

# Package ‘admix’

March 7, 2025

**Title** Package Admix for Admixture (aka Contamination) Models

**Version** 2.3.4

**Description** Implements techniques to estimate the unknown quantities related to two-component admixture models, where the two components can belong to any distribution (note that in the case of multinomial mixtures, the two components must belong to the same family). Estimation methods depend on the assumptions made on the unknown component density; see Bordes and Vandekerkhove (2010) <[doi:10.3103/S1066530710010023](https://doi.org/10.3103/S1066530710010023)>, Patra and Sen (2016) <[doi:10.1111/rssb.12148](https://doi.org/10.1111/rssb.12148)>, and Milhaud, Pommeret, Salhi, Vandekerkhove (2024) <[doi:10.3150/23-BEJ1593](https://doi.org/10.3150/23-BEJ1593)>. In practice, one can estimate both the mixture weight and the unknown component density in a wide variety of frameworks. On top of that, hypothesis tests can be performed in one and two-sample contexts to test the unknown component density (see Milhaud, Pommeret, Salhi and Vandekerkhove (2022) <[doi:10.1016/j.jspi.2021.05.010](https://doi.org/10.1016/j.jspi.2021.05.010)>, and Milhaud, Pommeret, Salhi, Vandekerkhove (2024) <[doi:10.3150/23-BEJ1593](https://doi.org/10.3150/23-BEJ1593)>). Finally, clustering of unknown mixture components is also feasible in a K-sample setting (see Milhaud, Pommeret, Salhi, Vandekerkhove (2024) <<https://jmlr.org/papers/v25/23-0914.html>>).

**License** GPL (>= 3)

**URL** <https://github.com/XavierMilhaud/admix-Rpackage>

**BugReports** <https://github.com/XavierMilhaud/admix-Rpackage/issues>

**Encoding** UTF-8

**RoxygenNote** 7.3.2

**Imports** base, cubature, EnvStats, fdrtool, graphics, Iso, MASS, orthopolynom, pracma, Rcpp, Rdpack, stats, utils

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**LinkingTo** Rcpp

**RdMacros** Rdpack

**Config/testthat/edition** 3

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**Author** Xavier Milhaud [aut, cre],  
 Pierre Vandekerkhove [ctb],  
 Denys Pommeret [ctb],  
 Yahia Salhi [ctb]

**Maintainer** Xavier Milhaud <xavier.milhaud.research@gmail.com>

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admix\_cluster *Clustering of K populations following admixture models*

**Description**

Create clusters on the unknown components related to the K populations following admixture models. Based on the K-sample test using Inversion - Best Matching (IBM) approach, see 'Details' below for further information.

**Usage**

```
admix_cluster(
  samples,
  admixMod,
  conf_level = 0.95,
  tune_penalty = TRUE,
  tabul_dist = NULL,
  echo = TRUE,
  ...
)
```

**Arguments**

- samples      A list of the K (K>1) samples to be studied, all following admixture distributions.
- admixMod     A list of objects of class [admix\\_model](#), containing useful information about distributions and parameters.
- conf\_level   (default to 0.95) The confidence level of the k-sample tests used in the clustering procedure.

tune_penalty	(default to TRUE) A boolean that allows to choose between a classical penalty term or an optimized penalty (embedding some tuning parameters, automatically optimized). Optimized penalty is particularly useful for low/mid-sized samples, or unbalanced sample sizes to detect alternatives to the null hypothesis (H0). It is recommended to use it.
tabul_dist	(default to NULL) Only useful for comparisons of detected clusters at different confidence levels. A list of the tabulated distributions of the stochastic integral used in the k-sample test, each element for each cluster previously detected.
echo	(default to TRUE) Display the remaining computation time.
...	Optional arguments to <a href="#">IBM_k_samples_test</a> ; namely 'n_sim_tab', 'parallel' and 'n_cpu'. These are crucial to speed-up the building of clusters.

### Value

An object of class [admix\\_cluster](#), containing 12 attributes: 1) the number of samples under study; 2) the sizes of samples; 3) the information about mixture components in each sample (distributions and parameters); 4) the number of detected clusters; 5) the list of p-values for each k-sample test at the origin of detected clusters; 6) the cluster affiliation for each sample; 7) the confidence level of statistical tests; 8) which samples in which cluster; 9) the size of clusters; 10) the estimated weights of the unknown component distributions inside each cluster (remind that estimated weights are consistent only if unknown components are tested to be identical, which is the case inside clusters); 11) the matrix of pairwise discrepancies across all samples; 12) the list of tabulated distributions used for statistical tests involved in building the clusters.

### Author(s)

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

### References

Milhaud X, Pommeret D, Salhi Y, Vandekerkhove P (2024). "Contamination-source based K-sample clustering." *Journal of Machine Learning Research*, **25**(287), 1–32. <https://jmlr.org/papers/v25/23-0914.html>.

### Examples

```
## Simulate mixture data:
mixt1 <- twoComp_mixt(n = 2600, weight = 0.8,
  comp.dist = list("gamma", "exp"),
  comp.param = list(list("shape" = 16, "scale" = 1/4),
    list("rate" = 1/3.5)))
mixt2 <- twoComp_mixt(n = 3000, weight = 0.7,
  comp.dist = list("gamma", "exp"),
  comp.param = list(list("shape" = 14, "scale" = 1/2),
    list("rate" = 1/5)))
mixt3 <- twoComp_mixt(n = 3500, weight = 0.6,
  comp.dist = list("gamma", "gamma"),
  comp.param = list(list("shape" = 16, "scale" = 1/4),
    list("shape" = 12, "scale" = 1/2)))
mixt4 <- twoComp_mixt(n = 4800, weight = 0.5,
```

```

comp.dist = list("gamma", "exp"),
comp.param = list(list("shape" = 14, "scale" = 1/2),
                  list("rate" = 1/7)))

data1 <- getmixtData(mixt1)
data2 <- getmixtData(mixt2)
data3 <- getmixtData(mixt3)
data4 <- getmixtData(mixt4)
## Define the admixture models:
admixMod1 <- admix_model(knownComp_dist = mixt1$comp.dist[[2]],
                        knownComp_param = mixt1$comp.param[[2]])
admixMod2 <- admix_model(knownComp_dist = mixt2$comp.dist[[2]],
                        knownComp_param = mixt2$comp.param[[2]])
admixMod3 <- admix_model(knownComp_dist = mixt3$comp.dist[[2]],
                        knownComp_param = mixt3$comp.param[[2]])
admixMod4 <- admix_model(knownComp_dist = mixt4$comp.dist[[2]],
                        knownComp_param = mixt4$comp.param[[2]])
## Clustering procedure:
admix_cluster(samples = list(data1, data2, data3, data4),
              admixMod = list(admixMod1, admixMod2, admixMod3, admixMod4),
              conf_level = 0.95, tune_penalty = TRUE, n_sim_tab = 30)

```

---

admix\_estim

*Estimate the unknown parameters of the admixture model(s)*


---

## Description

Estimate the component weights, the location shift parameter (in case of a symmetric unknown component density), and the unknown component distribution using different estimation techniques. We remind that the  $i$ -th admixture model has probability density function (pdf)  $l_i$  such that:  $l_i = p_i * f_i + (1-p_i) * g_i$ , where  $g_i$  is the known component density. The unknown quantities  $p_i$  and  $f_i$  then have to be estimated.

## Usage

```
admix_estim(samples, admixMod, est_method = c("PS", "BVdk", "IBM"), ...)
```

## Arguments

<code>samples</code>	A list of the $K$ ( $K > 0$ ) samples to be studied, all following admixture distributions.
<code>admixMod</code>	A list of objects of class <code>admix_model</code> , containing useful information about distributions and parameters.
<code>est_method</code>	The estimation method to be applied. Can be one of 'BVdk' (Bordes and Vandekerckhove estimator), 'PS' (Patra and Sen estimator), or 'IBM' (Inversion Best-Matching approach) in the continuous case (continuous random variable). Only 'IBM' for discrete random variables. The same estimation method is performed on each sample if several samples are provided.

... Optional arguments to `estim_PS`, `estim_BVdk` or `estim_IBM` depending on the choice made by the user for the estimation method.

### Details

For further details on the different estimation techniques, see references below on i) Patra and Sen estimator ; ii) Bordes and Vandekerkhove estimator ; iii) Inversion Best-Matching approach. Important note: estimation by 'IBM' requires at least two samples at hand, and provides unbiased estimators only if the distributions of unknown components are equal (meaning that it requires to perform previously this test between the pairs of samples, see `?admix_test`).

### Value

An object of class `admix_estim`, containing at least 5 attributes: 1) the number of samples under study; 2) the information about the mixture components (distributions and parameters); 3) the sizes of the samples; 4) the chosen estimation technique (one of 'BVdk', 'PS' or 'IBM'); 5) the estimated mixing proportions (weights of the unknown component distributions in the mixture model). In case of 'BVdk' estimation, one additional attribute corresponding to the estimated location shift parameter is included.

### Author(s)

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

### References

Patra RK, Sen B (2016). "Estimation of a two-component mixture model with applications to multiple testing." *Journal of the Royal Statistical Society Series B*, **78**(4), 869-893. Bordes L, Delmas C, Vandekerkhove P (2006). "Semiparametric Estimation of a Two-Component Mixture Model Where One Component Is Known." *Scandinavian Journal of Statistics*, **33**(4), 733–752. ISSN 03036898, 14679469, <http://www.jstor.org/stable/4616955>. Bordes L, Vandekerkhove P (2010). "Semiparametric two-component mixture model with a known component: An asymptotically normal estimator." *Mathematical Methods of Statistics*, **19**(1), 22–41. doi:10.3103/S1066530710010023. Milhaud X, Pommeret D, Salhi Y, Vandekerkhove P (2024). "Two-sample contamination model test." *Bernoulli*, **30**(1), 170–197. doi:10.3150/23BEJ1593.

### Examples

```
## Simulate mixture data:
mixt1 <- twoComp_mixt(n = 300, weight = 0.7,
  comp.dist = list("norm", "norm"),
  comp.param = list(list("mean" = -2, "sd" = 0.5),
    list("mean" = 0, "sd" = 1)))
mixt2 <- twoComp_mixt(n = 250, weight = 0.85,
  comp.dist = list("norm", "exp"),
  comp.param = list(list("mean" = -2, "sd" = 0.5),
    list("rate" = 1)))

data1 <- getmixtData(mixt1)
data2 <- getmixtData(mixt2)
## Define the admixture models:
admixMod1 <- admix_model(knownComp_dist = mixt1$comp.dist[[2]],
```

```

                                knownComp_param = mixt1$comp.param[[2]])
admixMod2 <- admix_model(knownComp_dist = mixt2$comp.dist[[2]],
                        knownComp_param = mixt2$comp.param[[2]])
# Estimation by different methods:
admix_estim(samples=list(data1), admixMod=list(admixMod1), est_method = "BVdk")
admix_estim(samples=list(data1,data2), admixMod=list(admixMod1,admixMod2), est_method = "PS")
admix_estim(samples=list(data1,data2), admixMod=list(admixMod1,admixMod2), est_method = "IBM")

```

---

admix\_model

*Create an object of class 'admix\_model'*


---

## Description

Create an admixture model, also known as (aka) a contamination model. Such a model is a two-component mixture model with one known component. Both the second component distribution and the mixing weight are unknown.

## Usage

```
admix_model(knownComp_dist, knownComp_param)
```

## Arguments

`knownComp_dist` (Character) The name of the distribution (specified as in R glossary) of the known component of the admixture model

`knownComp_param`

(Character) A vector of the names of the parameters (specified as in R glossary) involved in the chosen known distribution, with their values.

## Value

An object of class `admix_model`, containing 2 attributes: 1) a list that gives the information about the distributions involved in the two-component mixture model (the unknown and the known ones); 2) a list that gives the information about the corresponding parameters of those distributions.

## Author(s)

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

## Examples

```

admix_model(knownComp_dist = "norm", knownComp_param = list("mean"=0, "sd"=1))
admix_model(knownComp_dist = "exp", knownComp_param = list("rate"=2))
admix_model(knownComp_dist = "multinom", knownComp_param = list("size"=1, "prob"=c(0.2,0.8,0.1)))

```

admix\_test

*Equality test for the unknown components of admixture models***Description**

Perform hypothesis test between unknown components of a list of admixture models, where we remind that the  $i$ -th admixture model has probability density function (pdf)  $l_i$  such that:  $l_i = p_i * f_i + (1-p_i) * g_i$ , with  $g_i$  the known component density. The unknown quantities  $p_i$  and  $f_i$  are thus estimated, leading to the test given by the following null and alternative hypothesis:  $H_0: f_i = f_j$  for all  $i \neq j$  against  $H_1$ : there exists at least  $i \neq j$  such that  $f_i$  differs from  $f_j$ . The test can be performed using two methods, either the comparison of coefficients obtained through polynomial basis expansions of the component densities, or by the inner-convergence property obtained using the IBM approach. See 'Details' below for further information.

**Usage**

```
admix_test(
  samples,
  admixMod,
  test_method = c("poly", "icv"),
  conf_level = 0.95,
  ...
)
```

**Arguments**

samples	A list of the $K$ ( $K > 0$ ) samples to be studied, each one assumed to follow a mixture distribution.
admixMod	A list of objects of class <a href="#">admix_model</a> , containing useful information about distributions and parameters of the contamination / admixture models under study.
test_method	The testing method to be applied. Can be either 'poly' (polynomial basis expansion) or 'icv' (inner convergence from IBM). The same testing method is performed between all samples. In the one-sample case, only 'Poly' is available and the test is a gaussianity test. For further details, see section 'Details' below.
conf_level	The confidence level of the $K$ -sample test.
...	Depending on the choice made by the user for the test method ('poly' or 'icv'), optional arguments to <a href="#">gaussianity_test</a> or <a href="#">orthobasis_test</a> (in case of 'poly'), and to <a href="#">IBM_k_samples_test</a> in case of 'icv'.

**Details**

For further details on implemented hypothesis tests, see the references hereafter. .



**Value**

An object of class `admix_test`, containing 8 attributes: 1) the test decision (reject the null hypothesis or not); 2) the p-value of the test; 3) the confidence level of the test (1-alpha, where alpha denotes the level of the test or equivalently the type-I error); 4) the value of the test statistic; 5) the number of samples under study; 6) the respective size of each sample; 7) the information about mixture components (distributions and parameters); 8) the chosen testing method (either based on polynomial basis expansions, or on the inner convergence property; see given references).

**Author(s)**

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

**References**

Milhaud X, Pommeret D, Salhi Y, Vandekerkhove P (2024). “Contamination-source based K-sample clustering.” *Journal of Machine Learning Research*, **25**(287), 1–32. <https://jmlr.org/papers/v25/23-0914.html>. Milhaud X, Pommeret D, Salhi Y, Vandekerkhove P (2022). “Semiparametric two-sample admixture components comparison test: The symmetric case.” *Journal of Statistical Planning and Inference*, **216**, 135-150. ISSN 0378-3758, [doi:10.1016/j.jspi.2021.05.010](https://doi.org/10.1016/j.jspi.2021.05.010). Pommeret D, Vandekerkhove P (2019). “Semiparametric density testing in the contamination model.” *Electronic Journal of Statistics*, 4743–4793. [doi:10.1214/19EJS1650](https://doi.org/10.1214/19EJS1650).

**Examples**

```
##### Example with 2 samples
mixt1 <- twoComp_mixt(n = 380, weight = 0.7,
  comp.dist = list("norm", "norm"),
  comp.param = list(list("mean" = -2, "sd" = 0.5),
    list("mean" = 0, "sd" = 1)))
mixt2 <- twoComp_mixt(n = 350, weight = 0.85,
  comp.dist = list("norm", "norm"),
  comp.param = list(list("mean" = -2, "sd" = 0.5),
    list("mean" = -1, "sd" = 1)))

data1 <- getmixtData(mixt1)
data2 <- getmixtData(mixt2)
admixMod1 <- admix_model(knownComp_dist = mixt1$comp.dist[[2]],
  knownComp_param = mixt1$comp.param[[2]])
admixMod2 <- admix_model(knownComp_dist = mixt2$comp.dist[[2]],
  knownComp_param = mixt2$comp.param[[2]])
admix_test(samples = list(data1,data2), admixMod = list(admixMod1,admixMod2),
  conf_level = 0.95, test_method = "poly", ask_poly_param = FALSE, support = "Real")
```

**Description**

An evolving data frame of velocities for 4 dSph galaxies (namely Carina, Sextans, Sculptor and Fornax), from SIMBAD astronomical database.

**Usage**

```
allGalaxies
```

**Format**

Currently contains 8,862 rows and 3 columns, with information on:

**Target** Target identification; Galaxy-ID number

**HV** Weighted mean Heliocentric rest frame velocity

**Name** The name of the galaxy

**Source**

[https://vizier.u-strasbg.fr/viz-bin/VizieR-3?-source=J/AJ/137/3100/stars&-out.max=50&-out.form=HTML%20Table&-out.add=\\_r&-out.add=\\_RAJ,\\_DEJ&-out.add=\\_RA%2a-c.eq,\\_DE%2a-c.eq&-sort=\\_r&-oc.form=sexa](https://vizier.u-strasbg.fr/viz-bin/VizieR-3?-source=J/AJ/137/3100/stars&-out.max=50&-out.form=HTML%20Table&-out.add=_r&-out.add=_RAJ,_DEJ&-out.add=_RA%2a-c.eq,_DE%2a-c.eq&-sort=_r&-oc.form=sexa)

---

decontaminated_cdf	<i>Estimates the decontaminated CDF of the unknown component in an admixture</i>
--------------------	--

---

**Description**

Estimates the decontaminated cumulative distribution function (CDF) of the unknown component in an admixture model, using inversion of the admixture CDF. Recall that an admixture model follows the cumulative distribution function (CDF)  $L$ , where  $L = p * F + (1-p) * G$ , with  $g$  a known CDF and  $p$  and  $f$  unknown quantities.

**Usage**

```
decontaminated_cdf(sample1, estim.p, admixMod)
```

**Arguments**

sample1	Observations of the sample under study.
estim.p	The estimated weight of the unknown component distribution, related to the proportion of the unknown component in the admixture model studied.
admixMod	An object of class 'admix_model', containing useful information about distributions and parameters.

**Details**

The decontaminated CDF is obtained by inverting the admixture CDF, given by  $L = p \cdot F + (1-p) \cdot G$ , to isolate the unknown component  $F$  after having estimated  $p$ . This means that  $F = (1/\hat{p}) * (\hat{L} - (1-p) \cdot G)$ .

**Value**

The decontaminated CDF  $F$  of the admixture model, of class 'stepfun' (step function).

**Author(s)**

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

**Examples**

```
## Simulate mixture data:
mixt1 <- twoComp_mixt(n = 400, weight = 0.4,
  comp.dist = list("norm", "norm"),
  comp.param = list(list("mean" = 3, "sd" = 0.5),
    list("mean" = 0, "sd" = 1)))
mixt2 <- twoComp_mixt(n = 300, weight = 0.6,
  comp.dist = list("norm", "norm"),
  comp.param = list(list("mean" = 3, "sd" = 0.5),
    list("mean" = 5, "sd" = 2)))

data1 <- getmixtData(mixt1)
data2 <- getmixtData(mixt2)
## Define the admixture models:
admMod1 <- admix_model(knownComp_dist = mixt1$comp.dist[[2]],
  knownComp_param = mixt1$comp.param[[2]])
admMod2 <- admix_model(knownComp_dist = mixt2$comp.dist[[2]],
  knownComp_param = mixt2$comp.param[[2]])

## Estimation:
est <- admix_estim(samples = list(data1,data2),
  admMod = list(admMod1,admMod2), est_method = 'PS')
prop <- getmixingWeight(est)
## Determine the decontaminated version of the unknown CDF by inversion:
F1 <- decontaminated_cdf(sample1 = data1, estim.p = prop[1], admMod = admMod1)
F2 <- decontaminated_cdf(sample1 = data2, estim.p = prop[2], admMod = admMod2)
abs <- seq(from=-1, to=4, length.out=100)
plot(x=abs, y=F1(abs), xlim=c(-1,4), ylim=c(0,1), type="l")
par(new = TRUE)
plot(x=abs, y=F2(abs), xlim=c(-1,4), ylim=c(0,1), type="l", col="red")
```

---

decontaminated\_density

*Estimates the decontaminated density of the unknown component in an admixture*

---

**Description**

Estimate the decontaminated density of the unknown component in the admixture model under study, after inversion of the admixture cumulative distribution function. Recall that an admixture model follows the cumulative distribution function (CDF)  $L$ , where  $L = p \cdot F + (1-p) \cdot G$ , with  $g$  a known CDF and  $p$  and  $f$  unknown quantities.

**Usage**

```
decontaminated_density(sample1, estim.p, admixMod)
```

**Arguments**

sample1	Sample under study.
estim.p	The estimated weight of the unknown component distribution, related to the proportion of the unknown component in the admixture model studied.
admixMod	An object of class 'admix_model', containing useful information about distributions and parameters.

**Details**

The decontaminated density is obtained by inverting the admixture density, given by  $l = p \cdot f + (1-p) \cdot g$ , to isolate the unknown component  $f$  after having estimated  $p$ .

**Value**

An object of class 'decontaminated\_density', containing 2 attributes: 1) the decontaminated density function; 2) the type of support for the underlying distribution (either discrete or continuous, useful for plots).

**Author(s)**

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

**Examples**

```
## Simulate mixture data:
mixt1 <- twoComp_mixt(n = 400, weight = 0.4,
                    comp.dist = list("norm", "norm"),
                    comp.param = list(list("mean" = -2, "sd" = 0.5),
                                       list("mean" = 0, "sd" = 1)))

data1 <- getmixtData(mixt1)
## Define the admixture models:
admixMod1 <- admix_model(knownComp_dist = mixt1$comp.dist[[2]],
                       knownComp_param = mixt1$comp.param[[2]])

## Estimation:
est <- admix_estim(samples = list(data1), admixMod = list(admixMod1),
                 est_method = 'PS')

## Determine the decontaminated version of the unknown density by inversion:
decontaminated_density(sample1 = data1, estim.p = est$estimated_mixing_weights[1],
                      admixMod = admixMod1)
```

```
##### Discrete support:
mixt1 <- twoComp_mixt(n = 5000, weight = 0.6,
                     comp.dist = list("pois", "pois"),
                     comp.param = list(list("lambda" = 3),
                                       list("lambda" = 2)))
mixt2 <- twoComp_mixt(n = 4000, weight = 0.8,
                     comp.dist = list("pois", "pois"),
                     comp.param = list(list("lambda" = 3),
                                       list("lambda" = 4)))

data1 <- getmixtData(mixt1)
data2 <- getmixtData(mixt2)
## Define the admixture models:
admMod1 <- admix_model(knownComp_dist = mixt1$comp.dist[[2]],
                      knownComp_param = mixt1$comp.param[[2]])
admMod2 <- admix_model(knownComp_dist = mixt2$comp.dist[[2]],
                      knownComp_param = mixt2$comp.param[[2]])

## Estimation:
est <- admix_estim(samples = list(data1, data2),
                  admMod = list(admMod1, admMod2), est_method = 'IBM')
## Determine the decontaminated version of the unknown density by inversion:
decontaminated_density(sample1 = data1, estim.p = est$estimated_mixing_weights[1],
                      admMod = admMod1)

##### Finite discrete support:
mixt1 <- twoComp_mixt(n = 12000, weight = 0.6,
                     comp.dist = list("multinom", "multinom"),
                     comp.param = list(list("size" = 1, "prob" = c(0.3,0.4,0.3)),
                                       list("size" = 1, "prob" = c(0.6,0.3,0.1))))
mixt2 <- twoComp_mixt(n = 10000, weight = 0.8,
                     comp.dist = list("multinom", "multinom"),
                     comp.param = list(list("size" = 1, "prob" = c(0.3,0.4,0.3)),
                                       list("size" = 1, "prob" = c(0.2,0.6,0.2))))

data1 <- getmixtData(mixt1)
data2 <- getmixtData(mixt2)
## Define the admixture models:
admMod1 <- admix_model(knownComp_dist = mixt1$comp.dist[[2]],
                      knownComp_param = mixt1$comp.param[[2]])
admMod2 <- admix_model(knownComp_dist = mixt2$comp.dist[[2]],
                      knownComp_param = mixt2$comp.param[[2]])

## Estimation:
est <- admix_estim(samples = list(data1, data2),
                  admMod = list(admMod1, admMod2), est_method = 'IBM')
## Determine the decontaminated version of the unknown density by inversion:
decontaminated_density(sample1 = data1, estim.p = est$estimated_mixing_weights[1],
                      admMod = admMod1)
```

## Description

Estimates parameters in an admixture model where the unknown component is assumed to have a symmetric density. More precisely, estimates the two parameters (mixture weight and location shift) in the admixture model with pdf:  $l(x) = p*f(x-\mu) + (1-p)*g(x)$ ,  $x$  in  $\mathbb{R}$ , where  $g$  is the known component,  $p$  is the proportion and  $f$  is the unknown component with symmetric density. The localization shift parameter is denoted  $\mu$ , and the component weight  $p$ . See the reference below for further details.

## Usage

```
estim_BVdk(
  samples,
  admixMod,
  method = c("L-BFGS-B", "Nelder-Mead"),
  compute_var = FALSE
)
```

## Arguments

<code>samples</code>	The observed sample under study.
<code>admixMod</code>	An object of class <code>admix_model</code> , containing useful information about distributions and parameters.
<code>method</code>	The method used throughout the optimization process, either 'L-BFGS-B' or 'Nelder-Mead' (see <code>?optim</code> ).
<code>compute_var</code>	(default to FALSE) A boolean that indicates whether one computes the variance of the estimators of unknown mixing proportions and location shift parameter.

## Value

An object of class `estim_BVdk`, containing 8 attributes: 1) the number of sample under study (set to 1 here); 2) the sample size; 3) the information about mixture components (distributions and parameters); 4) the estimation method (Bordes and Vandekerkhove here, see the given reference); 5) the estimated mixing proportion (weight of the unknown component distribution); 6) the estimated location parameter of the unknown component distribution (with symmetric density); 7) the variance of the two estimators (respectively the mixing proportion and location shift); 8) the optimization method that was used.

## Author(s)

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

## References

Bordes L, Vandekerkhove P (2010). "Semiparametric two-component mixture model with a known component: An asymptotically normal estimator." *Mathematical Methods of Statistics*, **19**(1), 22–41. doi:10.3103/S1066530710010023.

## Examples

```
## Simulate mixture data:
mixt1 <- twoComp_mixt(n = 200, weight = 0.4,
                     comp.dist = list("norm", "norm"),
                     comp.param = list(list("mean" = -2, "sd" = 0.5),
                                       list("mean" = 0, "sd" = 1)))

## Retrieves the mixture data:
data1 <- getmixtData(mixt1)
## Define the admixture model:
admixMod <- admix_model(knownComp_dist = mixt1$comp.dist[[2]],
                       knownComp_param = mixt1$comp.param[[2]])
## Perform the estimation of parameters in real-life:
estim_BVdk(samples = data1, admixMod = admixMod, method = 'L-BFGS-B')

## Second example:
mixt2 <- twoComp_mixt(n = 200, weight = 0.65,
                     comp.dist = list("norm", "exp"),
                     comp.param = list(list("mean" = -1, "sd" = 0.5),
                                       list("rate" = 1)))

data2 <- getmixtData(mixt2)
admixMod2 <- admix_model(knownComp_dist = mixt2$comp.dist[[2]],
                        knownComp_param = mixt2$comp.param[[2]])
## Perform the estimation of parameters in real-life:
estim_BVdk(samples = data2, admixMod = admixMod2, method = 'L-BFGS-B',
            compute_var = TRUE)
```

---

estim_IBM	<i>Estimates weights of unknown components from 2 admixtures using IBM</i>
-----------	--

---

## Description

Estimation of the component weights from the Inversion - Best Matching (IBM) method, related to two admixture models with respective probability density function (pdf)  $l_1$  and  $l_2$ , such that:  $l_1 = p_1 * f_1 + (1-p_1) * g_1$  and  $l_2 = p_2 * f_2 + (1-p_2) * g_2$ , where  $g_1$  and  $g_2$  are the known component densities. For further details about IBM approach, see 'Details' below.

## Usage

```
estim_IBM(samples, admixMod, n.integ = 1000, compute_var = FALSE)
```

## Arguments

samples	A list of the two considered samples.
admixMod	A list of two objects of class <code>admix_model</code> , one for each sample.
n.integ	Number of data points generated for the distribution on which to integrate.
compute_var	(default to FALSE) A boolean that indicates whether one computes the variance of the estimators of unknown mixing proportions.

**Value**

An object of class `estim_IBM`, containing 7 attributes: 1) the number of samples under study; 2) the sizes of samples; 3) the information about mixture components (distributions and parameters) for each sample; 4) the estimation method (Inversion Best Matching here, see the given reference); 5) the estimated mixing proportions (weights of the unknown component distributions in each sample); 6) the arbitrary value of the mixing weight in the first admixture sample (in case of equal known components, see the given reference); 7) the support of integration that was used in the computations.

**Author(s)**

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

**References**

Milhaud X, Pommeret D, Salhi Y, Vandekerckhove P (2024). “Two-sample contamination model test.” *Bernoulli*, **30**(1), 170–197. doi:10.3150/23BEJ1593.

**Examples**

```
## Continuous support: simulate mixture data.
mixt1 <- twoComp_mixt(n = 1500, weight = 0.5,
  comp.dist = list("norm", "norm"),
  comp.param = list(list("mean" = 3, "sd" = 0.5),
    list("mean" = 0, "sd" = 1)))

data1 <- getmixtData(mixt1)
mixt2 <- twoComp_mixt(n = 2000, weight = 0.7,
  comp.dist = list("norm", "norm"),
  comp.param = list(list("mean" = 3, "sd" = 0.5),
    list("mean" = 5, "sd" = 2)))

data2 <- getmixtData(mixt2)
## Define the admixture models:
admMod1 <- admix_model(knownComp_dist = mixt1$comp.dist[[2]],
  knownComp_param = mixt1$comp.param[[2]])
admMod2 <- admix_model(knownComp_dist = mixt2$comp.dist[[2]],
  knownComp_param = mixt2$comp.param[[2]])
## Estimate the mixture weights of the two admixture models (provide only hat(theta)_n):
estim_IBM(samples = list(data1,data2),
  admixMod = list(admMod1,admMod2), n.integ = 1000)

## Example 2: multinomial distribution (discrete case).
mixt1 <- twoComp_mixt(n = 1500, weight = 0.8,
  comp.dist = list("multinom", "multinom"),
  comp.param = list(list("size" = 1, "prob" = c(0.2,0.3,0.5)),
    list("size" = 1, "prob" = c(0.1,0.6,0.3))))

data1 <- getmixtData(mixt1)
mixt2 <- twoComp_mixt(n = 2000, weight = 0.3,
  comp.dist = list("multinom", "multinom"),
  comp.param = list(list("size" = 1, "prob" = c(0.2,0.3,0.5)),
    list("size" = 1, "prob" = c(0.7,0.1,0.2))))

data2 <- getmixtData(mixt2)
```



```
## Define the admixture models:
admixMod1 <- admix_model(knownComp_dist = mixt1$comp.dist[[2]],
                        knownComp_param = mixt1$comp.param[[2]])
admixMod2 <- admix_model(knownComp_dist = mixt2$comp.dist[[2]],
                        knownComp_param = mixt2$comp.param[[2]])
## Estimate the mixture weights of the two admixture models (provide only hat(theta)_n):
estim_IBM(samples = list(data1,data2), admixMod = list(admixMod1,admixMod2),
           compute_var = TRUE)
```

---

estim\_PS

*Estimates in an admixture using Patra and Sen approach*


---

### Description

Estimation of both the weight and the distribution of the unknown component in an admixture model, by Patra and Sen approach. Remind that the admixture probability density function (pdf)  $l$  is given by  $l = p*f + (1-p)*g$ , where  $g$  is the known component of the two-component mixture,  $p$  is the unknown proportion of the unknown component distribution  $f$ . More information in 'Details' below concerning the estimation method.

### Usage

```
estim_PS(
  samples,
  admixMod,
  method = c("fixed", "lwr.bnd", "cv"),
  c.n = 0.1 * log(log(length(samples))),
  folds = 10,
  reps = 1,
  cn.s = NULL,
  cn.length = 100,
  gridsize = 1200
)
```

### Arguments

samples	Sample to be studied.
admixMod	An object of class <code>admix_model</code> , containing information about the known component distribution and its parameter(s).
method	One of 'lwr.bnd', 'fixed' or 'cv': depending on whether compute some lower bound of the mixing proportion, the estimate based on the value of 'c.n' or use cross-validation for choosing 'c.n' (tuning parameter).
c.n	(default to NULL) A positive number for the penalization, see reference below. If NULL, equals to $0.1 * \log(\log(n))$ .
folds	(optional, default to 10) Number of folds used for cross-validation.

reps	(optional, default to 1) Number of replications for cross-validation.
cn.s	(optional) A sequence of 'c.n' to be used for cross-validation (vector of values). Default is equally spaced grid of 100 values between $.001 \times \log(\log(n))$ and $0.2 \times \log(\log(n))$ .
cn.length	(optional, default to 100) Number of equally spaced tuning parameter (between $.001 \times \log(\log(n))$ and $0.2 \times \log(\log(n))$ ). Values to search from.
gridsize	(default to 600) Number of equally spaced points (between 0 and 1) to evaluate the distance function. Larger values are more computationally intensive but also lead to more accurate estimates.

### Value

An object of class `estim_PS`, containing 10 attributes: 1) the number of samples studied (1 in this case); 2) the sample size; 3) the information about component distributions of the admixture model; 4) the estimation method (Patra and Sen here); 5) the estimated mixing weight (estimate of the unknown component proportion); 6) the estimated decontaminated CDF; 7) an object of the class 'dist.fun' (that gives the distance); 8) the tuning parameter 'c.n'; 9) the lower bound of the estimated mixing proportion (if such an option has been chosen); 10) the number of observations.

### Author(s)

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

### References

Patra RK, Sen B (2016). "Estimation of a two-component mixture model with applications to multiple testing." *Journal of the Royal Statistical Society Series B*, **78**(4), 869-893.

### Examples

```
## Simulate mixture data:
mixt1 <- twoComp_mixt(n = 800, weight = 0.33,
                    comp.dist = list("gamma", "exp"),
                    comp.param = list(list("shape" = 2, "scale" = 0.5),
                                       list("rate" = 0.25)))

data1 <- getmixtData(mixt1)
## Define the admixture model:
admixMod1 <- admix_model(knownComp_dist = mixt1$comp.dist[[2]],
                       knownComp_param = mixt1$comp.param[[2]])

## Estimation step:
estim_PS(samples = data1, admixMod = admixMod1, method = 'fixed')
```

---

gaussianity\_test

*Gaussianity test in an admixture model*


---

### Description

Performs an hypothesis test to check for the gaussianity of the unknown mixture component, given that the known component has support on the real line. Recall that an admixture model has probability density function (pdf)  $l = p*f + (1-p)*g$ , where  $g$  is the known pdf and  $l$  is observed (others are unknown). This test requires optimization (to estimate the unknown parameters) as defined by Bordes & Vandekerkhove (2010), which means that the unknown mixture component must have a symmetric density.

### Usage

```
gaussianity_test(
  samples,
  admixMod,
  conf_level = 0.95,
  ask_poly_param = FALSE,
  K = 3,
  s = 0.25,
  support = c("Real", "Integer", "Positive", "Bounded.continuous"),
  ...
)
```

### Arguments

<code>samples</code>	Sample under study.
<code>admixMod</code>	An object of class <code>admix_model</code> , containing useful information about distributions and parameters.
<code>conf_level</code>	(default to 0.95) The confidence level. Equals $1-\alpha$ , where $\alpha$ is the level of the test (type-I error).
<code>ask_poly_param</code>	(default to FALSE) If TRUE, ask the user to choose both the order 'K' of expansion coefficients in the orthonormal polynomial basis, and the penalization rate 's' involved on the penalization rule for the test.
<code>K</code>	( $K > 0$ , default to 3) If not asked (see the previous argument), number of coefficients considered for the polynomial basis expansion.
<code>s</code>	(in $]0,1/2[$ , default to 0.25) If not asked (see the previous argument), normalization rate involved in the penalization rule for model selection. See the reference below.
<code>support</code>	Support of the probability distributions, useful to choose the appropriate polynomial orthonormal basis. One of 'Real', 'Integer', 'Positive', or 'Bounded.continuous'.
<code>...</code>	Optional arguments to <code>estim_BVdk</code> .

**Details**

Extensions to the case of non-Gaussian known components can be overcome thanks to basic transformations using cdf.

**Value**

An object of class `gaussianity_test`, containing 10 elements: 1) the number of populations under study (1 in this case); 2) the sample size; 3) the information about the known component distribution; 4) the reject decision of the test; 5) the confidence level of the test, 6) the p-value of the test; 7) the value of the test statistic; 8) the variance of the test statistic at each order in the polynomial orthobasis expansion; 9) the selected rank (order) for the test statistic; 10) a list of estimates (mixing weight, mean and standard deviation of the Gaussian unknown distribution).

**Author(s)**

Xavier Milhau [xavier.milhau.research@gmail.com](mailto:xavier.milhau.research@gmail.com)

**References**

Pommeret D, Vandekerkhove P (2019). “Semiparametric density testing in the contamination model.” *Electronic Journal of Statistics*, 4743–4793. doi:10.1214/19EJS1650.

**Examples**

```
##### Under the null hypothesis H0.
## Simulate mixture data:
mixt1 <- twoComp_mixt(n = 250, weight = 0.4,
                    comp.dist = list("norm", "exp"),
                    comp.param = list(list("mean" = -2, "sd" = 0.5),
                                       list("rate" = 1)))

data1 <- getmixtData(mixt1)
## Define the admixture models:
admixMod1 <- admix_model(knownComp_dist = mixt1$comp.dist[[2]],
                       knownComp_param = mixt1$comp.param[[2]])

## Performs the test:
gaussianity_test(samples = data1, admixMod = admixMod1,
                 conf_level = 0.95, K = 3, s = 0.1, support = "Real")
```

---

getmixingWeight

*Extractor for object of class 'admix\_estim'*

---

**Description**

Get the estimated unknown mixing proportion related to the weight of the unknown component distribution of the admixture model.

**Usage**

```
getmixingWeight(x)
```

**Arguments**

x                    An object of class 'admix\_estim'.

**Author(s)**

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

getmixtData

*Extractor for object of class 'twoComp\_mixt'*

**Description**

Get the mixture data generated from method 'twoComp\_mixt'.

**Usage**

```
getmixtData(x)
```

**Arguments**

x                    An object of class 'twoComp\_mixt'.

**Author(s)**

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

IBM\_k\_samples\_test

*Equality test of K unknown component distributions*

**Description**

Equality test of the unknown component distributions coming from  $K$  ( $K > 1$ ) admixture models, based on the Inversion - Best Matching (IBM) approach. Recall that we have  $K$  populations following admixture models, each one with probability density functions (pdf)  $l_k = p_k * f_k + (1 - p_k) * g_k$ , where  $g_k$  is the known pdf and  $l_k$  corresponds to the observed sample. Perform the following hypothesis test:  $H_0 : f_1 = \dots = f_K$  against  $H_1 : f_i$  differs from  $f_j$  ( $i$  different from  $j$ , and  $i, j$  in  $1, \dots, K$ ).

**Usage**

```

IBM_k_samples_test(
  samples,
  admixMod,
  conf_level = 0.95,
  sim_U = NULL,
  tune_penalty = TRUE,
  n_sim_tab = 100,
  parallel = FALSE,
  n_cpu = 2
)

```

**Arguments**

<code>samples</code>	A list of the K samples to be studied, all following admixture distributions.
<code>admixMod</code>	A list of objects of class <code>class admix_model</code> , containing useful information about distributions and parameters.
<code>conf_level</code>	The confidence level of the K-sample test.
<code>sim_U</code>	(default to NULL) Random draws of the inner convergence part of the contrast as defined in the IBM approach (see 'Details' below).
<code>tune_penalty</code>	(default to TRUE) A boolean that allows to choose between a classical penalty term or an optimized penalty (embedding some tuning parameters, automatically optimized). Optimized penalty is particularly useful for low or unbalanced sample sizes to detect alternatives to the null hypothesis (H0). It is recommended to set it to TRUE.
<code>n_sim_tab</code>	(default to 100) Number of simulated Gaussian processes when tabulating the inner convergence distribution in the 'icv' testing method using the IBM estimation approach.
<code>parallel</code>	(default to FALSE) Boolean to indicate whether parallel computations are performed (speed-up the tabulation).
<code>n_cpu</code>	(default to 2) Number of cores used when paralleling computations.

**Value**

An object of class `admix_test`, containing 17 attributes: 1) the number of samples for the test; 2) the sizes of each sample; 3) the information about component distributions for each sample; 4) the reject decision of the test; 5) the confidence level of the test (1-alpha, where alpha refers to the first-type error); 6) the test p-value; 7) the 95th-percentile of the contrast tabulated distribution; 8) the test statistic value; 9) the selected rank (number of terms involved in the test statistic); 10) the terms (pairwise contrasts) involved in the test statistic; 11) A boolean indicating whether the penalization corresponds to the null hypothesis has been considered; 12) the value of penalized test statistics; 13) the selected optimal 'gamma' parameter (see reference below); 14) the selected optimal constant involved in the penalization process (see also the reference); 15) the tabulated distribution of the contrast; 16) the estimated mixing proportions (not implemented yet, since that makes sense only in case of equal unknown component distributions); 17) the matrix of pairwise contrasts (distance between two samples).

**Author(s)**

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

**References**

Milhaud X, Pommeret D, Salhi Y, Vandekerkhove P (2024). “Contamination-source based K-sample clustering.” *Journal of Machine Learning Research*, **25**(287), 1–32. <https://jmlr.org/papers/v25/23-0914.html>.

**Examples**

```
##### Under the null hypothesis H0 (with K=3 populations):
## Simulate mixture data:
mixt1 <- twoComp_mixt(n = 450, weight = 0.4,
                    comp.dist = list("norm", "norm"),
                    comp.param = list(list("mean" = -2, "sd" = 0.5),
                                       list("mean" = 0, "sd" = 1)))
mixt2 <- twoComp_mixt(n = 380, weight = 0.7,
                    comp.dist = list("norm", "norm"),
                    comp.param = list(list("mean" = -2, "sd" = 0.5),
                                       list("mean" = 1, "sd" = 1)))
mixt3 <- twoComp_mixt(n = 400, weight = 0.8,
                    comp.dist = list("norm", "exp"),
                    comp.param = list(list("mean" = -2, "sd" = 0.5),
                                       list("rate" = 1)))

data1 <- getmixtData(mixt1)
data2 <- getmixtData(mixt2)
data3 <- getmixtData(mixt3)
## Define the admixture models:
admMod1 <- admix_model(knownComp_dist = mixt1$comp.dist[[2]],
                      knownComp_param = mixt1$comp.param[[2]])
admMod2 <- admix_model(knownComp_dist = mixt2$comp.dist[[2]],
                      knownComp_param = mixt2$comp.param[[2]])
admMod3 <- admix_model(knownComp_dist = mixt3$comp.dist[[2]],
                      knownComp_param = mixt3$comp.param[[2]])
## Perform the 3-samples test:
IBM_k_samples_test(samples = list(data1, data2, data3),
                  admixMod = list(admMod1, admMod2, admMod3),
                  conf_level = 0.95, sim_U = NULL, n_sim_tab = 8,
                  tune_penalty = FALSE, parallel = FALSE, n_cpu = 2)
```

**Description**

Tabulate the distribution related to the inner convergence part of the contrast, by simulating trajectories of Gaussian processes and applying some transformations. Useful to perform the test hypothesis, by retrieving the (1-alpha)-quantile of interest. See 'Details' below and the cited paper therein for further information.

**Usage**

```
IBM_tabul_stochasticInteg(
  samples,
  admixMod,
  min_size = NULL,
  n.varCovMat = 80,
  n_sim_tab = 100,
  parallel = FALSE,
  n_cpu = 2
)
```

**Arguments**

<code>samples</code>	A list of the two samples under study.
<code>admixMod</code>	A list of two objects of class 'admix_model', with information about distributions and parameters.
<code>min_size</code>	(optional, NULL by default) In the k-sample case, useful to provide the minimal size among all samples (needed to take into account the correction factor for variance-covariance assessment). Otherwise, useless.
<code>n.varCovMat</code>	(default to 80) Number of time points at which the Gaussian processes are simulated.
<code>n_sim_tab</code>	(default to 100) Number of simulated Gaussian processes when tabulating the inner convergence distribution in the 'icv' testing method using the IBM estimation approach.
<code>parallel</code>	(default to FALSE) Boolean to indicate whether parallel computations are performed (speed-up the tabulation).
<code>n_cpu</code>	(default to 2) Number of cores used when paralleling computations.

**Value**

A list with four elements, containing: 1) random draws of the contrast as defined in the reference given here; 2) estimated unknown component weights for the two admixture models; 3) the value of the the empirical contrast; 4) support that was used to evaluate the variance-covariance matrix of the empirical processes.

**Author(s)**

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)



## References

Milhaud X, Pommeret D, Salhi Y, Vandekerckhove P (2024). “Two-sample contamination model test.” *Bernoulli*, **30**(1), 170–197. doi:10.3150/23BEJ1593.

## Examples

```
## Simulate mixture data:
mixt1 <- twoComp_mixt(n = 1200, weight = 0.4,
                    comp.dist = list("norm", "norm"),
                    comp.param = list(list("mean" = -2, "sd" = 0.5),
                                       list("mean" = 0, "sd" = 1)))
mixt2 <- twoComp_mixt(n = 1000, weight = 0.7,
                    comp.dist = list("norm", "norm"),
                    comp.param = list(list("mean" = -2, "sd" = 0.5),
                                       list("mean" = 1, "sd" = 1)))

data1 <- getmixtData(mixt1)
data2 <- getmixtData(mixt2)
## Define the admixture models:
admixtureMod1 <- admix_model(knownComp_dist = mixt1$comp.dist[[2]],
                            knownComp_param = mixt1$comp.param[[2]])
admixtureMod2 <- admix_model(knownComp_dist = mixt2$comp.dist[[2]],
                            knownComp_param = mixt2$comp.param[[2]])
IBM_tabul_stochasticInteg(samples = list(data1, data2), admixtureMod = list(admixtureMod1, admixtureMod2),
                          min_size=NULL, n.varCovMat=20, n_sim_tab=2, parallel=FALSE, n_cpu=2)
```

---

milkyWay

*Heliocentric velocity for the Milky Way*

---

## Description

Heliocentric velocity for the Milky Way

## Usage

milkyWay

## Format

A data frame with 170,601 rows and 1 column:

**V1** Heliocentric velocity measurements of the Milky way

## Source

[https://www.aanda.org/articles/aa/full\\_html/2018/08/aa32905-18/aa32905-18.html](https://www.aanda.org/articles/aa/full_html/2018/08/aa32905-18/aa32905-18.html)

## References

Walker MG, Mateo M, Olszewski EW, Gnedin OY, Wang X, Sen B, Woodroofe M (2007). “Velocity Dispersion Profiles of Seven Dwarf Spheroidal Galaxies.” *The Astrophysical Journal*, **667**(1), L53–L56. ISSN 1538-4357, doi:10.1086/521998, <http://dx.doi.org/10.1086/521998>.

---

mortality\_sample      *Deaths statistics in 11 european countries*

---

## Description

Deaths statistics in 11 european countries

## Usage

mortality\_sample

## Format

Dataset providing the exposure-to-death (population size) and number of deaths for males in 11 european countries, between 1908 and 2020, with ages ranging from 30 years old to 85 years old. Exported from the Human Mortality Database (HMD). The two first lists relate to some subsample of the population size and number of deaths in those countries, with random sampling from the original dataset.

An evolving data frame of exposure-to-death and number of deaths in Belgium, Switzerland, Denmark, Spain, Finland, France, United Kingdom, Italia, The Netherlands, Norway and Sweden.

**XP** A list of eleven elements (one for each country) giving a subset of the exposure-to-death (or reduced population size), each element having 56 rows (ages 30-85) and 113 columns (period 1908-2020)

**DX** A list of eleven elements (one for each country) giving a subset of the number of deaths, each element having 56 rows (ages 30-85) and 113 columns (period 1908-2020)

**names** A list of eleven elements giving the names of the countries, in the same order as the elements in other lists

## Source

<https://www.mortality.org>

---

orthobasis_test	<i>Equality test of two unknown component distributions using polynomial expansions</i>
-----------------	---

---

### Description

Tests the null hypothesis ( $H_0: f_1=f_2$ ) using the decomposition of unknown component densities of two admixture distributions in an adequate orthonormal polynomial basis. Recall that we have two admixture models with respective probability density functions (pdf)  $l_1 = p_1*f_1 + (1-p_1)g_1$  and  $l_2 = p_2*f_2 + (1-p_2)*g_2$ , where  $g_1$  and  $g_2$  are the only known elements and  $l_1$  and  $l_2$  are observed. The admixture weights  $p_1$  and  $p_2$  thus have to be estimated. For further information on this method, see 'Details' below.

### Usage

```
orthobasis_test(
  samples,
  admixMod,
  conf_level = 0.95,
  est_method = c("BVdk", "PS"),
  ask_poly_param = FALSE,
  K = 3,
  s = 0.25,
  nb_echBoot = 100,
  support = c("Real", "Integer", "Positive", "Bounded.continuous", "Bounded.discrete"),
  bounds_supp = NULL,
  ...
)
```

### Arguments

samples	List of the two samples, each one following the mixture distribution given by $l = p*f + (1-p)*g$ , with $f$ and $p$ unknown and $g$ known.
admixMod	An object of class <code>admix_model</code> , containing useful information about distributions and parameters.
conf_level	The confidence level, default to 95 percent. Equals $1-\alpha$ , where $\alpha$ is the level of the test (type-I error).
est_method	Estimation method to get the component weights, either 'PS' (Patra and Sen estimation) or 'BVdk' (Bordes and Vendekerkhove estimation). Choosing 'PS' requires to specify the number of bootstrap samples.
ask_poly_param	(default to FALSE) If TRUE, ask the user to choose both the order 'K' of expansion coefficients in the orthonormal polynomial basis, and the penalization rate 's' involved on the penalization rule for the test.
K	( $K > 0$ , default to 3) If not asked (see the previous argument), number of coefficients considered for the polynomial basis expansion.

s	(in ]0,1/2[, default to 0.25) If not asked (see the previous argument), rate at which the normalization factor is set in the penalization rule for model selection (in ]0,1/2[). Low values of 's' favors the detection of alternative hypothesis. See reference below. [, default to 0.25) If not asked (see the previous argument), rate at which the normalization factor is set in the penalization rule for model selection (in ]: R:,%20default%20to%200.25)%20If%20not%20asked%20(see%20the%20previous%20argument),%20
nb_echBoot	(default to 100) Number of bootstrap samples, useful when choosing 'PS' estimation method.
support	Support of the probability distributions, useful to choose the appropriate polynomial orthonormal basis. One of 'Real', 'Integer', 'Positive', or 'Bounded.continuous'.
bounds_supp	(default to NULL) Useful if support = 'Bounded.continuous', a list of minimum and maximum bounds, specified as following: list( list(min.f1,min.g1,min.f2,min.g2) , list(max.f1,max.g1,max.f2,max.g2) )
...	Optional arguments to <code>estim_BVdk</code> or <code>estim_PS</code> , depending on the chosen argument 'est_method' (see above).

### Value

An object of class `orthobasis_test`, containing ten attributes: 1) the number of populations under study (2 in this case); 2) the sizes of samples; 3) the information about the known component distribution; 4) the reject decision of the test; 5) the confidence level of the test, 6) the p-value of the test; 7) the value of the test statistic; 8) the variance of the test statistic at each order in the polynomial orthobasis expansion; 9) the selected rank (order) for the test statistic; 10) a vector of estimates, related to the estimated mixing proportions in the two samples.

### Author(s)

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

### References

Milhaud X, Pommeret D, Salhi Y, Vandekerkhove P (2022). "Semiparametric two-sample admixture components comparison test: The symmetric case." *Journal of Statistical Planning and Inference*, **216**, 135-150. ISSN 0378-3758, [doi:10.1016/j.jspi.2021.05.010](https://doi.org/10.1016/j.jspi.2021.05.010).

### Examples

```
#### Under the null hypothesis H0.
mixt1 <- twoComp_mixt(n = 300, weight = 0.77,
                     comp.dist = list("norm", "exp"),
                     comp.param = list(list("mean" = 1, "sd" = 1),
                                       list("rate" = 0.33)))

data1 <- getmixtData(mixt1)
admixMod1 <- admix_model(knownComp_dist = mixt1$comp.dist[[2]],
                       knownComp_param = mixt1$comp.param[[2]])

mixt2 <- twoComp_mixt(n = 500, weight = 0.62,
                     comp.dist = list("norm", "norm"),
                     comp.param = list(list("mean" = 1, "sd" = 1),
```

```

                                list("mean" = -2, "sd" = 0.5)))
data2 <- getmixtData(mixt2)
admixMod2 <- admix_model(knownComp_dist = mixt2$comp.dist[[2]],
                        knownComp_param = mixt2$comp.param[[2]])
## Test procedure:
orthobasis_test(samples = list(data1,data2), admixMod = list(admixMod1,admixMod2),
                conf_level = 0.95, est_method = 'BVdk', support = 'Real')
```

---

```
plot.decontaminated_density
```

*Plot method for class 'decontaminated\_density'*

---

## Description

Plot the decontaminated density of the unknown component from some admixture model, after inversion of the admixture cumulative distribution functions.

## Usage

```
## S3 method for class 'decontaminated_density'
plot(x, x_val, add_plot = FALSE, ...)
```

## Arguments

x	An object of class 'decontaminated_density' (see ?decontaminated_density).
x_val	(numeric) A vector of points at which to evaluate the probability mass/density function.
add_plot	(default to FALSE) A boolean specifying if one plots the decontaminated density over an existing plot. Used for visual comparison purpose.
...	Arguments to be passed to generic method 'plot', such as graphical parameters (see par).

## Details

The decontaminated density is obtained by inverting the admixture density, given by  $l = p*f + (1-p)*g$ , to isolate the unknown component  $f$  after having estimated  $p$  and  $l$ .

## Value

The plot of the decontaminated density.

## Author(s)

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

**Examples**

```
##### Continuous support:
## Simulate mixture data:
mixt1 <- twoComp_mixt(n = 400, weight = 0.4,
                     comp.dist = list("norm", "norm"),
                     comp.param = list(list("mean" = 3, "sd" = 0.5),
                                       list("mean" = 0, "sd" = 1)))
mixt2 <- twoComp_mixt(n = 350, weight = 0.6,
                     comp.dist = list("norm", "norm"),
                     comp.param = list(list("mean" = 3, "sd" = 0.5),
                                       list("mean" = 5, "sd" = 2)))

data1 <- getmixtData(mixt1)
data2 <- getmixtData(mixt2)
## Define the admixture models:
admMod1 <- admix_model(knownComp_dist = mixt1$comp.dist[[2]],
                      knownComp_param = mixt1$comp.param[[2]])
admMod2 <- admix_model(knownComp_dist = mixt2$comp.dist[[2]],
                      knownComp_param = mixt2$comp.param[[2]])

## Estimation:
est <- admix_estim(samples = list(data1,data2),
                  admMod = list(admMod1,admMod2), est_method = 'PS')
prop <- getmixingWeight(est)
## Determine the decontaminated version of the unknown density by inversion:
res1 <- decontaminated_density(sample1 = data1, estim.p = prop[1],
                              admMod = admMod1)
res2 <- decontaminated_density(sample1 = data2, estim.p = prop[2],
                              admMod = admMod2)

## Use appropriate sequence of x values:
plot(x = res1, x_val = seq(from = 0, to = 6, length.out = 100), add_plot = FALSE)
plot(x = res2, col = "red", x_val = seq(from = 0, to = 6, length.out = 100), add_plot = TRUE)

##### Countable discrete support:
mixt1 <- twoComp_mixt(n = 4000, weight = 0.7,
                     comp.dist = list("pois", "pois"),
                     comp.param = list(list("lambda" = 3),
                                       list("lambda" = 2)))
mixt2 <- twoComp_mixt(n = 3500, weight = 0.85,
                     comp.dist = list("pois", "pois"),
                     comp.param = list(list("lambda" = 3),
                                       list("lambda" = 4)))

data1 <- getmixtData(mixt1)
data2 <- getmixtData(mixt2)
## Define the admixture models:
admMod1 <- admix_model(knownComp_dist = mixt1$comp.dist[[2]],
                      knownComp_param = mixt1$comp.param[[2]])
admMod2 <- admix_model(knownComp_dist = mixt2$comp.dist[[2]],
                      knownComp_param = mixt2$comp.param[[2]])

## Estimation:
est <- admix_estim(samples = list(data1,data2),
                  admMod = list(admMod1,admMod2), est_method = "IBM")
prop <- getmixingWeight(est)
## Determine the decontaminated version of the unknown density by inversion:
```

```

res1 <- decontaminated_density(sample1 = data1, estim.p = prop[1],
                              admixMod = admixMod1)
res2 <- decontaminated_density(sample1 = data2, estim.p = prop[2],
                              admixMod = admixMod2)

## Use appropriate sequence of x values:
plot(x = res1, x_val = seq(from = 0, to = 15, by = 1), add_plot = FALSE)
plot(x = res2, x_val = seq(from = 0, to = 15, by = 1), add_plot = TRUE, col = "red")

##### Finite discrete support:
mixt1 <- twoComp_mixt(n = 4000, weight = 0.7,
                    comp.dist = list("multinom", "multinom"),
                    comp.param = list(list("size" = 1, "prob" = c(0.3,0.4,0.3)),
                                       list("size" = 1, "prob" = c(0.6,0.3,0.1))))
mixt2 <- twoComp_mixt(n = 3500, weight = 0.85,
                    comp.dist = list("multinom", "multinom"),
                    comp.param = list(list("size" = 1, "prob" = c(0.3,0.4,0.3)),
                                       list("size" = 1, "prob" = c(0.2,0.6,0.2))))

data1 <- getmixtData(mixt1)
data2 <- getmixtData(mixt2)
## Define the admixture models:
admixMod1 <- admix_model(knownComp_dist = mixt1$comp.dist[[2]],
                       knownComp_param = mixt1$comp.param[[2]])
admixMod2 <- admix_model(knownComp_dist = mixt2$comp.dist[[2]],
                       knownComp_param = mixt2$comp.param[[2]])

## Estimation:
est <- admix_estim(samples = list(data1,data2),
                  admixMod = list(admixMod1,admixMod2), est_method = "IBM")
prop <- getmixingWeight(est)
## Determine the decontaminated version of the unknown density by inversion:
res1 <- decontaminated_density(sample1 = data1, estim.p = prop[1],
                              admixMod = admixMod1)
res2 <- decontaminated_density(sample1 = data2, estim.p = prop[2],
                              admixMod = admixMod2)

## Use appropriate sequence of x values:
plot(x = res1, x_val = seq(from=1, to=3, by=1), add_plot = FALSE)
plot(x = res2, x_val = seq(from=1, to=3, by=1), add_plot = TRUE, col = "red")

```

---

plot.twoComp\_mixt

*Plots several mixture densities on the same graph*


---

## Description

Plots the empirical densities of the samples with optional arguments to improve the visualization.

## Usage

```

## S3 method for class 'twoComp_mixt'
plot(x, add.plot = FALSE, ...)

```

**Arguments**

x	Object of class 'twoComp_mixt' from which the density will be plotted.
add.plot	(default to FALSE) Option to plot another mixture distribution on the same graph.
...	further classical arguments and graphical parameters for methods plot and hist.

**Value**

a plot with the densities of the samples provided as inputs.

**Author(s)**

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

---

print.admix\_cluster    *Print method for object of class 'admix\_cluster'*

---

**Description**

Print the main results when clustering the unknown component distributions coming from various admixture samples, i.e. the obtained clusters.

**Usage**

```
## S3 method for class 'admix_cluster'  
print(x, ...)
```

**Arguments**

x	An object of class 'admix_cluster' (see ?admix_clustering).
...	further arguments passed to or from other methods.

**Author(s)**

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)



---

print.admix\_estim      *Print the estimated parameters from K admixture models*

---

**Description**

Print the estimated parameters from K admixture models

**Usage**

```
## S3 method for class 'admix_estim'  
print(x, ...)
```

**Arguments**

x                      An object of class 'admix\_estim' (see ?admix\_estim).  
...                     further arguments passed to or from other methods.

**Author(s)**

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

---

print.admix\_model      *Print method for objects of class 'admix\_model'*

---

**Description**

Print an object of class 'admix\_mod'. An admixture model has probability density function (pdf)  $l_i$  such that:  $l_i = p_i * f_i + (1-p_i) * g_i$ , with  $g_i$  the known component density. The unknown quantities are therefore  $p_i$  and  $f_i$ .

**Usage**

```
## S3 method for class 'admix_model'  
print(x, ...)
```

**Arguments**

x                      An object of class 'admix\_model'.  
...                     A list of additional parameters belonging to the default method.

**Author(s)**

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

print.admix\_test      *Print method for objects 'admix\_test'*

---

**Description**

Print method for objects 'admix\_test'

**Usage**

```
## S3 method for class 'admix_test'  
print(x, ...)
```

**Arguments**

x                    An object of class 'admix\_test'.  
...                  A list of additional parameters belonging to the default method.

**Author(s)**

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

---

print.decontaminated\_density  
                          *Print method for object of class 'decontaminated\_density'*

---

**Description**

Print some overview of the decontaminated density function.

**Usage**

```
## S3 method for class 'decontaminated_density'  
print(x, ...)
```

**Arguments**

x                    An object of class 'decontaminated\_density' (see ?decontaminated\_density).  
...                  Arguments to be passed to generic method 'plot', such as graphical parameters  
                          (see par).

**Value**

More important information about the decontaminated density.

**Author(s)**

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

---

print.estim\_BVdk      *Print method for objects 'estim\_BVdk'*

---

**Description**

Print the results stored in an object of class 'estim\_BVdk'.

**Usage**

```
## S3 method for class 'estim_BVdk'  
print(x, ...)
```

**Arguments**

x                    An object of class 'estim\_BVdk'.  
...                  A list of additional parameters belonging to the default method.

**Author(s)**

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

---

print.estim\_IBM      *Print method for objects of class 'estim\_IBM'*

---

**Description**

Print the results stored in an object of class 'estim\_IBM'.

**Usage**

```
## S3 method for class 'estim_IBM'  
print(x, ...)
```

**Arguments**

x                    An object of class 'estim\_IBM'.  
...                  A list of additional parameters belonging to the default method.

**Author(s)**

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

---

print.estim\_PS            *Print method for objects of class 'estim\_PS'*

---

**Description**

Print all the attributes of objects of class 'estim\_PS'. Results of estimated quantities in an admixture using Patra and Sen approach

**Usage**

```
## S3 method for class 'estim_PS'  
print(x, ...)
```

**Arguments**

x                    An object of class 'estim\_PS'.  
...                  further arguments passed to or from other methods.

**Author(s)**

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

---

print.gaussianity\_test  
*Print method for objects 'gaussianity\_test'*

---

**Description**

Print method for objects 'gaussianity\_test'

**Usage**

```
## S3 method for class 'gaussianity_test'  
print(x, ...)
```

**Arguments**

x                    An object of class 'gaussianity\_test'.  
...                  A list of additional parameters belonging to the default method.

**Author(s)**

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

---

print.IBM\_test            *Print method for objects 'IBM\_test'*

---

**Description**

Print method for objects 'IBM\_test'

**Usage**

```
## S3 method for class 'IBM_test'  
print(x, ...)
```

**Arguments**

x                    An object of class 'IBM\_test'.  
...                  A list of additional parameters belonging to the default method.

**Author(s)**

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

---

print.orthobasis\_test    *Print method for objects of class 'orthobasis\_test'*

---

**Description**

Print method for objects of class 'orthobasis\_test'

**Usage**

```
## S3 method for class 'orthobasis_test'  
print(x, ...)
```

**Arguments**

x                    An object of class 'orthobasis\_test'.  
...                  A list of additional parameters belonging to the default method.

**Author(s)**

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

---

```
print.twoComp_mixt      Print method for objects 'twoComp_mixt'
```

---

### Description

Print an object of class 'twoComp\_mixt'. A two-component mixture model has probability density function (pdf)  $l$  such that:  $l = p * f + (1-p) * g$ , where  $p$  is the mixing proportion, and  $f$  and  $g$  are the component distributions.

### Usage

```
## S3 method for class 'twoComp_mixt'
print(x, ...)
```

### Arguments

`x` An object of class 'twoComp\_mixt'.  
`...` A list of additional parameters belonging to the default method.

### Author(s)

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

---

```
stmf_small      Short-term Mortality Fluctuations (STMF) data
```

---

### Description

Restricted to 6 countries: Belgium, France, Italy, Netherlands, Spain, Germany. Weekly death counts provide the most objective and comparable way of assessing the scale of short-term mortality elevations across countries and time. Extraction date from the Human Mortality Database (HMD): 09/21/2020.

### Usage

```
stmf_small
```

### Format

A data frame with 88146 rows and 19 variables:

**CountryCode** Mortality database country code

**Year** Year

**Week** Week number

**Sex** Gender ('m': male, 'f': female, 'b': both)

**D0\_14** Age range 0-14  
**D15\_64** Age range 15-64  
**D65\_74** Age range 65-74  
**D75\_84** Age range 75-84  
**D85p** Age range 85-+  
**DTotal** Count of deaths for all ages combined  
**R0\_14** Crude death rate for age range 0-14  
**R15\_64** Crude death rate for age range 15-64  
**R65\_74** Crude death rate for age range 65-74  
**R75\_84** Crude death rate for age range 75-84  
**R85p** Crude death rate for age range 85-+  
**RTotal** Crude death rate for all ages combined  
**Split** Indicates if data were split from aggregated age groups (0 if the original data has necessary detailed age scale). For example, if the original age scale was 0-4, 5-29, 30-65, 65+, then split will be equal to 1  
**SplitSex** Indicates if the original data are available by sex (0) or data are interpolated (1)  
**Forecast** Equals 1 for all years where forecasted population exposures were used to calculate weekly death rates

#### Source

<https://www.mortality.org>

---

summary.admix\_cluster *Summary method for object of class 'admix\_cluster'*

---

#### Description

Summarizes the results obtained when clustering the unknown component distributions coming from various admixture samples.

#### Usage

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

#### Arguments

object            An object of class 'admix\_cluster' (see ?admix\_clustering).  
 ...                further arguments passed to or from other methods.

#### Author(s)

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

---

summary.admix\_estim     *Results of estimated parameters from K admixture models*

---

### Description

Summarize the estimated weight(s) of the unknown component(s) in the admixture model(s) under study. Recall that an admixture model follows the cumulative distribution function (CDF)  $L$ , where  $L = p * F + (1 - p) * G$ , with  $G$  a known CDF, and  $p$  and  $F$  unknown quantities.

### Usage

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

### Arguments

object             An object of class 'admixture\_estim' (see ?admixture\_estim).  
 ...                further arguments passed to or from other methods.

### Author(s)

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

---

summary.admix\_test     *Summary method for 'admixture\_test' objects*

---

### Description

Print the decision (as well as other useful information) of the statistical test with null hypothesis corresponding to the equality of unknown component distributions in admixture models. More precisely, given two (or more) admixture models with cumulative distribution functions (CDF)  $L_1$  and  $L_2$ , where  $L_i = \pi_i * F_i + (1 - \pi_i) * G_i$   $i=1,2$  and  $G_i$  are the known CDFs, the function performs the test:  $H_0: F_1 = F_2$  versus  $H_1: F_1 \neq F_2$ .

### Usage

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

### Arguments

object             An object of class 'admixture\_test' (see ?admixture\_test).  
 ...                further arguments passed to or from other methods.

### Author(s)

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)



---

summary.estim\_BVdk      *Summary method for objects 'estim\_BVdk'*

---

**Description**

Summarizes the results stored in an object of class 'estim\_BVdk'.

**Usage**

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

**Arguments**

object            An object of class 'estim\_BVdk'.  
...                A list of additional parameters belonging to the default method.

**Author(s)**

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

---

summary.estim\_IBM      *Summary method for objects 'estim\_IBM'*

---

**Description**

Summarizes the results stored in an object of class 'estim\_IBM'.

**Usage**

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

**Arguments**

object            An object of class 'estim\_IBM'.  
...                A list of additional parameters belonging to the default method.

**Author(s)**

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

---

summary.estim\_PS      *Summary method for objects 'estim\_PS'*

---

**Description**

Summarizes the results stored in an object of class 'estim\_PS'.

**Usage**

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

**Arguments**

object      An object of class 'estim\_PS'.  
...      A list of additional parameters belonging to the default method.

**Author(s)**

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

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summary.gaussianity\_test  
*Summary method for objects 'gaussianity\_test'*

---

**Description**

Summary method for objects 'gaussianity\_test'

**Usage**

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

**Arguments**

object      An object of class 'gaussianity\_test'.  
...      A list of additional parameters belonging to the default method.

**Author(s)**

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

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summary.IBM\_test      *Summary method for objects 'IBM\_test'*

---

**Description**

Summary method for objects 'IBM\_test'

**Usage**

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

**Arguments**

object      An object of class 'IBM\_test'.  
...      A list of additional parameters belonging to the default method.

**Author(s)**

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

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summary.orthobasis\_test  
*Summary method for objects of class 'orthobasis\_test'*

---

**Description**

Summary method for objects of class 'orthobasis\_test'

**Usage**

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

**Arguments**

object      An object of class 'orthobasis\_test'.  
...      A list of additional parameters belonging to the default method.

**Author(s)**

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

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`twoComp_mixt`*Simulation of a two-component mixture model*

---

### Description

Simulate a two-component mixture model following the probability density function (pdf)  $l$  such that  $l = p*f + (1-p)*g$ , with  $f$  and  $g$  the mixture component distributions, and  $p$  the mixing weight.

### Usage

```
twoComp_mixt(  
  n = 1000,  
  weight = 0.5,  
  comp.dist = list("norm", "norm"),  
  comp.param = list(list(mean = 0, sd = 1), list(mean = 2, sd = 1))  
)
```

### Arguments

<code>n</code>	Number of observations to be simulated.
<code>weight</code>	Weight of the first component distribution (distribution $f$ ) in the mixture.
<code>comp.dist</code>	A list of two elements corresponding to the component distributions (specified with R native names) involved in the mixture model. These elements respectively refer to the two component distributions $f$ and $g$ .
<code>comp.param</code>	A list of two elements corresponding to the parameters of the component distributions, each element being a list itself. The names used in each list must correspond to the native R argument names for these distributions. These elements respectively refer to the parameters of $f$ and $g$ distributions of the mixture model.

### Value

An object of class `twoComp_mixt`, containing eight attributes: 1) the number of simulated observations, 2) the simulated mixture data, 3) the support of the distributions, 4) the name of the component distributions, 5) the name of the parameters of the component distributions and their values, 6) the mixing proportion, 7) the observations coming from the first component, 8) the observations coming from the second component.

### Author(s)

Xavier Milhaud [xavier.milhaud.research@gmail.com](mailto:xavier.milhaud.research@gmail.com)

**Examples**

```
## Mixture of continuous random variables:
sim.X <- twoComp_mixt(n = 2000, weight = 0.5,
                     comp.dist = list("norm", "norm"),
                     comp.param = list(list("mean"=3, "sd"=0.5),
                                         list("mean"=0, "sd"=1)))
sim.Y <- twoComp_mixt(n = 1200, weight = 0.7,
                     comp.dist = list("norm", "exp"),
                     comp.param = list(list("mean"=-3, "sd"=0.5),
                                         list("rate"=1)))

print(sim.X)
plot(sim.X, xlim=c(-5,5), ylim=c(0,0.5))
plot(sim.Y, add.plot = TRUE, xlim=c(-5,5), ylim=c(0,0.5), col = "red")

## Mixture of discrete random variables:
sim.X <- twoComp_mixt(n = 2000, weight = 0.5,
                     comp.dist = list("multinom", "multinom"),
                     comp.param = list(list("size"=1, "prob"=c(0.3,0.4,0.3)),
                                         list("size"=1, "prob"=c(0.1,0.2,0.7))))

print(sim.X)
plot(sim.X)
```

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