

Package ‘XPEB’

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Title Cross-Population Empirical Bayes

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Description This R package implements the cross-population empirical Bayes method, XPEB, described in Coram et al. 2015. XPEB takes as input P-value summary statistics from two GWAS, a target-GWAS from for example an ethnic minority population of primary interest and an auxiliary base-GWAS such as a larger GWAS in Europeans, and reprioritizes SNPs in the target population to compute local false discovery rates. XPEB also estimates the degree of overlap in the genetic architecture underlying the trait in the two populations.

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Depends R (>= 2.15.0)

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URL <http://med.stanford.edu/tanglab/software>

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run.xpeb	<i>Calculates the XPEB locfdr and overlap for a target and base-GWAS</i>
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Description

This function runs XPEB. It takes as input the target and base-GWAS files, containing the GWAS p-values for the target and base. It applies genomic control correction per user specification. Then it runs XPEB including trimming for LD based on base pair position. The function returns the XPEB locfdr and estimated overlap.

Usage

```
run.xpeb(path.target,path.base,n.target,n.base,gc.target=T,gc.base=T,n.iter=1e6)
```

Arguments

path.target	string indicating the path to the target-GWAS file.
path.base	string indicating the path to the base-GWAS file.
n.base	numeric, number of individuals in the base-GWAS
n.target	numeric, number of individuals in the target-GWAS.
gc.target	logical. Should genomic controls be applied to the target-GWAS? True by default.
gc.base	logical. Should genomic controls be applied to the base-GWAS? True by default.
n.iter	numeric: number of iterations for MCMC.

Value

locfdr	a data frame giving for each marker, the locfdr.
overlap	numeric: the overlap in genetic architecture between the two populations.

References

Marc A Coram, Sophie I Candille, Qing Duan, Katie Chan, Yun Li, Charles Kooperberg, Alex P Reiner, Hua Tang. An Ethnicity-Aware Approach for Mapping Complex Traits Using Multi-ethnic Data. American Journal of Human Genetics (submitted)

Examples

```
#Unzip the example files from the package and retrieve their path
#target-GWAS
path.target <- system.file("extdata", "target.gwas.txt.zip", package="XPEB")
unzip(path.target,exdir="TMPinput")
path.target <- "TMPinput/target.gwas.txt"
#base-GWAS
path.base <- system.file("extdata", "base.gwas.txt.zip", package="XPEB")
unzip(path.base,exdir="TMPinput")
path.base <- "TMPinput/base.gwas.txt"

#Run XPEB on the example files
res <- run.xpeb(path.target=path.target,path.base=path.base,n.target=1e4,n.base=1e5)

#print the overlap
print("The estimated overlap in genetic architecture is:", res$overlap, sep="")

#Save the locfdr calculation results to a text file
write.table(res$locfdr, file="locfdrResults.txt", sep="\t", quote=FALSE, row.names=FALSE)
```

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