
phenopackets-to-fhir

Release 0.0.1

Ksenia Zaytseva

Mar 03, 2020

CONTENTS:

1	Introduction	1
2	Converters	3
3	Validation	5
4	Mappings	7
4.1	HL7 Genomics Mappings	7
4.2	Phenopackets on FHIR Mappings	7
5	Indices and tables	11
	Python Module Index	13
	Index	15

INTRODUCTION

phenopackets-to-fhir is a service to convert derived phenopackets objects to FHIR resources. The service is a part of the ongoing work for [CHORD Metadata service](#). The phenopackets schemas are project-specific adaptations of [Phenopackets schema standard](#).

The package contains:

- json schemas for Phenopacket and its elements derived/based on [Phenopackets schema standard](#).
- functions to transform phenopackets objects to [FHIR](#) resources.
- mappings derived from [Phenopackets on FHIR Implementation Guide](#).

The conversion uses [Python SMART on FHIR client](#) that provides validation of generated FHIR resources.

CONVERTERS

`converters.resources.age_to_fhir(obj, mapping, field)`

Generic function to convert Phenopackets Age or AgeRange to FHIR Age.

Parameters

- **obj** – object to which field Age or AgeRange belongs to
- **mapping** – mapping from PHENOPACKETS_ON_FHIR
- **field** – name of the field that stores age

Returns age extension object

`converters.resources.biosample_to_fhir(obj)`

Converts Biosample to FHIR Specimen.

Parameters **obj** – Biosample json

Returns FHIR Specimen json

`converters.resources.check_disease_onset(disease)`

Phenopackets schema allows age to be represented by ISO8601 string, whereis Pheno-FHIR guide requires it to be represented by CodeableConcept. This function checks how age is represented in data.

Parameters **disease** – disease json object

Returns True/False

`converters.resources.codeable_concepts_fields(field_list, profile, obj)`

Converts a list of fields to FHIR CodeableConcepts and returns a list of extensions.

Parameters

- **field_list** – fields to convert to codeable concepts
- **profile** – name of an object in phenopackets mappings
- **obj** – object to which fields belong to

Returns list of extensions

`converters.resources.disease_to_fhir(obj)`

Converts Disease to FHIR Condition.

Parameters **obj** – Disease json

Returns FHIR Condition json

`converters.resources.fhir_codeable_concept(obj)`

Generic function to convert object to FHIR CodeableConcept.

`converters.resources.fhir_coding_util (obj)`

Genenric function to convert object to FHIR Coding.

`converters.resources.gene_to_fhir (obj)`

Convert Gene to Observation.component:gene property. GA4GH Phenopackets Implementation Guide provides a link to Genomics Reporting Implementation Guide (STU1) mapping <http://hl7.org/fhir/uv/genomics-reporting/StructureDefinition/region-studied> .

Parameters `obj` – gene json

Returns Observation.component:gene json

`converters.resources.hts_file_to_fhir (obj)`

Converts HTS file to FHIR DocumentReference.

Parameters `obj` – HTS file json

Returns FHIR DocumentReference json

`converters.resources.individual_to_fhir (obj)`

Converts Individual to FHIR Patient.

Parameters `obj` – Individual json

Returns FHIR Patient json

`converters.resources.phenopacket_to_fhir (obj)`

Converts Phenopacket to FHIR Composition.

Parameters `obj` – Phenopacket json

Returns FHIR Composition json

`converters.resources.phenotypic_feature_to_fhir (obj)`

Converts Phenotypic feature to FHIR Observation.

Parameters `obj` – PhenotypicFeature json

Returns FHIR Observation json

`converters.resources.procedure_to_fhir (obj)`

Converts Procedure to FHIR Specimen collection.

`converters.resources.variant_to_fhir (obj)`

Variant corresponds to Observation.component:variant. GA4GH Phenopackets Implementation Guide provides a link to Genomics Reporting Implementation Guide (STU1) mapping <http://hl7.org/fhir/uv/genomics-reporting/STU1/variant.html>.

Parameters `obj` – Variant json

Returns Observation.component:variant json

VALIDATION

`converters.validate.validate_schema(schema, data)`

Validates the instance against corresponding json schema.

Parameters

- **schema** – the json schema to validate with
- **data** – the instance to validate

Returns True if the instance is valid, False if not

Raises *ValidationError* if the instance is invalid

MAPPINGS

4.1 HL7 Genomics Mappings

```
# All fixed values provided by Phenopackets on FHIR Mapping guide
# Mappings from http://build.fhir.org/ig/HL7/genomics-reporting/index.html

HL7_GENOMICS_MAPPING = {
    "gene": {
        "url": "http://hl7.org/fhir/uv/genomics-reporting/StructureDefinition/region-
↪studied",
        "geneStudied_Code": {
            "system": "https://loinc.org",
            "id": "48018-6",
            "label": "Gene studied [ID]"
        },
        "geneStudiedValue": {
            "system": "https://www.genenames.org/"
        }
    },
    "variant": {
        "url": "http://hl7.org/fhir/uv/genomics-reporting/StructureDefinition/variant
↪",
        "variantLengthCode": {
            "system": "https://loinc.org",
            "id": "81300-6",
            "label": "Structural variant [Length]"
        }
    }
}
```

4.2 Phenopackets on FHIR Mappings

```
# All fixed values provided by Phenopackets on FHIR Mapping guide

PHENOPACKETS_ON_FHIR_MAPPING = {
    "individual": {
        "title": "Individual",
        "url": "http://ga4gh.org/fhir/phenopackets/StructureDefinition/Individual",
        "age": "http://ga4gh.org/fhir/phenopackets/StructureDefinition/individual-age
↪",
        "karyotypicSex": {
```

(continues on next page)

(continued from previous page)

```

        "url": "http://ga4gh.org/fhir/phenopackets/StructureDefinition/individual-
↪karyotypic-sex",
        "system": "http://ga4gh.org/fhir/phenopackets/CodeSystem/karyotypic-sex"
    },
    "taxonomy": "http://ga4gh.org/fhir/phenopackets/StructureDefinition/
↪individual-taxonomy"
},
"phenopacket": {
    "title": "Phenopacket",
    "code": {
        "system": "http://ga4gh.org/fhir/phenopackets/CodeSystem/document-type",
        "code": "phenopacket"
    },
    "url": "http://ga4gh.org/fhir/phenopackets/StructureDefinition/Phenopacket",
    "phenotypicFeatures": {
        "title": "Phenotypic Features",
        "code": {
            "system": "http://ga4gh.org/fhir/phenopackets/CodeSystem/section-type
↪",
            "version": "0.1.0",
            "code": "phenotypic-features",
            "display": "Phenotypic Features"
        }
    },
    "biosamples": {
        "title": "Biosamples",
        "code": {
            "system": "http://ga4gh.org/fhir/phenopackets/CodeSystem/section-
↪type",
            "version": "0.1.0",
            "code": "biosamples",
            "display": "Biosamples"
        }
    },
    "variants": {
        "title": "Variants",
        "code": {
            "system": "http://ga4gh.org/fhir/phenopackets/CodeSystem/section-type
↪",
            "version": "0.1.0",
            "code": "variants",
            "display": "Variants"
        }
    },
    "diseases": {
        "title": "Diseases",
        "code": {
            "system": "http://ga4gh.org/fhir/phenopackets/CodeSystem/section-type
↪",
            "version": "0.1.0",
            "code": "diseases",
            "display": "Diseases"
        }
    },
    "htsFiles": {
        "title": "HTS Files",
        "code": {

```

(continues on next page)

(continued from previous page)

```

        "system": "http://ga4gh.org/fhir/phenopackets/CodeSystem/section-type
↪",
        "version": "0.1.0",
        "code": "hts-files",
        "display": "HTS Files"
    }
},
"biosample": {
    "title": "Biosample",
    "url": "http://ga4gh.org/fhir/phenopackets/StructureDefinition/Biosample",
    "individualAgeAtCollection": "http://ga4gh.org/fhir/phenopackets/
↪StructureDefinition/biosample-individual-age-at-collection",
    "histologicalDiagnosis": "http://ga4gh.org/fhir/phenopackets/
↪StructureDefinition/biosample-histological-diagnosis",
    "tumorProgression": "http://ga4gh.org/fhir/phenopackets/StructureDefinition/
↪biosample-tumor-progression",
    "tumorGrade": "http://ga4gh.org/fhir/phenopackets/StructureDefinition/
↪biosample-tumor-grade",
    "diagnosticMarkers": "http://ga4gh.org/fhir/phenopackets/StructureDefinition/
↪biosample-diagnostic-markers",
    "isControlSample": "http://ga4gh.org/fhir/phenopackets/StructureDefinition/
↪biosample-control"
},
"phenotypicFeature": {
    "title": "Phenotypic Feature",
    "url": "http://ga4gh.org/fhir/phenopackets/StructureDefinition/
↪PhenotypicFeature",
    "severity": "http://ga4gh.org/fhir/phenopackets/StructureDefinition/
↪phenotypic-feature-severity",
    "modifier": "http://ga4gh.org/fhir/phenopackets/StructureDefinition/
↪phenotypic-feature-modifier",
    "onset": "http://ga4gh.org/fhir/phenopackets/StructureDefinition/phenotypic-
↪feature-onset",
    "evidence": {
        "url": "http://ga4gh.org/fhir/phenopackets/StructureDefinition/evidence",
        # fixed value
        "evidenceCode": "evidenceCode"
    }
},
"externalReference": {
    "url": "http://ga4gh.org/fhir/phenopackets/StructureDefinition/external-
↪reference",
    # fixed values
    "idUrl": "id",
    "descriptionUrl": "description"
},
"htsFile": {
    "url": "http://ga4gh.org/fhir/phenopackets/StructureDefinition/HtsFile",
    "genomeAssembly": "http://ga4gh.org/fhir/phenopackets/StructureDefinition/
↪htsfile-genome-assembly",
    # fixed value
    "status": "current",
    "htsFormat": "http://ga4gh.org/fhir/phenopackets/CodeSystem/hts-format"
},
"disease": {
    "url": "http://ga4gh.org/fhir/phenopackets/StructureDefinition/Disease",

```

(continues on next page)

(continued from previous page)

```
        "onset": "http://ga4gh.org/fhir/phenopackets/StructureDefinition/disease-onset
↪",
        "disease_stage": "http://ga4gh.org/fhir/phenopackets/StructureDefinition/
↪disease-tumor-stage",
    }
}
```

INDICES AND TABLES

- `genindex`
- `modindex`
- `search`

PYTHON MODULE INDEX

C

`converters.resources`, 3

`converters.validate`, 5

INDEX

A

`age_to_fhir()` (in module *converters.resources*), 3

B

`biosample_to_fhir()` (in module *converters.resources*), 3

C

`check_disease_onset()` (in module *converters.resources*), 3

`codeable_concepts_fields()` (in module *converters.resources*), 3

`converters.resources` (module), 3

`converters.validate` (module), 5

D

`disease_to_fhir()` (in module *converters.resources*), 3

F

`fhir_codeable_concept()` (in module *converters.resources*), 3

`fhir_coding_util()` (in module *converters.resources*), 3

G

`gene_to_fhir()` (in module *converters.resources*), 4

H

`hts_file_to_fhir()` (in module *converters.resources*), 4

I

`individual_to_fhir()` (in module *converters.resources*), 4

P

`phenopacket_to_fhir()` (in module *converters.resources*), 4

`phenotypic_feature_to_fhir()` (in module *converters.resources*), 4

`procedure_to_fhir()` (in module *converters.resources*), 4

V

`validate_schema()` (in module *converters.validate*), 5

`variant_to_fhir()` (in module *converters.resources*), 4