

# Package ‘MungeSumstats’

May 3, 2024

**Type** Package

**Title** Standardise summary statistics from GWAS

**Version** 1.12.0

**Description** The \*MungeSumstats\* package is designed to facilitate the standardisation of GWAS summary statistics. It reformats inputted summary statistics to include SNP, CHR, BP and can look up these values if any are missing. It also performs dozens of QC and filtering steps to ensure high data quality and minimise inter-study differences.

**URL** <https://github.com/neurogenomics/MungeSumstats>

**BugReports** <https://github.com/neurogenomics/MungeSumstats/issues>

**License** Artistic-2.0

**Depends** R(>= 4.1)

**Imports** magrittr, data.table, utils, R.utils, dplyr, stats,  
GenomicRanges, IRanges, GenomeInfoDb, BSgenome, Biostrings,  
stringr, VariantAnnotation, googleAuthR, httr, jsonlite,  
methods, parallel, rtracklayer(>= 1.59.1), RCurl

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SNPlocs.Hsapiens.dbSNP144.GRCh38,  
SNPlocs.Hsapiens.dbSNP155.GRCh37,  
SNPlocs.Hsapiens.dbSNP155.GRCh38,  
BSgenome.Hsapiens.1000genomes.hs37d5,  
BSgenome.Hsapiens.NCBI.GRCh38, BiocGenerics, S4Vectors,  
rmarkdown, markdown, knitr, testthat (>= 3.0.0), UpSetR,  
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---

api_query	<i>Wrapper for sending queries and payloads to API</i>
-----------	--

---

## Description

There are a number of different GET and POST endpoints in the GWAS database API. This is a generic way to access them

## Usage

```
api_query(
  path,
  query = NULL,
  access_token = check_access_token(),
  method = "GET",
  silent = TRUE,
  encode = "json",
  timeout = 300
)
```

## Arguments

path	Either a full query path (e.g. for get) or an endpoint (e.g. for post) queries
query	If post query, provide a list of arguments as the payload. NULL by default
access_token	Google OAuth2 access token. Used to authenticate level of access to data. By default, checks if already authenticated through <code>get_access_token</code> and if not then does not perform authentication.
method	GET (default) or POST, DELETE etc
silent	TRUE/FALSE to be passed to httr call. TRUE by default
encode	Default = json, see <code>httr::POST</code> for options
timeout	Default = 300, avoid increasing this, preferentially simplify the query first.

## Value

httr response object

---

axel	<i>axel downloader</i>
------	------------------------

---

### Description

R wrapper for axel, which enables multi-threaded download of a single large file.

### Usage

```
axel(  
  input_url,  
  output_path,  
  background = FALSE,  
  nThread = 1,  
  force_overwrite = FALSE,  
  quiet = TRUE,  
  alternate = TRUE,  
  check_certificates = FALSE  
)
```

### Arguments

input_url	input_url.
output_path	output_path.
background	Run in background
nThread	Number of threads to parallelize over.
force_overwrite	Overwrite existing file.
quiet	Run quietly.
alternate	alternate,
check_certificates	check_certificates

### Value

Path where the file has been downloaded

### See Also

<https://github.com/axel-download-accelerator/axel/>

Other downloaders: [downloader\(\)](#)

---

check_access_token	<i>Check if authentication has been made</i>
--------------------	--

---

**Description**

If a call to get\_access\_token() has been made then it will have generated mrbase.oauth. Pass the token if it is present, if not, return NULL and do not authenticate.

**Usage**

```
check_access_token()
```

**Value**

NULL or access\_token depending on current authentication state

---

check_allele_flip	<i>Ensure A1 &amp; A2 are correctly named, if GWAS SNP constructed as Alternative/Reference or Risk/Nonrisk alleles these SNPs will need to be converted to Reference/Alternative or Nonrisk/Risk. Here non-risk is defined as what's on the reference genome (this may not always be the case).</i>
-------------------	--

---

**Description**

Ensure A1 & A2 are correctly named, if GWAS SNP constructed as Alternative/Reference or Risk/Nonrisk alleles these SNPs will need to be converted to Reference/Alternative or Nonrisk/Risk. Here non-risk is defined as what's on the reference genome (this may not always be the case).

**Usage**

```
check_allele_flip(
  sumstats_dt,
  path,
  ref_genome,
  rsids,
  allele_flip_check,
  allele_flip_drop,
  allele_flip_z,
  allele_flip_frq,
  bi_allelic_filter,
  flip_frq_as_biallelic,
  imputation_ind,
  log_folder_ind,
  check_save_out,
```

```

    tabix_index,
    nThread,
    log_files,
    standardise_headers = FALSE,
    mapping_file,
    dbSNP
)

```

## Arguments

path	Filepath for the summary statistics file to be formatted. A dataframe or datatable of the summary statistics file can also be passed directly to MungeSumstats using the path parameter.
ref_genome	name of the reference genome used for the GWAS ("GRCh37" or "GRCh38"). Argument is case-insensitive. Default is NULL which infers the reference genome from the data.
allele_flip_check	Binary Should the allele columns be checked against reference genome to infer if flipping is necessary. Default is TRUE.
allele_flip_drop	Binary Should the SNPs for which neither their A1 or A2 base pair values match a reference genome be dropped. Default is TRUE.
allele_flip_z	Binary should the Z-score be flipped along with effect and FRQ columns like Beta? It is assumed to be calculated off the effect size not the P-value and so will be flipped i.e. default TRUE.
allele_flip_frq	Binary should the frequency (FRQ) column be flipped along with effect and z-score columns like Beta? Default TRUE.
bi_allelic_filter	Binary Should non-biallelic SNPs be removed. Default is TRUE.
flip_frq_as_biallelic	Binary Should non-bi-allelic SNPs frequency values be flipped as 1-p despite there being other alternative alleles? Default is FALSE but if set to TRUE, this allows non-bi-allelic SNPs to be kept despite needing flipping.
imputation_ind	Binary Should a column be added for each imputation step to show what SNPs have imputed values for differing fields. This includes a field denoting SNP allele flipping (flipped). On the flipped value, this denoted whether the alleles were switched based on MungeSumstats initial choice of A1, A2 from the input column headers and thus may not align with what the creator intended. <b>Note</b> these columns will be in the formatted summary statistics returned. Default is FALSE.
log_folder_ind	Binary Should log files be stored containing all filtered out SNPs (separate file per filter). The data is outputted in the same format specified for the resulting sumstats file. The only exception to this rule is if output is vcf, then log file saved as .tsv.gz. Default is FALSE.
tabix_index	Index the formatted summary statistics with <b>tabix</b> for fast querying.



nThread	Number of threads to use for parallel processes.
log_files	list of log file locations
standardise_headers	Run standardise_sumstats_column_headers_crossplatform first.
mapping_file	MungeSumstats has a pre-defined column-name mapping file which should cover the most common column headers and their interpretations. However, if a column header that is in your file is missing of the mapping we give is incorrect you can supply your own mapping file. Must be a 2 column dataframe with column names "Uncorrected" and "Corrected". See data(sumstatsColHeaders) for default mapping and necessary format.
dbSNP	version of dbSNP to be used for imputation (144 or 155).

**Value**

A list containing two data tables:

- sumstats\_dt: the modified summary statistics data.table object.
- rsids: snpsById, filtered to SNPs of interest if loaded already. Or else NULL.
- log\_files: log file list

---

check_allele_merge	<i>Ensure that A1:A2 or A1/A2 or A1&gt;A2 or A2&gt;A1 aren't merged into 1 column</i>
--------------------	---

---

**Description**

Ensure that A1:A2 or A1/A2 or A1>A2 or A2>A1 aren't merged into 1 column

**Usage**

```
check_allele_merge(sumstats_dt, path)
```

**Arguments**

sumstats_dt	data table obj of the summary statistics file for the GWAS
path	Filepath for the summary statistics file to be formatted

**Value**

list containing sumstats\_dt, the modified summary statistics data table object.

---

check\_bi\_allelic      *Remove non-biallelic SNPs*

---

## Description

Remove non-biallelic SNPs

## Usage

```
check_bi_allelic(
  sumstats_dt,
  path,
  ref_genome,
  bi_allelic_filter,
  rsids,
  log_folder_ind,
  check_save_out,
  tabix_index,
  nThread,
  log_files,
  dbSNP
)
```

## Arguments

path	Filepath for the summary statistics file to be formatted. A dataframe or datatable of the summary statistics file can also be passed directly to MungeSumstats using the path parameter.
ref_genome	name of the reference genome used for the GWAS ("GRCh37" or "GRCh38"). Argument is case-insensitive. Default is NULL which infers the reference genome from the data.
bi_allelic_filter	Binary Should non-biallelic SNPs be removed. Default is TRUE.
log_folder_ind	Binary Should log files be stored containing all filtered out SNPs (separate file per filter). The data is outputted in the same format specified for the resulting sumstats file. The only exception to this rule is if output is vcf, then log file saved as .tsv.gz. Default is FALSE.
tabix_index	Index the formatted summary statistics with <b>tabix</b> for fast querying.
nThread	Number of threads to use for parallel processes.
log_files	list of log file locations
dbSNP	version of dbSNP to be used for imputation (144 or 155).

**Value**

A list containing two data tables:

- `sumstats_dt`: the modified summary statistics data table object
- `rsids`: `snpsById`, filtered to SNPs of interest if loaded already. Or else NULL.
- `log_files`: log file list

---

<code>check_bp_range</code>	<i>Ensure that the Base-pair column values are all within the range for the chromosome</i>
-----------------------------	--

---

**Description**

Ensure that the Base-pair column values are all within the range for the chromosome

**Usage**

```
check_bp_range(
  sumstats_dt,
  path,
  ref_genome,
  log_folder_ind,
  imputation_ind,
  check_save_out,
  tabix_index,
  nThread,
  log_files
)
```

**Arguments**

<code>path</code>	Filepath for the summary statistics file to be formatted. A dataframe or datatable of the summary statistics file can also be passed directly to <code>MungeSumstats</code> using the <code>path</code> parameter.
<code>ref_genome</code>	name of the reference genome used for the GWAS ("GRCh37" or "GRCh38"). Argument is case-insensitive. Default is NULL which infers the reference genome from the data.
<code>log_folder_ind</code>	Binary Should log files be stored containing all filtered out SNPs (separate file per filter). The data is outputted in the same format specified for the resulting <code>sumstats</code> file. The only exception to this rule is if output is <code>vcf</code> , then log file saved as <code>.tsv.gz</code> . Default is <code>FALSE</code> .
<code>imputation_ind</code>	Binary Should a column be added for each imputation step to show what SNPs have imputed values for differing fields. This includes a field denoting SNP allele flipping (flipped). On the flipped value, this denoted whether the alleles were switched based on <code>MungeSumstats</code> initial choice of <code>A1</code> , <code>A2</code> from the input column headers and thus may not align with what the creator intended. <b>Note</b>

	these columns will be in the formatted summary statistics returned. Default is FALSE.
tabix_index	Index the formatted summary statistics with <b>tabix</b> for fast querying.
nThread	Number of threads to use for parallel processes.
log_files	list of log file locations

**Value**

list containing sumstats\_dt, the modified summary statistics data table object and the log file list

---

check_chr	<i>Standardize the CHR column</i>
-----------	-----------------------------------

---

**Description**

Maps chromosome names to the default Ensembl/NCBI naming style and removes SNPs with non-standard CHR entries. Optionally, also removes SNPs on user-specified chromosomes.

**Usage**

```
check_chr(
  sumstats_dt,
  log_files,
  check_save_out,
  rmv_chr,
  nThread,
  tabix_index,
  log_folder_ind
)
```

**Arguments**

sumstats_dt	data.table with summary statistics
log_files	list of locations for all log files
check_save_out	list of parameters for saved files
rmv_chr	Chromosomes to exclude from the formatted summary statistics file. Use NULL if no filtering is necessary. Default is c("X", "Y", "MT") which removes all non-autosomal SNPs.
nThread	Number of threads to use for parallel processes.
tabix_index	Index the formatted summary statistics with <b>tabix</b> for fast querying.
log_folder_ind	Binary Should log files be stored containing all filtered out SNPs (separate file per filter). The data is outputted in the same format specified for the resulting sumstats file. The only exception to this rule is if output is vcf, then log file saved as .tsv.gz. Default is FALSE.

**Value**

list containing the updated summary statistics data.table and the updated log file locations list

---

check_col_order	<i>Ensure that the first three columns are SNP, CHR, BP in that order and then A1, A2 if present</i>
-----------------	--

---

**Description**

Ensure that the first three columns are SNP, CHR, BP in that order and then A1, A2 if present

**Usage**

```
check_col_order(sumstats_dt, path)
```

**Arguments**

sumstats_dt	data table obj of the summary statistics file for the GWAS
path	Filepath for the summary statistics file to be formatted

**Value**

list containing sumstats\_dt, the modified summary statistics data table object

---

check_drop_indels	<i>Drop Indels from summary statistics</i>
-------------------	--

---

**Description**

Drop Indels from summary statistics

**Usage**

```
check_drop_indels(
  sumstats_dt,
  drop_indels,
  path,
  log_folder_ind,
  check_save_out,
  tabix_index,
  nThread,
  log_files
)
```

**Arguments**

sumstats_dt	data table obj of the summary statistics file for the GWAS
drop_indels	Binary, should any indels found in the sumstats be dropped? These can not be checked against a reference dataset and will have the same RS ID and position as SNPs which can affect downstream analysis. Default is False.
path	Filepath for the summary statistics file to be formatted. A dataframe or datatable of the summary statistics file can also be passed directly to MungeSumstats using the path parameter.
log_folder_ind	Binary Should log files be stored containing all filtered out SNPs (separate file per filter). The data is outputted in the same format specified for the resulting sumstats file. The only exception to this rule is if output is vcf, then log file saved as .tsv.gz. Default is FALSE.
tabix_index	Index the formatted summary statistics with <b>tabix</b> for fast querying.
nThread	Number of threads to use for parallel processes.

**Value**

list containing sumstats\_dt, the modified summary statistics data table object

**Source**

```
sumstats_dt <- MungeSumstats::formatted_example()
sumstats <- check_drop_indels(sumstats_dt
= sumstats_dt, drop_indels = TRUE)
```

---

check\_dup\_bp

*Ensure all rows have unique positions, drop those that don't*

---

**Description**

Ensure all rows have unique positions, drop those that don't

**Usage**

```
check_dup_bp(
  sumstats_dt,
  bi_allelic_filter,
  check_dups,
  indels,
  path,
  log_folder_ind,
  check_save_out,
  tabix_index,
  nThread,
  log_files
)
```

**Arguments**

bi_allelic_filter	Binary Should non-biallelic SNPs be removed. Default is TRUE.
check_dups	whether to check for duplicates - if formatting QTL datasets this should be set to FALSE otherwise keep as TRUE. Default is TRUE.
indels	Binary does your Sumstats file contain Indels? These don't exist in our reference file so they will be excluded from checks if this value is TRUE. Default is TRUE.
path	Filepath for the summary statistics file to be formatted. A dataframe or datatable of the summary statistics file can also be passed directly to MungeSumstats using the path parameter.
log_folder_ind	Binary Should log files be stored containing all filtered out SNPs (separate file per filter). The data is outputted in the same format specified for the resulting sumstats file. The only exception to this rule is if output is vcf, then log file saved as .tsv.gz. Default is FALSE.
tabix_index	Index the formatted summary statistics with <b>tabix</b> for fast querying.
nThread	Number of threads to use for parallel processes.
log_files	list of log file locations

**Value**

list containing sumstats\_dt, the modified summary statistics data table object and log files list

---

check_dup_col	<i>Ensure that no columns are duplicated</i>
---------------	--

---

**Description**

Ensure that no columns are duplicated

**Usage**

```
check_dup_col(sumstats_dt, path)
```

**Arguments**

sumstats_dt	data table obj of the summary statistics file for the GWAS
path	Filepath for the summary statistics file to be formatted

**Value**

list containing sumstats\_dt, the modified summary statistics data table object

---

check_dup_row	<i>Ensure all rows are unique based on SNP,CHR,BP,A1,A2, drop those that aren't</i>
---------------	---

---

### Description

Ensure all rows are unique based on SNP,CHR,BP,A1,A2, drop those that aren't

### Usage

```
check_dup_row(
  sumstats_dt,
  check_dups,
  path,
  log_folder_ind,
  check_save_out,
  tabix_index,
  nThread,
  log_files
)
```

### Arguments

check_dups	whether to check for duplicates - if formatting QTL datasets this should be set to FALSE otherwise keep as TRUE. Default is TRUE.
path	Filepath for the summary statistics file to be formatted. A dataframe or datatable of the summary statistics file can also be passed directly to MungeSumstats using the path parameter.
log_folder_ind	Binary Should log files be stored containing all filtered out SNPs (separate file per filter). The data is outputted in the same format specified for the resulting sumstats file. The only exception to this rule is if output is vcf, then log file saved as .tsv.gz. Default is FALSE.
tabix_index	Index the formatted summary statistics with <b>tabix</b> for fast querying.
nThread	Number of threads to use for parallel processes.
log_files	list of log file locations

### Value

list containing sumstats\_dt, the modified summary statistics data table object and log files list



---

check_dup_snp	<i>Ensure all rows have unique SNP IDs, drop those that don't</i>
---------------	---

---

### Description

Ensure all rows have unique SNP IDs, drop those that don't

### Usage

```
check_dup_snp(
  sumstats_dt,
  indels,
  path,
  log_folder_ind,
  check_save_out,
  tabix_index,
  nThread,
  log_files,
  bi_allelic_filter,
  check_dups
)
```

### Arguments

indels	Binary does your Sumstats file contain Indels? These don't exist in our reference file so they will be excluded from checks if this value is TRUE. Default is TRUE.
path	Filepath for the summary statistics file to be formatted. A dataframe or datatable of the summary statistics file can also be passed directly to MungeSumstats using the path parameter.
log_folder_ind	Binary Should log files be stored containing all filtered out SNPs (separate file per filter). The data is outputted in the same format specified for the resulting sumstats file. The only exception to this rule is if output is vcf, then log file saved as .tsv.gz. Default is FALSE.
tabix_index	Index the formatted summary statistics with <b>tabix</b> for fast querying.
nThread	Number of threads to use for parallel processes.
log_files	list of log file locations
bi_allelic_filter	Binary Should non-biallelic SNPs be removed. Default is TRUE.
check_dups	whether to check for duplicates - if formatting QTL datasets this should be set to FALSE otherwise keep as TRUE. Default is TRUE.

### Value

list containing sumstats\_dt, the modified summary statistics data table object and log files list

---

check\_effect\_columns\_nonzero

*Ensure that the standard error (se) is positive for all SNPs*

---

## Description

Ensure that the standard error (se) is positive for all SNPs

## Usage

```
check_effect_columns_nonzero(
  sumstats_dt,
  path,
  effect_columns_nonzero,
  log_folder_ind,
  check_save_out,
  tabix_index,
  nThread,
  log_files
)
```

## Arguments

path	Filepath for the summary statistics file to be formatted. A dataframe or datatable of the summary statistics file can also be passed directly to MungeSumstats using the path parameter.
effect_columns_nonzero	Binary should the effect columns in the data BETA,OR (odds ratio),LOG_ODDS,SIGNED_SUMSTAT be checked to ensure no SNP=0. Those that do are removed(if present in sumstats file). Default FALSE.
log_folder_ind	Binary Should log files be stored containing all filtered out SNPs (separate file per filter). The data is outputted in the same format specified for the resulting sumstats file. The only exception to this rule is if output is vcf, then log file saved as .tsv.gz. Default is FALSE.
tabix_index	Index the formatted summary statistics with <b>tabix</b> for fast querying.
nThread	Number of threads to use for parallel processes.
log_files	list of log file locations

## Value

list containing sumstats\_dt, the modified summary statistics data table object and the log file list

---

check_empty_cols	<i>Check for empty columns</i>
------------------	--------------------------------

---

**Description**

Empty columns contain only ".", NA, or 0

**Usage**

```
check_empty_cols(sumstats_dt, sampled_rows = NULL, verbose = TRUE)
```

**Arguments**

sampled_rows	First N rows to sample. Set NULL to use full sumstats_file. when determining whether cols are empty.
verbose	Print messages.

**Value**

empty\_cols

---

check_four_step_col	<i>Ensure that CHR:BP:A2:A1 aren't merged into 1 column</i>
---------------------	---

---

**Description**

Ensure that CHR:BP:A2:A1 aren't merged into 1 column

**Usage**

```
check_four_step_col(sumstats_dt, path)
```

**Arguments**

sumstats_dt	data table obj of the summary statistics file for the GWAS
path	Filepath for the summary statistics file to be formatted

**Value**

list containing sumstats\_dt, the modified summary statistics data table object

---

check_frq	<i>Ensure all SNPs have frq score above threshold</i>
-----------	---

---

### Description

Ensure all SNPs have frq score above threshold

### Usage

```
check_frq(
  sumstats_dt,
  path,
  FRQ_filter,
  log_folder_ind,
  check_save_out,
  tabix_index,
  nThread,
  log_files
)
```

### Arguments

path	Filepath for the summary statistics file to be formatted. A dataframe or datatable of the summary statistics file can also be passed directly to MungeSumstats using the path parameter.
FRQ_filter	numeric The minimum value permissible of the frequency(FRQ) of the SNP (i.e. Allele Frequency (AF)) (if present in sumstats file). By default no filtering is done, i.e. value of 0.
log_folder_ind	Binary Should log files be stored containing all filtered out SNPs (separate file per filter). The data is outputted in the same format specified for the resulting sumstats file. The only exception to this rule is if output is vcf, then log file saved as .tsv.gz. Default is FALSE.
tabix_index	Index the formatted summary statistics with <b>tabix</b> for fast querying.
nThread	Number of threads to use for parallel processes.
log_files	list of log file locations

### Value

list containing sumstats\_dt, the modified summary statistics data table object and the log file list

---

check_frq_maf	<i>Check that FRQ column refers to minor/effect allele frequency not major</i>
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---

**Description**

Check that FRQ column refers to minor/effect allele frequency not major

**Usage**

```
check_frq_maf(sumstats_dt, frq_is_maf)
```

**Arguments**

frq_is_maf	Conventionally the FRQ column is intended to show the minor/effect allele frequency (MAF) but sometimes the major allele frequency can be inferred as the FRQ column. This logical variable indicates that the FRQ column should be renamed to MAJOR_ALLELE_FRQ if the frequency values appear to relate to the major allele i.e. >0.5. By default this mapping won't occur i.e. is TRUE.
------------	---

**Value**

sumstats\_dt, the modified summary statistics data table object

---

check_info_score	<i>Ensure all SNPs have info score above threshold</i>
------------------	--

---

**Description**

Ensure all SNPs have info score above threshold

**Usage**

```
check_info_score(  
  sumstats_dt,  
  INFO_filter,  
  log_folder_ind,  
  check_save_out,  
  tabix_index,  
  nThread,  
  log_files  
)
```

**Arguments**

INFO_filter	numeric	The minimum value permissible of the imputation information score (if present in sumstats file). Default 0.9.
log_folder_ind	Binary	Should log files be stored containing all filtered out SNPs (separate file per filter). The data is outputted in the same format specified for the resulting sumstats file. The only exception to this rule is if output is vcf, then log file saved as .tsv.gz. Default is FALSE.
tabix_index		Index the formatted summary statistics with <b>tabix</b> for fast querying.
nThread		Number of threads to use for parallel processes.
log_files		list of log file locations.

**Value**

list containing sumstats\_dt, the modified summary statistics data table object and the log file list

---

check_ldsc_format	<i>Ensures that parameters are compatible with LDSC format</i>
-------------------	--

---

**Description**

Format summary statistics for direct input to Linkage Disequilibrium Score (LDSC) regression without the need to use their munge\_sumstats.py script first.

**Usage**

```
check_ldsc_format(
  sumstats_dt,
  save_format,
  convert_n_int,
  allele_flip_check,
  compute_z,
  compute_n
)
```

**Arguments**

sumstats_dt	data table obj of the summary statistics file for the GWAS.
save_format	Output format of sumstats. Options are NULL - standardised output format from MungeSumstats, LDSC - output format compatible with LDSC and openGWAS - output compatible with openGWAS VCFs. Default is NULL. <b>NOTE</b> - If LDSC format is used, the naming convention of A1 as the reference (genome build) allele and A2 as the effect allele will be reversed to match LDSC (A1 will now be the effect allele). See more info on this <a href="#">here</a> . Note that any effect columns (e.g. Z) will be in relation to A1 now instead of A2.

convert_n_int	Binary, if N (the number of samples) is not an integer, should this be rounded? Default is TRUE.
allele_flip_check	Binary Should the allele columns be checked against reference genome to infer if flipping is necessary. Default is TRUE.
compute_z	Whether to compute Z-score column. Default is FALSE. This can be computed from Beta and SE with (Beta/SE) or P ( $Z:=\text{sign}(\text{BETA})\cdot\sqrt{\text{stats::qchisq}(P,1,\text{lower}=\text{FALSE})}$ ). <b>Note</b> that imputing the Z-score from P for every SNP will not be perfectly correct and may result in a loss of power. This should only be done as a last resort. Use 'BETA' to impute by BETA/SE and 'P' to impute by SNP p-value.
compute_n	Whether to impute N. Default of 0 won't impute, any other integer will be imputed as the N (sample size) for every SNP in the dataset. <b>Note</b> that imputing the sample size for every SNP is not correct and should only be done as a last resort. N can also be inputted with "ldsc", "sum", "giant" or "metal" by passing one of these for this field or a vector of multiple. Sum and an integer value creates an N column in the output whereas giant, metal or ldsc create an Neff or effective sample size. If multiples are passed, the formula used to derive it will be indicated.

**Details**

[LDSC documentation.](#)

**Value**

Formatted summary statistics

**Source**

[LDSC GitHub](#)

---

check_miss_data	<i>Remove SNPs with missing data</i>
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---

**Description**

Remove SNPs with missing data

**Usage**

```
check_miss_data(
  sumstats_dt,
  path,
  log_folder_ind,
  check_save_out,
  tabix_index,
  nThread,
```

```

    log_files,
    drop_na_cols
  )

```

### Arguments

path	Filepath for the summary statistics file to be formatted. A dataframe or datatable of the summary statistics file can also be passed directly to MungeSumstats using the path parameter.
log_folder_ind	Binary Should log files be stored containing all filtered out SNPs (separate file per filter). The data is outputted in the same format specified for the resulting sumstats file. The only exception to this rule is if output is vcf, then log file saved as .tsv.gz. Default is FALSE.
tabix_index	Index the formatted summary statistics with <b>tabix</b> for fast querying.
nThread	Number of threads to use for parallel processes.
log_files	list of log file locations
drop_na_cols	A character vector of column names to be checked for missing values. Rows with missing values in any of these columns (if present in the dataset) will be dropped. If NULL, all columns will be checked for missing values. Default columns are SNP, chromosome, position, allele 1, allele2, effect columns (frequency, beta, Z-score, standard error, log odds, signed sumstats, odds ratio), p value and N columns.

### Value

list containing sumstats\_dt, the modified summary statistics data table object and a log file list.

---

check_multi_gwas	<i>Ensure that only one model in GWAS sumstats or only one trait tested</i>
------------------	---

---

### Description

Ensure that only one model in GWAS sumstats or only one trait tested

### Usage

```

check_multi_gwas(
  sumstats_dt,
  path,
  analysis_trait,
  ignore_multi_trait,
  mapping_file
)

```



**Arguments**

sumstats_dt	data table obj of the summary statistics file for the GWAS
path	Filepath for the summary statistics file to be formatted
analysis_trait	If multiple traits were studied, name of the trait for analysis from the GWAS. Default is NULL
mapping_file	MungeSumstats has a pre-defined column-name mapping file which should cover the most common column headers and their interpretations. However, if a column header that is in your file is missing of the mapping we give is incorrect you can supply your own mapping file. Must be a 2 column dataframe with column names "Uncorrected" and "Corrected". See data(sumstatsColHeaders) for default mapping and necessary format.

**Value**

list containing sumstats\_dt, the modified summary statistics data table object

---

check\_multi\_rs\_snp      *Ensure that SNP ids don't have multiple rs ids on one line*

---

**Description**

Ensure that SNP ids don't have multiple rs ids on one line

**Usage**

```
check_multi_rs_snp(
  sumstats_dt,
  path,
  remove_multi_rs_snp,
  imputation_ind,
  log_folder_ind,
  check_save_out,
  tabix_index,
  nThread,
  log_files
)
```

**Arguments**

path	Filepath for the summary statistics file to be formatted. A dataframe or datatable of the summary statistics file can also be passed directly to MungeSumstats using the path parameter.
remove_multi_rs_snp	Binary Sometimes summary statistics can have multiple RSIDs on one row (i.e. related to one SNP), for example "rs5772025_rs397784053". This can cause an error so by default, the first RS ID will be kept and the rest removed

e.g. "rs5772025". If you want to just remove these SNPs entirely, set it to TRUE. Default is FALSE.

imputation_ind	Binary Should a column be added for each imputation step to show what SNPs have imputed values for differing fields. This includes a field denoting SNP allele flipping (flipped). On the flipped value, this denoted whether the alleles were switched based on MungeSumstats initial choice of A1, A2 from the input column headers and thus may not align with what the creator intended. <b>Note</b> these columns will be in the formatted summary statistics returned. Default is FALSE.
log_folder_ind	Binary Should log files be stored containing all filtered out SNPs (separate file per filter). The data is outputted in the same format specified for the resulting sumstats file. The only exception to this rule is if output is vcf, then log file saved as .tsv.gz. Default is FALSE.
tabix_index	Index the formatted summary statistics with <b>tabix</b> for fast querying.
nThread	Number of threads to use for parallel processes.
log_files	list of log file locations

### Value

list containing sumstats\_dt, the modified summary statistics data table object and the log file list.

---

check_no_allele	<i>Ensure that A1 &amp; A2 are present, if not can find it with SNP and other allele</i>
-----------------	--

---

### Description

More care needs to be taken if one of A1/A2 is present, before imputing the other allele flipping needs to be checked

### Usage

```
check_no_allele(
  sumstats_dt,
  path,
  ref_genome,
  rsids,
  imputation_ind,
  allele_flip_check,
  log_folder_ind,
  check_save_out,
  tabix_index,
  nThread,
  log_files,
  bi_allelic_filter,
  dbSNP
)
```

**Arguments**

path	Filepath for the summary statistics file to be formatted. A dataframe or datatable of the summary statistics file can also be passed directly to MungeSumstats using the path parameter.
ref_genome	name of the reference genome used for the GWAS ("GRCh37" or "GRCh38"). Argument is case-insensitive. Default is NULL which infers the reference genome from the data.
imputation_ind	Binary Should a column be added for each imputation step to show what SNPs have imputed values for differing fields. This includes a field denoting SNP allele flipping (flipped). On the flipped value, this denoted whether the alleles were switched based on MungeSumstats initial choice of A1, A2 from the input column headers and thus may not align with what the creator intended. <b>Note</b> these columns will be in the formatted summary statistics returned. Default is FALSE.
allele_flip_check	Binary Should the allele columns be checked against reference genome to infer if flipping is necessary. Default is TRUE.
log_folder_ind	Binary Should log files be stored containing all filtered out SNPs (separate file per filter). The data is outputted in the same format specified for the resulting sumstats file. The only exception to this rule is if output is vcf, then log file saved as .tsv.gz. Default is FALSE.
tabix_index	Index the formatted summary statistics with <b>tabix</b> for fast querying.
nThread	Number of threads to use for parallel processes.
log_files	list of log file locations
bi_allelic_filter	Binary Should non-biallelic SNPs be removed. Default is TRUE.
dbSNP	version of dbSNP to be used for imputation (144 or 155).

**Value**

A list containing two data tables:

- `sumstats_dt`: the modified summary statistics data table object
- `rsids`: `snpById`, filtered to SNPs of interest if loaded already. Or else NULL.
- `allele_flip_check`: does the dataset require allele flip check
- `log_files`: log file list
- `bi_allelic_filter`: should multi-allelic SNPs be filtered out

---

check_no_chr_bp	<i>Ensure that CHR and BP are missing if SNP is present, can find them</i>
-----------------	--

---

### Description

Ensure that CHR and BP are missing if SNP is present, can find them

### Usage

```
check_no_chr_bp(
  sumstats_dt,
  path,
  ref_genome,
  rsids,
  imputation_ind,
  log_folder_ind,
  check_save_out,
  tabix_index,
  nThread,
  log_files,
  dbSNP
)
```

### Arguments

path	Filepath for the summary statistics file to be formatted. A dataframe or datatable of the summary statistics file can also be passed directly to MungeSumstats using the path parameter.
ref_genome	name of the reference genome used for the GWAS ("GRCh37" or "GRCh38"). Argument is case-insensitive. Default is NULL which infers the reference genome from the data.
imputation_ind	Binary Should a column be added for each imputation step to show what SNPs have imputed values for differing fields. This includes a field denoting SNP allele flipping (flipped). On the flipped value, this denoted whether the alleles were switched based on MungeSumstats initial choice of A1, A2 from the input column headers and thus may not align with what the creator intended. <b>Note</b> these columns will be in the formatted summary statistics returned. Default is FALSE.
log_folder_ind	Binary Should log files be stored containing all filtered out SNPs (separate file per filter). The data is outputted in the same format specified for the resulting sumstats file. The only exception to this rule is if output is vcf, then log file saved as .tsv.gz. Default is FALSE.
tabix_index	Index the formatted summary statistics with <b>tabix</b> for fast querying.
nThread	Number of threads to use for parallel processes.
log_files	list of log file locations
dbSNP	version of dbSNP to be used for imputation (144 or 155).

**Value**

A list containing two data tables:

- `sumstats_dt` : the modified summary statistics data table object
- `rsids` : `snpsById`, filtered to SNPs of interest if loaded already. Or else NULL
- `log_files` : log file list

---

<code>check_no_rs_snp</code>	<i>Ensure that SNP appears to be valid RSIDs (starts with rs)</i>
------------------------------	---

---

**Description**

Ensure that SNP appears to be valid RSIDs (starts with rs)

**Usage**

```
check_no_rs_snp(
  sumstats_dt,
  path,
  ref_genome,
  snp_ids_are_rs_ids,
  indels,
  imputation_ind,
  log_folder_ind,
  check_save_out,
  tabix_index,
  nThread,
  log_files,
  dbSNP
)
```

**Arguments**

<code>path</code>	Filepath for the summary statistics file to be formatted. A dataframe or datatable of the summary statistics file can also be passed directly to <code>MungeSumstats</code> using the <code>path</code> parameter.
<code>ref_genome</code>	name of the reference genome used for the GWAS ("GRCh37" or "GRCh38"). Argument is case-insensitive. Default is NULL which infers the reference genome from the data.
<code>snp_ids_are_rs_ids</code>	Binary Should the supplied SNP ID's be assumed to be RSIDs. If not, imputation using the SNP ID for other columns like base-pair position or chromosome will not be possible. If set to FALSE, the SNP RS ID will be imputed from the reference genome if possible. Default is TRUE.
<code>indels</code>	Binary does your Sumstats file contain Indels? These don't exist in our reference file so they will be excluded from checks if this value is TRUE. Default is TRUE.

imputation_ind	Binary Should a column be added for each imputation step to show what SNPs have imputed values for differing fields. This includes a field denoting SNP allele flipping (flipped). On the flipped value, this denoted whether the alleles were switched based on MungeSumstats initial choice of A1, A2 from the input column headers and thus may not align with what the creator intended. <b>Note</b> these columns will be in the formatted summary statistics returned. Default is FALSE.
log_folder_ind	Binary Should log files be stored containing all filtered out SNPs (separate file per filter). The data is outputted in the same format specified for the resulting sumstats file. The only exception to this rule is if output is vcf, then log file saved as .tsv.gz. Default is FALSE.
tabix_index	Index the formatted summary statistics with <b>tabix</b> for fast querying.
nThread	Number of threads to use for parallel processes.
log_files	list of log file locations
dbSNP	version of dbSNP to be used for imputation (144 or 155).

**Value**

list containing sumstats\_dt, the modified summary statistics data table object and the log file list.

---

check\_no\_snp

*Ensure that SNP is present if not can find it with CHR and BP*

---

**Description**

Ensure that SNP is present if not can find it with CHR and BP

**Usage**

```
check_no_snp(
  sumstats_dt,
  path,
  ref_genome,
  indels,
  imputation_ind,
  log_folder_ind,
  check_save_out,
  tabix_index,
  nThread,
  log_files,
  dbSNP,
  verbose = TRUE
)
```

**Arguments**

path	Filepath for the summary statistics file to be formatted. A dataframe or datatable of the summary statistics file can also be passed directly to MungeSumstats using the path parameter.
ref_genome	name of the reference genome used for the GWAS ("GRCh37" or "GRCh38"). Argument is case-insensitive. Default is NULL which infers the reference genome from the data.
indels	Binary does your Sumstats file contain Indels? These don't exist in our reference file so they will be excluded from checks if this value is TRUE. Default is TRUE.
imputation_ind	Binary Should a column be added for each imputation step to show what SNPs have imputed values for differing fields. This includes a field denoting SNP allele flipping (flipped). On the flipped value, this denoted whether the alleles were switched based on MungeSumstats initial choice of A1, A2 from the input column headers and thus may not align with what the creator intended. <b>Note</b> these columns will be in the formatted summary statistics returned. Default is FALSE.
log_folder_ind	Binary Should log files be stored containing all filtered out SNPs (separate file per filter). The data is outputted in the same format specified for the resulting sumstats file. The only exception to this rule is if output is vcf, then log file saved as .tsv.gz. Default is FALSE.
tabix_index	Index the formatted summary statistics with <b>tabix</b> for fast querying.
nThread	Number of threads to use for parallel processes.
log_files	list of log file locations
dbSNP	version of dbSNP to be used for imputation (144 or 155).
verbose	should messages be printed. Default it TRUE.

**Value**

list containing sumstats\_dt, the modified summary statistics data table object and the log files list

---

check_numeric	<i>Check numeric columns</i>
---------------	------------------------------

---

**Description**

Checks for any columns that should be numeric, and ensures that they are indeed numeric.

**Usage**

```
check_numeric(sumstats_dt, cols = c("P", "SE", "FRQ", "MAF", "BETA"))
```

**Arguments**

sumstats_dt	Summary stats with column names already standardised by <a href="#">format_sumstats</a> .
cols	Names of columns that should be numeric. If any of these columns are not actually present in sumstats_dt, they will be skipped.

**Value**

sumstats\_dt

---

 check\_n\_int
 

---



---

*Ensure that the N column is all integers*


---

**Description**

Ensure that the N column is all integers

**Usage**

```
check_n_int(sumstats_dt, path, convert_n_int, imputation_ind)
```

**Arguments**

sumstats_dt	data table obj of the summary statistics file for the GWAS
path	Filepath for the summary statistics file to be formatted
convert_n_int	Binary, if N (the number of samples) is not an integer, should this be rounded? Default is TRUE.
imputation_ind	Binary Should a column be added for each imputation step to show what SNPs have imputed values for differing fields. This includes a field denoting SNP allele flipping (flipped). <b>Note</b> these columns will be in the formatted summary statistics returned. Default is FALSE.

**Value**

list containing sumstats\_dt, the modified summary statistics data table object.

---

 check\_n\_num
 

---



---

*Ensure all SNPs have N less than X std dev below mean*


---

**Description**

In case some SNPs were genotyped by a specialized genotyping array and have substantially more samples than others. These will be removed.



**Usage**

```

check_n_num(
  sumstats_dt,
  path,
  N_std,
  N_dropNA = FALSE,
  log_folder_ind,
  check_save_out,
  tabix_index,
  nThread,
  log_files
)

```

**Arguments**

path	Filepath for the summary statistics file to be formatted. A dataframe or datatable of the summary statistics file can also be passed directly to MungeSumstats using the path parameter.
N_std	numeric The number of standard deviations above the mean a SNP's N is needed to be removed. Default is 5.
N_dropNA	Drop rows where N is missing. Default is TRUE.
log_folder_ind	Binary Should log files be stored containing all filtered out SNPs (separate file per filter). The data is outputted in the same format specified for the resulting sumstats file. The only exception to this rule is if output is vcf, then log file saved as .tsv.gz. Default is FALSE.
tabix_index	Index the formatted summary statistics with <b>tabix</b> for fast querying.
nThread	Number of threads to use for parallel processes.
log_files	list of log file locations

**Value**

list containing sumstats\_dt, the modified summary statistics data table object and the log file list

---

check\_on\_ref\_genome    *Ensure all SNPs are on the reference genome*

---

**Description**

Ensure all SNPs are on the reference genome

**Usage**

```

check_on_ref_genome(
  sumstats_dt,
  path,
  ref_genome,
  on_ref_genome,
  indels = indels,
  rsids,
  imputation_ind,
  log_folder_ind,
  check_save_out,
  tabix_index,
  nThread,
  log_files,
  dbSNP
)

```

**Arguments**

path	Filepath for the summary statistics file to be formatted. A dataframe or datatable of the summary statistics file can also be passed directly to MungeSumstats using the path parameter.
ref_genome	name of the reference genome used for the GWAS ("GRCh37" or "GRCh38"). Argument is case-insensitive. Default is NULL which infers the reference genome from the data.
on_ref_genome	Binary Should a check take place that all SNPs are on the reference genome by SNP ID. Default is TRUE.
indels	Binary does your Sumstats file contain Indels? These don't exist in our reference file so they will be excluded from checks if this value is TRUE. Default is TRUE.
imputation_ind	Binary Should a column be added for each imputation step to show what SNPs have imputed values for differing fields. This includes a field denoting SNP allele flipping (flipped). On the flipped value, this denoted whether the alleles were switched based on MungeSumstats initial choice of A1, A2 from the input column headers and thus may not align with what the creator intended. <b>Note</b> these columns will be in the formatted summary statistics returned. Default is FALSE.
log_folder_ind	Binary Should log files be stored containing all filtered out SNPs (separate file per filter). The data is outputted in the same format specified for the resulting sumstats file. The only exception to this rule is if output is vcf, then log file saved as .tsv.gz. Default is FALSE.
tabix_index	Index the formatted summary statistics with <b>tabix</b> for fast querying.
nThread	Number of threads to use for parallel processes.
log_files	list of log file locations
dbSNP	version of dbSNP to be used for imputation (144 or 155).

**Value**

A list containing two data tables:

- `sumstats_dt` : the modified summary statistics data table object
- `rsids` : `snpsById`, filtered to SNPs of interest if loaded already. Or else NULL
- `log_files` : log file list

---

<code>check_pos_se</code>	<i>Ensure that the standard error (se) is positive for all SNPs Also impute se if missing</i>
---------------------------	---

---

**Description**

Ensure that the standard error (se) is positive for all SNPs Also impute se if missing

**Usage**

```
check_pos_se(
  sumstats_dt,
  path,
  pos_se,
  log_folder_ind,
  imputation_ind,
  check_save_out,
  tabix_index,
  nThread,
  log_files,
  impute_se
)
```

**Arguments**

<code>path</code>	Filepath for the summary statistics file to be formatted. A dataframe or datatable of the summary statistics file can also be passed directly to <code>MungeSumstats</code> using the <code>path</code> parameter.
<code>pos_se</code>	Binary Should the standard Error (SE) column be checked to ensure it is greater than 0? Those that are, are removed (if present in <code>sumstats</code> file). Default TRUE.
<code>log_folder_ind</code>	Binary Should log files be stored containing all filtered out SNPs (separate file per filter). The data is outputted in the same format specified for the resulting <code>sumstats</code> file. The only exception to this rule is if output is <code>vcf</code> , then log file saved as <code>.tsv.gz</code> . Default is FALSE.
<code>imputation_ind</code>	Binary Should a column be added for each imputation step to show what SNPs have imputed values for differing fields. This includes a field denoting SNP allele flipping (flipped). On the flipped value, this denoted whether the alleles were switched based on <code>MungeSumstats</code> initial choice of A1, A2 from the input

	column headers and thus may not align with what the creator intended. <b>Note</b> these columns will be in the formatted summary statistics returned. Default is FALSE.
tabix_index	Index the formatted summary statistics with <code>tabix</code> for fast querying.
nThread	Number of threads to use for parallel processes.
log_files	list of log file locations
impute_se	Binary, whether the standard error should be imputed using other effect data if it isn't present in the sumstats. Note that this imputation is an approximation so could have an effect on downstream analysis. Use with caution. The different methods MungeSumstats will try and impute se (in this order or priority) are: <ol style="list-style-type: none"> <li>1. BETA / Z</li> <li>2. abs(BETA/ qnorm(P/2))</li> </ol> Default is FALSE.

**Value**

list containing `sumstats_dt`, the modified summary statistics data table object and the log file list

---

check_range_p_val	<i>Ensure that the p values are not &gt;1 and if so set to 1</i>
-------------------	--

---

**Description**

Ensure that the p values are not >1 and if so set to 1

**Usage**

```
check_range_p_val(sumstats_dt, convert_large_p, convert_neg_p, imputation_ind)
```

**Arguments**

sumstats_dt	data table obj of the summary statistics file for the GWAS
convert_large_p	Binary, should p-values >1 be converted to 1? P-values >1 should not be possible and can cause errors with LDSC/MAGMA and should be converted. Default is TRUE.
convert_neg_p	Binary, should p-values <0 be converted to 0? Negative p-values should not be possible and can cause errors with LDSC/MAGMA and should be converted. Default is TRUE.
imputation_ind	Binary Should a column be added for each imputation step to show what SNPs have imputed values for differing fields. This includes a field denoting SNP allele flipping (flipped). On the flipped value, this denoted whether the alleles were switched based on MungeSumstats initial choice of A1, A2 from the input column headers and thus may not align with what the creator intended. <b>Note</b> these columns will be in the formatted summary statistics returned. Default is FALSE.

**Value**

list containing `sumstats_dt`, the modified summary statistics data table object

**Source**

```
sumstats_dt <- MungeSumstats::formatted_example()
sumstats_dt$P[1:3] <- 5
sumstats_dt$P[6:10] <- -5
sumstats <- check_range_p_val(sumstats_dt = sumstats_dt,
  convert_large_p = TRUE,
  convert_neg_p = TRUE,
  imputation_ind = TRUE)
```

---

check_row_snp	<i>Ensure all rows have SNPs beginning with rs or SNP, drop those that don't</i>
---------------	--

---

**Description**

Ensure all rows have SNPs beginning with rs or SNP, drop those that don't

**Usage**

```
check_row_snp(
  sumstats_dt,
  path,
  log_folder_ind,
  check_save_out,
  tabix_index,
  nThread,
  log_files
)
```

**Arguments**

path	Filepath for the summary statistics file to be formatted. A dataframe or datatable of the summary statistics file can also be passed directly to <code>MungeSumstats</code> using the <code>path</code> parameter.
log_folder_ind	Binary Should log files be stored containing all filtered out SNPs (separate file per filter). The data is outputted in the same format specified for the resulting <code>sumstats</code> file. The only exception to this rule is if output is <code>vcf</code> , then log file saved as <code>.tsv.gz</code> . Default is <code>FALSE</code> .
tabix_index	Index the formatted summary statistics with <code>tabix</code> for fast querying.
nThread	Number of threads to use for parallel processes.
log_files	list of log file locations

**Value**

list containing `sumstats_dt`, the modified summary statistics data table object and log file list

---

check_save_path	<i>Check if save path and log folder is appropriate</i>
-----------------	---

---

### Description

Check if save path and log folder is appropriate

### Usage

```
check_save_path(
  save_path,
  log_folder,
  log_folder_ind,
  tabix_index,
  write_vcf = FALSE,
  verbose = TRUE
)
```

### Arguments

save_path	File path to save formatted data. Defaults to <code>tempfile(fileext=".tsv.gz")</code> .
log_folder	Filepath to the directory for the log files and the log of MungeSumstats messages to be stored. Default is a temporary directory. Note the name of the log files (log messages and log outputs) are now the same as the name of the file specified in the save path parameter with the extension <code>'_log_msg.txt'</code> and <code>'_log_output.txt'</code> respectively.
log_folder_ind	Binary Should log files be stored containing all filtered out SNPs (separate file per filter). The data is outputted in the same format specified for the resulting sumstats file. The only exception to this rule is if output is vcf, then log file saved as <code>.tsv.gz</code> . Default is FALSE.
tabix_index	Index the formatted summary statistics with <code>tabix</code> for fast querying.
write_vcf	Whether to write as VCF (TRUE) or tabular file (FALSE).
verbose	Print messages.

### Value

Corrected save\_path, the file type, the separator, corrected log\_folder, the log file extension.

---

check_signed_col	<i>Ensure that there is at least one signed column in summary statistics file Impute beta if user requests</i>
------------------	--

---

### Description

Ensure that there is at least one signed column in summary statistics file Impute beta if user requests

### Usage

```
check_signed_col(
  sumstats_dt,
  impute_beta,
  log_folder_ind,
  rsids,
  imputation_ind,
  check_save_out,
  tabix_index,
  log_files,
  nThread
)
```

### Arguments

sumstats_dt	data table obj of the summary statistics file for the GWAS
impute_beta	Binary, whether BETA should be imputed using other effect data if it isn't present in the sumstats. Note that this imputation is an approximation (for Z & SE approach) so could have an effect on downstream analysis. Use with caution. The different methods MungeSumstats will try and impute beta (in this order or priority) are: <ol style="list-style-type: none"> <li>1. log(OR)</li> <li>2. Z x SE</li> </ol> Default value is FALSE.
log_folder_ind	Binary Should log files be stored containing all filtered out SNPs (separate file per filter). The data is outputted in the same format specified for the resulting sumstats file. The only exception to this rule is if output is vcf, then log file saved as .tsv.gz. Default is FALSE.
imputation_ind	Binary Should a column be added for each imputation step to show what SNPs have imputed values for differing fields. This includes a field denoting SNP allele flipping (flipped). On the flipped value, this denoted whether the alleles were switched based on MungeSumstats initial choice of A1, A2 from the input column headers and thus may not align with what the creator intended. <b>Note</b> these columns will be in the formatted summary statistics returned. Default is FALSE.
tabix_index	Index the formatted summary statistics with <b>tabix</b> for fast querying.
log_files	list of log file locations
nThread	Number of threads to use for parallel processes.

**Value**

null

---

check_small_p_val	<i>Ensure that the non-negative p-values are not 5e-324 or lower, if so set to 0</i>
-------------------	--

---

**Description**

Ensure that the non-negative p-values are not 5e-324 or lower, if so set to 0

**Usage**

```
check_small_p_val(sumstats_dt, convert_small_p, imputation_ind)
```

**Arguments**

sumstats_dt	data table obj of the summary statistics file for the GWAS
convert_small_p	Binary, should non-negative p-values $\leq 5e-324$ be converted to 0? Small p-values pass the R limit and can cause errors with LDSC/MAGMA and should be converted. Default is TRUE.
imputation_ind	Binary Should a column be added for each imputation step to show what SNPs have imputed values for differing fields. This includes a field denoting SNP allele flipping (flipped). On the flipped value, this denoted whether the alleles were switched based on MungeSumstats initial choice of A1, A2 from the input column headers and thus may not align with what the creator intended. <b>Note</b> these columns will be in the formatted summary statistics returned. Default is FALSE.

**Value**

list containing sumstats\_dt, the modified summary statistics data table object

**Source**

```
sumstats_dt <- MungeSumstats::formatted_example() sumstats_dt$P[1:3] <- 5e-324 sumstats_dt$P[6:10]
<- "5e-324" sumstats <- check_small_p_val(sumstats_dt = sumstats_dt, convert_small_p
= TRUE, imputation_ind = TRUE)
```



---

 check\_strand\_ambiguous

*Remove SNPs with strand-ambiguous alleles*


---

### Description

Remove SNPs with strand-ambiguous alleles

### Usage

```
check_strand_ambiguous(
  sumstats_dt,
  path,
  ref_genome,
  strand_ambig_filter,
  log_folder_ind,
  check_save_out,
  tabix_index,
  nThread,
  log_files
)
```

### Arguments

path	Filepath for the summary statistics file to be formatted. A dataframe or datatable of the summary statistics file can also be passed directly to MungeSumstats using the path parameter.
ref_genome	name of the reference genome used for the GWAS ("GRCh37" or "GRCh38"). Argument is case-insensitive. Default is NULL which infers the reference genome from the data.
strand_ambig_filter	Binary Should SNPs with strand-ambiguous alleles be removed. Default is FALSE.
log_folder_ind	Binary Should log files be stored containing all filtered out SNPs (separate file per filter). The data is outputted in the same format specified for the resulting sumstats file. The only exception to this rule is if output is vcf, then log file saved as .tsv.gz. Default is FALSE.
tabix_index	Index the formatted summary statistics with <b>tabix</b> for fast querying.
nThread	Number of threads to use for parallel processes.
log_files	list of log file locations

### Value

list containing sumstats\_dt, the modified summary statistics data table object and the log file list

---

check_tabular	<i>Ensure valid tabular format</i>
---------------	------------------------------------

---

**Description**

Ensure valid tabular format

**Usage**

```
check_tabular(header)
```

**Arguments**

header	The summary statistics file for the GWAS
--------	--

**Value**

Whether the file is tabular

---

check_two_step_col	<i>Ensure that CHR:BP aren't merged into 1 column</i>
--------------------	---

---

**Description**

Ensure that CHR:BP aren't merged into 1 column

**Usage**

```
check_two_step_col(sumstats_dt, path)
```

**Arguments**

sumstats_dt	data table obj of the summary statistics file for the GWAS
path	Filepath for the summary statistics file to be formatted

**Value**

list containing sumstats\_dt, the modified summary statistics data table object

---

check_vcf	<i>Check if the inputted file is in VCF format</i>
-----------	--

---

**Description**

Check if the inputted file is in VCF format

**Usage**

```
check_vcf(header)
```

**Arguments**

header	Header of the GWAS summary statistics file.
--------	---

**Value**

Whether the file is vcf or not

---

check_vital_col	<i>Ensure that all necessary columns are in the summary statistics file</i>
-----------------	---

---

**Description**

Ensure that all necessary columns are in the summary statistics file

**Usage**

```
check_vital_col(sumstats_dt)
```

**Arguments**

sumstats_dt	data table obj of the summary statistics file for the GWAS
-------------	--

**Value**

null

---

check_zscore	<i>Check for Z-score column</i>
--------------	---------------------------------

---

### Description

The following ensures that a Z-score column is present. The Z-score formula we used here is a R implementation of the formula used in [LDSC's munge\\_sumstats.py](#):

### Usage

```
check_zscore(
  sumstats_dt,
  imputation_ind,
  compute_z = "BETA",
  force_new_z = FALSE,
  standardise_headers = FALSE,
  mapping_file
)
```

### Arguments

sumstats_dt	data table obj of the summary statistics file for the GWAS.
imputation_ind	Binary Should a column be added for each imputation step to show what SNPs have imputed values for differing fields. This includes a field denoting SNP allele flipping (flipped). <b>Note</b> these columns will be in the formatted summary statistics returned. Default is FALSE.
compute_z	Whether to compute Z-score column. Default is FALSE. This can be computed from Beta and SE with (Beta/SE) or P ( $Z := \text{sign}(\text{BETA}) * \sqrt{\text{stats}::\text{qchisq}(P, 1, \text{lower} = \text{FALSE})}$ ). <b>Note</b> that imputing the Z-score from P for every SNP will not be perfectly correct and may result in a loss of power. This should only be done as a last resort. Use 'BETA' to impute by BETA/SE and 'P' to impute by SNP p-value.
force_new_z	When a "Z" column already exists, it will be used by default. To override and compute a new Z-score column from P set force_new_z=TRUE.
standardise_headers	Run standardise_sumstats_column_headers_crossplatform first.
mapping_file	MungeSumstats has a pre-defined column-name mapping file which should cover the most common column headers and their interpretations. However, if a column header that is in your file is missing of the mapping we give is incorrect you can supply your own mapping file. Must be a 2 column dataframe with column names "Uncorrected" and "Corrected". See data(sumstatsColHeaders) for default mapping and necessary format.

**Details**

```
np.sqrt(chi2.isf(P, 1))
```

The R implementation is adapted from the `GenomicSEM::munge` function, after optimizing for speed using `data.table`:

```
sumstats_dt[,Z:=sign(BETA)*sqrt(stats::qchisq(P, 1, lower=FALSE))]
```

*NOTE*: `compute_z` is set to `TRUE` by default to ensure standardisation of the "Z" column (which can be computed differently in different datasets).

**Value**

```
list("sumstats_dt"=sumstats_dt)
```

---

column_dictionary	<i>Map column names to positions.</i>
-------------------	---------------------------------------

---

**Description**

Useful in situations where you need to specify columns by index instead of name (e.g. awk queries).

**Usage**

```
column_dictionary(file_path)
```

**Arguments**

file_path	Path to full summary stats file (or any really file you want to make a column dictionary for).
-----------	--

**Value**

Named list of column positions.

**Source**

Borrowed function from [echotabix](#).

```
eduAttainOkbayPth <- system.file("extdata", "eduAttainOkbay.txt", package = "MungeSumstats")
) tmp <- tempfile(fileext = ".tsv") file.copy(eduAttainOkbayPth, tmp) cdict <- MungeSumstats:::column_di
= tmp)
```

---

compute_nsize	<i>Check for N column if not present and user wants, impute N based on user's sample size. <b>NOTE</b> this will be the same value for each SNP which is not necessarily correct and may cause issues down the line. N can also be inputted with "ldsc", "sum", "giant" or "metal" by passing one or multiple of these.</i>
---------------	---

---

### Description

Check for N column if not present and user wants, impute N based on user's sample size. **NOTE** this will be the same value for each SNP which is not necessarily correct and may cause issues down the line. N can also be inputted with "ldsc", "sum", "giant" or "metal" by passing one or multiple of these.

### Usage

```
compute_nsize(
  sumstats_dt,
  imputation_ind = FALSE,
  compute_n = c("ldsc", "giant", "metal", "sum"),
  standardise_headers = FALSE,
  force_new = FALSE,
  return_list = TRUE
)
```

### Arguments

sumstats_dt	data table obj of the summary statistics file for the GWAS.
imputation_ind	Binary Should a column be added for each imputation step to show what SNPs have imputed values for differing fields. This includes a field denoting SNP allele flipping (flipped). <b>Note</b> these columns will be in the formatted summary statistics returned. Default is FALSE.
compute_n	How to compute per-SNP sample size (new column "N"). <ul style="list-style-type: none"> <li>• 0: N will not be computed.</li> <li>• &gt;0: If any number &gt;0 is provided, that value will be set as N for every row. <b>Note:</b> Computing N this way is incorrect and should be avoided if at all possible.</li> <li>• "sum": N will be computed as: cases (N_CAS) + controls (N_CON), so long as both columns are present.</li> <li>• "ldsc": N will be computed as effective sample size: <math>N_{eff} = (N_{CAS} + N_{CON}) * (N_{CAS} / (N_{CAS} + N_{CON})) / \text{mean}((N_{CAS} / (N_{CAS} + N_{CON})) * (N_{CAS} + N_{CON}))</math></li> <li>• "giant": N will be computed as effective sample size: <math>N_{eff} = 2 / (1/N_{CAS} + 1/N_{CON})</math>.</li> <li>• "metal": N will be computed as effective sample size: <math>N_{eff} = 4 / (1/N_{CAS} + 1/N_{CON})</math>.</li> </ul>

standardise_headers	Standardise headers first.
force_new	If "Neff" (or "N") already exists in sumstats_dt, replace it with the recomputed version.
return_list	Return the sumstats_dt within a named list (default: TRUE).

**Value**

```
list("sumstats_dt"=sumstats_dt)
```

**Examples**

```
sumstats_dt <- MungeSumstats::formatted_example()
sumstats_dt2 <- MungeSumstats::compute_nsize(sumstats_dt=sumstats_dt,
                                             compute_n=10000)
```

---

compute\_sample\_size    *Compute (effective) sample size*

---

**Description**

Computes sample sum (as new column "N") or effective sample size (ESS) (as new column "Neff"). Computing ESS is important as it takes into account the proportion of cases to controls (i.e. class imbalance) so as not to overestimate your statistical power.

**Usage**

```
compute_sample_size(
  sumstats_dt,
  method = c("ldsc", "giant", "metal", "sum"),
  force_new = FALSE,
  append_method_name = FALSE
)
```

**Arguments**

sumstats_dt	Summary statistics data.table.
method	Method for computing (effective) sample size. <ul style="list-style-type: none"> <li>"ldsc" :  <math display="block">Neff = (N_{CAS} + N_{CON}) * (N_{CAS} / (N_{CAS} + N_{CON})) / \text{mean}((N_{CAS} / (N_{CAS} + N_{CON}))[(N_{CAS} + N_{CON}) == \max(N_{CAS} + N_{CON})])</math> <a href="#">bulik/ldsc GitHub Issue</a> <a href="#">bulik/ldsc GitHub code</a> </li> <li>"giant" :  <math display="block">Neff = 2 / (1/N_{CAS} + 1/N_{CON})</math> <a href="#">Winkler et al. 2014, Nature</a> </li> </ul>

- "metal" :  

$$N_{eff} = 4 / (1/N_{CAS} + 1/N_{CON})$$
[Willer et al. 2010, Bioinformatics](#)
  - "sum" :  

$$N = N_{CAS} + N_{CON}$$
 Simple summation of cases and controls that does not account for class imbalance.
  - "<integer>" :  

$$N = \text{<integer>}$$
 If method is a positive integer, it will be used as N for every row.
- force\_new      If "Neff" (or "N") already exists in sumstats\_dt, replace it with the recomputed version.
- append\_method\_name      should Neff column have an indicator to explain the method that makes it., Default is FALSE unless multiple methods are passed

### Details

There are many different formulas for calculating ESS, but LDSC is probably the best method available here, as it doesn't assume that the proportion of controls:cases is 2:1 (as in GIANT) or 4:1 (as in METAL).

### Value

A data.table with a new column "Neff" or "N"

---

compute\_sample\_size\_n *Add user supplied sample size*

---

### Description

Add user supplied sample size

### Usage

```
compute_sample_size_n(sumstats_dt, method, force_new = FALSE)
```

### Arguments

- sumstats\_dt      Summary statistics data.table.
- method            Method for computing (effective) sample size.
- "ldsc" :  

$$N_{eff} = (N_{CAS} + N_{CON}) * (N_{CAS} / (N_{CAS} + N_{CON})) / \text{mean}((N_{CAS} / (N_{CAS} + N_{CON}))[(N_{CAS} + N_{CON}) == \text{max}(N_{CAS} + N_{CON})])$$
[bulik/ldsc GitHub Issue](#) [bulik/ldsc GitHub code](#)



- "giant" :  
 $N_{eff} = 2/(1/N_{CAS} + 1/N_{CON})$   
[Winkler et al. 2014, Nature](#)
- "metal" :  
 $N_{eff} = 4/(1/N_{CAS} + 1/N_{CON})$   
[Willer et al. 2010, Bioinformatics](#)
- "sum" :  
 $N = N_{CAS} + N_{CON}$   
 Simple summation of cases and controls that does not account for class imbalance.
- "<integer>" :  
 $N = \text{integer}$   
 If method is a positive integer, it will be used as N for every row.

force\_new      If "Neff" (or "N") already exists in sumstats\_dt, replace it with the recomputed version.

### Value

No return

---

compute\_sample\_size\_neff  
*Compute Neff/N*

---

### Description

Compute Neff/N

### Usage

```
compute_sample_size_neff(
  sumstats_dt,
  method,
  force_new = FALSE,
  append_method_name = FALSE
)
```

### Arguments

sumstats\_dt      Summary statistics data.table.

method            Method for computing (effective) sample size.

- "ldsc" :  
 $N_{eff} = (N_{CAS} + N_{CON}) * (N_{CAS} / (N_{CAS} + N_{CON})) / \text{mean}((N_{CAS} / (N_{CAS} + N_{CON}))[(N_{CAS} + N_{CON}) == \text{max}(N_{CAS} + N_{CON})])$   
[bulik/ldsc GitHub Issue](#) [bulik/ldsc GitHub code](#)

- "giant" :  
 $N_{eff} = 2 / (1/N_{CAS} + 1/N_{CON})$   
Winkler et al. 2014, Nature
  - "metal" :  
 $N_{eff} = 4 / (1/N_{CAS} + 1/N_{CON})$   
Willer et al. 2010, Bioinformatics
  - "sum" :  
 $N = N_{CAS} + N_{CON}$   
Simple summation of cases and controls that does not account for class imbalance.
  - "<integer>" :  
 $N = \text{integer}$   
If method is a positive integer, it will be used as N for every row.
- force\_new      If "Neff" (or "N") already exists in sumstats\_dt, replace it with the recomputed version.
- append\_method\_name      should Neff column have an indicator to explain the method that makes it., Default is FALSE unless multiple methods are passed

**Value**

No return

---

convert_sumstats	<i>Convert summary statistics to desired object type</i>
------------------	--

---

**Description**

Convert summary statistics to desired object type

**Usage**

```
convert_sumstats(
  sumstats_dt,
  return_format = c("data.table", "vranges", "granges")
)
```

**Arguments**

return\_format      Object type to convert to; "data.table", "GenomicRanges" or "VRanges"(default is "data.table").

**Value**

Summary statistics in the converted format

---

DF_to_dt	<i>DataFrame to data.table</i>
----------	--------------------------------

---

**Description**

Efficiently convert [DataFrame](#) to [data.table](#).

**Usage**

```
DF_to_dt(DF)
```

**Arguments**

DF [DataFrame](#) object.

**Value**

VCF data in [data.table](#) format.

**Source**

[Solution from Bioc forum](#)

---

downloader	<i>downloader wrapper</i>
------------	---------------------------

---

**Description**

R wrapper for [axel](#) (multi-threaded) and [download.file](#) (single-threaded) download functions.

**Usage**

```
downloader(  
  input_url,  
  output_path,  
  download_method = "axel",  
  background = FALSE,  
  force_overwrite = FALSE,  
  quiet = TRUE,  
  show_progress = TRUE,  
  continue = TRUE,  
  nThread = 1,  
  alternate = TRUE,  
  check_certificates = TRUE,  
  timeout = 10 * 60  
)
```

**Arguments**

input_url	input_url.
output_path	output_path.
download_method	"axel" (multi-threaded) or "download.file" (single-threaded) .
background	Run in background
force_overwrite	Overwrite existing file.
quiet	Run quietly.
show_progress	show_progress.
continue	continue.
nThread	Number of threads to parallelize over.
alternate	alternate,
check_certificates	check_certificates
timeout	How many seconds before giving up on download. Passed to download.file. Default: 10*60 (10min).

**Value**

Local path to downloaded file.

**Source**

**Suggestion to avoid 'proc\$get\_built\_file() : Build process failed'**

**See Also**

Other downloaders: [axel\(\)](#)

---

download\_vcf

*Download VCF file and its index file from Open GWAS*

---

**Description**

Ideally, we would use [gwasvcf](#) instead but it hasn't been made available on CRAN or Bioconductor yet, so we can't include it as a dep.

**Usage**

```
download_vcf(
  vcf_url,
  vcf_dir = tempdir(),
  vcf_download = TRUE,
  download_method = "download.file",
  force_new = FALSE,
  quiet = FALSE,
  timeout = 10 * 60,
  nThread = 1
)
```

**Arguments**

vcf_url	Remote URL to VCF file.
vcf_dir	Where to download the original VCF from Open GWAS. <i>WARNING:</i> This is set to tempdir() by default. This means the raw (pre-formatted) VCFs be deleted upon ending the R session. Change this to keep the raw VCF file on disk (e.g. vcf_dir="./raw_vcf").
vcf_download	Download the original VCF from Open GWAS.
download_method	"axel" (multi-threaded) or "download.file" (single-threaded) .
force_new	Overwrite a previously downloaded VCF with the same path name.
quiet	Run quietly.
timeout	How many seconds before giving up on download. Passed to download.file. Default: 10*60 (10min).
nThread	Number of threads to parallelize over.

**Value**

List containing the paths to the downloaded VCF and its index file.

**Examples**

```
#only run the examples if user has internet access:
if(try(is.character(getURL("www.google.com")))==TRUE){
  vcf_url <- "https://gwas.mrcieu.ac.uk/files/ieu-a-298/ieu-a-298.vcf.gz"
  out_paths <- download_vcf(vcf_url = vcf_url)
}
```

---

drop\_duplicate\_cols    *Drop duplicate columns*

---

**Description**

Drop columns with identical names (if any exist) within a data.table.

**Usage**

```
drop_duplicate_cols(dt)
```

**Arguments**

dt                    data.table

**Value**

Null output

---

drop\_duplicate\_rows    *Drop duplicate rows*

---

**Description**

Drop rows with duplicate values across all columns.

**Usage**

```
drop_duplicate_rows(dt, verbose = TRUE)
```

**Arguments**

dt                    data.table  
verbose                Print messages.

**Value**

Filtered dt.

---

 find\_sumstats

*Search Open GWAS for datasets matching criteria*


---

## Description

For each argument, searches for any datasets matching a case-insensitive substring search in the respective metadata column. Users can supply a single character string or a list/vector of character strings.

## Usage

```
find_sumstats(
  ids = NULL,
  traits = NULL,
  years = NULL,
  consortia = NULL,
  authors = NULL,
  populations = NULL,
  categories = NULL,
  subcategories = NULL,
  builds = NULL,
  pmids = NULL,
  min_sample_size = NULL,
  min_ncase = NULL,
  min_ncontrol = NULL,
  min_nsnp = NULL,
  include_NAs = FALSE,
  access_token = check_access_token()
)
```

## Arguments

ids	List of Open GWAS study IDs (e.g. c("prot-a-664", "ieu-b-4760")).
traits	List of traits (e.g. c("parkinson", "Alzheimer")).
years	List of years (e.g. seq(2015,2021) or c(2010, 2012, 2021)).
consortia	List of consortia (e.g. c("MRC-IEU", "Neale Lab")).
authors	List of authors (e.g. c("Elsworth", "Kunkle", "Neale")).
populations	List of populations (e.g. c("European", "Asian")).
categories	List of categories (e.g. c("Binary", "Continuous", "Disease", "Risk factor")).
subcategories	List of categories (e.g. c("neurological", "Immune", "cardio")).
builds	List of genome builds (e.g. c("hg19", "grch37")).
pmids	List of PubMed ID (exact matches only) (e.g. c(29875488, 30305740, 28240269)).
min_sample_size	Minimum total number of study participants (e.g. 5000).

min_ncase	Minimum number of case participants (e.g. 1000).
min_ncontrol	Minimum number of control participants (e.g. 1000).
min_nsnp	Minimum number of SNPs (e.g. 200000).
include_NAs	Include datasets with missing metadata for size criteria (i.e. min_sample_size, min_ncase, or min_ncontrol).
access_token	Google OAuth2 access token. Used to authenticate level of access to data

### Details

By default, returns metadata for all studies currently in Open GWAS database.

### Value

(Filtered) GWAS metadata table.

### Examples

```
# Only run the examples if user has internet access:
if(try(is.character(getURL("www.google.com"))==TRUE)){
### By ID
metagwas <- find_sumstats(ids = c(
  "ieu-b-4760",
  "prot-a-1725",
  "prot-a-664"
))
### By ID and sample size
metagwas <- find_sumstats(
  ids = c("ieu-b-4760", "prot-a-1725", "prot-a-664"),
  min_sample_size = 5000
)
### By criteria
metagwas <- find_sumstats(
  traits = c("alzheimer", "parkinson"),
  years = seq(2015, 2021)
)
}
```

---

formatted\_example      *Formatted example*

---

### Description

Returns an example of summary stats that have had their column names already standardised with [standardise\\_header](#).



**Usage**

```
formatted_example(
  path = system.file("extdata", "eduAttainOkbay.txt", package = "MungeSumstats"),
  formatted = TRUE,
  sorted = TRUE
)
```

**Arguments**

path	Path to raw example file. Default to built-in dataset.
formatted	Whether the column names should be formatted (default:TRUE).
sorted	Whether the rows should be sorted by genomic coordinates (default:TRUE).

**Value**

sumstats\_dt

**Examples**

```
sumstats_dt <- MungeSumstats::formatted_example()
```

---

format_sumstats	<i>Check that summary statistics from GWAS are in a homogeneous format</i>
-----------------	--

---

**Description**

Check that summary statistics from GWAS are in a homogeneous format

**Usage**

```
format_sumstats(
  path,
  ref_genome = NULL,
  convert_ref_genome = NULL,
  chain_source = "ensembl",
  local_chain = NULL,
  convert_small_p = TRUE,
  convert_large_p = TRUE,
  convert_neg_p = TRUE,
  compute_z = FALSE,
  force_new_z = FALSE,
  compute_n = 0L,
  convert_n_int = TRUE,
  impute_beta = FALSE,
  es_is_beta = TRUE,
  impute_se = FALSE,
```

```
analysis_trait = NULL,
ignore_multi_trait = FALSE,
INFO_filter = 0.9,
FRQ_filter = 0,
pos_se = TRUE,
effect_columns_nonzero = FALSE,
N_std = 5,
N_dropNA = TRUE,
chr_style = "Ensembl",
rmv_chr = c("X", "Y", "MT"),
on_ref_genome = TRUE,
infer_eff_direction = TRUE,
strand_ambig_filter = FALSE,
allele_flip_check = TRUE,
allele_flip_drop = TRUE,
allele_flip_z = TRUE,
allele_flip_frq = TRUE,
bi_allelic_filter = TRUE,
flip_frq_as_biallelic = FALSE,
snp_ids_are_rs_ids = TRUE,
remove_multi_rs_snp = FALSE,
frq_is_maf = TRUE,
indels = TRUE,
drop_indels = FALSE,
drop_na_cols = c("SNP", "CHR", "BP", "A1", "A2", "FRQ", "BETA", "Z", "OR", "LOG_ODDS",
  "SIGNED_SUMSTAT", "SE", "P", "N"),
dbSNP = 155,
check_dups = TRUE,
sort_coordinates = TRUE,
nThread = 1,
save_path = tempfile(fileext = ".tsv.gz"),
write_vcf = FALSE,
tabix_index = FALSE,
return_data = FALSE,
return_format = "data.table",
ldsc_format = FALSE,
save_format = NULL,
log_folder_ind = FALSE,
log_mungesumstats_msgs = FALSE,
log_folder = tempdir(),
imputation_ind = FALSE,
force_new = FALSE,
mapping_file = sumstatsColHeaders,
rmv_chrPrefix = NULL
)
```

**Arguments**

path	Filepath for the summary statistics file to be formatted. A dataframe or datatable of the summary statistics file can also be passed directly to MungeSumstats using the path parameter.
ref_genome	name of the reference genome used for the GWAS ("GRCh37" or "GRCh38"). Argument is case-insensitive. Default is NULL which infers the reference genome from the data.
convert_ref_genome	name of the reference genome to convert to ("GRCh37" or "GRCh38"). This will only occur if the current genome build does not match. Default is not to convert the genome build (NULL).
chain_source	source of the chain file to use in liftover, if converting genome build ("ucsc" or "ensembl"). Note that the UCSC chain files require a license for commercial use. The Ensembl chain is used by default ("ensembl").
local_chain	Path to local chain file to use instead of downloading. Default of NULL i.e. no local file to use. NOTE if passing a local chain file make sure to specify the path to convert from and to the correct build like GRCh37 to GRCh38. We can not sense check this for local files. The chain file can be submitted as a gz file (as downloaded from source) or unzipped.
convert_small_p	Binary, should non-negative p-values $\leq 5e-324$ be converted to 0? Small p-values pass the R limit and can cause errors with LDSC/MAGMA and should be converted. Default is TRUE.
convert_large_p	Binary, should p-values $>1$ be converted to 1? P-values $>1$ should not be possible and can cause errors with LDSC/MAGMA and should be converted. Default is TRUE.
convert_neg_p	Binary, should p-values $<0$ be converted to 0? Negative p-values should not be possible and can cause errors with LDSC/MAGMA and should be converted. Default is TRUE.
compute_z	Whether to compute Z-score column. Default is FALSE. This can be computed from Beta and SE with $(\text{Beta}/\text{SE})$ or $P(Z:=\text{sign}(\text{BETA})\sqrt{\text{stats::qchisq}(P,1,\text{lower}=\text{FALSE})})$ . <b>Note</b> that imputing the Z-score from P for every SNP will not be perfectly correct and may result in a loss of power. This should only be done as a last resort. Use 'BETA' to impute by BETA/SE and 'P' to impute by SNP p-value.
force_new_z	When a "Z" column already exists, it will be used by default. To override and compute a new Z-score column from P set <code>force_new_z=TRUE</code> .
compute_n	Whether to impute N. Default of 0 won't impute, any other integer will be imputed as the N (sample size) for every SNP in the dataset. <b>Note</b> that imputing the sample size for every SNP is not correct and should only be done as a last resort. N can also be inputted with "ldsc", "sum", "giant" or "metal" by passing one of these for this field or a vector of multiple. Sum and an integer value creates an N column in the output whereas giant, metal or ldsc create an Neff or effective sample size. If multiples are passed, the formula used to derive it will be indicated.

convert_n_int	Binary, if N (the number of samples) is not an integer, should this be rounded? Default is TRUE.
impute_beta	Binary, whether BETA should be imputed using other effect data if it isn't present in the sumstats. Note that this imputation is an approximation (for Z & SE approach) so could have an effect on downstream analysis. Use with caution. The different methods MungeSumstats will try and impute beta (in this order or priority) are: 1. log(OR) 2. Z x SE Default value is FALSE.
es_is_beta	Binary, whether to map ES to BETA. We take BETA to be any BETA-like value (including Effect Size). If this is not the case for your sumstats, change this to FALSE. Default is TRUE.
impute_se	Binary, whether the standard error should be imputed using other effect data if it isn't present in the sumstats. Note that this imputation is an approximation so could have an effect on downstream analysis. Use with caution. The different methods MungeSumstats will try and impute se (in this order or priority) are: 1. BETA / Z 2. abs(BETA/ qnorm(P/2)) Default is FALSE.
analysis_trait	If multiple traits were studied, name of the trait for analysis from the GWAS. Default is NULL.
ignore_multi_trait	If you have multiple traits (p-values) in the study but you want to ignore these and instead use a standard named p-value, set to TRUE. By default is FALSE which will check for multi-traits.
INFO_filter	numeric The minimum value permissible of the imputation information score (if present in sumstats file). Default 0.9.
FRQ_filter	numeric The minimum value permissible of the frequency(FRQ) of the SNP (i.e. Allele Frequency (AF)) (if present in sumstats file). By default no filtering is done, i.e. value of 0.
pos_se	Binary Should the standard Error (SE) column be checked to ensure it is greater than 0? Those that are, are removed (if present in sumstats file). Default TRUE.
effect_columns_nonzero	Binary should the effect columns in the data BETA,OR (odds ratio),LOG_ODDS,SIGNED_SUMSTAT be checked to ensure no SNP=0. Those that do are removed(if present in sumstats file). Default FALSE.
N_std	numeric The number of standard deviations above the mean a SNP's N is needed to be removed. Default is 5.
N_dropNA	Drop rows where N is missing.Default is TRUE.
chr_style	Chromosome naming style to use in the formatted summary statistics file ("NCBI", "UCSC", "dbSNP", or "Ensembl"). The NCBI and Ensembl styles both code chromosomes as 1-22, X, Y, MT; the UCSC style is chr1-chr22, chrX, chrY, chrM; and the dbSNP style is ch1-ch22, chX, chY, chMT. Default is Ensembl.
rmv_chr	Chromosomes to exclude from the formatted summary statistics file. Use NULL if no filtering is necessary. Default is c("X", "Y", "MT") which removes all non-autosomal SNPs.
on_ref_genome	Binary Should a check take place that all SNPs are on the reference genome by SNP ID. Default is TRUE.

infer_eff_direction	Binary Should a check take place to ensure the alleles match the effect direction? Default is TRUE.
strand_ambig_filter	Binary Should SNPs with strand-ambiguous alleles be removed. Default is FALSE.
allele_flip_check	Binary Should the allele columns be checked against reference genome to infer if flipping is necessary. Default is TRUE.
allele_flip_drop	Binary Should the SNPs for which neither their A1 or A2 base pair values match a reference genome be dropped. Default is TRUE.
allele_flip_z	Binary should the Z-score be flipped along with effect and FRQ columns like Beta? It is assumed to be calculated off the effect size not the P-value and so will be flipped i.e. default TRUE.
allele_flip_frq	Binary should the frequency (FRQ) column be flipped along with effect and z-score columns like Beta? Default TRUE.
bi_allelic_filter	Binary Should non-biallelic SNPs be removed. Default is TRUE.
flip_frq_as_biallelic	Binary Should non-bi-allelic SNPs frequency values be flipped as 1-p despite there being other alternative alleles? Default is FALSE but if set to TRUE, this allows non-bi-allelic SNPs to be kept despite needing flipping.
snp_ids_are_rs_ids	Binary Should the supplied SNP ID's be assumed to be RSIDs. If not, imputation using the SNP ID for other columns like base-pair position or chromosome will not be possible. If set to FALSE, the SNP RS ID will be imputed from the reference genome if possible. Default is TRUE.
remove_multi_rs_snp	Binary Sometimes summary statistics can have multiple RSIDs on one row (i.e. related to one SNP), for example "rs5772025_rs397784053". This can cause an error so by default, the first RS ID will be kept and the rest removed e.g."rs5772025". If you want to just remove these SNPs entirely, set it to TRUE. Default is FALSE.
frq_is_maf	Conventionally the FRQ column is intended to show the minor/effect allele frequency (MAF) but sometimes the major allele frequency can be inferred as the FRQ column. This logical variable indicates that the FRQ column should be renamed to MAJOR_ALLELE_FRQ if the frequency values appear to relate to the major allele i.e. >0.5. By default this mapping won't occur i.e. is TRUE.
indels	Binary does your Sumstats file contain Indels? These don't exist in our reference file so they will be excluded from checks if this value is TRUE. Default is TRUE.
drop_indels	Binary, should any indels found in the sumstats be dropped? These can not be checked against a reference dataset and will have the same RS ID and position as SNPs which can affect downstream analysis. Default is False.

drop_na_cols	A character vector of column names to be checked for missing values. Rows with missing values in any of these columns (if present in the dataset) will be dropped. If NULL, all columns will be checked for missing values. Default columns are SNP, chromosome, position, allele 1, allele2, effect columns (frequency, beta, Z-score, standard error, log odds, signed sumstats, odds ratio), p value and N columns.
dbSNP	version of dbSNP to be used for imputation (144 or 155).
check_dups	whether to check for duplicates - if formatting QTL datasets this should be set to FALSE otherwise keep as TRUE. Default is TRUE.
sort_coordinates	Whether to sort by coordinates of resulting sumstats
nThread	Number of threads to use for parallel processes.
save_path	File path to save formatted data. Defaults to tempfile(fileext=".tsv.gz").
write_vcf	Whether to write as VCF (TRUE) or tabular file (FALSE).
tabix_index	Index the formatted summary statistics with <b>tabix</b> for fast querying.
return_data	Return data.table, GRanges or VRanges directly to user. Otherwise, return the path to the save data. Default is FALSE.
return_format	If return_data is TRUE. Object type to be returned ("data.table", "vranges", "granges").
ldsc_format	DEPRECATED, do not use. Use save_format="LDSC" instead.
save_format	Output format of sumstats. Options are NULL - standardised output format from MungeSumstats, LDSC - output format compatible with LDSC and openGWAS - output compatible with openGWAS VCFs. Default is NULL. <b>NOTE</b> - If LDSC format is used, the naming convention of A1 as the reference (genome build) allele and A2 as the effect allele will be reversed to match LDSC (A1 will now be the effect allele). See more info on this <a href="#">here</a> . Note that any effect columns (e.g. Z) will be in relation to A1 now instead of A2.
log_folder_ind	Binary Should log files be stored containing all filtered out SNPs (separate file per filter). The data is outputted in the same format specified for the resulting sumstats file. The only exception to this rule is if output is vcf, then log file saved as .tsv.gz. Default is FALSE.
log_mungesumstats_msgs	Binary Should a log be stored containing all messages and errors printed by MungeSumstats in a run. Default is FALSE
log_folder	Filepath to the directory for the log files and the log of MungeSumstats messages to be stored. Default is a temporary directory. Note the name of the log files (log messages and log outputs) are now the same as the name of the file specified in the save path parameter with the extension '_log_msg.txt' and '_log_output.txt' respectively.
imputation_ind	Binary Should a column be added for each imputation step to show what SNPs have imputed values for differing fields. This includes a field denoting SNP allele flipping (flipped). On the flipped value, this denoted whether the alleles were switched based on MungeSumstats initial choice of A1, A2 from the input column headers and thus may not align with what the creator intended. <b>Note</b> these columns will be in the formatted summary statistics returned. Default is FALSE.

force_new	If a formatted file of the same names as save_path exists, formatting will be skipped and this file will be imported instead (default). Set force_new=TRUE to override this.
mapping_file	MungeSumstats has a pre-defined column-name mapping file which should cover the most common column headers and their interpretations. However, if a column header that is in your file is missing or the mapping we give is incorrect you can supply your own mapping file. Must be a 2 column dataframe with column names "Uncorrected" and "Corrected". See data(sumstatsColHeaders) for default mapping and necessary format.
rmv_chrPrefix	Is now deprecated, do. not use. Use chr_style instead - chr_style = 'Ensembl' will give the same result as rmv_chrPrefix=TRUE used to give.

### Value

The address for the modified sumstats file or the actual data dependent on user choice. Also, if log files wanted by the user, the return in both above instances are a list.

### Examples

```
# Pass path to Educational Attainment Okbay sumstat file to a temp directory

eduAttainOkbayPth <- system.file("extdata", "eduAttainOkbay.txt",
  package = "MungeSumstats"
)

## Call uses reference genome as default with more than 2GB of memory,
## which is more than what 32-bit Windows can handle so remove certain checks
## Using dbSNP = 144 for speed as it's smaller but you should use 155 unless
## you know what you are doing and need 144

is_32bit_windows <-
  .Platform$OS.type == "windows" && .Platform$r_arch == "i386"
if (!is_32bit_windows) {
  reformatted <- format_sumstats(
    path = eduAttainOkbayPth,
    ref_genome = "GRCh37",
    dbSNP = 144
  )
} else {
  reformatted <- format_sumstats(
    path = eduAttainOkbayPth,
    ref_genome = "GRCh37",
    on_ref_genome = FALSE,
    strand_ambig_filter = FALSE,
    bi_allelic_filter = FALSE,
    allele_flip_check = FALSE,
    dbSNP=144
  )
}
# returned location has the updated summary statistics file
```

---

get_access_token	<i>Get access token for OAuth2 access to MR Base</i>
------------------	--

---

**Description**

Get access token for OAuth2 access to MR Base

**Usage**

```
get_access_token()
```

**Value**

access token string

---

get_chain_file	<i>Download chain file for liftover</i>
----------------	---

---

**Description**

Download chain file for liftover

**Usage**

```
get_chain_file(
  from = c("hg38", "hg19"),
  to = c("hg19", "hg38"),
  chain_source = c("ucsc", "ensembl"),
  save_dir = tempdir(),
  verbose = TRUE
)
```

**Arguments**

from	genome build converted from ("hg38", "hg19")
to	genome build converted to ("hg19", "hg38")
chain_source	chain file source used ("ucsc" as default, or "ensembl")
save_dir	where is the chain file saved? Default is a temp directory
verbose	extra messages printed? Default is TRUE

**Value**

loaded chain file for liftover



**Source**

[UCSC chain files](#)

[Ensembl chain files](#)

---

```
get_eff_frq_allele_combns
```

*Get combinations of uncorrected allele and effect (and frq) columns*

---

**Description**

Get combinations of uncorrected allele and effect (and frq) columns

**Usage**

```
get_eff_frq_allele_combns(
  mapping_file = sumstatsColHeaders,
  eff_frq_cols = c("BETA", "OR", "LOG_ODDS", "SIGNED_SUMSTAT", "Z", "FRQ")
)
```

**Arguments**

mapping_file	MungeSumstats has a pre-defined column-name mapping file which should cover the most common column headers and their interpretations. However, if a column header that is in your file is missing of the mapping we give is incorrect you can supply your own mapping file. Must be a 2 column dataframe with column names "Uncorrected" and "Corrected". See <code>data(sumstatsColHeaders)</code> for default mapping and necessary format.
eff_frq_cols	Corrected effect or frequency column names found in a sumstats. Default of BETA, OR, LOG_ODDS, SIGNED_SUMSTAT, Z and FRQ.

**Value**

datatable containing uncorrected and corrected combinations

---

get_genome_build	<i>Infers the genome build of the summary statistics file (GRCh37 or GRCh38) from the data. Uses SNP (RSID) &amp; CHR &amp; BP to get genome build.</i>
------------------	---

---

**Description**

Infers the genome build of the summary statistics file (GRCh37 or GRCh38) from the data. Uses SNP (RSID) & CHR & BP to get genome build.

**Usage**

```

get_genome_build(
  sumstats,
  nThread = 1,
  sampled_snps = 10000,
  standardise_headers = TRUE,
  mapping_file = sumstatsColHeaders,
  dbSNP = 155,
  header_only = FALSE,
  allele_match_ref = FALSE,
  ref_genome = NULL,
  chr_filt = NULL
)

```

**Arguments**

sumstats	data table/data frame obj of the summary statistics file for the GWAS ,or file path to summary statistics file.
nThread	Number of threads to use for parallel processes.
sampled_snps	Downsample the number of SNPs used when inferring genome build to save time.
standardise_headers	Run standardise_sumstats_column_headers_crossplatform.
mapping_file	<b>MungeSumstats</b> has a pre-defined column-name mapping file which should cover the most common column headers and their interpretations. However, if a column header that is in your file is missing of the mapping we give is incorrect you can supply your own mapping file. Must be a 2 column dataframe with column names "Uncorrected" and "Corrected". See data(sumstatsColHeaders) for default mapping and necessary format.
dbSNP	version of dbSNP to be used (144 or 155). Default is 155.
header_only	Instead of reading in the entire sumstats file, only read in the first N rows where N=sampled_snps. This should help speed up cases where you have to read in sumstats from disk each time.
allele_match_ref	Instead of returning the genome_build this will return the propotion of matches to each genome build for each allele (A1,A2).
ref_genome	name of the reference genome used for the GWAS ("GRCh37" or "GRCh38"). Argument is case-insensitive. Default is NULL which infers the reference genome from the data.
chr_filt	Internal for testing - filter reference genomes and sumstats to specific chromosomes for testing. Pass a list of chroms in format: c("1","2"). Default is NULL i.e. no filtering

**Value**

ref\_genome the genome build of the data

---

get\_genome\_builds      *Infer genome builds*

---

### Description

Infers the genome build of summary statistics files (GRCh37 or GRCh38) from the data. Uses SNP (RSID) & CHR & BP to get genome build.

### Usage

```
get_genome_builds(
  sumstats_list,
  header_only = TRUE,
  sampled_snps = 10000,
  names_from_paths = FALSE,
  dbSNP = 155,
  nThread = 1,
  chr_filt = NULL
)
```

### Arguments

sumstats_list	A named list of paths to summary statistics, or a named list of data.table objects.
header_only	Instead of reading in the entire sumstats file, only read in the first N rows where N=sampled_snps. This should help speed up cases where you have to read in sumstats from disk each time.
sampled_snps	Downsample the number of SNPs used when inferring genome build to save time.
names_from_paths	Infer the name of each item in sumstats_list from its respective file path. Only works if sumstats_list is a list of paths.
dbSNP	version of dbSNP to be used (144 or 155). Default is 155.
nThread	Number of threads to use for parallel processes.
chr_filt	Internal for testing - filter reference genomes and sumstats to specific chromosomes for testing. Pass a list of chroms in format: c("1","2"). Default is NULL i.e. no filtering

### Details

Iterative version of get\_genome\_build.

### Value

ref\_genome the genome build of the data

**Examples**

```

# Pass path to Educational Attainment Okbay sumstat file to a temp directory

eduAttainOkbayPth <- system.file("extdata", "eduAttainOkbay.txt",
  package = "MungeSumstats"
)
sumstats_list <- list(ss1 = eduAttainOkbayPth, ss2 = eduAttainOkbayPth)

## Call uses reference genome as default with more than 2GB of memory,
## which is more than what 32-bit Windows can handle so remove certain checks
is_32bit_windows <-
  .Platform$OS.type == "windows" && .Platform$r_arch == "i386"
if (!is_32bit_windows) {

  #multiple sumstats can be passed at once to get all their genome builds:
  #ref_genomes <- get_genome_builds(sumstats_list = sumstats_list)
  #just passing first here for speed
  sumstats_list_quick <- list(ss1 = eduAttainOkbayPth)
  ref_genomes <- get_genome_builds(sumstats_list = sumstats_list_quick,
    dbSNP=144)
}

```

---

get_query_content	<i>Parse out json response from httr object</i>
-------------------	---

---

**Description**

Parse out json response from httr object

**Usage**

```
get_query_content(response)
```

**Arguments**

response	Output from httr
----------	------------------

**Value**

Parsed json output from query, often in form of data frame. If status code is not successful then return the actual response.

---

`get_unique_name_log_file`

*Simple function to ensure the new entry name to a list doesn't have the same name as another entry*

---

**Description**

Simple function to ensure the new entry name to a list doesn't have the same name as another entry

**Usage**

```
get_unique_name_log_file(name, log_files)
```

**Arguments**

<code>name</code>	proposed name for the entry
<code>log_files</code>	list of log file locations

**Value**

a unique name (character)

---

`get_vcf_sample_ids`     *Get VCF sample ID(s)*

---

**Description**

Get VCF sample ID(s)

**Usage**

```
get_vcf_sample_ids(path)
```

**Arguments**

<code>path</code>	Filepath for the summary statistics file to be formatted. A dataframe or datatable of the summary statistics file can also be passed directly to MungeSumstats using the path parameter.
-------------------	--

**Value**

`sample_id`

---

granges_to_dt	<i>GenomicRanges to data.table</i>
---------------	------------------------------------

---

**Description**

Convert a [GRanges](#) into a [data.table](#).

**Usage**

```
granges_to_dt(gr)
```

**Arguments**

gr                    A [GRanges](#) object.

**Value**

A [data.table](#) object.

**Source**

Code adapted from [GenomicDistributions](#).

---

gwasinfo	<i>Get list of studies with available GWAS summary statistics through API</i>
----------	---

---

**Description**

Get list of studies with available GWAS summary statistics through API

**Usage**

```
gwasinfo(id = NULL, access_token = check_access_token())
```

**Arguments**

id                    List of MR-Base IDs to retrieve. If NULL (default) retrieves all available datasets

access\_token        Google OAuth2 access token. Used to authenticate level of access to data

**Value**

Dataframe of details for all available studies

---

hg19ToHg38

*UCSC Chain file hg19 to hg38*

---

**Description**

UCSC Chain file hg19 to hg38, .chain.gz file, downloaded from <https://hgdownload.cse.ucsc.edu/goldenpath/hg19/liftOver/> on 09/10/21

**Format**

gunzipped chain file

**Details**

UCSC Chain file hg19 to hg38, .chain.gz file, downloaded on 09/10/21 To be used as a back up if the download from UCSC fails.

**hg19ToHg38.over.chain.gz**

NA

**Source**

The chain file was downloaded from <https://hgdownload.cse.ucsc.edu/goldenpath/hg19/liftOver/> `utils::download.file('ftp://hgdownload.cse.ucsc.edu/goldenPath/hg19/liftOver/hg19ToHg38.over.chain.gz')`

---

hg38ToHg19

*UCSC Chain file hg38 to hg19*

---

**Description**

UCSC Chain file hg38 to hg19, .chain.gz file, downloaded from <https://hgdownload.cse.ucsc.edu/goldenpath/hg19/liftOver/> on 09/10/21

**Format**

gunzipped chain file

**Details**

UCSC Chain file hg38 to hg19, .chain.gz file, downloaded on 09/10/21 To be used as a back up if the download from UCSC fails.

**hg38ToHg19.over.chain.gz**

NA

**Source**

The chain file was downloaded from [https://hgdownload.cse.ucsc.edu/goldenpath/hg38/liftOver/Utils::download.file\('ftp://hgdownload.cse.ucsc.edu/goldenPath/hg38/liftOver/hg38ToHg19.over.chain.](https://hgdownload.cse.ucsc.edu/goldenpath/hg38/liftOver/Utils::download.file('ftp://hgdownload.cse.ucsc.edu/goldenPath/hg38/liftOver/hg38ToHg19.over.chain.)

---

 ieu-a-298

*Local ieu-a-298 file from IEU Open GWAS*


---

**Description**

Local ieu-a-298 file from IEU Open GWAS, downloaded on 09/10/21.

**Format**

gunzipped tsv file

**Details**

Local ieu-a-298 file from IEU Open GWAS, downloaded on 09/10/21. This is done in case the download in the package vignette fails.

**ieu-a-298.tsv.gz**

NA

**Source**

The file was downloaded with: `MungeSumstats::import_sumstats(ids = "ieu-a-298", ref_genome = "GRCH37")`

---

 import\_sumstats

*Import full genome-wide GWAS summary statistics from Open GWAS*


---

**Description**

Requires internet access to run.



**Usage**

```
import_sumstats(
  ids,
  vcf_dir = tempdir(),
  vcf_download = TRUE,
  save_dir = tempdir(),
  write_vcf = FALSE,
  download_method = "download.file",
  quiet = TRUE,
  force_new = FALSE,
  force_new_vcf = FALSE,
  nThread = 1,
  parallel_across_ids = FALSE,
  ...
)
```

**Arguments**

<code>ids</code>	List of Open GWAS study IDs (e.g. <code>c("prot-a-664", "ieu-b-4760")</code> ).
<code>vcf_dir</code>	Where to download the original VCF from Open GWAS. <i>WARNING:</i> This is set to <code>tempdir()</code> by default. This means the raw (pre-formatted) VCFs be deleted upon ending the R session. Change this to keep the raw VCF file on disk (e.g. <code>vcf_dir="./raw_vcf"</code> ).
<code>vcf_download</code>	Download the original VCF from Open GWAS.
<code>save_dir</code>	Directory to save formatted summary statistics in.
<code>write_vcf</code>	Whether to write as VCF (TRUE) or tabular file (FALSE).
<code>download_method</code>	"axel" (multi-threaded) or "download.file" (single-threaded) .
<code>quiet</code>	Run quietly.
<code>force_new</code>	If a formatted file of the same names as <code>save_path</code> exists, formatting will be skipped and this file will be imported instead (default). Set <code>force_new=TRUE</code> to override this.
<code>force_new_vcf</code>	Overwrite a previously downloaded VCF with the same path name.
<code>nThread</code>	Number of threads to use for parallel processes.
<code>parallel_across_ids</code>	If <code>parallel_across_ids=TRUE</code> and <code>nThread&gt;1</code> , then each ID in <code>ids</code> will be processed in parallel.
<code>...</code>	Arguments passed on to <a href="#">format_sumstats</a>
	<code>path</code> Filepath for the summary statistics file to be formatted. A dataframe or datatable of the summary statistics file can also be passed directly to <code>MungeSumstats</code> using the <code>path</code> parameter.
	<code>ref_genome</code> name of the reference genome used for the GWAS ("GRCh37" or "GRCh38"). Argument is case-insensitive. Default is <code>NULL</code> which infers the reference genome from the data.

`convert_ref_genome` name of the reference genome to convert to ("GRCh37" or "GRCh38"). This will only occur if the current genome build does not match. Default is not to convert the genome build (NULL).

`chain_source` source of the chain file to use in liftover, if converting genome build ("ucsc" or "ensembl"). Note that the UCSC chain files require a license for commercial use. The Ensembl chain is used by default ("ensembl").

`local_chain` Path to local chain file to use instead of downloading. Default of NULL i.e. no local file to use. NOTE if passing a local chain file make sure to specify the path to convert from and to the correct build like GRCh37 to GRCh38. We can not sense check this for local files. The chain file can be submitted as a gz file (as downloaded from source) or unzipped.

`convert_small_p` Binary, should non-negative p-values  $\leq 5e-324$  be converted to 0? Small p-values pass the R limit and can cause errors with LDSC/MAGMA and should be converted. Default is TRUE.

`convert_large_p` Binary, should p-values  $> 1$  be converted to 1? P-values  $> 1$  should not be possible and can cause errors with LDSC/MAGMA and should be converted. Default is TRUE.

`convert_neg_p` Binary, should p-values  $< 0$  be converted to 0? Negative p-values should not be possible and can cause errors with LDSC/MAGMA and should be converted. Default is TRUE.

`compute_z` Whether to compute Z-score column. Default is FALSE. This can be computed from Beta and SE with  $(\text{Beta}/\text{SE})$  or  $P(Z := \text{sign}(\text{BETA}) * \sqrt{\text{stats::qchisq}(P, 1, \text{lower} = \text{FALSE})})$ . **Note** that imputing the Z-score from P for every SNP will not be perfectly correct and may result in a loss of power. This should only be done as a last resort. Use 'BETA' to impute by BETA/SE and 'P' to impute by SNP p-value.

`force_new_z` When a "Z" column already exists, it will be used by default. To override and compute a new Z-score column from P set `force_new_z=TRUE`.

`compute_n` Whether to impute N. Default of 0 won't impute, any other integer will be imputed as the N (sample size) for every SNP in the dataset. **Note** that imputing the sample size for every SNP is not correct and should only be done as a last resort. N can also be inputted with "ldsc", "sum", "giant" or "metal" by passing one of these for this field or a vector of multiple. Sum and an integer value creates an N column in the output whereas giant, metal or ldsc create an Neff or effective sample size. If multiples are passed, the formula used to derive it will be indicated.

`convert_n_int` Binary, if N (the number of samples) is not an integer, should this be rounded? Default is TRUE.

`impute_beta` Binary, whether BETA should be imputed using other effect data if it isn't present in the sumstats. Note that this imputation is an approximation (for Z & SE approach) so could have an effect on downstream analysis. Use with caution. The different methods MungeSumstats will try and impute beta (in this order or priority) are:

1.  $\log(\text{OR})$
  2.  $Z \times \text{SE}$
- Default value is FALSE.

`es_is_beta` Binary, whether to map ES to BETA. We take BETA to be any BETA-like value (including Effect Size). If this is not the case for your

sumstats, change this to FALSE. Default is TRUE.

`impute_se` Binary, whether the standard error should be imputed using other effect data if it isn't present in the sumstats. Note that this imputation is an approximation so could have an effect on downstream analysis. Use with caution. The different methods MungeSumstats will try and impute se (in this order or priority) are:

1. BETA / Z
  2. abs(BETA/ qnorm(P/2))
- Default is FALSE.

`analysis_trait` If multiple traits were studied, name of the trait for analysis from the GWAS. Default is NULL.

`ignore_multi_trait` If you have multiple traits (p-values) in the study but you want to ignore these and instead use a standard named p-value, set to TRUE. By default is FALSE which will check for multi-traits.

`INFO_filter` numeric The minimum value permissible of the imputation information score (if present in sumstats file). Default 0.9.

`FRQ_filter` numeric The minimum value permissible of the frequency(FRQ) of the SNP (i.e. Allele Frequency (AF)) (if present in sumstats file). By default no filtering is done, i.e. value of 0.

`pos_se` Binary Should the standard Error (SE) column be checked to ensure it is greater than 0? Those that are, are removed (if present in sumstats file). Default TRUE.

`effect_columns_nonzero` Binary should the effect columns in the data BETA,OR (odds ratio),LOG\_ODDS,SIGNED\_SUMSTAT be checked to ensure no SNP=0. Those that do are removed(if present in sumstats file). Default FALSE.

`N_std` numeric The number of standard deviations above the mean a SNP's N is needed to be removed. Default is 5.

`N_dropNA` Drop rows where N is missing. Default is TRUE.

`chr_style` Chromosome naming style to use in the formatted summary statistics file ("NCBI", "UCSC", "dbSNP", or "Ensembl"). The NCBI and Ensembl styles both code chromosomes as 1-22, X, Y, MT; the UCSC style is chr1-chr22, chrX, chrY, chrM; and the dbSNP style is ch1-ch22, chX, chY, chMT. Default is Ensembl.

`rmv_chrPrefix` Is now deprecated, do not use. Use `chr_style` instead - `chr_style = 'Ensembl'` will give the same result as `rmv_chrPrefix=TRUE` used to give.

`rmv_chr` Chromosomes to exclude from the formatted summary statistics file. Use NULL if no filtering is necessary. Default is `c("X", "Y", "MT")` which removes all non-autosomal SNPs.

`on_ref_genome` Binary Should a check take place that all SNPs are on the reference genome by SNP ID. Default is TRUE.

`infer_eff_direction` Binary Should a check take place to ensure the alleles match the effect direction? Default is TRUE.

`strand_ambig_filter` Binary Should SNPs with strand-ambiguous alleles be removed. Default is FALSE.

`allele_flip_check` Binary Should the allele columns be checked against reference genome to infer if flipping is necessary. Default is TRUE.

`allele_flip_drop` Binary Should the SNPs for which neither their A1 or A2 base pair values match a reference genome be dropped. Default is TRUE.

`allele_flip_z` Binary should the Z-score be flipped along with effect and FRQ columns like Beta? It is assumed to be calculated off the effect size not the P-value and so will be flipped i.e. default TRUE.

`allele_flip_frq` Binary should the frequency (FRQ) column be flipped along with effect and z-score columns like Beta? Default TRUE.

`bi_allelic_filter` Binary Should non-biallelic SNPs be removed. Default is TRUE.

`flip_frq_as_biallelic` Binary Should non-bi-allelic SNPs frequency values be flipped as 1-p despite there being other alternative alleles? Default is FALSE but if set to TRUE, this allows non-bi-allelic SNPs to be kept despite needing flipping.

`snp_ids_are_rs_ids` Binary Should the supplied SNP ID's be assumed to be RSIDs. If not, imputation using the SNP ID for other columns like base-pair position or chromosome will not be possible. If set to FALSE, the SNP RS ID will be imputed from the reference genome if possible. Default is TRUE.

`remove_multi_rs_snp` Binary Sometimes summary statistics can have multiple RSIDs on one row (i.e. related to one SNP), for example "rs5772025\_rs397784053". This can cause an error so by default, the first RS ID will be kept and the rest removed e.g."rs5772025". If you want to just remove these SNPs entirely, set it to TRUE. Default is FALSE.

`frq_is_maf` Conventionally the FRQ column is intended to show the minor/effect allele frequency (MAF) but sometimes the major allele frequency can be inferred as the FRQ column. This logical variable indicates that the FRQ column should be renamed to MAJOR\_ALLELE\_FRQ if the frequency values appear to relate to the major allele i.e. >0.5. By default this mapping won't occur i.e. is TRUE.

`indels` Binary does your Sumstats file contain Indels? These don't exist in our reference file so they will be excluded from checks if this value is TRUE. Default is TRUE.

`drop_indels` Binary, should any indels found in the sumstats be dropped? These can not be checked against a reference dataset and will have the same RS ID and position as SNPs which can affect downstream analysis. Default is False.

`drop_na_cols` A character vector of column names to be checked for missing values. Rows with missing values in any of these columns (if present in the dataset) will be dropped. If NULL, all columns will be checked for missing values. Default columns are SNP, chromosome, position, allele 1, allele2, effect columns (frequency, beta, Z-score, standard error, log odds, signed sumstats, odds ratio), p value and N columns.

`dbSNP` version of dbSNP to be used for imputation (144 or 155).

`check_dups` whether to check for duplicates - if formatting QTL datasets this should be set to FALSE otherwise keep as TRUE. Default is TRUE.

`sort_coordinates` Whether to sort by coordinates of resulting sumstats

`save_path` File path to save formatted data. Defaults to `tempfile(fileext=".tsv.gz")`.

- `tabix_index` Index the formatted summary statistics with `tabix` for fast querying.
- `return_data` Return data.table, GRanges or VRanges directly to user. Otherwise, return the path to the save data. Default is FALSE.
- `return_format` If `return_data` is TRUE. Object type to be returned ("data.table", "vranges", "granges").
- `ldsc_format` DEPRECATED, do not use. Use `save_format="LDSC"` instead.
- `save_format` Output format of sumstats. Options are NULL - standardised output format from MungeSumstats, LDSC - output format compatible with LDSC and openGWAS - output compatible with openGWAS VCFs. Default is NULL. **NOTE** - If LDSC format is used, the naming convention of A1 as the reference (genome build) allele and A2 as the effect allele will be reversed to match LDSC (A1 will now be the effect allele). See more info on this [here](#). Note that any effect columns (e.g. Z) will be in relation to A1 now instead of A2.
- `log_folder_ind` Binary Should log files be stored containing all filtered out SNPs (separate file per filter). The data is outputted in the same format specified for the resulting sumstats file. The only exception to this rule is if output is vcf, then log file saved as .tsv.gz. Default is FALSE.
- `log_mungesumstats_msgs` Binary Should a log be stored containing all messages and errors printed by MungeSumstats in a run. Default is FALSE
- `log_folder` Filepath to the directory for the log files and the log of MungeSumstats messages to be stored. Default is a temporary directory. Note the name of the log files (log messages and log outputs) are now the same as the name of the file specified in the save path parameter with the extension '\_log\_msg.txt' and '\_log\_output.txt' respectively.
- `imputation_ind` Binary Should a column be added for each imputation step to show what SNPs have imputed values for differing fields. This includes a field denoting SNP allele flipping (flipped). On the flipped value, this denoted whether the alleles were switched based on MungeSumstats initial choice of A1, A2 from the input column headers and thus may not align with what the creator intended. **Note** these columns will be in the formatted summary statistics returned. Default is FALSE.
- `mapping_file` MungeSumstats has a pre-defined column-name mapping file which should cover the most common column headers and their interpretations. However, if a column header that is in your file is missing of the mapping we give is incorrect you can supply your own mapping file. Must be a 2 column dataframe with column names "Uncorrected" and "Corrected". See `data(sumstatsColHeaders)` for default mapping and necessary format.

## Value

Either a named list of data objects or paths, depending on the arguments passed to `format_sumstats`.

## Examples

```
#only run the examples if user has internet access:
if(try(is.character(getURL("www.google.com")))==TRUE){
### Search by criteria
```

```

metagwas <- find_sumstats(
  traits = c("parkinson", "alzheimer"),
  min_sample_size = 5000
)
### Only use a subset for testing purposes
ids <- (dplyr::arrange(metagwas, nsnp))$id

### Default usage
## You can supply \code{import_sumstats()}
## with a list of as many OpenGWAS IDs as you want,
## but we'll just give one to save time.

## Call uses reference genome as default with more than 2GB of memory,
## which is more than what 32-bit Windows can handle so remove certain checks
## commented out down to runtime
# datasets <- import_sumstats(ids = ids[1])
}

```

---

index\_tabular

*Tabix-index file: table*


---

## Description

Convert summary stats file to tabix format.

## Usage

```

index_tabular(
  path,
  chrom_col = "CHR",
  start_col = "BP",
  end_col = start_col,
  overwrite = TRUE,
  remove_tmp = TRUE,
  verbose = TRUE
)

```

## Arguments

path	Path to GWAS summary statistics file.
chrom_col	Name of the chromosome column in <code>sumstats_dt</code> (e.g. "CHR").
start_col	Name of the starting genomic position column in <code>sumstats_dt</code> (e.g. "POS", "start").
end_col	Name of the ending genomic position column in <code>sumstats_dt</code> (e.g. "POS", "end"). Can be the same as <code>start_col</code> when <code>sumstats_dt</code> only contains SNPs that span 1 base pair (bp) each.
overwrite	A logical(1) indicating whether <code>dest</code> should be over-written, if it already exists.
remove_tmp	Remove the temporary uncompressed version of the file ( <i>.tsv</i> ).
verbose	Print messages.

**Value**

Path to tabix-indexed tabular file

**Source**

Borrowed function from [echotabix](#).

**See Also**

Other tabix: [index\\_vcf\(\)](#)

**Examples**

```
sumstats_dt <- MungeSumstats::formatted_example()
path <- tempfile(fileext = ".tsv")
MungeSumstats::write_sumstats(sumstats_dt = sumstats_dt, save_path = path)
indexed_file <- MungeSumstats::index_tabular(path = path)
```

---

index\_vcf

*Tabix-index file: VCF*

---

**Description**

Convert summary stats file to tabix format

**Usage**

```
index_vcf(path, verbose = TRUE)
```

**Arguments**

path	Path to VCF.
verbose	Print messages.

**Value**

Path to tabix-indexed tabular file

**Source**

Borrowed function from [echotabix](#).

**See Also**

Other tabix: [index\\_tabular\(\)](#)

**Examples**

```

eduAttainOkbayPth <- system.file("extdata", "eduAttainOkbay.txt",
                                package = "MungeSumstats")
sumstats_dt <- data.table::fread(eduAttainOkbayPth, nThread = 1)
sumstats_dt <-
MungeSumstats::standardise_sumstats_column_headers_crossplatform(
  sumstats_dt = sumstats_dt)$sumstats_dt
sumstats_dt <- MungeSumstats::sort_coords(sumstats_dt = sumstats_dt)
path <- tempfile(fileext = ".tsv")
MungeSumstats::write_sumstats(sumstats_dt = sumstats_dt, save_path = path)

indexed_file <- MungeSumstats::index_tabular(path = path)

```

---

infer\_effect\_column    *Infer if effect relates to a1 or A2 if ambiguously named*

---

**Description**

Three checks are made to infer which allele the effect/frequency information relates to if they are ambiguous (named A1 and A2 or equivalent):

1. Check if ambiguous naming conventions are used (i.e. allele 1 and 2 or equivalent). If not exit, otherwise continue to next checks. This can be checked by using the mapping file and splitting A1/A2 mappings by those that contain 1 or 2 (ambiguous) or doesn't contain 1 or 2 e.g. effect, tested (unambiguous so fine for MSS to handle as is).
2. Look for effect column/frequency column where the A1/A2 explicitly mentioned, if found then we know the direction and should update A1/A2 naming so A2 is the effect column. We can look for such columns by getting every combination of A1/A2 naming and effect/frq naming.
3. If note found in 2, a final check should be against the reference genome, whichever of A1 and A2 has more of a match with the reference genome should be taken as **not** the effect allele. There is an assumption in this but is still better than guessing the ambiguous allele naming.

**Usage**

```

infer_effect_column(
  sumstats_dt,
  dbSNP = 155,
  sampled_snps = 10000,
  mapping_file = sumstatsColHeaders,
  nThread = nThread,
  ref_genome = NULL,
  on_ref_genome = TRUE,
  infer_eff_direction = TRUE,
  return_list = TRUE
)

```



**Arguments**

sumstats_dt	data table obj of the summary statistics file for the GWAS.
dbSNP	version of dbSNP to be used for imputation (144 or 155).
sampled_snps	Downsample the number of SNPs used when inferring genome build to save time.
mapping_file	MungeSumstats has a pre-defined column-name mapping file which should cover the most common column headers and their interpretations. However, if a column header that is in your file is missing of the mapping we give is incorrect you can supply your own mapping file. Must be a 2 column dataframe with column names "Uncorrected" and "Corrected". See data(sumstatsColHeaders) for default mapping and necessary format.
nThread	Number of threads to use for parallel processes.
ref_genome	name of the reference genome used for the GWAS ("GRCh37" or "GRCh38"). Argument is case-insensitive. Default is NULL which infers the reference genome from the data.
on_ref_genome	Binary Should a check take place that all SNPs are on the reference genome by SNP ID. Default is TRUE.
infer_eff_direction	Binary Should a check take place to ensure the alleles match the effect direction? Default is TRUE.
return_list	Return the sumstats_dt within a named list (default: TRUE).

**Value**

list containing sumstats\_dt, the modified summary statistics data table object

**Examples**

```
sumstats <- MungeSumstats::formatted_example()
#for speed, don't run on_ref_genome part of check (on_ref_genome = FALSE)
sumstats_dt2<-infer_effect_column(sumstats_dt=sumstats,on_ref_genome = FALSE)
```

---

is\_tabix

*Is tabix*


---

**Description**

Is a file bgz-compressed and tabix-indexed.

**Usage**

```
is_tabix(path)
```

**Arguments**

path	Path to file.
------	---------------

**Value**

logical: whether the file is tabix-indexed or not.  
 logical

---

legacy_ids	<i>Convert current IDs to legacy IDs</i>
------------	--

---

**Description**

Convert current IDs to legacy IDs

**Usage**

```
legacy_ids(x)
```

**Arguments**

x                    Vector of ids

**Value**

vector of back compatible ids

---

liftover	<i>Genome build liftover</i>
----------	------------------------------

---

**Description**

Transfer genomic coordinates from one genome build to another.

**Usage**

```
liftover(
  sumstats_dt,
  convert_ref_genome,
  ref_genome,
  chain_source = "ensembl",
  imputation_ind = TRUE,
  chrom_col = "CHR",
  start_col = "BP",
  end_col = start_col,
  as_granges = FALSE,
  style = "NCBI",
  local_chain = NULL,
  verbose = TRUE
)
```

**Arguments**

sumstats_dt	data table obj of the summary statistics file for the GWAS.
convert_ref_genome	name of the reference genome to convert to ("GRCh37" or "GRCh38"). This will only occur if the current genome build does not match. Default is not to convert the genome build (NULL).
ref_genome	name of the reference genome used for the GWAS ("GRCh37" or "GRCh38"). Argument is case-insensitive. Default is NULL which infers the reference genome from the data.
chain_source	chain file source used ("ucsc" as default, or "ensembl")
imputation_ind	Binary Should a column be added for each imputation step to show what SNPs have imputed values for differing fields. This includes a field denoting SNP allele flipping (flipped). On the flipped value, this denoted whether the alleles were switched based on MungeSumstats initial choice of A1, A2 from the input column headers and thus may not align with what the creator intended. <b>Note</b> these columns will be in the formatted summary statistics returned. Default is FALSE.
chrom_col	Name of the chromosome column in sumstats_dt (e.g. "CHR").
start_col	Name of the starting genomic position column in sumstats_dt (e.g. "POS", "start").
end_col	Name of the ending genomic position column in sumstats_dt (e.g. "POS", "end"). Can be the same as start_col when sumstats_dt only contains SNPs that span 1 base pair (bp) each.
as_granges	Return results as <a href="#">GRanges</a> instead of a <a href="#">data.table</a> (default: FALSE).
style	Style to return <a href="#">GRanges</a> object in (e.g. "NCBI" = 4; "UCSC" = "chr4"); (default: "NCBI").
local_chain	Path to local chain file to use instead of downloading. Default of NULL i.e. no local file to use. <b>NOTE</b> if passing a local chain file make sure to specify the path to convert from and to the correct build like GRCh37 to GRCh38. We can not sense check this for local files. The chain file can be submitted as a gz file (as downloaded from source) or unzipped.
verbose	Print messages.

**Value**

Lifted summary stats in [data.table](#) or [GRanges](#) format.

**Source**

[liftOver](#)

[UCSC chain files](#)

[Ensembl chain files](#)

## Examples

```
sumstats_dt <- MungeSumstats::formatted_example()

sumstats_dt_hg38 <- liftover(sumstats_dt=sumstats_dt,
                             ref_genome = "hg19",
                             convert_ref_genome="hg38")
```

---

list_sumstats	<i>List munged summary statistics</i>
---------------	---------------------------------------

---

## Description

Searches for and lists local GWAS summary statistics files munged by [format\\_sumstats](#) or [import\\_sumstats](#).

## Usage

```
list_sumstats(
  save_dir = getwd(),
  pattern = "*.tsv.gz$",
  ids_from_file = TRUE,
  verbose = TRUE
)
```

## Arguments

save_dir	Top-level directory to recursively search for summary statistics files within.
pattern	Regex pattern to search for files with.
ids_from_file	Try to extract dataset IDs from file names. If FALSE, will infer IDs from the directory names instead.
verbose	Print messages.

## Value

Named vector of summary stats paths.

## Examples

```
save_dir <- system.file("extdata", package = "MungeSumstats")
munged_files <- MungeSumstats::list_sumstats(save_dir = save_dir)
```

---

load\_ref\_genome\_data *Load the reference genome data for SNPs of interest*

---

### Description

Load the reference genome data for SNPs of interest

### Usage

```
load_ref_genome_data(  
  snps,  
  ref_genome,  
  dbSNP = c(144, 155),  
  msg = NULL,  
  chr_filt = NULL  
)
```

### Arguments

snps	Character vector SNPs by rs_id from sumstats file of interest.
ref_genome	Name of the reference genome used for the GWAS (GRCh37 or GRCh38)
dbSNP	version of dbSNP to be used (144 or 155)
msg	Optional name of the column missing from the dataset in question. Default is NULL
chr_filt	Internal for testing - filter reference genomes and sumstats to specific chromosomes for testing. Pass a list of chroms in format: c("1","2"). Default is NULL i.e. no filtering.

### Value

data table of snpsById, filtered to SNPs of interest.

### Source

```
sumstats_dt <- formatted_example() rsids <- MungeSumstats:::load_ref_genome_data(snps  
= sumstats_dt$SNP, ref_genome = "GRCH37", dbSNP=144)
```

---

load_snp_loc_data	<i>Loads the SNP locations and alleles for Homo sapiens extracted from NCBI dbSNP Build 144. Reference genome version is dependent on user input.</i>
-------------------	---

---

### Description

Loads the SNP locations and alleles for Homo sapiens extracted from NCBI dbSNP Build 144. Reference genome version is dependent on user input.

### Usage

```
load_snp_loc_data(ref_genome, dbSNP = c(144, 155), msg = NULL)
```

### Arguments

ref_genome	name of the reference genome used for the GWAS (GRCh37 or GRCh38)
dbSNP	version of dbSNP to be used (144 or 155)
msg	Optional name of the column missing from the dataset in question

### Value

SNP\_LOC\_DATA SNP positions and alleles for Homo sapiens extracted from NCBI dbSNP Build 144

### Examples

```
SNP_LOC_DATA <- load_snp_loc_data("GRCH37", dbSNP=144)
```

---

logs_example	<i>Example logs file</i>
--------------	--------------------------

---

### Description

Example logs file produced by [format\\_sumstats](#).

### Usage

```
logs_example(read = FALSE)
```

### Arguments

read	Whether to read the logs file into memory.
------	--

**Value**

Path to logs file.

**Source**

```
eduAttainOkbayPth <- system.file("extdata", "eduAttainOkbay.txt", package = "MungeSumstats")
sumstats_dt <- data.table::fread(eduAttainOkbayPth) ##### Introduce values that need
to be fixed ##### sumstats_dt$Pval[10:15] <- 5 sumstats_dt$Pval[20:22] <- -5 sumstats_dt$Pval[23:25]
<- "5e-324" ss_path <- tempfile() data.table::fwrite(sumstats_dt, ss_path) log_folder
<- tempdir() reformatted <- MungeSumstats::format_sumstats(path = ss_path, ref_genome
= "GRCh37", log_folder = log_folder, log_mungesumstats_msgs = TRUE, log_folder_ind =
TRUE,) file.copy(reformatted$log_files$MungeSumstats_log_msg, "inst/extdata", overwrite
= TRUE)
```

---

make_allele_upper	<i>Ensure A1 and A2 are upper case</i>
-------------------	--

---

**Description**

Ensure A1 and A2 are upper case

**Usage**

```
make_allele_upper(sumstats_dt, log_files)
```

**Arguments**

log\_files      list of log file locations

**Value**

list containing sumstats\_dt, the modified summary statistics data table object and the log file list

---

messenger	<i>Print messages</i>
-----------	-----------------------

---

**Description**

Print messages with option to silence.

**Usage**

```
messenger(..., v = TRUE)
```

**Arguments**

...            Message input.  
v                Whether to print messages.

**Value**

Null output.

---

message\_parallel        *Send messages to console even from within parallel processes*

---

**Description**

Send messages to console even from within parallel processes

**Usage**

message\_parallel(...)

**Value**

A message

---

parse\_dropped\_chrom    *Parse number of SNPs dropped due to being on chrom X, Y or MT*

---

**Description**

Support function for [parse\\_logs](#).

**Usage**

parse\_dropped\_chrom(1)

**Arguments**

1                Lines of text from log file.

**Value**

Numeric



---

parse\_dropped\_duplicates

*Parse number of SNPs dropped due to being duplicates*

---

**Description**

Support function for [parse\\_logs](#).

**Usage**

parse\_dropped\_duplicates(1)

**Arguments**

1                    Lines of text from log file.

**Value**

Numeric

---

parse\_dropped\_INFO

*Parse number of SNPs dropped due to being below the INFO threshold*

---

**Description**

Support function for [parse\\_logs](#).

**Usage**

parse\_dropped\_INFO(1)

**Arguments**

1                    Lines of text from log file.

**Value**

Numeric

---

parse\_dropped\_nonA1A2 *Parse number of SNPs dropped due to not matching the ref genome A1 or A2*

---

**Description**

Support function for [parse\\_logs](#).

**Usage**

```
parse_dropped_nonA1A2(1)
```

**Arguments**

1                    Lines of text from log file.

**Value**

Numeric

---

parse\_dropped\_nonBiallelic  
*Parse number of SNPs dropped due to not being bi-allelic*

---

**Description**

Support function for [parse\\_logs](#).

**Usage**

```
parse_dropped_nonBiallelic(1)
```

**Arguments**

1                    Lines of text from log file.

**Value**

Numeric

---

*parse\_dropped\_nonRef*    *Parse number of SNPs dropped due to being in the ref genome*

---

**Description**

Support function for [parse\\_logs](#).

**Usage**

`parse_dropped_nonRef(1)`

**Arguments**

1                    Lines of text from log file.

**Value**

Numeric

---

*parse\_flipped*                    *Parse number of SNPs flipped to align with the ref genome*

---

**Description**

Support function for [parse\\_logs](#).

**Usage**

`parse_flipped(1)`

**Arguments**

1                    Lines of text from log file.

**Value**

Numeric

parse\_genome\_build      *Genome build inferred from the summary statistics*

---

**Description**

Support function for [parse\\_logs](#).

**Usage**

```
parse_genome_build(1)
```

**Arguments**

1                      Lines of text from log file.

**Value**

Character

---

parse\_idStandard      *Standardised IEU MRC OpenGWAS ID*

---

**Description**

Support function for [parse\\_logs](#).

**Usage**

```
parse_idStandard(1)
```

**Arguments**

1                      Lines of text from log file.

**Value**

Character

---

parse_logs	<i>Parse data from log files</i>
------------	----------------------------------

---

**Description**

Parses data from the log files generated by [format\\_sumstats](#) or [import\\_sumstats](#) when the argument `log_mungesumstats_msgs` is set to TRUE.

**Usage**

```
parse_logs(  
  save_dir = getwd(),  
  pattern = "MungeSumstats_log_msg.txt$",  
  verbose = TRUE  
)
```

**Arguments**

<code>save_dir</code>	Top-level directory to recursively search for log files within.
<code>pattern</code>	Regex pattern to search for files with.
<code>verbose</code>	Print messages.

**Value**

[data.table](#) of parsed log data.

**Examples**

```
save_dir <- system.file("extdata", package = "MungeSumstats")  
log_data <- MungeSumstats::parse_logs(save_dir = save_dir)
```

---

parse_pval_large	<i>Parse number of SNPs with p-values &gt;1</i>
------------------	---

---

**Description**

Support function for [parse\\_logs](#).

**Usage**

```
parse_pval_large(1)
```

**Arguments**

1	Lines of text from log file.
---	------------------------------

**Value**

Numeric

---

parse_pval_neg	<i>Parse number of SNPs with p-values &lt;0</i>
----------------	---

---

**Description**Support function for [parse\\_logs](#).**Usage**

parse\_pval\_neg(1)

**Arguments**

1                    Lines of text from log file.

**Value**

Numeric

---

parse_pval_small	<i>Parse number of SNPs with non-negative p-values <math>\leq 5e-324</math></i>
------------------	---

---

**Description**Support function for [parse\\_logs](#).**Usage**

parse\_pval\_small(1)

**Arguments**

1                    Lines of text from log file.

**Value**

Numeric

---

parse_report	<i>Parse "Summary statistics report" metrics</i>
--------------	--

---

**Description**

Support function for [parse\\_logs](#).

**Usage**

```
parse_report(1, entry = 1, line = 1)
```

**Arguments**

1                    Lines of text from log file.

**Value**

Numeric

---

parse_snps_freq_05	<i>Parse number/percent of SNPs with <i>FREQ</i> values &gt;0.5</i>
--------------------	---

---

**Description**

Support function for [parse\\_logs](#).

**Usage**

```
parse_snps_freq_05(1, percent = FALSE)
```

**Arguments**

1                    Lines of text from log file.

**Value**

Numeric

---

parse_snps_not_formatted	<i>Parse number of SNPs not correctly formatted</i>
--------------------------	---

---

**Description**

Support function for [parse\\_logs](#).

**Usage**

```
parse_snps_not_formatted(1)
```

**Arguments**

1	Lines of text from log file.
---	------------------------------

**Value**

Numeric

---

parse_time	<i>Parse the total time taken the munge the file</i>
------------	--

---

**Description**

Support function for [parse\\_logs](#).

**Usage**

```
parse_time(1)
```

**Arguments**

1	Lines of text from log file.
---	------------------------------

**Value**

Character



---

```
preview_sumstats      Preview formatted sum stats saved to disk
```

---

**Description**

Prints the first n lines of the sum stats.

**Usage**

```
preview_sumstats(save_path, nrows = 5L)
```

**Arguments**

save\_path        File path to save formatted data. Defaults to tempfile(fileext=".tsv.gz").

**Value**

No return

---

```
raw_ALSvcf           GWAS Amyotrophic lateral sclerosis ieu open GWAS project - Subset
```

---

**Description**

VCF (VCFv4.2) of the GWAS Amyotrophic lateral sclerosis ieu open GWAS project Dataset: ebi-a-GCST005647. A subset of 99 SNPs

**Format**

vcf document with 528 items relating to 99 SNPs

**Details**

A VCF file (VCFv4.2) of the GWAS Amyotrophic lateral sclerosis ieu open GWAS project has been subsetted here to act as an example summary statistic file in VCF format which has some issues in the formatting. MungeSumstats can correct these issues and produced a standardised summary statistics format.

**ALSvcf.vcf**

NA

**Source**

The summary statistics VCF (VCFv4.2) file was downloaded from <https://gwas.mrcieu.ac.uk/datasets/ebi-a-GCST005647/> and formatted to a .rda with the following: #Get example VCF dataset, use GWAS Amyotrophic lateral sclerosis ALS\_GWAS\_VCF <- readLines("ebi-a-GCST005647.vcf.gz") #Subset to just the first 99 SNPs ALSvcf <- ALS\_GWAS\_VCF[1:528] writeLines(ALSvcf, "inst/extdata/ALSvcf.v")

---

raw_eduAttainOkbay	<i>GWAS Educational Attainment Okbay 2016 - Subset</i>
--------------------	--

---

### Description

GWAS Summary Statistics on Educational Attainment by Okbay et al 2016: PMID: 27898078  
 PMCID: PMC5509058 DOI: 10.1038/ng1216-1587b. A subset of 93 SNPs

### Format

txt document with 94 items

### Details

GWAS Summary Statistics on Educational Attainment by Okbay et al 2016 has been subsetted here to act as an example summary statistic file which has some issues in the formatting. MungeSumstats can correct these issues.

### eduAttainOkbay.txt

NA

### Source

The summary statistics file was downloaded from <https://www.nature.com/articles/ng.3552> and formatted to a .rda with the following: #Get example dataset, use Educational-Attainment\_Okbay\_2016  
 link<-"Educational-Attainment\_Okbay\_2016/EduYears\_Discovery\_5000.txt" eduAttainOkbay<-readLines(link)  
 #There is an issue where values end with .0, this 0 is removed in func #There are also SNPs  
 not on ref genome or arebi/tri allelic #So need to remove these in this dataset as its used  
 for testing tmp <- tempfile() writelines(eduAttainOkbay, con=tmp) eduAttainOkbay <- data.table::fread(tm  
 #DT read removes the .0's #remove those not on ref genome and withbi/tri allelic rmv <-  
 c("rs192818565", "rs79925071", "rs1606974", "rs1871109", "rs73074378", "rs7955289") eduAttainOkbay  
 <- eduAttainOkbay[!MarkerName data.table::fwrite(eduAttainOkbay, file=tmp, sep="\t")  
 eduAttainOkbay <- readLines(tmp) writelines(eduAttainOkbay, "inst/extdata/eduAttainOkbay.txt")

---

read_header	<i>Read in file header</i>
-------------	----------------------------

---

### Description

Read in file header

### Usage

```
read_header(path, n = 2L, skip_vcf_metadata = FALSE, nThread = 1)
```

**Arguments**

path	Filepath for the summary statistics file to be formatted. A dataframe or datatable of the summary statistics file can also be passed directly to MungeSumstats using the path parameter.
n	integer. The (maximal) number of lines to read. Negative values indicate that one should read up to the end of input on the connection.
skip_vcf_metadata	logical, should VCF metadata be ignored
nThread	Number of threads to use for parallel processes.

**Value**

First n lines of the VCF header

**Examples**

```
path <- system.file("extdata", "eduAttain0kbay.txt",
  package = "MungeSumstats")
header <- read_header(path = path)
```

---

read\_sumstats

*Determine summary statistics file type and read them into memory*


---

**Description**

Determine summary statistics file type and read them into memory

**Usage**

```
read_sumstats(
  path,
  nrows = Inf,
  standardise_headers = FALSE,
  samples = 1,
  sampled_rows = 10000L,
  nThread = 1,
  mapping_file = sumstatsColHeaders
)
```

**Arguments**

path	Filepath for the summary statistics file to be formatted. A dataframe or datatable of the summary statistics file can also be passed directly to MungeSumstats using the path parameter.
nrows	integer. The (maximal) number of lines to read. If Inf, will read in all rows.

standardise_headers	Standardise headers first.
samples	Which samples to use: <ul style="list-style-type: none"> <li>• 1 : Only the first sample will be used (<i>DEFAULT</i>).</li> <li>• NULL : All samples will be used.</li> <li>• c("&lt;sample_id1&gt;", "&lt;sample_id2&gt;", ...) : Only user-selected samples will be used (case-insensitive).</li> </ul>
sampld_rows	First N rows to sample. Set NULL to use full sumstats_file. when determining whether cols are empty.
nThread	Number of threads to use for parallel processes.
mapping_file	MungeSumstats has a pre-defined column-name mapping file which should cover the most common column headers and their interpretations. However, if a column header that is in your file is missing of the mapping we give is incorrect you can supply your own mapping file. Must be a 2 column dataframe with column names "Uncorrected" and "Corrected". See data(sumstatsColHeaders) for default mapping and necessary format.

**Value**

data.table of formatted summary statistics

**Examples**

```
path <- system.file("extdata", "eduAttain0kbay.txt",
  package = "MungeSumstats"
)
eduAttain0kbay <- read_sumstats(path = path)
```

---

read_vcf	<i>Read in VCF file</i>
----------	-------------------------

---

**Description**

Read in a VCF file as a [VCF](#) or a [data.table](#). Can optionally save the VCF/data.table as well.

**Usage**

```
read_vcf(
  path,
  as_datatable = TRUE,
  save_path = NULL,
  tabix_index = FALSE,
  samples = 1,
  which = NULL,
  use_params = TRUE,
  sampled_rows = 10000L,
```

```

download = TRUE,
vcf_dir = tempdir(),
download_method = "download.file",
force_new = FALSE,
mt_thresh = 100000L,
nThread = 1,
verbose = TRUE
)

```

## Arguments

path	Path to local or remote VCF file.
as_data_table	Return the data as a <a href="#">data.table</a> (default: TRUE) or a <a href="#">VCF</a> (FALSE).
save_path	File path to save formatted data. Defaults to <code>tempfile(fileext=".tsv.gz")</code> .
tabix_index	Index the formatted summary statistics with <a href="#">tabix</a> for fast querying.
samples	Which samples to use: <ul style="list-style-type: none"> <li>• 1 : Only the first sample will be used (<i>DEFAULT</i>).</li> <li>• NULL : All samples will be used.</li> <li>• <code>c("&lt;sample_id1&gt;","&lt;sample_id2&gt;","...")</code> : Only user-selected samples will be used (case-insensitive).</li> </ul>
which	Genomic ranges to be added if supplied. Default is NULL.
use_params	When TRUE (default), increases the speed of reading in the VCF by omitting columns that are empty based on the head of the VCF (NAs only). NOTE that that this requires the VCF to be sorted, bgzip-compressed, tabix-indexed, which <a href="#">read_vcf</a> will attempt to do.
sampled_rows	First N rows to sample. Set NULL to use full <code>sumstats_file</code> . when determining whether cols are empty.
download	Download the VCF (and its index file) to a temp folder before reading it into R. This is important to keep TRUE when <code>nThread&gt;1</code> to avoid making too many queries to remote file.
vcf_dir	Where to download the original VCF from Open GWAS. <i>WARNING</i> : This is set to <code>tempdir()</code> by default. This means the raw (pre-formatted) VCFs be deleted upon ending the R session. Change this to keep the raw VCF file on disk (e.g. <code>vcf_dir="/raw_vcf"</code> ).
download_method	"axel" (multi-threaded) or "download.file" (single-threaded) .
force_new	If a formatted file of the same names as <code>save_path</code> exists, formatting will be skipped and this file will be imported instead (default). Set <code>force_new=TRUE</code> to override this.
mt_thresh	When the number of rows (variants) in the VCF is <code>&lt; mt_thresh</code> , only use single-threading for reading in the VCF. This is because the overhead of parallelisation outweighs the speed benefits when VCFs are small.
nThread	Number of threads to use for parallel processes.
verbose	Print messages.

**Value**

The VCF file in data.table format.

**Source**

```
##### Benchmarking ##### library(VCFwrenchR) library(VariantAnnotation) path <- "https://gwas.mrcieu.ac.uk/files/ieua-298/ieua-298.vcf.gz"
vcf <- VariantAnnotation::readVcf(file = path) N <- 1e5 vcf_sub <- vcf[1:N,] res <- microbenchmark::microbenchmark(
  "vcf2df"={dat1 <- MungeSumstats::vcf2df(vcf = vcf_sub)}, "VCFwrenchR"={dat2 <- as.data.frame(x = vcf_sub)}, "VRanges"={dat3 <- data.table::as.data.table(methods::as(vcf_sub, "VRanges"))},
  times=1)
```

[Discussion on VariantAnnotation GitHub](#)

[Discussion on VariantAnnotation GitHub](#)

**Examples**

```
##### Local file #####
path <- system.file("extdata", "ALSvcf.vcf", package="MungeSumstats")
sumstats_dt <- read_vcf(path = path)

##### Remote file #####
## Small GWAS (0.2Mb)
# path <- "https://gwas.mrcieu.ac.uk/files/ieua-298/ieua-298.vcf.gz"
# sumstats_dt2 <- read_vcf(path = path)

## Large GWAS (250Mb)
# path <- "https://gwas.mrcieu.ac.uk/files/ubm-a-2929/ubm-a-2929.vcf.gz"
# sumstats_dt3 <- read_vcf(path = path, nThread=11)

### Very large GWAS (500Mb)
# path <- "https://gwas.mrcieu.ac.uk/files/ieua-1124/ieua-1124.vcf.gz"
# sumstats_dt4 <- read_vcf(path = path, nThread=11)
```

---

read\_vcf\_genome

*Read VCF genome*

---

**Description**

Get the genome build of a remote or local VCF file.

**Usage**

```
read_vcf_genome(
  header = NULL,
  validate = FALSE,
  default_genome = "HG19/GRCh37",
  verbose = TRUE
)
```

**Arguments**

header	Header extracted by <a href="#">scanVcfHeader</a> .
validate	Validate genome name using <a href="#">mapGenomeBuilds</a> .
default_genome	When no genome can be extracted, default to this genome build.
verbose	Print messages.

**Value**

genome

---

read_vcf_info	<i>Read VCF: INFO column</i>
---------------	------------------------------

---

**Description**

Parse INFO column in VCF file.

**Usage**

```
read_vcf_info(sumstats_dt)
```

**Arguments**

sumstats_dt	Summary stats data.table.
-------------	---------------------------

**Value**

Null output.

---

read_vcf_markername	<i>Read VCF: MarkerName column</i>
---------------------	------------------------------------

---

**Description**

Parse MarkerName/SNP column in VCF file.

**Usage**

```
read_vcf_markername(sumstats_dt)
```

**Arguments**

sumstats_dt	Summary stats data.table.
-------------	---------------------------

**Value**

Null output.

---

read\_vcf\_parallel      *Read VCF: parallel*

---

### Description

Read a VCF file across 1 or more threads in parallel. If `tilewidth` is not specified, the size of each chunk will be determined by total genome size divided by `ntile`. By default, `ntile` is equal to the number of threads, `nThread`. For further discussion on how this function was optimised, see [here](#) and [here](#).

### Usage

```
read_vcf_parallel(
  path,
  samples = 1,
  which = NULL,
  use_params = TRUE,
  as_datatable = TRUE,
  sampled_rows = 10000L,
  include_xy = FALSE,
  download = TRUE,
  vcf_dir = tempdir(),
  download_method = "download.file",
  force_new = FALSE,
  tilewidth = NULL,
  mt_thresh = 100000L,
  nThread = 1,
  ntile = nThread,
  verbose = TRUE
)
```

### Arguments

<code>path</code>	Path to local or remote VCF file.
<code>samples</code>	Which samples to use: <ul style="list-style-type: none"> <li>• 1 : Only the first sample will be used (<i>DEFAULT</i>).</li> <li>• NULL : All samples will be used.</li> <li>• c("&lt;sample_id1&gt;",&lt;sample_id2&gt;,...) : Only user-selected samples will be used (case-insensitive).</li> </ul>
<code>which</code>	Genomic ranges to be added if supplied. Default is NULL.
<code>use_params</code>	When TRUE (default), increases the speed of reading in the VCF by omitting columns that are empty based on the head of the VCF (NAs only). NOTE that that this requires the VCF to be sorted, bgzip-compressed, tabix-indexed, which <a href="#">read_vcf</a> will attempt to do.
<code>as_datatable</code>	Return the data as a <a href="#">data.table</a> (default: TRUE) or a <a href="#">VCF</a> (FALSE).



sampled_rows	First N rows to sample. Set NULL to use full sumstats_file. when determining whether cols are empty.
download	Download the VCF (and its index file) to a temp folder before reading it into R. This is important to keep TRUE when nThread>1 to avoid making too many queries to remote file.
vcf_dir	Where to download the original VCF from Open GWAS. <i>WARNING:</i> This is set to tempdir() by default. This means the raw (pre-formatted) VCFs be deleted upon ending the R session. Change this to keep the raw VCF file on disk (e.g. vcf_dir="./raw_vcf").
download_method	"axel" (multi-threaded) or "download.file" (single-threaded) .
force_new	If a formatted file of the same names as save_path exists, formatting will be skipped and this file will be imported instead (default). Set force_new=TRUE to override this.
tilewidth	The desired tile width. The effective tile width might be slightly different but is guaranteed to never be more than the desired width.
mt_thresh	When the number of rows (variants) in the VCF is < mt_thresh, only use single-threading for reading in the VCF. This is because the overhead of parallelisation outweighs the speed benefits when VCFs are small.
nThread	Number of threads to use for parallel processes.
ntile	The number of tiles to generate.
verbose	Print messages.

**Value**

VCF file.

**Source**

```
path <- "https://gwas.mrcieu.ac.uk/files/ieu-a-298/ieu-a-298.vcf.gz" ##### Single-threaded
#### vcf <- MungeSumstats:::read_vcf_parallel(path = path) ##### Parallel ##### vcf2 <-
MungeSumstats:::read_vcf_parallel(path = path, nThread=11)
```

---

read_vcf_pval	<i>Read VCF: p-value column</i>
---------------	---------------------------------

---

**Description**

Parse p-value column in VCF file.

**Usage**

```
read_vcf_pval(sumstats_dt)
```

**Arguments**

sumstats\_dt      Summary stats data.table.

**Value**

Null output.

---

register\_cores      *Register cores*

---

**Description**

Register a multi-threaded instances using **BiocParallel**.

**Usage**

```
register_cores(workers = 1, progressbar = TRUE)
```

**Arguments**

workers            integer(1) Number of workers. Defaults to the maximum of 1 or the number of cores determined by detectCores minus 2 unless environment variables R\_PARALLELLY\_AVAILABLECORES\_FALLBACK or BIOCPARALLEL\_WORKER\_NUMBER are set otherwise. For a SOCK cluster, workers can be a character() vector of host names.

progressbar       logical(1) Enable progress bar (based on plyr:::progress\_text).

**Value**

Null output.

---

remove\_empty\_cols      *Remove empty columns*

---

**Description**

Remove columns that are empty or contain all the same values in a data.table.

**Usage**

```
remove_empty_cols(sumstats_dt, sampled_rows = NULL, verbose = TRUE)
```

**Arguments**

sampled_rows	First N rows to sample. Set NULL to use full sumstats_file. when determining whether cols are empty.
verbose	Print messages.

**Value**

Null output.

---

report_summary	<i>Report info on current state of the summary statistics</i>
----------------	---

---

**Description**

Prints report.

**Usage**

```
report_summary(sumstats_dt, orig_dims = NULL)
```

**Arguments**

sumstats_dt	data table obj of the summary statistics file for the GWAS.
-------------	---

**Value**

No return

---

select_api	<i>Toggle API address between development and release</i>
------------	---

---

**Description**

From ieugwasr.

**Usage**

```
select_api(where = "public", verbose = TRUE)
```

**Arguments**

where	Which API to use. Choice between "local", "release", "test". Default = "local"
-------	--

**Value**

No return

---

select_vcf_fields	Select VCF fields
-------------------	-------------------

---

### Description

Select non-empty columns from each VCF field type.

### Usage

```
select_vcf_fields(
  path,
  sampled_rows = 10000L,
  which = NULL,
  samples = NULL,
  nThread = 1,
  verbose = TRUE
)
```

### Arguments

path	Path to local or remote VCF file.
sampled_rows	First N rows to sample. Set NULL to use full sumstats_file. when determining whether cols are empty.
which	Genomic ranges to be added if supplied. Default is NULL.
samples	Which samples to use: <ul style="list-style-type: none"> <li>• 1 : Only the first sample will be used (<i>DEFAULT</i>).</li> <li>• NULL : All samples will be used.</li> <li>• c("&lt;sample_id1&gt;", "&lt;sample_id2&gt;", ...) : Only user-selected samples will be used (case-insensitive).</li> </ul>
nThread	Number of threads to use for parallel processes.
verbose	Print messages.

### Value

ScanVcfParam object.

---

sort_coords	<i>Sort sum stats</i>
-------------	-----------------------

---

### Description

Sort summary statistics table by genomic coordinates.

### Usage

```
sort_coords(
  sumstats_dt,
  sort_coordinates = TRUE,
  sort_method = c("data.table", "GenomicRanges")
)
```

### Arguments

sumstats_dt	<a href="#">data.table</a> obj of the summary statistics file for the GWAS.
sort_method	Method to sort coordinates by: <ul style="list-style-type: none"> <li>• "data.table" (default) Uses <a href="#">setorderv</a>, which is much faster than "GenomicRanges" but less robust to variations in some sum stats files.</li> <li>• "GenomicRanges" Uses <a href="#">sort.GenomicRanges</a>, which is more robust to variations in sum stats files but much slower than the "data.table" method.</li> </ul>
sort_coords	Whether to sort by coordinates.

### Value

Sorted sumstats\_dt

---

sort_coords_datatable	<i>Sort sum stats: data.table</i>
-----------------------	-----------------------------------

---

### Description

Sort summary statistics table by genomic coordinates using a fast data.table-native strategy

### Usage

```
sort_coords_datatable(
  sumstats_dt,
  chr_col = "CHR",
  start_col = "BP",
  end_col = start_col
)
```

**Arguments**

sumstats\_dt     [data.table](#) obj of the summary statistics file for the GWAS.  
 chr\_col         Chromosome column name.  
 start\_col        Genomic end position column name.

**Value**

Sorted sumstats\_dt

---

sort\_coord\_genomicranges

*Sort sum stats: GenomicRanges*

---

**Description**

Sort summary statistics table by genomic coordinates using a slower (but in some cases more robust) GenomicRanges strategy

**Usage**

```
sort_coord_genomicranges(sumstats_dt)
```

**Arguments**

sumstats\_dt     [data.table](#) obj of the summary statistics file for the GWAS.

**Value**

Sorted sumstats\_dt

---

standardise\_header

*Standardise the column headers in the Summary Statistics files*

---

**Description**

Use a reference data table of common column header names (stored in sumstatsColHeaders or user inputted mapping file) to convert them to a standard set, i.e. chromosome -> CHR. This function does not check that all the required column headers are present. The amended header is written directly back into the file

**Usage**

```
standardise_header(
  sumstats_dt,
  mapping_file = sumstatsColHeaders,
  uppercase_unmapped = TRUE,
  return_list = TRUE
)
```

**Arguments**

`sumstats_dt` data table obj of the summary statistics file for the GWAS.

`mapping_file` MungeSumstats has a pre-defined column-name mapping file which should cover the most common column headers and their interpretations. However, if a column header that is in your file is missing of the mapping we give is incorrect you can supply your own mapping file. Must be a 2 column dataframe with column names "Uncorrected" and "Corrected". See `data(sumstatsColHeaders)` for default mapping and necessary format.

`uppercase_unmapped` For columns that could not be identified in the `mapping_file`, return them in the same format they were input as (without forcing them to uppercase).

`return_list` Return the `sumstats_dt` within a named list (default: TRUE).

**Value**

list containing `sumstats_dt`, the modified summary statistics data table object

**Examples**

```
sumstats_dt <- data.table::fread(system.file("extdata", "eduAttain0kbay.txt",
                                             package = "MungeSumstats"))
sumstats_dt2 <- standardise_header(sumstats_dt=sumstats_dt)
```

---

`sumstatsColHeaders`      *Summary Statistics Column Headers*

---

**Description**

List of uncorrected column headers often found in GWAS Summary Statistics column headers. Note the effect allele will always be the A2 allele, this is the approach done for VCF(<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC>) This is enforced with the column header corrections here and also the check allele flipping test.

**Usage**

```
data("sumstatsColHeaders")
```

**Format**

dataframe with 2 columns

**Source**

```
The code to prepare the .Rda file from the marker file is: # Most the data in the below table
comes from the LDSC github wiki data("sumstatsColHeaders") # Make additions to sumstatsColHeaders
using github version of MungeSumstats-# shown is an example of adding columns for Standard
Error (SE) #se_cols <- data.frame("Uncorrected"=c("SE", "se", "STANDARD.ERROR", # "STANDARD_ERROR", "STAND
"Corrected"=rep("SE", 5)) #sumstatsColHeaders <- rbind(sumstatsColHeaders, se_cols)
#Once additions are made, order & save the new mapping dataset #now sort ordering -important
for logic that # uncorrected=corrected comes first sumstatsColHeaders$ordering <- sumstatsColHeaders$Unc
sumstatsColHeaders <- sumstatsColHeaders[order(sumstatsColHeaders$Corrected, sumstatsColHeaders$order
= TRUE), ] rownames(sumstatsColHeaders)<-1:nrow(sumstatsColHeaders) sumstatsColHeaders$ordering
<- NULL #manually move FRWQUENCY to above MAR - github issue 95 frequency <- sumstatsColHeaders[sumstatsCo
maf <- sumstatsColHeaders[sumstatsColHeaders$Uncorrected=="MAF", ] if(as.integer(rownames(frequency))>
sumstatsColHeaders[as.integer(rownames(frequency)), ] <- maf sumstatsColHeaders[as.integer(rownames(ma
<- frequency } usethis::use_data(sumstatsColHeaders, overwrite = TRUE, internal=TRUE)
save(sumstatsColHeaders, file="data/sumstatsColHeaders.rda") # You will need to restart
your r session for effects to take account
```

---

supported\_suffixes      *List supported file formats*

---

**Description**

List supported file formats

**Usage**

```
supported_suffixes(
  tabular = TRUE,
  tabular_compressed = TRUE,
  vcf = TRUE,
  vcf_compressed = TRUE
)
```

**Arguments**

```
tabular            Include tabular formats.
tabular_compressed            Include compressed tabular formats.

vcf                Include Variant Call Format.
vcf_compressed    Include compressed Variant Call Format.
```

**Value**

File formats



---

to_granges	<i>To GRanges</i>
------------	-------------------

---

### Description

Convert a [data.table](#) to [GRanges](#).

### Usage

```
to_granges(
  sumstats_dt,
  seqnames.field = "CHR",
  start.field = "BP",
  end.field = "BP",
  style = c("NCBI", "UCSC")
)
```

### Arguments

sumstats_dt	data table obj of the summary statistics file for the GWAS.
seqnames.field	A character vector of recognized names for the column in df that contains the chromosome name (a.k.a. sequence name) associated with each genomic range. Only the first name in seqnames.field that is found in colnames(df) is used. If no one is found, then an error is raised.
start.field	A character vector of recognized names for the column in df that contains the start positions of the genomic ranges. Only the first name in start.field that is found in colnames(df) is used. If no one is found, then an error is raised.
end.field	A character vector of recognized names for the column in df that contains the end positions of the genomic ranges. Only the first name in start.field that is found in colnames(df) is used. If no one is found, then an error is raised.
style	GRanges style to convert to, "NCBI" or "UCSC".

### Value

GRanges object

---

to_vranges	<i>Convert to VRanges</i>
------------	---------------------------

---

### Description

Convert to VRanges

**Usage**

```
to_vranges(sumstats_dt)
```

**Arguments**

sumstats\_dt      data table obj of the summary statistics file for the GWAS.

**Value**

VRanges object

---

unlist_dt	<i>Unlist a data.table</i>
-----------	----------------------------

---

**Description**

Identify columns that are lists and turn them into vectors.

**Usage**

```
unlist_dt(dt, verbose = TRUE)
```

**Arguments**

dt                      data.table  
verbose                Print messages.

**Value**

dt with list columns turned into vectors.

---

validate_parameters	<i>Ensure that the input parameters are logical</i>
---------------------	---

---

**Description**

Ensure that the input parameters are logical

**Usage**

```
validate_parameters(  
  path,  
  ref_genome,  
  convert_ref_genome,  
  convert_small_p,  
  es_is_beta,  
  compute_z,  
  compute_n,  
  convert_n_int,  
  analysis_trait,  
  INFO_filter,  
  FRQ_filter,  
  pos_se,  
  effect_columns_nonzero,  
  N_std,  
  N_dropNA,  
  chr_style,  
  rmv_chr,  
  on_ref_genome,  
  infer_eff_direction,  
  strand_ambig_filter,  
  allele_flip_check,  
  allele_flip_drop,  
  allele_flip_z,  
  allele_flip_frq,  
  bi_allelic_filter,  
  flip_frq_as_biallelic,  
  snp_ids_are_rs_ids,  
  remove_multi_rs_snp,  
  frq_is_maf,  
  indels,  
  drop_indels,  
  check_dups,  
  dbSNP,  
  write_vcf,  
  return_format,  
  ldsc_format,  
  save_format,  
  imputation_ind,  
  log_folder_ind,  
  log_mungesumstats_msgs,  
  mapping_file,  
  tabix_index,  
  chain_source,  
  local_chain,  
  drop_na_cols,  
  rmv_chrPrefix
```

)

**Arguments**

path	Filepath for the summary statistics file to be formatted. A dataframe or datatable of the summary statistics file can also be passed directly to MungeSumstats using the path parameter.
ref_genome	name of the reference genome used for the GWAS ("GRCh37" or "GRCh38"). Argument is case-insensitive. Default is NULL which infers the reference genome from the data.
convert_ref_genome	name of the reference genome to convert to ("GRCh37" or "GRCh38"). This will only occur if the current genome build does not match. Default is not to convert the genome build (NULL).
convert_small_p	Binary, should non-negative p-values $\leq 5e-324$ be converted to 0? Small p-values pass the R limit and can cause errors with LDSC/MAGMA and should be converted. Default is TRUE.
es_is_beta	Binary, whether to map ES to BETA. We take BETA to be any BETA-like value (including Effect Size). If this is not the case for your sumstats, change this to FALSE. Default is TRUE.
compute_z	Whether to compute Z-score column. Default is FALSE. This can be computed from Beta and SE with $(\text{Beta}/\text{SE})$ or $P (Z:=\text{sign}(\text{BETA}) * \sqrt{\text{stats::qchisq}(P,1,\text{lower}=\text{FALSE})})$ . <b>Note</b> that imputing the Z-score from P for every SNP will not be perfectly correct and may result in a loss of power. This should only be done as a last resort. Use 'BETA' to impute by BETA/SE and 'P' to impute by SNP p-value.
compute_n	Whether to impute N. Default of 0 won't impute, any other integer will be imputed as the N (sample size) for every SNP in the dataset. <b>Note</b> that imputing the sample size for every SNP is not correct and should only be done as a last resort. N can also be inputted with "ldsc", "sum", "giant" or "metal" by passing one of these for this field or a vector of multiple. Sum and an integer value creates an N column in the output whereas giant, metal or ldsc create an Neff or effective sample size. If multiples are passed, the formula used to derive it will be indicated.
convert_n_int	Binary, if N (the number of samples) is not an integer, should this be rounded? Default is TRUE.
analysis_trait	If multiple traits were studied, name of the trait for analysis from the GWAS. Default is NULL.
INFO_filter	numeric The minimum value permissible of the imputation information score (if present in sumstats file). Default 0.9.
FRQ_filter	numeric The minimum value permissible of the frequency(FRQ) of the SNP (i.e. Allele Frequency (AF)) (if present in sumstats file). By default no filtering is done, i.e. value of 0.
pos_se	Binary Should the standard Error (SE) column be checked to ensure it is greater than 0? Those that are, are removed (if present in sumstats file). Default TRUE.

effect_columns_nonzero	Binary should the effect columns in the data BETA,OR (odds ratio),LOG_ODDS,SIGNED_SUMSTAT be checked to ensure no SNP=0. Those that do are removed(if present in sum-stats file). Default FALSE.
N_std	numeric The number of standard deviations above the mean a SNP's N is needed to be removed. Default is 5.
N_dropNA	Drop rows where N is missing.Default is TRUE.
chr_style	Chromosome naming style to use in the formatted summary statistics file ("NCBI", "UCSC", "dbSNP", or "Ensembl"). The NCBI and Ensembl styles both code chromosomes as 1-22, X, Y, MT; the UCSC style is chr1-chr22, chrX, chrY, chrM; and the dbSNP style is ch1-ch22, chX, chY, chMT. Default is Ensembl.
rmv_chr	Chromosomes to exclude from the formatted summary statistics file. Use NULL if no filtering is necessary. Default is c("X", "Y", "MT") which removes all non-autosomal SNPs.
on_ref_genome	Binary Should a check take place that all SNPs are on the reference genome by SNP ID. Default is TRUE.
infer_eff_direction	Binary Should a check take place to ensure the alleles match the effect direction? Default is TRUE.
strand_ambig_filter	Binary Should SNPs with strand-ambiguous alleles be removed. Default is FALSE.
allele_flip_check	Binary Should the allele columns be checked against reference genome to infer if flipping is necessary. Default is TRUE.
allele_flip_drop	Binary Should the SNPs for which neither their A1 or A2 base pair values match a reference genome be dropped. Default is TRUE.
allele_flip_z	Binary should the Z-score be flipped along with effect and FRQ columns like Beta? It is assumed to be calculated off the effect size not the P-value and so will be flipped i.e. default TRUE.
allele_flip_frq	Binary should the frequency (FRQ) column be flipped along with effect and z-score columns like Beta? Default TRUE.
bi_allelic_filter	Binary Should non-biallelic SNPs be removed. Default is TRUE.
flip_frq_as_biallelic	Binary Should non-bi-allelic SNPs frequency values be flipped as 1-p despite there being other alternative alleles? Default is FALSE but if set to TRUE, this allows non-bi-allelic SNPs to be kept despite needing flipping.
snp_ids_are_rs_ids	Binary Should the supplied SNP ID's be assumed to be RSIDs. If not, imputation using the SNP ID for other columns like base-pair position or chromosome will not be possible. If set to FALSE, the SNP RS ID will be imputed from the reference genome if possible. Default is TRUE.

remove_multi_rs_snp	Binary Sometimes summary statistics can have multiple RSIDs on one row (i.e. related to one SNP), for example "rs5772025_rs397784053". This can cause an error so by default, the first RS ID will be kept and the rest removed e.g. "rs5772025". If you want to just remove these SNPs entirely, set it to TRUE. Default is FALSE.
frq_is_maf	Conventionally the FRQ column is intended to show the minor/effect allele frequency (MAF) but sometimes the major allele frequency can be inferred as the FRQ column. This logical variable indicates that the FRQ column should be renamed to MAJOR_ALLELE_FRQ if the frequency values appear to relate to the major allele i.e. >0.5. By default this mapping won't occur i.e. is TRUE.
indels	Binary does your Sumstats file contain Indels? These don't exist in our reference file so they will be excluded from checks if this value is TRUE. Default is TRUE.
drop_indels	Binary, should any indels found in the sumstats be dropped? These can not be checked against a reference dataset and will have the same RS ID and position as SNPs which can affect downstream analysis. Default is False.
check_dups	whether to check for duplicates - if formatting QTL datasets this should be set to FALSE otherwise keep as TRUE. Default is TRUE.
dbSNP	version of dbSNP to be used for imputation (144 or 155).
write_vcf	Whether to write as VCF (TRUE) or tabular file (FALSE).
return_format	If return_data is TRUE. Object type to be returned ("data.table", "vranges", "granges").
ldsc_format	DEPRECATED, do not use. Use save_format="LDSC" instead.
save_format	Output format of sumstats. Options are NULL - standardised output format from MungeSumstats, LDSC - output format compatible with LDSC and openGWAS - output compatible with openGWAS VCFs. Default is NULL. <b>NOTE</b> - If LDSC format is used, the naming convention of A1 as the reference (genome build) allele and A2 as the effect allele will be reversed to match LDSC (A1 will now be the effect allele). See more info on this <a href="#">here</a> . Note that any effect columns (e.g. Z) will be in relation to A1 now instead of A2.
imputation_ind	Binary Should a column be added for each imputation step to show what SNPs have imputed values for differing fields. This includes a field denoting SNP allele flipping (flipped). On the flipped value, this denoted whether the alleles were switched based on MungeSumstats initial choice of A1, A2 from the input column headers and thus may not align with what the creator intended. <b>Note</b> these columns will be in the formatted summary statistics returned. Default is FALSE.
log_folder_ind	Binary Should log files be stored containing all filtered out SNPs (separate file per filter). The data is outputted in the same format specified for the resulting sumstats file. The only exception to this rule is if output is vcf, then log file saved as .tsv.gz. Default is FALSE.
log_mungesumstats_msgs	Binary Should a log be stored containing all messages and errors printed by MungeSumstats in a run. Default is FALSE
mapping_file	MungeSumstats has a pre-defined column-name mapping file which should cover the most common column headers and their interpretations. However, if a column header that is in your file is missing of the mapping we give is incorrect

you can supply your own mapping file. Must be a 2 column dataframe with column names "Uncorrected" and "Corrected". See `data(sumstatsColHeaders)` for default mapping and necessary format.

tabix_index	Index the formatted summary statistics with <code>tabix</code> for fast querying.
chain_source	source of the chain file to use in liftover, if converting genome build ("ucsc" or "ensembl"). Note that the UCSC chain files require a license for commercial use. The Ensembl chain is used by default ("ensembl").
local_chain	Path to local chain file to use instead of downloading. Default of NULL i.e. no local file to use. NOTE if passing a local chain file make sure to specify the path to convert from and to the correct build like GRCh37 to GRCh38. We can not sense check this for local files. The chain file can be submitted as a gz file (as downloaded from source) or unzipped.
drop_na_cols	A character vector of column names to be checked for missing values. Rows with missing values in any of these columns (if present in the dataset) will be dropped. If NULL, all columns will be checked for missing values. Default columns are SNP, chromosome, position, allele 1, allele2, effect columns (frequency, beta, Z-score, standard error, log odds, signed sumstats, odds ratio), p value and N columns.
rmv_chrPrefix	Is now deprecated, do. not use. Use <code>chr_style</code> instead - <code>chr_style = 'Ensembl'</code> will give the same result as <code>rmv_chrPrefix=TRUE</code> used to give.

**Value**

No return

---

vcf2df	<i>VCF to DF</i>
--------	------------------

---

**Description**

Function to convert a **VariantAnnotation** CollapsedVCF/ExpandedVCF object to a `data.frame`.

**Usage**

```
vcf2df(
  vcf,
  add_sample_names = TRUE,
  add_rowranges = TRUE,
  drop_empty_cols = TRUE,
  unique_cols = TRUE,
  unique_rows = TRUE,
  unlist_cols = TRUE,
  sampled_rows = NULL,
  verbose = TRUE
)
```

**Arguments**

vcf	Variant Call Format (VCF) file imported into R as a <b>VariantAnnotation CollapsedVCF/ ExpandedVCF</b> object.
add_sample_names	Append sample names to column names (e.g. "EZ" -> "EZ_ubm-a-2929").
add_rowranges	Include rowRanges from VCF as well.
drop_empty_cols	Drop columns that are filled entirely with: NA, ".", or "".
unique_cols	Only keep uniquely named columns.
unique_rows	Only keep unique rows.
unlist_cols	If any columns are lists instead of vectors, unlist them. Required to be TRUE when unique_rows=TRUE.
sampled_rows	First N rows to sample. Set NULL to use full sumstats_file. when determining whether cols are empty.
verbose	Print messages.

**Value**

data.frame version of VCF

**Source**

[Original code source](#)

**vcfR:**

```
if(!require("pinfsc50")) install.packages("pinfsc50") vcf_file <- system.file("extdata", "pinf_sc50.vcf.gz",
package = "pinfsc50") vcf <- read.vcfR( vcf_file, verbose = FALSE ) vcf_df_list <- vcfR::vcfR2tidy(vcf,
single_frame=TRUE) vcf_df <- data.table::data.table(vcf_df_list$dat)
```

**Examples**

```
#### VariantAnnotation ####
# path <- "https://github.com/brentp/vcfanno/raw/master/example/exac.vcf.gz"
path <- system.file("extdata", "ALSvcf.vcf",
                    package = "MungeSumstats")

vcf <- VariantAnnotation::readVcf(file = path)
vcf_df <- MungeSumstats::vcf2df(vcf = vcf)
```



---

write_sumstats	<i>Write sum stats file to disk</i>
----------------	-------------------------------------

---

## Description

Write sum stats file to disk

## Usage

```
write_sumstats(
  sumstats_dt,
  save_path,
  ref_genome = NULL,
  sep = "\t",
  write_vcf = FALSE,
  save_format = NULL,
  tabix_index = FALSE,
  nThread = 1,
  return_path = FALSE,
  save_path_check = FALSE
)
```

## Arguments

sumstats_dt	data table obj of the summary statistics file for the GWAS.
save_path	File path to save formatted data. Defaults to <code>tempfile(fileext=".tsv.gz")</code> .
ref_genome	name of the reference genome used for the GWAS ("GRCh37" or "GRCh38"). Argument is case-insensitive. Default is NULL which infers the reference genome from the data.
sep	The separator between columns. Defaults to the character in the set <code>[\t   ; :]</code> that separates the sample of rows into the most number of lines with the same number of fields. Use NULL or "" to specify no separator; i.e. each line a single character column like <code>base::readLines</code> does.
write_vcf	Whether to write as VCF (TRUE) or tabular file (FALSE).
save_format	Output format of sumstats. Options are NULL - standardised output format from MungeSumstats, LDSC - output format compatible with LDSC and openGWAS - output compatible with openGWAS VCFs. Default is NULL. <b>NOTE</b> - If LDSC format is used, the naming convention of A1 as the reference (genome build) allele and A2 as the effect allele will be reversed to match LDSC (A1 will now be the effect allele). See more info on this <a href="#">here</a> . Note that any effect columns (e.g. Z) will be in relation to A1 now instead of A2.
tabix_index	Index the formatted summary statistics with <code>tabix</code> for fast querying.
nThread	The number of threads to use. Experiment to see what works best for your data on your hardware.

`return_path` Return `save_path`. This will have been modified in some cases (e.g. after compressing and tabix-indexing a previously un-compressed file).

`save_path_check` Ensure path name is valid (given the other arguments) before writing (default: FALSE).

**Value**

If `return_path=TRUE`, returns `save_path`. Else returns NULL.

**Source**

**VariantAnnotation::writeVcf has some unexpected/silent file renaming behavior**

**Examples**

```
path <- system.file("extdata", "eduAttain0kbay.txt",
  package = "MungeSumstats"
)
eduAttain0kbay <- read_sumstats(path = path)
write_sumstats(
  sumstats_dt = eduAttain0kbay,
  save_path = tempfile(fileext = ".tsv.gz")
)
```

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