Package 'ADDO'

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Title a comprehensive toolkit to detect, classify and visualise additive and non-additive Quantitative Trait Loci

Description A highly-efficient tool designed to detect, classify and visualize quantitative trait loci (QTLs) with additive and non-additive effects. ADDO implements a mixed-model transformation to control for population structure and unequal relatedness that accounts for both additive and dominant genetic covariance among individuals, and decomposes single nucleotide polymorphism (SNP) effects into additive, partial dominance, dominance and over-dominance categories. A matrix multiplication approach is used to accelerate the computation.

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Depends R (>= 3.0.1), data.table, parallel, bigmemory, mvtnorm, MASS, GenABEL, emma

License GPL-3

URL https://github.com/LeileiCui/ADDO

LazyData true

RoxygenNote 6.1.1

NeedsCompilation no

R topics documented:

ADDO_AddDom1_QC *Quality Control of Phenotype and Genotype (STEP1 of The Add-Dom Model)*

Description

Quality control of Phenotype and Genotype (Input file format: PLINK or GenABEL) (1) Discard phenotypes with <200 individuals or logical variables; (2) Remove extreme values over threefold sd from the mean; (3) Remove genotypes with MAF<0.05 or missing rate>0.1; (4) Normalized phenotypes using "quantile" or "-log2" transforming; (5) Histogram Plot of the raw, clean, residual, normalized and transformed phenotypes; (6) Calculate kinship matrix using GenABEL, EMMA, EMMAX, GEMMA, GCTA, HOMEBREW_AFW or HOMEBREW_AS; (7) Summary the mean, sd and sum of each phenotype.

Usage

```
ADDO_AddDom1_QC(indir = indir, outdir = outdir,
  Input_name = Input_name, Input_type = "PLINK",
  Kinship_type = Kinship_type, PheList_Choose = F, PheList = PheList,
  Phe_ResDone = F, Phe_NormDone = F, Normal_method = "QUANTILE",
  covariates_sum = covariates_sum, covariates_types = covariates_types,
  Phe_IndMinimum = 200, Phe_Extreme = 5, GT_maf = 0.05,
  GT_missing = 0.1, num_nodes = 10)
```

Arguments

indir	A character. The input directory where contains the input bPLINK or GenABEL data.
outdir	A character. The output directory where generates the folder: "1_PheGen".
Input_name	A character. The prefixes of the input files.
Input_type	A character. The format of input data. Please select from "PLINK" or "GenABEL".
Kinship_type	A character. The method to generate kinship matrix. Please select from "GenABEL","EMMA","EMMAX","GEMMA", "GCTA", "GCTA_ad", "HOMEBREW_AFW" or "HOMEBREW_AS".
PheList_Choose	A logic variable. T: Investigate specified phenotypes; F: Investigate all phenofiles.
PheList	A vector of character. Please specifie a list like c("id","cov1","cov2","phe1","phe2"), when "PheList_Choose=F".
Phe_ResDone	A logic variable. T: The input data has already been residualize, won't correct the covariates effect; F: Correct the covariates effect.
Phe_NormDone	A logic variable. T: The input data has already been normalized, won't implement Log Transforming; F: Implement Log Transforming.
Normal_method	A character. When choose "Phe_NormDone = F", the specified normalized method will be needed, "LOG2" or "QUANTILE".
covariates_sum	A numeric variable. The sum of all covariates.

`covariates_types`
: A vector of character. The type of all covariates. Please select from "n" and "f". "f" stands for factorization.

`Phe_IndMinimum`
: A numeric variable. Remove phenotypes without enough available individuals.

`Phe_Extreme`
: A numeric variable. Phenotype QC2: Remove extreme phenotype values over -/+ Phe_Extreme*sd from mean.

`GT_maf`
: A numeric variable. Genotype QC1: Remove genotypes with MAF<GT_maf.

`GT_missing`
: A numeric variable. Genotype QC2: Remove genotypes with rate>GT_missing.

`num_nodes`
: A numeric variable. The number of cores used parallelly.

Details

NOTE1: PLINK Input Format (1) Genotype File, named "file.bed", "file.bim" & "file.fam" (2) Phenotype File, named "file.phe" (1st column name should be "id"; The covariates columns should be prior than phenotypes; The sex column should coded as female=0 and male=1) (3) Covariates File, named "file.covs" (1st column is phenotype names; 2nd column is corresponding covariates separated by ","). NOTE2: GenABEL Input Format (1) file.ABEL.dat (Just contain one GenABEL type variable named "dat") (2) file.covs (1st column is phenotype name; 2nd column is corresponding covariates and all covariates should be separated by ",") NOTE3: Required Softwares: plink (v.1.90) & gcta64 (or emma/emmax-kin/gemma, only required when specified)

Value

a folder named "1_PheGen" with phenotypes and genotypes after QC.

Author(s)

Leilei Cui and Bin Yang

Examples

```
covariates_types = c("n","f")
names(covariates_types) = c("sex","batch")
ADDO_AddDom1_QC(indir=indir, outdir=outdir, Input_name="TEST", Kinship_type="GCTA_ad", Ph
```

ADDO_AddDom2_Pvalue

Detection and Classification of QTLs with Various Inheritance Categories (STEP2 of The Add-Dom Model)

Description

Select significant QTLs using a matrix operation strategy and estimate the logP of each QTLs with 4 different models as well as their "tAdd" and "tDom" for inheritance categories classification. (1) Run the whole PLINK file or Run the separated PLINK files if the genotypes are massive ("Run_separated = F"); (2) Additive Recode Model (AA:0/AB:1/BB:2) vs Null Model; (3) Dominant Recode Model (AA:0/AB:1/BB:0) vs Null Model; (4) Add+Dom Recode Model (AA:0 0/AB:1 1/BB:2 0) vs Null Model; (5) Add+Dom Reocde Model (AA:0 0/AB:1 1/BB:2 0) vs Additive Model.

Usage

```
ADDO_AddDom2_Pvalue(indir = indir, outdir = outdir,
  Input_name = Input_name, Kinship_type = Kinship_type,
  VarComponent_Method = VarComponent_Method, PheList_Choose = F,
  PheList = PheList, Run_separated = F,
  covariates_sum = covariates_sum, Phe_IndMinimum = 200,
  GT_IndMinimum = 10, matrix_acceleration = T, logP_threshold = 1,
  num_nodes = 10)
```

Arguments

indir	A character. The input directory where contains the input bPLINK or GenABEL data.
outdir	A character. The output directory where generates the folder: "2_Pvalue".
Input_name	A character. The prefixes of the input files.
Kinship_type	A character. The method to generate kinship matrix. Please select from "GenABEL","EMMA","EMMAX","GEMMA", "GCTA", "GCTA_ad", "HOMEBREW_AFW" or "HOMEBREW_AS".
VarComponent_Method	A character. The method to estimate variance components. Please select from "EMMA_a", "GCTA_a" or "GCTA_ad" (When VarComponent_Method is "GCTA_ad", the Kinship_type must be "GCTA_ad").
PheList_Choose	A logic variable. T: Just investigate specified phenotypes; F: Investigate all phenotypes.
PheList	A vector of character. When choose "PheList_Choose=F", the specified phenotype list must be specified.
Run_separated	A logic variable. T: Run the separated genotype files; F: Run the whole genotype file.
covariates_sum	A numeric variable. The sum of all covariates.
Phe_IndMinimum	A numeric variable. Remove phenotypes without enough available individuals.
GT_IndMinimum	A numeric variable. Remove loci with available individuals <GT_IndMinimum for all three genotypes.
matrix_acceleration	A logic variable. T: Implement the matrix acceleration to select significant loci before mixed model; F: Didn't implement the matrix acceleration.
logP_threshold	A numeric variable. The -logP threshold to select significant loci.
num_nodes	A numeric variable. The number of cores used parallelly.

Value

a folder named "2_Pvalue" with various statistics of each significant SNP for all phenotypes.

Author(s)

Leilei Cui and Bin Yang

Examples

```
ADDO_AddDom2_Pvalue(indir=indir, outdir=outdir, Input_name="TEST", Kinship_type="GCTA_ad"
```

`ADDO_AddDom3_Plot` *Visulization of Various 4in1 Figures (STEP3 of The Add-Dom Model)*

Description

Visualizing additive and non-additive QTLs detected by four different models from ADDO_AddDom2_Pvalue. (1) 4in1 Manhattan Plot; (2) 4in1 QQ Plot using all loci with or without those loci located in the chromosome contains Peak SNP; (3) 4in1 Regional Manhattan Plot of the Peak SNP; (4) 4in1 Genotype Boxplot of the Peak SNP.

Usage

```
ADDO_AddDom3_Plot(outdir = outdir, PheList_Choose = F,
  PheList = PheList, covariates_sum = covariates_sum,
  RegionMan_chr_whole = F, RegionMan_chr_region = RegionMan_chr_region,
  Down_sampling = F, Down_sampling_logP = 1,
  Down_sampling_distance = 10, chrs_sum = chrs_sum, num_nodes = 10)
```

Arguments

`outdir`	A character. The output directory where generates the folder: "3_Plot".
`PheList_Choose`	A logic variable. T: Just investigate specified phenotypes; F: Investigate all phenofiles.
`PheList`	A vector of character. When choose "PheList_Choose=F", the specified phenotype list must be specified.
`covariates_sum`	A numeric variable. The sum of all covariates.
`RegionMan_chr_whole`	A logic variable. T: Draw a whole chromosome; F: Draw the specified region.
`RegionMan_chr_region`	A numeric variable. The length of specified region around the Peak SNP.
`Down_sampling`	A logic variable. T: Down-sampling points with low logP to speed up the plotting progress; F: Darwing with all loci.
`Down_sampling_logP`	A numeric variable. The threshold for down-sampling points for rapid rendering of the Manhattan Plots, when Down_sampling is true.
`Down_sampling_distance`	A numeric variable. The distance of points for equidistant sampling, when Down_sampling is true.
`chrs_sum`	A numeric variable. The sum of all chromosomes.
`num_nodes`	A numeric variable. The number of cores used parallelly.

Value

a folder named "3_Plot" with various plots.

Author(s)

Leilei Cui and Bin Yang

Examples

```
ADDO_AddDom3_Plot(outdir=outdir, covariates_sum=2, RegionMan_chr_whole=F, RegionMan_chr_r
```

`ADDO_AddDom4_IntePlot`

Visulization of An Integrated Figure (STEP4 of The Add-Dom Model)

Description

Visualizing additive and non-additive QTLs by an integrated plot.

Usage

```
ADDO_AddDom4_IntePlot(outdir = outdir, PheList_Choose = F,
  PheList = PheList, covariates_sum = covariates_sum,
  RegionMan_chr_whole = F, RegionMan_chr_region = RegionMan_chr_region,
  Down_sampling = F, Down_sampling_logP = 1,
  Down_sampling_distance = 10, Plot_model = "NvsAD",
  chrs_sum = chrs_sum, num_nodes = 10)
```

Arguments

`outdir`	A character. The output directory where generates the folder: "3_Plot".
`PheList_Choose`	A logic variable. T: Just investigate specified phenotypes; F: Investigate all phenofiles.
`PheList`	A vector of character. When choose "PheList_Choose=F", the specified phenotype list must be specified.
`covariates_sum`	A numeric variable. The sum of all covariates.
`RegionMan_chr_whole`	A logic variable. T: Draw a whole chromosome; F: Draw the specified region.
`RegionMan_chr_region`	A numeric variable. The length of specified region around the Peak SNP.
`Down_sampling`	A logic variable. T: Down-sampling points with low logP to speed up the plotting progress; F: Darwing with all loci.
`Down_sampling_logP`	A numeric variable. The threshold for down-sampling points for rapid rendering of the Manhattan Plots, when Down_sampling is true.

Down_sampling_distance
: A numeric variable. The distance of points for equidistant sampling, when Down_sampling is true.

Plot_model
: A character. The model to be mainly focused in the integrated plot. Please select from choose "AvsAD" or "NvsAD" or "NvsA" or "NvsD".

chrs_sum
: A numeric variable. The sum of all chromosomes.

num_nodes
: A numeric variable. The number of cores used parallelly.

Value

a folder named "3_Plot" with various plots.

Author(s)

Leilei Cui and Bin Yang

Examples

```
ADDO_AddDom4_IntePlot(outdir=outdir, covariates_sum=2, RegionMan_chr_whole=F, RegionMan_c
```

ADDO_Heterotic1_QC *Quality Control of Phenotype and Genotype (STEP1 of The Heterotic Model)*

Description

Quality control of Phenotype and Genotype (Input file format: PLINK or GenABEL) (1) Discard phenotypes with <200 individuals or logical variables; (2) Remove extreme values over threefold sd from the mean; (3) Remove genotypes with MAF<0.05 or missing rate>0.1; (4) Normalized phenotypes using "quantile" or "-log2" transforming; (5) Histogram Plot of the raw, clean, residual, normalized and transformed phenotypes; (6) Calculate kinship matrix using GenABEL, EMMA, EMMAX, GEMMA, GCTA, HOMEBREW_AFW or HOMEBREW_AS; (7) Summary the mean, sd and sum of each phenotype.

Usage

```
ADDO_Heterotic1_QC(indir = indir, outdir = outdir,
  Input_name = Input_name, Input_type = "PLINK",
  Kinship_type = Kinship_type, PheList_Choose = F, PheList = PheList,
  Phe_ResDone = F, Phe_NormDone = F, Normal_method = "QUANTILE",
  covariates_sum = covariates_sum, covariates_types = covariates_types,
  Phe_IndMinimum = 200, Phe_Extreme = 5, GT_maf = 0.05,
  GT_missing = 0.1, num_nodes = 10)
```

Arguments

indir	A character. The input directory where contains the input bPLINK or GenABEL data.
outdir	A character. The output directory where generates the folder: "1_PheGen".
Input_name	A character. The prefixes of the input files.
Input_type	A character. The format of input data. Please select from "PLINK" or "GenABEL".
Kinship_type	A character. The method to generate kinship matrix. Please select from "GenABEL","EMMA","EMMAX","GEMMA", "GCTA", "GCTA_ad", "HOMEBREW_AFW" or "HOMEBREW_AS".
PheList_Choose	A logic variable. T: Investigate specified phenotypes; F: Investigate all phenofiles.
PheList	A vector of character. Please specifie a list like c("id","cov1","cov2","phe1","phe2"), when "PheList_Choose=F".
Phe_ResDone	A logic variable. T: The input data has already been residualize, won't correct the covariates effect; F: Correct the covariates effect.
Phe_NormDone	A logic variable. T: The input data has already been normalized, won't implement Log Transforming; F: Implement Log Transforming.
Normal_method	A character. When choose "Phe_NormDone = F", the specified normalized method will be needed, "LOG2" or "QUANTILE".
covariates_sum	A numeric variable. The sum of all covariates.
covariates_types	A vector of character. The type of all covariates. Please select from "n" and "f". "f" stands for factorization.
Phe_IndMinimum	A numeric variable. Remove phenotypes without enough available individuals.
Phe_Extreme	A numeric variable. Phenotype QC2: Remove extreme phenotype values over -/+ Phe_Extreme*sd from mean.
GT_maf	A numeric variable. Genotype QC1: Remove genotypes with MAF<GT_maf.
GT_missing	A numeric variable. Genotype QC2: Remove genotypes with rate>GT_missing.
num_nodes	A numeric variable. The number of cores used parallelly.

Details

NOTE1: PLINK Input Format (1) Genotype File, named "file.bed", "file.bim" & "file.fam" (2) Phenotype File, named "file.phe" (1st column name should be "id"; The covariates columns should be prior than phenotypes; The sex column should coded as female=0 and male=1) (3) Covariates File, named "file.covs" (1st column is phenotype names; 2nd column is corresponding covariates separated by ","). NOTE2: GenABEL Input Format (1) file.ABEL.dat (Just contain one GenABEL type variable named "dat") (2) file.covs (1st column is phenotype name; 2nd column is corresponding covariates and all covariates should be separated by ",") NOTE3: Required Softwares: plink (v.1.90) & gcta64 (or emma/emmax-kin/gemma, only required when specified)

Value

a folder named "1_PheGen" with phenotypes and genotypes after QC.

Author(s)

Leilei Cui and Bin Yang

Examples

```
covariates_types = c("n","f")
names(covariates_types) = c("sex","batch")
ADDO_Heterotic1_QC(indir=indir, outdir=outdir, Input_name="TEST", Kinship_type="GCTA_ad",
```

ADDO_Heterotic2_Pvalue

Pvalue calculation and Verfication of Overdominance QTLs (STEP2 of The Heterotic Model)

Description

P-value Calculation and Verfication of overdominance (or heterotic) QTLs (1) Run the whole PLINK file or Run the separated PLINK files ("Run_separated = F"); (2) Indicate Reocde Model (AA:1 0 0/AB:0 1 0/BB:0 0 1) without the "1" column of covariance matrix; (3) Estimate two T-statistics (t(AB-AA) and t(AB-BB)) to measure the deviation between the effect of heterozygote (AB) and that of two homozygotes (AA and BB); (4) Generate the P-value based on MVN distribution using the minor(abs(t(AB-AA)),abs(t(AB-BB))) from SNPs with t(AB-AA)*t(AB-BB)>0.

Usage

```
ADDO_Heterotic2_Pvalue(indir = indir, outdir = outdir,
  Input_name = Input_name, Kinship_type = Kinship_type,
  VarComponent_Method = VarComponent_Method, PheList_Choose = F,
  PheList = PheList, Run_separated = F,
  covariates_sum = covariates_sum, Phe_IndMinimum = 200,
  GT_IndMinimum = 10, num_nodes = 10)
```

Arguments

`indir`	A character. The input directory where contains the input bPLINK or GenABEL data.
`outdir`	A character. The output directory where generates the folder: "2_Pvalue".
`Input_name`	A character. The prefixes of the input files.
`Kinship_type`	A character. The method to generate kinship matrix. Please select from "GenABEL","EMMA","EMMAX","GEMMA", "GCTA", "GCTA_ad", "HOMEBREW_AFW" or "HOMEBREW_AS".
`VarComponent_Method`	A character. The method to estimate variance components. Please select from "EMMA_a", "GCTA_a" or "GCTA_ad" (When VarComponent_Method is "GCTA_ad", the Kinship_type must be "GCTA_ad").
`PheList_Choose`	A logic variable. T: Just investigate specified phenotypes; F: Investigate all phenotypes.

`PheList` A vector of character. When choose "PheList_Choose=F", the specified phenotype list must be specified.

`Run_separated` A logic variable. T: Run the separated genotype files; F: Run the whole genotype file.

`covariates_sum` A numeric variable. The sum of all covariates.

`Phe_IndMinimum` A numeric variable. Remove phenotypes without enough available individuals.

`GT_IndMinimum` A numeric variable. Remove loci with available individuals <GT_IndMinimum for all three genotypes.

`num_nodes` A numeric variable. The number of cores used parallelly.

Value

a folder named "2_Pvalue" with various statistics of each significant SNP for all phenotypes.

Author(s)

Leilei Cui and Bin Yang

Examples

```
ADDO_Heterotic2_Pvalue(indir=indir, outdir=outdir, Input_name="TEST", Kinship_type="GCTA_
```

ADDO_Heterotic3_Plot

Visulization of Various Different Figures (STEP3 of The Heterotic Model)

Description

Visualizing overdominance QTLs by various plots.

Usage

```
ADDO_Heterotic3_Plot(outdir = outdir, PheList_Choose = F,
  PheList = PheList, covariates_sum = covariates_sum,
  RegionMan_chr_whole = F, RegionMan_chr_region = RegionMan_chr_region,
  Down_sampling = F, Down_sampling_logP = 1,
  Down_sampling_distance = 10, chrs_sum = chrs_sum, num_nodes = 10)
```

Arguments

`outdir` A character. The output directory where generates the folder: "3_Plot".

`PheList_Choose` A logic variable. T: Just investigate specified phenotypes; F: Investigate all phenofiles.

`PheList` A vector of character. When choose "PheList_Choose=F", the specified phenotype list must be specified.

`covariates_sum` A numeric variable. The sum of all covariates.

`RegionMan_chr_whole` A logic variable. T: Draw a whole chromosome; F: Draw the specified region.

`RegionMan_chr_region` A numeric variable. The length of specified region around the Peak SNP.

`Down_sampling` A logic variable. T: Down-sampling points with low logP to speed up the plotting progress; F: Darwing with all loci.

`Down_sampling_logP` A numeric variable. The threshold for down-sampling points for rapid rendering of the Manhattan Plots, when Down_sampling is true.

`Down_sampling_distance` A numeric variable. The distance of points for equidistant sampling, when Down_sampling is true.

`chrs_sum` A numeric variable. The sum of all chromosomes.

`num_nodes` A numeric variable. The number of cores used parallelly.

Value

a folder named "3_Plot" with various plots.

Author(s)

Leilei Cui and Bin Yang

Examples

```
ADDO_Heterotic3_Plot(outdir=outdir, covariates_sum=2, RegionMan_chr_whole=F, RegionMan_ch
```

ADDO_Heterotic4_IntePlot

Visulization of An Integrated Figure (STEP4 of The Heterotic Model)

Description

Visualizing overdominance QTLs by an integrated plot.

Usage

```
ADDO_Heterotic4_IntePlot(outdir = outdir, PheList_Choose = F,
  PheList = PheList, covariates_sum = covariates_sum,
  RegionMan_chr_whole = F, RegionMan_chr_region = RegionMan_chr_region,
  Down_sampling = F, Down_sampling_logP = 1,
  Down_sampling_distance = 10, chrs_sum = chrs_sum, num_nodes = 10)
```

Arguments

`outdir`	A character. The output directory where generates the folder: "3_Plot".
`PheList_Choose`	A logic variable. T: Just investigate specified phenotypes; F: Investigate all phenofiles.
`PheList`	A vector of character. When choose "PheList_Choose=F", the specified phenotype list must be specified.
`covariates_sum`	A numeric variable. The sum of all covariates.
`RegionMan_chr_whole`	A logic variable. T: Draw a whole chromosome; F: Draw the specified region.
`RegionMan_chr_region`	A numeric variable. The length of specified region around the Peak SNP.
`Down_sampling`	A logic variable. T: Down-sampling points with low logP to speed up the plotting progress; F: Darwing with all loci.
`Down_sampling_logP`	A numeric variable. The threshold for down-sampling points for rapid rendering of the Manhattan Plots, when Down_sampling is true.
`Down_sampling_distance`	A numeric variable. The distance of points for equidistant sampling, when Down_sampling is true.
`chrs_sum`	A numeric variable. The sum of all chromosomes.
`num_nodes`	A numeric variable. The number of cores used parallelly.

Value

a folder named "3_Plot" with various plots.

Author(s)

Leilei Cui and Bin Yang

Examples

```
ADDO_Heterotic4_IntePlot(outdir=outdir, covariates_sum=2, RegionMan_chr_whole=F, RegionMa
```

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plotGWAS *A Flexible Function to draw Manhattan Plot*

Description

Manhattan Plot for whole genome association analyses for single or multiple traits

Usage

```
plotGWAS(chrs = chrs, traitIdx = 1, plotcolor = c("darkgreen"),
  alldat = alldat, y_limit = "", main = "", cex_points = 1,
  cex_lab = 3.1, cex_axis = 3)
```

Arguments

chrs	A vector of numbers or characters indicating the chromosomes of markers.
traitIdx	A numeric variable indicating the index of trait to plot.
plotcolor	A vector of characters specify the colors used to plot the signatures on each chromosome.
alldat	A dataframe with columns containing SNP, chr, pos and association strength (-log10 P value) of markers for one or more traits.
y_limit	A numeric variable detail the range of y axis.
main	A character specifies the title of the plot.
cex_points	A numeric value specifies the cex of points in the plot.
cex_lab	A numeric value specifies the cex of labels in the plot.
cex_axis	A numeric value specifies the cex of axis in the plot.

Value

a figure

Author(s)

Bin Yang and Leilei Cui

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plotRegion *A Flexible Function for Manhattan Plot*

Description

Plot the GWAS results for a single trait on one particular chromosome, or specific region on one chromosome

Usage

```
plotRegion(chrs = chrs, traitIdx = 1, alldat = alldat, from = NULL,
  to = NULL, main = "", ldinfo = ldinfo, ylim = NULL,
  cex_points = 2.5, cex_points_peak = 4, cex_lab = 1.3,
  cex_axis = 1.3, cex_main = 1.4)
```

Arguments

chrs	A vector of numbers or characters indicating the chromosomes of markers.
traitIdx	A numeric variable indicating the index of trait to plot.
alldat	A dataframe with columns containing SNP, chr, pos and association strength (-log10 P value) of markers for one or more traits.
from	A character specify the name of SNP.
to	A character specify the name of SNP.
main	A character specifies the title of the plot.
ldinfo	A data frame generated using –r2 –ld-snp command in PLINK .

ylim	A vector of two numeric variables specify the range of y axis..
cex_points	A numeric variable specify the cex of points to plot.
cex_points_peak	A numeric variable specify the cex of point for the lmost significant marker to plot..
cex_lab	A numeric value specifies the cex of labels in the plot.
cex_axis	A numeric value specifies the cex of axis in the plot.
cex_main	AA numeric value specifies the cex of title in the plot.

Value

a figure

Author(s)

Bin Yang and Leilei Cui

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