

# Package ‘BiocHail’

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**Title** basilisk and hail

**Version** 1.7.1

**Description** Use hail via basilisk when appropriate, or via reticulate.  
This package can be used in terra.bio to interact with UK Biobank resources processed by hail.is.

**License** Artistic-2.0

**Encoding** UTF-8

**Depends** R (>= 4.3.0), graphics, stats, utils

**Imports** reticulate, basilisk, BiocFileCache, methods, dplyr,  
BiocGenerics

**Suggests** knitr, testthat, BiocStyle, ggplot2, DT

**VignetteBuilder** knitr

**biocViews** Infrastructure

**RoxygenNote** 7.3.2

**URL** <https://github.com/vjcitn/BiocHail>

**BugReports** <https://github.com/vjcitn/BiocHail/issues>

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---

as.data.frame	<i>S3 support</i>
---------------	-------------------

---

### Description

S3 support

### Usage

```
as.data.frame(x, row.names = NULL, optional = FALSE, ...)
```

### Arguments

x	entity coercible to data.frame
row.names	character or NULL
optional	logical
...	any args

**Value**

data.frame

**Examples**

```
hl <- hail_init()
annopath <- path_1kg_annotations()
tab <- hl$import_table(annopath, impute = TRUE)$key_by("Sample")
as.data.frame(tab$head(3L))
```

---

as.data.frame.default *S3 support*

---

**Description**

S3 support

**Usage**

```
## Default S3 method:
as.data.frame(x, row.names = NULL, optional = FALSE, ...)
```

**Arguments**

x	entity coercible to data.frame
row.names	character or NULL
optional	logical
...	any args

**Value**

data.frame

**Examples**

```
hl <- hail_init()
annopath <- path_1kg_annotations()
tab <- hl$import_table(annopath, impute = TRUE)$key_by("Sample")
as.data.frame(tab$head(3L))
```

---

```
as.data.frame.hail.table.Table
      convert hail.table.Table to R data frame
```

---

**Description**

convert hail.table.Table to R data frame

**Usage**

```
## S3 method for class 'hail.table.Table'
as.data.frame(x, row.names = NULL, optional = FALSE, ...)
```

**Arguments**

x	instance of "hail.table.Table"
row.names	not used
optional	not used
...	not used

**Value**

data.frame

**Note**

only use on small table because collect is used

**Examples**

```
h1 <- hail_init()
annopath <- path_1kg_annotations()
tab <- h1$import_table(annopath, impute = TRUE)$key_by("Sample")
as.data.frame(tab$head(3L))
```

---

```
bare_hail      bare interface to hail using reticulate
```

---

**Description**

bare interface to hail using reticulate

**Usage**

```
bare_hail()
```

**Value**

python reference to hail module

**Note**

'/home/jupyter/.local/share/r-miniconda/envs/r-reticulate/bin/pip3 install...' is used to ensure that reticulate's python ecosystem is what we want

**Examples**

```
# assumes terra
if (nchar(Sys.getenv("WORKSPACE_NAMESPACE"))>0) {
  hl = bare_hail()
  hl$init(idempotent=TRUE, spark_conf=list(
    'spark.hadoop.fs.gs.requester.pays.mode'= 'CUSTOM',
    'spark.hadoop.fs.gs.requester.pays.buckets'= 'ukb-diverse-pops-public',
    'spark.hadoop.fs.gs.requester.pays.project.id'= Sys.getenv("GOOGLE_PROJECT")))
  hl$read_matrix_table('gs://ukb-diverse-pops-public/sumstats_release/results_full.mt')$describe()
  ## Not run:
  # this is supposed to get us some LD data but xx.shape fails, issue filed
  hli = reticulate::import("hail.linalg")
  upa = reticulate::import("ukbb_pan_ancestry")
  xx = hli$BlockMatrix$read(upa$get_ld_matrix_path('AFR'))

  ## End(Not run)
}
```

---

colnames,hail.table.Table-method

*extract field names from hail.table.Table*

---

**Description**

extract field names from hail.table.Table

**Usage**

```
## S4 method for signature 'hail.table.Table'
colnames(x, do.NULL = TRUE, prefix = "col")
```

**Arguments**

x	hail.table.Table instance
do.NULL	ignored
prefix	ignored

**Value**

character vector

**Examples**

```

hl <- hail_init()
annopath <- path_1kg_annotations()
tab <- hl$import_table(annopath, impute = TRUE)$key_by("Sample")
colnames(tab)

```

---

filter

*s3 support*


---

**Description**

s3 support

**Usage**

```
filter(.data, ..., .by = NULL, .preserve = FALSE)
```

**Arguments**

<code>.data</code>	instance of <code>hail.table.Table</code>
<code>...</code>	should include named components ‘filter’ which is a logical vector with same number of rows as ‘.data’, ‘hl’, a reference to a hail environment (Module), and ‘placeholder’ an arbitrary character(1)
<code>.by</code>	not used
<code>.preserve</code>	not used

**Value**

filtered `hail.table.Table` reference

**Examples**

```

hl <- hail_init()
annopath <- path_1kg_annotations()
tab <- hl$import_table(annopath, impute = TRUE)$key_by("Sample")
pick <- rep(FALSE, 3500)
pick[seq_len(10)] <- TRUE
ft <- filter(tab, filter = pick, hl = hl)
ft$count()
ft$head(2L)$collect()

```

---

`filter.hail.table.Table`*filter rows of a hail Table*

---

**Description**

filter rows of a hail Table

**Usage**

```
## S3 method for class 'hail.table.Table'  
filter(.data, ..., .by = NULL, .preserve = FALSE)
```

**Arguments**

<code>.data</code>	instance of <code>hail.table.Table</code>
<code>...</code>	should include named components 'filter' which is a logical vector with same number of rows as <code>.data</code> , 'hl', a reference to a hail environment (Module), and 'placeholder' an arbitrary character(1)
<code>.by</code>	not used
<code>.preserve</code>	not used

**Value**

filtered `hail.table.Table` reference

**Note**

writes one line of table to disk to retrieve field names

FIXME: uses disk because I don't know how to create a `BooleanExpression` except by importing.

**Examples**

```
hl <- hail_init()  
annopath <- path_1kg_annotations()  
tab <- hl$import_table(annopath, impute = TRUE)$key_by("Sample")  
pick <- rep(FALSE, 3500)  
pick[seq_len(10)] <- TRUE  
ft <- filter(tab, filter = pick, hl = hl)  
ft$count()  
ft$head(2L)$collect()
```

---

get\_1kg                      *interface to 1kg import*

---

### Description

interface to 1kg import

### Usage

```
get_1kg(
  hl,
  retrieve_import_write = FALSE,
  path_1kg_zip = osn_1kg_path(),
  folder = tempdir(),
  cache = BiocFileCache::BiocFileCache()
)
```

### Arguments

hl	hail object
retrieve_import_write	logical(1) if TRUE, use hl.utils.get_1kg to retrieve data, otherwise acquire a previously written zip file, either from a cache, or, if no file found in cache, from web, followed by caching
path_1kg_zip	character(1) path to zip of MatrixTable, defaults to 'osn_1kg_path()'.
folder	character(1) destination of 1kg.mt as retrieved using hl.utils.get_1kg, import_vcf, write
cache	a BiocFileCache-type cache

### Value

"hail.matrixtable.MatrixTable" instance

### Note

overwrite is permitted in the import\_vcf.write event

### Examples

```
hl <- hail_init()
mt <- get_1kg(hl)
mt
mt$rows()$select()$show(5L) # must use integer
annopath <- path_1kg_annotations()
tab <- hl$import_table(annopath, impute = TRUE)$key_by("Sample")
tab$describe()
tab$show(width = 100L)
```



---

get_key	<i>S3 generic for get_key</i>
---------	-------------------------------

---

**Description**

S3 generic for get\_key

**Usage**

```
get_key(x)
```

**Arguments**

x                    anything

**Value**

typically a list

**Examples**

```
hl <- hail_init()
annopath <- path_1kg_annotatons()
tab <- hl$import_table(annopath, impute = TRUE)$key_by("Sample")
get_key(tab)
```

---

get_key.hail.table.Table	<i>S3 method for get_key</i>
--------------------------	------------------------------

---

**Description**

S3 method for get\_key

**Usage**

```
## S3 method for class 'hail.table.Table'
get_key(x)
```

**Arguments**

x                    instance of hail.table.Table

**Value**

a list with elements names (names of keys) and key\_df (data.frame of key values, with column names)

**Examples**

```
hl <- hail_init()
annopath <- path_1kg_annotatons()
tab <- hl$import_table(annopath, impute = TRUE)$key_by("Sample")
get_key(tab)
```

---

```
get_ukbb_sumstat_10kloci_mt
      interface to a small subset of UKBB summary stats in MatrixTable
      format
```

---

**Description**

interface to a small subset of UKBB summary stats in MatrixTable format

**Usage**

```
get_ukbb_sumstat_10kloci_mt(
  hl,
  folder = tempdir(),
  cache = BiocFileCache::BiocFileCache(),
  timeout.ukbb = 3600
)
```

**Arguments**

hl	hail object
folder	character(1) destination of 1kg.mt as retrieved using hl.utils.get_1kg, import_vcf, write
cache	a BiocFileCache-type cache
timeout.ukbb	numeric(1) defaults to 3600 for timeout setting in ‘options()’; option value is reset on exit

**Value**

"hail.matrixtable.MatrixTable" instance

**Note**

The loci were selected using a .000345 of over 28 million loci recorded in the UKBB pan-ancestry record. The sample is made available a) to assess some issues with data volume (the full resource is about 12.78 TB according to [this doc](<https://pan-dev.ukbb.broadinstitute.org/docs/hail-format/index.html>), and b) to provide full information on the scope of phenotypes and populations available.

This function will unzip 5GB of MatrixTable data. It may be desirable to cache the unzipped image to a persistent location. If this has been done and the environment variable ‘HAIL\_UKBB\_SUMSTAT\_10K\_PATH’ has been set to this location, this function will use the MatrixTable content found there.

**Examples**

```
hl <- hail_init()
ss <- get_ukbb_sumstat_10kloci_mt(hl)
# consider saving the unzipped image and recaching
ss$count()
```

---

hail_init	<i>initialize hail, using more options</i>
-----------	--

---

**Description**

initialize hail, using more options

**Usage**

```
hail_init(
  quiet = FALSE,
  min_block_size = 0L,
  branching_factor = 50L,
  default_reference = "GRCh37",
  global_seed = 1234L,
  log = tempfile(),
  spark_conf = NULL,
  gcs_requester_pays_configuration = NULL
)
```

**Arguments**

quiet	logical(1) defaults to FALSE
min_block_size	integer(1) defaults to 0L
branching_factor	integer(1) defaults to 50L
default_reference	character(1) defaults to "GRCh37", for compatibility with earlier 'hail_init'
global_seed	integer(1) defaults to 1234L
log	character(1) target folder for logging, defaults to tempfile()
spark_conf	list, defaults to NULL
gcs_requester_pays_configuration	list, defaults to NULL

**Value**

python reference to hail module

**Note**

hail object may be passed around. See hail documentation for details on all args.

**Examples**

```
proj = Sys.getenv("GOOGLE_PROJECT")
buck = Sys.getenv("GCS_BUCKET")
if (nchar(buck)>0) {
  # conf = list(proj, c(buck)) doesn't seem to generate tuple[str,Sequence[str]]
  hl <- hail_init() #gcs_requester_pays_configuration=conf
  hl$default_reference()
}
```

---

hail_init_simple	<i>initialize hail</i>
------------------	------------------------

---

**Description**

initialize hail

**Usage**

```
hail_init_simple()
```

**Value**

python reference to hail module

**Note**

hail object may be passed around

**Examples**

```
hc <- hail_init_simple()
hc
```

---

hail_stop	<i>stop hail</i>
-----------	------------------

---

**Description**

stop hail

**Usage**

```
hail_stop(hl)
```

**Arguments**

hl                    a hail object produced by hail\_init()

**Value**

result of stop() method for Hail module

**Examples**

```
hail_stop
```

---

kg_3202	<i>data.frame with metadata about 3202 samples genotyped against T2T reference</i>
---------	--

---

**Description**

data.frame with metadata about 3202 samples genotyped against T2T reference

**Usage**

```
data("kg_3202")
```

**Format**

data.frame

**Value**

data.frame

**Note**

Source: index files described at ‘<https://www.internationalgenome.org/data-portal/data-collection/30x-grch38>‘

**Examples**

```
data(kg_3202)
dim(kg_3202)
```

---

multipop_df	<i>pheno_data component harvesting from columns of summary stats MatrixTable allowing for info on multiple populations in the pheno_data component</i>
-------------	--

---

**Description**

pheno\_data component harvesting from columns of summary stats MatrixTable allowing for info on multiple populations in the pheno\_data component

**Usage**

```
multipop_df(
  x,
  top2get = c("trait_type", "phenocode", "description", "modifier", "coding_description",
             "coding"),
  pheno2get = c("n_cases", "n_controls", "heritability", "pop")
)
```

**Arguments**

x	Struct - a single element of the list returned by mt\$cols()\$collect()
top2get	character() vector of general fields to retrieve
pheno2get	character() vector of fields to be retrieved for each subpopulation

**Value**

data.frame

**Examples**

```
# following are too time-consuming but can be of interest
# if (nchar(Sys.getenv("HAIL_UKBB_SUMSTAT_10K_PATH"))>0) {
#   hl = hail_init()
#   ss = get_ukbb_sumstat_10kloci_mt(hl)
#   sscol = ss$cols()$collect() # may take a bit of time
#   print(length(sscol))
#   multipop_df(sscol[[1]])
# }
#

# if (nchar(Sys.getenv("HAIL_UKBB_SUMSTAT_10K_PATH"))>0) {
# # to get an overview of all phenotype-cohort combinations in a searchable table
# mmm = lapply(sscol, multipop_df )
```

```

# mymy = do.call(rbind, mmm) # over 16k rows
# DT::datatable(mymy)
# }
#

# this runs quickly and is demonstrative
hl <- hail_init()
litzip <- system.file("extdata", "myss2.zip", package = "BioHail")
td <- tempdir()
unzip(litzip, exdir = td)
ntab <- hl$read_matrix_table(paste0(td, "/myss2.mt"))
ntab$describe()
nt2 <- ntab$col$collect()
multipop_df(nt2[[1]]) # must select one element

```

---

osn_1kg_path	<i>Open Storage Network path to a zip of hail MatrixTable with some 1kg data for the Hail.is GWAS tutorial</i>
--------------	--

---

### Description

Open Storage Network path to a zip of hail MatrixTable with some 1kg data for the Hail.is GWAS tutorial

### Usage

```
osn_1kg_path()
```

### Value

character(1) URL to zip

### Examples

```
osn_1kg_path()
```

---

osn_ukbb_sumst10k_path	<i>Open Storage Network path to a zip of hail MatrixTable with a small subset of UKBB summary statistics as of 12/25/2022</i>
------------------------	---

---

### Description

Open Storage Network path to a zip of hail MatrixTable with a small subset of UKBB summary statistics as of 12/25/2022

**Usage**

```
osn_ukbb_sumst10k_path()
```

**Value**

character(1) path to zip

**Examples**

```
osn_ukbb_sumst10k_path()
```

---

`path_1kg_annotations` *generate path to installed annotations file*

---

**Description**

generate path to installed annotations file

**Usage**

```
path_1kg_annotations()
```

**Value**

character(1) path to annotations

**Note**

.txt file retrieved from extraction on '[https://storage.googleapis.com/hail-1kg/tutorial\\_data.tar](https://storage.googleapis.com/hail-1kg/tutorial_data.tar)'

**Examples**

```
path_1kg_annotations()
```



---

pcs_191k	<i>HWE-normalized PCA scores for 3202 thousand-genomes samples genotyped with the telomere-to-telomere reference</i>
----------	--

---

**Description**

HWE-normalized PCA scores for 3202 thousand-genomes samples genotyped with the telomere-to-telomere reference

**Usage**

```
data("pcs_191k")
```

**Format**

data.frame

**Value**

data.frame

**Note**

The genotypes are from a 5

**Examples**

```
data(pcs_191k)
dim(pcs_191k)
```

---

pcs_38k	<i>HWE-normalized PCA scores for 3202 thousand-genomes samples genotyped with the telomere-to-telomere reference</i>
---------	--

---

**Description**

HWE-normalized PCA scores for 3202 thousand-genomes samples genotyped with the telomere-to-telomere reference

**Usage**

```
data("pcs_38k")
```

**Format**

data.frame

**Value**

data.frame

**Note**

The genotypes are from a 1

**Examples**

```
data(pcs_38k)
dim(pcs_38k)
```

---

pheno_data_sec_2df	<i>pheno_data component harvesting from columns of summary stats MatrixTable</i>
--------------------	--

---

**Description**

pheno\_data component harvesting from columns of summary stats MatrixTable

**Usage**

```
pheno_data_sec_2df(
  m,
  section = 1,
  toget = c("n_cases", "n_controls", "heritability", "pop"),
  verbose = FALSE
)
```

**Arguments**

m	Struct returned from mt\$cols()\$collect()
section	numeric(1) element of pheno_data list to be transformed to data.frame
toget	character() vector of field names to retrieve
verbose	logical(1) if TRUE (NOT default) will message that there are multiple 'pheno_data' components returned

**Value**

1 row data.frame

**Note**

applies top2df to the pheno\_data component of input

---

rg_update	<i>update the reference genome for a hail instance</i>
-----------	--

---

**Description**

update the reference genome for a hail instance

**Usage**

```
rg_update(
  hc,
  init = "GRCh38",
  newjson = system.file("json/t2tAnVIL.json", package = "BiocHail")
)
```

**Arguments**

hc	hail context
init	character(1) valid name for a reference genome, defaults to "GRCh38"
newjson	character(1) path to a json spec of a reference genome [needs doc]

**Value**

a python list; the function is used for its side effect

**Examples**

```
hl <- hail_init()
rg_update(hl)
```

---

rownames, hail.table.Table-method	<i>acquire row names of a Hail Table, assuming key has been set</i>
-----------------------------------	---

---

**Description**

acquire row names of a Hail Table, assuming key has been set

**Usage**

```
## S4 method for signature 'hail.table.Table'
rownames(x, do.NULL = TRUE, prefix = "row")
```

**Arguments**

x instance of `hail.table.Table`  
do.NULL not used  
prefix not used

**Value**

character()  
character vector

**Note**

To try example, run `example("rownames,hail.table.Table-method")`

**Examples**

```
h1 <- hail_init()
annopath <- path_1kg_annotiations()
tab <- h1$import_table(annopath, impute = TRUE)$key_by("Sample")
rt <- rownames(tab)
length(rt)
head(rt)
```

---

top2df	<i>top-level annotation harvesting from columns of summary statistics MatrixTable</i>
--------	---

---

**Description**

top-level annotation harvesting from columns of summary statistics MatrixTable

**Usage**

```
top2df(
  x,
  toget = c("trait_type", "phenocode", "description", "modifier", "coding_description")
)
```

**Arguments**

x a Struct returned from `mt$cols()$collect()` – which can be slow  
toget character() vector of field names to retrieve

**Value**

1-row data.frame

**Note**

python None are transformed to NA

---

ukbb\_init

*initialize ukbb*

---

**Description**

initialize ukbb

**Usage**

```
ukbb_init()
```

**Value**

python module reference

**Note**

ukbb module may be passed around

**Examples**

```
ukbb <- ukbb_init()
names(ukbb)
```

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