

# Package ‘RonFHIR’

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**Type** Package

**Title** Read and Search Interface to the 'HL7 FHIR' REST API

**Version** 0.4.0

**Description**

R on FHIR is an easy to use wrapper around the 'HL7 FHIR' REST API (STU 3 and R4). It provides tools to easily read and search resources on a FHIR server and brings the results into the R environment. R on FHIR is based on the FhirClient of the official 'HL7 FHIR .NET API', also made by Firely.

**License** BSD 3-clause License + file LICENSE

**Imports** R6, httr, jsonlite, utils, stringr

**Suggests** testthat

**Encoding** UTF-8

**LazyData** true

**Depends** R (>= 3.1.0)

**NeedsCompilation** no

**RoxygenNote** 6.0.1

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fhirBulkClient	<i>fhirBulkClient</i>
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## Description

Bulk data client in R for FHIR STU 3.

## Usage

```
bulkclient <- fhirBulkClient$new(endpoint, tokenURL = NULL, token = NULL)

bulkclient$patientExport(criteria = NULL)
bulkclient$groupExport(groupId, criteria = NULL)
bulkclient$wholeSystemExport(criteria = NULL)
bulkclient$getBulkStatus()
bulkclient$downloadBulk(requestNumber, returnType = "parsed" ,deleteFromQueue = TRUE)
bulkclient$deleteBulkRequest(requestNumber)
bulkclient$retrieveToken(jwt, scopes, tokenURL = NULL)
bulkclient$setToken(token)

print(bulkclient)
```

## Arguments

**bulkclient** A fhirBulkClient object.

**endpoint** The URL of the server to connect to.

**tokenURL** Authorization server's endpoint.

**token** Acces token.

**criteria** The search parameters to filter the Resources on. Each given string is a combined key/value pair (separated by '=').

**groupId** Id of the Group resource.

**requestNumber** Number of the request in the queue.

**returnType** Specify the return type. This can be "parsed" or "ndjson".

**deleteFromQueue** If the request needs to be deleted from the queue after it's been downloaded.

**jwt** JSON Web Token signed with the app's private key (RSA SHA-256).

**scopes** Desired scope(s).

## Details

`$new()` Creates a new fhirBulkClient using a given endpoint. If the endpoint does not end with a slash (/), it will be added.

`$patientExport()` Request all data on all patients. Possible to filter the results with the `_output-Format`, `_since` and `_type` parameters. The request will be added to the queue.

`$groupExport()` Request all data of a patientgroup. Possible to filter the results with the `_outputFormat`, `_since` and `_type` parameters. The request will be added to the queue.

`$wholeSystemExport()` Request all data. Possible to filter the results with the `_outputFormat`, `_since` and `_type` parameters. The request will be added to the queue.

`$getBulkStatus()` Update and return the queue to see the progress of your requests.

`$downloadBulk()` Download a request from the queue.

`$deleteBulkRequest()` Cancel a request from the queue.

`$retrieveToken()` Retrieve a token from the authentication server.

`$setToken` Set a token.

`print(p)` or `p$print()` Shows which endpoint is configured.

## Examples

```
## Not run:
# Read your private key
privatekey <- openssl::read_key("PrivateKey.pem")

# Create your claim
claim <- jose::jwt_claim(iss = "ServiceURL",
                        sub = "ClientID",
                        aud = "TokenURL",

                        # expiration date as epoch (5 minutes)
                        exp = as.integer(as.POSIXct( Sys.time() + 300)),

                        # 'random' number
                        jti = charToRaw(as.character(runif(1, 0.5, 100000000000))))

# Sign your claim with your private key
jwt <- jose::jwt_encode_sig(claim, privatekey)

# Define your scope(s)
scopes <- c("system/*.read", "system/CommunicationRequest.write")

# Create a new fhirBulkClient
bulkclient <- fhirBulkClient$new("FHIRBulkServerURL", tokenURL = "TokenURL")

# Retrieve your token
token <- bulkclient$retrieveToken(jwt, scopes)

# Set your token
bulkclient$setToken(token$access_token)

# Request a download for Patient Cohort 3
bulkclient$groupExport(3)

# Request the progress of the requests
bulkclient$getBulkStatus()

# When the downloads are available, download the bulkdata
```

```

patient_cohort_3 <- bulkclient$downloadBulk(1)

View(patient_cohort_3)

## End(Not run)

```

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fhirClient

*fhirClient*


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## Description

Read and search only client in R for FHIR STU 3 and R4. Based on [the official HL7 FHIR .NET API](#).

## Usage

```

client <- fhirClient$new(endpoint, token = NULL)

client$read(location, summaryType = NULL, returnType = "parsed")
client$search(resourceType, criteria = NULL, includes = NULL, pageSize = NULL, summaryType = NULL, returnType = "parsed")
client$searchById(resourceType, id, includes = NULL, summaryType = NULL, returnType = "parsed")
client$wholeSystemSearch(criteria = NULL, includes = NULL, pageSize = NULL, summaryType = NULL, returnType = "parsed")
client$searchParams(params, resourceType = NULL, returnType = "parsed")
client$continue(bundle)

client$setToken(token)

client$endpoint
client$authUrl
client$tokenUrl
client$registerUrl
client$token

print(client)

```

## Arguments

- client** A fhirClient object.
- endpoint** The URL of the server to connect to.
- token** An ouath 2.0 Token (httr Token 2.0)
- resourceType** The type of resource to search for.
- id** The id of the Resource to search for.
- summaryType** Whether to include only return a summary of the Resource(s).
- location** The url of the Resource to fetch. This can be a Resource id url or a version-specific.

**criteria** The search parameters to filter the Resources on. Each given string is a combined key/value pair (separated by '=').

**includes** Paths to include in the search.

**pageSize** Asks server to limit the number of entries per page returned.

**query** A searchParams object containing the search parameters.

**bundle** The bundle as received from the last response.

**returnType** Specify the return type. This can be "parsed", "json" or "xml".

## Details

`$new()` Creates a new fhirClient using a given endpoint. If the endpoint does not end with a slash (/), it will be added.

`$read()` Fetches a typed Resource from a FHIR resource endpoint.

`$search()` Search for Resources of a certain type that match the given criteria.

`$searchById()` Search for Resources based on a Resource's id.

`$wholeSystemSearch()` Search for Resources across the whole server that match the given criteria.

`$searchByQuery()` Search for Resources based on a searchParams object.

`$continue()` Uses the FHIR paging mechanism to go navigate around a series of paged result Bundles.

`$setToken()` Saves an Oauth 2.0 token in a variable.

`$endpoint` Returns the endpoint.

`$authUrl` Returns the authorization server's OAuth authorization endpoint.

`$tokenUrl` Returns the authorization server's OAuth token endpoint.

`$registerUrl` Returns the endpoint where the client can register.

`$token` Returns the initialized token.

`print(p)` or `p$print()` Shows which endpoint is configured.

## Examples

```
## Not run:
# Setting up a fhirClient
client <- fhirClient$new("https://vonk.fire.ly")
# Read
client$read("Patient/example")

# Search
bundle <- client$search("Patient", c("name=Peter", "address-postalcode=3999"))

while(!is.null(bundle)){
  # Do something useful
  bundle <- client$continue(bundle)
}

## End(Not run)
```

```

## Not run:
# Using OAuth 2.0
client <- fhirClient$new("https://vonk.fire.ly")

# Retrieving a token

client_id <- "id"
client_secret <- "secret"
app_name <- "TestApp"
scopes <- c("patient/*.read")

app <- httr::oauth_app(appname = app_name, client_id, client_secret)
oauth_endpoint <- httr::oauth_endpoint(
  authorize = paste(client$authUrl, "?aud=", client$endpoint, sep=""),
  access = client$tokenUrl)

token <- httr::oauth2.0_token(endpoint = oauth_endpoint, app = app, scope = scopes)

# Set a token and read a patient resource
client$setToken(token$credentials$access_token)

client$read("Patient/example")

# Token refresh
token <- token$refresh()

client$setToken(token$credentials$access_token)

## End(Not run)

```

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searchParams

*searchParams*

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## Description

An alternative way to specify a query is by creating a searchParams object and pass this to the `fhirClient`'s `searchByQuery`. The searchParams class has a set of fluent calls to allow you to easily construct more complex queries. Based on [the official HL7 FHIR .NET API](#).

## Usage

```

query <- searchParams$new()

query$select(elements)
query$where(criteria)
query$include(path)
query$orderBy(paramName, sortOrder = "asc")
query$limitTo(count)

```

```

query$countOnly()
query$summaryOnly()
query$textOnly()
query$dataOnly()

```

### Arguments

**query** A searchParams object that contains all specified search criteria.

**elements** Elements defined at the root level in the Resource.

**criteria** The search parameters to filter the Resources on. Each given string is a combined key/value pair (separated by '=').

**path** Paths to include in the search.

**paramName** Name of the parameter to order by.

**sortOrder** Direction of the order. Can be asc or desc (ascending and descending).

**count** The number of returned Resources per page.

### Details

`$new()` Creates a new searchParams object.

`$select()` Specify the elements to be returned as part of a Resource.

`$where()` Specify on which parameters to filter.

`$include()` Specify the paths to include.

`$orderBy()` Specify the order to return the results.

`$limitTo()` Specify how many Resources should be returned in a single page of a Bundle.

`$countOnly()` Specify to just return a count of the matching Resources, without returning the actual matches.

`$summaryOnly()` Specify to return only those elements marked as "summary" in the base definition of the Resource(s).

`$textOnly()` Specify to return only the "text" element, the 'id' element, the 'meta' element, and only top-level mandatory elements.

`$dataOnly()` Specify to remove the text element.

### Examples

```

## Not run:
# Setting up a fhirClient
client <- fhirClient$new("http://vonk.furore.com")

# Creating a new searchParams object
query <- searchParams$new()
query$select(c("name", "birthDate"))$where("given:exact=Peter")$orderBy("family")

peters <- client$searchByQuery(query, "Patient")
# equivalent:

```

```
# client$search("Patient", c("_elements=name,birthDate","given:exact=Peter", "_sort=family"))

while(!is.null(bundle)){
  # Do something useful
  peters <- client$continue(peters)
}

## End(Not run)
```

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