

# Package: HIBAG (via r-universe)

July 14, 2024

**Type** Package

**Title** HLA Genotype Imputation with Attribute Bagging

**Version** 1.41.1

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**Depends** R (>= 3.2.0)

**Imports** methods, RcppParallel

**Suggests** parallel, ggplot2, reshape2, gdsfmt, SNPRelate, SeqArray, knitr, markdown, rmarkdown, Rsamtools

**LinkingTo** RcppParallel (>= 5.0.0)

**Description** Imputes HLA classical alleles using GWAS SNP data, and it relies on a training set of HLA and SNP genotypes. HIBAG can be used by researchers with published parameter estimates instead of requiring access to large training sample datasets. It combines the concepts of attribute bagging, an ensemble classifier method, with haplotype inference for SNPs and HLA types. Attribute bagging is a technique which improves the accuracy and stability of classifier ensembles using bootstrap aggregating and random variable selection.

**License** GPL-3

**LazyData** yes

**VignetteBuilder** knitr

**SystemRequirements** C++11, GNU make

**ByteCompile** TRUE

**biocViews** Genetics, StatisticalMethod

**URL** <https://github.com/zhengxwen/HIBAG>,  
<https://hibag.s3.amazonaws.com/index.html>

**Repository** <https://bioc.r-universe.dev>

**RemoteUrl** <https://github.com/bioc/HIBAG>

**RemoteRef** HEAD

**RemoteSha** 82c88fdb5a5ca74afe216f1dd2aa68eea7b3a305

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HIBAG-package	<i>HLA Genotype Imputation with Attribute Bagging</i>
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## Description

To impute HLA types from unphased SNP data using an attribute bagging method.

## Details

Package:	HIBAG
Type:	R/Bioconductor Package
License:	GPL version 3
Kernel Version:	v1.5

HIBAG is a state of the art software package for imputing HLA types using SNP data, and it uses the R statistical programming language. HIBAG is highly accurate, computationally tractable, and can be used by researchers with published parameter estimates instead of requiring access to large training sample datasets. It combines the concepts of attribute bagging, an ensemble classifier method, with haplotype inference for SNPs and HLA types. Attribute bagging is a technique which improves the accuracy and stability of classifier ensembles using bootstrap aggregating and random variable selection.

### Features:

- 1) HIBAG can be used by researchers with published parameter estimates ([https://hibag.s3.amazonaws.com/hlares\\_index.html](https://hibag.s3.amazonaws.com/hlares_index.html)) instead of requiring access to large training sample datasets.
- 2) A typical HIBAG parameter file contains only haplotype frequencies at different SNP subsets rather than individual training genotypes.
- 3) SNPs within the xMHC region (chromosome 6) are used for imputation.
- 4) HIBAG employs unphased genotypes of unrelated individuals as a training set.
- 5) HIBAG supports parallel computing with R.

## Author(s)

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## References

Zheng X, Shen J, Cox C, Wakefield J, Ehm M, Nelson M, Weir BS; HIBAG – HLA Genotype Imputation with Attribute Bagging. The Pharmacogenomics Journal. doi: 10.1038/tpj.2013.18. <https://www.nature.com/articles/tpj201318>

## Examples

```
# HLA_Type_Table data
head(HLA_Type_Table)
dim(HLA_Type_Table) # 60 13

# HapMap_CEU_Geno data
summary(HapMap_CEU_Geno)

#####

# make a "hlaAlleleClass" object
hla.id <- "A"
hla <- hlaAllele(HLA_Type_Table$sample.id,
  H1 = HLA_Type_Table[, paste(hla.id, ".1", sep="")],
  H2 = HLA_Type_Table[, paste(hla.id, ".2", sep="")],
  locus=hla.id, assembly="hg19")

# divide HLA types randomly
set.seed(100)
hlatab <- hlaSplitAllele(hla, train.prop=0.5)
names(hlatab)
# "training" "validation"
summary(hlatab$training)
summary(hlatab$validation)

# SNP predictors within the flanking region on each side
region <- 500 # kb
snpid <- hlaFlankingSNP(HapMap_CEU_Geno$snp.id, HapMap_CEU_Geno$snp.position,
  hla.id, region*1000, assembly="hg19")
length(snpid) # 275

# training and validation genotypes
train.geno <- hlaGenoSubset(HapMap_CEU_Geno,
  snp.sel=match(snpid, HapMap_CEU_Geno$snp.id),
  samp.sel=match(hlatab$training$value$sample.id,
    HapMap_CEU_Geno$sample.id))
test.geno <- hlaGenoSubset(HapMap_CEU_Geno,
  samp.sel=match(hlatab$validation$value$sample.id,
    HapMap_CEU_Geno$sample.id))

# train a HIBAG model
set.seed(100)
# please use "nclassifier=100" when you use HIBAG for real data
model <- hlaAttrBagging(hlatab$training, train.geno, nclassifier=4,
  verbose.detail=TRUE)
```

```

summary(model)

# validation
pred <- hlaPredict(model, test.geno)
summary(pred)

# compare
(comp <- hlaCompareAllele(hlatab$validation, pred, allele.limit=model,
  call.threshold=0))
(comp <- hlaCompareAllele(hlatab$validation, pred, allele.limit=model,
  call.threshold=0.5))

# save the parameter file
mobj <- hlaModelToObj(model)
save(mobj, file="HIBAG_model.RData")
save(test.geno, file="testgeno.RData")
save(hlatab, file="HLASplit.RData")

# Clear Workspace
hlaClose(model) # release all resources of model
rm(list = ls())

#####

# NOW, load a HIBAG model from the parameter file
mobj <- get(load("HIBAG_model.RData"))
model <- hlaModelFromObj(mobj)

# validation
test.geno <- get(load("testgeno.RData"))
hlatab <- get(load("HLASplit.RData"))

pred <- hlaPredict(model, test.geno)
# compare
(comp <- hlaCompareAllele(hlatab$validation, pred, allele.limit=model,
  call.threshold=0.5))

#####

# import a PLINK BED file
#
bed.fn <- system.file("extdata", "HapMap_CEU.bed", package="HIBAG")
fam.fn <- system.file("extdata", "HapMap_CEU.fam", package="HIBAG")
bim.fn <- system.file("extdata", "HapMap_CEU.bim", package="HIBAG")
hapmap.ceu <- hlaBED2Geno(bed.fn, fam.fn, bim.fn, assembly="hg19")

#####

# predict
#
pred <- hlaPredict(model, hapmap.ceu, type="response")

```

```
head(pred$value)
#   sample.id allele1 allele2      prob
# 1   NA10859   01:01   03:01 0.9999992
# 2   NA11882   01:01   29:02 1.0000000
# ...

# delete the temporary files
unlink(c("HIBAG_model.RData", "testgeno.RData", "HLASplit.RData"), force=TRUE)
```

---

HapMap_CEU_Geno	<i>SNP genotypes of a study simulated from HapMap CEU genotypic data</i>
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---

**Description**

An object of [hlaSNPGenoClass](#) of 60 samples and 1564 SNPs.

**Usage**

HapMap\_CEU\_Geno

**Value**

A list

**References**

[https://www.ncbi.nlm.nih.gov/variation/news/NCBI\\_retiring\\_HapMap/](https://www.ncbi.nlm.nih.gov/variation/news/NCBI_retiring_HapMap/)

The International HapMap Consortium. A second generation human haplotype map of over 3.1 million SNPs. Nature 449, 851-861. 2007.

---

hlaAASeqClass	<i>Class of HLA Amino Acid Sequence Type</i>
---------------	--

---

**Description**

The definition of a class for HLA protein amino acid sequences.

Value

There are following components:

locus	HLA locus
pos.start	the starting position in basepair
pos.end	the end position in basepair
value	a data frame
assembly	the human genome reference, such like "hg19"
start.position	the start position
reference	reference sequence

The component value includes:

sample.id	sample ID
allele1	amino acid or nucleotide sequence
allele2	amino acid or nucleotide sequence
P1, ..., Pn	if applicable, a matrix of posterior probability, row – sample, column – position of amino acid

Author(s)

Xiuwen Zheng

See Also

[hlaConvSequence](#)

---

hlaAllele	<i>A list of HLA/KIR types</i>
-----------	--------------------------------

---

Description

Return an object of [hlaAlleleClass](#), which contains HLA/KIR types.

Usage

```
hlaAllele(sample.id, H1, H2, max.resolution="", locus="any", assembly="auto",
  locus.pos.start=NA_integer_, locus.pos.end=NA_integer_, prob=NULL,
  na.rm=TRUE)
```

**Arguments**

sample.id	sample IDs
H1	a vector of HLA/KIR alleles
H2	a vector of HLA/KIR alleles
max.resolution	"2-digit", "1-field", "4-digit", "2-field", "6-digit", "3-field", "8-digit", "4-field", "allele", "protein", "full", "none", or "": "allele" = "2-digit"; "protein" = "4-digit"; "full", "none" or "" for no limit on resolution
locus	the name of HLA locus: "A", "B", "C", "DRB1", "DRB5", "DQA1", "DQB1", "DPB1", KIR locus, or "any", where "any" indicates any other multiallelic locus; see <a href="#">hlaLocInfo</a> for possible locus names
assembly	the human genome reference: "hg18", "hg19" (default), "hg38"; "auto" refers to "hg19"; "auto-silent" refers to "hg19" without any warning
locus.pos.start	the starting position in basepair
locus.pos.end	the end position in basepair
prob	the probabilities assigned to the samples
na.rm	if TRUE, remove the samples without valid HLA types

**Details**

The format of H1 and H2 is "allele group : different protein : synonymous mutations in exons : synonymous mutations in introns"L, where the suffix L is express level (N, null; L, low; S, secreted; A, aberrant; Q: questionable). For example, "44:02:01:02L". If max.resolution is specified, the HLA alleles will be trimmed with a possible maximum resolution.

**Value**

Return a [hlaAlleleClass](#) object, and it is a list:

locus	HLA locus
pos.start	the starting position in basepair
pos.end	the end position in basepair
value	a data frame
assembly	the human genome reference, such like "hg19"

The component value includes:

sample.id	sample ID
allele1	HLA allele
allele2	HLA allele
prob	the posterior probability

**Author(s)**

Xiuwen Zheng



See Also

[hlaAlleleDigit](#), [hlaAlleleSubset](#), [hlaLociInfo](#), [hlaAlleleToVCF](#)

Examples

```
head(HLA_Type_Table)
dim(HLA_Type_Table) # 60 13

# make a "hlaAlleleClass" object
hla.id <- "A"
hla <- hlaAllele(HLA_Type_Table$sample.id,
  H1 = HLA_Type_Table[, paste(hla.id, ".1", sep="")],
  H2 = HLA_Type_Table[, paste(hla.id, ".2", sep="")],
  locus=hla.id, assembly="hg19")
summary(hla)

# encode other loci
hlaAllele("HD0010", "1", "2", locus="NewLocus")
```

---

hlaAlleleClass	<i>Class of HLA/KIR Type</i>
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---

Description

The definition of a class for HLA/KIR types, returned from [hlaAllele](#).

Value

There are following components:

locus	HLA/KIR locus
pos.start	the starting position in basepair
pos.end	the end position in basepair
value	a data frame
assembly	the human genome reference, such like "hg19"
postprob	if applicable, a matrix of all posterior probabilities
~	

The component value includes:

sample.id	sample ID
allele1	HLA allele
allele2	HLA allele
prob	if applicable, the posterior probability

**Author(s)**

Xiuwen Zheng

**See Also**

[hlaAllele](#)

---

hlaAlleleDigit	<i>Trim HLA alleles</i>
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---

**Description**

Trim HLA alleles to specified width.

**Usage**

```
hlaAlleleDigit(obj, max.resolution=NA_character_, rm.suffix=FALSE)
```

**Arguments**

obj	should be a <a href="#">hlaAlleleClass</a> object or characters
max.resolution	"2-digit", "1-field", "4-digit", "2-field", "6-digit", "3-field", "8-digit", "4-field", "allele", "protein", "full", "none", or "": "allele" = "2-digit"; "protein" = "4-digit"; "full", "none" or "" for no limit on resolution
rm.suffix	whether remove the non-digit suffix in the last field, e.g., for "01:22N", "N" is a non-digit suffix

**Details**

If max.resolution is specified, the HLA alleles will be trimmed with the maximum resolution. See <https://hla.alleles.org/nomenclature/naming.html> for the HLA nomenclature.

**Value**

Return a [hlaAlleleClass](#) object if obj is [hlaAlleleClass](#)-type, or characters if obj is character-type.

**Author(s)**

Xiuwen Zheng

**See Also**

[hlaAllele](#)

**Examples**

```

head(HLA_Type_Table)
dim(HLA_Type_Table) # 60 13

# make a "hlaAlleleClass" object
hla.id <- "A"
hla <- hlaAllele(HLA_Type_Table$sample.id,
  H1 = HLA_Type_Table[, paste(hla.id, ".1", sep="")],
  H2 = HLA_Type_Table[, paste(hla.id, ".2", sep="")],
  locus = hla.id, assembly="hg19")
summary(hla)

hla2 <- hlaAlleleDigit(hla, "2-digit")
summary(hla2)

```

---

hlaAlleleSubset	<i>Get a subset of HLA/KIR types</i>
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---

**Description**

Get a subset of HLA/KIR types from an object of [hlaAlleleClass](#).

**Usage**

```
hlaAlleleSubset(hla, samp.sel=NULL)
```

**Arguments**

hla	an object of <a href="#">hlaAlleleClass</a>
samp.sel	a logical vector, or an integer vector of indices

**Value**

Return [hlaAlleleClass](#).

**Author(s)**

Xiuwen Zheng

**See Also**

[hlaAllele](#), [hlaAlleleDigit](#)

Examples

```
head(HLA_Type_Table)
dim(HLA_Type_Table) # 60 13

# make a "hlaAlleleClass" object
hla.id <- "A"
hla <- hlaAllele(HLA_Type_Table$sample.id,
  H1 = HLA_Type_Table[, paste(hla.id, ".1", sep="")],
  H2 = HLA_Type_Table[, paste(hla.id, ".2", sep="")],
  locus=hla.id, assembly="hg19")
summary(hla)

subhla <- hlaAlleleSubset(hla, 1:100)
summary(subhla)
```

---

hlaAlleleToVCF	<i>Convert HLA alleles to VCF</i>
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---

Description

To convert the HLA allele data to a VCF file.

Usage

```
hlaAlleleToVCF(hla, outfn, DS=TRUE, allele.list=FALSE, prob.cutoff=NaN,
  verbose=TRUE)
```

Arguments

hla	an object of <a href="#">hlaAlleleClass</a> for HLA alleles, or a list of hlaAlleleClass objects
outfn	a VCF file name or a connection; if outfn ends with ".gz" or ".xz", gzfile or xzfile will be used to compress the output file
DS	if TRUE, output dosages in the DS field
allele.list	a logical value or a character vector for a list of alleles; when it is a logical value, if TRUE and dosage is available, use all possible alleles in the dosages; otherwise, use the alleles predicted at least once
prob.cutoff	a probability threshold for setting the output alleles and dosages to missing; the output VCF file contains all samples in hla ignoring prob.cutoff
verbose	if TRUE, show information

Value

Return outfn.

Author(s)

Xiuwen Zheng

## References

Zheng X, Shen J, Cox C, Wakefield J, Ehm M, Nelson M, Weir BS; HIBAG – HLA Genotype Imputation with Attribute Bagging. Pharmacogenomics Journal. doi: 10.1038/tpj.2013.18. <https://www.nature.com/articles/tpj201318>

## See Also

[hlaAttrBagging](#), [hlaAllele](#)

## Examples

```
# make a "hlaAlleleClass" object
hla.id <- "A"
hla <- hlaAllele(HLA_Type_Table$sample.id,
  H1 = HLA_Type_Table[, paste(hla.id, ".1", sep="")],
  H2 = HLA_Type_Table[, paste(hla.id, ".2", sep="")],
  locus=hla.id, assembly="hg19")

# SNP predictors within the flanking region on each side
region <- 500 # kb
snpid <- hlaFlankingSNP(HapMap_CEU_Geno$snp.id, HapMap_CEU_Geno$snp.position,
  hla.id, region*1000, assembly="hg19")
length(snpid) # 275

# train a HIBAG model
set.seed(100)
# please use "nclassifier=100" when you use HIBAG for real data
model <- hlaAttrBagging(hla, HapMap_CEU_Geno, nclassifier=2)
summary(model)

# validation
pred <- hlaPredict(model, HapMap_CEU_Geno)
summary(pred)

# output to standard output with dosages
hlaAlleleToVCF(hlaAlleleSubset(pred, 1:4), stdout())
```

## Description

Perform statistical association tests via Pearson's Chi-squared test, Fisher's exact test and logistic regressions.

**Usage**

```
## S3 method for class 'hlaAlleleClass'
hlaAssocTest(hla, formula, data,
  model=c("dominant", "additive", "recessive", "genotype"),
  model.fit=c("glm"), prob.threshold=NaN, use.prob=FALSE, showOR=FALSE,
  verbose=TRUE, ...)
## S3 method for class 'hlaAASeqClass'
hlaAssocTest(hla, formula, data,
  model=c("dominant", "additive", "recessive", "genotype"),
  model.fit=c("glm"), prob.threshold=NaN, use.prob=FALSE, showOR=FALSE,
  show.all=FALSE, verbose=TRUE, ...)
```

**Arguments**

hla	an object of <a href="#">hlaAlleleClass</a>
formula	an object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted, e.g., $y \sim 1$ , $y \sim h + a$
data	an optional data frame, list or environment containing the variables in the model. If not found in data, the variables are taken from <code>environment(formula)</code>
model	dominant, additive, recessive or genotype models: "dominant" is default
model.fit	"glm" – generalized linear regression
prob.threshold	the probability threshold to exclude individuals with low confidence scores
use.prob	if TRUE, use the posterior probabilities as weights in glm models
showOR	show odd ratio (OR) instead of log OR if TRUE
show.all	if TRUE, show both significant and non-significant results; if FALSE, only show significant results
verbose	if TRUE, show information
...	optional arguments to <a href="#">glm</a> or <a href="#">nlme</a> call

**Details**

model	description (given a specific HLA allele h)
dominant	[-/-] vs. [-/h,h/h] (0 vs. 1 in design matrix)
additive	[-] vs. [h] in Chi-squared and Fisher's exact test, the allele dosage in regressions (0: -/-, 1: -/h, 2: h/h)
recessive	[-/-,-/h] vs. [h/h] (0 vs. 1 in design matrix)
genotype	[-/-], [-/h], [h/h] (0 vs. 1 in design matrix)

In allelic associations, Chi-squared and Fisher exact tests are performed on the cross tabulation, which is constructed according to the specified model (dominant, additive, recessive and genotype).

In amino acid associations, Fisher exact test is performed on a cross tabulation with the numbers of each amino acid stratified by response variable (e.g., disease status).

In linear and logistic regressions, 95% confidence intervals are calculated based on asymptotic normality. The option `use.prob=TRUE` might be useful in the sensitivity analysis.

**Value**

Return a `data.frame` with

<code>[-]</code>	the number of haplotypes not carrying the specified HLA allele
<code>[h]</code>	the number of haplotype carrying the specified HLA allele
<code>%.[-], ...</code>	case/disease proportion in the group <code>[-]</code> , ...
<code>[-/-]</code>	the number of individuals or haplotypes not carrying the specified HLA allele
<code>[-/h]</code>	the number of individuals or haplotypes carrying one specified HLA allele
<code>[-/h]</code>	the number of individuals or haplotypes carrying two specified HLA alleles
<code>[-/h, h/h]</code>	the number of individuals or haplotypes carrying one or two specified HLA alleles
<code>[-/-, -/h]</code>	the number of individuals or haplotypes carrying at most one specified HLA allele
<code>%.[-/-], ...</code>	case/disease proportion in the group <code>[-/-]</code> , ...
<code>avg.[-/-], ...</code>	outcome average in the group <code>[-/-]</code> , ...
<code>chisq.st</code>	the value the chi-squared test statistic
<code>chisq.p</code>	the p-value for the Chi-squared test
<code>fisher.p</code>	the p-value for the Fisher's exact test
<code>h.est</code>	the coefficient estimate of HLA allele
<code>h.25%, h.75%</code>	the 95% confidence interval for HLA allele
<code>h.pval</code>	p value for HLA allele

**Author(s)**

Xiuwen Zheng

**See Also**

[hlaConvSequence](#), [summary.hlaAASeqClass](#)

**Examples**

```
hla.id <- "A"
hla <- hlaAllele(HLA_Type_Table$sample.id,
  H1 = HLA_Type_Table[, paste(hla.id, ".1", sep="")],
  H2 = HLA_Type_Table[, paste(hla.id, ".2", sep="")],
  locus=hla.id, assembly="hg19")

set.seed(1000)
n <- nrow(hla$value)
dat <- data.frame(case = c(rep(0, n/2), rep(1, n/2)), y = rnorm(n),
  pc1 = rnorm(n))

hlaAssocTest(hla, case ~ 1, data=dat)
hlaAssocTest(hla, case ~ 1, data=dat, model="additive")
```

```

hlaAssocTest(hla, case ~ 1, data=dat, model="recessive")
hlaAssocTest(hla, case ~ 1, data=dat, model="genotype")

hlaAssocTest(hla, y ~ 1, data=dat)
hlaAssocTest(hla, y ~ 1, data=dat, model="genotype")

hlaAssocTest(hla, case ~ h, data=dat)
hlaAssocTest(hla, case ~ h + pc1, data=dat)
hlaAssocTest(hla, case ~ h + pc1, data=dat, showOR=TRUE)

hlaAssocTest(hla, y ~ h, data=dat)
hlaAssocTest(hla, y ~ h + pc1, data=dat)
hlaAssocTest(hla, y ~ h + pc1, data=dat, showOR=TRUE)

hlaAssocTest(hla, case ~ h, data=dat, model="additive")
hlaAssocTest(hla, case ~ h, data=dat, model="recessive")
hlaAssocTest(hla, case ~ h, data=dat, model="genotype")

```

---

hlaAttrBagClass	<i>The class of HIBAG model</i>
-----------------	---------------------------------

---

## Description

The class of a HIBAG model, and its instance is returned from [hlaAttrBagging](#).

## Value

Return a list of:

n.samp	the total number of training samples
n.snp	the total number of candidate SNP predictors
sample.id	the sample IDs
snp.id	the SNP IDs
snp.position	SNP position in basepair
snp.allele	a vector of characters with the format of "A allele/B allele"
snp.allele.freq	the allele frequencies
hla.locus	the name of HLA locus
hla.allele	the HLA alleles used in the model
hla.freq	the HLA allele frequencies
assembly	the human genome reference, such like "hg19"
model	internal use
appendix	an optional list: platform – supported platform(s); information – other information, like training sets, authors; warning – any warning message
matching	matching proportion in the training set



**Author(s)**

Xiuwen Zheng

**See Also**[hlaAttrBagging](#), [hlaParallelAttrBagging](#), [hlaAttrBagObj](#)

---

hlaAttrBagging*Build a HIBAG model*

---

**Description**

To build a HIBAG model for predicting HLA types with SNP markers.

**Usage**

```
hlaAttrBagging(hla, snp, nclassifier=100L, mtry=c("sqrt", "all", "one"),
  prune=TRUE, na.rm=TRUE, mono.rm=TRUE, maf=NaN, nthread=1L, verbose=TRUE,
  verbose.detail=FALSE)
```

**Arguments**

hla	the training HLA types, an object of <a href="#">hlaAlleleClass</a>
snp	the training SNP genotypes, an object of <a href="#">hlaSNPGenoClass</a>
nclassifier	the total number of individual classifiers
mtry	a character or a numeric value, the number of variables randomly sampled as candidates for each selection. See details
prune	if TRUE, to perform a parsimonious forward variable selection, otherwise, exhaustive forward variable selection. See details
na.rm	if TRUE, remove the samples with missing HLA alleles
mono.rm	if TRUE, remove monomorphic SNPs
maf	MAF threshold for SNP filter, excluding any SNP with MAF < maf
nthread	specify the number of threads used in the model building; if TRUE, use the number of threads returned from <code>RcppParallel::defaultNumThreads()</code> (by default using all threads)
verbose	if TRUE, show information
verbose.detail	if TRUE, show more information

## Details

mtry (the number of variables randomly sampled as candidates for each selection, "sqrt" by default): "sqrt", using the square root of the total number of candidate SNPs; "all", using all candidate SNPs; "one", using one SNP; an integer, specifying the number of candidate SNPs;  $0 < r < 1$ , the number of candidate SNPs is  $r * \text{the total number of SNPs}$ .

prune: there is no significant difference on accuracy between parsimonious and exhaustive forward variable selections. If prune=TRUE, the searching algorithm performs a parsimonious forward variable selection: if a new SNP predictor reduces the current out-of-bag accuracy, then it is removed from the candidate SNP set for future searching. Parsimonious selection helps to improve the computational efficiency by reducing the searching times on non-informative SNP markers.

[hlaParallelAttrBagging](#) extends hlaAttrBagging to allow parallel computing with multiple compute nodes in a cluster. An autosave function is available in [hlaParallelAttrBagging](#) when an new individual classifier is built internally without completing the ensemble.

## Value

Return an object of [hlaAttrBagClass](#):

n.samp	the total number of training samples
n.snp	the total number of candidate SNP predictors
sample.id	the sample IDs
snp.id	the SNP IDs
snp.position	SNP position in basepair
snp.allele	a vector of characters with the format of "A allele/B allele"
snp.allele.freq	the allele frequencies
hla.locus	the name of HLA locus
hla.allele	the HLA alleles used in the model
hla.freq	the HLA allele frequencies
assembly	the human genome reference, such like "hg19"
model	internal use
matching	matching proportion in the training set

## Author(s)

Xiuwen Zheng

## References

Zheng X, Shen J, Cox C, Wakefield J, Ehm M, Nelson M, Weir BS; HIBAG – HLA Genotype Imputation with Attribute Bagging. Pharmacogenomics Journal. doi: 10.1038/tpj.2013.18. <https://www.nature.com/articles/tpj201318>

**See Also**

[hlaClose](#), [hlaParallelAttrBagging](#), [summary.hlaAttrBagClass](#), [predict.hlaAttrBagClass](#), [hlaPredict](#), [hlaSetKernelTarget](#)

**Examples**

```
# make a "hlaAlleleClass" object
hla.id <- "A"
hla <- hlaAllele(HLA_Type_Table$sample.id,
  H1 = HLA_Type_Table[, paste(hla.id, ".1", sep="")],
  H2 = HLA_Type_Table[, paste(hla.id, ".2", sep="")],
  locus=hla.id, assembly="hg19")

# divide HLA types randomly
set.seed(100)
hlatab <- hlaSplitAllele(hla, train.prop=0.5)
names(hlatab)
# "training" "validation"
summary(hlatab$training)
summary(hlatab$validation)

# SNP predictors within the flanking region on each side
region <- 500 # kb
snpid <- hlaFlankingSNP(HapMap_CEU_Geno$snp.id, HapMap_CEU_Geno$snp.position,
  hla.id, region*1000, assembly="hg19")
length(snpid) # 275

# training and validation genotypes
train.geno <- hlaGenoSubset(HapMap_CEU_Geno,
  snp.sel=match(snpid, HapMap_CEU_Geno$snp.id),
  samp.sel=match(hlatab$training$value$sample.id,
    HapMap_CEU_Geno$sample.id))
test.geno <- hlaGenoSubset(HapMap_CEU_Geno,
  samp.sel=match(hlatab$validation$value$sample.id,
    HapMap_CEU_Geno$sample.id))

# train a HIBAG model
set.seed(100)
# please use "nclassifier=100" when you use HIBAG for real data
model <- hlaAttrBagging(hlatab$training, train.geno, nclassifier=4,
  verbose.detail=TRUE)
summary(model)

# validation
pred <- hlaPredict(model, test.geno)
summary(pred)

# compare
(comp <- hlaCompareAllele(hlatab$validation, pred, allele.limit=model,
  call.threshold=0))
(comp <- hlaCompareAllele(hlatab$validation, pred, allele.limit=model,
  call.threshold=0.5))
```

```

# save the parameter file
mobj <- hlaModelToObj(model)
save(mobj, file="HIBAG_model.RData")
save(test.geno, file="testgeno.RData")
save(hlatab, file="HLASplit.RData")

# Clear Workspace
hlaClose(model) # release all resources of model
rm(list = ls())

#####

# NOW, load a HIBAG model from the parameter file
mobj <- get(load("HIBAG_model.RData"))
model <- hlaModelFromObj(mobj)

# validation
test.geno <- get(load("testgeno.RData"))
hlatab <- get(load("HLASplit.RData"))

pred <- hlaPredict(model, test.geno, type="response")
summary(pred)

# compare
(comp <- hlaCompareAllele(hlatab$validation, pred, allele.limit=model,
  call.threshold=0))
(comp <- hlaCompareAllele(hlatab$validation, pred, allele.limit=model,
  call.threshold=0.5))

# delete the temporary files
unlink(c("HIBAG_model.RData", "testgeno.RData", "HLASplit.RData"), force=TRUE)

```

---

hlaAttrBagObj

*The class of HIBAG object*


---

## Description

The class of a HIBAG object, which can be saved in the .RData file.

## Value

A list of:

n.samp	the total number of training samples
n.snp	the total number of candidate SNP predictors
sample.id	the sample IDs

snp.id	the SNP IDs
snp.position	SNP position in basepair
snp.allele	a vector of characters with the format of "A allele/B allele"
snp.allele.freq	the allele frequencies
hla.locus	the name of HLA locus
hla.allele	the HLA alleles used in the model
hla.freq	the HLA allele frequencies
assembly	the human genome reference, such like "hg19"
classifiers	a list of all classifiers (described as follows)
matching	matching proportion in the training set
appendix	platform – supported platform(s); information – other information, like training sets, authors; warning – any warning message

classifiers has the following components:

samp.num	the number of copies of samples in a bootstrap sample
haplos	a data.frame of haplotype frequencies
.	freq – haplotype frequency
.	hla – a HLA allele
.	haplo – a SNP haplotype, with an entry value 0 standing for B (ZERO A allele), 1 for A (ONE A allele)
snpidx	the SNP indices used in this classifier
outofbag.acc	the out-of-bag accuracy of this classifier

### Author(s)

Xiuwen Zheng

### See Also

[hlaAttrBagging](#), [hlaParallelAttrBagging](#), [hlaModelToObj](#), [hlaModelFiles](#), [hlaAttrBagClass](#)

---

hlaBED2Geno

*Convert from PLINK BED format*

---

### Description

To convert a PLINK BED file to an object of [hlaSNPGenoClass](#).

### Usage

```
hlaBED2Geno(bed.fn, fam.fn, bim.fn, rm.invalid.allele=FALSE,
            import.chr="xMHC", assembly="auto", verbose=TRUE)
```

**Arguments**

bed.fn	binary file, genotype information
fam.fn	family, individual information, etc
bim.fn	extended MAP file: two extra cols = allele names
rm.invalid.allele	if TRUE, remove SNPs with non-standard alleles (except A,G,C,T)
import.chr	the chromosome, "1" .. "22", "X", "Y", "XY", "MT", "xMHC", or "", where "xMHC" implies the extended MHC on chromosome 6, and "" for all SNPs; "6" for all SNPs on chromosome 6 for HLA; "19" for all SNPs on chromosome 19 for KIR
assembly	the human genome reference: "hg18", "hg19" (default), "hg38"; "auto" refers to "hg19"; "auto-silent" refers to "hg19" without any warning
verbose	if TRUE, show information

**Value**

Return an object of [hlaSNPGenoClass](#).

**Author(s)**

Xiuwen Zheng

**See Also**

[hlaGeno2PED](#), [hlaGDS2Geno](#)

**Examples**

```
# Import a PLINK BED file
bed.fn <- system.file("extdata", "HapMap_CEU.bed", package="HIBAG")
fam.fn <- system.file("extdata", "HapMap_CEU.fam", package="HIBAG")
bim.fn <- system.file("extdata", "HapMap_CEU.bim", package="HIBAG")

hapmap.ceu <- hlaBED2Geno(bed.fn, fam.fn, bim.fn, assembly="hg19")
summary(hapmap.ceu)

# Or

hapmap.ceu <- hlaBED2Geno(bed.fn, fam.fn, bim.fn, assembly="hg19",
  rm.invalid.allele=TRUE, import.chr="6")
summary(hapmap.ceu)
```

---

hlaCheckAllele	<i>Check SNP alleles</i>
----------------	--------------------------

---

**Description**

Check SNP reference and non-reference alleles.

**Usage**

```
hlaCheckAllele(allele1, allele2)
```

**Arguments**

allele1	two alleles for the first individual, like c("A/G", "C/G")
allele2	two alleles for the second individual, like c("A/G", "C/G")

**Value**

Return a logical vector, where TRUE indicates the alleles are matching at that locus.

**Author(s)**

Xiuwen Zheng

**See Also**

[hlaCheckSNPs](#)

**Examples**

```
hlaCheckAllele(c("A/G", "T/G", "0/A"), c("G/A", "C/A", "G/0"))
```

---

hlaCheckSNPs	<i>Check the SNP predictors in a HIBAG model</i>
--------------	--

---

**Description**

Check the SNP predictors in a HIBAG model, by calculating the overlapping between the model and SNP genotypes.

**Usage**

```
hlaCheckSNPs(model, object,  
  match.type=c("Position", "Pos+Allele", "RefSNP+Position", "RefSNP"), verbose=TRUE)
```

**Arguments**

model	an object of <a href="#">hlaAttrBagClass</a> , or an object of <a href="#">hlaAttrBagObj</a>
object	a genotype object of <a href="#">hlaSNPGenoClass</a> , or a character vector like c("rs2523442", "rs9257863", ...)
match.type	"RefSNP+Position" (by default) – using both of RefSNP IDs and positions; "RefSNP" – using RefSNP IDs only; "Position" – using positions only
verbose	if TRUE, show information

**Value**

Return a `data.frame` for individual classifiers:

NumOfValidSNP	the number of non-missing SNPs in an individual classifier
NumOfSNP	the number of SNP predictors in an individual classifier
fraction	NumOfValidSNP / NumOfSNP

**Author(s)**

Xiuwen Zheng

**See Also**

[hlaAttrBagging](#), [predict.hlaAttrBagClass](#)

**Examples**

```
# make a "hlaAlleleClass" object
hla.id <- "DQB1"
hla <- hlaAllele(HLA_Type_Table$sample.id,
  H1 = HLA_Type_Table[, paste(hla.id, ".1", sep="")],
  H2 = HLA_Type_Table[, paste(hla.id, ".2", sep="")],
  locus=hla.id, assembly="hg19")

# training genotypes
region <- 100 # kb
snpid <- hlaFlankingSNP(HapMap_CEU_Geno$snp.id, HapMap_CEU_Geno$snp.position,
  hla.id, region*1000, assembly="hg19")
train.geno <- hlaGenoSubset(HapMap_CEU_Geno,
  snp.sel = match(snpid, HapMap_CEU_Geno$snp.id))

# train a HIBAG model
set.seed(1000)
model <- hlaAttrBagging(hla, train.geno, nclassifier=2)
print(model)

hlaCheckSNPs(model, train.geno)

# close the HIBAG model explicitly
hlaClose(model)
```



---

hlaClose	<i>Dispose a model object</i>
----------	-------------------------------

---

**Description**

Release all resources stored in the [hlaAttrBagClass](#) object. The HIBAG package allows up to 256 [hlaAttrBagClass](#) objects stored in memory.

**Usage**

```
hlaClose(model)
```

**Arguments**

model	an object of <a href="#">hlaAttrBagClass</a>
-------	--

**Value**

None.

**Author(s)**

Xiuwen Zheng

**See Also**

[hlaAttrBagging](#), [summary.hlaAttrBagClass](#)

---

hlaCombineAllele	<i>Combine two datasets of HLA types</i>
------------------	--

---

**Description**

Combine two objects of [hlaAlleleClass](#).

**Usage**

```
hlaCombineAllele(H1, H2)
```

**Arguments**

H1	the first <a href="#">hlaAlleleClass</a> object
H2	the second <a href="#">hlaAlleleClass</a> object

**Value**

Return [hlaAlleleClass](#).

**Author(s)**

Xiuwen Zheng

**See Also**[hlaAllele](#), [hlaAlleleSubset](#)**Examples**

```

head(HLA_Type_Table)
dim(HLA_Type_Table) # 60 13

# make a "hlaAlleleClass" object
hla.id <- "C"
hla <- hlaAllele(HLA_Type_Table$sample.id,
  HLA_Type_Table[, paste(hla.id, ".1", sep="")],
  HLA_Type_Table[, paste(hla.id, ".2", sep="")],
  locus=hla.id, assembly="hg19")
summary(hla)

subhla1 <- hlaAlleleSubset(hla, 1:100)
summary(subhla1)
subhla2 <- hlaAlleleSubset(hla, 201:300)
summary(subhla2)

H <- hlaCombineAllele(subhla1, subhla2)
summary(H)

```

---

hlaCombineModelObj

---

*Combine two HIBAG models together*


---

**Description**

Merge two objects of [hlaAttrBagObj](#) together, which is useful for building an ensemble model in parallel.

**Usage**

```
hlaCombineModelObj(obj1, obj2)
```

**Arguments**

obj1                    an object of [hlaAttrBagObj](#)  
 obj2                    an object of [hlaAttrBagObj](#)

**Value**

Return an object of [hlaAttrBagObj](#).

**Author(s)**

Xiuwen Zheng

**See Also**[hlaAttrBagging](#), [hlaModelFiles](#)**Examples**

```
# make a "hlaAlleleClass" object
hla.id <- "A"
hla <- hlaAllele(HLA_Type_Table$sample.id,
  H1 = HLA_Type_Table[, paste(hla.id, ".1", sep="")],
  H2 = HLA_Type_Table[, paste(hla.id, ".2", sep="")],
  locus=hla.id, assembly="hg19")

# SNP predictors within the flanking region on each side
region <- 500 # kb
snpid <- hlaFlankingSNP(HapMap_CEU_Geno$snp.id, HapMap_CEU_Geno$snp.position,
  hla.id, region*1000, assembly="hg19")
length(snpid) # 275

# training genotypes
train.geno <- hlaGenoSubset(HapMap_CEU_Geno,
  snp.sel = match(snpid, HapMap_CEU_Geno$snp.id))

# train a HIBAG model
set.seed(100)
m1 <- hlaAttrBagging(hla, train.geno, nclassifier=1)
m2 <- hlaAttrBagging(hla, train.geno, nclassifier=1)

m1.obj <- hlaModelToObj(m1)
m2.obj <- hlaModelToObj(m2)

m.obj <- hlaCombineModelObj(m1.obj, m2.obj)
summary(m.obj)
```

hlaCompareAllele

*Evaluate prediction accuracies***Description**

To evaluate the overall accuracy, sensitivity, specificity, positive predictive value, negative predictive value.

**Usage**

```
hlaCompareAllele(TrueHLA, PredHLA, allele.limit=NULL, call.threshold=NaN,
  match.threshold=NaN, max.resolution="", output.individual=FALSE,
  verbose=TRUE)
```

**Arguments**

TrueHLA	an object of <code>hlaAlleleClass</code> , the true HLA types
PredHLA	an object of <code>hlaAlleleClass</code> , the predicted HLA types
allele.limit	a list of HLA alleles, the validation samples are limited to those having HLA alleles in <code>allele.limit</code> , or NULL for no limit. <code>allele.limit</code> could be character-type, <code>hlaAttrBagClass</code> or <code>hlaAttrBagObj</code>
call.threshold	the call threshold for posterior probability, i.e., call or no call is determined by whether <code>prob &gt;= call.threshold</code> or not
match.threshold	the matching threshold for SNP haplotype similarity, e.g., use 1% quantile of matching statistics of a training model
max.resolution	"2-digit", "4-digit", "6-digit", "8-digit", "allele", "protein", "2", "4", "6", "8", "full" or "": "allele" = "2-digit", "protein" = "4-digit", "full" and "" indicating no limit on resolution
output.individual	if TRUE, output accuracy for each individual
verbose	if TRUE, show information

**Value**

Return a `list(overall, confusion, detail)`, or `list(overall, confusion, detail, individual)` if `output.individual=TRUE`.

`overall` (data.frame):

<code>total.num.ind</code>	the total number of individuals
<code>crt.num.ind</code>	the number of individuals with correct HLA types
<code>crt.num.haplo</code>	the number of chromosomes with correct HLA alleles
<code>acc.ind</code>	the proportion of individuals with correctly predicted HLA types (i.e., both of alleles are correct, the accuracy of an individual is 0 or 1.)
<code>acc.haplo</code>	the proportion of chromosomes with correctly predicted HLA alleles (i.e., the accuracy of an individual is 0, 0.5 or 1, since an individual has two alleles.)
<code>call.threshold</code>	call threshold, if it is NaN, no call threshold is executed
<code>n.call</code>	the number of individuals with call
<code>call.rate</code>	overall call rate

`confusion` (matrix): a confusion matrix.

`detail` (data.frame):

<code>allele</code>	HLA alleles
<code>train.num</code>	the number of training haplotypes
<code>train.freq</code>	the training haplotype frequencies
<code>valid.num</code>	the number of validation haplotypes
<code>valid.freq</code>	the validation haplotype frequencies

call.rate	the call rates for HLA alleles
accuracy	allele accuracy
sensitivity	sensitivity
specificity	specificity
ppv	positive predictive value
npv	negative predictive value
miscall	the most likely miss-called alleles
miscall.prop	the proportions of the most likely miss-called allele in all miss-called alleles

individual (data.frame):

sample.id	sample id
true.hla	the true HLA type
pred.hla	the prediction of HLA type
accuracy	accuracy, 0, 0.5, or 1

**Author(s)**

Xiuwen Zheng

**See Also**

[hlaAttrBagging](#), [predict.hlaAttrBagClass](#), [hlaReport](#)

**Examples**

```
# make a "hlaAlleleClass" object
hla.id <- "A"
hla <- hlaAllele(HLA_Type_Table$sample.id,
  H1 = HLA_Type_Table[, paste(hla.id, ".1", sep="")],
  H2 = HLA_Type_Table[, paste(hla.id, ".2", sep="")],
  locus=hla.id, assembly="hg19")

# divide HLA types randomly
set.seed(100)
hlatab <- hlaSplitAllele(hla, train.prop=0.5)
names(hlatab)
# "training" "validation"
summary(hlatab$training)
summary(hlatab$validation)

# SNP predictors within the flanking region on each side
region <- 500 # kb
snpid <- hlaFlankingSNP(HapMap_CEU_Geno$snp.id, HapMap_CEU_Geno$snp.position,
  hla.id, region*1000, assembly="hg19")
length(snpid) # 275

# training and validation genotypes
train.geno <- hlaGenoSubset(HapMap_CEU_Geno,
```

```

snp.sel=match(snpid, HapMap_CEU_Geno$snp.id),
samp.sel=match(hlatab$training$value$sample.id,
HapMap_CEU_Geno$sample.id))
test.geno <- hlaGenoSubset(HapMap_CEU_Geno,
  samp.sel=match(hlatab$validation$value$sample.id,
HapMap_CEU_Geno$sample.id))

# train a HIBAG model
set.seed(100)
model <- hlaAttrBagging(hlatab$training, train.geno, nclassifier=4,
  verbose.detail=TRUE)
summary(model)

# validation
pred <- hlaPredict(model, test.geno)
# compare
(comp <- hlaCompareAllele(hlatab$validation, pred, allele.limit=model,
  call.threshold=0))
(comp <- hlaCompareAllele(hlatab$validation, pred, allele.limit=model,
  call.threshold=0.5))

```

hlaConvSequence

*Conversion From HLA Alleles to Amino Acid Sequences***Description**

Convert (P-coded or G-coded) HLA alleles to amino acid sequences.

**Usage**

```

hlaConvSequence(hla=character(), locus=NULL,
  method=c("protein", "protein_reference"),
  code=c("exact", "P.code", "G.code", "P.code.merge", "G.code.merge"),
  region=c("auto", "all", "P.code", "G.code"), release=c("v3.22.0"),
  replace=NULL)

```

**Arguments**

hla	characters, or an object of <a href="#">hlaAlleleClass</a> , at least 4-digit or 2-field (P-coded) HLA alleles
locus	"A", "B", "C", "DRB1", "DQA1", "DQB1", "DPB1" or "DPA1"
method	"protein": returns protein sequence alignments, "protein_reference": returns the protein sequence alignment reference
code	"exact": requires full resolution; "P.code": allows ambiguous alleles according to P code; "G.code": allows ambiguous alleles according to G code; "P.code.merge" and "G.code.merge" merge multiple ambiguous allele sequences by masking unknown or ambiguous amino acid an asterisk

region	"all": returns all amino acid or nucleotide sequences; "P.code", "G.code": returns the exon 2 and 3 for HLA class I, and the exon 2 for HLA class II alleles; "auto": region="all" if code=="exact", region="P.code" if code=="P.code" "P.code.merge", region="G.code" if code=="G.code" "G.code.merge"
release	"v3.22.0" – IPD-IMGT/HLA 3.22.0 database (2015-10-07)
replace	NULL, or a character vector, e.g., c("09:02"="107:01"), any "09:02" will be replaced by "107:01". Due to the change of HLA nomenclature from 2010, HLA-DPB1*09:02 is replaced by DPB1*107:01

## Details

The P or G codes for reporting of ambiguous allele typings can be found: [http://hla.alleles.org/alleles/p\\_groups.html](http://hla.alleles.org/alleles/p_groups.html) or [http://hla.alleles.org/alleles/g\\_groups.html](http://hla.alleles.org/alleles/g_groups.html). The protein sequences for each HLA alleles could be found: [http://hla.alleles.org/alleles/text\\_index.html](http://hla.alleles.org/alleles/text_index.html).

Due to allelic ambiguity, multiple alleles are assigned to a 2-field P-coded allele or 3-field G-coded allele. For HLA Class I alleles, identity in the 'antigen binding domains' is based on identical protein sequences as encoded by exons 2 and 3. For HLA Class II alleles this is based on identical protein sequences as encoded by exon 2. P codes and G codes encode the same protein sequence for the peptide binding domains (exon 2 and 3 for HLA class I and exon 2 only for HLA class II alleles).

1. the sequence is displayed as a hyphen "-" where it is identical to the reference.
2. an insertion or deletion is represented by a period ".".
3. an unknown or ambiguous position in the alignment is represented by an asterisk "\*".
4. a capital X is used for the 'stop' codons in protein alignments.

<http://hla.alleles.org/alleles/formats.html>

HLA class I and II sequence alignments (Text Index): [http://hla.alleles.org/alleles/text\\_index.html](http://hla.alleles.org/alleles/text_index.html)

WARNING: if you are not familiar with HLA nomenclature, you might consult with the package author or anyone who is familiar with HLA sequence alignments.

## Value

Return an object of `hlaAASeqClass` or a list of characters. NULL or NA in the list indicates no matching.

## Author(s)

Xiuwen Zheng

## References

The licence and disclaimer of distributed HLA data: Creative Commons Attribution-NoDerivs Licence (<http://hla.alleles.org/terms.html>).

Robinson J, Halliwell JA, Hayhurst JH, Flicek P, Parham P, Marsh SGE: The IPD and IMGT/HLA database: allele variant databases. Nucleic Acids Research. 2015 43:D423-431

Robinson J, Malik A, Parham P, Bodmer JG, Marsh SGE: IMGT/HLA - a sequence database for the human major histocompatibility complex. Tissue Antigens. 2000 55:280-7

## See Also

[hlaAlleleSubset](#)

## Examples

```
hlaConvSequence(locus="A", method="protein_reference")

# exact match
hlaConvSequence(c("01:01", "02:02", "01:01:01G", "01:01:01:01", "07"),
  locus="A")

# allow ambiguity
hlaConvSequence(c("01:01", "02:02", "01:01:01G", "01:01:01:01", "07"),
  locus="A", code="P.code")
hlaConvSequence(c("01:01", "02:02", "01:01:01G", "01:01:01:01", "07"),
  locus="A", code="P.code.merge")

hlaConvSequence(locus="DPB1", method="protein_reference")
hlaConvSequence(c("09:01", "09:02", locus="DPB1", replace=c("09:02"="107:01"))
hlaConvSequence(c("09:01", "09:02", locus="DPB1", code="P.code",
  replace=c("09:02"="107:01"))
hlaConvSequence(c("09:01", "09:02", locus="DPB1", code="P.code.merge",
  replace=c("09:02"="107:01"))

hlaConvSequence(locus="DQB1", method="protein_reference")
hlaConvSequence(c("05:01:01:01", "06:01:01"), locus="DQB1")
hlaConvSequence(c("05:01", "06:01"), locus="DQB1", code="P.code")
hlaConvSequence(c("05:01", "06:01"), locus="DQB1", code="P.code.merge")

hla.id <- "A"
hla <- hlaAllele(HLA_Type_Table$sample.id,
  H1 = HLA_Type_Table[, paste(hla.id, ".1", sep="")],
  H2 = HLA_Type_Table[, paste(hla.id, ".2", sep="")],
  locus=hla.id, assembly="hg19")

(v <- hlaConvSequence(hla, code="P.code.merge"))
summary(v)

v <- hlaConvSequence(hla, code="P.code.merge", region="all")
summary(v)

hla.id <- "DQB1"
hla <- hlaAllele(HLA_Type_Table$sample.id,
```



```

H1 = HLA_Type_Table[, paste(hla.id, ".1", sep=""),
H2 = HLA_Type_Table[, paste(hla.id, ".2", sep=""),
locus=hla.id, assembly="hg19")

(v <- hlaConvSequence(hla, code="P.code.merge"))
summary(v)

v <- hlaConvSequence(hla, code="P.code.merge", region="all")
summary(v)

```

---

hlaDistance	<i>Distance matrix of HLA alleles</i>
-------------	---------------------------------------

---

## Description

To calculate the distance matrix of HLA alleles from a HIBAG model.

## Usage

```
hlaDistance(model)
```

## Arguments

model                      a model of [hlaAttrBagClass](#) or [hlaAttrBagObj](#)

## Value

Return a distance matrix with row and column names for HLA alleles.

## Author(s)

Xiuwen Zheng

## Examples

```

# make a "hlaAlleleClass" object
hla.id <- "A"
hla <- hlaAllele(HLA_Type_Table$sample.id,
  H1 = HLA_Type_Table[, paste(hla.id, ".1", sep=""),
  H2 = HLA_Type_Table[, paste(hla.id, ".2", sep=""),
  locus=hla.id, assembly="hg19")

# flanking genotypes
train.geno <- hlaGenoSubsetFlank(HapMap_CEU_Geno, hla.id, 500000)
summary(train.geno)

# train a HIBAG model
set.seed(100)
model <- hlaAttrBagging(hla, train.geno, nclassifier=10)
summary(model)

```

```
# distance matrix
d <- hlaDistance(model)

# draw
p <- hclust(as.dist(d))
plot(p, xlab="HLA alleles")
```

---

hlaFlankingSNP

*SNP IDs or SNP genotypes in Flanking Region*


---

## Description

To get SNPs in the flanking region of a specified HLA/KIR locus.

## Usage

```
hlaFlankingSNP(snp.id, position, locus, flank.bp=500000L, assembly="auto",
               pos.mid=NA_integer_)
hlaGenoSubsetFlank(genoobj, locus="any", flank.bp=500000L, assembly="auto",
                  pos.mid=NA_integer_)
```

## Arguments

snp.id	a vector of SNP IDs
genoobj	a genotype object of <a href="#">hlaSNPGenoClass</a>
position	a vector of positions
locus	the name of HLA locus, or "any" for other genes and using pos.mid
flank.bp	the size of flanking region on each side in basepair
assembly	the human genome reference: "hg18", "hg19" (default), "hg38"; "auto" refers to "hg19"; "auto-silent" refers to "hg19" without any warning
pos.mid	the middle position of the flanking region

## Details

hla.id is "A", "B", "C", "DRB1", "DRB5", "DQA1", "DQB1", "DPB1" or "any".

## Value

Return selected SNP IDs from snp.id.

## Author(s)

Xiuwen Zheng

**See Also**

[hlaGenoSubset](#), [hlaLociInfo](#)

**Examples**

```
# make a "hlaAlleleClass" object
hla.id <- "A"
hla <- hlaAllele(HLA_Type_Table$sample.id,
  H1 = HLA_Type_Table[, paste(hla.id, ".1", sep="")],
  H2 = HLA_Type_Table[, paste(hla.id, ".2", sep="")],
  locus=hla.id, assembly="hg19")

# training genotypes
region <- 500 # kb
snpid <- hlaFlankingSNP(HapMap_CEU_Geno$snp.id, HapMap_CEU_Geno$snp.position,
  hla.id, region*1000, assembly="hg19")
train.geno <- hlaGenoSubset(HapMap_CEU_Geno,
  snp.sel = match(snpid, HapMap_CEU_Geno$snp.id))
summary(train.geno)

# or using hlaGenoSubsetFlank
train.geno <- hlaGenoSubsetFlank(HapMap_CEU_Geno, hla.id, region*1000)
summary(train.geno)

## customize positions
snpid <- hlaFlankingSNP(HapMap_CEU_Geno$snp.id, HapMap_CEU_Geno$snp.position,
  "any", 500*1000, pos.mid=29954010)
```

---

hlaGDS2Geno

*Import genotypes from a GDS file*


---

**Description**

To convert a SNPRelate or SeqArray GDS file to an object of hlaSNPGenoClass.

**Usage**

```
hlaGDS2Geno(gds.fn, rm.invalid.allele=FALSE, import.chr="xMHC", assembly="auto",
  verbose=TRUE)
```

**Arguments**

gds.fn	a file name for the GDS file defined in the SNPRelate or SeqArray package
rm.invalid.allele	if TRUE, remove SNPs with non-standard alleles (except A,G,C,T)
import.chr	the chromosome, "1" .. "22", "X", "Y", "XY", "MT", "xMHC", or "", where "xMHC" implies the extended MHC on chromosome 6, and "" for all SNPs

assembly            the human genome reference: "hg18", "hg19" (default), "hg38"; "auto" refers to "hg19"; "auto-silent" refers to "hg19" without any warning

verbose            if TRUE, show information

**Value**

Return an object of [hlaSNPGenoClass](#).

**Author(s)**

Xiuwen Zheng

**See Also**

[hlaGeno2PED](#), [hlaBED2Geno](#)

**Examples**

```
# Import a SNP GDS file
fn <- system.file("extdata", "HapMap_CEU_Chr6.gds", package="HIBAG")

geno <- hlaGDS2Geno(fn, assembly="hg18", rm.invalid.allele=TRUE)

summary(geno)
```

---

hlaGeno2PED	<i>Convert to PLINK PED format</i>
-------------	------------------------------------

---

**Description**

Convert an object of [hlaSNPGenoClass](#) to a file of PLINK PED format.

**Usage**

```
hlaGeno2PED(geno, out.fn)
```

**Arguments**

geno            a genotype object of [hlaSNPGenoClass](#)

out.fn          the file name of output ped file

**Details**

Two files ".map" and ".ped" are created.

**Value**

None.

Author(s)

Xiuwen Zheng

See Also

[hlaBED2Geno](#)

Examples

```
# make a "hlaAlleleClass" object
hla.id <- "A"
hla <- hlaAllele(HLA_Type_Table$sample.id,
  H1 = HLA_Type_Table[, paste(hla.id, ".1", sep="")],
  H2 = HLA_Type_Table[, paste(hla.id, ".2", sep="")],
  max.resolution="4-digit", locus=hla.id, assembly="hg19")

# training genotypes
region <- 500 # kb
snpid <- hlaFlankingSNP(HapMap_CEU_Geno$snp.id, HapMap_CEU_Geno$snp.position,
  hla.id, region*1000, assembly="hg19")

train.geno <- hlaGenoSubset(HapMap_CEU_Geno,
  snp.sel = match(snpid, HapMap_CEU_Geno$snp.id))

hlaGeno2PED(train.geno, "test")

# delete the temporary files
unlink(c("test.map", "test.ped"), force=TRUE)
```

---

hlaGenoAFreq	<i>Allele Frequency</i>
--------------	-------------------------

---

Description

To calculate the allele frequencies from genotypes or haplotypes.

Usage

```
hlaGenoAFreq(obj)
```

Arguments

obj                    an object of [hlaSNPGenoClass](#)

Value

Return allele frequencies.

**Author(s)**

Xiuwen Zheng

**See Also**

[hlaGenoAFreq](#), [hlaGenoMFreq](#), [hlaGenoMRate](#), [hlaGenoMRate\\_Samp](#)

**Examples**

```
summary(HapMap_CEU_Geno)

summary(hlaGenoAFreq(HapMap_CEU_Geno))
```

---

hlaGenoCombine	<i>Combine two genotypic data sets into one</i>
----------------	---

---

**Description**

To combine two genotypic data sets into one dataset.

**Usage**

```
hlaGenoCombine(geno1, geno2,
  match.type=c("Position", "Pos+Allele", "RefSNP+Position", "RefSNP"),
  allele.check=TRUE, same.strand=FALSE, verbose=TRUE)
```

**Arguments**

geno1	the first genotype object of <a href="#">hlaSNPGenoClass</a>
geno2	the second genotype object of <a href="#">hlaSNPGenoClass</a>
match.type	"RefSNP+Position" (by default) – using both of RefSNP IDs and positions; "RefSNP" – using RefSNP IDs only; "Position" – using positions only
allele.check	if TRUE, call <a href="#">hlaGenoSwitchStrand</a> to check and then switch allele pairs if needed
same.strand	TRUE assuming alleles are on the same strand (e.g., forward strand); otherwise, FALSE not assuming whether on the same strand or not
verbose	show information, if TRUE

**Details**

The function merges two SNP dataset geno1 and geno2, and returns a SNP dataset consisting of the SNP intersect between geno1 and geno2, and having the same SNP information (allele and position) as geno1.

**Value**

An object of [hlaSNPGenoClass](#).

**Author(s)**

Xiuwen Zheng

**See Also**[hlaMakeSNPGeno](#), [hlaGenoSubset](#)**Examples**

```
# import a PLINK BED file
bed.fn <- system.file("extdata", "HapMap_CEU.bed", package="HIBAG")
fam.fn <- system.file("extdata", "HapMap_CEU.fam", package="HIBAG")
bim.fn <- system.file("extdata", "HapMap_CEU.bim", package="HIBAG")
hapmap.ceu <- hlaBED2Geno(bed.fn, fam.fn, bim.fn, assembly="hg19")

# combine two datasets together
geno <- hlaGenoCombine(HapMap_CEU_Geno, hapmap.ceu)
summary(geno)
```

hlaGenoLD

*Composite Linkage Disequilibrium***Description**

To calculate composite linkage disequilibrium ( $r^2$ ) between HLA locus and SNP markers.

**Usage**

```
hlaGenoLD(hla, geno)
```

**Arguments**

hla	an object of <a href="#">hlaAlleleClass</a>
geno	an object of <a href="#">hlaSNPGenoClass</a> , or a vector or matrix for SNP data

**Value**

Return a vector of linkage disequilibrium ( $r^2$ ) for each SNP marker.

**Author(s)**

Xiuwen Zheng

**References**

Weir BS, Cockerham CC: Complete characterization of disequilibrium at two loci; in Feldman MW (ed): Mathematical Evolutionary Theory. Princeton, NJ: Princeton University Press, 1989.

Zaykin, D. V., Pudovkin, A., and Weir, B. S. (2008). Correlation-based inference for linkage disequilibrium with multiple alleles. *Genetics* 180, 533-545.

## Examples

```
# plot linkage disequilibrium
ymax <- 0.16
plot(NaN, NaN, xlab="SNP Position (in KB)",
      ylab="Composite Linkage Disequilibrium (r2)",
      xlim=range(HapMap_CEU_Geno$snp.position)/1000, ylim=c(0, ymax),
      main="Major Histocompatibility Complex")

hla.list <- c("A", "C", "DQA1")
col.list <- 1:3

# for-loop
for (i in 1:3)
{
  hla.id <- hla.list[i]

  # make a "hlaAlleleClass" object
  hla <- hlaAllele(HLA_Type_Table$sample.id,
    H1 = HLA_Type_Table[, paste(hla.id, ".1", sep="")],
    H2 = HLA_Type_Table[, paste(hla.id, ".2", sep="")],
    locus=hla.id, assembly="hg19")

  # linkage disequilibrium between HLA locus and SNP markers
  ld <- hlaGenoLD(hla, HapMap_CEU_Geno)

  # draw
  points(HapMap_CEU_Geno$snp.position/1000, ld, pch="*", col=i)
  x <- (hla$pos.start/1000 + hla$pos.end/1000)/2
  abline(v=x, col=col.list[i], lty=3, lwd=2.5)
  points(x, ymax, pch=25, col=7, bg=col.list[i], cex=1.5)
}
legend("topleft", col=col.list, pt.bg=col.list, text.col=col.list, pch=25,
      legend=paste("HLA -", hla.list))
```

---

hlaGenoMFreq

*Minor Allele Frequency*


---

## Description

To calculate the minor allele frequencies from genotypes or haplotypes.

## Usage

```
hlaGenoMFreq(obj)
```

## Arguments

obj                    an object of [hlaSNPGenoClass](#)



**Value**

Return minor allele frequencies.

**Author(s)**

Xiuwen Zheng

**See Also**

[hlaGenoAFreq](#), [hlaGenoMFreq](#), [hlaGenoMRate](#), [hlaGenoMRate\\_Samp](#)

**Examples**

```
summary(HapMap_CEU_Geno)
```

```
summary(hlaGenoMFreq(HapMap_CEU_Geno))
```

---

hlaGenoMRate	<i>Missing Rates Per SNP</i>
--------------	------------------------------

---

**Description**

To calculate the missing rates from genotypes or haplotypes per SNP.

**Usage**

```
hlaGenoMRate(obj)
```

**Arguments**

obj                    an object of [hlaSNPGenoClass](#)

**Value**

Return missing rates per SNP.

**Author(s)**

Xiuwen Zheng

**See Also**

[hlaGenoAFreq](#), [hlaGenoMFreq](#), [hlaGenoMRate](#), [hlaGenoMRate\\_Samp](#)

**Examples**

```
summary(HapMap_CEU_Geno)
```

```
summary(hlaGenoMRate(HapMap_CEU_Geno))
```

---

hlaGenoMRate_Samp	<i>Missing Rates Per Sample</i>
-------------------	---------------------------------

---

**Description**

To calculate the missing rates from genotypes or haplotypes per sample.

**Usage**

```
hlaGenoMRate_Samp(obj)
```

**Arguments**

obj                    an object of [hlaSNPGenoClass](#)

**Value**

Return missing rates per sample.

**Author(s)**

Xiuwen Zheng

**See Also**

[hlaGenoAFreq](#), [hlaGenoMFreq](#), [hlaGenoMRate](#), [hlaGenoMRate\\_Samp](#)

**Examples**

```
summary(HapMap_CEU_Geno)

summary(hlaGenoMRate_Samp(HapMap_CEU_Geno))
```

---

hlaGenoSubset	<i>Get a subset of genotypes</i>
---------------	----------------------------------

---

**Description**

To get a subset of genotypes from a [hlaSNPGenoClass](#) object.

**Usage**

```
hlaGenoSubset(genoobj, samp.sel=NULL, snp.sel=NULL, snp.id=NULL)
```

**Arguments**

genoobj	a genotype object of <a href="#">hlaSNPGenoClass</a>
samp.sel	a logical vector, or an integer vector of indices
snp.sel	a logical vector, or an integer vector of indices
snp.id	SNP IDs to be selected, or NULL

**Details**

genoobj\$genotype is a numeric matrix, with an entry value 0 standing for BB (ZERO A allele), 1 for AB (ONE A allele), 2 for AA (TWO A alleles) and others for missing values (missing genotypes are usually set to be NA).

**Value**

Return a [hlaSNPGenoClass](#) object, and it is a list:

genotype	a genotype matrix, “# of SNPs” - by - “# of individuals”
sample.id	a vector of sample IDs
snp.id	a vector of SNP IDs
snp.position	a vector of SNP positions in basepair
snp.allele	a vector of characters with the format of “A allele/B allele”
assembly	optional, human genome information

**Author(s)**

Xiuwen Zheng

**See Also**

[hlaMakeSNPGeno](#), [hlaGenoCombine](#)

**Examples**

```
summary(HapMap_CEU_Geno)

geno <- hlaGenoSubset(HapMap_CEU_Geno,
  snp.sel = (hlaGenoMFreq(HapMap_CEU_Geno)>0.10))
summary(geno)
```

---

hlaGenoSwitchStrand	<i>Allele flipping if needed</i>
---------------------	----------------------------------

---

### Description

Determine the ordered pair of A and B alleles, using the allele information provided by template.

### Usage

```
hlaGenoSwitchStrand(target, template,  
    match.type=c("Position", "Pos+Allele", "RefSNP+Position", "RefSNP"),  
    same.strand=FALSE, verbose=TRUE)
```

### Arguments

target	an object of <a href="#">hlaSNPGenoClass</a>
template	a genotypic object of <a href="#">hlaSNPGenoClass</a> , a model object of <a href="#">hlaAttrBagClass</a> or a model object of <a href="#">hlaAttrBagObj</a>
match.type	"RefSNP+Position" (by default) – using both of RefSNP IDs and positions; "RefSNP" – using RefSNP IDs only; "Position" – using positions only
same.strand	TRUE assuming alleles are on the same strand (e.g., forward strand); otherwise, FALSE not assuming whether on the same strand or not
verbose	show information, if TRUE

### Details

The A/B pairs of target are determined using the information from template.

### Value

Return a [hlaSNPGenoClass](#) object consisting of the SNP intersect between target and template.

### Author(s)

Xiuwen Zheng

### See Also

[hlaMakeSNPGeno](#), [hlaGenoSubset](#)

**Examples**

```
summary(HapMap_CEU_Geno)
# A/C A/G C/T G/T
# 136 655 632 141

# import a PLINK BED file
bed.fn <- system.file("extdata", "HapMap_CEU.bed", package="HIBAG")
fam.fn <- system.file("extdata", "HapMap_CEU.fam", package="HIBAG")
bim.fn <- system.file("extdata", "HapMap_CEU.bim", package="HIBAG")
hapmap.ceu <- hlaBED2Geno(bed.fn, fam.fn, bim.fn, assembly="hg19")
summary(hapmap.ceu)
# A/C A/G A/T C/G C/T G/T
# 332 1567 64 111 1510 348

# combine two datasets together
geno <- hlaGenoSwitchStrand(HapMap_CEU_Geno, hapmap.ceu)
summary(geno)
# There are 1564 SNPs in common.
# The allele pairs of 763 SNPs need to be switched.
# A/C A/G C/T G/T
# 104 505 496 109
```

hlaLDMatrix

*Composite Linkage Disequilibrium in a Region***Description**

To calculate composite linkage disequilibrium ( $r^2$ ) among SNPs within a region.

**Usage**

```
hlaLDMatrix(geno, loci=NULL, maf=0.01, assembly="auto", draw=TRUE,
  verbose=TRUE)
```

**Arguments**

geno	an object of <a href="#">hlaSNPGenoClass</a>
maf	MAF filter $\geq$ maf
loci	NULL or a character vector, e.g., "A", "B"
assembly	the human genome reference: "hg18", "hg19" (default), "hg38"; "auto" refers to "hg19"; "auto-silent" refers to "hg19" without any warning
draw	if TRUE, return a ggplot2 object
verbose	if TRUE, show information

**Value**

Return a ggplot2 object if draw=TRUE or a matrix correlation.

**Author(s)**

Xiuwen Zheng

**References**

Weir BS, Cockerham CC: Complete characterization of disequilibrium at two loci; in Feldman MW (ed): Mathematical Evolutionary Theory. Princeton, NJ: Princeton University Press, 1989.

**Examples**

```
region <- 500*1000 # basepair
geno <- hlaGenoSubsetFlank(HapMap_CEU_Geno, "A", region)
summary(geno)

hlaLDMatrix(geno, "A")
```

---

hlaLociInfo

*HLA/KIR Locus Information*


---

**Description**

To get the starting and ending positions in basepair of HLA/KIR loci.

**Usage**

```
hlaLociInfo(assembly=c("auto", "auto-silent", "hg18", "hg19", "hg38",
  "unknown"))
```

**Arguments**

assembly            the human genome reference: "hg18", "hg19" (default), "hg38"; "auto" refers to "hg19"; "auto-silent" refers to "hg19" without any warning

**Value**

Return a data frame include the genomic locations.

**Author(s)**

Xiuwen Zheng

**References**

NCBI Resources: <https://www.ncbi.nlm.nih.gov/gene>, HLA Nomenclature: <http://hla.alleles.org/genes/index.html>

**Examples**

```
hlaLociInfo()
```

---

hlaMakeSNPGeno	<i>Make a SNP genotype object</i>
----------------	-----------------------------------

---

## Description

To create a [hlaSNPGenoClass](#) object (SNP genotypic object).

## Usage

```
hlaMakeSNPGeno(genotype, sample.id, snp.id, snp.position,
  A.allele, B.allele, assembly="auto")
```

## Arguments

genotype	a genotype matrix, “# of SNPs” - by - “# of individuals”
sample.id	a vector of sample IDs
snp.id	a vector of SNP IDs
snp.position	a vector of SNP positions
A.allele	a vector of A alleles, A is usually defined as a minor or alternative allele
B.allele	a vector of B alleles, B is usually defined as a major or reference allele
assembly	the human genome reference: "hg18", "hg19" (default), "hg38"; "auto" refers to "hg19"; "auto-silent" refers to "hg19" without any warning

## Details

genotype is a numeric matrix, with an entry value 0 standing for BB (ZERO A allele), 1 for AB (ONE A allele), 2 for AA (TWO A alleles) and others for missing values (missing genotypes are usually set to be NA).

## Value

Return a [hlaSNPGenoClass](#) object, and it is a list:

genotype	a genotype matrix, “# of SNPs” - by - “# of individuals”
sample.id	a vector of sample IDs
snp.id	a vector of SNP IDs
snp.position	a vector of SNP positions in basepair
snp.allele	a vector of characters with the format of “A allele/B allele”
assembly	the human genome reference

## Author(s)

Xiuwen Zheng

**See Also**

[hlaGenoSubset](#), [hlaGenoCombine](#)

**Examples**

```
summary(HapMap_CEU_Geno)

allele <- strsplit(HapMap_CEU_Geno$snp.allele, "/")
A.allele <- sapply(allele, function(x) { x[1] })
B.allele <- sapply(allele, function(x) { x[2] })

geno <- hlaMakeSNPGeno(HapMap_CEU_Geno$genotype, HapMap_CEU_Geno$sample.id,
  HapMap_CEU_Geno$snp.id, HapMap_CEU_Geno$snp.position, A.allele, B.allele,
  assembly="hg19")

summary(geno)
```

---

hlaModelFiles	<i>Load a model object from files</i>
---------------	---------------------------------------

---

**Description**

To load HIBAG models from a list of files, and merge all together.

**Usage**

```
hlaModelFiles(fn.list, action.missingfile=c("ignore", "stop"), verbose=TRUE)
```

**Arguments**

fn.list	a vector of file names
action.missingfile	"ignore", ignore the missing files, by default; "stop", stop if missing
verbose	if TRUE, show information

**Value**

Return [hlaAttrBagObj](#).

**Author(s)**

Xiuwen Zheng

**See Also**

[hlaAttrBagging](#), [hlaModelToObj](#)



## Examples

```
# make a "hlaAlleleClass" object
hla.id <- "C"
hla <- hlaAllele(HLA_Type_Table$sample.id,
  H1 = HLA_Type_Table[, paste(hla.id, ".1", sep="")],
  H2 = HLA_Type_Table[, paste(hla.id, ".2", sep="")],
  locus=hla.id, assembly="hg19")

# training genotypes
region <- 100 # kb
snpid <- hlaFlankingSNP(HapMap_CEU_Geno$snp.id, HapMap_CEU_Geno$snp.position,
  hla.id, region*1000, assembly="hg19")
train.geno <- hlaGenoSubset(HapMap_CEU_Geno,
  snp.sel = match(snpid, HapMap_CEU_Geno$snp.id),
  samp.sel = match(hla$value$sample.id, HapMap_CEU_Geno$sample.id))

#
# train HIBAG models
#
set.seed(1000)

model1 <- hlaAttrBagging(hla, train.geno, nclassifier=1)
mobj1 <- hlaModelToObj(model1)
save(mobj1, file="tm1.RData")

model2 <- hlaAttrBagging(hla, train.geno, nclassifier=1)
mobj2 <- hlaModelToObj(model2)
save(mobj2, file="tm2.RData")

model3 <- hlaAttrBagging(hla, train.geno, nclassifier=1)
mobj3 <- hlaModelToObj(model3)
save(mobj3, file="tm3.RData")

# load all of mobj1, mobj2 and mobj3
mobj <- hlaModelFiles(c("tm1.RData", "tm2.RData", "tm3.RData"))
summary(mobj)

# delete the temporary files
unlink(c("tm1.RData", "tm2.RData", "tm3.RData"), force=TRUE)
```

hlaModelFromObj

*Conversion between the in-memory model and the object that can be saved in a file*

## Description

Build a model [hlaAttrBagClass](#) from an object of [hlaAttrBagObj](#) which is stored in an R object file, or convert [hlaAttrBagClass](#) to [hlaAttrBagObj](#).

**Usage**

```
hlaModelFromObj(obj)
hlaModelToObj(model)
```

**Arguments**

obj	an object of <a href="#">hlaAttrBagObj</a>
model	an object of <a href="#">hlaAttrBagClass</a>

**Value**

`hlaModelFromObj` returns `hlaAttrBagClass`, and `hlaModelToObj` returns `hlaAttrBagObj`.

**Author(s)**

Xiuwen Zheng

**See Also**

[hlaAttrBagging](#)

**Examples**

```
# make a "hlaAlleleClass" object
hla.id <- "DQB1"
hla <- hlaAllele(HLA_Type_Table$sample.id,
  H1 = HLA_Type_Table[, paste(hla.id, ".1", sep="")],
  H2 = HLA_Type_Table[, paste(hla.id, ".2", sep="")],
  locus=hla.id, assembly="hg19")

# training genotypes
region <- 100 # kb
snpid <- hlaFlankingSNP(HapMap_CEU_Geno$snp.id, HapMap_CEU_Geno$snp.position,
  hla.id, region*1000, assembly="hg19")
train.geno <- hlaGenoSubset(HapMap_CEU_Geno,
  snp.sel = match(snpid, HapMap_CEU_Geno$snp.id))

# train a HIBAG model
set.seed(1000)
model <- hlaAttrBagging(hla, train.geno, nclassifier=2)
print(model)

mobj <- hlaModelToObj(model)

is(model)
is(mobj)

# close the HIBAG model explicitly
hlaClose(model)
```

---

hlaOutOfBag	<i>Out-of-bag estimation of overall accuracy, per-allele sensitivity, etc</i>
-------------	---

---

**Description**

Out-of-bag estimation of overall accuracy, per-allele sensitivity, specificity, positive predictive value, negative predictive value and call rate.

**Usage**

```
hlaOutOfBag(model, hla, snp, call.threshold=NaN, verbose=TRUE)
```

**Arguments**

model	an object of <a href="#">hlaAttrBagClass</a> or <a href="#">hlaAttrBagObj</a>
hla	the training HLA types, an object of <a href="#">hlaAlleleClass</a>
snp	the training SNP genotypes, an object of <a href="#">hlaSNPGenoClass</a>
call.threshold	the specified call threshold; if NaN, no threshold is used
verbose	if TRUE, show information

**Value**

Return [hlaAlleleClass](#).

**Author(s)**

Xiuwen Zheng

**See Also**

[hlaCompareAllele](#), [hlaReport](#)

**Examples**

```
# make a "hlaAlleleClass" object
hla.id <- "A"
hla <- hlaAllele(HLA_Type_Table$sample.id,
  H1 = HLA_Type_Table[, paste(hla.id, ".1", sep="")],
  H2 = HLA_Type_Table[, paste(hla.id, ".2", sep="")],
  locus=hla.id, assembly="hg19")

# SNP predictors within the flanking region on each side
region <- 500 # kb
snpid <- hlaFlankingSNP(HapMap_CEU_Geno$snp.id, HapMap_CEU_Geno$snp.position,
  hla.id, region*1000, assembly="hg19")
length(snpid) # 275

# training and validation genotypes
```

```

geno <- hlaGenoSubset(HapMap_CEU_Geno,
  snp.sel = match(snpid, HapMap_CEU_Geno$snp.id),
  samp.sel = match(hla$value$sample.id, HapMap_CEU_Geno$sample.id))

# train a HIBAG model
set.seed(100)
# please use "nclassifier=100" when you use HIBAG for real data
model <- hlaAttrBagging(hla, geno, nclassifier=4)
summary(model)

# out-of-bag estimation
(comp <- hlaOutOfBag(model, hla, geno, call.threshold=NaN, verbose=TRUE))

# report
hlaReport(comp, type="txt")

hlaReport(comp, type="tex")

hlaReport(comp, type="html")

```

---

hlaParallelAttrBagging

*Build a HIBAG model via parallel computation*


---

## Description

To build a HIBAG model for predicting HLA types via parallel computation.

## Usage

```

hlaParallelAttrBagging(cl, hla, snp, auto.save="",
  nclassifier=100L, mtry=c("sqrt", "all", "one"), prune=TRUE, na.rm=TRUE,
  mono.rm=TRUE, maf=NaN, stop.cluster=FALSE, verbose=TRUE,
  verbose.detail=FALSE)

```

## Arguments

cl	NULL, FALSE, TRUE, an integer, or a cluster object created by the <a href="#">parallel-package</a> ; if NULL or FALSE, use the serial implementation; if TRUE, use the number of threads returned from <code>RcppParallel::defaultNumThreads()</code> (by default using all threads); if an integer, specify the number of threads; When cl is TRUE or an integer, the multithreading implementation will be used; when cl is a cluster, the multi-processing implementation will be used where each individual classifier is built within a child process
hla	training HLA types, an object of <a href="#">hlaAlleleClass</a>
snp	training SNP genotypes, an object of <a href="#">hlaSNPGenoClass</a>
auto.save	specify a autosaved file name for an R object (.rda, .RData or .rds); "", no file saving; see details

nclassifier	the total number of individual classifiers
mtry	a character or a numeric value, the number of variables randomly sampled as candidates for each selection. See details
prune	if TRUE, to perform a parsimonious forward variable selection, otherwise, exhaustive forward variable selection. See details
na.rm	if TRUE, remove the samples with missing HLA types
mono.rm	if TRUE, remove monomorphic SNPs
maf	MAF threshold for SNP filter, excluding any SNP with $MAF < maf$
stop.cluster	TRUE: stop cluster nodes after completing the calculation
verbose	if TRUE, show information
verbose.detail	if TRUE, show more information

### Details

mtry (the number of variables randomly sampled as candidates for each selection): "sqrt", using the square root of the total number of candidate SNPs; "all", using all candidate SNPs; "one", using one SNP; an integer, specifying the number of candidate SNPs;  $0 < r < 1$ , the number of candidate SNPs is "r \* the total number of SNPs".

prune: there is no significant difference on accuracy between parsimonious and exhaustive forward variable selections. If prune = TRUE, the searching algorithm performs a parsimonious forward variable selection: if a new SNP predictor reduces the current out-of-bag accuracy, then it is removed from the candidate SNP set for future searching. Parsimonious selection helps to improve the computational efficiency by reducing the searching times of non-informative SNP markers.

An autosave function is available in hlaParallelAttrBagging when an new individual classifier is built internally without completing the ensemble.

### Value

Return an object of [hlaAttrBagClass](#) if `auto.save=""`, and NULL otherwise.

### Author(s)

Xiuwen Zheng

### References

Zheng X, Shen J, Cox C, Wakefield J, Ehm M, Nelson M, Weir BS; HIBAG – HLA Genotype Imputation with Attribute Bagging. Pharmacogenomics Journal. doi: 10.1038/tpj.2013.18. <https://www.nature.com/articles/tpj201318>

### See Also

[hlaAttrBagging](#), [hlaClose](#), [hlaSetKernelTarget](#)

**Examples**

```

# make a "hlaAlleleClass" object
hla.id <- "A"
hla <- hlaAllele(HLA_Type_Table$sample.id,
  H1 = HLA_Type_Table[, paste(hla.id, ".1", sep="")],
  H2 = HLA_Type_Table[, paste(hla.id, ".2", sep="")],
  locus=hla.id, assembly="hg19")

# divide HLA types randomly
set.seed(100)
hlatab <- hlaSplitAllele(hla, train.prop=0.5)
names(hlatab)
# "training" "validation"
summary(hlatab$training)
summary(hlatab$validation)

# SNP predictors within the flanking region on each side
region <- 500 # kb
snpid <- hlaFlankingSNP(HapMap_CEU_Geno$snp.id, HapMap_CEU_Geno$snp.position,
  hla.id, region*1000, assembly="hg19")
length(snpid) # 275

# training and validation genotypes
train.geno <- hlaGenoSubset(HapMap_CEU_Geno,
  snp.sel = match(snpid, HapMap_CEU_Geno$snp.id),
  samp.sel = match(hlatab$training$value$sample.id,
    HapMap_CEU_Geno$sample.id))
test.geno <- hlaGenoSubset(HapMap_CEU_Geno,
  samp.sel=match(hlatab$validation$value$sample.id,
    HapMap_CEU_Geno$sample.id))

#####
# Multithreading

set.seed(100)

# train a HIBAG model in parallel with 2 cores
# please use "nclassifier=100" when you use HIBAG for real data
model <- hlaParallelAttrBagging(2, hlatab$training, train.geno, nclassifier=4)

#####
# Multicore & autosave

library(parallel)

# choose an appropriate cluster size, e.g., 2
cl <- makeCluster(2)
set.seed(100)

# train a HIBAG model in parallel

```

```

# please use "nclassifier=100" when you use HIBAG for real data
hlaParallelAttrBagging(cl, hlab$training, train.geno, nclassifier=4,
  auto.save="tmp_model.RData", stop.cluster=TRUE)

mobj <- get(load("tmp_model.RData"))
summary(mobj)
model <- hlaModelFromObj(mobj)

# validation
pred <- hlaPredict(model, test.geno)
summary(pred)

# compare
hlaCompareAllele(hlab$validation, pred, allele.limit=model)$overall

# since 'stop.cluster=TRUE' used in 'hlaParallelAttrBagging'
# need a new cluster
cl <- makeCluster(2)

pred <- hlaPredict(model, test.geno, cl=cl)
summary(pred)

# stop parallel nodes
stopCluster(cl)

# delete the temporary file
unlink(c("tmp_model.RData"), force=TRUE)

```

hlaPredict

*HIBAG model prediction (in parallel)***Description**

To predict HLA type based on a HIBAG model (in parallel).

**Usage**

```

hlaPredict(object, snp, cl=FALSE,
  type=c("response+dosage", "response", "prob", "response+prob"),
  vote=c("prob", "majority"), allele.check=TRUE,
  match.type=c("Position", "Pos+Allele", "RefSNP+Position", "RefSNP"),
  same.strand=FALSE, verbose=TRUE, verbose.match=TRUE)
## S3 method for class 'hlaAttrBagClass'
predict(object, snp, cl=FALSE,
  type=c("response+dosage", "response", "prob", "response+prob"),
  vote=c("prob", "majority"), allele.check=TRUE,
  match.type=c("Position", "Pos+Allele", "RefSNP+Position", "RefSNP"),
  same.strand=FALSE, verbose=TRUE, verbose.match=TRUE, ...)

```

**Arguments**

<code>object</code>	a model of <a href="#">hlaAttrBagClass</a>
<code>snp</code>	a genotypic object of <a href="#">hlaSNPGenoClass</a>
<code>cl</code>	FALSE, TRUE, an integer, or a cluster object created by the <a href="#">parallel-package</a> ; if FALSE, use the serial implementation; if TRUE, use the number of threads returned from <code>RcppParallel::defaultNumThreads()</code> (by default using all threads); if an integer, specify the number of threads
<code>type</code>	"response+dosage": return the best-guess types and dosages for each allele (by default); "response": return the best-guess types with its posterior probability; "prob": return a matrix for all posterior probabilities; "response+prob": return the best-guess, dosages and all posterior probabilities
<code>vote</code>	"prob" (default behavior) – make a prediction based on the averaged posterior probabilities from all individual classifiers; "majority" – majority voting from all individual classifiers, where each classifier votes for an HLA type
<code>allele.check</code>	if TRUE, check and then switch allele pairs if needed
<code>match.type</code>	"Position" – use positions only (by default); "RefSNP+Position" – use both of SNP IDs and positions; "RefSNP" – using SNP IDs only
<code>same.strand</code>	TRUE assuming alleles are on the same strand (e.g., forward strand); otherwise, FALSE not assuming whether on the same strand or not
<code>verbose</code>	if TRUE, show information
<code>verbose.match</code>	if TRUE, show missing SNP proportions for different <code>match.type</code>
<code>...</code>	unused

**Details**

If more than 50% of SNP predictors are missing, a warning will be given.

When `match.type="RefSNP+Position"`, the matching of SNPs requires both SNP IDs and positions. A lower missing fraction maybe gained by matching SNP IDs or positions only. Call `hlaPredict(..., match.type="RefSNP")` or `hlaPredict(..., match.type="Position")` for this purpose. It could be safe to assume that the SNPs with the same positions on the same genome reference (e.g., hg19) are the same variant albeit the different SNP IDs. Any concern about SNP mismatching should be emailed to the genotyping platform provider.

**Value**

Return a [hlaAlleleClass](#) object with posterior probabilities of predicted HLA types, or a matrix of pairwise possible HLA types with all posterior probabilities. If `type = "response+prob"`, return a [hlaAlleleClass](#) object with a matrix of `postprob` for the probabilities of all pairs of alleles. If a probability matrix is returned, `colnames` is `sample.id` and `rownames` is an unordered pair of HLA alleles.

**Author(s)**

Xiuwen Zheng



**See Also**

[hlaAttrBagging](#), [hlaAllele](#), [hlaCompareAllele](#), [hlaParallelAttrBagging](#), [hlaSetKernelTarget](#), [hlaAlleleToVCF](#)

**Examples**

```
# make a "hlaAlleleClass" object
hla.id <- "A"
hla <- hlaAllele(HLA_Type_Table$sample.id,
  H1 = HLA_Type_Table[, paste(hla.id, ".1", sep="")],
  H2 = HLA_Type_Table[, paste(hla.id, ".2", sep="")],
  locus=hla.id, assembly="hg19")

# divide HLA types randomly
set.seed(100)
hlatab <- hlaSplitAllele(hla, train.prop=0.5)
names(hlatab)
# "training" "validation"
summary(hlatab$training)
summary(hlatab$validation)

# SNP predictors within the flanking region on each side
region <- 500 # kb
snpid <- hlaFlankingSNP(HapMap_CEU_Geno$snp.id, HapMap_CEU_Geno$snp.position,
  hla.id, region*1000, assembly="hg19")
length(snpid) # 275

# training and validation genotypes
train.geno <- hlaGenoSubset(HapMap_CEU_Geno,
  snp.sel=match(snpid, HapMap_CEU_Geno$snp.id),
  samp.sel=match(hlatab$training$value$sample.id,
    HapMap_CEU_Geno$sample.id))
test.geno <- hlaGenoSubset(HapMap_CEU_Geno,
  samp.sel=match(hlatab$validation$value$sample.id,
    HapMap_CEU_Geno$sample.id))

# train a HIBAG model
set.seed(100)
model <- hlaAttrBagging(hlatab$training, train.geno, nclassifier=4,
  verbose.detail=TRUE)
summary(model)

# validation
pred <- hlaPredict(model, test.geno, type="response+dosage")
pred

head(pred$value)
pred$dosage[, 1:4] # a dosage matrix

# compare
(comp <- hlaCompareAllele(hlatab$validation, pred, allele.limit=model,
  call.threshold=0))
```

```
(comp <- hlaCompareAllele(hlatab$validation, pred, allele.limit=model,
  call.threshold=0.5))
```

hlaPredMerge

*Merge prediction results from multiple HIBAG models*

## Description

Return an object of [hlaAlleleClass](#), which contains predicted HLA types.

## Usage

```
hlaPredMerge(..., weight=NULL, equivalence=NULL, use.matching=TRUE,
  ret.dosage=TRUE, ret.postprob=FALSE, max.resolution="", rm.suffix=FALSE,
  verbose=TRUE)
```

## Arguments

...	The object(s) of <a href="#">hlaAlleleClass</a> , having a field of 'postprob', and returned by <code>hlaPredict(..., type="response+prob")</code>
weight	the weight used for each prediction; if NULL, equal weights to be used; or set the weight vector to be the training sample sizes
equivalence	a data.frame with two columns, the first column for new equivalent alleles, and the second for the alleles possibly exist in the object(s) passed to this function; there is no replace if the allele is not found in the second column
use.matching	if TRUE, use actual probabilities (i.e., poster prob. * matching) for merging; otherwise, use poster prob. instead. <code>use.matching=TRUE</code> is recommended.
ret.dosage	if TRUE, return dosages
ret.postprob	if TRUE, return average posterior probabilities
max.resolution	"2-digit", "1-field", "4-digit", "2-field", "6-digit", "3-field", "8-digit", "4-field", "allele", "protein", "full", "none", or "": "allele" = "2-digit"; "protein" = "4-digit"; "full", "none" or "" for no limit on resolution
rm.suffix	whether remove the non-digit suffix in the last field, e.g., for "01:22N", "N" is a non-digit suffix
verbose	if TRUE, show information

## Details

Calculate a new probability matrix for each pair of HLA alleles, by averaging (posterior) probabilities from all models with specified weights. If equivalence is specified, multiple alleles might be collapsed into one class.

## Value

Return a [hlaAlleleClass](#) object.

**Author(s)**

Xiuwen Zheng

**See Also**

[hlaAttrBagging](#), [hlaAllele](#), [predict.hlaAttrBagClass](#)

**Examples**

```
# make a "hlaAlleleClass" object
hla.id <- "A"
hla <- hlaAllele(HLA_Type_Table$sample.id,
  H1 = HLA_Type_Table[, paste(hla.id, ".1", sep="")],
  H2 = HLA_Type_Table[, paste(hla.id, ".2", sep="")],
  locus=hla.id, assembly="hg19")

# divide HLA types randomly
set.seed(100)
hlatab <- hlaSplitAllele(hla, train.prop=0.5)
names(hlatab)
# "training" "validation"
summary(hlatab$training)
summary(hlatab$validation)

# SNP predictors within the flanking region on each side
region <- 500 # kb
snpid <- hlaFlankingSNP(HapMap_CEU_Geno$snp.id, HapMap_CEU_Geno$snp.position,
  hla.id, region*1000, assembly="hg19")
length(snpid) # 275

# training and validation genotypes
train.geno <- hlaGenoSubset(HapMap_CEU_Geno,
  snp.sel=match(snpid, HapMap_CEU_Geno$snp.id),
  samp.sel=match(hlatab$training$value$sample.id,
    HapMap_CEU_Geno$sample.id))
test.geno <- hlaGenoSubset(HapMap_CEU_Geno,
  samp.sel=match(hlatab$validation$value$sample.id,
    HapMap_CEU_Geno$sample.id))

# train HIBAG models
set.seed(100)

# please use "nclassifier=100" when you use HIBAG for real data
m1 <- hlaAttrBagging(hlatab$training, train.geno, nclassifier=2,
  verbose.detail=TRUE)
m2 <- hlaAttrBagging(hlatab$training, train.geno, nclassifier=2,
  verbose.detail=TRUE)

# validation
pd1 <- hlaPredict(m1, test.geno, type="response+prob")
pd2 <- hlaPredict(m2, test.geno, type="response+prob")
```

```

hlaCompareAllele(hlatab$validation, pd1)$overall
hlaCompareAllele(hlatab$validation, pd2)$overall

# merge predictions from multiple models, by voting from all classifiers
pd <- hlaPredMerge(pd1, pd2)
pd

hlaCompareAllele(hlatab$validation, pd)$overall

# collapse to 2-digit
pd <- hlaPredMerge(pd1, pd2, max.resolution="2-digit", ret.postprob=FALSE)
pd

```

---

hlaPublish	<i>Finalize a HIBAG model</i>
------------	-------------------------------

---

## Description

Finalize a HIBAG model by removing unused SNP predictors and adding appendix information (platform, training set, authors, warning, etc)

## Usage

```
hlaPublish(mobj, platform=NULL, information=NULL, warning=NULL,
           rm.unused.snp=TRUE, anonymize=TRUE, verbose=TRUE)
```

## Arguments

mobj	an object of <a href="#">hlaAttrBagObj</a> or <a href="#">hlaAttrBagClass</a>
platform	the text of platform information
information	the other information, like authors
warning	any warning message
rm.unused.snp	if TRUE, remove unused SNPs from the model
anonymize	if TRUE, remove sample IDs
verbose	if TRUE, show information

## Value

Returns a new object of [hlaAttrBagObj](#).

## Author(s)

Xiuwen Zheng

## See Also

[hlaModelFromObj](#), [hlaModelToObj](#)

**Examples**

```

# make a "hlaAlleleClass" object
hla.id <- "A"
hla <- hlaAllele(HLA_Type_Table$sample.id,
  H1 = HLA_Type_Table[, paste(hla.id, ".1", sep="")],
  H2 = HLA_Type_Table[, paste(hla.id, ".2", sep="")],
  locus=hla.id, assembly="hg19")

# training genotypes
region <- 250 # kb
snpid <- hlaFlankingSNP(HapMap_CEU_Geno$snp.id, HapMap_CEU_Geno$snp.position,
  hla.id, region*1000, assembly="hg19")
train.geno <- hlaGenoSubset(HapMap_CEU_Geno,
  snp.sel = match(snpid, HapMap_CEU_Geno$snp.id),
  samp.sel = match(hla$value$sample.id, HapMap_CEU_Geno$sample.id))

#
# train a HIBAG model
#
set.seed(1000)

# please use "nclassifier=100" when you use HIBAG for real data
model <- hlaAttrBagging(hla, train.geno, nclassifier=2, verbose.detail=TRUE)
summary(model)
length(model$snp.id)

mobj <- hlaPublish(model,
  platform = "Illumina 1M Duo",
  information = "Training set -- HapMap Phase II")
model2 <- hlaModelFromObj(mobj)
length(mobj$snp.id)
mobj$appendix
summary(mobj)

p1 <- hlaPredict(model, train.geno)
p2 <- hlaPredict(model2, train.geno)

# check
cbind(p1$value, p2$value)

```

hlaReport

*Format a report***Description**

Create a report for evaluating prediction accuracies.

**Usage**

```
hlaReport(object, export.fn="", type=c("txt", "tex", "html", "markdown"),
          header=TRUE)
```

**Arguments**

object	an object returned by <a href="#">hlaCompareAllele</a>
export.fn	a file name for output, or "" for stdout
type	"txt" – tab-delimited text format; "tex" – tex format using the 'longtable' package; "html" – html file
header	if TRUE, output the header of text file associated corresponding format

**Value**

None.

**Author(s)**

Xiuwen Zheng

**See Also**

[hlaCompareAllele](#)

**Examples**

```
# make a "hlaAlleleClass" object
hla.id <- "A"
hla <- hlaAllele(HLA_Type_Table$sample.id,
  H1 = HLA_Type_Table[, paste(hla.id, ".1", sep="")],
  H2 = HLA_Type_Table[, paste(hla.id, ".2", sep="")],
  locus=hla.id, assembly="hg19")

# divide HLA types randomly
set.seed(100)
hlatab <- hlaSplitAllele(hla, train.prop=0.5)
names(hlatab)
# "training" "validation"
summary(hlatab$training)
summary(hlatab$validation)

# SNP predictors within the flanking region on each side
region <- 500 # kb
snpid <- hlaFlankingSNP(HapMap_CEU_Geno$snp.id, HapMap_CEU_Geno$snp.position,
  hla.id, region*1000, assembly="hg19")
length(snpid) # 275

# training and validation genotypes
train.geno <- hlaGenoSubset(HapMap_CEU_Geno,
  snp.sel = match(snpid, HapMap_CEU_Geno$snp.id),
```

```

    samp.sel = match(hlatab$training$value$sample.id,
    HapMap_CEU_Geno$sample.id))
test.geno <- hlaGenoSubset(HapMap_CEU_Geno,
    samp.sel=match(hlatab$validation$value$sample.id,
    HapMap_CEU_Geno$sample.id))

# train a HIBAG model
set.seed(100)
# please use "nclassifier=100" when you use HIBAG for real data
model <- hlaAttrBagging(hlatab$training, train.geno, nclassifier=4,
    verbose.detail=TRUE)
summary(model)

# validation
pred <- hlaPredict(model, test.geno)
# compare
(comp <- hlaCompareAllele(hlatab$validation, pred, allele.limit=model,
    call.threshold=0))

# report
hlaReport(comp, type="txt")

hlaReport(comp, type="tex")

hlaReport(comp, type="html")

hlaReport(comp, type="markdown")

```

---

hlaReportPlot

*Format a report with figures*


---

## Description

Create figures for evaluating prediction accuracies.

## Usage

```

hlaReportPlot(PredHLA=NULL, TrueHLA=NULL, model=NULL,
    fig=c("matching", "call.rate", "call.threshold"), match.threshold=NaN,
    log_scale=TRUE)

```

## Arguments

PredHLA	NULL, an object of <a href="#">hlaAlleleClass</a> , the predicted HLA types
TrueHLA	NULL, an object of <a href="#">hlaAlleleClass</a> , the true HLA types
model	NULL, or a model of <a href="#">hlaAttrBagClass</a>

`fig` "matching": violin plot for matching measurements; "call.rate": relationship between accuracy and call rate; "call.threshold": relationship between accuracy and call threshold

`match.threshold` the threshold for matching proportion

`log_scale` if TRUE, use log scale for matching violin plot

**Value**

Return a ggplot2 object.

**Author(s)**

Xiuwen Zheng

**See Also**

[hlaReport](#)

**Examples**

```
# make a "hlaAlleleClass" object
hla.id <- "A"
hla <- hlaAllele(HLA_Type_Table$sample.id,
  H1 = HLA_Type_Table[, paste(hla.id, ".1", sep="")],
  H2 = HLA_Type_Table[, paste(hla.id, ".2", sep="")],
  locus=hla.id, assembly="hg19")

# divide HLA types randomly
set.seed(100)
hlatab <- hlaSplitAllele(hla, train.prop=0.5)
names(hlatab)
# "training" "validation"
summary(hlatab$training)
summary(hlatab$validation)

# SNP predictors within the flanking region on each side
region <- 500 # kb
snpid <- hlaFlankingSNP(HapMap_CEU_Geno$snp.id, HapMap_CEU_Geno$snp.position,
  hla.id, region*1000, assembly="hg19")
length(snpid) # 275

# training and validation genotypes
train.geno <- hlaGenoSubset(HapMap_CEU_Geno,
  snp.sel = match(snpid, HapMap_CEU_Geno$snp.id),
  samp.sel = match(hlatab$training$value$sample.id,
    HapMap_CEU_Geno$sample.id))
test.geno <- hlaGenoSubset(HapMap_CEU_Geno,
  samp.sel=match(hlatab$validation$value$sample.id,
    HapMap_CEU_Geno$sample.id))

# train a HIBAG model
```



```

set.seed(100)
# please use "nclassifier=100" when you use HIBAG for real data
model <- hlaAttrBagging(hlatab$training, train.geno, nclassifier=4,
  verbose.detail=TRUE)
summary(model)

# validation
pred <- hlaPredict(model, test.geno)

# visualize
hlaReportPlot(pred, fig="matching")

hlaReportPlot(model=model, fig="matching")

hlaReportPlot(pred, model=model, fig="matching")

hlaReportPlot(pred, hlatab$validation, fig="call.rate")

hlaReportPlot(pred, hlatab$validation, fig="call.threshold")

```

---

hlaSampleAllele	<i>Get sample IDs from HLA types with a filter</i>
-----------------	--

---

## Description

Get sample IDs from HLA types limited to a set of HLA alleles.

## Usage

```
hlaSampleAllele(TrueHLA, allele.limit=NULL, max.resolution="")
```

## Arguments

TrueHLA	an object of <a href="#">hlaAlleleClass</a>
allele.limit	a list of HLA alleles, the validation samples are limited to those having HLA alleles in allele.limit, or NULL for no limit. allele.limit could be character-type, <a href="#">hlaAttrBagClass</a> or <a href="#">hlaAttrBagObj</a>
max.resolution	"2-digit", "4-digit", "6-digit", "8-digit", "allele", "protein", "2", "4", "6", "8", "full" or "": "allele" = "2-digit", "protein" = "4-digit", "full" and "" mean no limit on resolution

## Value

Return a list of sample IDs.

## Author(s)

Xiuwen Zheng

**See Also**[hlaCompareAllele](#)**Examples**

```
# make a "hlaAlleleClass" object
hla.id <- "A"
hla <- hlaAllele(HLA_Type_Table$sample.id,
  HLA_Type_Table[, paste(hla.id, ".1", sep="")],
  HLA_Type_Table[, paste(hla.id, ".2", sep="")],
  locus=hla.id, assembly="hg19")
summary(hla)

hlaSampleAllele(hla)

hlaSampleAllele(hla, allele.limit=c(
  "01:01", "02:01", "02:06", "03:01", "11:01", "23:01"))
```

---

hlaSetKernelTarget	<i>Set the CPU target</i>
--------------------	---------------------------

---

**Description**

Set the CPU target that the HIBAG algorithm is built on.

**Usage**

```
hlaSetKernelTarget(cpu=c("max", "auto.avx2", "base",
  "sse2", "sse4", "avx", "avx2", "avx512f", "avx512bw", "avx512vpopcnt"))
```

**Arguments**

cpu	Specify the Intel/AMD CPU flag; "max" by default
-----	--

**Details**

If `cpu="max"`, the kernel target will be automatically determined according to the CPU capabilities to maximize the algorithm efficiency. When `cpu="auto.avx2"`, "avx2" is used instead of "avx512f", "avx512bw", "avx512vpopcnt" even if the CPU supports the AVX512F, AVX512BW or AVX512VPOPCNT intrinsics, since the CPU may reduce the frequency of the cores dynamically to keep power usage of AVX512 within bounds; if AVX2 is not applicable, other target will be automatically determined.

The HIBAG algorithm is optimized using different SIMD instruction sets to leverage the efficiency of the target Intel/AMD platform. The higher version of the C++ compiler is needed to enable the compilation of AVX2 and AVX512F intrinsics, e.g., GCC  $\geq$  v6.0. If the compiler does not support the CPU target, the implementation on that target will be disabled.

**Value**

Return a character vector for describing the CPU capabilities, the compiler information and the supported implementation.

**Author(s)**

Xiuwen Zheng

**See Also**

[hlaAttrBagging](#), [hlaParallelAttrBagging](#), [predict.hlaAttrBagClass](#), [hlaPredict](#)

**Examples**

```
hlaSetKernelTarget("auto")
```

---

hlaSNPGenoClass	<i>The class of SNP genotypes</i>
-----------------	-----------------------------------

---

**Description**

The class of SNP genotypes, and its instance is returned from [hlaMakeSNPGeno](#).

**Value**

There are five components:

genotype	a genotype matrix, “# of SNPs”-by-“# of individuals”; 0 standing for BB (ZERO A allele), 1 for AB (ONE A allele), 2 for AA (TWO A alleles) and NA for missing values (other values have no meaning)
sample.id	a vector of sample IDs
snp.id	a vector of SNP IDs
snp.position	a vector of SNP positions in basepair
snp.allele	a vector of characters with a format of “A allele/B allele”; B is usually defined as a major or reference allele, while A is defined as a minor or alternative allele
assembly	the human genome reference, such like "hg19"

**Author(s)**

Xiuwen Zheng

**See Also**

[hlaMakeSNPGeno](#)

---

`hlaSNPID`*Get SNP IDs and positions*

---

**Description**

Get the information of SNP ID with or without position.

**Usage**

```
hlaSNPID(obj, type=c("Position", "Pos+Allele", "RefSNP+Position", "RefSNP"))
```

**Arguments**

<code>obj</code>	a genotypic object of <a href="#">hlaSNPGenoClass</a> , a model object of <a href="#">hlaAttrBagClass</a> or a model object of <a href="#">hlaAttrBagObj</a>
<code>type</code>	"RefSNP+Position" (by default), "RefSNP" or "Position"

**Value**

If `type = "RefSNP+Position"`, return `paste(obj$snp.id, obj$snp.position, sep="-")`; if `type = "RefSNP"`, return `obj$snp.id`; if `type = "Position"`, return `obj$snp.position`; if `type = "Pos+Allele"`, return `paste(obj$snp.position, obj$snp.allele, sep="-")`.

**Author(s)**

Xiuwen Zheng

**See Also**

[hlaGenoSwitchStrand](#), [hlaGenoCombine](#)

**Examples**

```
x <- hlaSNPID(HapMap_CEU_Geno)
head(x)

x <- hlaSNPID(HapMap_CEU_Geno, "RefSNP")
head(x)

x <- hlaSNPID(HapMap_CEU_Geno, "Position")
head(x)
```

---

hlaSplitAllele	<i>Divide the samples randomly</i>
----------------	------------------------------------

---

**Description**

Divide the samples to the training and validation sets randomly.

**Usage**

```
hlaSplitAllele(HLA, train.prop=0.5)
```

**Arguments**

HLA	an object of <a href="#">hlaAlleleClass</a>
train.prop	the proportion of training set

**Details**

The algorithm tries to divide each HLA alleles into training and validation sets randomly with a training proportion train.prop.

**Value**

Return a list:

training	an object of <a href="#">hlaAlleleClass</a>
validation	an object of <a href="#">hlaAlleleClass</a>

**Author(s)**

Xiuwen Zheng

**See Also**

[hlaAllele](#)

**Examples**

```
# make a "hlaAlleleClass" object
hla.id <- "A"
hla <- hlaAllele(HLA_Type_Table$sample.id,
  H1 = HLA_Type_Table[, paste(hla.id, ".1", sep="")],
  H2 = HLA_Type_Table[, paste(hla.id, ".2", sep="")],
  locus=hla.id, assembly="hg19")

# divide HLA types randomly
set.seed(100)
hlatab <- hlaSplitAllele(hla, train.prop=0.5)
names(hlatab)
```

```
# "training"    "validation"
summary(hlatab$training)
summary(hlatab$validation)
```

---

hlaSubModelObj	<i>Get a subset of individual classifiers</i>
----------------	---

---

## Description

Get the first n individual classifiers.

## Usage

```
hlaSubModelObj(obj, n)
```

## Arguments

obj	an object of <a href="#">hlaAttrBagObj</a>
n	an integer, get the first n individual classifiers

## Value

Return an object of [hlaAttrBagObj](#).

## Author(s)

Xiuwen Zheng

## See Also

[hlaAttrBagging](#)

## Examples

```
# make a "hlaAlleleClass" object
hla.id <- "C"
hla <- hlaAllele(HLA_Type_Table$sample.id,
  H1 = HLA_Type_Table[, paste(hla.id, ".1", sep="")],
  H2 = HLA_Type_Table[, paste(hla.id, ".2", sep="")],
  locus=hla.id, assembly="hg19")

# training genotypes
region <- 50 # kb
snpid <- hlaFlankingSNP(HapMap_CEU_Geno$snp.id, HapMap_CEU_Geno$snp.position,
  hla.id, region*1000, assembly="hg19")
train.geno <- hlaGenoSubset(HapMap_CEU_Geno,
  snp.sel = match(snpid, HapMap_CEU_Geno$snp.id))

# train a HIBAG model
```

```

set.seed(1000)
# please use "nclassifier=100" when you use HIBAG for real data
model <- hlaAttrBagging(hla, train.geno, nclassifier=2, verbose.detail=TRUE)
mobj <- hlaModelToObj(model)
summary(mobj)

newmobj <- hlaSubModelObj(mobj, 1)
summary(newmobj)

```

---

hlaUniqueAllele	<i>Get unique HLA alleles</i>
-----------------	-------------------------------

---

## Description

Get unique HLA alleles, which are in ascending order.

## Usage

```
hlaUniqueAllele(hla, all=NA)
```

## Arguments

hla	character-type HLA alleles, a <a href="#">hlaAlleleClass</a> object, a <code>link{hlaAttrBagClass}</code> object, or a <code>link{hlaAttrBagObj}</code> object
all	when hla is a <code>hlaAlleleClass</code> object and <code>all=TRUE</code> , return all HLA alleles if <code>hla\$dosage</code> or <code>hla\$postprob</code> exists; otherwise, only return the alleles in <code>hla\$value</code>

## Details

Each HLA allele name has a unique number corresponding to up to four sets of digits separated by colons. The name designation depends on the sequence of the allele and that of its nearest relative. The digits before the first colon describe the type, which often corresponds to the serological antigen carried by an allotype. The next set of digits are used to list the subtypes, numbers being assigned in the order in which DNA sequences have been determined. Alleles whose numbers differ in the two sets of digits must differ in one or more nucleotide substitutions that change the amino acid sequence of the encoded protein. Alleles that differ only by synonymous nucleotide substitutions (also called silent or non-coding substitutions) within the coding sequence are distinguished by the use of the third set of digits. Alleles that only differ by sequence polymorphisms in the introns or in the 5' or 3' untranslated regions that flank the exons and introns are distinguished by the use of the fourth set of digits.

In addition to the unique allele number there are additional optional suffixes that may be added to an allele to indicate its expression status. Alleles that have been shown not to be expressed, 'Null' alleles have been given the suffix 'N'. Those alleles which have been shown to be alternatively expressed may have the suffix 'L', 'S', 'C', 'A' or 'Q'.

<http://hla.alleles.org/nomenclature/index.html>

Value

Return a character vector of HLA alleles

Author(s)

Xiuwen Zheng

See Also

[hlaAllele](#), [hlaAlleleDigit](#)

Examples

```
# make a "hlaAlleleClass" object
hla.id <- "A"
hla <- hlaAllele(HLA_Type_Table$sample.id,
  H1 = HLA_Type_Table[, paste(hla.id, ".1", sep="")],
  H2 = HLA_Type_Table[, paste(hla.id, ".2", sep="")],
  locus=hla.id, assembly="hg19")
summary(hla)
hlaUniqueAllele(hla)

hlaUniqueAllele(c("01", "01:03", "01:01", "03:05", "03:01G",
  "03:05P", "03:104:01", "104:01"))
```

---

HLA_Type_Table	<i>Four-digit HLA types of a study simulated from HapMap CEU</i>
----------------	--

---

Description

A data.frame object including HLA-A, B, C, DRB1, DQA1 and DQB1 loci of 60 samples.

Usage

HLA\_Type\_Table

Value

A data.frame

References

A high-resolution HLA and SNP haplotype map for disease association studies in the extended human MHC. de Bakker PI, McVean G, Sabeti PC, Miretti MM, Green T, Marchini J, Ke X, Monsuur AJ, Whittaker P, Delgado M, Morrison J, Richardson A, Walsh EC, Gao X, Galver L, Hart J, Hafler DA, Pericak-Vance M, Todd JA, Daly MJ, Trowsdale J, Wijmenga C, Vyse TJ, Beck S, Murray SS, Carrington M, Gregory S, Deloukas P, Rioux JD. Nat Genet. 2006 Oct;38(10):1166-72. Epub 2006 Sep 24.



---

plot.hlaAttrBagObj      *Plot a HIBAG model*

---

## Description

To show a scatterplot of the numbers of individual classifiers and SNP positions.

## Usage

```
## S3 method for class 'hlaAttrBagObj'
plot(x, snp.col="gray33", snp.pch=1, snp.sz=1,
      locus.col="blue", locus.lty=1L, locus.lty2=2L, addplot=NULL,
      assembly="auto", ...)
## S3 method for class 'hlaAttrBagClass'
plot(x, ...)
```

## Arguments

x	an object of <a href="#">hlaAttrBagObj</a>
snp.col	the color of SNP uses
snp.pch	the point type of SNP uses
snp.sz	the point size of SNP uses
locus.col	the color of text and line for HLA locus
locus.lty	the type of line for the bounds of HLA locus
locus.lty2	the type of line for HLA locus
addplot	NULL for creating a plot, or a ggplot object to be appended
assembly	the human genome reference: "hg18", "hg19" (default), "hg38"; "auto" refers to "hg19"; "auto-silent" refers to "hg19" without any warning
...	further arguments passed to or from other methods

## Value

None

## Author(s)

Xiuwen Zheng

## See Also

[print.hlaAttrBagObj](#), [summary.hlaAttrBagObj](#)

## Examples

```
# make a "hlaAlleleClass" object
hla.id <- "C"
hla <- hlaAllele(HLA_Type_Table$sample.id,
  H1 = HLA_Type_Table[, paste(hla.id, ".1", sep="")],
  H2 = HLA_Type_Table[, paste(hla.id, ".2", sep="")],
  locus=hla.id, assembly="hg19")

# training genotypes
region <- 100 # kb
snpid <- hlaFlankingSNP(HapMap_CEU_Geno$snp.id, HapMap_CEU_Geno$snp.position,
  hla.id, region*1000, assembly="hg19")
train.geno <- hlaGenoSubset(HapMap_CEU_Geno,
  snp.sel = match(snpid, HapMap_CEU_Geno$snp.id))

# train a HIBAG model
set.seed(1000)
# please use "nclassifier=100" when you use HIBAG for real data
model <- hlaAttrBagging(hla, train.geno, nclassifier=2, verbose.detail=TRUE)
plot(model)
```

---

`print.hlaAttrBagClass` Summarize a “`hlaAttrBagClass`” or “`hlaAttrBagObj`” object.

---

## Description

Summarize an object of [hlaAttrBagClass](#) or [hlaAttrBagObj](#).

## Usage

```
## S3 method for class 'hlaAttrBagClass'
print(x, ...)
## S3 method for class 'hlaAttrBagObj'
print(x, ...)
## S3 method for class 'hlaAttrBagClass'
summary(object, show=TRUE, ...)
## S3 method for class 'hlaAttrBagObj'
summary(object, show=TRUE, ...)
```

## Arguments

<code>x</code>	an object of <a href="#">hlaAttrBagClass</a> or <a href="#">hlaAttrBagObj</a>
<code>object</code>	an object of <a href="#">hlaAttrBagClass</a> or <a href="#">hlaAttrBagObj</a>
<code>show</code>	if TRUE, show information
<code>...</code>	further arguments passed to or from other methods

**Value**

print returns NULL.

summary.hlaAttrBagClass and summary.hlaAttrBagObj return a list:

num.classifier	the total number of classifiers
num.snp	the total number of SNPs
snp.id	SNP IDs
snp.position	SNP position in basepair
snp.hist	the number of classifier for each SNP, and it could be used for SNP importance
info	a data.frame for the average number of SNPs (num.snp), haplotypes (num.haplo), out-of-bag accuracies (accuracy) among all classifiers: mean, standard deviation, min, max

**Author(s)**

Xiuwen Zheng

**See Also**

[plot.hlaAttrBagClass](#), [plot.hlaAttrBagObj](#)

**Examples**

```
# make a "hlaAlleleClass" object
hla.id <- "C"
hla <- hlaAllele(HLA_Type_Table$sample.id,
  H1 = HLA_Type_Table[, paste(hla.id, ".1", sep="")],
  H2 = HLA_Type_Table[, paste(hla.id, ".2", sep="")],
  locus=hla.id, assembly="hg19")

# training genotypes
region <- 100 # kb
snpid <- hlaFlankingSNP(HapMap_CEU_Geno$snp.id, HapMap_CEU_Geno$snp.position,
  hla.id, region*1000, assembly="hg19")
train.geno <- hlaGenoSubset(HapMap_CEU_Geno,
  snp.sel = match(snpid, HapMap_CEU_Geno$snp.id))

# train a HIBAG model
set.seed(1000)
# please use "nclassifier=100" when you use HIBAG for real data
model <- hlaAttrBagging(hla, train.geno, nclassifier=2, verbose.detail=TRUE)
print(model)
```

---

`summary.hlaAlleleClass`*Summarize a “hlaAlleleClass” or “hlaAASeqClass” object*

---

## Description

Show the information of a [hlaAlleleClass](#) or [hlaAASeqClass](#) object.

## Usage

```
## S3 method for class 'hlaAlleleClass'
summary(object, verbose=TRUE, ...)
## S3 method for class 'hlaAASeqClass'
summary(object, poly.only=TRUE, head=0L,
        verbose=TRUE, ...)
## S3 method for class 'hlaAlleleClass'
print(x, ...)
```

## Arguments

<code>object</code>	an object of <a href="#">hlaAlleleClass</a> or <a href="#">hlaAASeqClass</a>
<code>x</code>	an object of <a href="#">hlaAlleleClass</a> or <a href="#">hlaAASeqClass</a>
<code>poly.only</code>	if TRUE, only show the amino acid positions with polymorphism; otherwise, show all sequences
<code>head</code>	show the first head rows of cross tabulation, or 0L for all rows
<code>verbose</code>	if TRUE, show information
<code>...</code>	further arguments passed to or from other methods

## Value

Return a `data.frame` of count and frequency for each HLA allele, if object is `hlaAlleleClass`; a matrix of cross tabulation of amino acids at each position, if object is `hlaAASeqClass`.

## Author(s)

Xiuwen Zheng

## See Also

[hlaAllele](#), [hlaConvSequence](#)

---

```
summary.hlaSNPGenoClass
```

*Summarize a SNP dataset*

---

**Description**

Summarize the genotypic dataset.

**Usage**

```
## S3 method for class 'hlaSNPGenoClass'
summary(object, show=TRUE, ...)
## S3 method for class 'hlaSNPGenoClass'
print(x, ...)
```

**Arguments**

object	a genotype object of <a href="#">hlaSNPGenoClass</a>
x	a genotype object of <a href="#">hlaSNPGenoClass</a>
show	if TRUE, print information
...	further arguments passed to or from other methods

**Value**

None.

**Author(s)**

Xiuwen Zheng

**See Also**

[hlaMakeSNPGeno](#), [hlaGenoSubset](#)

**Examples**

```
summary(HapMap_CEU_Geno)
```

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