Package ‘BiocFHIR’

July 15, 2025

Title Illustration of FHIR ingestion and transformation using R

Version 1.11.0

Date 2022-11-29

Description FHIR R4 bundles in JSON format are derived from https://synthea.mitre.org/downloads. Transformation inspired by a kaggle notebook published by Dr Alexander Scarlat, https://www.kaggle.com/code/drscarlat/fhir-starter-parse-healthcare-bundles-into-tables. This is a very limited illustration of some basic parsing and reorganization processes. Additional tooling will be required to move beyond the Synthea data illustrations.

License Artistic-2.0

Encoding UTF-8

Depends R (>= 4.2)

Imports DT, shiny, jsonlite, graph, tidyr, visNetwork, dplyr, utils, methods, BiocBaseUtils

Suggests knitr, testthat, rjsoncons, igraph, BiocStyle

VignetteBuilder knitr

biocViews Infrastructure, DataImport, DataRepresentation

RoxygenNote 7.3.2

URL `https://github.com/vjcitn/BiocFHIR`

BugReports `https://github.com/vjcitn/BiocFHIR/issues`

git_url https://git.bioconductor.org/packages/BiocFHIR

git_branch devel

git_last_commit 6a27e5d

git_last_commit_date 2025-04-30

Repository Bioconductor 3.22

Date/Publication 2025-07-15

Author Vincent Carey [aut, cre] (ORCID: <`https://orcid.org/0000-0003-4046-0063`>)

Maintainer Vincent Carey `<stvjc@channing.harvard.edu>`

Contents

`add_procedures` *update a fhir graph on patients and conditions with procedures*

Description

update a fhir graph on patients and conditions with procedures

Usage

```
add_procedures(fhirgraph, listOfProcessedBundles)
```

Arguments

`fhirgraph`	instance of BiocFHIR.FHIRgraph
`listOfProcessedBundles`	list

Value

instance of BiocFHIR.FHIRgraph

Examples

```
data("allin")
g <- make_condition_graph(allin)
g <- add_procedures(g, allin)
g
```

`allin` *collection of synthea FHIR documents ingested*

Description

collection of synthea FHIR documents ingested

Usage

```
data("allin", package = "BiocFHIR")
```

Format

list

Examples

```
data("allin", package="BiocFHIR")
allin[[1]]
```

`available_retention_schemas` *list available 'retention schemas'*

Description

list available 'retention schemas'

Usage

```
available_retention_schemas()
```

Value

character vector

Examples

```
available_retention_schemas()
```

`build_proccond_igraph` *build graph with patients, conditions and procedures*

Description

build graph with patients, conditions and procedures

Usage

```
build_proccond_igraph(listOfBundles)
```

Arguments

`listOfBundles`	list of processed FHIR bundles, processed with ‘process_fhir_bundle‘

Value

instance of visIgraph from visNetworks

Examples

```
data("allin")
build_proccond_igraph( allin )
```

`display_proccond_igraph` *make network visualization*

Description

make network visualization

Usage

```
display_proccond_igraph(igraph)
```

Arguments

`igraph`	instance of igraph produced by ‘build_procond_igraph‘

Value

visIGraph instance

Examples

```
data("allin")
g <- build_proccond_igraph( allin )
if (interactive()) {
 display_proccond_igraph( g )
}
```

`FHIRtabs` *table app*

Description

table app

Usage

```
FHIRtabs()
```

Value

No value returned.

Examples

```
if (interactive()) {
 FHIRtabs()
}
```

`FHIR_ResourceTypes` *FHIR Resource types recognized in package*

Description

FHIR Resource types recognized in package

Usage

```
FHIR_ResourceTypes()
```

Value

vector of strings

Examples

```
FHIR_ResourceTypes() # Oct 2022
```

`FHIR_retention_schemas` *collection of FHIR Resource components to be retained*

Description

collection of FHIR Resource components to be retained

Usage

```
FHIR_retention_schemas()
```

Value

list of vectors of strings

Examples

```
FHIR_retention_schemas() # Oct 2022
```

`freq_app` *produce interactive tables with FHIR resources from a list of ingested bundles*

Description

produce interactive tables with FHIR resources from a list of ingested bundles

Usage

```
freq_app(blist)
```

Arguments

`blist`	list of ingested bundles

Value

side-effects of shiny app invocation

Examples

```
if (interactive()) {
tset = make_test_json_set()
bl = lapply(tset, process_fhir_bundle)
freq_app(bl)
}
```

`getHumanName` *get human name from a BiocFHIR.Patient instance*

Description

get human name from a BiocFHIR.Patient instance

Usage

```
getHumanName(Patient)
```

Arguments

`Patient`	BiocFHIR.Patient instance

Value

string with name components concatenated

Examples

```
testf <- system.file("json/Vince741_Rogahn59_6fa3d4ab-c0b6-424a-89d8-7d9105129296.json",
   package="BiocFHIR")
tbun <- process_fhir_bundle(testf)
getHumanName(tbun$Patient)
```

`make_condition_graph` *create graph with links from patients to conditions*

Description

create graph with links from patients to conditions

Usage

```
make_condition_graph(listOfProcessedBundles, keep_with_condition_only = TRUE)
```

Arguments

`listOfProcessedBundles`	list with elements generated by ‘process_fhir_bundle‘
`keep_with_condition_only`	logical(1) omit bundles that lack a "Condition" element, defaults to TRUE

Value

instance of BiocFHIR.FHIRgraph

Examples

```
data("allin")
make_condition_graph(allin, TRUE)
```

`make_test_json_set` *produce 50 json FHIR files in a folder*

Description

produce 50 json FHIR files in a folder

Usage

```
make_test_json_set(target = paste0(tempdir(), "/jsontest"), reuse = TRUE)
```

Arguments

`target`	character(1) a path, defaults to ‘jsontest‘ under ‘tempdir()‘; the contents of synthfhir.zip, in inst/zip of BiocFHIR, will be deposted there.
`reuse`	logical(1) if TRUE, just use what is there, if folder already exists

Value

a vector of paths to FHIR JSON, invisibly

Examples

```
z <- make_test_json_set()
z[1:3]
```

`print.BiocFHIR.FHIRgraph` *show a combination of graph and patient attributes*

Description

show a combination of graph and patient attributes

Usage

```
## S3 method for class 'BiocFHIR.FHIRgraph'
print(x, ...)
```

Arguments

`x`	instance of BiocFHIR.FHIRgraph
`...`	not used

Value

print method

Examples

```
data("allin")
make_condition_graph(allin)
```

`print.FHIR.bundle` *print method*

Description

print method

Usage

```
## S3 method for class 'FHIR.bundle'
print(x, ...)
```

Arguments

`x`	BiocFHIR FHIR.bundle instance
`...`	not used

Value

print method

`process_AllergyIntolerance` *extract information from retained fields in AllergyIntolerance component of FHIR Bundle, produce simple data.frame*

Description

extract information from retained fields in AllergyIntolerance component of FHIR Bundle, produce simple data.frame

Usage

```
process_AllergyIntolerance(AllergyIntolerance)
```

Arguments

`AllergyIntolerance`	component of FHIR.bundle instance

Value

data.frame

Examples

```
testf <- system.file("json/Vince741_Rogahn59_6fa3d4ab-c0b6-424a-89d8-7d9105129296.json",
   package="BiocFHIR")
tbun <- process_fhir_bundle(testf)
process_AllergyIntolerance(tbun$AllergyIntolerance)
```

`process_CarePlan` *extract information from retained fields in CarePlan component of FHIR Bundle, produce simple data.frame*

Description

extract information from retained fields in CarePlan component of FHIR Bundle, produce simple data.frame

Usage

```
process_CarePlan(CarePlan)
```

Arguments

`CarePlan`	component of FHIR.bundle instance

Value

data.frame

Note

Nov 13 2022, added code to refine the 'category' data processing.

Examples

```
testf <- system.file("json/Vince741_Rogahn59_6fa3d4ab-c0b6-424a-89d8-7d9105129296.json",
   package="BiocFHIR")
tbun <- process_fhir_bundle(testf)
process_CarePlan(tbun$CarePlan)
```

`process_Claim` *extract information from retained fields in Claim component of FHIR Bundle, produce simple data.frame*

Description

extract information from retained fields in Claim component of FHIR Bundle, produce simple data.frame

Usage

```
process_Claim(Claim)
```

Arguments

`Claim`	component of FHIR.bundle instance

Value

data.frame

Examples

```
testf <- system.file("json/Vince741_Rogahn59_6fa3d4ab-c0b6-424a-89d8-7d9105129296.json",
   package="BiocFHIR")
tbun <- process_fhir_bundle(testf)
process_Claim(tbun$Claim)
```

`process_Condition` *extract information from retained fields in Condition component of FHIR Bundle, produce simple data.frame*

Description

extract information from retained fields in Condition component of FHIR Bundle, produce simple data.frame

Usage

```
process_Condition(Condition)
```

Arguments

`Condition`	component of FHIR.bundle instance

Value

data.frame

Examples

```
testf <- system.file("json/Vince741_Rogahn59_6fa3d4ab-c0b6-424a-89d8-7d9105129296.json",
   package="BiocFHIR")
tbun <- process_fhir_bundle(testf)
process_Condition(tbun$Condition)
```

`process_Encounter` *extract information from retained fields in Encounter component of FHIR Bundle, produce simple data.frame*

Description

extract information from retained fields in Encounter component of FHIR Bundle, produce simple data.frame

Usage

```
process_Encounter(Encounter)
```

Arguments

`Encounter`	component of FHIR.bundle instance

Value

data.frame

Examples

```
testf <- system.file("json/Vince741_Rogahn59_6fa3d4ab-c0b6-424a-89d8-7d9105129296.json",
   package="BiocFHIR")
tbun <- process_fhir_bundle(testf)
process_Encounter(tbun$Encounter)
```

`process_fhir_bundle` *process a bundle of FHIR R4 JSON*

Description

process a bundle of FHIR R4 JSON

Usage

```
process_fhir_bundle(json_file, schemas = FHIR_retention_schemas())
```

Arguments

`json_file`	character(1) path to text in JSON format
`schemas`	list of character vectors defining expected fields, defaults to FHIR_retention_schemas()

Value

instance of FHIR.bundle, extending list

Note

If one encounters the error "Element ... lacks field", the schemas argument can be modified by removing the noted field from the schema.

Examples

```
testf = system.file("json/Vince741_Rogahn59_6fa3d4ab-c0b6-424a-89d8-7d9105129296.json",
   package="BiocFHIR")
tbun = process_fhir_bundle(testf)
tbun
```

`process_Immunization` *extract information from retained fields in Immunization component of FHIR Bundle, produce simple data.frame*

Description

extract information from retained fields in Immunization component of FHIR Bundle, produce simple data.frame

Usage

```
process_Immunization(Immunization)
```

Arguments

`Immunization`	component of FHIR.bundle instance

Value

data.frame

Examples

```
testf <- system.file("json/Vince741_Rogahn59_6fa3d4ab-c0b6-424a-89d8-7d9105129296.json",
   package="BiocFHIR")
tbun <- process_fhir_bundle(testf)
process_Immunization(tbun$Immunization)
```

`process_MedicationRequest` *extract information from retained fields in MedicationRequest component of FHIR Bundle, produce simple data.frame*

Description

extract information from retained fields in MedicationRequest component of FHIR Bundle, produce simple data.frame

Usage

```
process_MedicationRequest(MedicationRequest)
```

Arguments

`MedicationRequest`	component of FHIR.bundle instance

Value

data.frame

Examples

```
testf <- system.file("json/Vince741_Rogahn59_6fa3d4ab-c0b6-424a-89d8-7d9105129296.json",
   package="BiocFHIR")
tbun <- process_fhir_bundle(testf)
process_MedicationRequest(tbun$MedicationRequest)
```

`process_Observation` *extract information from retained fields in Observation component of FHIR Bundle, produce simple data.frame*

Description

extract information from retained fields in Observation component of FHIR Bundle, produce simple data.frame

Usage

```
process_Observation(Observation)
```

Arguments

`Observation`	component of FHIR.bundle instance

Value

data.frame

Examples

```
testf <- system.file("json/Vince741_Rogahn59_6fa3d4ab-c0b6-424a-89d8-7d9105129296.json",
   package="BiocFHIR")
tbun <- process_fhir_bundle(testf)
process_Observation(tbun$Observation)
```

`process_Patient` *flatten information in Patient component of a bundle to a one-line data.frame*

Description

flatten information in Patient component of a bundle to a one-line data.frame

Usage

```
process_Patient(Patient)
```

Arguments

`Patient`	element of FHIR.bundle instance

Value

data.frame

Examples

```
testf <- system.file("json/Vince741_Rogahn59_6fa3d4ab-c0b6-424a-89d8-7d9105129296.json",
   package="BiocFHIR")
tbun <- process_fhir_bundle(testf)
tpat <- process_Patient(tbun$Patient)
head(names(tpat))
tags <- c("identifier.system3", "identifier.value3")
tpat[tags,,FALSE]
tags2 <- grep("extension.extension", rownames(tpat), value=TRUE)
tpat[tags2,,FALSE]
```

`process_Procedure` *extract information from retained fields in Procedure component of FHIR Bundle, produce simple data.frame*

Description

extract information from retained fields in Procedure component of FHIR Bundle, produce simple data.frame

Usage

```
process_Procedure(Procedure)
```

Arguments

`Procedure`	component of FHIR.bundle instance

Value

data.frame

Examples

```
testf <- system.file("json/Vince741_Rogahn59_6fa3d4ab-c0b6-424a-89d8-7d9105129296.json",
   package="BiocFHIR")
tbun <- process_fhir_bundle(testf)
process_Procedure(tbun$Procedure)
```

`stack_fhir` *convert data of a given FHIR type in a list of bundles to a data.frame*

Description

convert data of a given FHIR type in a list of bundles to a data.frame

Usage

```
stack_fhir(blist, type, droperr = TRUE)
```

Arguments

`blist`	list of FHIR bundles imported with process_fhir_bundle
`type`	character(1) type, in names(blist[[1]]), e.g.
`droperr`	logical(1) exclude records for which process_[type] fails, defaults to TRUE

Value

data.frame

Examples

```
jj = make_test_json_set()
b2 = lapply(jj[1:2], process_fhir_bundle)
ss = stack_fhir(b2, "Procedure")
head(ss,2)
```

`summarise_bundles` *produce tables summarizing FHIR data*

Description

produce tables summarizing FHIR data

Usage

```
summarise_bundles(
  blist,
  resource = "Condition",
  selection_map = summary_selections()
)
```

Arguments

`blist`	list of ingested bundles
`resource`	character(1) FHIR resource name
`selection_map`	character() named vector of single strings selected for summarisation

Value

data.frame

`summary_selections` *vector of fields to be selected for summarization*

Description

vector of fields to be selected for summarization

Usage

```
summary_selections()
```

Value

named vector of strings

Index