

# Package ‘BiocFHIR’

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**Title** Illustration of FHIR ingestion and transformation using R

**Version** 1.1.0

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**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 Scarlet, <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, igraph, utils, methods, BiocBaseUtils

**Suggests** knitr, testthat, rjsoncons

**VignetteBuilder** knitr

**biocViews** Infrastructure, DataImport, DataRepresentation

**RoxygenNote** 7.2.1

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

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

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**Author** Vincent Carey [aut, cre]

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

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add_procedures	<i>update a fhir graph on patients and conditions with procedures</i>
----------------	---

---

**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	<i>collection of synthea FHIR documents ingested</i>
-------	--

---

**Description**

collection of synthea FHIR documents ingested

**Usage**

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

**Format**

list

**Examples**

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

---

available_retention_schemas	<i>list available 'retention schemas'</i>
-----------------------------	---

---

**Description**

list available 'retention schemas'

**Usage**

```
available_retention_schemas()
```

**Value**

character vector

**Examples**

```
available_retention_schemas()
```

---

build\_prococond\_igraph *build graph with patients, conditions and procedures*

---

**Description**

build graph with patients, conditions and procedures

**Usage**

```
build_prococond_igraph(listOfBundles)
```

**Arguments**

listOfBundles list of processed FHIR bundles, processed with ‘process\_fhir\_bundle‘

**Value**

instance of visIgraph from visNetworks

**Examples**

```
data("allin")
build_prococond_igraph( allin )
```

---

display\_prococond\_igraph  
*make network visualization*

---

**Description**

make network visualization

**Usage**

```
display_prococond_igraph(igraph)
```

**Arguments**

igraph instance of igraph produced by ‘build\_prococond\_igraph‘

**Value**

visIgraph instance

**Examples**

```
data("allin")
g <- build_procond_igraph( allin )
if (interactive()) {
  display_procond_igraph( g )
}
```

---

FHIRtabs	<i>table app</i>
----------	------------------

---

**Description**

table app

**Usage**

```
FHIRtabs()
```

**Value**

No value returned.

**Examples**

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

---

FHIR_ResourceTypes	<i>FHIR Resource types recognized in package</i>
--------------------	--

---

**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
```

---

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(), "/jstest"), reuse = TRUE)
```

**Arguments**

target  
character(1) a path, defaults to 'jstest' under 'tempdir()'; the contents of syn-  
thfhir.zip, in inst/zip of BiocFHIR, will be deposited 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	<i>extract information from retained fields in CarePlan component of FHIR Bundle, produce simple data.frame</i>
------------------	---

---

**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

**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	<i>extract information from retained fields in Claim component of FHIR Bundle, produce simple data.frame</i>
---------------	--

---

**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	<i>extract information from retained fields in Condition component of FHIR Bundle, produce simple data.frame</i>
-------------------	--

---

**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	<i>flatten information in Patient component of a bundle to a one-line data.frame</i>
-----------------	--

---

**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	<i>extract information from retained fields in Procedure component of FHIR Bundle, produce simple data.frame</i>
-------------------	--

---

**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)
```



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