Description

This function computes local fdr values by using a two-components mixture model with a semi-parametric density estimation. The code is freely inspired from the density function. For a simple use, we recommand the default setting (most parameters are optional).

Usage

```
kerfdr(pv,x=NULL,trans=c("probit","log","none"),f0=NULL,localfdr=NULL,pi1="storey",lambda=0.5,b
```

Arguments

`pv`	the vector of raw p-values.
`x`	a transformation of `pv`. It can be given by the user or (if `NULL`) computed via the `trans` parameter
`trans`	the transformation to apply on `pv` to produce `x`: `"probit"` (by default) returns `qnorm(pv)` and `"log"` returns `log10(pv)`.
`f0`	the sample density under the null hypothesis. Can be specified by the user. If `NULL` (by default) the density under H0 is determined according to `trans`: if `trans = "probit"` then `f0` is a standard Gaussian distribution; if `trans = "log"` then `f0` is a standard Exponential distribution; if `trans = "none"` then `f0` is a standard Uniform distribution
`localfdr`	values to initiate the iterative algorithm. If `NULL` (by default) initial values are then sampled in a Uniform distribution [0,1]
`pi1`	a priori proportion of alternative hypothesis or a method (string) to compute it; by default it uses the method proposed by Storey and Tibshirani (2003).
`lambda`	p-value threshold for the Storey's calculation of `pi1` (0.5 by default). See qvalue for more details.
`bw`	a bandwidth value or a method to determine it among `"nrd0", "nrd", "ucv", "bcv", "sj-ste", "sj-dpi"`. See bandwidth for more details.
`kernel`	the kernel used (string) among `"gaussian"` (by default), `"epanechnikov", "rectangular", "triangular", "biweight","cosine"`. For more details on kernels: http://stat.genopole.cnrs.fr/sg/software/kerfdr/kernels
`truncat`	an interval on p-values to deal with truncated distributions such as those obtained with Monte-Carlo simulations.
`plot`	if `TRUE`, it returns graphics of local fdr estimations. Some plots are inspired from qvalue.
`cuts`	vector of significance values to use in `summary` (see below)

Value

A list of parameters (`pv, x, pi1, bw, f0` ...) and the following results:

`f`	the observed mixture density
`f1`	the estimated density under H1
`localfdr`	the local fdr values resulting from the algorithm
`summary`	a summary table comparing the number of significant calls for the raw p-values, Bonferroni and Benjamini-Hochberg corrections and for the calculated local fdr, using a set of cutoffs given by `cuts`

Author(s)

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References

http://stat.genopole.cnrs.fr/sg/software/kerfdr, Robin et al (2007), Strimmer (2008), Guedj et al (under review)

Examples

```
# Example 1: kerfdr with different plots
n = 10000
pi0 = 0.8
# plot in a probit scale (default)
pv = 1-pnorm(c(rnorm(n*pi0), rnorm(n*(1-pi0), 4)))
res = kerfdr(pv)
res$pi0
res$summary
# plot in a log scale
kerfdr(pv, trans = "log")
# plot in the raw p-values scale
kerfdr(pv, trans = "none")
# Example 2: truncation on a vector of null p-values (resulting local fdr should be 1 for each point)
n = 10000
pv = runif(n)
# truncation on [0.1;0.9]
pv[which(pv < 0.1)] = 0.1
pv[which(pv > 0.9)] = 0.9
# kerfdr WITHOUT taking the truncation into account (local fdr is hence badly estimated)
kerfdr(pv, trans = "log")
# kerfdr by taking the truncation into account (local fdr is then well estimated)
kerfdr(pv, truncat = c(0.1, 0.9), trans = "log")
```