Assignment4-Q1-mlr3

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R-Markdown Notebook for classifying the Breast-Cancer data using mlr3

Environment

First we shall load the necessary packages

Data

We shall now load the data and summarise it

```
data <- read.csv(file = "breast-cancer.csv", stringsAsFactors = TRUE)
str(data)
```

```
## 'data.frame':    569 obs. of  32 variables:
##  $ id                     : int  842302 842517 84300903 84348301 84358402 843786 844359 84458202 844981 8450100
01 ...
##  $ diagnosis              : Factor w/ 2 levels "B","M": 2 2 2 2 2 2 2 2 2 2 ...
##  $ radius_mean            : num  18 20.6 19.7 11.4 20.3 ...
##  $ texture_mean           : num  10.4 17.8 21.2 20.4 14.3 ...
##  $ perimeter_mean         : num  122.8 132.9 130 77.6 135.1 ...
##  $ area_mean              : num  1001 1326 1203 386 1297 ...
##  $ smoothness_mean        : num  0.1184 0.0847 0.1096 0.1425 0.1003 ...
##  $ compactness_mean       : num  0.2776 0.0786 0.1599 0.2839 0.1328 ...
##  $ concavity_mean         : num  0.3001 0.0869 0.1974 0.2414 0.198 ...
##  $ concave.points_mean    : num  0.1471 0.0702 0.1279 0.1052 0.1043 ...
##  $ symmetry_mean          : num  0.242 0.181 0.207 0.26 0.181 ...
##  $ fractal_dimension_mean : num  0.0787 0.0567 0.06 0.0974 0.0588 ...
##  $ radius_se              : num  1.095 0.543 0.746 0.496 0.757 ...
##  $ texture_se             : num  0.905 0.734 0.787 1.156 0.781 ...
##  $ perimeter_se           : num  8.59 3.4 4.58 3.44 5.44 ...
##  $ area_se                : num  153.4 74.1 94 27.2 94.4 ...
##  $ smoothness_se          : num  0.0064 0.00522 0.00615 0.00911 0.01149 ...
##  $ compactness_se         : num  0.049 0.0131 0.0401 0.0746 0.0246 ...
##  $ concavity_se           : num  0.0537 0.0186 0.0383 0.0566 0.0569 ...
##  $ concave.points_se      : num  0.0159 0.0134 0.0206 0.0187 0.0188 ...
##  $ symmetry_se            : num  0.03 0.0139 0.0225 0.0596 0.0176 ...
##  $ fractal_dimension_se   : num  0.00619 0.00353 0.00457 0.00921 0.00511 ...
##  $ radius_worst           : num  25.4 25 23.6 14.9 22.5 ...
##  $ texture_worst          : num  17.3 23.4 25.5 26.5 16.7 ...
##  $ perimeter_worst        : num  184.6 158.8 152.5 98.9 152.2 ...
##  $ area_worst             : num  2019 1956 1709 568 1575 ...
##  $ smoothness_worst       : num  0.162 0.124 0.144 0.21 0.137 ...
##  $ compactness_worst      : num  0.666 0.187 0.424 0.866 0.205 ...
##  $ concavity_worst        : num  0.712 0.242 0.45 0.687 0.4 ...
##  $ concave.points_worst   : num  0.265 0.186 0.243 0.258 0.163 ...
##  $ symmetry_worst         : num  0.46 0.275 0.361 0.664 0.236 ...
##  $ fractal_dimension_worst: num  0.1189 0.089 0.0876 0.173 0.0768 ...
```

```
skim(data)
```

Data summary

Name	data
Number of rows	569
Number of columns	32
_____	
Column type frequency:	
factor	1
numeric	31

_____

Group variables	None

Variable type: factor

skim_variable	n_missing	complete_rate	ordered	n_unique	top_counts
diagnosis	0	1	FALSE	2	B: 357, M: 212

Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100	hist
id	0	1	30371831.43	125020585.61	8670.00	869218.00	906024.00	8813129.00	911320502.00	
radius_mean	0	1	14.13	3.52	6.98	11.70	13.37	15.78	28.11	
texture_mean	0	1	19.29	4.30	9.71	16.17	18.84	21.80	39.28	
perimeter_mean	0	1	91.97	24.30	43.79	75.17	86.24	104.10	188.50	
area_mean	0	1	654.89	351.91	143.50	420.30	551.10	782.70	2501.00	
smoothness_mean	0	1	0.10	0.01	0.05	0.09	0.10	0.11	0.16	
compactness_mean	0	1	0.10	0.05	0.02	0.06	0.09	0.13	0.35	
concavity_mean	0	1	0.09	0.08	0.00	0.03	0.06	0.13	0.43	
concave.points_mean	0	1	0.05	0.04	0.00	0.02	0.03	0.07	0.20	
symmetry_mean	0	1	0.18	0.03	0.11	0.16	0.18	0.20	0.30	
fractal_dimension_mean	0	1	0.06	0.01	0.05	0.06	0.06	0.07	0.10	
radius_se	0	1	0.41	0.28	0.11	0.23	0.32	0.48	2.87	
texture_se	0	1	1.22	0.55	0.36	0.83	1.11	1.47	4.88	
perimeter_se	0	1	2.87	2.02	0.76	1.61	2.29	3.36	21.98	
area_se	0	1	40.34	45.49	6.80	17.85	24.53	45.19	542.20	
smoothness_se	0	1	0.01	0.00	0.00	0.01	0.01	0.01	0.03	
compactness_se	0	1	0.03	0.02	0.00	0.01	0.02	0.03	0.14	
concavity_se	0	1	0.03	0.03	0.00	0.02	0.03	0.04	0.40	
concave.points_se	0	1	0.01	0.01	0.00	0.01	0.01	0.01	0.05	
symmetry_se	0	1	0.02	0.01	0.01	0.02	0.02	0.02	0.08	
fractal_dimension_se	0	1	0.00	0.00	0.00	0.00	0.00	0.00	0.03	
radius_worst	0	1	16.27	4.83	7.93	13.01	14.97	18.79	36.04	
texture_worst	0	1	25.68	6.15	12.02	21.08	25.41	29.72	49.54	
perimeter_worst	0	1	107.26	33.60	50.41	84.11	97.66	125.40	251.20	
area_worst	0	1	880.58	569.36	185.20	515.30	686.50	1084.00	4254.00	
smoothness_worst	0	1	0.13	0.02	0.07	0.12	0.13	0.15	0.22	
compactness_worst	0	1	0.25	0.16	0.03	0.15	0.21	0.34	1.06	
concavity_worst	0	1	0.27	0.21	0.00	0.11	0.23	0.38	1.25	
concave.points_worst	0	1	0.11	0.07	0.00	0.06	0.10	0.16	0.29	
symmetry_worst	0	1	0.29	0.06	0.16	0.25	0.28	0.32	0.66	
fractal_dimension_worst	0	1	0.08	0.02	0.06	0.07	0.08	0.09	0.21	

Test/train

We need to separate test from train as early as possible. First we create a new classification task object necessary for MLR3 processes. The target is the 'diagnosis' variable, defined in the task.

```
bc_task <- TaskClassif$new(id = "breast_cancer_task", backend = data, target = "diagnosis")
bc_task
```

```
## <TaskClassif:breast_cancer_task> (569 x 32)
## * Target: diagnosis
## * Properties: twoclass
## * Features (31):
##   - dbl (30): area_mean, area_se, area_worst, compactness_mean,
##     compactness_se, compactness_worst, concave.points_mean,
##     concave.points_se, concave.points_worst, concavity_mean,
##     concavity_se, concavity_worst, fractal_dimension_mean,
##     fractal_dimension_se, fractal_dimension_worst, perimeter_mean,
##     perimeter_se, perimeter_worst, radius_mean, radius_se,
##     radius_worst, smoothness_mean, smoothness_se, smoothness_worst,
##     symmetry_mean, symmetry_se, symmetry_worst, texture_mean,
##     texture_se, texture_worst
##   - int (1): id
```

```
bc_task$nrow
```

```
## [1] 569
```

Next, splitting the data into training and testing sets using mlr3::prediction function. Specifying 70% of the task to the train set, 30% to test set.

```
set.seed(7903)

split <- mlr3::partition(bc_task, ration = 0.7) #70% goes to train, %30 goes to test
split
```

```
## $train
##   [1]   1   2   3   4   5   9  10  11  13  14  15  17  18  19  23  24  25  26
##  [19]  27  29  31  35  36  39  40  41  43  44  46  48  54  57  65  71  73  76
##  [37]  78  79  83  87  92  95  96 100 101 106 109 118 119 120 122 127 128 130
##  [55] 132 133 135 136 142 157 162 163 165 168 169 172 178 182 185 187 194 195
##  [73] 197 199 200 204 206 208 211 213 215 220 224 230 240 253 254 255 257 258
##  [91] 261 263 265 275 278 281 283 298 301 303 322 329 330 340 352 353 354 367
## [109] 369 370 371 373 374 380 390 393 394 409 415 434 436 442 445 447 450 461
## [127] 462 469 490 493 502 504 510 513 515 518 536 537 565 566 567 568  21  38
## [145]  49  51  56  59  60  61  64  67  68  69  70  72  82  85  91  93  94  97
## [163]  98  99 102 103 104 105 107 111 113 115 116 117 121 124 126 129 137 138
## [181] 140 144 145 146 149 151 156 158 160 164 174 175 176 184 186 188 189 190
## [199] 192 196 201 205 207 209 210 212 217 218 221 223 225 226 227 228 229 232
## [217] 233 235 239 243 244 247 249 250 267 268 269 271 272 274 276 279 282 285
## [235] 287 290 291 292 293 294 295 296 297 299 300 302 304 305 306 307 309 310
## [253] 311 316 317 319 321 325 326 328 332 333 334 339 341 342 346 347 348 349
## [271] 350 351 355 356 357 358 359 363 364 365 368 372 378 382 384 385 387 388
## [289] 389 391 392 395 396 398 399 402 403 404 405 406 407 408 410 411 412 414
## [307] 416 417 420 421 423 424 425 426 427 429 432 437 439 440 443 448 451 453
## [325] 454 459 460 464 465 466 470 471 474 475 478 483 486 489 491 492 494 495
## [343] 497 498 501 503 505 506 508 512 514 516 519 520 523 524 525 526 527 528
## [361] 529 530 531 532 538 539 542 543 544 546 547 548 549 551 552 553 554 556
## [379] 559 561 569
##
## $test
##   [1]   6   7   8  12  16  28  30  32  33  34  37  42  45  55  58  63  66  74
##  [19]  84  86  88 123 139 147 173 181 183 191 198 202 203 214 216 219 231 234
##  [37] 237 238 245 251 256 259 260 262 264 266 273 284 318 324 331 336 338 344
##  [55] 366 386 401 418 431 433 452 480 488 499 500 517 522 534 563 564  20  22
##  [73]  47  50  52  53  62  75  77  80  81  89  90 108 110 112 114 125 131 134
##  [91] 141 143 148 150 152 153 154 155 159 161 166 167 170 171 177 179 180 193
## [109] 222 236 241 242 246 248 252 270 277 280 286 288 289 308 312 313 314 315
## [127] 320 323 327 335 337 343 345 360 361 362 375 376 377 379 381 383 397 400
## [145] 413 419 422 428 430 435 438 441 444 446 449 455 456 457 458 463 467 468
## [163] 472 473 476 477 479 481 482 484 485 487 496 507 509 511 521 533 535 540
## [181] 541 545 550 555 557 558 560 562
```

Preprocessing

The recipe will be as follows:

- diagnosis is the target
- id is the identifier
- up-sample the minority class
- normalise the numeric predictors
- experiment with dimensional reduction to 5 components

```
#what mlr pipe operations are available?
as.data.table(mlr_pipeops)
```

```
##                              key
##   1:                       boxcox
##   2:                       branch
##   3:                        chunk
##   4:                 classbalancing
##   5:                    classifavg
##   6:                   classweights
##   7:                      colapply
##   8:                 collapsefactors
##   9:                      colroles
## 10:                         copy
## 11:                  datefeatures
## 12:                       encode
## 13:                  encodeimpact
## 14:                    encodelmer
## 15:                  featureunion
## 16:                       filter
## 17:                    fixfactors
## 18:                      histbin
## 19:                          ica
## 20:                imputeconstant
## 21:                    imputehist
## 22:                 imputelearner
## 23:                   imputemean
## 24:                 imputemedian
## 25:                   imputemode
## 26:                    imputeoor
## 27:                 imputesample
## 28:                    kernelpca
## 29:                      learner
## 30:                   learner_cv
## 31:                      missind
## 32:                  modelmatrix
## 33:            multiplicityexply
## 34:            multiplicityimply
## 35:                       mutate
## 36:                          nmf
## 37:                          nop
## 38:                     ovrsplit
## 39:                     ovrunite
## 40:                          pca
## 41:                        proxy
## 42:                   quantilebin
## 43:               randomprojection
## 44:                randomresponse
## 45:                      regravg
## 46:              removeconstants
## 47:                renamecolumns
## 48:                    replicate
## 49:                        scale
## 50:                  scalemaxabs
## 51:                   scalerange
## 52:                       select
## 53:                        smote
## 54:                   spatialsign
## 55:                    subsample
## 56:                  targetinvert
## 57:                  targetmutate
## 58: targettrafoscalerange
## 59:               textvectorizer
## 60:                    threshold
## 61:                tunethreshold
## 62:                      unbranch
## 63:                       vtreat
```

```
## 64:           yeojohnson
##                          key
##                                                                         label
##  1:                          Box-Cox Transformation of Numeric Features
##  2:                                                      Path Branching
##  3:                                      Chunk Input into Multiple Outputs
##  4:                                                      Class Balancing
##  5:                                                Majority Vote Prediction
##  6:                                      Class Weights for Sample Weighting
##  7:                                    Apply a Function to each Column of a Task
##  8:                                                        Collapse Factors
##  9:                                              Change Column Roles of a Task
## 10:                                                Copy Input Multiple Times
## 11:                                                    Preprocess Date Features
## 12:                                                            Factor Encoding
## 13:                                    Conditional Target Value Impact Encoding
## 14:                                    Impact Encoding with Random Intercept Models
## 15:                                      Aggregate Features from Multiple Inputs
## 16:                                                          Feature Filtering
## 17:                                                          Fix Factor Levels
## 18:                          Split Numeric Features into Equally Spaced Bins
## 19:                                          Independent Component Analysis
## 20:                                              Impute Features by a Constant
## 21:                                      Impute Numerical Features by Histogram
## 22:                                      Impute Features by Fitting a Learner
## 23:                                      Impute Numerical Features by their Mean
## 24:                                    Impute Numerical Features by their Median
## 25:                                          Impute Features by their Mode
## 26:                                                      Out of Range Imputation
## 27:                                              Impute Features by Sampling
## 28:                                        Kernelized Principle Component Analysis
## 29:                                              Wrap a Learner into a PipeOp
## 30: Wrap a Learner into a PipeOp with Cross-validated Predictions as Features
## 31:                                              Add Missing Indicator Columns
## 32:                          Transform Columns by Constructing a Model Matrix
## 33:                                                    Explicate a Multiplicity
## 34:                                                    Implicate a Multiplicity
## 35:                                              Add Features According to Expressions
## 36:                                              Non-negative Matrix Factorization
## 37:                                                    Simply Push Input Forward
## 38:                          Split a Classification Task into Binary Classification Tasks
## 39:                                            Unite Binary Classification Tasks
## 40:                                                Principle Component Analysis
## 41:                              Wrap another PipeOp or Graph as a Hyperparameter
## 42:                                    Split Numeric Features into Quantile Bins
## 43:                          Project Numeric Features onto a Randomly Sampled Subspace
## 44:                                      Generate a Randomized Response Prediction
## 45:                                              Weighted Prediction Averaging
## 46:                                                Remove Constant Features
## 47:                                                            Rename Columns
## 48:                                          Replicate the Input as a Multiplicity
## 49:                                          Center and Scale Numeric Features
## 50:             Scale Numeric Features with Respect to their Maximum Absolute Value
## 51:                  Linearly Transform Numeric Features to Match Given Boundaries
## 52:                                    Remove Features Depending on a Selector
## 53:                                                            SMOTE Balancing
## 54:                                                Normalize Data Row-wise
## 55:                                                                Subsampling
## 56:                                              Invert Target Transformations
## 57:                                              Transform a Target by a Function
## 58:                  Linearly Transform a Numeric Target to Match Given Boundaries
## 59:                                  Bag-of-word Representation of Character Features
## 60:                          Change the Threshold of a Classification Prediction
## 61:                            Tune the Threshold of a Classification Prediction
## 62:                                                    Unbranch Different Paths
## 63:                                              Interface to the vtreat Package
## 64:                          Yeo-Johnson Transformation of Numeric Features
##                                                                         label
##                      packages                               tags
##  1:      mlr3pipelines,bestNormalize              data transform
##  2:              mlr3pipelines                                meta
##  3:              mlr3pipelines                                meta
##  4:              mlr3pipelines      imbalanced data,data transform
##  5:          mlr3pipelines,stats                          ensemble
##  6:              mlr3pipelines      imbalanced data,data transform
```

```
##  7:                   mlr3pipelines                            data transform
##  8:                   mlr3pipelines                            data transform
##  9:                   mlr3pipelines                            data transform
## 10:                   mlr3pipelines                                      meta
## 11:                   mlr3pipelines                            data transform
## 12:             mlr3pipelines,stats              encode,data transform
## 13:                   mlr3pipelines              encode,data transform
## 14:       mlr3pipelines,lme4,nloptr              encode,data transform
## 15:                   mlr3pipelines                                  ensemble
## 16:                   mlr3pipelines feature selection,data transform
## 17:                   mlr3pipelines            robustify,data transform
## 18:          mlr3pipelines,graphics                            data transform
## 19:           mlr3pipelines,fastICA                            data transform
## 20:                   mlr3pipelines                                  missings
## 21:          mlr3pipelines,graphics                                  missings
## 22:                   mlr3pipelines                                  missings
## 23:                   mlr3pipelines                                  missings
## 24:             mlr3pipelines,stats                                  missings
## 25:                   mlr3pipelines                                  missings
## 26:                   mlr3pipelines                                  missings
## 27:                   mlr3pipelines                                  missings
## 28:           mlr3pipelines,kernlab                            data transform
## 29:                   mlr3pipelines                                   learner
## 30:                   mlr3pipelines  learner,ensemble,data transform
## 31:                   mlr3pipelines            missings,data transform
## 32:             mlr3pipelines,stats                            data transform
## 33:                   mlr3pipelines                              multiplicity
## 34:                   mlr3pipelines                              multiplicity
## 35:                   mlr3pipelines                            data transform
## 36:           mlr3pipelines,MASS,NMF                            data transform
## 37:                   mlr3pipelines                                      meta
## 38:                   mlr3pipelines    target transform,multiplicity
## 39:                   mlr3pipelines            multiplicity,ensemble
## 40:                   mlr3pipelines                            data transform
## 41:                   mlr3pipelines                                      meta
## 42:             mlr3pipelines,stats                            data transform
## 43:                   mlr3pipelines                            data transform
## 44:                   mlr3pipelines                                  abstract
## 45:                   mlr3pipelines                                  ensemble
## 46:                   mlr3pipelines            robustify,data transform
## 47:                   mlr3pipelines                            data transform
## 48:                   mlr3pipelines                              multiplicity
## 49:                   mlr3pipelines                            data transform
## 50:                   mlr3pipelines                            data transform
## 51:                   mlr3pipelines                            data transform
## 52:                   mlr3pipelines feature selection,data transform
## 53:       mlr3pipelines,smotefamily  imbalanced data,data transform
## 54:                   mlr3pipelines                            data transform
## 55:                   mlr3pipelines                            data transform
## 56:                   mlr3pipelines                                  abstract
## 57:                   mlr3pipelines                          target transform
## 58:                   mlr3pipelines                          target transform
## 59: mlr3pipelines,quanteda,stopwords                            data transform
## 60:                   mlr3pipelines                          target transform
## 61:             mlr3pipelines,bbotk                          target transform
## 62:                   mlr3pipelines                                      meta
## 63:            mlr3pipelines,vtreat  encode,missings,data transform
## 64:       mlr3pipelines,bestNormalize                            data transform
##                         packages                                      tags
##                                   feature_types input.num output.num
##  1:                     numeric,integer          1          1
##  2:                                  NA          1         NA
##  3:                                  NA          1         NA
##  4: logical,integer,numeric,character,factor,ordered,...         1          1
##  5:                                  NA         NA          1
##  6: logical,integer,numeric,character,factor,ordered,...         1          1
##  7: logical,integer,numeric,character,factor,ordered,...         1          1
##  8:                        factor,ordered          1          1
##  9: logical,integer,numeric,character,factor,ordered,...         1          1
## 10:                                  NA          1         NA
## 11:                             POSIXct          1          1
## 12:                        factor,ordered          1          1
## 13:                        factor,ordered          1          1
## 14:                        factor,ordered          1          1
## 15:                                  NA         NA          1
```

```
## 16: logical,integer,numeric,character,factor,ordered,...          1          1
## 17:                                        factor,ordered          1          1
## 18:                                       numeric,integer          1          1
## 19:                                       numeric,integer          1          1
## 20: logical,integer,numeric,character,factor,ordered,...          1          1
## 21:                                       integer,numeric          1          1
## 22:                                 logical,factor,ordered          1          1
## 23:                                       numeric,integer          1          1
## 24:                                       numeric,integer          1          1
## 25:             factor,integer,logical,numeric,ordered          1          1
## 26:           character,factor,integer,numeric,ordered          1          1
## 27:             factor,integer,logical,numeric,ordered          1          1
## 28:                                       numeric,integer          1          1
## 29:                                                    NA          1          1
## 30: logical,integer,numeric,character,factor,ordered,...          1          1
## 31: logical,integer,numeric,character,factor,ordered,...          1          1
## 32: logical,integer,numeric,character,factor,ordered,...          1          1
## 33:                                                    NA          1         NA
## 34:                                                    NA         NA          1
## 35: logical,integer,numeric,character,factor,ordered,...          1          1
## 36:                                       numeric,integer          1          1
## 37:                                                    NA          1          1
## 38:                                                    NA          1          1
## 39:                                                    NA          1          1
## 40:                                       numeric,integer          1          1
## 41:                                                    NA         NA          1
## 42:                                       numeric,integer          1          1
## 43:                                       numeric,integer          1          1
## 44:                                                    NA          1          1
## 45:                                                    NA         NA          1
## 46: logical,integer,numeric,character,factor,ordered,...          1          1
## 47: logical,integer,numeric,character,factor,ordered,...          1          1
## 48:                                                    NA          1          1
## 49:                                       numeric,integer          1          1
## 50:                                       numeric,integer          1          1
## 51:                                       numeric,integer          1          1
## 52: logical,integer,numeric,character,factor,ordered,...          1          1
## 53: logical,integer,numeric,character,factor,ordered,...          1          1
## 54:                                       numeric,integer          1          1
## 55: logical,integer,numeric,character,factor,ordered,...          1          1
## 56:                                                    NA          2          1
## 57:                                                    NA          1          2
## 58:                                                    NA          1          2
## 59:                                             character          1          1
## 60:                                                    NA          1          1
## 61:                                                    NA          1          1
## 62:                                                    NA         NA          1
## 63: logical,integer,numeric,character,factor,ordered,...          1          1
## 64:                                       numeric,integer          1          1
##                                            feature_types input.num output.num
##     input.type.train  input.type.predict output.type.train output.type.predict
##  1:             Task                Task              Task                Task
##  2:                *                   *                 *                   *
##  3:             Task                Task              Task                Task
##  4:       TaskClassif         TaskClassif       TaskClassif         TaskClassif
##  5:             NULL   PredictionClassif              NULL   PredictionClassif
##  6:       TaskClassif         TaskClassif       TaskClassif         TaskClassif
##  7:             Task                Task              Task                Task
##  8:             Task                Task              Task                Task
##  9:             Task                Task              Task                Task
## 10:                *                   *                 *                   *
## 11:             Task                Task              Task                Task
## 12:             Task                Task              Task                Task
## 13:             Task                Task              Task                Task
## 14:             Task                Task              Task                Task
## 15:             Task                Task              Task                Task
## 16:             Task                Task              Task                Task
## 17:             Task                Task              Task                Task
## 18:             Task                Task              Task                Task
## 19:             Task                Task              Task                Task
## 20:             Task                Task              Task                Task
## 21:             Task                Task              Task                Task
## 22:             Task                Task              Task                Task
## 23:             Task                Task              Task                Task
## 24:             Task                Task              Task                Task
```

```
## 25:            Task             Task             Task             Task
## 26:            Task             Task             Task             Task
## 27:            Task             Task             Task             Task
## 28:            Task             Task             Task             Task
## 29:       TaskClassif       TaskClassif             NULL    PredictionClassif
## 30:       TaskClassif       TaskClassif       TaskClassif       TaskClassif
## 31:            Task             Task             Task             Task
## 32:            Task             Task             Task             Task
## 33:             [*]              [*]                *                *
## 34:               *                *              [*]              [*]
## 35:            Task             Task             Task             Task
## 36:            Task             Task             Task             Task
## 37:               *                *                *                *
## 38:       TaskClassif       TaskClassif     [TaskClassif]     [TaskClassif]
## 39:          [NULL] [PredictionClassif]           NULL    PredictionClassif
## 40:            Task             Task             Task             Task
## 41:               *                *                *                *
## 42:            Task             Task             Task             Task
## 43:            Task             Task             Task             Task
## 44:            NULL       Prediction             NULL       Prediction
## 45:            NULL    PredictionRegr             NULL    PredictionRegr
## 46:            Task             Task             Task             Task
## 47:            Task             Task             Task             Task
## 48:               *                *              [*]              [*]
## 49:            Task             Task             Task             Task
## 50:            Task             Task             Task             Task
## 51:            Task             Task             Task             Task
## 52:            Task             Task             Task             Task
## 53:            Task             Task             Task             Task
## 54:            Task             Task             Task             Task
## 55:            Task             Task             Task             Task
## 56:       NULL,NULL function,Prediction           NULL       Prediction
## 57:            Task             Task        NULL,Task    function,Task
## 58:        TaskRegr         TaskRegr    NULL,TaskRegr    function,TaskRegr
## 59:            Task             Task             Task             Task
## 60:            NULL PredictionClassif             NULL    PredictionClassif
## 61:            Task             Task             NULL       Prediction
## 62:               *                *                *                *
## 63:            Task             Task             Task             Task
## 64:            Task             Task             Task             Task
##      input.type.train  input.type.predict output.type.train output.type.predict
```

```r
# Define the SVM learner with a radial kernel
learner <- lrn("classif.svm", kernel = "radial")
```

The "step_umap() creates a specification of a recipe step that will project a set of features into a smaller space." While this is not available in mlr3, the PCA (principal component analysis) po is also able to reduce the dimensionality of a dataset while retaining most of its original information.

Next, creating a pipeline with Smote, Scaling, PCA, and assigning ID as a name variable (in place of 'id' variable).

```r
# Create a pipeline
smote <- PipeOpSmote$new(id="Smote", param_vals = list(dup_size=1))
scale <- PipeOpScale$new(id = "Normalise", param_vals = list()) #full syntax
pca <- po("pca") #abbreviated syntax
col_role <- po("colroles", param_vals = list(new_role = list(id = "name"))) ### id not work

# Define the SVM learner with probability estimates
learner_po <- po("learner", learner = lrn("classif.svm", kernel = "radial", predict_type = "prob"))

#pipeline
graph <- col_role %>>%
  smote %>>%
  scale %>>%
  pca %>>%
  learner_po

graph$plot() #visualising the pipeline
```

```
        ┌─────────────┐
        │  <INPUT>    │
        └─────────────┘
               ▼
        ┌─────────────┐
        │  colroles   │
        └─────────────┘
               ▼
        ┌─────────────┐
        │   Smote     │
        └─────────────┘
               ▼
        ┌─────────────┐
        │  Normalise  │
        └─────────────┘
               ▼
        ┌─────────────┐
        │    pca      │
        └─────────────┘
               ▼
        ┌─────────────┐
        │ classif.svm │
        └─────────────┘
               ▼
        ┌─────────────┐
        │  <OUTPUT>   │
        └─────────────┘
```
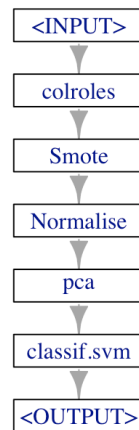
```
glrn <- GraphLearner$new(graph) #creating a new graphlearner object
```

```
#print the parameters available to tune

print(glrn$param_set$ids())
```

```
##  [1] "colroles.new_role"        "Smote.K"
##  [3] "Smote.dup_size"           "Normalise.center"
##  [5] "Normalise.scale"          "Normalise.robust"
##  [7] "Normalise.affect_columns" "pca.center"
##  [9] "pca.scale."               "pca.rank."
## [11] "pca.affect_columns"       "classif.svm.cachesize"
## [13] "classif.svm.class.weights" "classif.svm.coef0"
## [15] "classif.svm.cost"         "classif.svm.cross"
## [17] "classif.svm.decision.values" "classif.svm.degree"
## [19] "classif.svm.epsilon"      "classif.svm.fitted"
## [21] "classif.svm.gamma"        "classif.svm.kernel"
## [23] "classif.svm.nu"           "classif.svm.scale"
## [25] "classif.svm.shrinking"    "classif.svm.tolerance"
## [27] "classif.svm.type"
```

From the above parameters available to tune, we can tune the scaling/centering ability (mean/sd) and robust scaling (median). PCA rank will also be used to tune the model.

Modeling (SVM)

First, setting up the tuning space. Using mlr3tuning::AutoTuner, we can specify which method of tuning to use, the learner object, how many times to resample and through what method, when to stop searching for a model, how to measure model success, and the hyperparameter search space.

I will explore PCA between 5 and 15, thus trying all instances of 5, 10 and 15 principal components in training the model in one go.

```
as.data.table(mlr_measures) #show all available measures. Wanting ROC/AUC
```

```
##               key                              label
## 1:            aic                Akaike Information Criterion
## 2:            bic              Bayesian Information Criterion
## 3:    classif.acc                     Classification Accuracy
## 4:    classif.auc                    Area Under the ROC Curve
## 5:   classif.bacc                          Balanced Accuracy
## 6: classif.bbrier                          Binary Brier Score
## 7:     classif.ce                        Classification Error
## 8:  classif.costs            Cost-sensitive Classification
## 9:    classif.dor                        Diagnostic Odds Ratio
```

```
## 10:      classif.fbeta                                      F-beta score
## 11:        classif.fdr                              False Discovery Rate
## 12:         classif.fn                                   False Negatives
## 13:        classif.fnr                               False Negative Rate
## 14:       classif.fomr                               False Omission Rate
## 15:         classif.fp                                   False Positives
## 16:        classif.fpr                               False Positive Rate
## 17:    classif.logloss                                          Log Loss
## 18:  classif.mauc_au1p       Weighted average 1 vs. 1 multiclass AUC
## 19:  classif.mauc_au1u                Average 1 vs. 1 multiclass AUC
## 20:  classif.mauc_aunp    Weighted average 1 vs. rest multiclass AUC
## 21:  classif.mauc_aunu             Average 1 vs. rest multiclass AUC
## 22:     classif.mbrier                            Multiclass Brier Score
## 23:        classif.mcc            Matthews Correlation Coefficient
## 24:        classif.npv                   Negative Predictive Value
## 25:        classif.ppv                   Positive Predictive Value
## 26:      classif.prauc                      Precision-Recall Curve
## 27:  classif.precision                                       Precision
## 28:     classif.recall                                          Recall
## 29: classif.sensitivity                                     Sensitivity
## 30: classif.specificity                                     Specificity
## 31:         classif.tn                                   True Negatives
## 32:        classif.tnr                               True Negative Rate
## 33:         classif.tp                                   True Positives
## 34:        classif.tpr                               True Positive Rate
## 35:      debug_classif                     Debug Classification Measure
## 36:          oob_error                             Out-of-bag Error
## 37:          regr.bias                                            Bias
## 38:          regr.ktau                                  Kendall's tau
## 39:           regr.mae                         Mean Absolute Error
## 40:          regr.mape                 Mean Absolute Percent Error
## 41:         regr.maxae                             Max Absolute Error
## 42:         regr.medae                         Median Absolute Error
## 43:         regr.medse                          Median Squared Error
## 44:           regr.mse                             Mean Squared Error
## 45:          regr.msle                         Mean Squared Log Error
## 46:         regr.pbias                                    Percent Bias
## 47:           regr.rae                        Relative Absolute Error
## 48:          regr.rmse                        Root Mean Squared Error
## 49:         regr.rmsle                    Root Mean Squared Log Error
## 50:          regr.rrse                    Root Relative Squared Error
## 51:           regr.rse                         Relative Squared Error
## 52:           regr.rsq                                       R Squared
## 53:           regr.sae                        Sum of Absolute Errors
## 54:         regr.smape        Symmetric Mean Absolute Percent Error
## 55:          regr.srho                                  Spearman's rho
## 56:           regr.sse                         Sum of Squared Errors
## 57:  selected_features Absolute or Relative Frequency of Selected Features
## 58:        sim.jaccard                      Jaccard Similarity Index
## 59:            sim.phi                    Phi Coefficient Similarity
## 60:          time_both                                    Elapsed Time
## 61:       time_predict                                    Elapsed Time
## 62:         time_train                                    Elapsed Time
##               key                                                   label
##       task_type           packages predict_type task_properties
##  1:      <NA>              mlr3          <NA>
##  2:      <NA>              mlr3          <NA>
##  3:   classif mlr3,mlr3measures      response
##  4:   classif mlr3,mlr3measures          prob        twoclass
##  5:   classif mlr3,mlr3measures      response
##  6:   classif mlr3,mlr3measures          prob        twoclass
##  7:   classif mlr3,mlr3measures      response
##  8:   classif              mlr3      response
##  9:   classif mlr3,mlr3measures      response        twoclass
## 10:   classif mlr3,mlr3measures      response        twoclass
## 11:   classif mlr3,mlr3measures      response        twoclass
## 12:   classif mlr3,mlr3measures      response        twoclass
## 13:   classif mlr3,mlr3measures      response        twoclass
## 14:   classif mlr3,mlr3measures      response        twoclass
## 15:   classif mlr3,mlr3measures      response        twoclass
## 16:   classif mlr3,mlr3measures      response        twoclass
## 17:   classif mlr3,mlr3measures          prob
## 18:   classif mlr3,mlr3measures          prob
## 19:   classif mlr3,mlr3measures          prob
## 20:   classif mlr3,mlr3measures          prob
```

```
## 21:    classif mlr3,mlr3measures         prob
## 22:    classif mlr3,mlr3measures         prob
## 23:    classif mlr3,mlr3measures     response       twoclass
## 24:    classif mlr3,mlr3measures     response       twoclass
## 25:    classif mlr3,mlr3measures     response       twoclass
## 26:    classif mlr3,mlr3measures         prob       twoclass
## 27:    classif mlr3,mlr3measures     response       twoclass
## 28:    classif mlr3,mlr3measures     response       twoclass
## 29:    classif mlr3,mlr3measures     response       twoclass
## 30:    classif mlr3,mlr3measures     response       twoclass
## 31:    classif mlr3,mlr3measures     response       twoclass
## 32:    classif mlr3,mlr3measures     response       twoclass
## 33:    classif mlr3,mlr3measures     response       twoclass
## 34:    classif mlr3,mlr3measures     response       twoclass
## 35:      <NA>            mlr3     response
## 36:      <NA>            mlr3         <NA>
## 37:      regr mlr3,mlr3measures     response
## 38:      regr mlr3,mlr3measures     response
## 39:      regr mlr3,mlr3measures     response
## 40:      regr mlr3,mlr3measures     response
## 41:      regr mlr3,mlr3measures     response
## 42:      regr mlr3,mlr3measures     response
## 43:      regr mlr3,mlr3measures     response
## 44:      regr mlr3,mlr3measures     response
## 45:      regr mlr3,mlr3measures     response
## 46:      regr mlr3,mlr3measures     response
## 47:      regr mlr3,mlr3measures     response
## 48:      regr mlr3,mlr3measures     response
## 49:      regr mlr3,mlr3measures     response
## 50:      regr mlr3,mlr3measures     response
## 51:      regr mlr3,mlr3measures     response
## 52:      regr mlr3,mlr3measures     response
## 53:      regr mlr3,mlr3measures     response
## 54:      regr mlr3,mlr3measures     response
## 55:      regr mlr3,mlr3measures     response
## 56:      regr mlr3,mlr3measures     response
## 57:      <NA>            mlr3         <NA>
## 58:      <NA> mlr3,mlr3measures         <NA>
## 59:      <NA> mlr3,mlr3measures         <NA>
## 60:      <NA>            mlr3         <NA>
## 61:      <NA>            mlr3         <NA>
## 62:      <NA>            mlr3         <NA>
##     task_type         packages predict_type task_properties
```

```
#set what we are measuring our model on - model assessment
measure = msr("classif.auc") #"classif.auc" refers to the Area Under the Receiver Operating Characteristic (ROC)
Curve (AUC) as a classification measure.

#search space - what parameters are allowed to be tuned
search_space = ps(
  Normalise.scale = p_lgl(),
  Normalise.robust = p_lgl(),
  Normalise.center = p_lgl(),
  pca.rank. = p_int(lower=5,upper=15)) #exploring the number of principal components within this range (b/w 5 and
15).

# Train the learner on the training Task
tune <- mlr3tuning::AutoTuner$new(tuner = tnr("grid_search", resolution = 5), #tuner - which method - gridsearch,
gaussian, random search. Lots of options. Here, will use grid search.
                  learner = glrn, #learner is glrn as defined previously
                  resampling = rsmp("cv", folds = 10), #10 fold cross vailidation
                  terminator = trm("evals", n_evals = 50), #terminate - when to stop. eg after 50 models
                  measure = measure,
                  search_space = search_space
                  )
```

Now, using the tune object, we can train our model using the split$train as our identifiers of our training data within the bc_task data.

```
trained_model_1 = tune$train(task = bc_task, row_ids = split$train)
```

```
## INFO  [21:04:17.204] [bbotk] Starting to optimize 4 parameter(s) with '<TunerGridSearch>' and '<TerminatorEval
s> [n_evals=50, k=0]'
## INFO  [21:04:17.227] [bbotk] Evaluating 1 configuration(s)
```

```
## INFO  [21:04:17.307] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:04:17.334] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:04:17.746] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:04:17.987] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:04:18.217] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:04:18.454] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:04:18.689] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:04:18.927] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:04:19.340] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:04:19.577] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:04:19.819] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:04:20.055] [mlr3] Finished benchmark
## INFO  [21:04:20.085] [bbotk] Result of batch 1:
## INFO  [21:04:20.087] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:04:20.087] [bbotk]            FALSE            FALSE            FALSE         13   0.9854092
## INFO  [21:04:20.087] [bbotk]  warnings errors runtime_learners                              uhash
## INFO  [21:04:20.087] [bbotk]         0      0            2.64 88f86a9d-747b-4aa0-aa68-ae3efbd8774a
## INFO  [21:04:20.087] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:04:20.120] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:04:20.124] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:04:20.357] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:04:20.642] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:04:20.885] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:04:21.407] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:04:21.694] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:04:21.932] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:04:22.175] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:04:22.418] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:04:22.654] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:04:22.889] [mlr3] Finished benchmark
## INFO  [21:04:22.918] [bbotk] Result of batch 2:
## INFO  [21:04:22.919] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:04:22.919] [bbotk]            FALSE            FALSE            FALSE         10   0.9881509
## INFO  [21:04:22.919] [bbotk]  warnings errors runtime_learners                              uhash
## INFO  [21:04:22.919] [bbotk]         0      0           2.676 188db308-c991-4b87-a5c0-60e173d30ff0
## INFO  [21:04:22.920] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:04:22.953] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:04:22.957] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:04:23.193] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:04:23.429] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:04:23.666] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:04:23.903] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:04:24.146] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:04:24.441] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:04:24.690] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:04:24.933] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
```

```
## INFO  [21:04:25.200] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:04:25.444] [mlr3] Finished benchmark
## INFO  [21:04:25.473] [bbotk] Result of batch 3:
## INFO  [21:04:25.474] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:04:25.474] [bbotk]             TRUE             TRUE            FALSE         15   0.9906982
## INFO  [21:04:25.474] [bbotk]  warnings errors runtime_learners                                uhash
## INFO  [21:04:25.474] [bbotk]         0      0            2.406 e4c8e1a3-b39e-43e6-ace8-661f912f2ecf
## INFO  [21:04:25.475] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:04:25.506] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:04:25.511] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:04:25.754] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:04:25.992] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:04:26.231] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:04:26.471] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:04:26.710] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:04:26.950] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:04:27.208] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:04:27.456] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:04:27.696] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:04:27.939] [mlr3] Finished benchmark
## INFO  [21:04:27.968] [bbotk] Result of batch 4:
## INFO  [21:04:27.969] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:04:27.969] [bbotk]             TRUE             TRUE             TRUE         13    0.991635
## INFO  [21:04:27.969] [bbotk]  warnings errors runtime_learners                                uhash
## INFO  [21:04:27.969] [bbotk]         0      0            2.348 54e4f764-1310-440e-af97-fa5a702695ab
## INFO  [21:04:27.970] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:04:28.012] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:04:28.016] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:04:28.249] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:04:28.487] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:04:28.728] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:04:29.039] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:04:29.284] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:04:29.525] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:04:29.765] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:04:30.008] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:04:30.248] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:04:30.487] [mlr3] Finished benchmark
## INFO  [21:04:30.516] [bbotk] Result of batch 5:
## INFO  [21:04:30.517] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:04:30.517] [bbotk]             TRUE            FALSE            FALSE         13   0.9923426
## INFO  [21:04:30.517] [bbotk]  warnings errors runtime_learners                                uhash
## INFO  [21:04:30.517] [bbotk]         0      0            2.393 14b4c7f5-5975-427e-affd-4d71e7bfbecf
## INFO  [21:04:30.518] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:04:30.551] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:04:30.555] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:04:30.799] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:04:31.035] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:04:31.274] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:04:31.514] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
```

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_task' (iter 5/10)
## INFO  [21:04:31.758] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:04:32.013] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:04:32.257] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:04:32.498] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:04:32.748] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:04:32.988] [mlr3] Finished benchmark
## INFO  [21:04:33.055] [bbotk] Result of batch 6:
## INFO  [21:04:33.056] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:04:33.056] [bbotk]             TRUE             TRUE            FALSE         13    0.9915734
## INFO  [21:04:33.056] [bbotk]  warnings errors runtime_learners                                   uhash
## INFO  [21:04:33.056] [bbotk]         0      0            2.347 570c978f-2f50-4d67-8104-b113b2d88132
## INFO  [21:04:33.057] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:04:33.090] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:04:33.094] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:04:33.343] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:04:33.584] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:04:33.826] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:04:34.070] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:04:34.316] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:04:34.560] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:04:34.805] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:04:35.049] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:04:35.294] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:04:35.538] [mlr3] Finished benchmark
## INFO  [21:04:35.578] [bbotk] Result of batch 7:
## INFO  [21:04:35.580] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:04:35.580] [bbotk]             TRUE            FALSE             TRUE         13    0.9916821
## INFO  [21:04:35.580] [bbotk]  warnings errors runtime_learners                                   uhash
## INFO  [21:04:35.580] [bbotk]         0      0            2.364 137ef918-5fad-421c-b032-bacc4fcedc9d
## INFO  [21:04:35.580] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:04:35.613] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:04:35.617] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:04:35.856] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:04:36.097] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:04:36.337] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:04:36.595] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:04:36.842] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:04:37.094] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:04:37.557] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:04:37.795] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:04:38.034] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:04:38.270] [mlr3] Finished benchmark
## INFO  [21:04:38.298] [bbotk] Result of batch 8:
## INFO  [21:04:38.299] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:04:38.299] [bbotk]             TRUE            FALSE            FALSE         15    0.9887853
## INFO  [21:04:38.299] [bbotk]  warnings errors runtime_learners                                   uhash
## INFO  [21:04:38.299] [bbotk]         0      0            2.577 d0f0e932-6ac5-438b-b44a-836ff93753df
## INFO  [21:04:38.300] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:04:38.332] [mlr3] Running benchmark with 10 resampling iterations
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## INFO  [21:04:38.336] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:04:38.557] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:04:38.780] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:04:38.999] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:04:39.229] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:04:39.446] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:04:39.669] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:04:39.893] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:04:40.111] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:04:40.338] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:04:40.562] [mlr3] Finished benchmark
## INFO  [21:04:40.591] [bbotk] Result of batch 9:
## INFO  [21:04:40.592] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:04:40.592] [bbotk]             TRUE             TRUE             TRUE         5    0.9885513
## INFO  [21:04:40.592] [bbotk]  warnings errors runtime_learners                                 uhash
## INFO  [21:04:40.592] [bbotk]         0      0            2.149 a4fed183-2b2e-4ae3-a0dd-cccd83ede963
## INFO  [21:04:40.593] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:04:40.625] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:04:40.629] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:04:40.851] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:04:41.068] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:04:41.289] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:04:41.514] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:04:41.740] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:04:41.959] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:04:42.184] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:04:42.410] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:04:42.638] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:04:42.863] [mlr3] Finished benchmark
## INFO  [21:04:42.892] [bbotk] Result of batch 10:
## INFO  [21:04:42.893] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:04:42.893] [bbotk]            FALSE             TRUE             TRUE         7    0.9875177
## INFO  [21:04:42.893] [bbotk]  warnings errors runtime_learners                                 uhash
## INFO  [21:04:42.893] [bbotk]         0      0            2.158 3e591aeb-e6b4-4e4e-91de-a5274569e64b
## INFO  [21:04:42.894] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:04:42.925] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:04:42.929] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:04:43.159] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:04:43.385] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:04:43.617] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:04:43.853] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:04:44.088] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:04:44.323] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:04:44.559] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:04:44.794] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:04:45.021] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
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_task' (iter 10/10)
## INFO  [21:04:45.259] [mlr3] Finished benchmark
## INFO  [21:04:45.289] [bbotk] Result of batch 11:
## INFO  [21:04:45.362] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:04:45.362] [bbotk]            FALSE            FALSE             TRUE        13   0.9852663
## INFO  [21:04:45.362] [bbotk]  warnings errors runtime_learners                                  uhash
## INFO  [21:04:45.362] [bbotk]         0      0           2.251 c491b99c-03a1-40e6-83e9-5ccf35b3e1c8
## INFO  [21:04:45.364] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:04:45.400] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:04:45.405] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:04:45.642] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:04:45.888] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:04:46.127] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:04:46.367] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:04:46.612] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:04:46.855] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:04:47.098] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:04:47.333] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:04:47.575] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:04:47.817] [mlr3] Finished benchmark
## INFO  [21:04:47.846] [bbotk] Result of batch 12:
## INFO  [21:04:47.847] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:04:47.847] [bbotk]             TRUE            FALSE             TRUE        15   0.9920768
## INFO  [21:04:47.847] [bbotk]  warnings errors runtime_learners                                  uhash
## INFO  [21:04:47.847] [bbotk]         0      0           2.333 85de1c8e-a0d7-49c3-9fb2-0079d2417d0e
## INFO  [21:04:47.848] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:04:47.881] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:04:47.885] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:04:48.107] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:04:48.331] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:04:48.546] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:04:48.771] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:04:48.994] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:04:49.219] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:04:49.443] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:04:49.659] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:04:49.882] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:04:50.105] [mlr3] Finished benchmark
## INFO  [21:04:50.133] [bbotk] Result of batch 13:
## INFO  [21:04:50.135] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:04:50.135] [bbotk]            FALSE            FALSE             TRUE         5   0.9890084
## INFO  [21:04:50.135] [bbotk]  warnings errors runtime_learners                                  uhash
## INFO  [21:04:50.135] [bbotk]         0      0           2.141 dc9bb8b8-1815-4e47-bab0-de8a305c06c9
## INFO  [21:04:50.136] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:04:50.168] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:04:50.172] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:04:50.408] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:04:50.644] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:04:50.878] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:04:51.117] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
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## INFO  [21:04:51.356] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:04:51.623] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:04:51.854] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:04:52.098] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:04:52.339] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:04:52.582] [mlr3] Finished benchmark
## INFO  [21:04:52.611] [bbotk] Result of batch 14:
## INFO  [21:04:52.612] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:04:52.612] [bbotk]            FALSE             TRUE            FALSE         15   0.9907065
## INFO  [21:04:52.612] [bbotk]  warnings errors runtime_learners                                 uhash
## INFO  [21:04:52.612] [bbotk]         0      0            2.335 b0b80da8-8416-4e71-8757-062a87a6a527
## INFO  [21:04:52.613] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:04:52.645] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:04:52.649] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:04:52.880] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:04:53.102] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:04:53.334] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:04:53.572] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:04:53.809] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:04:54.035] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:04:54.272] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:04:54.508] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:04:54.745] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:04:54.981] [mlr3] Finished benchmark
## INFO  [21:04:55.010] [bbotk] Result of batch 15:
## INFO  [21:04:55.011] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:04:55.011] [bbotk]            FALSE             TRUE             TRUE         10   0.9881615
## INFO  [21:04:55.011] [bbotk]  warnings errors runtime_learners                                 uhash
## INFO  [21:04:55.011] [bbotk]         0      0            2.257 fc3d9289-318b-4d94-82c3-7243156b8e4b
## INFO  [21:04:55.012] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:04:55.044] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:04:55.048] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:04:55.284] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:04:55.517] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:04:55.745] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:04:55.986] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:04:56.226] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:04:56.469] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:04:56.709] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:04:56.951] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:04:57.191] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:04:57.431] [mlr3] Finished benchmark
## INFO  [21:04:57.460] [bbotk] Result of batch 16:
## INFO  [21:04:57.461] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:04:57.461] [bbotk]            FALSE             TRUE            FALSE         13   0.9870674
## INFO  [21:04:57.461] [bbotk]  warnings errors runtime_learners                                 uhash
## INFO  [21:04:57.461] [bbotk]         0      0            2.304 e23f5405-df24-4243-a277-8913acce5564
## INFO  [21:04:57.462] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:04:57.494] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:04:57.498] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
```

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                   _task' (iter 1/10)
## INFO  [21:04:57.778] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:04:58.018] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:04:58.239] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:04:58.478] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:04:58.717] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:04:58.953] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:04:59.185] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:04:59.415] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:04:59.651] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:04:59.888] [mlr3] Finished benchmark
## INFO  [21:04:59.917] [bbotk] Result of batch 17:
## INFO  [21:04:59.918] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:04:59.918] [bbotk]            FALSE            TRUE            FALSE         10   0.9877462
## INFO  [21:04:59.918] [bbotk]  warnings errors runtime_learners                                 uhash
## INFO  [21:04:59.918] [bbotk]        0      0           2.311 8c1e9d5c-ca79-4aa6-9cd6-ae91b94491e8
## INFO  [21:04:59.919] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:04:59.951] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:04:59.955] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:05:00.183] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:05:00.413] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:05:00.636] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:05:00.861] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:05:01.093] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:05:01.323] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:05:01.553] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:05:01.784] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:05:02.014] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:05:02.243] [mlr3] Finished benchmark
## INFO  [21:05:02.272] [bbotk] Result of batch 18:
## INFO  [21:05:02.273] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:05:02.273] [bbotk]            FALSE            TRUE             TRUE          5   0.9894477
## INFO  [21:05:02.273] [bbotk]  warnings errors runtime_learners                                 uhash
## INFO  [21:05:02.273] [bbotk]        0      0           2.208 8d3aab45-be1a-400f-9426-37e23c282946
## INFO  [21:05:02.274] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:05:02.306] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:05:02.310] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:05:02.543] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:05:02.778] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:05:03.010] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:05:03.246] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:05:03.517] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:05:03.756] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:05:03.989] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:05:04.243] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:05:04.487] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
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## INFO  [21:05:04.733] [mlr3] Finished benchmark
## INFO  [21:05:04.763] [bbotk] Result of batch 19:
## INFO  [21:05:04.765] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:05:04.765] [bbotk]            FALSE           FALSE             TRUE       10   0.9866606
## INFO  [21:05:04.765] [bbotk]  warnings errors runtime_learners                                uhash
## INFO  [21:05:04.765] [bbotk]         0      0            2.337 ede248aa-6f47-46fe-ad79-673798318715
## INFO  [21:05:04.766] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:05:04.798] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:05:04.802] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:05:05.045] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:05:05.281] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:05:05.575] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:05:05.865] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:05:06.222] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:05:06.472] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:05:06.723] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:05:06.970] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:05:07.215] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:05:07.460] [mlr3] Finished benchmark
## INFO  [21:05:07.497] [bbotk] Result of batch 20:
## INFO  [21:05:07.499] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:05:07.499] [bbotk]             TRUE            TRUE             TRUE       10   0.9901713
## INFO  [21:05:07.499] [bbotk]  warnings errors runtime_learners                                uhash
## INFO  [21:05:07.499] [bbotk]         0      0            2.573 34832202-825b-4e9b-b9f7-03d0a3c943a9
## INFO  [21:05:07.500] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:05:07.533] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:05:07.538] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:05:07.777] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:05:08.016] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:05:08.257] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:05:08.506] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:05:08.754] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:05:09.004] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:05:09.252] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:05:09.498] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:05:10.016] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:05:10.255] [mlr3] Finished benchmark
## INFO  [21:05:10.283] [bbotk] Result of batch 21:
## INFO  [21:05:10.285] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:05:10.285] [bbotk]             TRUE           FALSE             TRUE       10   0.9907693
## INFO  [21:05:10.285] [bbotk]  warnings errors runtime_learners                                uhash
## INFO  [21:05:10.285] [bbotk]         0      0            2.634 92182b22-9986-4841-9d3a-8f2377381c7c
## INFO  [21:05:10.286] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:05:10.318] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:05:10.322] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:05:10.545] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:05:10.763] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:05:10.983] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:05:11.204] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:05:11.430] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
```

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_task' (iter 6/10)
## INFO  [21:05:11.661] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:05:11.881] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:05:12.106] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:05:12.329] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:05:12.547] [mlr3] Finished benchmark
## INFO  [21:05:12.576] [bbotk] Result of batch 22:
## INFO  [21:05:12.577] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:05:12.577] [bbotk]             TRUE            FALSE             TRUE          7    0.9909042
## INFO  [21:05:12.577] [bbotk]  warnings errors runtime_learners                                  uhash
## INFO  [21:05:12.577] [bbotk]         0      0            2.15 ee66b774-1c83-4c29-97d8-3a34e42f8071
## INFO  [21:05:12.578] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:05:12.616] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:05:12.620] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:05:12.845] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:05:13.079] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:05:13.313] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:05:13.545] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:05:13.781] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:05:14.020] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:05:14.250] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:05:14.486] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:05:14.723] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:05:14.953] [mlr3] Finished benchmark
## INFO  [21:05:14.982] [bbotk] Result of batch 23:
## INFO  [21:05:14.984] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:05:14.984] [bbotk]            FALSE             TRUE             TRUE         15    0.9910601
## INFO  [21:05:14.984] [bbotk]  warnings errors runtime_learners                                  uhash
## INFO  [21:05:14.984] [bbotk]         0      0           2.255 57b7b51b-1fd9-45ed-832d-00ccc3efde91
## INFO  [21:05:14.984] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:05:15.018] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:05:15.023] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:05:15.248] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:05:15.474] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:05:15.711] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:05:15.966] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:05:16.344] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:05:16.655] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:05:16.910] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:05:17.149] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:05:17.497] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:05:17.720] [mlr3] Finished benchmark
## INFO  [21:05:17.749] [bbotk] Result of batch 24:
## INFO  [21:05:17.750] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:05:17.750] [bbotk]             TRUE            FALSE            FALSE         10    0.9940749
## INFO  [21:05:17.750] [bbotk]  warnings errors runtime_learners                                  uhash
## INFO  [21:05:17.750] [bbotk]         0      0           2.609 852e80e0-f4e4-46e4-bd2c-0cd4674c53c1
## INFO  [21:05:17.751] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:05:17.783] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:05:17.788] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
```

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## INFO  [21:05:18.014] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:05:18.241] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:05:18.456] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:05:18.687] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:05:18.919] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:05:19.140] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:05:19.372] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:05:19.603] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:05:19.822] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:05:20.052] [mlr3] Finished benchmark
## INFO  [21:05:20.080] [bbotk] Result of batch 25:
## INFO  [21:05:20.082] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:05:20.082] [bbotk]             TRUE             TRUE            FALSE          7   0.9905737
## INFO  [21:05:20.082] [bbotk]  warnings errors runtime_learners                                   uhash
## INFO  [21:05:20.082] [bbotk]         0      0            2.185 2e9785bf-16ec-406c-80a7-1f6ed2526864
## INFO  [21:05:20.082] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:05:20.114] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:05:20.118] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:05:20.340] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:05:20.554] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:05:20.777] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:05:21.004] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:05:21.219] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:05:21.444] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:05:21.669] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:05:21.885] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:05:22.118] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:05:22.349] [mlr3] Finished benchmark
## INFO  [21:05:22.378] [bbotk] Result of batch 26:
## INFO  [21:05:22.379] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:05:22.379] [bbotk]            FALSE            FALSE            FALSE          5   0.9890382
## INFO  [21:05:22.379] [bbotk]  warnings errors runtime_learners                                   uhash
## INFO  [21:05:22.379] [bbotk]         0      0            2.154 3fb06812-d3cc-4f1a-beb4-2eb335b6822d
## INFO  [21:05:22.380] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:05:22.412] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:05:22.416] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:05:22.657] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:05:22.886] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:05:23.123] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:05:23.366] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:05:23.599] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:05:23.853] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:05:24.096] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:05:24.341] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:05:24.575] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:05:24.890] [mlr3] Finished benchmark
```

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## INFO  [21:05:24.920] [bbotk] Result of batch 27:
## INFO  [21:05:24.921] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:05:24.921] [bbotk]            FALSE            FALSE             TRUE        15    0.9917045
## INFO  [21:05:24.921] [bbotk]  warnings errors runtime_learners                                  uhash
## INFO  [21:05:24.921] [bbotk]         0      0            2.396 764117fe-afbe-45d6-87c6-24e4c74ad295
## INFO  [21:05:24.922] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:05:24.955] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:05:24.959] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:05:25.204] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:05:25.430] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:05:25.665] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:05:25.905] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:05:26.132] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:05:26.372] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:05:26.611] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:05:26.839] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:05:27.079] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:05:27.317] [mlr3] Finished benchmark
## INFO  [21:05:27.346] [bbotk] Result of batch 28:
## INFO  [21:05:27.347] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:05:27.347] [bbotk]            FALSE             TRUE             TRUE        13    0.9856037
## INFO  [21:05:27.347] [bbotk]  warnings errors runtime_learners                                  uhash
## INFO  [21:05:27.347] [bbotk]         0      0            2.279 3548effd-fa39-46e1-ab0c-5050e3da977e
## INFO  [21:05:27.348] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:05:27.380] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:05:27.384] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:05:27.608] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:05:27.823] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:05:28.047] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:05:28.274] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:05:28.495] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:05:28.723] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:05:28.953] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:05:29.171] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:05:29.401] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:05:29.630] [mlr3] Finished benchmark
## INFO  [21:05:29.659] [bbotk] Result of batch 29:
## INFO  [21:05:29.660] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:05:29.660] [bbotk]             TRUE             TRUE            FALSE         5    0.9877011
## INFO  [21:05:29.660] [bbotk]  warnings errors runtime_learners                                  uhash
## INFO  [21:05:29.660] [bbotk]         0      0            2.166 a08e07dc-062b-432a-9a14-807fd6a78982
## INFO  [21:05:29.661] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:05:29.693] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:05:29.697] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:05:29.912] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:05:30.140] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:05:30.366] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:05:30.595] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:05:30.820] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
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## INFO   [21:05:31.062] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO   [21:05:31.293] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO   [21:05:31.514] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO   [21:05:31.747] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO   [21:05:32.026] [mlr3] Finished benchmark
## INFO   [21:05:32.055] [bbotk] Result of batch 30:
## INFO   [21:05:32.057] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO   [21:05:32.057] [bbotk]            FALSE             TRUE            FALSE          7    0.9868201
## INFO   [21:05:32.057] [bbotk]  warnings errors runtime_learners                                    uhash
## INFO   [21:05:32.057] [bbotk]         0      0            2.242 c090c0d8-89c5-48aa-8a34-ecd7a2c6ea80
## INFO   [21:05:32.058] [bbotk] Evaluating 1 configuration(s)
## INFO   [21:05:32.090] [mlr3] Running benchmark with 10 resampling iterations
## INFO   [21:05:32.094] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO   [21:05:32.340] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO   [21:05:32.581] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO   [21:05:32.829] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO   [21:05:33.075] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO   [21:05:33.322] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO   [21:05:33.578] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO   [21:05:33.828] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO   [21:05:34.077] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO   [21:05:34.333] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO   [21:05:34.584] [mlr3] Finished benchmark
## INFO   [21:05:34.614] [bbotk] Result of batch 31:
## INFO   [21:05:34.615] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO   [21:05:34.615] [bbotk]             TRUE             TRUE             TRUE         15     0.991189
## INFO   [21:05:34.615] [bbotk]  warnings errors runtime_learners                                    uhash
## INFO   [21:05:34.615] [bbotk]         0      0            2.406 5311550b-5347-4bf4-b748-905787d78a14
## INFO   [21:05:34.616] [bbotk] Evaluating 1 configuration(s)
## INFO   [21:05:34.648] [mlr3] Running benchmark with 10 resampling iterations
## INFO   [21:05:34.652] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO   [21:05:34.864] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO   [21:05:35.096] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO   [21:05:35.323] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO   [21:05:35.541] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO   [21:05:35.776] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO   [21:05:36.008] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO   [21:05:36.225] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO   [21:05:36.461] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO   [21:05:36.693] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO   [21:05:36.924] [mlr3] Finished benchmark
## INFO   [21:05:36.957] [bbotk] Result of batch 32:
## INFO   [21:05:36.958] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO   [21:05:36.958] [bbotk]             TRUE            FALSE            FALSE          5    0.9935599
## INFO   [21:05:36.958] [bbotk]  warnings errors runtime_learners                                    uhash
## INFO   [21:05:36.958] [bbotk]         0      0            2.187 94a37d81-b016-4b1a-8797-3379d4be1e9d
## INFO   [21:05:36.959] [bbotk] Evaluating 1 configuration(s)
## INFO   [21:05:36.991] [mlr3] Running benchmark with 10 resampling iterations
## INFO   [21:05:36.995] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO   [21:05:37.213] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
```

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_task' (iter 2/10)
## INFO  [21:05:37.451] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:05:37.685] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:05:37.920] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:05:38.150] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:05:38.390] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:05:38.627] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:05:38.850] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:05:39.089] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:05:39.378] [mlr3] Finished benchmark
## INFO  [21:05:39.407] [bbotk] Result of batch 33:
## INFO  [21:05:39.408] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:05:39.408] [bbotk]             TRUE             TRUE             TRUE          7    0.9913273
## INFO  [21:05:39.408] [bbotk]  warnings errors runtime_learners                                 uhash
## INFO  [21:05:39.408] [bbotk]        0      0            2.303 32a2b951-1140-4483-9472-5d39e278d8b3
## INFO  [21:05:39.409] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:05:39.441] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:05:39.445] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:05:39.696] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:05:39.928] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:05:40.175] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:05:40.423] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:05:40.655] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:05:40.904] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:05:41.152] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:05:41.383] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:05:41.632] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:05:41.879] [mlr3] Finished benchmark
## INFO  [21:05:41.909] [bbotk] Result of batch 34:
## INFO  [21:05:41.910] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:05:41.910] [bbotk]            FALSE            FALSE            FALSE         15    0.9901431
## INFO  [21:05:41.910] [bbotk]  warnings errors runtime_learners                                 uhash
## INFO  [21:05:41.910] [bbotk]        0      0            2.356 683ffcfd-f9a0-4e4a-8d6b-727b7b5b47b9
## INFO  [21:05:41.911] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:05:41.943] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:05:41.947] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:05:42.177] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:05:42.395] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:05:42.628] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:05:42.864] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:05:43.085] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:05:43.323] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:05:43.558] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:05:43.779] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:05:44.016] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:05:44.251] [mlr3] Finished benchmark
## INFO  [21:05:44.281] [bbotk] Result of batch 35:
```

```
## INFO  [21:05:44.282] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:05:44.282] [bbotk]            FALSE            FALSE            FALSE       7    0.987706
## INFO  [21:05:44.282] [bbotk]  warnings errors runtime_learners                                  uhash
## INFO  [21:05:44.282] [bbotk]        0      0             2.228 048709cf-29cd-4e3b-87de-19002b0284a7
## INFO  [21:05:44.283] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:05:44.315] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:05:44.319] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:05:44.551] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:05:44.769] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:05:45.002] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:05:45.239] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:05:45.476] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:05:45.698] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:05:45.939] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:05:46.177] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:05:46.449] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:05:46.671] [mlr3] Finished benchmark
## INFO  [21:05:46.700] [bbotk] Result of batch 36:
## INFO  [21:05:46.702] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:05:46.702] [bbotk]            FALSE            FALSE             TRUE       7   0.9877971
## INFO  [21:05:46.702] [bbotk]  warnings errors runtime_learners                                  uhash
## INFO  [21:05:46.702] [bbotk]        0      0             2.276 b2ea058e-f90e-49e2-885c-473a290271a7
## INFO  [21:05:46.702] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:05:46.744] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:05:46.750] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:05:46.977] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:05:47.213] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:05:47.432] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:05:47.668] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:05:47.907] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:05:48.134] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:05:48.367] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:05:48.605] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:05:48.838] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:05:49.063] [mlr3] Finished benchmark
## INFO  [21:05:49.093] [bbotk] Result of batch 37:
## INFO  [21:05:49.094] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:05:49.094] [bbotk]            FALSE             TRUE            FALSE       5   0.9887176
## INFO  [21:05:49.094] [bbotk]  warnings errors runtime_learners                                  uhash
## INFO  [21:05:49.094] [bbotk]        0      0             2.225 22d52188-82db-4cf2-89ae-29df12155d96
## INFO  [21:05:49.095] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:05:49.127] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:05:49.131] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:05:49.372] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:05:49.611] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:05:49.827] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:05:50.075] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:05:50.317] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:05:50.551] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
```

```
_task' (iter 7/10)
## INFO  [21:05:50.781] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:05:51.028] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:05:51.268] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:05:51.490] [mlr3] Finished benchmark
## INFO  [21:05:51.520] [bbotk] Result of batch 38:
## INFO  [21:05:51.521] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:05:51.521] [bbotk]             TRUE            FALSE            FALSE         7   0.9891253
## INFO  [21:05:51.521] [bbotk]  warnings errors runtime_learners                                 uhash
## INFO  [21:05:51.521] [bbotk]         0      0            2.274 303fb7c6-28c2-4fd9-9538-54b30505b2e4
## INFO  [21:05:51.522] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:05:51.570] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:05:51.576] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:05:51.813] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:05:52.056] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:05:52.293] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:05:52.514] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:05:52.756] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:05:52.997] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:05:53.238] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:05:53.471] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:05:53.952] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:05:54.182] [mlr3] Finished benchmark
## INFO  [21:05:54.212] [bbotk] Result of batch 39:
## INFO  [21:05:54.213] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:05:54.213] [bbotk]             TRUE            FALSE             TRUE         5   0.9933444
## INFO  [21:05:54.213] [bbotk]  warnings errors runtime_learners                                 uhash
## INFO  [21:05:54.213] [bbotk]         0      0            2.523 09297067-6b95-4d2b-baaa-38bcca4b62b5
## INFO  [21:05:54.214] [bbotk] Evaluating 1 configuration(s)
## INFO  [21:05:54.246] [mlr3] Running benchmark with 10 resampling iterations
## INFO  [21:05:54.250] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 1/10)
## INFO  [21:05:54.476] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 2/10)
## INFO  [21:05:54.698] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 3/10)
## INFO  [21:05:54.937] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 4/10)
## INFO  [21:05:55.171] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 5/10)
## INFO  [21:05:55.394] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 6/10)
## INFO  [21:05:55.622] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 7/10)
## INFO  [21:05:55.847] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 8/10)
## INFO  [21:05:56.076] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 9/10)
## INFO  [21:05:56.304] [mlr3] Applying learner 'colroles.Smote.Normalise.pca.classif.svm' on task 'breast_cancer
_task' (iter 10/10)
## INFO  [21:05:56.531] [mlr3] Finished benchmark
## INFO  [21:05:56.568] [bbotk] Result of batch 40:
## INFO  [21:05:56.569] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## INFO  [21:05:56.569] [bbotk]             TRUE             TRUE            FALSE        10   0.9914717
## INFO  [21:05:56.569] [bbotk]  warnings errors runtime_learners                                 uhash
## INFO  [21:05:56.569] [bbotk]         0      0              2.2 46245752-5a71-4023-9a97-f8af2f0815d1
## INFO  [21:05:56.574] [bbotk] Finished optimizing after 40 evaluation(s)
## INFO  [21:05:56.574] [bbotk] Result:
## INFO  [21:05:56.575] [bbotk]  Normalise.scale Normalise.robust Normalise.center pca.rank. learner_param_vals
## INFO  [21:05:56.575] [bbotk]             TRUE            FALSE            FALSE        10          <list[7]>
## INFO  [21:05:56.575] [bbotk]   x_domain classif.auc
## INFO  [21:05:56.575] [bbotk]  <list[4]>   0.9940749
```

```
trained_model_1$model
```

```
## $learner
## <GraphLearner:colroles.Smote.Normalise.pca.classif.svm>
## * Model: list
## * Parameters: colroles.new_role=<list>, Smote.dup_size=1,
##   Normalise.center=FALSE, Normalise.scale=TRUE, Normalise.robust=FALSE,
##   pca.rank.=10, classif.svm.kernel=radial
## * Packages: mlr3, mlr3pipelines, smotefamily, mlr3learners, e1071
## * Predict Types:  response, [prob]
## * Feature Types: logical, integer, numeric, character, factor, ordered,
##   POSIXct
## * Properties: featureless, hotstart_backward, hotstart_forward,
##   importance, loglik, missings, multiclass, oob_error,
##   selected_features, twoclass, weights
##
## $tuning_instance
## <TuningInstanceSingleCrit>
## * State:  Optimized
## * Objective: <ObjectiveTuning:colroles.Smote.Normalise.pca.classif.svm_on_breast_cancer_task>
## * Search Space:
##                 id    class lower upper nlevels
## 1:  Normalise.scale ParamLgl    NA    NA       2
## 2: Normalise.robust ParamLgl    NA    NA       2
## 3: Normalise.center ParamLgl    NA    NA       2
## 4:        pca.rank. ParamInt     5    15      11
## * Terminator: <TerminatorEvals>
## * Result:
##    Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
## 1:            TRUE            FALSE            FALSE        10   0.9940749
## * Archive:
##     Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
##  1:           FALSE            FALSE            FALSE        13   0.9854092
##  2:           FALSE            FALSE            FALSE        10   0.9881509
##  3:            TRUE             TRUE            FALSE        15   0.9906982
##  4:            TRUE             TRUE             TRUE        13   0.9916350
##  5:            TRUE            FALSE            FALSE        13   0.9923426
##  6:            TRUE             TRUE            FALSE        13   0.9915734
##  7:            TRUE            FALSE             TRUE        13   0.9916821
##  8:            TRUE            FALSE            FALSE        15   0.9887853
##  9:            TRUE             TRUE             TRUE         5   0.9885513
## 10:           FALSE             TRUE             TRUE         7   0.9875177
## 11:           FALSE            FALSE             TRUE        13   0.9852663
## 12:            TRUE            FALSE             TRUE        15   0.9920768
## 13:           FALSE            FALSE             TRUE         5   0.9890084
## 14:           FALSE             TRUE            FALSE        15   0.9907065
## 15:           FALSE             TRUE             TRUE        10   0.9881615
## 16:           FALSE             TRUE            FALSE        13   0.9870674
## 17:           FALSE             TRUE            FALSE        10   0.9877462
## 18:           FALSE             TRUE             TRUE         5   0.9894477
## 19:           FALSE            FALSE             TRUE        10   0.9866606
## 20:            TRUE             TRUE             TRUE        10   0.9901713
## 21:            TRUE            FALSE             TRUE        10   0.9907693
## 22:            TRUE            FALSE             TRUE         7   0.9909042
## 23:           FALSE             TRUE             TRUE        15   0.9910601
## 24:            TRUE            FALSE            FALSE        10   0.9940749
## 25:            TRUE             TRUE            FALSE         7   0.9905737
## 26:           FALSE            FALSE            FALSE         5   0.9890382
## 27:           FALSE            FALSE             TRUE        15   0.9917045
## 28:           FALSE             TRUE             TRUE        13   0.9856037
## 29:            TRUE             TRUE            FALSE         5   0.9877011
## 30:           FALSE             TRUE            FALSE         7   0.9868201
## 31:            TRUE             TRUE             TRUE        15   0.9911890
## 32:            TRUE            FALSE            FALSE         5   0.9935599
## 33:            TRUE             TRUE             TRUE         7   0.9913273
## 34:           FALSE            FALSE            FALSE        15   0.9901431
## 35:           FALSE            FALSE            FALSE         7   0.9877060
## 36:           FALSE            FALSE             TRUE         7   0.9877971
## 37:           FALSE             TRUE            FALSE         5   0.9887176
## 38:            TRUE            FALSE            FALSE         7   0.9891253
## 39:            TRUE            FALSE             TRUE         5   0.9933444
## 40:            TRUE             TRUE            FALSE        10   0.9914717
##     Normalise.scale Normalise.robust Normalise.center pca.rank. classif.auc
```

If we just want to visualise the best model's tuning results, we can specify this.

```
trained_model_1$tuning_result
```

```
##    Normalise.scale Normalise.robust Normalise.center pca.rank.
## 1:           TRUE            FALSE            FALSE        10
##    learner_param_vals  x_domain classif.auc
## 1:          <list[7]> <list[4]>   0.9940749
```

The best tuning results show scaling true, but no centering, a PCA rank of 5 (5 principal components), and a final classif auc of 0.9956.

Predicitons on test data

Based on our trained model, we can now make predictions on our data using the $predict() function.

```
predictions <- tune$predict(task = bc_task, row_ids = split$test)

predictions
```

```
## <PredictionClassif> for 188 observations:
##     row_ids truth response       prob.B       prob.M
##           6     M        M 3.197761e-02 0.968022393
##           7     M        M 5.102822e-05 0.999948972
##           8     M        M 1.350497e-01 0.864950322
## ---
##         558     B        B 9.905641e-01 0.009435855
##         560     B        B 8.930365e-01 0.106963515
##         562     B        B 9.792291e-01 0.020770908
```

Just printing the confusion matrix makes the outcome of the best model clear:

```
predictions$confusion
```

```
##         truth
## response   B   M
##        B 111   4
##        M   7  66
```

```
confusion_matrix(predictions$truth, predictions$response, predictions$positive, na_value = NaN, relative = FALSE)
```

```
##         truth
## response   B   M
##        B 111   4
##        M   7  66
## acc :  0.9415; ce  :  0.0585; dor :  261.6429; f1  :  0.9528
## fdr :  0.0348; fnr :  0.0593; fomr:  0.0959; fpr :  0.0571
## mcc :  0.8764; npv :  0.9041; ppv :  0.9652; tnr :  0.9429
## tpr :  0.9407
```

```
as.data.table(predictions)
```

```
##      row_ids truth response       prob.B       prob.M
##   1:       6     M        M 3.197761e-02 0.9680223927
##   2:       7     M        M 5.102822e-05 0.9999489718
##   3:       8     M        M 1.350497e-01 0.8649503224
##   4:      12     M        M 1.368026e-02 0.9863197431
##   5:      16     M        M 1.951610e-03 0.9980483904
##  ---
## 184:     555     B        M 4.813370e-01 0.5186629943
## 185:     557     B        B 9.997064e-01 0.0002935784
## 186:     558     B        B 9.905641e-01 0.0094358554
## 187:     560     B        B 8.930365e-01 0.1069635145
## 188:     562     B        B 9.792291e-01 0.0207709076
```

```
predictions$score(measure)
```

```
## classif.auc
##   0.9901937
```

Alluvial Chart

We can print the confusion matrix as an alluvial chart, visualing the number of correctly predicted vs incorrectly predicted observations.

```
dataCm <- as.data.frame(predictions$confusion)
dataCm
```

```
##   response truth Freq
## 1        B     B  111
## 2        M     B    7
## 3        B     M    4
## 4        M     M   66
```

```
dataCm$missclassified <- dataCm$response != dataCm$truth

ggplot(data = dataCm, mapping = aes(y = Freq, axis1 = response, axis2 = truth, label = after_stat(stratum))) +
  ggalluvial::geom_alluvium(aes(fill = missclassified, colour = missclassified), show.legend = TRUE) +
  ggalluvial::geom_stratum(width = 0.2) +
  geom_text(stat = "stratum", reverse = TRUE) +
  scale_x_discrete(limits = c("Prediction", "Actual"), expand = c(0.0, 0.0)) +
  ggtitle("Classification of Breast-cancer diagnoses") +
  scale_fill_manual(values = c("green","red")) +
  theme_bw()
```

```
## Warning in to_lodes_form(data = data, axes = axis_ind, discern =
## params$discern): Some strata appear at multiple axes.

## Warning in to_lodes_form(data = data, axes = axis_ind, discern =
## params$discern): Some strata appear at multiple axes.

## Warning in to_lodes_form(data = data, axes = axis_ind, discern =
## params$discern): Some strata appear at multiple axes.
```