Package ‘BiocFHIR’

March 25, 2024

Title Illustration of FHIR ingestion and transformation using R

Version 1.4.0

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.

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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 7.2.2

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

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

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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**

```r
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

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

FHIRtabs

<table>
<thead>
<tr>
<th>table app</th>
</tr>
</thead>
</table>

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_fhirBundle)
  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**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Patient</td>
<td>BiocFHIR.Patient instance</td>
</tr>
</tbody>
</table>

**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**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>listOfProcessedBundles</td>
<td>list with elements generated by 'process_fhir_bundle'</td>
</tr>
<tr>
<td>keep_with_condition_only</td>
<td>logical(1) omit bundles that lack a &quot;Condition&quot; element, defaults to TRUE</td>
</tr>
</tbody>
</table>

**Value**
instance of BiocFHIR.FHIRgraph
Examples

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

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

Description
produce 50 json FHIR files in a folder

Usage
```r
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 deposed 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
```r
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
```r
## S3 method for class 'BiocFHIR.FHIRgraph'
print(x, ...)
```
print.FHIR.bundle

Arguments

  x           instance of BiocFHIR.FHIRgraph
  ...          not used

Value

  print method

Examples

data("allin")
make_condition_graph(allin)

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
CarePlancomponent of FHIR.bundle instance
process_Claim

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

**Description**

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

**Usage**

```r
process_Condition(Condition)
```

**Arguments**

- **Condition**: component of FHIR.bundle instance

**Value**

data.frame

**Examples**

```r
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

**Description**

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

**Usage**

```r
process_Encounter(Encounter)
```

**Arguments**

- **Encounter**: component of FHIR.bundle instance
process_fhir_bundle

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
process_Observation

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**

```r
process_Patient(Patient)
```

**Arguments**

- **Patient** element of FHIR.bundle instance

**Value**

data.frame

**Examples**

```r
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**

```r
process_Procedure(Procedure)
```
stack_fhir

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)
summary_selections

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
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