

# Package ‘GA4GHclient’

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**Type** Package

**Title** A Bioconductor package for accessing GA4GH API data servers

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**Description** GA4GHclient provides an easy way to access public data servers through Global Alliance for Genomics and Health (GA4GH) genomics API. It provides low-level access to GA4GH API and translates response data into Bioconductor-based class objects.

**License** GPL (>= 2)

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GA4GHclient-package    *A Bioconductor package for accessing GA4GH API data server*

---

### Description

GA4GHclient provides an easy way to access public data servers through Global Alliance for Genomics and Health (GA4GH) genomics API. It provides low-level access to GA4GH API and translates response data into Bioconductor-based class objects.

### Author(s)

Welliton Souza, Benilton Carvalho, Cristiane Rocha

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---

getBiosample            *getBiosample function*

---

### Description

Get a biosample by its ID.

### Usage

```
getBiosample(host, biosampleId)
```

### Arguments

host                    URL of GA4GH API data server.

biosampleId            ID of the biosample requested.

### Details

This function requests GET `host/datasets/biosampleId`.

### Value

[DataFrame](#) object.

### References

[Official documentation](#).

### See Also

[DataFrame](#), [searchBiosamples](#)

## Examples

```
host <- "http://1kgenomes.ga4gh.org/"
## Not run:
datasetId <- searchDatasets(host, nrows = 1)$id
biosampleId <- searchBiosamples(host, datasetId, nrows = 1)$id
getBiosample(host, biosampleId)

## End(Not run)
```

---

getCallSet

*getCallSet function*

---

## Description

Get a call set by its ID.

## Usage

```
getCallSet(host, callSetId)
```

## Arguments

host	URL of GA4GH API data server.
callSetId	The ID of the CallSet to be retrieved.

## Details

This request maps to GET `host/callsets/callSetId`.

## Value

[DataFrame](#) object.

## References

[Official documentation](#).

## See Also

[DataFrame](#), [searchCallSets](#)

## Examples

```
host <- "http://1kgenomes.ga4gh.org/"
## Not run:
datasetId <- searchDatasets(host, nrows = 1)$id
variantSetId <- searchVariantSets(host, datasetId, nrows = 1)$id
callSetId <- searchCallSets(host, variantSetId, nrows = 1)$id
getCallSet(host, callSetId)

## End(Not run)
```

---

getDataset	<i>getDataset function</i>
------------	----------------------------

---

## Description

Get a dataset by its ID.

## Usage

```
getDataset(host, datasetId)
```

## Arguments

host	URL of GA4GH API data server.
datasetId	The ID of the dataset to be retrieved.

## Details

This function requests GET `host/datasets/datasetId`.

## Value

[DataFrame](#) object.

## References

[Official documentation.](#)

## See Also

[DataFrame](#), [searchDatasets](#)

## Examples

```
host <- "http://1kgenomes.ga4gh.org/"
## Not run:
datasetId <- searchDatasets(host, nrows = 1)$id
getDataset(host, datasetId)

## End(Not run)
```

---

getExpressionLevel     *getExpressionLevel function*

---

### Description

Get an expression level by its ID.

### Usage

```
getExpressionLevel(host, expressionLevelId)
```

### Arguments

host                    URL of GA4GH API data server.  
expressionLevelId      ID of the expression level.

### Details

This function requests GET `host/expressionlevels/expressionLevelId`.

### Value

[DataFrame](#) object.

### References

[Official documentation](#).

### See Also

[DataFrame](#), [searchExpressionLevels](#)

### Examples

```
host <- "http://1kgenomes.ga4gh.org/"  
## Not run:  
datasetId <- searchDatasets(host, nrows = 1)$id  
rnaQuantificationSetId <- searchRnaQuantificationSets(host, datasetId, nrow = 1)$id  
rnaQuantificationId <- searchRnaQuantifications(host, rnaQuantificationSetId, nrows = 1)$id  
expressionLevelId <- searchExpressionLevels(host, rnaQuantificationId, nrows = 1)$id  
getExpressionLevel(host, expressionLevelId)  
  
## End(Not run)
```

---

getFeature	<i>getFeature function</i>
------------	----------------------------

---

### Description

Get a feature set by its ID (a line of genomic feature file).

### Usage

```
getFeature(host, featureId)
```

### Arguments

host	URL of GA4GH API data server.
featureId	The ID of the feature to be retrieved.

### Details

This function requests GET `host/features/featureId`.

### Value

[DataFrame](#) object.

### References

[Official documentation.](#)

### See Also

[DataFrame](#), [searchFeatures](#)

### Examples

```
host <- "http://1kgenomes.ga4gh.org/"
## Not run:
datasetId <- searchDatasets(host, nrows = 1)$id
featureSetId <- searchFeatureSets(host, datasetId, nrows = 1)$id
featureId <- searchFeatures(host, featureSetId, nrows = 1)$id
getFeature(host, featureId)

## End(Not run)
```

---

getFeatureSet	<i>getFeatureSet function</i>
---------------	-------------------------------

---

## Description

Get a feature set by its ID.

## Usage

```
getFeatureSet(host, featureSetId)
```

## Arguments

host	URL of GA4GH API data server.
featureSetId	The ID of the FeatureSet to be retrieved.

## Details

This function requests GET `host/featuresets/featureSetId`.

## Value

[DataFrame](#) object.

## References

[Official documentation](#).

## See Also

[DataFrame](#), [searchFeatureSets](#)

## Examples

```
host <- "http://1kgenomes.ga4gh.org/"
## Not run:
datasetId <- searchDatasets(host, nrows = 1)$id
featureSetId <- searchFeatureSets(host, datasetId, nrows = 1)$id
getFeatureSet(host, featureSetId)

## End(Not run)
```



---

getIndividual	<i>getIndividual function</i>
---------------	-------------------------------

---

**Description**

Get an individual by its ID.

**Usage**

```
getIndividual(host, individualId)
```

**Arguments**

host	URL of GA4GH API data server.
individualId	ID of the individual requested.

**Details**

This function requests GET `host/individuals/individualId`.

**Value**

[DataFrame](#) object.

**References**

[Official documentation](#).

**See Also**

[DataFrame](#), [searchIndividuals](#)

**Examples**

```
host <- "http://1kgenomes.ga4gh.org/"
## Not run:
datasetId <- searchDatasets(host, nrows = 1)$id
individualId <- searchIndividuals(host, datasetId, nrows = 1)$id
getIndividual(host, individualId)

## End(Not run)
```

---

getReadGroupSet	<i>getReadGroupSet function</i>
-----------------	---------------------------------

---

## Description

Get a read group set by its ID.

## Usage

```
getReadGroupSet(host, readGroupId)
```

## Arguments

`host` URL of GA4GH API data server.  
`readGroupId` The ID of the ReadGroupSet to be retrieved.

## Details

This function requests GET `host/readgroupsets/readGroupId`.

## Value

[DataFrame](#) object.

## References

[Official documentation](#).

## See Also

[DataFrame](#), [searchReadGroupSets](#)

## Examples

```
host <- "http://1kgenomes.ga4gh.org/"
## Not run:
datasetId <- searchDatasets(host, nrows = 1)$id
readGroupId <- searchReadGroupSets(host, datasetId, nrows = 1)$id
getReadGroupSet(host, readGroupId)

## End(Not run)
```

---

getReference	<i>getReference function</i>
--------------	------------------------------

---

## Description

Get a reference by its ID.

## Usage

```
getReference(host, referenceId)
```

## Arguments

host	URL of GA4GH API data server.
referenceId	The ID of the Reference to be retrieved.

## Details

This function requests GET `host/references/referenceId`.

## Value

[DataFrame](#) object.

## References

[Official documentation](#).

## See Also

[DataFrame](#), [searchReferences](#)

## Examples

```
host <- "http://1kgenomes.ga4gh.org/"
## Not run:
referenceSetId <- searchReferenceSets(host, nrows = 1)$id
referenceId <- searchReferences(host, referenceSetId, nrows = 1)$id
getReference(host, referenceId)

## End(Not run)
```

getReferenceSet      *getReferenceSet function*

---

### Description

Get a reference set by its ID.

### Usage

```
getReferenceSet(host, referenceSetId)
```

### Arguments

host                      URL of GA4GH API data server.  
referenceSetId    The ID of the ReferenceSet to be retrieved.

### Details

This function requests GET `host/referencesets/referenceSetId`.

### Value

[DataFrame](#) object.

### References

[Official documentation](#).

### See Also

[DataFrame](#), [searchReferenceSets](#)

### Examples

```
host <- "http://1kgenomes.ga4gh.org/"  
## Not run:  
referenceSetId <- searchReferenceSets(host, nrows = 1)$id  
getReferenceSet(host, referenceSetId)  
  
## End(Not run)
```

---

getRnaQuantification *getRnaQuantification function*

---

## Description

Get an RNA quantification by its ID.

## Usage

```
getRnaQuantification(host, rnaQuantificationId)
```

## Arguments

host                   URL of GA4GH API data server.  
rnaQuantificationId    ID of the RNA quantification requested.

## Details

This function requests GET `host/rnaquantifications/rnaQuantificationId`.

## Value

[DataFrame](#) object.

## References

[Official documentation](#).

## See Also

[DataFrame](#), [searchRnaQuantifications](#)

## Examples

```
host <- "http://1kgenomes.ga4gh.org/"  
## Not run:  
datasetId <- searchDatasets(host, nrows = 1)$id  
rnaQuantificationSetId <- searchRnaQuantificationSets(host, datasetId, nrows = 1)$id  
rnaQuantificationId <- searchRnaQuantifications(host, rnaQuantificationSetId, nrows = 1)$id  
getRnaQuantification(host, rnaQuantificationId)  
  
## End(Not run)
```

---

```
getRnaQuantificationSet  
    getRnaQuantificationSet function
```

---

### Description

Get an RNA quantification set by its ID.

### Usage

```
getRnaQuantificationSet(host, rnaQuantificationSetId)
```

### Arguments

host	URL of GA4GH API data server.
rnaQuantificationSetId	ID of the RNA quantification set requested.

### Details

This function requests GET `host/rnaquantificationsets/rnaQuantificationSetId`.

### Value

[DataFrame](#) object.

### References

[Official documentation](#).

### See Also

[DataFrame](#), [searchRnaQuantificationSets](#)

### Examples

```
host <- "http://1kgenomes.ga4gh.org/"  
## Not run:  
datasetId <- searchDatasets(host, nrows = 1)$id  
rnaQuantificationSetId <- searchRnaQuantificationSets(host, datasetId, nrows = 1)$id  
getRnaQuantificationSet(host, rnaQuantificationSetId)  
  
## End(Not run)
```

---

getVariant	<i>getVariant function</i>
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---

### Description

Get a variant by its ID with all call sets for this variant.

### Usage

```
getVariant(host, variantId, asVCF = TRUE)
```

### Arguments

host	URL of GA4GH API data server.
variantId	The ID of the Variant to be retrieved.
asVCF	If TRUE the function will return an <a href="#">VCF</a> with header (default), otherwise it will return an <a href="#">DataFrame</a> .

### Details

This function requests GET `host/variants/variantId`.

### Value

[VCF](#) object (when `asVCF = TRUE`) or [DataFrame](#) object (otherwise).

### References

[Official documentation](#).

### See Also

[DataFrame](#), [searchVariants](#), [searchVariantsByGRanges](#), [VCF](#), [makeVCFFromGA4GHResponse](#)

### Examples

```
host <- "http://1kgenomes.ga4gh.org/"
## Not run:
datasetId <- searchDatasets(host, nrows = 1)$id
variantSetId <- searchVariantSets(host, datasetId, nrows = 1)$id
variantId <- searchVariants(host, variantSetId, "1", 15031, 15031)$id
getVariant(host, variantId)

getVariant(host, variantId, asVCF = FALSE)

## End(Not run)
```

---

`getVariantAnnotationSet`*Gets getVariantAnnotationSet function*

---

### Description

Get a variant annotation set by its ID.

### Usage

```
getVariantAnnotationSet(host, variantAnnotationSetId)
```

### Arguments

<code>host</code>	URL of GA4GH API data server.
<code>variantAnnotationSetId</code>	ID of variant annotation set.

### Details

This function requests GET `host/variantannotationsets/variantAnnotationSetId`.

### Value

[DataFrame](#) object.

### References

[Official documentation](#).

### See Also

[DataFrame](#), [searchVariantAnnotationSets](#)

### Examples

```
host <- "http://1kgenomes.ga4gh.org/"
## Not run:
datasetId <- searchDatasets(host, nrows = 1)$id
variantSetId <- searchVariantSets(host, datasetId, nrows = 2)$id[2]
id <- searchVariantAnnotationSets(host, variantSetId, nrows = 1)$id
getVariantAnnotationSet(host, variantAnnotationSetId = id)

## End(Not run)
```



---

getVariantSet	<i>getVariantSet</i> function.
---------------	--------------------------------

---

### Description

Get a variant set by its ID.

### Usage

```
getVariantSet(host, variantSetId, asVCFHeader = TRUE)
```

### Arguments

host	URL of GA4GH API data server.
variantSetId	The ID of the VariantSet to be retrieved.
asVCFHeader	If TRUE the function will return an <a href="#">VCFHeader</a> object (default), otherwise it will return an <a href="#">DataFrame</a> .

### Details

This function requests GET `host/variantsets/variantSetId`.

### Value

[DataFrame](#) object. It can be converted into [VCFHeader](#) object.

### See Also

[DataFrame](#), [searchVariantSets](#), [VCFHeader](#), [makeVCFHeaderFromGA4GHResponse](#)

### Examples

```
host <- "http://1kgenomes.ga4gh.org/"
## Not run:
datasetId <- searchDatasets(host, nrows = 1)$id
variantSetId <- searchVariantSets(host, datasetId, nrows = 1)$id
getVariantSet(host, variantSetId)

getVariantSet(host, variantSetId, asVCF = FALSE)

## End(Not run)
```

---

 HGVSnames

*Generate genomic variant data to HGVS nomenclature*


---

### Description

This function follows the official reference HGVS nomenclature. At this moment, it supports only 'substitution' and 'indel' for DNA sequences.

### Usage

```
HGVSnames(start, ref, alt, type = "g", seqnames = NA_character_)
```

### Arguments

start	genomic location of start
ref	reference sequence
alt	alternate sequence
type	Sequence type to be used as prefix. Allowed options are: <ul style="list-style-type: none"> <li>• g genomic (default);</li> <li>• m mitochondrial;</li> <li>• c coding DNA;</li> <li>• n non-coding DNA.</li> </ul>
seqnames	name of sequence (e.g. chr1, 1). It is optional.

### Value

Genomic coordinates of variants formatted as HGVS nomenclature.

### References

[Sequence Variant Nomenclature.](#)

### Examples

```
start <- c(45576, "88+1", 6775, 6775, 145, 9002, 4, 12345611, 58347698)
ref <- c("A", "G", "T", "TCA", "CGA", "AAAAAAAA", "GC", "G", "A")
alt <- c("C", "T", "GA", "C", "TGG", "TTT", "TG", "A", "*")
type <- c("g", "c", "g", "g", "c", "g", "g", "g", "g")
seqnames <- c("", "", NA, NA, NA, NA, NA, "chr11", NA)
HGVSnames(start, ref, alt, type, seqnames)
```

---

listReferenceBases      *listReferenceBases function*

---

## Description

Get the sequence bases of a reference genome by genomic range.

## Usage

```
listReferenceBases(host, referenceId, start = 1, end = NA_integer_)
```

## Arguments

host	URL of GA4GH API data server.
referenceId	The ID of the Reference to be retrieved.
start	The start position (1-based) of this query. Defaults to 0. Genomic positions are non-negative integers less than reference length. Requests spanning the join of circular genomes are represented as two requests one on each side of the join (position 1).
end	The end position (1-based, inclusive) of this query. Defaults to the length of this Reference.

## Details

This function requests POST `host/listreferencebases`.

## Value

[BString](#) object.

## See Also

[searchReferenceSets](#), [searchReferences](#)

## Examples

```
host <- "http://1kgenomes.ga4gh.org/"
## Not run:
referenceSetId <- searchReferenceSets(host, nrows = 1)$id
referenceId <- searchReferences(host, referenceSetId, nrows = 1)$id
listReferenceBases(host, referenceId, start = 1, end = 100)

## End(Not run)
```

```
makeVCFFromGA4GHResponse  
    makeVCFFromGA4GHResponse function
```

---

**Description**

Convert DataFrame output from [searchVariants](#) and [getVariant](#) functions to [VCF](#) class.

**Usage**

```
makeVCFFromGA4GHResponse(variants)
```

**Arguments**

variants            DataFrame generated by [searchVariants](#).

**Value**

[VCF](#) object.

**See Also**

[searchVariants](#), [getVariant](#), [VCF](#), [DataFrame](#)

**Examples**

```
host <- "http://1kgenomes.ga4gh.org/"  
## Not run:  
datasetId <- searchDatasets(host, nrows = 1)$id  
variantSetId <- searchVariantSets(host, datasetId, nrows = 1)$id  
variants <- searchVariants(host, variantSetId, referenceName = "1",  
    start = 15000, end = 16000)  
variants  
  
makeVCFFromGA4GHResponse(variants)  
  
## End(Not run)
```

---

```
makeVCFHeaderFromGA4GHResponse  
    makeVCFHeaderFromGA4GHResponse function
```

---

**Description**

Convert DataFrame output from [getVariantSet](#) function to [VCFHeader](#) class.

**Usage**

```
makeVCFHeaderFromGA4GHResponse(variantSet)
```

**Arguments**

variantSet      DataFrame generated by [getVariantSet](#) function.

**Value**

[VCFHeader](#) object.

**See Also**

[getVariantSet](#), [VCFHeader](#), [DataFrame](#)

**Examples**

```
host <- "http://1kgenomes.ga4gh.org/"
## Not run:
datasetId <- searchDatasets(host, nrows = 1)$id
variantSetId <- searchVariantSets(host, datasetId, nrows = 1)$id
variantId <- searchVariants(host, variantSetId, "1", 15031, 15031)$id
variant <- getVariant(host, variantId)

makeVCFFromGA4GHRresponse(variant)

## End(Not run)
```

---

searchBiosamples	<i>searchBiosamples</i> function
------------------	----------------------------------

---

**Description**

This function gets Biosamples matching the search criteria.

**Usage**

```
searchBiosamples(host, datasetId, name = NA_character_,
  individualId = NA_character_, nrows = Inf, responseSize = NA_integer_)
```

**Arguments**

host	URL of GA4GH API data server.
datasetId	Id of the dataset to search.
name	Returns Biosamples with the given name found by case-sensitive string matching.
individualId	Returns Biosamples for the provided individual ID.
nrows	Number of rows of the data frame returned by this function. If not defined, the function will return all entries. If the number of available entries is less than the value of this parameter, the function will silently return only the available entries.
responseSize	Specifies the number of entries to be returned by the server until reach the number of rows defined in nrows parameter or until get all available entries. If not defined, the server will return the allowed maximum response size. Increasing this the value of this parameter will reduce the number of requests and reducing the time required. The will not respect this parameter if the value is larger than its maximum response size.

**Details**

This function requests to /biosamples/search.

**Value**

[DataFrame](#) object. NULL means no registry found.

**References**

[Official documentation.](#)

**See Also**

[DataFrame](#), [getBiosample](#)

**Examples**

```
host <- "http://1kgenomes.ga4gh.org/"
## Not run:
datasetId <- searchDatasets(host, nrows = 1)$id
searchBiosamples(host, datasetId, nrows = 10)

## End(Not run)
```

---

searchCallSets

*searchCallSets function*

---

**Description**

Search for call sets (sample columns of VCF files).

**Usage**

```
searchCallSets(host, variantSetId, name = NA_character_,
  biosampleId = NA_character_, nrows = Inf, responseSize = NA_integer_)
```

**Arguments**

host	URL of GA4GH API data server.
variantSetId	The VariantSet to search.
name	Only return call sets with this name (case-sensitive, exact match).
biosampleId	Return only call sets generated from the provided BioSample ID.
nrows	Number of rows of the data frame returned by this function. If not defined, the function will return all entries. If the number of available entries is less than the value of this parameter, the function will silently return only the available entries.
responseSize	Specifies the number of entries to be returned by the server until reach the number of rows defined in nrows parameter or until get all available entries. If not defined, the server will return the allowed maximum response size. Increasing this the value of this parameter will reduce the number of requests and reducing the time required. The will not respect this parameter if the value is larger than its maximum response size.

**Details**

This function requests POST `host/callsets/search`.

**Value**

`DataFrame` object.

**See Also**

`DataFrame`, `getCallSet`

**Examples**

```
host <- "http://1kgenomes.ga4gh.org/"
## Not run:
datasetId <- searchDatasets(host, nrows = 1)$id
variantSetId <- searchVariantSets(host, datasetId, nrows = 1)$id
searchCallSets(host, variantSetId)

## End(Not run)
```

---

`searchDatasets`*searchDatasets function*

---

**Description**

Search for datasets.

**Usage**

```
searchDatasets(host, nrows = Inf, responseSize = NA_integer_)
```

**Arguments**

<code>host</code>	URL of GA4GH API data server.
<code>nrows</code>	Number of rows of the data frame returned by this function. If not defined, the function will return all entries. If the number of available entries is less than the value of this parameter, the function will silently return only the available entries.
<code>responseSize</code>	Specifies the number of entries to be returned by the server until reach the number of rows defined in <code>nrows</code> parameter or until get all available entries. If not defined, the server will return the allowed maximum response size. Increasing this the value of this parameter will reduce the number of requests and reducing the time required. The will not respect this parameter if the value is larger than its maximum response size.

**Details**

This function requests to POST `/datasets/search`.

**Value**

[DataFrame](#) object. NULL means no registry found.

**See Also**

[DataFrame](#), [getDataset](#)

**Examples**

```
host <- "http://1kgenomes.ga4gh.org/"
## Not run:
searchDatasets(host)

## End(Not run)
```

---

searchExpressionLevels

*searchExpressionLevels function*

---

**Description**

This function gets expression levels matching the search criteria.

**Usage**

```
searchExpressionLevels(host, rnaQuantificationId, nrows = Inf,
  responseSize = NA_integer_)
```

**Arguments**

host	URL of GA4GH API data server.
rnaQuantificationId	Id of the rnaQuantification to restrict search to.
nrows	Number of rows of the data frame returned by this function. If not defined, the function will return all entries. If the number of available entries is less than the value of this parameter, the function will silently return only the available entries.
responseSize	Specifies the number of entries to be returned by the server until reach the number of rows defined in nrows parameter or until get all available entries. If not defined, the server will return the allowed maximum response size. Increasing this the value of this parameter will reduce the number of requests and reducing the time required. The will not respect this parameter if the value is larger than its maximum response size.

**Details**

This function requests to /expressionlevels/search.

**Value**

[DataFrame](#) object. NULL means no registry found.



## References

[Official documentation.](#)

## See Also

[DataFrame](#), [getExpressionLevel](#), [searchRnaQuantificationSets](#)

## Examples

```
host <- "http://1kgenomes.ga4gh.org/"
## Not run:
datasetId <- searchDatasets(host, nrows = 1)$id
rnaQuantificationSetId <- searchRnaQuantificationSets(host, datasetId, nrow = 1)$id
rnaQuantificationId <- searchRnaQuantifications(host, rnaQuantificationSetId, nrows = 1)$id
searchExpressionLevels(host, rnaQuantificationId, nrows = 10)

## End(Not run)
```

---

searchFeatures	<i>searchFeatures function</i>
----------------	--------------------------------

---

## Description

Search for features (lines of genomic feature files).

## Usage

```
searchFeatures(host, featureSetId, name = NA_character_,
  geneSymbol = NA_character_, parentId = NA_character_,
  referenceName = NA_character_, start = NA_integer_, end = NA_integer_,
  featureTypes = character(), nrows = Inf, responseSize = NA_integer_)
```

## Arguments

host	URL of GA4GH API data server.
featureSetId	The annotation set to search within. Either featureSetId or parentId must be non-empty.
name	Only returns features with this name (case-sensitive, exact match).
geneSymbol	Only return features with matching the provided gene symbol (case-sensitive, exact match). This field may be replaced with a more generic representation in a future version.
parentId	Restricts the search to direct children of the given parent feature ID. Either feature_set_id or parent_id must be non-empty.
referenceName	Only return features on the reference with this name (matched to literal reference name as imported from the GFF3).
start	Required, if name or symbol not provided. The beginning of the window (0-based, inclusive) for which overlapping features should be returned. Genomic positions are non-negative integers less than reference length. Requests spanning the join of circular genomes are represented as two requests one on each side of the join (position 0).

end	Required, if name or symbol not provided. The end of the window (0-based, exclusive) for which overlapping features should be returned.
featureTypes	TODO: To be replaced with a fully featured ontology search once the Metadata definitions are rounded out. If specified, this query matches only annotations whose feature_type matches one of the provided ontology terms.
nrows	Number of rows of the data frame returned by this function. If not defined, the function will return all entries. If the number of available entries is less than the value of this parameter, the function will silently return only the available entries.
responseSize	Specifies the number of entries to be returned by the server until reach the number of rows defined in nrows parameter or until get all available entries. If not defined, the server will return the allowed maximum response size. Increasing this the value of this parameter will reduce the number of requests and reducing the time required. The will not respect this parameter if the value is larger than its maximum response size.

### Details

This function requests POST `host/features/search`.

### Value

[DataFrame](#) object.

### References

[Official documentation](#).

### See Also

[DataFrame](#), [getFeature](#)

### Examples

```
host <- "http://1kgenomes.ga4gh.org/"
## Not run:
datasetId <- searchDatasets(host, nrows = 1)$id
featureSetId <- searchFeatureSets(host, datasetId, nrows = 1)$id
searchFeatures(host, featureSetId, nrows = 10)

## End(Not run)
```

---

searchFeatureSets      *searchFeatureSets function*

---

### Description

Search for feature sets (genomic features, e.g. GFF files).

### Usage

```
searchFeatureSets(host, datasetId, nrows = Inf, responseSize = NA_integer_)
```

## Arguments

host	URL of GA4GH API data server.
datasetId	The Dataset to search.
nrows	Number of rows of the data frame returned by this function. If not defined, the function will return all entries. If the number of available entries is less than the value of this parameter, the function will silently return only the available entries.
responseSize	Specifies the number of entries to be returned by the server until reach the number of rows defined in nrows parameter or until get all available entries. If not defined, the server will return the allowed maximum response size. Increasing this the value of this parameter will reduce the number of requests and reducing the time required. The will not respect this parameter if the value is larger than its maximum response size.

## Details

This function requests POST `host/featuresets/search`.

## Value

[DataFrame](#) object.

## References

[Official documentation](#).

## See Also

[DataFrame](#), [getFeatureSet](#)

## Examples

```
host <- "http://1kgenomes.ga4gh.org/"
## Not run:
datasetId <- searchDatasets(host, nrows = 1)$id
searchFeatureSets(host, datasetId)

## End(Not run)
```

---

searchIndividuals      *searchIndividuals function*

---

## Description

This function gets individuals matching the search criteria.

## Usage

```
searchIndividuals(host, datasetId, name = NA_character_, nrows = Inf,
  responseSize = NA_integer_)
```

## Arguments

host	URL of GA4GH API data server.
datasetId	Id of the dataset to search.
name	Returns Individuals with the given name found by case-sensitive string matching.
nrows	Number of rows of the data frame returned by this function. If not defined, the function will return all entries. If the number of available entries is less than the value of this parameter, the function will silently return only the available entries.
responseSize	Specifies the number of entries to be returned by the server until reach the number of rows defined in nrows parameter or until get all available entries. If not defined, the server will return the allowed maximum response size. Increasing this the value of this parameter will reduce the number of requests and reducing the time required. The will not respect this parameter if the value is larger than its maximum response size.

## Details

This function requests to `/individuals/search`.

## Value

`DataFrame` object. NULL means no registry found.

## References

[Official documentation](#).

## See Also

`DataFrame`, `getIndividual`

## Examples

```
host <- "http://1kgenomes.ga4gh.org/"
## Not run:
datasetId <- searchDatasets(host, nrows = 1)$id
searchIndividuals(host, datasetId, nrows = 10)

## End(Not run)
```

---

searchPhenotypeAssociations  
*searchPhenotypeAssociations function*

---

## Description

This function gets a list of phenotype associations matching the search criteria.

**Usage**

```
searchPhenotypeAssociations(host, phenotypeAssociationSetId,
  featureIds = character(), phenotypeIds = character(), nrows = Inf,
  responseSize = NA_integer_)
```

**Arguments**

host	URL of GA4GH API data server.
phenotypeAssociationSetId	Id of the PhenotypeAssociationSet to search.
featureIds	Ids of the features. At least one featureId or phenotypeId must be provided.
phenotypeIds	Ids of the phenotypes. At least one featureId or phenotypeId must be provided.
nrows	Number of rows of the data frame returned by this function. If not defined, the function will return all entries. If the number of available entries is less than the value of this parameter, the function will silently return only the available entries.
responseSize	Specifies the number of entries to be returned by the server until reach the number of rows defined in nrows parameter or until get all available entries. If not defined, the server will return the allowed maximum response size. Increasing this the value of this parameter will reduce the number of requests and reducing the time required. The will not respect this parameter if the value is larger than its maximum response size.

**Details**

This function requests to `/featurephenotypeassociations/search`.

**Value**

[DataFrame](#) object. NULL means no registry found.

**References**

[Official documentation](#).

**See Also**

[DataFrame](#), [searchPhenotypeAssociationSets](#)

**Examples**

```
host <- "http://1kgenomes.ga4gh.org/"
## Not run:
datasetId <- searchDatasets(host, nrows = 1)$id
id <- searchPhenotypeAssociationSets(host, datasetId, nrows = 1)$id
searchPhenotypeAssociations(host, id, nrows = 10)

## End(Not run)
```

---

searchPhenotypeAssociationSets  
*searchPhenotypeAssociationSets function*

---

### Description

This function gets a list of association sets matching the search criteria.

### Usage

```
searchPhenotypeAssociationSets(host, datasetId, nrows = Inf,  
  responseSize = NA_integer_)
```

### Arguments

host	URL of GA4GH API data server.
datasetId	Id of the dataset to search.
nrows	Number of rows of the data frame returned by this function. If not defined, the function will return all entries. If the number of available entries is less than the value of this parameter, the function will silently return only the available entries.
responseSize	Specifies the number of entries to be returned by the server until reach the number of rows defined in nrows parameter or until get all available entries. If not defined, the server will return the allowed maximum response size. Increasing this the value of this parameter will reduce the number of requests and reducing the time required. The will not respect this parameter if the value is larger than its maximum response size.

### Details

This function requests to /phenotypeassociationsets/search.

### Value

[DataFrame](#) object. NULL means no registry found.

### References

[Official documentation.](#)

### See Also

[DataFrame](#)

### Examples

```
host <- "http://1kgenomes.ga4gh.org/"  
## Not run:  
datasetId <- searchDatasets(host, nrows = 1)$id  
searchPhenotypeAssociationSets(host, datasetId, nrows = 10)  
  
## End(Not run)
```

---

searchReadGroupSets    *searchReadGroupSets function*

---

## Description

Search for read group sets (sequence alignment, e.g BAM files).

## Usage

```
searchReadGroupSets(host, datasetId, name = NA_character_,  
  biosampleId = NA_character_, nrows = Inf, responseSize = NA_integer_)
```

## Arguments

host	URL of GA4GH API data server.
datasetId	The dataset to search.
name	Only return read group sets with this name (case-sensitive, exact match).
biosampleId	Specifying the id of a BioSample record will return only readgroups with the given biosampleId.
nrows	Number of rows of the data frame returned by this function. If not defined, the function will return all entries. If the number of available entries is less than the value of this parameter, the function will silently return only the available entries.
responseSize	Specifies the number of entries to be returned by the server until reach the number of rows defined in nrows parameter or until get all available entries. If not defined, the server will return the allowed maximum response size. Increasing this the value of this parameter will reduce the number of requests and reducing the time required. The will not respect this parameter if the value is larger than its maximum response size.

## Details

This function requests POST `host/readgroupsets/search`

## Value

[DataFrame](#) object.

## See Also

[DataFrame](#), [getReadGroupSet](#)

## Examples

```
host <- "http://1kgenomes.ga4gh.org/"  
## Not run:  
datasetId <- searchDatasets(host, nrows = 1)$id  
searchReadGroupSets(host, datasetId, nrows = 1)  
  
## End(Not run)
```

---

searchReads	<i>searchReads function</i>
-------------	-----------------------------

---

### Description

Search for reads by genomic range (bases of aligned sequences)

### Usage

```
searchReads(host, readGroupIds, referenceId = NA_character_,
            start = NA_integer_, end = NA_integer_, nrows = Inf,
            responseSize = NA_integer_)
```

### Arguments

host	URL of GA4GH API data server.
readGroupIds	The ReadGroups to search. At least one id must be specified.
referenceId	The reference to query. Leaving blank returns results from all references, including unmapped reads - this could be very large.
start	The start position (1-based) of this query. If a reference is specified, this defaults to 0. Genomic positions are non-negative integers less than reference length. Requests spanning the join of circular genomes are represented as two requests one on each side of the join (position 1).
end	The end position (1-based, exclusive) of this query. If a reference is specified, this defaults to the reference's length.
nrows	Number of rows of the data frame returned by this function. If not defined, the function will return all entries. If the number of available entries is less than the value of this parameter, the function will silently return only the available entries.
responseSize	Specifies the number of entries to be returned by the server until reach the number of rows defined in nrows parameter or until get all available entries. If not defined, the server will return the allowed maximum response size. Increasing this the value of this parameter will reduce the number of requests and reducing the time required. The will not respect this parameter if the value is larger than its maximum response size.

### Details

This function requests POST `host/reads/search`.

### Value

[DataFrame](#) object.

### References

[Official documentation](#).

### See Also

[DataFrame](#)



**Examples**

```

host <- "http://1kgenomes.ga4gh.org/"
## Not run:
readGroupIds <- "WyIxa2dlbm9tZXMiLCJyZ3MiLCJIRzAzMjcwIiwirVJSMTgxMzI5I10"
referenceSetId <- searchReferenceSets(host, nrows = 1)$id
referenceId <- searchReferences(host, referenceSetId, nrows = 1)$id
searchReads(host, readGroupIds, referenceId, start = 15000, end = 16000)

## End(Not run)

```

---

searchReferences	<i>searchReferences function</i>
------------------	----------------------------------

---

**Description**

Search for references (genome sequences, e.g. chromosomes).

**Usage**

```

searchReferences(host, referenceSetId, md5checksum = NA_character_,
  accession = NA_character_, nrows = Inf, responseSize = NA_integer_)

```

**Arguments**

host	URL of GA4GH API data server.
referenceSetId	The ReferenceSet to search.
md5checksum	If specified, return the references for which the md5checksum matches this string (case-sensitive, exact match). See ReferenceSet::md5checksum for details.
accession	If specified, return the references for which the accession matches this string (case-sensitive, exact match).
nrows	Number of rows of the data frame returned by this function. If not defined, the function will return all entries. If the number of available entries is less than the value of this parameter, the function will silently return only the available entries.
responseSize	Specifies the number of entries to be returned by the server until reach the number of rows defined in nrows parameter or until get all available entries. If not defined, the server will return the allowed maximum response size. Increasing this the value of this parameter will reduce the number of requests and reducing the time required. The will not respect this parameter if the value is larger than its maximum response size.

**Details**

This function requests POST `host/references/search`.

**Value**

[DataFrame](#) object.

**References**

[Official documentation.](#)

**See Also**

[DataFrame](#), [getReference](#)

**Examples**

```
host <- "http://1kgenomes.ga4gh.org/"
## Not run:
referenceSetId <- searchReferenceSets(host, nrows = 1)$id
searchReferences(host, referenceSetId)

## End(Not run)
```

---

searchReferenceSets    *searchReferenceSets function*

---

**Description**

Search for reference sets (reference genomes).

**Usage**

```
searchReferenceSets(host, md5checksum = NA_character_,
  accession = NA_character_, assemblyId = NA_character_, nrows = Inf,
  responseSize = NA_integer_)
```

**Arguments**

host	URL of GA4GH API data server.
md5checksum	If unset, return the reference sets for which the md5checksum matches this string (case-sensitive, exact match). See ReferenceSet::md5checksum for details.
accession	If unset, return the reference sets for which the accession matches this string (case-sensitive, exact match).
assemblyId	If unset, return the reference sets for which the assemblyId matches this string (case-sensitive, exact match).
nrows	Number of rows of the data frame returned by this function. If not defined, the function will return all entries. If the number of available entries is less than the value of this parameter, the function will silently return only the available entries.
responseSize	Specifies the number of entries to be returned by the server until reach the number of rows defined in nrows parameter or until get all available entries. If not defined, the server will return the allowed maximum response size. Increasing this the value of this parameter will reduce the number of requests and reducing the time required. The will not respect this parameter if the value is larger than its maximum response size.

**Details**

This function requests POST `host/references/search`.

**Value**

`DataFrame` object.

**References**

[Official documentation](#).

**See Also**

`DataFrame`, `getReferenceSet`

**Examples**

```
host <- "http://1kgenomes.ga4gh.org/"
## Not run:
searchReferenceSets(host)

## End(Not run)
```

---

searchRnaQuantifications

*searchRnaQuantifications function*

---

**Description**

This function gets a list of `RnaQuantifications` matching the search criteria.

**Usage**

```
searchRnaQuantifications(host, rnaQuantificationSetId,
  biosampleId = NA_character_, nrows = Inf, responseSize = NA_integer_)
```

**Arguments**

<code>host</code>	URL of GA4GH API data server.
<code>rnaQuantificationSetId</code>	IReturn only Rna Quantifications which belong to this set.
<code>biosampleId</code>	Return only RNA quantifications regarding the specified biosample.
<code>nrows</code>	Number of rows of the data frame returned by this function. If not defined, the function will return all entries. If the number of available entries is less than the value of this this parameter, the function will silently return only the available entries.
<code>responseSize</code>	Specifies the number of entries to be returned by the server until reach the number of rows defined in <code>nrows</code> parameter or until get all available entries. If not defined, the server will return the allowed maximum reponse size. Increasing this the value of this parameter will reduce the number of requests and reducing the time required. The will not respect this parameter if the value if larger than its maximum response size.

## Details

This function requests to /rnaquantifications/search.

## Value

[DataFrame](#) object. NULL means no registry found.

## References

[Official documentation.](#)

## See Also

[DataFrame](#)

## Examples

```
host <- "http://1kgenomes.ga4gh.org/"
## Not run:
datasetId <- searchDatasets(host, nrows = 1)$id
id <- searchRnaQuantificationSets(host, datasetId, nrows = 1)$id
searchRnaQuantifications(host, rnaQuantificationSetId = id)

## End(Not run)
```

---

searchRnaQuantificationSets

*searchRnaQuantificationSets function*

---

## Description

This function gets a list of RNA quantification sets matching the search criteria.

## Usage

```
searchRnaQuantificationSets(host, datasetId, nrows = Inf,
  responseSize = NA_integer_)
```

## Arguments

host	URL of GA4GH API data server.
datasetId	Id of the dataset to search.
nrows	Number of rows of the data frame returned by this function. If not defined, the function will return all entries. If the number of available entries is less than the value of this parameter, the function will silently return only the available entries.
responseSize	Specifies the number of entries to be returned by the server until reach the number of rows defined in nrows parameter or until get all available entries. If not defined, the server will return the allowed maximum response size. Increasing this the value of this parameter will reduce the number of requests and reducing the time required. The will not respect this parameter if the value is larger than its maximum response size.

## Details

This function requests to /rnaquantificationsets/search.

## Value

[DataFrame](#) object. NULL means no registry found.

## References

[Official documentation.](#)

## See Also

[DataFrame](#), [getRnaQuantificationSet](#)

## Examples

```
host <- "http://1kgenomes.ga4gh.org/"
## Not run:
datasetId <- searchDatasets(host, nrows = 1)$id
searchRnaQuantificationSets(host, datasetId, nrows = 1)

## End(Not run)
```

---

searchVariantAnnotations

*searchVariantAnnotations function*

---

## Description

Search for annotated variants by genomic range.

## Usage

```
searchVariantAnnotations(host, variantAnnotationSetId,
  referenceName = NA_character_, referenceId = NA_character_,
  start = NA_integer_, end = NA_integer_, effects = list(), nrows = Inf,
  responseSize = NA_integer_)
```

## Arguments

host	URL of GA4GH API data server.
variantAnnotationSetId	Required. The ID of the variant annotation set to search over.
referenceName	Only return variants with reference alleles on the reference with this name. One of this field or reference_id is required.
referenceId	Only return variants with reference alleles on the reference with this ID. One of this field or reference_name is required.

start	Required if reference_name or reference_id supplied. The beginning of the window (1-based, inclusive) for which variants with overlapping reference alleles should be returned. Genomic positions are non-negative integers less than reference length. Requests spanning the join of circular genomes are represented as two requests one on each side of the join (position 1).
end	Required if reference_name or reference_id supplied. The end of the window (1-based, exclusive) for which variants with overlapping reference alleles should be returned.
effects	This filter allows variant, transcript combinations to be extracted by effect type(s). Only return variant annotations including any of these effects and only return transcript effects including any of these effects. Exact matching across all fields of the Sequence Ontology OntologyTerm is required. (A transcript effect may have multiple SO effects which will all be reported.) If empty, return all variant annotations.
nrows	Number of rows of the data frame returned by this function. If not defined, the function will return all entries. If the number of available entries is less than the value of this this parameter, the function will silently return only the available entries.
responseSize	Specifies the number of entries to be returned by the server until reach the number of rows defined in nrows parameter or until get all available entries. If not defined, the server will return the allowed maximum reponse size. Increasing this the value of this parameter will reduce the number of requests and reducing the time required. The will not respect this parameter if the value if larger than its maximum response size.

### Details

This function requests POST `host/variantannotations/search`.

### Value

[DataFrame](#) object.

### References

[Official documentation](#).

### See Also

[DataFrame](#)

### Examples

```
host <- "http://1kgenomes.ga4gh.org/"
## Not run:
datasetId <- searchDatasets(host, nrows = 1)$id
variantSetId <- searchVariantSets(host, datasetId, nrows = 2)$id[2]
id <- searchVariantAnnotationSets(host, variantSetId, nrows = 1)$id
searchVariantAnnotations(host, variantAnnotationSetId = id,
  referenceName = "1", start = 15000, end = 16000)

## End(Not run)
```

---

searchVariantAnnotationSets  
*searchVariantAnnotationSets function*

---

## Description

Search for variant annotation sets (annotated VCF files).

## Usage

```
searchVariantAnnotationSets(host, variantSetId, nrows = Inf,  
  responseSize = NA_integer_)
```

## Arguments

host	URL of GA4GH API data server.
variantSetId	Required. The VariantSet to search.
nrows	Number of rows of the data frame returned by this function. If not defined, the function will return all entries. If the number of available entries is less than the value of this parameter, the function will silently return only the available entries.
responseSize	Specifies the number of entries to be returned by the server until reach the number of rows defined in nrows parameter or until get all available entries. If not defined, the server will return the allowed maximum response size. Increasing this the value of this parameter will reduce the number of requests and reducing the time required. The will not respect this parameter if the value is larger than its maximum response size.

## Details

This function maps to POST `host/variantannotationsets/search`.

## Value

[DataFrame](#) object.

## References

[Official documentation](#).

## See Also

[DataFrame](#)

## Examples

```
host <- "http://1kgenomes.ga4gh.org/"  
## Not run:  
datasetId <- searchDatasets(host, nrows = 1)$id  
variantSetId <- searchVariantSets(host, datasetId, nrows = 2)$id[2]  
searchVariantAnnotationSets(host, variantSetId)  
  
## End(Not run)
```

---

searchVariants      *searchVariants function*

---

### Description

Search for variants by genomic ranges (lines of VCF files).

### Usage

```
searchVariants(host, variantSetId, referenceName, start, end,
  callSetIds = character(), nrows = Inf, responseSize = NA_integer_,
  asVCF = TRUE)
```

### Arguments

host	URL of GA4GH API data server.
variantSetId	The variant set to search.
referenceName	Required. Only return variants on this reference.
start	Required. The beginning of the window (1-based, inclusive) for which overlapping variants should be returned. Genomic positions are non-negative integers less than reference length. Requests spanning the join of circular genomes are represented as two requests one on each side of the join (position 1).
end	Required. The end of the window (1-based, inclusive) for which overlapping variants should be returned.
callSetIds	Only return variant calls which belong to callsets with these IDs. If unspecified, return all variants and no variant call objects.
nrows	Number of rows of the data frame returned by this function. If not defined, the function will return all entries. If the number of available entries is less than the value of this parameter, the function will silently return only the available entries.
responseSize	Specifies the number of entries to be returned by the server until reach the number of rows defined in nrows parameter or until get all available entries. If not defined, the server will return the allowed maximum response size. Increasing this the value of this parameter will reduce the number of requests and reducing the time required. The will not respect this parameter if the value is larger than its maximum response size.
asVCF	If TRUE the function will return an <a href="#">VCF</a> with header (default), otherwise it will return a <code>DataFrame</code> .

### Details

This function maps to POST `host/variants/search`.

### Value

[VCF](#) object (when `asVCF = TRUE`) or `DataFrame` object (otherwise).

### References

[Official documentation](#).



**See Also**

[DataFrame](#), [getVariant](#), [searchVariantsByGRanges](#), [VCF](#), [makeVCFFromGA4GHResponse](#)

**Examples**

```
host <- "http://1kgenomes.ga4gh.org/"
## Not run:
datasetId <- searchDatasets(host, nrows = 1)$id
variantSetId <- searchVariantSets(host, datasetId, nrows = 1)$id
searchVariants(host, variantSetId, referenceName = "1",
  start = 15000, end = 16000)

searchVariants(host, variantSetId, referenceName = "1",
  start = 15000, end = 16000, asVCF = FALSE)

## End(Not run)
```

---

searchVariantsByGRanges

*searchVariantsByGranges function*

---

**Description**

Search for variants by genomic ranges (lines of VCF files)

**Usage**

```
searchVariantsByGRanges(host, variantSetId, granges, callSetIds = character(),
  nrows = Inf, responseSize = NA_integer_, asVCF = FALSE)
```

**Arguments**

host	URL of GA4GH API data server.
variantSetId	The variant set to search.
granges	A GRanges object containing one or more genomic ranges.
callSetIds	Only return variant calls which belong to callsets with these IDs. If unspecified, return all variants and no variant call objects.
nrows	Number of rows of the data frame returned by this function. If not defined, the function will return all entries. If the number of available entries is less than the value of this parameter, the function will silently return only the available entries.
responseSize	Specifies the number of entries to be returned by the server until reach the number of rows defined in nrows parameter or until get all available entries. If not defined, the server will return the allowed maximum response size. Increasing this the value of this parameter will reduce the number of requests and reducing the time required. The will not respect this parameter if the value is larger than its maximum response size.
asVCF	If TRUE the function will return a list of <a href="#">VCF</a> object with headers (default), otherwise it will return a list of <a href="#">DataFrame</a> objects.

**Details**

This function maps to the body of POST `host/variants/search`.

**Value**

List of [VCF](#) objects (when `asVCF = TRUE`) or a list of [DataFrame](#) objects (otherwise). Each row in `GRanges` object will be a element of the list.

**References**

[Official documentation](#).

**See Also**

[DataFrame](#), [searchVariants](#) [getVariant](#), [VCF](#)

**Examples**

```
library(GenomicRanges)
host <- "http://1kgenomes.ga4gh.org/"
## Not run:
datasetId <- searchDatasets(host, nrows = 1)$id
variantSetId <- searchVariantSets(host, datasetId, nrows = 1)$id[1]
granges <- GRanges(seqnames = "1", IRanges(start = 15000, end = 16000))
searchVariantsByGRanges(host, variantSetId, granges)

## End(Not run)
```

---

searchVariantSets      *searchVariantSets function*

---

**Description**

Search for for variant sets (VCF files).

**Usage**

```
searchVariantSets(host, datasetId, nrows = Inf, responseSize = NA_integer_)
```

**Arguments**

<code>host</code>	URL of GA4GH API data server.
<code>datasetId</code>	Id of the dataset to search.
<code>nrows</code>	Number of rows of the data frame returned by this function. If not defined, the function will return all entries. If the number of available entries is less than the value of this this parameter, the function will silently return only the available entries.
<code>responseSize</code>	Specifies the number of entries to be returned by the server until reach the number of rows defined in <code>nrows</code> parameter or until get all available entries. If not defined, the server will return the allowed maximum reponse size. Increasing this the value of this parameter will reduce the number of requests and reducing the time required. The will not respect this parameter if the value if larger than its maximum response size.

### **Details**

This request maps to the body of POST `host/variantsets/search`.

### **Value**

[DataFrame](#) object.

### **References**

[Official documentation](#).

### **See Also**

[DataFrame](#), [getVariantSet](#)

### **Examples**

```
host <- "http://1kgenomes.ga4gh.org/"
## Not run:
datasetId <- searchDatasets(host, nrows = 1)$id
searchVariantSets(host, datasetId)

## End(Not run)
```

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