

# Package ‘BiocFHIR’

July 30, 2025

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

**Version** 1.10.0

**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 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, 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>

**git\_url** <https://git.bioconductor.org/packages/BiocFHIR>

**git\_branch** RELEASE\_3\_21

**git\_last\_commit** 6ea9bf3

**git\_last\_commit\_date** 2025-04-15

**Repository** Bioconductor 3.21

**Date/Publication** 2025-07-30

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

---

**Description**

build graph with patients, conditions and procedures

**Usage**

```
build_procond_igraph(listOfBundles)
```

**Arguments**

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

**Value**

instance of visIgraph from visNetworks

**Examples**

```
data("allin")
build_procond_igraph( allin )
```

---

`display_procond_igraph`  
*make network visualization*

---

**Description**

make network visualization

**Usage**

```
display_procond_igraph(igraph)
```

**Arguments**

`igraph` instance of igraph produced by ‘build\_procond\_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
```

---

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 | <i>get human name from a BiocFHIR.Patient instance</i> |
|--------------|--------------------------------------------------------|

---

**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 | <i>create graph with links from patients to conditions</i> |
|----------------------|------------------------------------------------------------|

---

**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 syn-thfir.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 | <i>print method</i> |
|-------------------|---------------------|

---

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

---

**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 | <i>process a bundle of FHIR R4 JSON</i> |
|---------------------|-----------------------------------------|

---

**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
```



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

---

**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)
```

---

|            |                                                                               |
|------------|-------------------------------------------------------------------------------|
| stack_fhir | <i>convert data of a given FHIR type in a list of bundles to a data.frame</i> |
|------------|-------------------------------------------------------------------------------|

---

**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 | <i>produce tables summarizing FHIR data</i> |
|-------------------|---------------------------------------------|

---

**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 | <i>vector of fields to be selected for summarization</i> |
|--------------------|----------------------------------------------------------|

---

**Description**

vector of fields to be selected for summarization

**Usage**

```
summary_selections()
```

**Value**

named vector of strings

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