG00000134531 normalized expression for indicated transcript
ENSG00000134897 normalized expression for indicated transcript
ENSG00000135074 normalized expression for indicated transcript
ENSG00000135245 normalized expression for indicated transcript
ENSG00000135272 normalized expression for indicated transcript
ENSG00000135362 normalized expression for indicated transcript
ENSG00000135363 normalized expression for indicated transcript
ENSG00000135916 normalized expression for indicated transcript
ENSG00000136026 normalized expression for indicated transcript
ENSG00000136193 normalized expression for indicated transcript
ENSG00000136231 normalized expression for indicated transcript
ENSG00000136997 normalized expression for indicated transcript
ENSG00000137193 normalized expression for indicated transcript
ENSG00000137198 normalized expression for indicated transcript
ENSG00000138722 normalized expression for indicated transcript
ENSG00000139318 normalized expression for indicated transcript
ENSG00000140287 normalized expression for indicated transcript
ENSG00000144036 normalized expression for indicated transcript
ENSG00000144647 normalized expression for indicated transcript
ENSG00000144677 normalized expression for indicated transcript
ENSG00000145476 normalized expression for indicated transcript
ENSG00000145545 normalized expression for indicated transcript
ENSG00000146243 normalized expression for indicated transcript
ENSG00000146373 normalized expression for indicated transcript
ENSG00000147044 normalized expression for indicated transcript
ENSG00000147180 normalized expression for indicated transcript
ENSG00000148444 normalized expression for indicated transcript
ENSG00000148484 normalized expression for indicated transcript
ENSG00000149131 normalized expression for indicated transcript
ENSG00000150760 normalized expression for indicated transcript
ENSG00000150782 normalized expression for indicated transcript

ENSG00000151135 normalized expression for indicated transcript
ENSG00000151208 normalized expression for indicated transcript
ENSG00000151458 normalized expression for indicated transcript
ENSG00000152409 normalized expression for indicated transcript
ENSG00000152580 normalized expression for indicated transcript
ENSG00000152767 normalized expression for indicated transcript
ENSG00000152778 normalized expression for indicated transcript
ENSG00000153563 normalized expression for indicated transcript
ENSG00000154217 normalized expression for indicated transcript
ENSG00000154743 normalized expression for indicated transcript
ENSG00000154760 normalized expression for indicated transcript
ENSG00000154874 normalized expression for indicated transcript
ENSG00000156381 normalized expression for indicated transcript
ENSG00000157107 normalized expression for indicated transcript
ENSG00000157240 normalized expression for indicated transcript
ENSG00000157873 normalized expression for indicated transcript
ENSG00000157978 normalized expression for indicated transcript
ENSG00000158691 normalized expression for indicated transcript
ENSG00000159339 normalized expression for indicated transcript
ENSG00000159403 normalized expression for indicated transcript
ENSG00000159788 normalized expression for indicated transcript
ENSG00000160685 normalized expression for indicated transcript
ENSG00000160781 normalized expression for indicated transcript
ENSG00000161509 normalized expression for indicated transcript
ENSG00000162433 normalized expression for indicated transcript
ENSG00000162614 normalized expression for indicated transcript
ENSG00000162676 normalized expression for indicated transcript
ENSG00000163412 normalized expression for indicated transcript
ENSG00000163702 normalized expression for indicated transcript
ENSG00000163814 normalized expression for indicated transcript
ENSG00000164086 normalized expression for indicated transcript
ENSG00000164172 normalized expression for indicated transcript
ENSG00000164442 normalized expression for indicated transcript
ENSG00000165272 normalized expression for indicated transcript
ENSG00000166165 normalized expression for indicated transcript
ENSG00000166435 normalized expression for indicated transcript
ENSG00000166987 normalized expression for indicated transcript

ENSG00000167291 normalized expression for indicated transcript
ENSG00000167565 normalized expression for indicated transcript
ENSG00000167851 normalized expression for indicated transcript
ENSG00000168026 normalized expression for indicated transcript
ENSG00000168209 normalized expression for indicated transcript
ENSG00000168502 normalized expression for indicated transcript
ENSG00000168939 normalized expression for indicated transcript
ENSG00000169203 normalized expression for indicated transcript
ENSG00000169247 normalized expression for indicated transcript
ENSG00000169504 normalized expression for indicated transcript
ENSG00000169860 normalized expression for indicated transcript
ENSG00000169991 normalized expression for indicated transcript
ENSG00000170035 normalized expression for indicated transcript
ENSG00000170180 normalized expression for indicated transcript
ENSG00000170456 normalized expression for indicated transcript
ENSG00000170522 normalized expression for indicated transcript
ENSG00000170909 normalized expression for indicated transcript
ENSG00000171121 normalized expression for indicated transcript
ENSG00000171222 normalized expression for indicated transcript
ENSG00000171476 normalized expression for indicated transcript
ENSG00000171813 normalized expression for indicated transcript
ENSG00000171962 normalized expression for indicated transcript
ENSG00000172197 normalized expression for indicated transcript
ENSG00000172236 normalized expression for indicated transcript
ENSG00000173083 normalized expression for indicated transcript
ENSG00000173530 normalized expression for indicated transcript
ENSG00000173926 normalized expression for indicated transcript
ENSG00000174059 normalized expression for indicated transcript
ENSG00000174080 normalized expression for indicated transcript
ENSG00000174130 normalized expression for indicated transcript
ENSG00000174738 normalized expression for indicated transcript
ENSG00000175265 normalized expression for indicated transcript
ENSG00000175352 normalized expression for indicated transcript
ENSG00000176597 normalized expression for indicated transcript
ENSG00000179222 normalized expression for indicated transcript
ENSG00000179630 normalized expression for indicated transcript
ENSG00000179639 normalized expression for indicated transcript

ENSG00000179820 normalized expression for indicated transcript
ENSG00000180096 normalized expression for indicated transcript
ENSG00000180596 normalized expression for indicated transcript
ENSG00000180902 normalized expression for indicated transcript
ENSG00000181104 normalized expression for indicated transcript
ENSG00000182866 normalized expression for indicated transcript
ENSG00000182871 normalized expression for indicated transcript
ENSG00000183087 normalized expression for indicated transcript
ENSG00000183091 normalized expression for indicated transcript
ENSG00000184371 normalized expression for indicated transcript
ENSG00000185129 normalized expression for indicated transcript
ENSG00000185201 normalized expression for indicated transcript
ENSG00000185245 normalized expression for indicated transcript
ENSG00000185291 normalized expression for indicated transcript
ENSG00000185304 normalized expression for indicated transcript
ENSG00000185710 normalized expression for indicated transcript
ENSG00000185883 normalized expression for indicated transcript
ENSG00000185986 normalized expression for indicated transcript
ENSG00000186130 normalized expression for indicated transcript
ENSG00000186854 normalized expression for indicated transcript
ENSG00000187010 normalized expression for indicated transcript
ENSG00000187627 normalized expression for indicated transcript
ENSG00000187653 normalized expression for indicated transcript
ENSG00000187837 normalized expression for indicated transcript
ENSG00000188002 normalized expression for indicated transcript
ENSG00000188107 normalized expression for indicated transcript
ENSG00000188211 normalized expression for indicated transcript
ENSG00000188636 normalized expression for indicated transcript
ENSG00000188738 normalized expression for indicated transcript
ENSG00000188856 normalized expression for indicated transcript
ENSG00000189164 normalized expression for indicated transcript
ENSG00000189223 normalized expression for indicated transcript
ENSG00000196155 normalized expression for indicated transcript
ENSG00000196189 normalized expression for indicated transcript
ENSG00000196415 normalized expression for indicated transcript
ENSG00000196565 normalized expression for indicated transcript
ENSG00000197081 normalized expression for indicated transcript

ENSG00000197121 normalized expression for indicated transcript
ENSG00000197253 normalized expression for indicated transcript
ENSG00000197256 normalized expression for indicated transcript
ENSG00000197321 normalized expression for indicated transcript
ENSG00000197561 normalized expression for indicated transcript
ENSG00000197728 normalized expression for indicated transcript
ENSG00000197860 normalized expression for indicated transcript
ENSG00000197937 normalized expression for indicated transcript
ENSG00000197951 normalized expression for indicated transcript
ENSG00000198743 normalized expression for indicated transcript
ENSG00000198838 normalized expression for indicated transcript
ENSG00000199347 normalized expression for indicated transcript
ENSG00000200243 normalized expression for indicated transcript
ENSG00000201801 normalized expression for indicated transcript
ENSG00000203872 normalized expression for indicated transcript
ENSG00000204172 normalized expression for indicated transcript
ENSG00000205571 normalized expression for indicated transcript
ENSG00000205593 normalized expression for indicated transcript
ENSG00000208772 normalized expression for indicated transcript
ENSG00000213085 normalized expression for indicated transcript
ENSG00000213261 normalized expression for indicated transcript
ENSG00000213626 normalized expression for indicated transcript
ENSG00000213722 normalized expression for indicated transcript
ENSG00000213906 normalized expression for indicated transcript
ENSG00000213967 normalized expression for indicated transcript
ENSG00000214016 normalized expression for indicated transcript
ENSG00000214425 normalized expression for indicated transcript
ENSG00000216316 normalized expression for indicated transcript
ENSG00000220008 normalized expression for indicated transcript
ENSG00000223345 normalized expression for indicated transcript
ENSG00000224080 normalized expression for indicated transcript
ENSG00000225138 normalized expression for indicated transcript
ENSG00000226471 normalized expression for indicated transcript
ENSG00000227097 normalized expression for indicated transcript
ENSG00000227191 normalized expression for indicated transcript
ENSG00000227615 normalized expression for indicated transcript
ENSG00000228049 normalized expression for indicated transcript

ENSG00000229153 normalized expression for indicated transcript
ENSG00000230076 normalized expression for indicated transcript
ENSG00000231160 normalized expression for indicated transcript
ENSG00000231721 normalized expression for indicated transcript
ENSG00000233927 normalized expression for indicated transcript
ENSG00000233974 normalized expression for indicated transcript
ENSG00000234883 normalized expression for indicated transcript
ENSG00000236876 normalized expression for indicated transcript
ENSG00000237298 normalized expression for indicated transcript
ENSG00000237892 normalized expression for indicated transcript
ENSG00000238160 normalized expression for indicated transcript
ENSG00000239437 normalized expression for indicated transcript
ENSG00000241399 normalized expression for indicated transcript
ENSG00000241489 normalized expression for indicated transcript
ENSG00000241529 normalized expression for indicated transcript
ENSG00000244405 normalized expression for indicated transcript
ENSG00000247627 normalized expression for indicated transcript
ENSG00000249592 normalized expression for indicated transcript
ENSG00000250116 normalized expression for indicated transcript
ENSG00000250251 normalized expression for indicated transcript
ENSG00000251079 normalized expression for indicated transcript
ENSG00000253210 normalized expression for indicated transcript
ENSG00000253276 normalized expression for indicated transcript
ENSG00000254415 normalized expression for indicated transcript
ENSG00000259276 normalized expression for indicated transcript
ENSG00000260727 normalized expression for indicated transcript
ENSG00000261377 normalized expression for indicated transcript
ENSG00000264885 normalized expression for indicated transcript
ENSG00000264895 normalized expression for indicated transcript
ENSG00000267136 normalized expression for indicated transcript
ENSG00000267551 normalized expression for indicated transcript
ENSG00000267702 normalized expression for indicated transcript
ENSG00000268001 normalized expression for indicated transcript
ENSG00000268573 normalized expression for indicated transcript
ENSG00000270554 normalized expression for indicated transcript
ENSG00000270562 normalized expression for indicated transcript
ENSG00000271646 normalized expression for indicated transcript
ENSG00000273018 normalized expression for indicated transcript
ENSG00000273033 normalized expression for indicated transcript

Source

<doi:10.1186/s13045-024-01553-6>

auc_mcm	<i>AUC for cure prediction using mean score imputation</i>
---------	--

Description

This function calculates the AUC for cure prediction using the mean score imputation (MSI) method proposed by Asano et al (2014).

Usage

```
auc_mcm(object, newdata, cure_cutoff = 5, model_select = "AIC")
```

Arguments

object	a mixturecure object resulting from curegmifs, cureem, cv_curegmifs, or cv_cureem.
newdata	an optional data.frame that minimally includes the incidence and/or latency variables to use for predicting the response. If omitted, the training data are used.
cure_cutoff	cutoff value for cure, used to produce a proxy for the unobserved cure status (default is 5 representing 5 years). Users should be careful to note the time scale of their data and adjust this according to the time scale and clinical application.
model_select	either a case-sensitive parameter for models fit using curegmifs or cureem or any numeric step along the solution path can be selected. The default is model_select = "AIC" which calculates the predicted values using the coefficients from the model achieving the minimum AIC. The complete list of options are:

- "AIC" for the minimum AIC (default).
- "mAIC" for the minimum modified AIC.
- "cAIC" for the minimum corrected AIC.
- "BIC", for the minimum BIC.
- "mBIC" for the minimum modified BIC.
- "EBIC" for the minimum extended BIC.
- "logLik" for the step that maximizes the log-likelihood.
- n where n is any numeric value from the solution path.

This option has no effect for objects fit using cv_curegmifs or cv_cureem.

Value

Returns the AUC value for cure prediction using the mean score imputation (MSI) method.

References

Asano, J., Hirakawa, H., Hamada, C. (2014) Assessing the prediction accuracy of cure in the Cox proportional hazards cure model: an application to breast cancer data. *Pharmaceutical Statistics*, **13**:357–363.

See Also

[concordance_mcm](#)

Examples

```
library(survival)
withr::local_seed(1234)
temp <- generate_cure_data(n = 100, j = 10, n_true = 10, a = 1.8)
training <- temp$training
testing <- temp$testing
fit <- curegmifs(Surv(Time, Censor) ~ .,
  data = training, x_latency = training,
  model = "weibull", thresh = 1e-4, maxit = 2000,
  epsilon = 0.01, verbose = FALSE
)
auc_mcm(fit, model_select = "cAIC")
auc_mcm(fit, newdata = testing)
```

coef.mixturecure	<i>Extract model coefficients from a fitted mixturecure object</i>
------------------	--

Description

coef.mixturecure is a generic function which extracts the model coefficients from a fitted mixturecure model object fit using curegmifs, cureem, cv_curegmifs, or cv_cureem.

Usage

```
## S3 method for class 'mixturecure'
coef(object, model_select = "AIC", ...)
```

Arguments

object	a mixturecure object resulting from curegmifs, cureem, cv_curegmifs, or cv_cureem.
model_select	either a case-sensitive parameter for models fit using curegmifs or cureem or any numeric step along the solution path can be selected. The default is model_select = "AIC" which calculates the predicted values using the coefficients from the model achieving the minimum AIC. The complete list of options are: • "AIC" for the minimum AIC (default).

- "mAIC" for the minimum modified AIC.
- "cAIC" for the minimum corrected AIC.
- "BIC", for the minimum BIC.
- "mBIC" for the minimum modified BIC.
- "EBIC" for the minimum extended BIC.
- "logLik" for the step that maximizes the log-likelihood.
- n where n is any numeric value from the solution path.

This option has no effect for objects fit using `cv_curegmifs` or `cv_cureem`.

... other arguments.

Value

rate	estimated rate parameter when fitting a Weibull or exponential mixture cure model.
shape	estimated shape parameter when fitting a Weibull mixture cure model.
b0	estimated intercept for the incidence portion of the mixture cure model.
beta_inc	the vector of coefficient estimates for the incidence portion of the mixture cure model.
beta_lat	the vector of coefficient estimates for the latency portion of the mixture cure model.
p_uncured	a vector of probabilities from the incidence portion of the fitted model representing the P(uncured).

See Also

[curegmifs](#), [cureem](#), [summary.mixturecure](#), [plot.mixturecure](#), [predict.mixturecure](#)

Examples

```
library(survival)
withr::local_seed(1234)
temp <- generate_cure_data(n = 100, j = 10, n_true = 10, a = 1.8)
training <- temp$training
fit <- curegmifs(Surv(Time, Censor) ~ .,
  data = training, x_latency = training,
  model = "weibull", thresh = 1e-4, maxit = 2000,
  epsilon = 0.01, verbose = FALSE
)
coef(fit)
```

concordance_mcm	<i>C-statistic for mixture cure models</i>
-----------------	--

Description

This function calculates the C-statistic using the cure status weighting (CSW) method proposed by Asano and Hirakawa (2017).

Usage

```
concordance_mcm(object, newdata, cure_cutoff = 5, model_select = "AIC")
```

Arguments

- | | |
|--------------|--|
| object | a mixturecure object resulting from curegmifs, cureem, cv_curegmifs, or cv_cureem. |
| newdata | an optional data.frame that minimally includes the incidence and/or latency variables to use for predicting the response. If omitted, the training data are used. |
| cure_cutoff | cutoff value for cure, used to produce a proxy for the unobserved cure status (default is 5 representing 5 years). Users should be careful to note the time scale of their data and adjust this according to the time scale and clinical application. |
| model_select | either a case-sensitive parameter for models fit using curegmifs or cureem or any numeric step along the solution path can be selected. The default is model_select = "AIC" which calculates the predicted values using the coefficients from the model achieving the minimum AIC. The complete list of options are: <ul style="list-style-type: none"> • "AIC" for the minimum AIC (default). • "mAIC" for the minimum modified AIC. • "cAIC" for the minimum corrected AIC. • "BIC", for the minimum BIC. • "mBIC" for the minimum modified BIC. • "EBIC" for the minimum extended BIC. • "logLik" for the step that maximizes the log-likelihood. • model_select = n where n is any numeric value from the solution path. |

This option has no effect for objects fit using cv_curegmifs or cv_cureem.

Value

value of C-statistic for the cure models.

References

Asano, J. and Hirakawa, H. (2017) Assessing the prediction accuracy of a cure model for censored survival data with long-term survivors: Application to breast cancer data. *Journal of Biopharmaceutical Statistics*, **27**:6, 918–932.

See Also[auc_mcm](#)**Examples**

```
library(survival)
withr::local_seed(1234)
temp <- generate_cure_data(n = 100, j = 10, n_true = 10, a = 1.8)
training <- temp$training
testing <- temp$testing
fit <- curegmifs(Surv(Time, Censor) ~ .,
  data = training, x_latency = training,
  model = "weibull", thresh = 1e-4, maxit = 2000,
  epsilon = 0.01, verbose = FALSE
)
concordance_mcm(fit, model_select = "cAIC")
concordance_mcm(fit, newdata = testing, model_select = "cAIC")
```

cure_estimate

*Estimate cured fraction***Description**

Estimates the cured fraction using a Kaplan-Meier fitted object.

Usage

```
cure_estimate(object)
```

Arguments

object a survfit object.

Value

estimated proportion of cured observations

See Also[survfit](#), [sufficient_fu_test](#), [nonzerocure_test](#)**Examples**

```
library(survival)
withr::local_seed(1234)
temp <- generate_cure_data(n = 100, j = 10, n_true = 10, a = 1.8)
training <- temp$training
km_fit <- survfit(Surv(Time, Censor) ~ 1, data = training)
cure_estimate(km_fit)
```

cureem

*Fit penalized mixture cure model using the E-M algorithm***Description**

Fits penalized parametric and semi-parametric mixture cure models (MCM) using the E-M algorithm with user-specified penalty parameters. The lasso (L1), MCP, and SCAD penalty are supported for the Cox MCM while only lasso is currently supported for parametric MCMs.

Usage

```
cureem(
  formula,
  data,
  subset,
  x_latency = NULL,
  model = c("cox", "weibull", "exponential"),
  penalty = c("lasso", "MCP", "SCAD"),
  penalty_factor_inc = NULL,
  penalty_factor_lat = NULL,
  thresh = 0.001,
  scale = TRUE,
  maxit = NULL,
  inits = NULL,
  lambda_inc = 0.1,
  lambda_lat = 0.1,
  gamma_inc = 3,
  gamma_lat = 3,
  na.action = na.omit,
  ...
)
```

Arguments

formula	an object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted. The response must be a survival object as returned by the Surv function while the variables on the right side of the formula are the covariates that are included in the incidence portion of the model.
data	a data.frame in which to interpret the variables named in the formula or in the subset argument. Rows with missing data are omitted (only na.action = na.omit is operational) therefore users may want to impute missing data prior to calling this function.
subset	an optional expression indicating which subset of observations to be used in the fitting process, either a numeric or factor variable should be used in subset, not a character variable. All observations are included by default.

<code>x_latency</code>	specifies the variables to be included in the latency portion of the model and can be either a matrix of predictors, a model formula with the right hand side specifying the latency variables, or the same data.frame passed to the data parameter. Note that when using the model formula syntax for <code>x_latency</code> it cannot handle <code>x_latency = ~ ..</code>
<code>model</code>	type of regression model to use for the latency portion of mixture cure model. Can be "cox", "weibull", or "exponential" (default is "cox").
<code>penalty</code>	type of penalty function. Can be "lasso", "MCP", or "SCAD" (default is "lasso").
<code>penalty_factor_inc</code>	vector of binary indicators representing the penalty to apply to each incidence coefficient: 0 implies no shrinkage and 1 implies shrinkage. If not supplied, 1 is applied to all incidence variables.
<code>penalty_factor_lat</code>	vector of binary indicators representing the penalty to apply to each latency coefficient: 0 implies no shrinkage and 1 implies shrinkage. If not supplied, 1 is applied to all latency variables.
<code>thresh</code>	small numeric value. The iterative process stops when the differences between successive expected penalized complete-data log-likelihoods for both incidence and latency components are less than this specified level of tolerance (default is 10^{-3}).
<code>scale</code>	logical, if TRUE the predictors are centered and scaled.
<code>maxit</code>	integer specifying the maximum number of passes over the data for each lambda. If not specified, 100 is applied when <code>penalty = "lasso"</code> and 1000 is applied when <code>penalty = "MCP"</code> or <code>penalty = "SCAD"</code> .
<code>inits</code>	an optional list specifying the initial values. This includes: • <code>itct</code> the incidence intercept. • <code>b_u</code> a numeric vector for the unpenalized incidence coefficients for the incidence portion of the model. • <code>beta_u</code> a numeric vector for unpenalized latency coefficients in the incidence portion of the model. • <code>lambda</code> a numeric value for the rate parameter when fitting either a Weibull or exponential MCM using <code>model = "weibull"</code> or <code>model = "exponential"</code>. • <code>alpha</code> a numeric value for the shape parameter when fitting a Weibull MCM using <code>model = "weibull"</code>. • <code>survprob</code> a numeric vector for the latency survival probabilities $S_u(t_i w_i)$ for $i=1,...,N$ when fitting a Cox MCM <code>model = "cox"</code>. Penalized coefficients are initialized to zero. If <code>inits</code> is not specified or improperly specified, initialization is automatically provided by the function.
<code>lambda_inc</code>	numeric value for the penalization parameter λ for variables in the incidence portion of the model.
<code>lambda_lat</code>	numeric value for the penalization parameter λ for variables in the latency portion of the model.
<code>gamma_inc</code>	numeric value for the penalization parameter γ for variables in the incidence portion of the model when <code>penalty = "MCP"</code> or <code>penalty = "SCAD"</code> (default is 3).

<code>gamma_lat</code>	numeric value for the penalization parameter γ for variables in the latency portion of the model when <code>penalty = "MCP"</code> or <code>penalty = "SCAD"</code> (default is 3).
<code>na.action</code>	this function requires complete data so <code>"na.omit"</code> is invoked. Users can impute missing data as an alternative prior to model fitting.
<code>...</code>	additional arguments.

Value

<code>b_path</code>	Matrix representing the solution path of the coefficients in the incidence portion of the model. Row is step and column is variable.
<code>beta_path</code>	Matrix representing the solution path of the coefficients in the latency portion of the model. Row is step and column is variable.
<code>b0_path</code>	Vector representing the solution path of the intercept in the incidence portion of the model.
<code>logLik_inc</code>	Vector representing the expected penalized complete-data log-likelihood for the incidence portion of the model for each step in the solution path.
<code>logLik_lat</code>	Vector representing the expected penalized complete-data log-likelihood for the latency portion of the model for each step in the solution path.
<code>x_incidence</code>	Matrix representing the design matrix of the incidence predictors.
<code>x_latency</code>	Matrix representing the design matrix of the latency predictors.
<code>y</code>	Vector representing the survival object response as returned by the <code>Surv</code> function
<code>model</code>	Character string indicating the type of regression model used for the latency portion of mixture cure model ("weibull" or "exponential").
<code>scale</code>	Logical value indicating whether the predictors were centered and scaled.
<code>method</code>	Character string indicating the EM algorithm was used in fitting the mixture cure model.
<code>rate_path</code>	Vector representing the solution path of the rate parameter for the Weibull or exponential density in the latency portion of the model.
<code>alpha_path</code>	Vector representing the solution path of the shape parameter for the Weibull density in the latency portion of the model.
<code>call</code>	the matched call.

References

Archer, K. J., Fu, H., Mrozek, K., Nicolet, D., Mims, A. S., Uy, G. L., Stock, W., Byrd, J. C., Hiddemann, W., Braess, J., Spiekermann, K., Metzeler, K. H., Herold, T., Eisfeld, A.-K. (2024) Identifying long-term survivors and those at higher or lower risk of relapse among patients with cytogenetically normal acute myeloid leukemia using a high-dimensional mixture cure model. *Journal of Hematology & Oncology*, **17**:28.

See Also

[cv_cureem](#)

Examples

```
library(survival)
withr::local_seed(1234)
temp <- generate_cure_data(n = 80, j = 100, n_true = 10, a = 1.8)
training <- temp$training
fit <- cureem(Surv(Time, Censor) ~ .,
  data = training, x_latency = training,
  model = "cox", penalty = "lasso", lambda_inc = 0.1,
  lambda_lat = 0.1, gamma_inc = 6, gamma_lat = 10
)
```

curegmifs	<i>Fit penalized parametric mixture cure model using the GMIFS algorithm</i>
-----------	--

Description

Fits a penalized Weibull or exponential mixture cure model using the generalized monotone incremental forward stagewise (GMIFS) algorithm (Hastie et al 2007) and yields solution paths for parameters in the incidence and latency portions of the model.

Usage

```
curegmifs(
  formula,
  data,
  subset,
  x_latency = NULL,
  model = c("weibull", "exponential"),
  penalty_factor_inc = NULL,
  penalty_factor_lat = NULL,
  epsilon = 0.001,
  thresh = 1e-05,
  scale = TRUE,
  maxit = 10000,
  inits = NULL,
  verbose = TRUE,
  suppress_warning = FALSE,
  na.action = na.omit,
  ...
)
```

Arguments

formula	an object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted. The response must be a survival object as returned by the Surv function while the variables on the right side of
---------	---

	the formula are the covariates that are included in the incidence portion of the model.
<code>data</code>	a <code>data.frame</code> in which to interpret the variables named in the formula or in the <code>subset</code> argument. Rows with missing data are omitted (only <code>na.action = na.omit</code> is operational) therefore users may want to impute missing data prior to calling this function.
<code>subset</code>	an optional expression indicating which subset of observations to be used in the fitting process, either a numeric or factor variable should be used in <code>subset</code> , not a character variable. All observations are included by default.
<code>x_latency</code>	specifies the variables to be included in the latency portion of the model and can be either a matrix of predictors, a model formula with the right hand side specifying the latency variables, or the same <code>data.frame</code> passed to the <code>data</code> parameter. Note that when using the model formula syntax for <code>x_latency</code> it cannot handle <code>x_latency = ~ ..</code>
<code>model</code>	type of regression model to use for the latency portion of mixture cure model. Can be "weibull" or "exponential"; default is "weibull".
<code>penalty_factor_inc</code>	vector of binary indicators representing the penalty to apply to each incidence coefficient: 0 implies no shrinkage and 1 implies shrinkage. If not supplied, 1 is applied to all incidence variables.
<code>penalty_factor_lat</code>	vector of binary indicators representing the penalty to apply to each latency coefficient: 0 implies no shrinkage and 1 implies shrinkage. If not supplied, 1 is applied to all latency variables.
<code>epsilon</code>	small numeric value reflecting the incremental value used to update a coefficient at a given step (default is 0.001).
<code>thresh</code>	small numeric value. The iterative process stops when the differences between successive expected penalized log-likelihoods for both incidence and latency components are less than this specified level of tolerance (default is 10^{-5}).
<code>scale</code>	logical, if TRUE the predictors are centered and scaled.
<code>maxit</code>	integer specifying the maximum number of steps to run in the iterative algorithm (default is 10^4).
<code>inits</code>	an optional list specifying the initial values as follows: • <code>itct</code> a numeric value for the unpenalized incidence intercept. • <code>b_u</code> a numeric vector for the unpenalized incidence coefficients. • <code>beta_u</code> a numeric vector for unpenalized latency coefficients. • <code>lambda</code> a numeric value for the rate parameter. • <code>alpha</code> a numeric value for the shape parameter when <code>model = "weibull"</code>. If not supplied or improperly supplied, initialization is automatically provided by the function.
<code>verbose</code>	logical, if TRUE running information is printed to the console (default is FALSE).
<code>suppress_warning</code>	logical, if TRUE, suppresses echoing the warning that the maximum number of iterations was reached so that the algorithm may not have converged. Instead, warning is returned as part of the output with this message.

na.action	this function requires complete data so "na.omit" is invoked. Users can impute missing data as an alternative prior to model fitting.
...	additional arguments.

Value

b_path	Matrix representing the solution path of the coefficients in the incidence portion of the model. Row is step and column is variable.
beta_path	Matrix representing the solution path of the coefficients in the latency portion of the model. Row is step and column is variable.
b0_path	Vector representing the solution path of the intercept in the incidence portion of the model.
rate_path	Vector representing the solution path of the rate parameter for the Weibull or exponential density in the latency portion of the model.
logLik	Vector representing the log-likelihood for each step in the solution path.
x_incidence	Matrix representing the design matrix of the incidence predictors.
x_latency	Matrix representing the design matrix of the latency predictors.
y	Vector representing the survival object response as returned by the Surv function
model	Character string indicating the type of regression model used for the latency portion of mixture cure model ("weibull" or "exponential").
scale	Logical value indicating whether the predictors were centered and scaled.
alpha_path	Vector representing the solution path of the shape parameter for the Weibull density in the latency portion of the model.
call	the matched call.
warning	message indicating whether the maximum number of iterations was achieved which may indicate the model did not converge.

References

- Fu, H., Nicolet, D., Mrozek, K., Stone, R. M., Eisfeld, A. K., Byrd, J. C., Archer, K. J. (2022) Controlled variable selection in Weibull mixture cure models for high-dimensional data. *Statistics in Medicine*, **41**(22), 4340–4366.
- Hastie, T., Taylor J., Tibshirani R., Walther G. (2007) Forward stagewise regression and the monotone lasso. *Electron J Stat*, **1**:1–29.

See Also

[cv_curegmifs](#)

Examples

```
library(survival)
withr::local_seed(1234)
temp <- generate_cure_data(n = 100, j = 10, n_true = 10, a = 1.8)
training <- temp$training
```

```
fit <- curegmifs(Surv(Time, Censor) ~ .,
  data = training, x_latency = training,
  model = "weibull", thresh = 1e-4, maxit = 2000, epsilon = 0.01,
  verbose = FALSE
)
```

cv_cureem

Fit penalized mixture cure model using the E-M algorithm with cross-validation for parameter tuning

Description

Fits penalized parametric and semi-parametric mixture cure models (MCM) using the E-M algorithm with k-fold cross-validation for parameter tuning. The lasso (L1), MCP and SCAD penalty are supported for the Cox MCM while only lasso is currently supported for parametric MCMs. When FDR controlled variable selection is used, the model-X knockoffs method is applied and indices of selected variables are returned.

Usage

```
cv_cureem(
  formula,
  data,
  subset,
  x_latency = NULL,
  model = c("cox", "weibull", "exponential"),
  penalty = c("lasso", "MCP", "SCAD"),
  penalty_factor_inc = NULL,
  penalty_factor_lat = NULL,
  fdr_control = FALSE,
  fdr = 0.2,
  grid_tuning = FALSE,
  thresh = 0.001,
  scale = TRUE,
  maxit = NULL,
  inits = NULL,
  lambda_inc_list = NULL,
  lambda_lat_list = NULL,
  nlambda_inc = NULL,
  nlambda_lat = NULL,
  gamma_inc = 3,
  gamma_lat = 3,
  lambda_min_ratio_inc = 0.1,
  lambda_min_ratio_lat = 0.1,
  n_folds = 5,
  measure_inc = c("c", "auc"),
```

```

    one_se = FALSE,
    cure_cutoff = 5,
    parallel = FALSE,
    seed = NULL,
    verbose = TRUE,
    na.action = na.omit,
    ...
  )

```

Arguments

formula	an object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted. The response must be a survival object as returned by the Surv function while the variables on the right side of the formula are the covariates that are included in the incidence portion of the model.
data	a data.frame in which to interpret the variables named in the formula or in the subset argument. Rows with missing data are omitted (only na.action = na.omit is operational) therefore users may want to impute missing data prior to calling this function.
subset	an optional expression indicating which subset of observations to be used in the fitting process, either a numeric or factor variable should be used in subset, not a character variable. All observations are included by default.
x_latency	specifies the variables to be included in the latency portion of the model and can be either a matrix of predictors, a model formula with the right hand side specifying the latency variables, or the same data.frame passed to the data parameter. Note that when using the model formula syntax for x_latency it cannot handle <code>x_latency = ~ ..</code>
model	type of regression model to use for the latency portion of mixture cure model. Can be "cox", "weibull", or "exponential" (default is "cox").
penalty	type of penalty function. Can be "lasso", "MCP", or "SCAD" (default is "lasso").
penalty_factor_inc	vector of binary indicators representing the penalty to apply to each incidence coefficient: 0 implies no shrinkage and 1 implies shrinkage. If not supplied, 1 is applied to all incidence variables.
penalty_factor_lat	vector of binary indicators representing the penalty to apply to each latency coefficient: 0 implies no shrinkage and 1 implies shrinkage. If not supplied, 1 is applied to all latency variables.
fdr_control	logical, if TRUE, model-X knockoffs are used for FDR-controlled variable selection and indices of selected variables are returned (default is FALSE).
fdr	numeric value in (0, 1) range specifying the target FDR level to use for variable selection when fdr_control = TRUE (default is 0.2).
grid_tuning	logical, if TRUE a 2-D grid tuning approach is used to select the optimal pair of λ_b and λ_β penalty parameters for the incidence and latency portions of the model, respectively. Otherwise the λ_b and λ_β are selected from a 1-D sequence and are equal to one another (default is FALSE).

thresh	small numeric value. The iterative process stops when the differences between successive expected penalized complete-data log-likelihoods for both incidence and latency components are less than this specified level of tolerance (default is 10^{-3}).
scale	logical, if TRUE the predictors are centered and scaled.
maxit	maximum number of passes over the data for each lambda. If not specified, 100 is applied when penalty = "lasso" and 1000 is applied when penalty = "MCP" or penalty = "SCAD".
inits	an optional list specifying the initial values to be used for model fitting as follows: • itct the incidence intercept. • b_u a numeric vector for the unpenalized incidence coefficients for the incidence portion of the model. • beta_u a numeric vector for unpenalized latency coefficients in the incidence portion of the model. • lambda a numeric value for the rate parameter when fitting either a Weibull or exponential MCM using model = "weibull" or model = "exponential". • alpha a numeric value for the shape parameter when fitting a Weibull MCM using model = "weibull". • survprob a numeric vector for the latency survival probabilities $S_u(t_i w_i)$ for $i=1, \dots, N$ when fitting a Cox MCM model = "cox". Penalized coefficients are initialized to zero. If inits is not specified or improperly specified, initialization is automatically provided by the function.
lambda_inc_list	a numeric vector used to search for the optimal λ_b tuning parameter. If not supplied, the function computes a λ_b sequence based on nlambda_inc and lambda_min_ratio_inc. If grid_tuning = FALSE, the same sequence should be used for both λ_b and λ_β .
lambda_lat_list	a numeric vector used to search for the optimal λ_β tuning parameter. If not supplied, the function computes a λ_β sequence based on nlambda_lat and lambda_min_ratio_lat. If grid_tuning = FALSE, the same sequence should be used for both λ_b and λ_β .
nlambda_inc	an integer specifying the number of values to search for the optimal λ_b tuning parameter; default is 10 if grid_tuning = TRUE and 50 otherwise.
nlambda_lat	an integer specifying the number of values to search for the optimal λ_β tuning parameter; default is 10 if grid_tuning = TRUE and 50 otherwise.
gamma_inc	numeric value for the penalization parameter γ for variables in the incidence portion of the model when penalty = "MCP" or penalty = "SCAD" (default is 3).
gamma_lat	numeric value for the penalization parameter γ for variables in the latency portion of the model when penalty = "MCP" or penalty = "SCAD" (default is 3).
lambda_min_ratio_inc	numeric value in (0,1) representing the smallest value for λ_b as a fraction of lambda_max_inc, the data-derived entry value at which essentially all penalized variables in the incidence portion of the model have a coefficient estimate of 0 (default is 0.1).

lambda_min_ratio_lat	numeric value in (0,1) representing the smallest value for λ_β as a fraction of lambda_max_lat, the data-derived entry value at essentially all penalized variables in the latency portion of the model have a coefficient estimate of 0 (default is 0.1).
n_folds	an integer specifying the number of folds for the k-fold cross-validation procedure (default is 5).
measure_inc	character string specifying the evaluation criterion used in selecting the optimal λ_b which can be either • "c" specifying to use the C-statistic for cure status weighting (CSW) method proposed by Asano and Hirakawa (2017) to select both λ_b and λ_β • "auc" specifying to use the AUC for cure prediction using the mean score imputation (MSI) method proposed by Asano et al. (2014) to select λ_b while the C-statistic with CSW is used for λ_β.
one_se	logical, if TRUE then the one standard error rule is applied for selecting the optimal parameters. The one standard error rule selects the most parsimonious model having evaluation criterion no more than one standard error worse than that of the best evaluation criterion (default is FALSE).
cure_cutoff	numeric value representing the cutoff time value that represents subjects not experiencing the event by this time are cured. This value is used to produce a proxy for the unobserved cure status when calculating C-statistic and AUC (default is 5 representing 5 years). Users should be careful to note the time scale of their data and adjust this according to the time scale and clinical application.
parallel	logical. If TRUE, parallel processing is performed for K-fold CV using foreach and the doParallel package is required.
seed	optional integer representing the random seed. Setting the random seed fosters reproducibility of the results.
verbose	logical, if TRUE running information is printed to the console (default is FALSE).
na.action	this function requires complete data so "na.omit" is invoked. Users can impute missing data as an alternative prior to model fitting.
...	additional arguments.

Value

b0	Estimated intercept for the incidence portion of the model.
b	Estimated coefficients for the incidence portion of the model.
beta	Estimated coefficients for the latency portion of the model.
alpha	Estimated shape parameter if the Weibull model is fit.
rate	Estimated rate parameter if the Weibull or exponential model is fit.
logLik_inc	Expected penalized complete-data log-likelihood for the incidence portion of the model.
logLik_lat	Expected penalized complete-data log-likelihood for the latency portion of the model.

selected_lambda_inc
Value of λ_b selected using cross-validation. NULL when fdr_control is TRUE.

selected_lambda_lat
Value of λ_β selected using cross-validation. NULL when fdr_control is TRUE.

max_c
Maximum C-statistic achieved.

max_auc
Maximum AUC for cure prediction achieved; only output when measure_inc="auc".

selected_index_inc
Indices of selected variables for the incidence portion of the model when fdr_control=TRUE.
If no variables are selected, int(0) will be returned.

selected_index_lat
Indices of selected variables for the latency portion of the model when fdr_control=TRUE.
If no variables are selected, int(0) will be returned.

call
the matched call.

References

Archer, K. J., Fu, H., Mrozek, K., Nicolet, D., Mims, A. S., Uy, G. L., Stock, W., Byrd, J. C., Hiddemann, W., Braess, J., Spiekermann, K., Metzeler, K. H., Herold, T., Eisfeld, A.-K. (2024) Identifying long-term survivors and those at higher or lower risk of relapse among patients with cytogenetically normal acute myeloid leukemia using a high-dimensional mixture cure model. *Journal of Hematology & Oncology*, **17**:28.

See Also

[cureem](#)

Examples

```
## Not run:
library(survival)
withr::local_seed(1234)
temp <- generate_cure_data(n = 200, j = 25, n_true = 5, a = 1.8, rho = 0.2)
training <- temp$training
# Fit a penalized Cox MCM selecting parameters using 2-fold CV
fit.cv <- cv_cureem(Surv(Time, Censor) ~ .,
  data = training,
  x_latency = training, fdr_control = FALSE,
  grid_tuning = FALSE, nlambda_inc = 10, nlambda_lat = 10,
  n_folds = 2, seed = 23, verbose = FALSE
)
fit.cv.fdr <- cv_cureem(Surv(Time, Censor) ~ .,
  data = training,
  x_latency = training, model = "weibull", penalty = "lasso",
  fdr_control = TRUE, grid_tuning = FALSE, nlambda_inc = 10,
  nlambda_lat = 10, n_folds = 2, seed = 23, verbose = TRUE
)

## End(Not run)
```

cv_curegmifs	<i>Fit a penalized parametric mixture cure model using the generalized monotone incremental forward stagewise (GMIFS) algorithm (Hastie et al 2007) with cross-validation for model selection</i>
--------------	---

Description

Fits a penalized Weibull or exponential mixture cure model using the generalized monotone incremental forward stagewise (GMIFS) algorithm with k-fold cross-validation to select the optimal iteration step along the solution path. When FDR controlled variable selection is used, the model-X knockoffs method is applied and indices of selected variables are returned.

Usage

```
cv_curegmifs(
  formula,
  data,
  subset,
  x_latency = NULL,
  model = c("weibull", "exponential"),
  penalty_factor_inc = NULL,
  penalty_factor_lat = NULL,
  fdr_control = FALSE,
  fdr = 0.2,
  epsilon = 0.001,
  thresh = 1e-05,
  scale = TRUE,
  maxit = 10000,
  inits = NULL,
  n_folds = 5,
  measure_inc = c("c", "auc"),
  one_se = FALSE,
  cure_cutoff = 5,
  parallel = FALSE,
  seed = NULL,
  verbose = TRUE,
  na.action = na.omit,
  ...
)
```

Arguments

formula	an object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted. The response must be a survival object as returned by the Surv function while the variables on the right side of the formula are the covariates that are included in the incidence portion of the model.
---------	---

<code>data</code>	a <code>data.frame</code> in which to interpret the variables named in the formula or in the <code>subset</code> argument. Rows with missing data are omitted (only <code>na.action = na.omit</code> is operational) therefore users may want to impute missing data prior to calling this function.
<code>subset</code>	an optional expression indicating which subset of observations to be used in the fitting process, either a numeric or factor variable should be used in <code>subset</code> , not a character variable. All observations are included by default.
<code>x_latency</code>	specifies the variables to be included in the latency portion of the model and can be either a matrix of predictors, a model formula with the right hand side specifying the latency variables, or the same <code>data.frame</code> passed to the <code>data</code> parameter. Note that when using the model formula syntax for <code>x_latency</code> it cannot handle <code>x_latency = ~ ..</code>
<code>model</code>	type of regression model to use for the latency portion of mixture cure model. Can be "weibull" or "exponential"; default is "weibull".
<code>penalty_factor_inc</code>	vector of binary indicators representing the penalty to apply to each incidence coefficient: 0 implies no shrinkage and 1 implies shrinkage. If not supplied, 1 is applied to all incidence variables.
<code>penalty_factor_lat</code>	vector of binary indicators representing the penalty to apply to each latency coefficient: 0 implies no shrinkage and 1 implies shrinkage. If not supplied, 1 is applied to all latency variables.
<code>fdr_control</code>	logical, if TRUE, model-X knockoffs are used for FDR-controlled variable selection and indices of selected variables are returned (default is FALSE).
<code>fdr</code>	numeric value in (0, 1) range specifying the target FDR level to use for variable selection when <code>fdr_control = TRUE</code> (default is 0.2).
<code>epsilon</code>	small numeric value reflecting incremental value used to update a coefficient at a given step (default is 0.001).
<code>thresh</code>	small numeric value. The iterative process stops when the differences between successive expected penalized complete-data log-likelihoods for both incidence and latency components are less than this specified level of tolerance (default is 10^{-5}).
<code>scale</code>	logical, if TRUE the predictors are centered and scaled.
<code>maxit</code>	integer specifying the maximum number of steps to run in the iterative algorithm (default is 10^4).
<code>inits</code>	an optional list specifying the initial values as follows: • <code>itct</code> a numeric value for the unpenalized incidence intercept. • <code>b_u</code> a numeric vector for the unpenalized incidence coefficients. • <code>beta_u</code> a numeric vector for unpenalized latency coefficients. • <code>lambda</code> a numeric value for the rate parameter. • <code>alpha</code> a numeric value for the shape parameter when <code>model = "weibull"</code>. If <code>inits</code> is not specified or improperly supplied, initialization is automatically provided by the function.

n_folds	an integer specifying the number of folds for the k-fold cross-validation procedure (default is 5).
measure_inc	character string specifying the evaluation criterion used in selecting the optimal λ_b which can be either • "c" specifying to use the C-statistic for cure status weighting (CSW) method proposed by Asano and Hirakawa (2017) to select both λ_b and λ_β • "auc" specifying to use the AUC for cure prediction using the mean score imputation (MSI) method proposed by Asano et al. (2014) to select λ_b while the C-statistic with CSW is used for λ_β.
one_se	logical, if TRUE then the one standard error rule is applied for selecting the optimal parameters. The one standard error rule selects the most parsimonious model having evaluation criterion no more than one standard error worse than that of the best evaluation criterion (default is FALSE).
cure_cutoff	numeric value representing the cutoff time value that represents subjects not experiencing the event by this time are cured. This value is used to produce a proxy for the unobserved cure status when calculating C-statistic and AUC (default is 5 representing 5 years). Users should be careful to note the time scale of their data and adjust this according to the time scale and clinical application.
parallel	logical. If TRUE, parallel processing is performed for K-fold CV using foreach and the doParallel package is required.
seed	optional integer representing the random seed. Setting the random seed fosters reproducibility of the results.
verbose	logical, if TRUE running information is printed to the console (default is FALSE).
na.action	this function requires complete data so "na.omit" is invoked. Users can impute missing data as an alternative prior to model fitting.
...	additional arguments.

Value

b0	Estimated intercept for the incidence portion of the model.
b	Estimated coefficients for the incidence portion of the model.
beta	Estimated coefficients for the latency portion of the model.
alpha	Estimated shape parameter if the Weibull model is fit.
rate	Estimated rate parameter if the Weibull or exponential model is fit.
logLik	Log-likelihood value.
selected_step_inc	Iteration step selected for the incidence portion of the model using cross-validation. NULL when fdr_control is TRUE.
selected_step_lat	Iteration step selected for the latency portion of the model using cross-validation. NULL when fdr_control is TRUE.
max_c	Maximum C-statistic achieved
max_auc	Maximum AUC for cure prediction achieved; only output when measure_inc = "auc".

`selected_index_inc`
 Indices of selected variables for the incidence portion of the model when `fdr_control = TRUE`. If none selected, `int(0)` will be returned.

`selected_index_lat`
 Indices of selected variables for the latency portion of the model when `fdr_control = TRUE`. If none selected, `int(0)` will be returned.

`call`
 the matched call.

References

Fu, H., Nicolet, D., Mrozek, K., Stone, R. M., Eisefeld, A. K., Byrd, J. C., Archer, K. J. (2022) Controlled variable selection in Weibull mixture cure models for high-dimensional data. *Statistics in Medicine*, **41**(22), 4340–4366.

Hastie, T., Taylor J., Tibshirani R., Walther G. (2007) Forward stagewise regression and the monotone lasso. *Electron J Stat*, **1**:1–29.

See Also

[curegmifs](#)

Examples

```
## Not run:
library(survival)
withr::local_seed(123)
temp <- generate_cure_data(n = 100, j = 15, n_true = 3, a = 1.8, rho = 0.1)
training <- temp$training

fit.cv <- cv_curegmifs(Surv(Time, Censor) ~ .,
  data = training,
  x_latency = training, fdr_control = FALSE,
  maxit = 450, epsilon = 0.01, n_folds = 2, thresh = 1e-4,
  seed = 23, verbose = TRUE
)

## End(Not run)
```

dim.mixturecure

Dimension method for mixturecure objects

Description

Dimension method for mixturecure objects.

Usage

```
## S3 method for class 'mixturecure'
dim(x)
```

Arguments

`x` An object of class 'mixturecure'.

Value

`nobs` number of subjects in the dataset.
`p_incidence` number of variables in the incidence portion of the model.
`p_latency` number of variables in the latency portion of the model.

Examples

```
library(survival)
withr::local_seed(1234)
temp <- generate_cure_data(n = 100, j = 10, n_true = 10, a = 1.8)
training <- temp$training
fit <- curegmifs(Surv(Time, Censor) ~ .,
  data = training, x_latency = training,
  model = "weibull", thresh = 1e-4, maxit = 2000,
  epsilon = 0.01, verbose = FALSE
)
dim(fit)
```

family.mixturecure	<i>Return model family and fitting algorithm for mixturecure model fits</i>
--------------------	---

Description

Return model family and fitting algorithm formixturecure model fits.

Usage

```
## S3 method for class 'mixturecure'
family(object, ...)
```

Arguments

`object` an object of class mixturecure
`...` other arguments.

Value

the parametric or semi-parametric model fit and the fitting algorithm.

Examples

```
library(survival)
withr::local_seed(1234)
temp <- generate_cure_data(n = 100, j = 10, n_true = 10, a = 1.8)
training <- temp$training
fit <- curegmifs(Surv(Time, Censor) ~ .,
  data = training, x_latency = training,
  model = "weibull", thresh = 1e-4, maxit = 2000,
  epsilon = 0.01, verbose = FALSE
)
family(fit)
```

formula.mixturecure	<i>Extract model formula for mixturecure object</i>
---------------------	---

Description

Extract the model formula for 'mixturecure' object

Usage

```
## S3 method for class 'mixturecure'
formula(x, ...)
```

Arguments

x	an object from class 'mixturecure'.
...	other arguments.

Value

a formula representing the incidence and variables for the latency portion of the model

Examples

```
library(survival)
withr::local_seed(1234)
temp <- generate_cure_data(n = 100, j = 10, n_true = 10, a = 1.8)
training <- temp$training
fit <- curegmifs(Surv(Time, Censor) ~ .,
  data = training, x_latency = training,
  model = "weibull", thresh = 1e-4, maxit = 2000,
  epsilon = 0.01, verbose = FALSE
)
formula(fit)
```

generate_cure_data	<i>Simulate data under a mixture cure model</i>
--------------------	---

Description

Simulate data under a mixture cure model.

Usage

```
generate_cure_data(
  n = 400,
  j = 500,
  nonp = 2,
  train_prop = 0.75,
  n_true = 10,
  a = 1,
  rho = 0.5,
  itct_mean = 0.5,
  cens_ub = 20,
  alpha = 1,
  lambda = 2,
  same_signs = FALSE,
  model = "weibull"
)
```

Arguments

n	an integer denoting the total sample size.
j	an integer denoting the number of penalized predictors which is the same for both the incidence and latency portions of the model.
nonp	an integer denoting the number of unpenalized predictors (which is the same for both the incidence and latency portions of the model).
train_prop	a numeric value in [0, 1) representing the fraction of ‘n’ to be used in forming the training dataset.
n_true	an integer less than ‘j’ denoting the number of variables truly associated with the outcome (i.e., the number of covariates with nonzero parameter values) among the penalized predictors.
a	a numeric value denoting the effect size (signal amplitude) which is the same for both the incidence and latency portions of the model.
rho	a numeric value in [0, 1) representing the correlation between adjacent covariates in the same block.
itct_mean	a numeric value representing the expectation of the incidence intercept which controls the cure rate.
cens_ub	a numeric value representing the upper bound on the censoring time distribution which follows a uniform distribution on (0, cens_ub].

alpha	a numeric value representing the shape parameter in the Weibull density.
lambda	a numeric value representing the rate parameter in the Weibull density.
same_signs	logical, if TRUE the incidence and latency coefficients have the same signs.
model	type of regression model to use for the latency portion of mixture cure model. Can be one of the following: • "weibull" to generate times from a Weibull distribution. • "GG" to generate times from a generalized gamma distribution. • "Gompertz" to generate times from a Gompertz distribution. • "nonparametric" to generate times non-parametrically. • "GG_baseline" to generate times from a generalized gamma baseline distribution.

Value

training	training data.frame which includes Time, Censor, and covariates. Variables prefixed with "U" indicates unpenalized covariates and is equal to the value passed to nonp (default is 2). Variables prefixed with "X" indicates penalized covariates and is equal to the value passed to j.
training_y	the true status for the training set: uncured = 1; cured = 0
testing	testing data.frame which includes Time, Censor, Y (the true uncured = 1; cured = 0 status), and covariates. Variables prefixed with "U" indicates unpenalized covariates and is equal to the value passed to nonp (default is 2). Variables prefixed with "X" indicates penalized covariates and is equal to the value passed to j.
testing_y	the true status for the testing set: uncured = 1; cured = 0
parameters	a list including: the indices of true incidence signals (nonzero_b), indices of true latency signals (nonzero_beta), unpenalized incidence parameter values (b_u), unpenalized latency parameter values (beta_u), parameter values for the true incidence signals among penalized covariates (b_p_nz), parameter values for the true latency signals among penalized covariates (beta_p_nz), parameter value for the incidence intercept (itct)

Examples

```
library(survival)
withr::local_seed(1234)
# This dataset has 2 penalized features associated with the outcome,
# 3 penalized features not associated with the outcome (noise features), and 1
# unpenalized noise feature.
data <- generate_cure_data(n = 1000, j = 5, n_true = 2, nonp = 1, a = 2)
# Extract the training data
training <- data$training
# Extract the testing data
testing <- data$testing
# To identify the features truly associated with incidence
names(training)[grep("^X", names(training))][data$parameters$nonzero_b]
# To identify the features truly associated with latency
```

```

names(training)[grep("^X", names(training))][data$parameters$nonzero_beta]
# Fit the model to the training data
fitem <- cureem(Surv(Time, Censor) ~ ., data = training,
  x_latency = training)
# Examine the estimated coefficients at the (default) minimum AIC
coef(fitem)
# As the penalty increases, the coefficients for the noise variables shrink
# to or remain at zero, while the truly associated features have coefficient
# paths that depart from zero. This shows the model's ability to distinguish
# signal from noise.
plot(fitem, label = TRUE)

```

logLik.mixturecure	<i>Log-likelihood for fitted mixture cure model</i>
--------------------	---

Description

This function returns the log-likelihood for a user-specified model criterion or step for a `curegmifs`, `cureem`, `cv_curegmifs` or `cv_cureem` fitted object.

Usage

```

## S3 method for class 'mixturecure'
logLik(object, model_select = "AIC", ...)

```

Arguments

<code>object</code>	a <code>mixturecure</code> object resulting from <code>curegmifs</code> , <code>cureem</code> , <code>cv_curegmifs</code> , <code>cv_cureem</code> .
<code>model_select</code>	either a case-sensitive parameter for models fit using <code>curegmifs</code> or <code>cureem</code> or any numeric step along the solution path can be selected. The default is <code>model_select = "AIC"</code> which calculates the predicted values using the coefficients from the model achieving the minimum AIC. The complete list of options are: • "AIC" for the minimum AIC (default). • "mAIC" for the minimum modified AIC. • "cAIC" for the minimum corrected AIC. • "BIC", for the minimum BIC. • "mBIC" for the minimum modified BIC. • "EBIC" for the minimum extended BIC. • "logLik" for the step that maximizes the log-likelihood. • n where n is any numeric value from the solution path. This option has no effect for objects fit using <code>cv_curegmifs</code> or <code>cv_cureem</code> .
<code>...</code>	other arguments.

Value

log-likelihood of the fitted mixture cure model using the specified criteria.

Examples

```
library(survival)
withr::local_seed(1234)
temp <- generate_cure_data(n = 100, j = 10, n_true = 10, a = 1.8)
training <- temp$training
fit <- curegmifs(Surv(Time, Censor) ~ .,
  data = training, x_latency = training,
  model = "weibull", thresh = 1e-4, maxit = 2000,
  epsilon = 0.01, verbose = FALSE
)
logLik(fit, model_select = "AIC")
```

nobs.mixturecure	<i>Number of observations in mixturecure object</i>
------------------	---

Description

Number of observations in fitted ‘mixturecure’ object.

Usage

```
## S3 method for class 'mixturecure'
nobs(object, ...)
```

Arguments

object	An object of class ‘mixturecure’.
...	other arguments.

Value

number of subjects in the dataset.

Examples

```
library(survival)
withr::local_seed(1234)
temp <- generate_cure_data(n = 100, j = 10, n_true = 10, a = 1.8)
training <- temp$training
fit <- curegmifs(Surv(Time, Censor) ~ .,
  data = training, x_latency = training,
  model = "weibull", thresh = 1e-4, maxit = 2000,
  epsilon = 0.01, verbose = FALSE
)
nobs(fit)
```

nonzerocure_test	<i>Non-parametric test for a non-zero cured fraction</i>
------------------	--

Description

Tests the null hypothesis that the proportion of observations susceptible to the event = 1 against the alternative that the proportion of observations susceptible to the event is < 1. If the null hypothesis is rejected, there is a significant cured fraction.

Usage

```
nonzerocure_test(object, reps = 1000, seed = NULL, plot = FALSE, b = NULL)
```

Arguments

object	a survfit object.
reps	number of simulations on which to base the p-value (default = 1000).
seed	optional random seed.
plot	logical. If TRUE a histogram of the estimated susceptible proportions over all simulations is produced.
b	optional. If specified the maximum observed time for the uniform distribution for generating the censoring times. If not specified, an exponential model is used for generating the censoring times (default).

Value

proportion_susceptible	estimated proportion of susceptibles
proportion_cured	estimated proportion of those cured
p_value	p-value testing the null hypothesis that the proportion of susceptibles = 1 (cured fraction = 0) against the alternative that the proportion of susceptibles < 1 (non-zero cured fraction)
time_95_percent_of_events	estimated time at which 95 events should have occurred

References

Maller, R. A. and Zhou, X. (1996) *Survival Analysis with Long-Term Survivors*. John Wiley & Sons.

See Also

[survfit](#), [cure_estimate](#), [sufficient_fu_test](#)

Examples

```
library(survival)
withr::local_seed(1234)
temp <- generate_cure_data(n = 100, j = 10, n_true = 10, a = 1.8)
training <- temp$training
km_fit <- survfit(Surv(Time, Censor) ~ 1, data = training)
nonzerocure_test(km_fit)
```

npar_mixturecure	<i>Number of parameters in fitted mixture cure model</i>
------------------	--

Description

This function returns the number of parameters in a user-specified model criterion or step for a curegmifs, cureem, cv_curegmifs or cv_cureem fitted object.

Usage

```
npar_mixturecure(object, model_select = "AIC")
```

Arguments

object a mixturecure object resulting from curegmifs, cureem, cv_curegmifs, cv_cureem.

model_select either a case-sensitive parameter for models fit using curegmifs or cureem or any numeric step along the solution path can be selected. The default is model_select = "AIC" which calculates the predicted values using the coefficients from the model achieving the minimum AIC. The complete list of options are:

- "AIC" for the minimum AIC (default).
- "mAIC" for the minimum modified AIC.
- "cAIC" for the minimum corrected AIC.
- "BIC", for the minimum BIC.
- "mBIC" for the minimum modified BIC.
- "EBIC" for the minimum extended BIC.
- "logLik" for the step that maximizes the log-likelihood.
- n where n is any numeric value from the solution path.

This option has no effect for objects fit using cv_curegmifs or cv_cureem.

Value

number of paramaters of the fitted mixture cure model using the specified criteria.

pediatric_flt3	<i>Pediatric acute myeloid leukemia patients with FLT3-ITD rearrangement data</i>
----------------	---

Description

Event-free survival for 246 pediatric acute myeloid leukemia patients having a FLT3-ITD rearrangement along with expression of 200 transcripts from RNA-sequencing.

Usage

```
pediatric_flt3
```

Format

A data frame with 246 rows (subjects) and 202 columns:

efs event-free survival

status censoring indicator: 1 = event; 0 = censored

ENSG00000229807.12 normalized expression for indicated transcript

ENSG00000211459.2 normalized expression for indicated transcript

ENSG00000264063.1 normalized expression for indicated transcript

ENSG00000264462.1 normalized expression for indicated transcript

ENSG00000227195.11 normalized expression for indicated transcript

ENSG00000198795.11 normalized expression for indicated transcript

ENSG00000177133.11 normalized expression for indicated transcript

ENSG00000257883.1 normalized expression for indicated transcript

ENSG00000189223.15 normalized expression for indicated transcript

ENSG00000210082.2 normalized expression for indicated transcript

ENSG00000142611.17 normalized expression for indicated transcript

ENSG00000054598.9 normalized expression for indicated transcript

ENSG00000147180.17 normalized expression for indicated transcript

ENSG00000275708.1 normalized expression for indicated transcript

ENSG00000227063.5 normalized expression for indicated transcript

ENSG00000179455.10 normalized expression for indicated transcript

ENSG00000243478.9 normalized expression for indicated transcript

ENSG00000239839.7 normalized expression for indicated transcript

ENSG00000274253.5 normalized expression for indicated transcript

ENSG00000198840.2 normalized expression for indicated transcript

ENSG00000186407.7 normalized expression for indicated transcript

ENSG00000198763.3 normalized expression for indicated transcript
ENSG00000107562.16 normalized expression for indicated transcript
ENSG00000188536.13 normalized expression for indicated transcript
ENSG00000164821.5 normalized expression for indicated transcript
ENSG00000255833.2 normalized expression for indicated transcript
ENSG00000107447.8 normalized expression for indicated transcript
ENSG00000237541.4 normalized expression for indicated transcript
ENSG00000274618.2 normalized expression for indicated transcript
ENSG00000206172.8 normalized expression for indicated transcript
ENSG00000198886.2 normalized expression for indicated transcript
ENSG00000122592.8 normalized expression for indicated transcript
ENSG00000038427.16 normalized expression for indicated transcript
ENSG00000134755.17 normalized expression for indicated transcript
ENSG00000248527.1 normalized expression for indicated transcript
ENSG00000273018.7 normalized expression for indicated transcript
ENSG00000261377.5 normalized expression for indicated transcript
ENSG00000074964.17 normalized expression for indicated transcript
ENSG00000118113.12 normalized expression for indicated transcript
ENSG00000086548.9 normalized expression for indicated transcript
ENSG00000172037.14 normalized expression for indicated transcript
ENSG00000198744.5 normalized expression for indicated transcript
ENSG00000198899.2 normalized expression for indicated transcript
ENSG00000186818.12 normalized expression for indicated transcript
ENSG00000154864.13 normalized expression for indicated transcript
ENSG00000227081.5 normalized expression for indicated transcript
ENSG00000101425.14 normalized expression for indicated transcript
ENSG00000158473.8 normalized expression for indicated transcript
ENSG00000102362.15 normalized expression for indicated transcript
ENSG00000212907.2 normalized expression for indicated transcript
ENSG00000121807.6 normalized expression for indicated transcript
ENSG00000138829.12 normalized expression for indicated transcript
ENSG00000185052.12 normalized expression for indicated transcript
ENSG00000111057.11 normalized expression for indicated transcript
ENSG00000228253.1 normalized expression for indicated transcript
ENSG00000188153.14 normalized expression for indicated transcript
ENSG00000166681.14 normalized expression for indicated transcript
ENSG00000198888.2 normalized expression for indicated transcript

ENSG00000276141.4 normalized expression for indicated transcript
ENSG00000230076.1 normalized expression for indicated transcript
ENSG00000260314.3 normalized expression for indicated transcript
ENSG00000187164.20 normalized expression for indicated transcript
ENSG00000212443.1 normalized expression for indicated transcript
ENSG00000251692.8 normalized expression for indicated transcript
ENSG00000198727.2 normalized expression for indicated transcript
ENSG00000131401.11 normalized expression for indicated transcript
ENSG00000225345.3 normalized expression for indicated transcript
ENSG00000197253.13 normalized expression for indicated transcript
ENSG00000163737.4 normalized expression for indicated transcript
ENSG00000204010.3 normalized expression for indicated transcript
ENSG00000174403.16 normalized expression for indicated transcript
ENSG00000249790.3 normalized expression for indicated transcript
ENSG00000239559.2 normalized expression for indicated transcript
ENSG00000142192.21 normalized expression for indicated transcript
ENSG00000151650.8 normalized expression for indicated transcript
ENSG00000198712.1 normalized expression for indicated transcript
ENSG00000124469.12 normalized expression for indicated transcript
ENSG00000105854.13 normalized expression for indicated transcript
ENSG00000197629.6 normalized expression for indicated transcript
ENSG00000278588.2 normalized expression for indicated transcript
ENSG00000196565.15 normalized expression for indicated transcript
ENSG00000241743.4 normalized expression for indicated transcript
ENSG00000174059.17 normalized expression for indicated transcript
ENSG00000150760.13 normalized expression for indicated transcript
ENSG00000133742.14 normalized expression for indicated transcript
ENSG00000210196.2 normalized expression for indicated transcript
ENSG00000204860.5 normalized expression for indicated transcript
ENSG00000131398.15 normalized expression for indicated transcript
ENSG00000106080.11 normalized expression for indicated transcript
ENSG00000198786.2 normalized expression for indicated transcript
ENSG00000248334.6 normalized expression for indicated transcript
ENSG00000169908.12 normalized expression for indicated transcript
ENSG00000171509.16 normalized expression for indicated transcript
ENSG00000008438.5 normalized expression for indicated transcript
ENSG00000130147.16 normalized expression for indicated transcript

ENSG00000180071.20 normalized expression for indicated transcript
ENSG00000168329.14 normalized expression for indicated transcript
ENSG00000147689.16 normalized expression for indicated transcript
ENSG00000136193.17 normalized expression for indicated transcript
ENSG00000170180.22 normalized expression for indicated transcript
ENSG00000146373.16 normalized expression for indicated transcript
ENSG00000172236.18 normalized expression for indicated transcript
ENSG00000244734.4 normalized expression for indicated transcript
ENSG00000239552.2 normalized expression for indicated transcript
ENSG00000125618.17 normalized expression for indicated transcript
ENSG00000273983.1 normalized expression for indicated transcript
ENSG00000250361.9 normalized expression for indicated transcript
ENSG00000277775.2 normalized expression for indicated transcript
ENSG00000138119.17 normalized expression for indicated transcript
ENSG00000128422.17 normalized expression for indicated transcript
ENSG00000160883.11 normalized expression for indicated transcript
ENSG00000275895.7 normalized expression for indicated transcript
ENSG00000169877.10 normalized expression for indicated transcript
ENSG00000163736.4 normalized expression for indicated transcript
ENSG00000161944.16 normalized expression for indicated transcript
ENSG00000095917.14 normalized expression for indicated transcript
ENSG00000022556.16 normalized expression for indicated transcript
ENSG00000152078.10 normalized expression for indicated transcript
ENSG00000165092.13 normalized expression for indicated transcript
ENSG00000170458.14 normalized expression for indicated transcript
ENSG00000070182.21 normalized expression for indicated transcript
ENSG00000157445.15 normalized expression for indicated transcript
ENSG00000206737.1 normalized expression for indicated transcript
ENSG00000225217.1 normalized expression for indicated transcript
ENSG00000198336.9 normalized expression for indicated transcript
ENSG00000177469.13 normalized expression for indicated transcript
ENSG00000198695.2 normalized expression for indicated transcript
ENSG00000113763.12 normalized expression for indicated transcript
ENSG00000223609.11 normalized expression for indicated transcript
ENSG00000206177.7 normalized expression for indicated transcript
ENSG00000164684.13 normalized expression for indicated transcript
ENSG00000197632.9 normalized expression for indicated transcript

ENSG00000177575.13 normalized expression for indicated transcript
ENSG00000004939.15 normalized expression for indicated transcript
ENSG00000121053.6 normalized expression for indicated transcript
ENSG00000259207.9 normalized expression for indicated transcript
ENSG00000158352.16 normalized expression for indicated transcript
ENSG00000198046.12 normalized expression for indicated transcript
ENSG00000225630.1 normalized expression for indicated transcript
ENSG00000070808.16 normalized expression for indicated transcript
ENSG00000012223.13 normalized expression for indicated transcript
ENSG00000085265.11 normalized expression for indicated transcript
ENSG00000158578.21 normalized expression for indicated transcript
ENSG00000112077.17 normalized expression for indicated transcript
ENSG00000272398.6 normalized expression for indicated transcript
ENSG00000116667.15 normalized expression for indicated transcript
ENSG00000101916.12 normalized expression for indicated transcript
ENSG00000184293.7 normalized expression for indicated transcript
ENSG00000244040.7 normalized expression for indicated transcript
ENSG00000229344.1 normalized expression for indicated transcript
ENSG00000142405.22 normalized expression for indicated transcript
ENSG00000171051.9 normalized expression for indicated transcript
ENSG00000183023.18 normalized expression for indicated transcript
ENSG00000257178.5 normalized expression for indicated transcript
ENSG00000244682.7 normalized expression for indicated transcript
ENSG00000166025.18 normalized expression for indicated transcript
ENSG00000204613.11 normalized expression for indicated transcript
ENSG00000214188.9 normalized expression for indicated transcript
ENSG00000179869.15 normalized expression for indicated transcript
ENSG00000136315.4 normalized expression for indicated transcript
ENSG00000119919.11 normalized expression for indicated transcript
ENSG00000123384.14 normalized expression for indicated transcript
ENSG00000104918.8 normalized expression for indicated transcript
ENSG00000287431.1 normalized expression for indicated transcript
ENSG00000227827.3 normalized expression for indicated transcript
ENSG00000164047.6 normalized expression for indicated transcript
ENSG00000137571.11 normalized expression for indicated transcript
ENSG00000143416.21 normalized expression for indicated transcript
ENSG00000253578.1 normalized expression for indicated transcript

ENSG00000120708.17 normalized expression for indicated transcript
ENSG00000220842.6 normalized expression for indicated transcript
ENSG00000110077.14 normalized expression for indicated transcript
ENSG00000198722.14 normalized expression for indicated transcript
ENSG00000121316.11 normalized expression for indicated transcript
ENSG00000123689.6 normalized expression for indicated transcript
ENSG00000198938.2 normalized expression for indicated transcript
ENSG00000163430.12 normalized expression for indicated transcript
ENSG00000258227.7 normalized expression for indicated transcript
ENSG00000233101.10 normalized expression for indicated transcript
ENSG00000163220.11 normalized expression for indicated transcript
ENSG00000100985.7 normalized expression for indicated transcript
ENSG00000166947.15 normalized expression for indicated transcript
ENSG00000275713.2 normalized expression for indicated transcript
ENSG00000143546.10 normalized expression for indicated transcript
ENSG00000136929.13 normalized expression for indicated transcript
ENSG00000103313.13 normalized expression for indicated transcript
ENSG00000186529.16 normalized expression for indicated transcript
ENSG00000109321.11 normalized expression for indicated transcript
ENSG00000104177.18 normalized expression for indicated transcript
ENSG00000257335.8 normalized expression for indicated transcript
ENSG00000197993.9 normalized expression for indicated transcript
ENSG00000134460.18 normalized expression for indicated transcript
ENSG00000211892.4 normalized expression for indicated transcript
ENSG00000180044.5 normalized expression for indicated transcript
ENSG00000268555.2 normalized expression for indicated transcript
ENSG00000266402.3 normalized expression for indicated transcript
ENSG00000163221.9 normalized expression for indicated transcript
ENSG00000225101.6 normalized expression for indicated transcript
ENSG00000197249.14 normalized expression for indicated transcript
ENSG00000093134.15 normalized expression for indicated transcript

Source

<<https://www.cancer.gov/ccg/research/genome-sequencing/target/studied-cancers/acute-myeloid-leukemia#targets-aml-project>>

plot.mixturecure	<i>Plot fitted mixture cure model</i>
------------------	---------------------------------------

Description

This function plots either the coefficient path, the AIC, the cAIC, the BIC, or the log-likelihood for a fitted curegmifs or cureem object. This function produces a lollipop plot of the coefficient estimates for a fitted cv_curegmifs or cv_cureem object.

Usage

```
## S3 method for class 'mixturecure'
plot(
  x,
  type = c("trace", "AIC", "BIC", "logLik", "cAIC", "mAIC", "mBIC", "EBIC"),
  xlab = NULL,
  ylab = NULL,
  label = FALSE,
  main = NULL,
  ...
)
```

Arguments

x	a mixturecure object resulting from curegmifs or cureem, cv_curegmifs or cv_cureem.
type	a case-sensitive parameter indicating what to plot on the y-axis. The complete list of options are: • "trace" plots the coefficient path for the fitted object (default). • "AIC" plots the AIC against step of model fit. • "mAIC" plots the modified AIC against step of model fit. • "cAIC" plots the corrected AIC against step of model fit. • "BIC", plots the BIC against step of model fit. • "mBIC" plots the modified BIC against step of model fit. • "EBIC" plots the extended BIC against step of model fit. • "logLik" plots the log-likelihood against step of model fit. This option has no effect for objects fit using cv_curegmifs or cv_cureem.
xlab	a default x-axis label will be used which can be changed by specifying a user-defined x-axis label.
ylab	a default y-axis label will be used which can be changed by specifying a user-defined y-axis label.
label	logical. If TRUE the variable names will appear in a legend. Applicable only when type = "trace". Be reminded that this works well only for small to moderate numbers of variables. For many predictors, the plot will be cluttered. The

	variables may be more easily identified using the coef function indicating the step of interest.
main	a default main title will be used which can be changed by specifying a user-defined main title. This option is not used for cv_curegmifs or cv_cureem fitted objects.
...	other arguments.

Value

this function has no returned value but is called for its side effects

See Also

[curegmifs](#), [cureem](#), [coef.mixturecure](#), [summary.mixturecure](#), [predict.mixturecure](#)

Examples

```
library(survival)
withr::local_seed(1234)
temp <- generate_cure_data(n = 100, j = 10, n_true = 10, a = 1.8)
training <- temp$training
fit <- curegmifs(Surv(Time, Censor) ~ .,
  data = training, x_latency = training,
  model = "weibull", thresh = 1e-4, maxit = 2000,
  epsilon = 0.01, verbose = FALSE
)
plot(fit)
```

predict.mixturecure	<i>Predicted probabilities for susceptibles, linear predictor for latency, and risk class for latency for mixture cure fit</i>
---------------------	--

Description

This function returns a list that includes the predicted probabilities for susceptibles as well as the linear predictor for the latency distribution and a dichotomous risk for latency for a curegmifs, cureem, cv_curegmifs or cv_cureem fitted object.

Usage

```
## S3 method for class 'mixturecure'
predict(object, newdata, model_select = "AIC", ...)
```

Arguments

object	a mixturecure object resulting from curegmifs, cureem, cv_curegmifs, or cv_cureem.
newdata	an optional data.frame that minimally includes the incidence and/or latency variables to use for predicting the response. If omitted, the training data are used.
model_select	either a case-sensitive parameter for models fit using curegmifs or cureem or any numeric step along the solution path can be selected. The default is model_select = "AIC" which calculates the predicted values using the coefficients from the model achieving the minimum AIC. The complete list of options are: • "AIC" for the minimum AIC (default). • "mAIC" for the minimum modified AIC. • "cAIC" for the minimum corrected AIC. • "BIC", for the minimum BIC. • "mBIC" for the minimum modified BIC. • "EBIC" for the minimum extended BIC. • "logLik" for the step that maximizes the log-likelihood. • n where n is any numeric value from the solution path. This option has no effect for objects fit using cv_curegmifs or cv_cureem.
...	other arguments

Value

p_uncured	a vector of probabilities from the incidence portion of the fitted model representing the P(uncured).
linear_latency	a vector for the linear predictor from the latency portion of the model.
latency_risk	a dichotomous class representing low (below the median) versus high risk for the latency portion of the model.

See Also

[curegmifs](#), [cureem](#), [coef.mixturecure](#), [summary.mixturecure](#), [plot.mixturecure](#)

Examples

```
library(survival)
withr::local_seed(1234)
temp <- generate_cure_data(n = 100, j = 10, n_true = 10, a = 1.8)
training <- temp$training
fit <- curegmifs(Surv(Time, Censor) ~ .,
  data = training, x_latency = training,
  model = "weibull", thresh = 1e-4, maxit = 2000,
  epsilon = 0.01, verbose = FALSE
)
predict_train <- predict(fit)
names(predict_train)
testing <- temp$testing
predict_test <- predict(fit, newdata = testing)
```

print.mixturecure	<i>Print the contents of a mixture cure fitted object</i>
-------------------	---

Description

This function prints the first several incidence and latency coefficients, the rate (when fitting an exponential or Weibull mixture cure model), and alpha (when fitting a Weibull mixture cure model). This function returns the fitted object invisible to the user.

Usage

```
## S3 method for class 'mixturecure'
print(x, max = 6, ...)
```

Arguments

x	a mixturecure object resulting from curegmifs, cureem, cv_cureem, or cv_curegmifs.
max	maximum number of rows in a matrix or elements in a vector to display
...	other arguments.

Value

prints coefficient estimates for the incidence portion of the model and if included, prints the coefficient estimates for the latency portion of the model. Also prints rate for exponential and Weibull models and scale (alpha) for the Weibull mixture cure model. Returns all objects fit using cureem, curegmifs, cv_cureem, or cv_curegmifs.

Note

The contents of a mixturecure fitted object differ depending upon whether the EM (cureem) or GMIFS (curegmifs) algorithm is used for model fitting or if cross-validation is used. Also, the output differs depending upon whether x_latency is specified in the model (i.e., variables are included in the latency portion of the model fit) or only terms on the right hand side of the equation are included (i.e., variables are included in the incidence portion of the model).

See Also

[curegmifs](#), [cureem](#), [coef.mixturecure](#), [summary.mixturecure](#), [plot.mixturecure](#), [predict.mixturecure](#)

Examples

```
library(survival)
withr::local_seed(1234)
temp <- generate_cure_data(n = 100, j = 10, n_true = 10, a = 1.8)
training <- temp$training
fit <- curegmifs(Surv(Time, Censor) ~ .,
  data = training, x_latency = training,
  model = "weibull", thresh = 1e-4, maxit = 2000,
```

```

    epsilon = 0.01, verbose = FALSE
  )
  print(fit)

```

sufficient_fu_test	<i>Test for sufficient follow-up</i>
--------------------	--------------------------------------

Description

Tests for sufficient follow-up using a Kaplan-Meier fitted object.

Usage

```
sufficient_fu_test(object)
```

Arguments

object a survfit object.

Value

p_value	p-value from testing the null hypothesis that there was not sufficient follow-up against the alternative that there was sufficient follow-up
n_n	total number of events that occurred at time > pmax(0, 2*(last observed event time)-(last observed time)) and < the last observed event time
N	number of observations in the dataset

References

Maller, R. A. and Zhou, X. (1996) *Survival Analysis with Long-Term Survivors*. John Wiley & Sons.

See Also

[survfit](#), [cure_estimate](#), [nonzerocure_test](#)

Examples

```

library(survival)
withr::local_seed(1234)
temp <- generate_cure_data(n = 100, j = 10, n_true = 10, a = 1.8)
training <- temp$training
km_fit <- survfit(Surv(Time, Censor) ~ 1, data = training)
sufficient_fu_test(km_fit)

```

summary.mixturecure	<i>Summarize a fitted mixture cure object</i>
---------------------	---

Description

summary method for a mixturecure object fit using curegmifs, cureem, cv_curegmifs, or cv_cureem.

Usage

```
## S3 method for class 'mixturecure'
summary(object, ...)
```

Arguments

object	a mixturecure object resulting from curegmifs, cureem, cv_curegmifs, or cv_cureem.
...	other arguments.

Value

prints the number of non-zero coefficients from the incidence and latency portions of the fitted mixture cure model when using the minimum AIC to select the final model. When fitting a model using curegmifs or cureem the summary function additionally prints results associated with the following model selection methods: the step and value that maximizes the log-likelihood; the step and value that minimizes the AIC, modified AIC (mAIC), corrected AIC (cAIC), BIC, modified BIC (mBIC), and extended BIC (EBIC). This information can be used to guide the user in the selection of a final model from the solution path.

See Also

[curegmifs](#), [cureem](#), [coef.mixturecure](#), [plot.mixturecure](#), [predict.mixturecure](#)

Examples

```
library(survival)
withr::local_seed(1234)
temp <- generate_cure_data(n = 100, j = 10, n_true = 10, a = 1.8)
training <- temp$training
fit <- curegmifs(Surv(Time, Censor) ~ .,
  data = training, x_latency = training,
  model = "weibull", thresh = 1e-4, maxit = 2000,
  epsilon = 0.01, verbose = FALSE
)
summary(fit)
```

Index

- * **datasets**
 - amltest, [2](#)
 - amltrain, [12](#)
 - pediatric_flt3, [49](#)
- * **htest**
 - nonzerocure_test, [47](#)
 - sufficient_fu_test, [59](#)
- * **methods**
 - coef.mixturecure, [22](#)
 - dim.mixturecure, [40](#)
 - family.mixturecure, [41](#)
 - formula.mixturecure, [42](#)
 - logLik.mixturecure, [45](#)
 - nobs.mixturecure, [46](#)
 - plot.mixturecure, [55](#)
 - predict.mixturecure, [56](#)
 - print.mixturecure, [58](#)
 - summary.mixturecure, [60](#)
- * **models**
 - cureem, [26](#)
 - curegmifs, [29](#)
 - cv_cureem, [32](#)
 - cv_curegmifs, [37](#)
- * **regression**
 - cureem, [26](#)
 - curegmifs, [29](#)
 - cv_cureem, [32](#)
 - cv_curegmifs, [37](#)
- * **univar**
 - auc_mcm, [21](#)
 - concordance_mcm, [24](#)
 - cure_estimate, [25](#)

amltest, [2](#)
amltrain, [12](#)
auc_mcm, [21](#), [25](#)

coef.mixturecure, [22](#), [56–58](#), [60](#)
coefficients (coef.mixturecure), [22](#)
concordance_mcm, [22](#), [24](#)

cure_estimate, [25](#), [47](#), [59](#)
cureem, [23](#), [26](#), [36](#), [56–58](#), [60](#)
curegmifs, [23](#), [29](#), [40](#), [56–58](#), [60](#)
cv_cureem, [28](#), [32](#)
cv_curegmifs, [31](#), [37](#)

dim.mixturecure, [40](#)

family.mixturecure, [41](#)
formula.mixturecure, [42](#)

generate_cure_data, [43](#)

logLik.mixturecure, [45](#)

nobs.mixturecure, [46](#)
nonzerocure_test, [25](#), [47](#), [59](#)
npar_mixturecure, [48](#)

pediatric_flt3, [49](#)
plot.mixturecure, [23](#), [55](#), [57](#), [58](#), [60](#)
predict.mixturecure, [23](#), [56](#), [56](#), [58](#), [60](#)
print.mixturecure, [58](#)

sufficient_fu_test, [25](#), [47](#), [59](#)
summary.mixturecure, [23](#), [56–58](#), [60](#)
survfit, [25](#), [47](#), [59](#)