

Package ‘CollapsABEL’

May 29, 2015

Type Package

Title An R package for quantitative CDH analysis

Version 0.0.1

Date 2015-05-20

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Depends R (>= 2.15.0), txtutils, manqq2, ggplot2,
mice, magrittr, rentrez,
haplo.stats, dplyr, stringr, XML, xlsx

Description QCDH

License GPL

URL <https://bitbucket.org/kindlychung/collapsabel/overview>

BugReports <https://bitbucket.org/kindlychung/collapsabel/issues>

Suggests testthat

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baseName	<i>Basename of a FilePath object</i>
----------	--------------------------------------

Description

 Basename of a FilePath object

Usage

```
## S4 method for signature 'FilePath'
baseName(fp)
```

Arguments

 fp

Value

 character vector of basenames

Author(s)

 kaiyin

Examples

```
fp = filePath(R.home())
baseName(fp)
```

bimCorrectTypes	<i>Correct types of bim data.frame</i>
-----------------	----------------------------------------

Description

CHR, BP and GDIST columns should be integers.

Usage

```
bimCorrectTypes(bim_dat)
```

Arguments

bim_dat	data.frame read from a .bim file
---------	----------------------------------

Value

data.frame

Author(s)

kaiyin

bim_fam_info	<i>.bim and .fam file information functions</i>
--------------	-------------------------------------------------

Description

These two functions bimInfo, famInfo are generated by a factory function. They are similar to readInfo, only with pre-determined colnames (since they are really known).

Usage

```
bimInfo(filename)
```

```
famInfo(filename)
```

checkFileExist	<i>Stop when any file does not exist</i>
----------------	------------------------------------------

Description

Stop when any file does not exist

Usage

```
checkFileExist(files)
```

Arguments

files	character vector. File paths you want to check.
-------	-------------------------------------------------

Author(s)

kaiyin

Examples

```
\donotrun{
  checkFileExist(R.home())
  checkFileExist(sapply(1:5, function(i) tempfile()))
  checkFileExist(sapply(1:5, function(i) tempdir()))
}
```

df2ffdf	<i>Converts a data frame to an ffd</i>
---------	----------------------------------------

Description

Converts a data frame to an ffd

Usage

```
df2ffdf(df, ...)
```

Arguments

df	the data.frame you want to convert.
----	-------------------------------------

Value

an ffd object.

Examples

```
require(ff)
d = data.frame(x = rnorm(10), y = sapply(65:74, function(i) rawToChar(as.raw(i))))
d.ffd = df2ffdf(d)
class(d.ffd)
d1 = ff::as.ram(d.ffd)
all(d1 == d) # true
```

dirName	<i>Directory name of a file path</i>
---------	--------------------------------------

Description

Directory name of a file path

Usage

```
## S4 method for signature 'FilePath'
dirName(fp)
```

Arguments

fp FilePath object

Value

character vector of directories

Author(s)

kaiyin

Examples

```
fp = filePath(R.home())
dirName(fp)
```

famCorrectTypes	<i>Correct types of fam data.frame</i>
-----------------	----------------------------------------

Description

SEX and PHE columns should be integers.

Usage

```
famCorrectTypes(fam_dat)
```

Arguments

fam_dat data.frame read from a .fam file

Value

data.frame

Author(s)

kaiyin

filePath

Constructor for FilePath class

Description

Constructor for FilePath class

Usage

filePath(s)

Arguments

s character, path to file or dir

Value

FilePath object

Author(s)

kaiyin

FilePath-class

An S4 class to represent a file path

Description

This class comes with a validation function, making sure that the file exists.

Slots

path character, file or dir path

Author(s)

kaiyin

ifLen	<i>IfLen macro</i>
-------	--------------------

Description

Check whether a object has non-zero length, and eval expression accordingly.

Usage

```
ifLen(df = stop("df not supplied"), body1 = stop("body1 not supplied"),  
      body2 = { })
```

Arguments

df	An object which can be passed to length
body1	If length(df) is not zero, then this clause is evaluated, otherwise, body2 is evaluated.
body2	See above.

Author(s)

kaiyin

Examples

```
ifLen(c(1, 2), { print('yes!') }, {print("no!")})
```

ifLet	<i>IfLet macro</i>
-------	--------------------

Description

Eval expression x, assign it to a variable, and if that is TRUE, continue to eval expression1, otherwise eval expression2. Inspired by the clojure if-let macro.

Usage

```
ifLet(sym_str = stop("sym_str not supplied"), x = stop("x not supplied"),  
      body1 = stop("body1 not supplied"), body2 = { })
```

Arguments

sym_str	a string that will be converted to a symbol to hold value of x
x	the predicate to be evaluateated, and to be assigned to a temporary variable as described in sym_str
body1	expression to be evaluated when the temporary variable is TRUE.
body2	expression to be evaluated when the temporary variable is FALSE.

Author(s)

kaiyin

Examples

```
ifLet("..temp..", TRUE, {print(paste("true.", as.character(..temp..))}),
{print(paste("false.", as.character(..temp..))})})
```

ifLetLen

*IfLetLen macro***Description**

Similar to ifLet, but conditioned on whether the length of the result of eval(x) is 0.

Usage

```
ifLetLen(sym_str = stop("sym_str not supplied"), x = stop("x not supplied"),
body1 = stop("body1 not supplied"), body2 = { })
```

Arguments

x	the predicate to be evaluated, and to be assigned to a temporary var called ..temp..
body1	expression to be evaluated when ..temp.. is TRUE.
body2	expression to be evaluated when ..temp.. is FALSE.

Author(s)

kaiyin

Examples

```
ifLetLen("..temp..", 1:3, {print(paste("true.", as.character(..temp..))}),
{print(paste("false.", as.character(..temp..))})})
```

isSetup,PlInfo-method	<i>Check if a directory containing .bed .fam and .bim files is properly setup</i>
-----------------------	-----------------------------------------------------------------------------------

Description

Check if a directory containing .bed .fam and .bim files is properly setup

Usage

```
## S4 method for signature 'PlInfo'
isSetup(pl_info)
```


Arguments

pl_info PlInfo object

Value

TRUE or FALSE

Author(s)

kaiyin

Examples

```
# see examples in plInfo
```

loadBim

Load plink bim file (in ff format) into R

Description

Load plink bim file (in ff format) into R

Arguments

pl_info PlInfo object

Value

ffdf object

Author(s)

kaiyin

Examples

```
# see examples in plInfo
```

loadFam	<i>Load plink fam file (in ff format) into R</i>
---------	--------------------------------------------------

Description

Load plink fam file (in ff format) into R

Arguments

pl_info PInfo object

Value

ffdf object

Author(s)

kaiyin

Examples

```
# see examples in plInfo
```

loadFFDF	<i>Load ffdf directory</i>
----------	----------------------------

Description

Load ffdf directory

Usage

```
## S4 method for signature 'FilePath'
loadFFDF(dir)

## S4 method for signature 'character'
loadFFDF(dir)
```

Arguments

dir the ffdf directory to be loaded

Value

an ffdf object

Author(s)

kaiyin

Examples

```
\donotrunc{
iris_ff = df2ffdf(iris)
save.ffdf(iris_ff, dir = "iris_ff")
rm(iris_ff)
# error: object "iris_ff" not found
head(iris_ff)
iris_ff = loadFFDF("iris_ff")
# print out head of iris data, in ffdf format
head(iris_ff)
}
```

loadFrq

*Load plink frq file (in ff format) into R***Description**

Load plink frq file (in ff format) into R

Arguments

pl_info PInfo object

Value

ffdf object

Author(s)

kaiyin

Examples

```
# see examples in plInfo
```

loading_functions

*Loading function for .bim .fam and .frq data***Description**

These three S4 methods loadBim, loadFam, loadFrq are generated by a factory function. They all receive an PInfo object as parameter. In a properly setup plink directory, .bim .fam and .frq files should have been converted to ff format. These three functions load the corresponding ff backing files on disk.

Author(s)

kaiyin

nonExistentFiles, character-method

Non-existent files from a vector of filenames

Description

This function receives a vector of filenames as parameter, and returns a vector of non-existent files among them.

Usage

```
## S4 method for signature 'character'
nonExistentFiles(filenames)
```

Arguments

filenames character A vector of filenames

Value

A character vector of file paths that do not exist.

Author(s)

kaiyin

Examples

```
\donotrun{
nonExistentFiles(R.home())
nonExistentFiles(sapply(1:5, function(i) tempfile()))
nonExistentFiles(sapply(1:5, function(i) tempdir()))
}
```

plInfo

Info about plink bed files

Description

Info about plink bed files, including the root directory, paths of plink .bed, .bim, .fam and .frq files, ff backing directories for .bim, .fam and .frq files. This function is a constructor for PlInfo s4 class.

Usage

```
plInfo(bedstem)
```

Arguments

bedstem path of bed file excluding extension name

Value

a PLInfo object

Author(s)

kaiyin

Examples

```
\donotrunc{
pl_info = plInfo("/Users/kaiyin/EclipseWorkspace/collapsabel2/tests/testthat/mmp13")
isSetup(pl_info) # false
setup(pl_info)
isSetup(pl_info) # true
bim_ff = loadMyBim(pl_info)
head(bim_ff)
fam_ff = loadFam(pl_info)
head(fam_ff)
summary(fam_ff[, "IID"])
which(fam_ff[, "IID"] == "10425")
frq_ff = loadFrq(pl_info)
head(frq_ff)
}
```

plinkr

A wrapper for plink

Description

A wrapper for plink.

Usage

```
plinkr(D = NULL, K = NULL, a1_allele = NULL, a2_allele = NULL,
adjust = NULL, all = NULL, all_pheno = NULL, allele1234 = NULL,
alleleACGT = NULL, allele_count = NULL, allow_extra_chr = NULL,
allow_no_sex = NULL, alt_group = NULL, alt_snp = NULL,
annotate = NULL, annotate_snp_field = NULL, aperm = NULL,
assoc = NULL, attrib = NULL, attrib_indiv = NULL, autosome = NULL,
autosome_num = NULL, autosome_xy = NULL, bcf = NULL, bd = NULL,
bed = NULL, beta = NULL, bfile = NULL, bgen = NULL,
biallelic_only = NULL, bim = NULL, blocks = NULL,
blocks_inform_frac = NULL, blocks_max_kb = NULL, blocks_min_maf = NULL,
blocks_recomb_highci = NULL, blocks_strong_highci = NULL,
blocks_strong_lowci = NULL, bmerge = NULL, border = NULL,
bp_space = NULL, case_only = NULL, cc = NULL, cell = NULL,
cfile = NULL, chap = NULL, check_sex = NULL, chr = NULL,
chr_set = NULL, ci = NULL, clump = NULL, clump_allow_overlap = NULL,
clump_annotate = NULL, clump_best = NULL, clump_field = NULL,
clump_index_first = NULL, clump_kb = NULL, clump_p1 = NULL,
clump_p2 = NULL, clump_r2 = NULL, clump_range = NULL,
clump_range_border = NULL, clump_replicate = NULL,
```

```

clump_snp_field = NULL, clump_verbose = NULL, cluster = NULL,
cluster_missing = NULL, cm_map = NULL, cnv_blue = NULL,
cnv_border = NULL, cnv_brown = NULL, cnv_check_no_overlap = NULL,
cnv_count = NULL, cnv_del = NULL, cnv_disrupt = NULL,
cnv_drop_no_segment = NULL, cnv_dup = NULL, cnv_enrichment_test = NULL,
cnv_exclude = NULL, cnv_exclude_off_by_1 = NULL,
cnv_freq_excludue_above = NULL, cnv_freq_excludue_below = NULL,
cnv_freq_excludue_exact = NULL, cnv_freq_exclude_above = NULL,
cnv_freq_exclude_below = NULL, cnv_freq_exclude_exact = NULL,
cnv_freq_includue_exact = NULL, cnv_freq_include_exact = NULL,
cnv_freq_method2 = NULL, cnv_freq_overlap = NULL, cnv_green = NULL,
cnv_indiv_perm = NULL, cnv_intersect = NULL, cnv_kb = NULL,
cnv_list = NULL, cnv_make_map = NULL, cnv_max_kb = NULL,
cnv_max_score = NULL, cnv_max_sites = NULL, cnv_overlap = NULL,
cnv_red = NULL, cnv_region_overlap = NULL, cnv_report_regions = NULL,
cnv_score = NULL, cnv_seglist = NULL, cnv_sites = NULL,
cnv_subset = NULL, cnv_test = NULL, cnv_test_1sided = NULL,
cnv_test_2sided = NULL, cnv_test_region = NULL, cnv_test_window = NULL,
cnv_track = NULL, cnv_union_overlap = NULL, cnv_unique = NULL,
cnv_verbose_report_regions = NULL, cnv_write = NULL,
cnv_write_freq = NULL, complement_sets = NULL,
compound_genotypes = NULL, compress = NULL, condition = NULL,
condition_list = NULL, consensus_match = NULL, const_fid = NULL,
control = NULL, counts = NULL, covar = NULL, covar_name = NULL,
covar_number = NULL, cow = NULL, d = NULL, data = NULL,
debug = NULL, decompress = NULL, dfam = NULL, distance = NULL,
distance_exp = NULL, distance_matrix = NULL, dog = NULL,
dominant = NULL, dosage = NULL, double_id = NULL, dprime = NULL,
dummy = NULL, dummy_coding = NULL, each_versus_others = NULL,
each_vs_others = NULL, epistasis = NULL, epistasis_summary_merge = NULL,
exclude = NULL, exclude_before_extract = NULL, exclude_snp = NULL,
exclude_snps = NULL, extract = NULL, fam = NULL, family = NULL,
fast_epistasis = NULL, fid = NULL, file = NULL,
fill_missing_a2 = NULL, filter = NULL, filter_cases = NULL,
filter_controls = NULL, filter_females = NULL, filter_founders = NULL,
filter_males = NULL, filter_nonfounders = NULL, fisher = NULL,
flip = NULL, flip_scan = NULL, flip_scan_threshold = NULL,
flip_scan_verbose = NULL, flip_scan_window = NULL,
flip_scan_window_kb = NULL, flip_subset = NULL, freq = NULL,
freqx = NULL, from = NULL, from_bp = NULL, from_kb = NULL,
from_mb = NULL, frqx = NULL, fst = NULL, gap = NULL, gates = NULL,
gc = NULL, gen = NULL, gene = NULL, gene_all = NULL,
gene_list = NULL, gene_list_border = NULL, gene_report = NULL,
gene_report_empty = NULL, gene_report_snp_field = NULL,
gene_subset = NULL, genedrop = NULL, genepi = NULL, geno = NULL,
genome = NULL, genome_full = NULL, genome_lists = NULL,
genome_minimal = NULL, genotypic = NULL, gfile = NULL, gplink = NULL,
grm = NULL, grm_bin = NULL, grm_gz = NULL, group_avg = NULL,
groupdist = NULL, gxe = NULL, hap... = NULL, hap = NULL,
hap_assoc = NULL, hap_freq = NULL, hap_impute = NULL,
hap_max_phase = NULL, hap_min_phase_prob = NULL, hap_miss = NULL,
hap_phase = NULL, hap_phase_wide = NULL, hap_pp = NULL,

```

```
hap_snps = NULL, hap_tdt = NULL, hap_window = NULL,
hard_call_threshold = NULL, hardy2 = NULL, hardy = NULL, help = NULL,
het = NULL, hethom = NULL, hide_covar = NULL, homog = NULL,
homozyg = NULL, homozyg_density = NULL, homozyg_gap = NULL,
homozyg_group = NULL, homozyg_het = NULL,
homozyg_include_missing = NULL, homozyg_kb = NULL, homozyg_match = NULL,
homozyg_snp = NULL, homozyg_verbose = NULL, homozyg_window_het = NULL,
homozyg_window_kb = NULL, homozyg_window_missing = NULL,
homozyg_window_snp = NULL, homozyg_window_threshold = NULL,
horse = NULL, hwe = NULL, hwe_all = NULL, ibc = NULL, ibm = NULL,
ibs_matrix = NULL, ibs_test = NULL, id_delim = NULL, id_dict = NULL,
id_match = NULL, iid = NULL, impossible = NULL, impute_sex = NULL,
ind_major = NULL, indep = NULL, indep_pairphase = NULL,
indep_pairwise = NULL, independent_effect = NULL, indiv_sort = NULL,
inter_chr = NULL, interaction = NULL, je_cellmin = NULL, keep = NULL,
keep_allele_order = NULL, keep_autoconv = NULL,
keep_before_remove = NULL, keep_cluster_names = NULL,
keep_clusters = NULL, keep_fam = NULL, lambda = NULL, lasso = NULL,
lasso_select_covars = NULL, ld = NULL, ld_snp = NULL,
ld_snp_list = NULL, ld_snps = NULL, ld_window = NULL,
ld_window_kb = NULL, ld_window_r2 = NULL, ld_xchr = NULL,
lfile = NULL, liability = NULL, linear = NULL, list = NULL,
list_23_indels = NULL, list_all = NULL, logistic = NULL,
lookup... = NULL, lookup = NULL, lookup_gene = NULL,
lookup_list = NULL, loop_assoc = NULL, maf = NULL, maf_succ = NULL,
make_bed = NULL, make_founders = NULL, make_grm = NULL,
make_grm_bin = NULL, make_grm_gz = NULL, make_just_bim = NULL,
make_just_fam = NULL, make_perm_pheno = NULL, make_pheno = NULL,
make_rel = NULL, make_set = NULL, make_set_border = NULL,
make_set_collapse_group = NULL, make_set_complement_all = NULL,
make_set_complement_group = NULL, map = NULL, mat = NULL,
match = NULL, match_type = NULL, matrix = NULL, max = NULL,
max_maf = NULL, mc = NULL, mcc = NULL, mcovar = NULL,
mds_cluster = NULL, mds_plot = NULL, me = NULL, me_exclude_one = NULL,
memory = NULL, mendel = NULL, mendel_duos = NULL,
mendel_multigen = NULL, merge = NULL, merge_equal_pos = NULL,
merge_list = NULL, merge_mode = NULL, merge_x = NULL,
meta_analysis = NULL, meta_analysis..._field = NULL, mfilter = NULL,
mh = NULL, mhf = NULL, min = NULL, mind = NULL,
mishap_window = NULL, missing = NULL, missing_code = NULL,
missing_genotype = NULL, missing_phenotype = NULL,
missing_var_code = NULL, mlma = NULL, mlma_loco = NULL,
mlma_no_adj_covar = NULL, model = NULL, model_dom = NULL,
model_gen = NULL, model_rec = NULL, model_trend = NULL, mouse = NULL,
mperm = NULL, mperm_save = NULL, mperm_save_all = NULL, mphenotype = NULL,
must_have_sex = NULL, mwithin = NULL, neighbour = NULL, no_fid = NULL,
no_parents = NULL, no_pheno = NULL, no_sex = NULL, no_snp = NULL,
no_x_sex = NULL, nonfounders = NULL, nop = NULL, not_chr = NULL,
nudge = NULL, null_group = NULL, null_snp = NULL,
oblig_cluster = NULL, oblig_clusters = NULL, oblig_missing = NULL,
out = NULL, output_chr = NULL, output_missing_genotype = NULL,
output_missing_phenotype = NULL, oxford_pheno_name = NULL,
```

```

parallel = NULL, parameters = NULL, parentdt1 = NULL,
parentdt2 = NULL, pat = NULL, pca = NULL, pca_cluster_names = NULL,
pca_clusters = NULL, ped = NULL, pedigree = NULL, perm = NULL,
perm_batch_size = NULL, perm_count = NULL, pfilter = NULL,
pheno = NULL, pheno_merge = NULL, pheno_name = NULL, pick1 = NULL,
plist = NULL, poo = NULL, pool_size = NULL, ppc = NULL,
ppc_gap = NULL, proxy... = NULL, proxy_assoc = NULL,
proxy_b_kb = NULL, proxy_b_maxsnp = NULL, proxy_b_r2 = NULL,
proxy_b_threshold = NULL, proxy_b_window = NULL, proxy_dosage = NULL,
proxy_drop = NULL, proxy_flanking = NULL, proxy_genotype = NULL,
proxy_genotypic_concordance = NULL, proxy_glm = NULL,
proxy_impute = NULL, proxy_impute_threshold = NULL, proxy_kb = NULL,
proxy_list = NULL, proxy_maf = NULL, proxy_maxsnp = NULL,
proxy_mhf = NULL, proxy_r2 = NULL, proxy_r2_no_filter = NULL,
proxy_replace = NULL, proxy_show_proxies = NULL,
proxy_sub_maxsnp = NULL, proxy_sub_r2 = NULL, proxy_tdt = NULL,
proxy_verbose = NULL, proxy_window = NULL, prune = NULL,
q_score_file = NULL, q_score_range = NULL, qfam... = NULL,
qmatch = NULL, qq_plot = NULL, qt = NULL, qt_means = NULL,
qual_genotype... = NULL, qual_genotype_max_threshold = NULL,
qual_genotype_scores = NULL, qual_genotype_threshold = NULL,
qual_max_threshold = NULL, qual_scores = NULL, qual_threshold = NULL,
r2 = NULL, r = NULL, range = NULL, rank = NULL, read_dists = NULL,
read_freq = NULL, read_genome = NULL, read_genome_list = NULL,
read_genome_minimal = NULL, recessive = NULL, recode12 = NULL,
recode = NULL, recodeA = NULL, recodeAD = NULL, recodeHV = NULL,
recode_allele = NULL, recode_beagle = NULL, recode_bimbam = NULL,
recode_fastphase = NULL, recode_lgen = NULL, recode_rlist = NULL,
recode_structure = NULL, recode_vcf = NULL, recode_whap = NULL,
reference = NULL, reference_allele = NULL, regress_distance = NULL,
regress_pcs = NULL, regress_rel = NULL, rel_check = NULL,
rel_cutoff = NULL, remove = NULL, remove_cluster_names = NULL,
remove_clusters = NULL, remove_fam = NULL, rerun = NULL, rice = NULL,
sample = NULL, score = NULL, score_no_mean_imputation = NULL,
script = NULL, seed = NULL, set = NULL, set_by_all = NULL,
set_collapse_all = NULL, set_hh_missing = NULL, set_max = NULL,
set_me_missing = NULL, set_missing_nonsnp_ids = NULL,
set_missing_snp_ids = NULL, set_missing_var_ids = NULL,
set_names = NULL, set_p = NULL, set_r2 = NULL, set_r2_phase = NULL,
set_table = NULL, set_test = NULL, sex = NULL, sheep = NULL,
show_tags = NULL, silent = NULL, simulate = NULL,
simulate_haps = NULL, simulate_label = NULL, simulate_missing = NULL,
simulate_n = NULL, simulate_ncases = NULL, simulate_ncontrols = NULL,
simulate_prevalence = NULL, simulate_qt = NULL, simulate_tags = NULL,
snp = NULL, snps = NULL, snps_only = NULL, specific_haplotype = NULL,
split_x = NULL, standard_beta = NULL, subset = NULL,
swap_parents = NULL, swap_sibs = NULL, swap_unrel = NULL, tab = NULL,
tag_kb = NULL, tag_mode2 = NULL, tag_r2 = NULL, tail_pheno = NULL,
tdt = NULL, test_all = NULL, test_mishap = NULL, test_missing = NULL,
test_snp = NULL, tests = NULL, tfam = NULL, tfile = NULL,
thin = NULL, thin_count = NULL, threads = NULL, to = NULL,
to_bp = NULL, to_kb = NULL, to_mb = NULL, tped = NULL,

```



```

transpose = NULL, trend = NULL, tucc = NULL, twolocus = NULL,
unbounded = NULL, unrelated_heritability = NULL, update_alleles = NULL,
update_chr = NULL, update_cm = NULL, update_ids = NULL,
update_map = NULL, update_name = NULL, update_parents = NULL,
update_sex = NULL, vcf = NULL, vcf_filter = NULL,
vcf_half_call = NULL, vcf_idspace_to = NULL, vcf_min_qual = NULL,
vegas = NULL, version = NULL, vif = NULL, whap = NULL,
window = NULL, with_freqs = NULL, with_phenotype = NULL,
with_reference = NULL, within = NULL, write_cluster = NULL,
write_covar = NULL, write_dosage = NULL, write_set = NULL,
write_set_r2 = NULL, write_snplist = NULL, xchr_model = NULL,
zero_cluster = NULL, zero_cms = NULL, one = NULL, twothreefile = NULL,
stdout = "", stderr = "", wait = TRUE)

```

Arguments

D	Same as plink -D
K	Same as plink -K
a1_allele	Same as plink -a1-allele
a2_allele	Same as plink -a2-allele
adjust	Same as plink -adjust
all	Same as plink -all
all_pheno	Same as plink -all-pheno
allele1234	Same as plink -allele1234
alleleACGT	Same as plink -alleleACGT
allele_count	Same as plink -allele-count
allow_extra_chr	Same as plink -allow-extra-chr
allow_no_sex	Same as plink -allow-no-sex
alt_group	Same as plink -alt-group
alt_snp	Same as plink -alt-snp
annotate	Same as plink -annotate
annotate_snp_field	Same as plink -annotate-snp-field
aperm	Same as plink -aperm
assoc	Same as plink -assoc
attrib	Same as plink -attrib
attrib_indiv	Same as plink -attrib-indiv
autosome	Same as plink -autosome
autosome_num	Same as plink -autosome-num
autosome_xy	Same as plink -autosome-xy
bcf	Same as plink -bcf
bd	Same as plink -bd
bed	Same as plink -bed
beta	Same as plink -beta

bfile	Same as plink -bfile
bgen	Same as plink -bgen
biallelic_only	Same as plink -biallelic-only
bim	Same as plink -bim
blocks	Same as plink -blocks
blocks_inform_frac	Same as plink -blocks-inform-fraction
blocks_max_kb	Same as plink -blocks-max-kb
blocks_min_maf	Same as plink -blocks-min-maf
blocks_recomb_highci	Same as plink -blocks-recomb-highci
blocks_strong_highci	Same as plink -blocks-strong-highci
blocks_strong_lowci	Same as plink -blocks-strong-lowci
bmerge	Same as plink -bmerge
border	Same as plink -border
bp_space	Same as plink -bp-space
case_only	Same as plink -case-only
cc	Same as plink -cc
cell	Same as plink -cell
cfile	Same as plink -cfile
chap	Same as plink -chap
check_sex	Same as plink -check-sex
chr	Same as plink -chr
chr_set	Same as plink -chr-set
ci	Same as plink -ci
clump	Same as plink -clump
clump_allow_overlap	Same as plink -clump-allow-overlap
clump_annotate	Same as plink -clump-annotate
clump_best	Same as plink -clump-best
clump_field	Same as plink -clump-field
clump_index_first	Same as plink -clump-index-first
clump_kb	Same as plink -clump-kb
clump_p1	Same as plink -clump-p1
clump_p2	Same as plink -clump-p2
clump_r2	Same as plink -clump-r2
clump_range	Same as plink -clump-range
clump_range_border	Same as plink -clump-range-border

clump_replicate	Same as plink --clump-replicate
clump_snp_field	Same as plink --clump-snp-field
clump_verbose	Same as plink --clump-verbose
cluster	Same as plink --cluster
cluster_missing	Same as plink --cluster-missing
cm_map	Same as plink --cm-map
cnv_blue	Same as plink --cnv-blue
cnv_border	Same as plink --cnv-border
cnv_brown	Same as plink --cnv-brown
cnv_check_no_overlap	Same as plink --cnv-check-no-overlap
cnv_count	Same as plink --cnv-count
cnv_del	Same as plink --cnv-del
cnv_disrupt	Same as plink --cnv-disrupt
cnv_drop_no_segment	Same as plink --cnv-drop-no-segment
cnv_dup	Same as plink --cnv-dup
cnv_enrichment_test	Same as plink --cnv-enrichment-test
cnv_exclude	Same as plink --cnv-exclude
cnv_exclude_off_by_1	Same as plink --cnv-exclude-off-by-1
cnv_freq_excldue_above	Same as plink --cnv-freq-excldue-above
cnv_freq_excldue_below	Same as plink --cnv-freq-excldue-below
cnv_freq_excldue_exact	Same as plink --cnv-freq-excldue-exact
cnv_freq_exclude_above	Same as plink --cnv-freq-exclude-above
cnv_freq_exclude_below	Same as plink --cnv-freq-exclude-below
cnv_freq_exclude_exact	Same as plink --cnv-freq-exclude-exact
cnv_freq_incldue_exact	Same as plink --cnv-freq-incldue-exact
cnv_freq_include_exact	Same as plink --cnv-freq-include-exact
cnv_freq_method2	Same as plink --cnv-freq-method2
cnv_freq_overlap	Same as plink --cnv-freq-overlap

cnv_green	Same as plink --cnv-green
cnv_indiv_perm	Same as plink --cnv-indiv-perm
cnv_intersect	Same as plink --cnv-intersect
cnv_kb	Same as plink --cnv-kb
cnv_list	Same as plink --cnv-list
cnv_make_map	Same as plink --cnv-make-map
cnv_max_kb	Same as plink --cnv-max-kb
cnv_max_score	Same as plink --cnv-max-score
cnv_max_sites	Same as plink --cnv-max-sites
cnv_overlap	Same as plink --cnv-overlap
cnv_red	Same as plink --cnv-red
cnv_region_overlap	Same as plink --cnv-region-overlap
cnv_report_regions	Same as plink --cnv-report-regions
cnv_score	Same as plink --cnv-score
cnv_seglist	Same as plink --cnv-seglist
cnv_sites	Same as plink --cnv-sites
cnv_subset	Same as plink --cnv-subset
cnv_test	Same as plink --cnv-test
cnv_test_1sided	Same as plink --cnv-test-1sided
cnv_test_2sided	Same as plink --cnv-test-2sided
cnv_test_region	Same as plink --cnv-test-region
cnv_test_window	Same as plink --cnv-test-window
cnv_track	Same as plink --cnv-track
cnv_union_overlap	Same as plink --cnv-union-overlap
cnv_unique	Same as plink --cnv-unique
cnv_verbose_report_regions	Same as plink --cnv-verbose-report-regions
cnv_write	Same as plink --cnv-write
cnv_write_freq	Same as plink --cnv-write-freq
complement_sets	Same as plink --complement-sets
compound_genotypes	Same as plink --compound-genotypes
compress	Same as plink --compress
condition	Same as plink --condition
condition_list	Same as plink --condition-list

consensus_match	Same as plink --consensus-match
const_fid	Same as plink --const-fid
control	Same as plink --control
counts	Same as plink --counts
covar	Same as plink --covar
covar_name	Same as plink --covar-name
covar_number	Same as plink --covar-number
cow	Same as plink --cow
d	Same as plink --d
data	Same as plink --data
debug	Same as plink --debug
decompress	Same as plink --decompress
dfam	Same as plink --dfam
distance	Same as plink --distance
distance_exp	Same as plink --distance-exp
distance_matrix	Same as plink --distance-matrix
dog	Same as plink --dog
dominant	Same as plink --dominant
dosage	Same as plink --dosage
double_id	Same as plink --double-id
dprime	Same as plink --dprime
dummy	Same as plink --dummy
dummy_coding	Same as plink --dummy-coding
each_versus_others	Same as plink --each-versus-others
each_vs_others	Same as plink --each-vs-others
epistasis	Same as plink --epistasis
epistasis_summary_merge	Same as plink --epistasis-summary-merge
exclude	Same as plink --exclude
exclude_before_extract	Same as plink --exclude-before-extract
exclude_snp	Same as plink --exclude-snp
exclude_snps	Same as plink --exclude-snps
extract	Same as plink --extract
fam	Same as plink --fam
family	Same as plink --family
fast_epistasis	Same as plink --fast-epistasis
fid	Same as plink --fid
file	Same as plink --file

fill_missing_a2	Same as plink --fill-missing-a2
filter	Same as plink --filter
filter_cases	Same as plink --filter-cases
filter_controls	Same as plink --filter-controls
filter_females	Same as plink --filter-females
filter_founders	Same as plink --filter-founders
filter_males	Same as plink --filter-males
filter_nonfounders	Same as plink --filter-nonfounders
fisher	Same as plink --fisher
flip	Same as plink --flip
flip_scan	Same as plink --flip-scan
flip_scan_threshold	Same as plink --flip-scan-threshold
flip_scan_verbose	Same as plink --flip-scan-verbose
flip_scan_window	Same as plink --flip-scan-window
flip_scan_window_kb	Same as plink --flip-scan-window-kb
flip_subset	Same as plink --flip-subset
freq	Same as plink --freq
freqx	Same as plink --freqx
from	Same as plink --from
from_bp	Same as plink --from-bp
from_kb	Same as plink --from-kb
from_mb	Same as plink --from-mb
frqx	Same as plink --frqx
fst	Same as plink --fst
gap	Same as plink --gap
gates	Same as plink --gates
gc	Same as plink --gc
gen	Same as plink --gen
gene	Same as plink --gene
gene_all	Same as plink --gene-all
gene_list	Same as plink --gene-list
gene_list_border	Same as plink --gene-list-border
gene_report	Same as plink --gene-report
gene_report_empty	Same as plink --gene-report-empty

gene_report_snp_field	
	Same as plink --gene-report-snp-field
gene_subset	Same as plink --gene-subset
genedrop	Same as plink --genedrop
genepi	Same as plink --genepi
geno	Same as plink --geno
genome	Same as plink --genome
genome_full	Same as plink --genome-full
genome_lists	Same as plink --genome-lists
genome_minimal	Same as plink --genome-minimal
genotypic	Same as plink --genotypic
gfile	Same as plink --gfile
gplink	Same as plink --gplink
grm	Same as plink --grm
grm_bin	Same as plink --grm-bin
grm_gz	Same as plink --grm-gz
group_avg	Same as plink --group-avg
groupdist	Same as plink --groupdist
gxe	Same as plink --gxe
hap...	Same as plink --hap...
hap	Same as plink --hap
hap_assoc	Same as plink --hap-assoc
hap_freq	Same as plink --hap-freq
hap_impute	Same as plink --hap-impute
hap_max_phase	Same as plink --hap-max-phase
hap_min_phase_prob	
	Same as plink --hap-min-phase-prob
hap_miss	Same as plink --hap-miss
hap_phase	Same as plink --hap-phase
hap_phase_wide	Same as plink --hap-phase-wide
hap_pp	Same as plink --hap-pp
hap_snps	Same as plink --hap-snps
hap_tdt	Same as plink --hap-tdt
hap_window	Same as plink --hap-window
hard_call_threshold	
	Same as plink --hard-call-threshold
hardy2	Same as plink --hardy2
hardy	Same as plink --hardy
help	Same as plink --help
het	Same as plink --het
hethom	Same as plink --hethom

hide_covar	Same as plink --hide-covar
homog	Same as plink --homog
homozyg	Same as plink --homozyg
homozyg_density	Same as plink --homozyg-density
homozyg_gap	Same as plink --homozyg-gap
homozyg_group	Same as plink --homozyg-group
homozyg_het	Same as plink --homozyg-het
homozyg_include_missing	Same as plink --homozyg-include-missing
homozyg_kb	Same as plink --homozyg-kb
homozyg_match	Same as plink --homozyg-match
homozyg_snp	Same as plink --homozyg-snp
homozyg_verbose	Same as plink --homozyg-verbose
homozyg_window_het	Same as plink --homozyg-window-het
homozyg_window_kb	Same as plink --homozyg-window-kb
homozyg_window_missing	Same as plink --homozyg-window-missing
homozyg_window_snp	Same as plink --homozyg-window-snp
homozyg_window_threshold	Same as plink --homozyg-window-threshold
horse	Same as plink --horse
hwe	Same as plink --hwe
hwe_all	Same as plink --hwe-all
ibc	Same as plink --ibc
ibm	Same as plink --ibm
ibs_matrix	Same as plink --ibs-matrix
ibs_test	Same as plink --ibs-test
id_delim	Same as plink --id-delim
id_dict	Same as plink --id-dict
id_match	Same as plink --id-match
iid	Same as plink --iid
impossible	Same as plink --impossible
impute_sex	Same as plink --impute-sex
ind_major	Same as plink --ind-major
indep	Same as plink --indep
indep_pairphase	Same as plink --indep-pairphase
indep_pairwise	Same as plink --indep-pairwise

independent_effect	Same as plink --independent-effect
indiv_sort	Same as plink --indiv-sort
inter_chr	Same as plink --inter-chr
interaction	Same as plink --interaction
je_cellmin	Same as plink --je-cellmin
keep	Same as plink --keep
keep_allele_order	Same as plink --keep-allele-order
keep_autoconv	Same as plink --keep-autoconv
keep_before_remove	Same as plink --keep-before-remove
keep_cluster_names	Same as plink --keep-cluster-names
keep_clusters	Same as plink --keep-clusters
keep_fam	Same as plink --keep-fam
lambda	Same as plink --lambda
lasso	Same as plink --lasso
lasso_select_covars	Same as plink --lasso-select-covars
ld	Same as plink --ld
ld_snp	Same as plink --ld-snp
ld_snp_list	Same as plink --ld-snp-list
ld_snps	Same as plink --ld-snps
ld_window	Same as plink --ld-window
ld_window_kb	Same as plink --ld-window-kb
ld_window_r2	Same as plink --ld-window-r2
ld_xchr	Same as plink --ld-xchr
lfile	Same as plink --lfile
liability	Same as plink --liability
linear	Same as plink --linear
list	Same as plink --list
list_23_indels	Same as plink --list-23-indels
list_all	Same as plink --list-all
logistic	Same as plink --logistic
lookup...	Same as plink --lookup...
lookup	Same as plink --lookup
lookup_gene	Same as plink --lookup-gene
lookup_list	Same as plink --lookup-list
loop_assoc	Same as plink --loop-assoc
maf	Same as plink --maf
maf_succ	Same as plink --maf-succ

<code>make_bed</code>	Same as <code>plink --make-bed</code>
<code>make_founders</code>	Same as <code>plink --make-founders</code>
<code>make_grm</code>	Same as <code>plink --make-grm</code>
<code>make_grm_bin</code>	Same as <code>plink --make-grm-bin</code>
<code>make_grm_gz</code>	Same as <code>plink --make-grm-gz</code>
<code>make_just_bim</code>	Same as <code>plink --make-just-bim</code>
<code>make_just_fam</code>	Same as <code>plink --make-just-fam</code>
<code>make_perm_pheno</code>	Same as <code>plink --make-perm-pheno</code>
<code>make_pheno</code>	Same as <code>plink --make-pheno</code>
<code>make_rel</code>	Same as <code>plink --make-rel</code>
<code>make_set</code>	Same as <code>plink --make-set</code>
<code>make_set_border</code>	Same as <code>plink --make-set-border</code>
<code>make_set_collapse_group</code>	Same as <code>plink --make-set-collapse-group</code>
<code>make_set_complement_all</code>	Same as <code>plink --make-set-complement-all</code>
<code>make_set_complement_group</code>	Same as <code>plink --make-set-complement-group</code>
<code>map</code>	Same as <code>plink --map</code>
<code>mat</code>	Same as <code>plink --mat</code>
<code>match</code>	Same as <code>plink --match</code>
<code>match_type</code>	Same as <code>plink --match-type</code>
<code>matrix</code>	Same as <code>plink --matrix</code>
<code>max</code>	Same as <code>plink --max</code>
<code>max_maf</code>	Same as <code>plink --max-maf</code>
<code>mc</code>	Same as <code>plink --mc</code>
<code>mcc</code>	Same as <code>plink --mcc</code>
<code>mcovar</code>	Same as <code>plink --mcovar</code>
<code>mds_cluster</code>	Same as <code>plink --mds-cluster</code>
<code>mds_plot</code>	Same as <code>plink --mds-plot</code>
<code>me</code>	Same as <code>plink --me</code>
<code>me_exclude_one</code>	Same as <code>plink --me-exclude-one</code>
<code>memory</code>	Same as <code>plink --memory</code>
<code>mendel</code>	Same as <code>plink --mendel</code>
<code>mendel_duos</code>	Same as <code>plink --mendel-duos</code>
<code>mendel_multigen</code>	Same as <code>plink --mendel-multigen</code>
<code>merge</code>	Same as <code>plink --merge</code>
<code>merge_equal_pos</code>	Same as <code>plink --merge-equal-pos</code>

merge_list	Same as plink --merge-list
merge_mode	Same as plink --merge-mode
merge_x	Same as plink --merge-x
meta_analysis	Same as plink --meta-analysis
meta_analysis_..._field	Same as plink --meta-analysis-...-field
mfilter	Same as plink --mfilter
mh	Same as plink --mh
mhf	Same as plink --mhf
min	Same as plink --min
mind	Same as plink --mind
mishap_window	Same as plink --mishap-window
missing	Same as plink --missing
missing_code	Same as plink --missing-code
missing_genotype	Same as plink --missing-genotype
missing_phenotype	Same as plink --missing-phenotype
missing_var_code	Same as plink --missing-var-code
mlma	Same as plink --mlma
mlma_loco	Same as plink --mlma-loco
mlma_no_adj_covar	Same as plink --mlma-no-adj-covar
model	Same as plink --model
model_dom	Same as plink --model-dom
model_gen	Same as plink --model-gen
model_rec	Same as plink --model-rec
model_trend	Same as plink --model-trend
mouse	Same as plink --mouse
mperm	Same as plink --mperm
mperm_save	Same as plink --mperm-save
mperm_save_all	Same as plink --mperm-save-all
mpheno	Same as plink --mpheno
must_have_sex	Same as plink --must-have-sex
mwithin	Same as plink --mwithin
neighbour	Same as plink --neighbour
no_fid	Same as plink --no-fid
no_parents	Same as plink --no-parents
no_pheno	Same as plink --no-pheno
no_sex	Same as plink --no-sex
no_snp	Same as plink --no-snp

no_x_sex	Same as plink --no-x-sex
nonfounders	Same as plink --nonfounders
nop	Same as plink --nop
not_chr	Same as plink --not-chr
nudge	Same as plink --nudge
null_group	Same as plink --null-group
null_snp	Same as plink --null-snp
oblig_cluster	Same as plink --oblig-cluster
oblig_clusters	Same as plink --oblig-clusters
oblig_missing	Same as plink --oblig-missing
out	Same as plink --out
output_chr	Same as plink --output-chr
output_missing_genotype	Same as plink --output-missing-genotype
output_missing_phenotype	Same as plink --output-missing-phenotype
oxford_pheno_name	Same as plink --oxford-pheno-name
parallel	Same as plink --parallel
parameters	Same as plink --parameters
parentdt1	Same as plink --parentdt1
parentdt2	Same as plink --parentdt2
pat	Same as plink --pat
pca	Same as plink --pca
pca_cluster_names	Same as plink --pca-cluster-names
pca_clusters	Same as plink --pca-clusters
ped	Same as plink --ped
pedigree	Same as plink --pedigree
perm	Same as plink --perm
perm_batch_size	Same as plink --perm-batch-size
perm_count	Same as plink --perm-count
pfilter	Same as plink --pfilter
pheno	Same as plink --pheno
pheno_merge	Same as plink --pheno-merge
pheno_name	Same as plink --pheno-name
pick1	Same as plink --pick1
plist	Same as plink --plist
poo	Same as plink --poo
pool_size	Same as plink --pool-size
ppc	Same as plink --ppc

ppc_gap	Same as plink --ppc-gap
proxy_...	Same as plink --proxy-...
proxy_assoc	Same as plink --proxy-assoc
proxy_b_kb	Same as plink --proxy-b-kb
proxy_b_maxsnp	Same as plink --proxy-b-maxsnp
proxy_b_r2	Same as plink --proxy-b-r2
proxy_b_threshold	Same as plink --proxy-b-threshold
proxy_b_window	Same as plink --proxy-b-window
proxy_dosage	Same as plink --proxy-dosage
proxy_drop	Same as plink --proxy-drop
proxy_flanking	Same as plink --proxy-flanking
proxy_geno	Same as plink --proxy-geno
proxy_genotypic_concordance	Same as plink --proxy-genotypic-concordance
proxy_glm	Same as plink --proxy-glm
proxy_impute	Same as plink --proxy-impute
proxy_impute_threshold	Same as plink --proxy-impute-threshold
proxy_kb	Same as plink --proxy-kb
proxy_list	Same as plink --proxy-list
proxy_maf	Same as plink --proxy-maf
proxy_maxsnp	Same as plink --proxy-maxsnp
proxy_mhf	Same as plink --proxy-mhf
proxy_r2	Same as plink --proxy-r2
proxy_r2_no_filter	Same as plink --proxy-r2-no-filter
proxy_replace	Same as plink --proxy-replace
proxy_show_proxies	Same as plink --proxy-show-proxies
proxy_sub_maxsnp	Same as plink --proxy-sub-maxsnp
proxy_sub_r2	Same as plink --proxy-sub-r2
proxy_tdt	Same as plink --proxy-tdt
proxy_verbose	Same as plink --proxy-verbose
proxy_window	Same as plink --proxy-window
prune	Same as plink --prune
q_score_file	Same as plink --q-score-file
q_score_range	Same as plink --q-score-range
qfam...	Same as plink --qfam...
qmatch	Same as plink --qmatch
qq_plot	Same as plink --qq-plot

qt	Same as plink --qt
qt_means	Same as plink --qt-means
qual_geno_...	Same as plink --qual-gen-...
qual_geno_max_threshold	Same as plink --qual-gen-max-threshold
qual_geno_scores	Same as plink --qual-gen-scores
qual_geno_threshold	Same as plink --qual-gen-threshold
qual_max_threshold	Same as plink --qual-max-threshold
qual_scores	Same as plink --qual-scores
qual_threshold	Same as plink --qual-threshold
r2	Same as plink --r2
r	Same as plink --r
range	Same as plink --range
rank	Same as plink --rank
read_dists	Same as plink --read-dists
read_freq	Same as plink --read-freq
read_genome	Same as plink --read-genome
read_genome_list	Same as plink --read-genome-list
read_genome_minimal	Same as plink --read-genome-minimal
recessive	Same as plink --recessive
recodel2	Same as plink --recodel2
recodel	Same as plink --recodel
recodelA	Same as plink --recodelA
recodelAD	Same as plink --recodelAD
recodelHV	Same as plink --recodelHV
recodel_allele	Same as plink --recodel-allele
recodel_beagle	Same as plink --recodel-beagle
recodel_bimbam	Same as plink --recodel-bimbam
recodel_fastphase	Same as plink --recodel-fastphase
recodel_lgen	Same as plink --recodel-lgen
recodel_rlist	Same as plink --recodel-rlist
recodel_structure	Same as plink --recodel-structure
recodel_vcf	Same as plink --recodel-vcf
recodel_whap	Same as plink --recodel-whap
reference	Same as plink --reference

reference_allele	Same as plink --reference-allele
regress_distance	Same as plink --regress-distance
regress_pcs	Same as plink --regress-pcs
regress_rel	Same as plink --regress-rel
rel_check	Same as plink --rel-check
rel_cutoff	Same as plink --rel-cutoff
remove	Same as plink --remove
remove_cluster_names	Same as plink --remove-cluster-names
remove_clusters	Same as plink --remove-clusters
remove_fam	Same as plink --remove-fam
rerun	Same as plink --rerun
rice	Same as plink --rice
sample	Same as plink --sample
score	Same as plink --score
score_no_mean_imputation	Same as plink --score-no-mean-imputation
script	Same as plink --script
seed	Same as plink --seed
set	Same as plink --set
set_by_all	Same as plink --set-by-all
set_collapse_all	Same as plink --set-collapse-all
set_hh_missing	Same as plink --set-hh-missing
set_max	Same as plink --set-max
set_me_missing	Same as plink --set-me-missing
set_missing_nonsnp_ids	Same as plink --set-missing-nonsnp-ids
set_missing_snp_ids	Same as plink --set-missing-snp-ids
set_missing_var_ids	Same as plink --set-missing-var-ids
set_names	Same as plink --set-names
set_p	Same as plink --set-p
set_r2	Same as plink --set-r2
set_r2_phase	Same as plink --set-r2-phase
set_table	Same as plink --set-table
set_test	Same as plink --set-test
sex	Same as plink --sex
sheep	Same as plink --sheep

show_tags	Same as plink --show-tags
silent	Same as plink --silent
simulate	Same as plink --simulate
simulate_haps	Same as plink --simulate-haps
simulate_label	Same as plink --simulate-label
simulate_missing	Same as plink --simulate-missing
simulate_n	Same as plink --simulate-n
simulate_ncases	Same as plink --simulate-ncases
simulate_ncontrols	Same as plink --simulate-ncontrols
simulate_prevalence	Same as plink --simulate-prevalence
simulate_qt	Same as plink --simulate-qt
simulate_tags	Same as plink --simulate-tags
snp	Same as plink --snp
snps	Same as plink --snps
snps_only	Same as plink --snps-only
specific_haplotype	Same as plink --specific-haplotype
split_x	Same as plink --split-x
standard_beta	Same as plink --standard-beta
subset	Same as plink --subset
swap_parents	Same as plink --swap-parents
swap_sibs	Same as plink --swap-sibs
swap_unrel	Same as plink --swap-unrel
tab	Same as plink --tab
tag_kb	Same as plink --tag-kb
tag_mode2	Same as plink --tag-mode2
tag_r2	Same as plink --tag-r2
tail_pheno	Same as plink --tail-pheno
tdt	Same as plink --tdt
test_all	Same as plink --test-all
test_mishap	Same as plink --test-mishap
test_missing	Same as plink --test-missing
test_snp	Same as plink --test-snp
tests	Same as plink --tests
tfam	Same as plink --tfam
tfile	Same as plink --tfile
thin	Same as plink --thin
thin_count	Same as plink --thin-count

threads	Same as plink --threads
to	Same as plink --to
to_bp	Same as plink --to-bp
to_kb	Same as plink --to-kb
to_mb	Same as plink --to-mb
tped	Same as plink --tped
transpose	Same as plink --transpose
trend	Same as plink --trend
tucc	Same as plink --tucc
twolocus	Same as plink --twolocus
unbounded	Same as plink --unbounded
unrelated_heritability	Same as plink --unrelated-heritability
update_alleles	Same as plink --update-alleles
update_chr	Same as plink --update-chr
update_cm	Same as plink --update-cm
update_ids	Same as plink --update-ids
update_map	Same as plink --update-map
update_name	Same as plink --update-name
update_parents	Same as plink --update-parents
update_sex	Same as plink --update-sex
vcf	Same as plink --vcf
vcf_filter	Same as plink --vcf-filter
vcf_half_call	Same as plink --vcf-half-call
vcf_idspace_to	Same as plink --vcf-idspace-to
vcf_min_qual	Same as plink --vcf-min-qual
vegas	Same as plink --vegas
version	Same as plink --version
vif	Same as plink --vif
whap	Same as plink --whap
window	Same as plink --window
with_freqs	Same as plink --with-freqs
with_phenotype	Same as plink --with-phenotype
with_reference	Same as plink --with-reference
within	Same as plink --within
write_cluster	Same as plink --write-cluster
write_covar	Same as plink --write-covar
write_dosage	Same as plink --write-dosage
write_set	Same as plink --write-set
write_set_r2	Same as plink --write-set-r2
write_snplist	Same as plink --write-snplist

xchr_model	Same as plink --xchr-model
zero_cluster	Same as plink --zero-cluster
zero_cms	Same as plink --zero-cms
one	Same as plink --1
twothreefile	Same as plink --23file
stdout	Passed to system2, see its documentation.
stderr	Passed to system2, see its documentation.
wait	Logical. If FALSE, the plink process will fork into the background.

See Also

[getPlinkParam](#)

readBim	<i>Read plink .bim files</i>
---------	------------------------------

Description

Read plink .bim files

Usage

```
readBim(filename, cn_select = "..all")
```

Arguments

filename	.bim file path
cn_select	a character vector for selected colnames

Value

a data.frame

Author(s)

kaiyin

Examples

```
\donotrunc{
bim = readBim("/Users/kaiyin/EclipseWorkspace/collapsabel2/tests/testthat/mmp13.bim",
cn_select = "..all")
head(bim)
summary(bim)
bim_info = bimInfo("/Users/kaiyin/EclipseWorkspace/collapsabel2/tests/testthat/mmp13.bim")
bim_info@cnames
bim1 = bim_info@read_fun(bim_info, c("CHR", "SNP", "BP"))
head(bim1)
}
```

readFam	<i>Read plink .fam files</i>
---------	------------------------------

Description

Read plink .fam files

Usage

```
readFam(filename, cn_select = "..all")
```

Arguments

filename	.fam file path
cn_select	a character vector for selected colnames

Value

a data.frame

Author(s)

kaiyin

Examples

```
\donotrun{
fam = readFam("/Users/kaiyin/EclipseWorkspace/collapsabel2/tests/testthat/mmp13.fam", cn_select = "..all")
head(fam)
summary(fam)
fam_info = famInfo("/Users/kaiyin/EclipseWorkspace/collapsabel2/tests/testthat/mmp13.fam")
fam_info@cnames
fam1 = fam_info@read_fun(fam_info, c("FID", "IID"))
head(fam1)
}
```

readInfo	<i>ReadInfo constructor</i>
----------	-----------------------------

Description

This function takes a file path as parameter, assuming the file is whitespace delimited, not quoted, and has a header line. It returns a ReadInfo object.

Usage

```
## S4 method for signature 'character,missing'
readInfo(filename)
```

```
## S4 method for signature 'character,character'
readInfo(filename, cnames)
```

Arguments

filename Path of the file to read

Value

ReadInfo object

Author(s)

kaiyin

Examples

```
\donotrunc{
ri = readInfo("/Users/kaiyin/EclipseWorkspace/collapsabel2/tests/testthat/mmp13.frq")
getSlots("ReadInfo")
ri@cnames
ri@filename
ri@header
frq = ri@read_fun(ri, cn_select = "..all")
head(frq)
print(ri@cnames)
frq1 = ri@read_fun(ri, ri@cnames[1:4])
head(frq1)
}
```

ReadInfo-class	<i>An S4 class to represent information about a whitespace-delimited text file to be read into R</i>
----------------	------------------------------------------------------------------------------------------------------

Description

An S4 class to represent information about a whitespace-delimited text file to be read into R

Slots

filename Path of the file

cnames character vector of column names

header logical. Whether the first line is header

read_fun function. The function to be used when reading this file

saveFFDF	<i>Save an R data.frame to ff format</i>
----------	------------------------------------------

Description

Save an R data.frame to ff format

Usage

```
## S4 method for signature 'data.frame,character,logical'
saveFFDF(df, dir, overwrite)

## S4 method for signature 'data.frame,character,missing'
saveFFDF(df, dir, overwrite)
```

Arguments

df	data.frame to be saved
dir	ff directory
overwrite	logical. Default to TRUE

Author(s)

kaiyin

Examples

```
\donotrun{
  saveFFDF(iris, "/tmp/iris")
  iris1 = loadFFDF("/tmp/iris")
  iris1[1, 1] == 5.1
}
```

setup,PlInfo-method	<i>Setup up a directory containing plink files</i>
---------------------	----------------------------------------------------

Description

Setup up a directory containing plink files

Usage

```
## S4 method for signature 'PlInfo'
setup(pl_info)
```

Arguments

pl_info

Author(s)

kaiyin

Examples

```
# see examples in plInfo
```

strConcat*Concatenate a vector of strings*

Description

Concatenate a vector of strings

Usage

```
## S4 method for signature 'character,character'
strConcat(ss, sep)
```

```
## S4 method for signature 'character,missing'
strConcat(ss, sep)
```

Arguments

ss	vector of strings
sep	a length-1 string used as separator, default to ""

Value

a string

Author(s)

kaiyin

Examples

```
strConcat(letters)
strConcat(letters, " ")
```

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