

# Introduction

The MMCI convector processes data from the CRC-cohort from MMCI and converts them into a chosen standard, FHIR or OMOP. After successful conversion, a set of quality checks is run. The tool also provides Wizzard, which questions the user and, based on provided information, recommends a better standard.

## System Requirements

**Operating system:** Windows 10

**Programming Language:** Python 3.7.9.+

Python libraries are listed in setup.py.

## Installation

Clone Repository:

```
git clone https://github.com/linartova/data-quality.git
```

```
cd data-quality
```

Install Dependencies:

```
pip install -r requirements.txt
```

Run the tool:

```
cd mmci-convector
```

```
python gui.py
```

# Using the tool

This section describes running FHIR or OMOP conversions on data storage and input data. Then, there is a description of the step-by-step wizard, including questions for the user. Last, a table compares the converted fields and input files and more information about quality checks.

## Prerequisites

The user must have the FHIR server and the OMOP CDM database to run the conversion and QC on both standards. In the case of missing data elements, the OMOP CDM database must have disabled null constraints.

### FHIR server

The recommended FHIR server is Blaze, which runs as a Java jar and is downloaded [here](#).

### OMOP CDM database

To use the OMOP conversion and QC tool, the user must download and set the OMOP CDM database. The tutorial is [here](#). Recommended RDBMS is PostgreSQL.

### Input file with data

The input file must be in XML. The tool uses the script "mmci\_convertor/input\_validation.py" to validate the XML input. The correct example of the input is in test\_data.xml. In case of incorrect input, a short hint will appear.

Input data are described further in this documentation. Additional data will not be converted.

## Step-by-step wizard

In the MMCI convector, the user can answer the set of questions. In the end, the answers will be evaluated and summarized, and the user will see the recommendation of which standard will be the best. The questionnaire will have two parts: the general questions and questions about which quality checks the user demands. There will also be a table with a comparison of quality checks.

## Questions about general usage

**What is the use case of the data?** If it includes Data exchange, then the FHIR is the best option. If it is a Longitudinal analysis, then use OMOP.

**Does the user have a license for SNOMED CT?** The vast majority of OMOP use SNOMED CT, so if the user needs a license, it is better to go for FHIR, where the license is unnecessary.

**What technical solution is better for data storage?** FHIR uses a server with RESTfull API, and data are stored in Resources and files in JSON and XML formats. On the other hand, the OMOP CDM uses an SQL database for data storage with all the concepts and vocabularies that must be downloaded. The OHDSI also provides many open-source tools in R.

**Does the user have additional data that needs conversion as well?** If the user needs to convert more data not converted in the MMCI convector, then it is usually faster and more developer-friendly in FHIR. On the other hand, if the user knows OMOP, the conversion of the OHDSI open-source tool can be accelerated [].

**What is the size of the data set?** In FHIR, the large amount of data can cause performance issues. The OMOP using SQL database is a better choice for extensive data.

**Does the user need a storage model or an interoperability model?** For the final storage model, where data will not be changed again, the OMOP is the best solution. For repeatable data exchange between many facilities, the FHIR is the best.

**Does the user need to customize the input data and minimize data loss?** The best option is FHIR. The FHIR implements only a minimal model and is designed to provide many extensions and specifications. This goal is thanks to "profiling". Each facility has its profile, which can be found in Simplifier.

**Does the user need the global model with standardized vocabularies and codes to simplify data?** Then, the best option is OMOP.

**Is it beneficial to use the OHDSI open-source tools?** On the OMOP CDM works, OHDSI provides tools such as White Rabbit for ETL, Achilles for database visualization, and the Data quality dashboard with many data quality checks.

**Is it necessary to add custom constraints?** The FHIR is the way to go.

## Conversion

In the tables below, the user can see how the data are mapped in the tool.

Tables list all elements from the input XML in the first row. Then, the blue rows are mapped into OMOP or FHIR, depending on the specific table.

BasicData FHIR				
Tag	Attribute	FHIR resource	FHIR object	Correction
2_2	Participation in clinical study			
22_4	KRAS exon 4 (codons 117 or 146) mutation status			
4_3	Time of recurrence (metastasis diagnosis)			
20_3	KRAS exon 2 (codons 12 or 13)			
6_3	Timestamp of last update of vital status			
87_1	BRAF, PIC3CA, HER2 mutation status			
24_4	NRAS exon 3 (codons 59 or 61)			
61_5	Liver imaging			
31_3	CT			
14_3	Microsatellite instability			
16_3	Risk situation (only HNPCC)			
85_1	Biological sex	Patient	gender	
3_1	Age at diagnosis (rounded to years)	Patient	birthDate	Dataelement_51_3 - Dataelement_3_1
21_5	KRAS exon 3 (codons 59 or 61)			

5_2	Vital status			
7_2	Overall survival status			
25_3	NRAS exon 4 (codons 117 or 146)			
88_1	Colonoscopy			
23_5	NRAS exon 2 (codons 12 or 13)			
63_4	Lung imaging			
30_3	MRI			
51_3	Date of diagnosis	Condition	recordedDate, onsetDateTime	
15_2	Mismatch repair gene expression			
Identifier		Patient	Identifier	

BasicData OMOP CDM				
Tag	Attribute	OHDSI table	OHDSI attribute	Correction
2_2	Participation in clinical study			
22_4	KRAS exon 4 (codons 117 or 146) mutation status			
4_3	Time of recurrence (metastasis diagnosis)			
20_3	KRAS exon 2 (codons 12 or 13)			
6_3	Timestamp of last update of vital status	OBSERVATION PERIOD	observation_period_end_date	
87_1	BRAF, PIC3CA, HER2 mutation status			
24_4	NRAS exon 3 (codons 59 or 61)			
61_5	Liver imaging	PROCEDURE OCCURRENCE	procedure_concept_id, procedure_source_value	mapping on right description
31_3	CT	PROCEDURE OCCURRENCE	procedure_concept_id, procedure_source_value	mapping on right description
14_3	Microsatellite instability			
16_3	Risk situation (only HNPCC)			
85_1	Biological sex	PERSON	gender_concept_id, gender_source_value	
3_1	Age at diagnosis (rounded to years)	PERSON	year_of_birth	

21_5	KRAS exon 3 (codons 59 or 61)			
5_2	Vital status			
7_2	Overall survival status			
25_3	NRAS exon 4 (codons 117 or 146)			
88_1	Colonoscopy	PROCEDURE OCCURRENCE	procedure_concept_id, procedure_source_value	mapping on right descriptio n
23_5	NRAS exon 2 (codons 12 or 13)			
63_4	Lung imaging	PROCEDURE OCCURRENCE	procedure_concept_id, procedure_source_value	mapping on right descriptio n
30_3	MRI	PROCEDURE OCCURRENCE	procedure_concept_id, procedure_source_value	mapping on right descriptio n
51_3	Date of diagnosis	PERSON	year_of_birth	calculatio n
		CONDITION OCCURRENCE	condition_start_date	
		PROCEDURE OCCURRENCE	procedure_date	only for diagnosti c procedur es
15_2	Mismatch repair gene expression			
Identifier		PERSON	person_source_value	

Pharmacotherapy OMOP CDM				
Tag	Attribute	OHDSI table	OHDSI attribute	Correction
10_2	Date of start of pharmacotherapy	DRUG EXPOSURE	drug_exposure_start_date, drug_exposure_start_datetime	
11_2	Date of end of pharmacotherapy	DRUG EXPOSURE	drug_exposure_end_date, drug_exposure_end_datetime	
59_5	Scheme of pharmacotherapy	DRUG EXPOSURE	drug_concept_id, drug_source_value	mapping

81_3	Other pharmacotherapy scheme	DRUG EXPOSURE	drug_source_value	only if scheme is other
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Surgery OMOP CDM				
Tag	Attribute	OHDSI table	OHDSI attribute	Correction
8_3	Time difference between initial diagnosis and surgery	PROCEDURE OCCURRENCE	procedure_date	
49_1	Surgery type	PROCEDURE OCCURRENCE	procedure_concept_id, procedure_source_value	mapping into right values
67_1	Other surgery type	PROCEDURE OCCURRENCE	procedure_concept_id, procedure_source_value	only if Dataelement_49_1 is "Other"
9_2	Surgery radicality			
93_1	Location of the tumor			

Sample FHIR			
Tag	Attribute	FHIR resource	FHIR object
56_2	Sample ID		
54_2	Material type	Specimen	type
55_2	Preservation mode		
89_3	Year of sample collection	Specimen	collection.collectedDateTime

Sample OMOP CDM				
Tag	Attribute	OHDSI table	OHDSI attribute	Correction
56_2	Sample ID	SPECIMEN	specimen_source_id	
54_2	Material type	SPECIMEN	specimen_concept_id, specimen_source_value	mapping on right description
55_2	Preservation mode			

89_3	Year of sample collection	OBSERVATION PERIOD	observation_start_date	choose the oldest date
		SPECIMEN	specimen_date	

Histopathology FHIR				
Tag	Attribute	FHIR resource	FHIR object	Correction
75_1	Distant metastasis			
83_1	Grade			
70_2	Stage			
92_1	Localization of primary tumor	Condition	code	mapping on right description
73_3	UICC version			
58_2	Availability invasion front digital imaging			
71_1	Primary Tumor			
77_1	Regional lymph nodes			
68_2	Localization of metastasis			
91_1	Morphology			
53_3	WHO version			
57_3	Availability digital imaging			
82_1	Biological material from recurrence available			

Histopathology OMOP CDM				
Tag	Attribute	OHDSI table	OHDSI attribute	Correction
75_1	Distant metastasis			
83_1	Grade			
70_2	Stage			
92_1	Localization of primary tumor	CONDITION OCCURRENCE	condition_concept_id, condition_source_value	mapping on right description
73_3	UICC version			
58_2	Availability invasion front digital imaging			
71_1	Primary Tumor			
77_1	Regional lymph nodes			
68_2	Localization of metastasis			
91_1	Morphology			
53_3	WHO version			
57_3	Availability digital			



	imaging			
82_1	Biological material from recurrence available			

Radiation therapy OMOP CDM				
Tag	Attribute	OHDSI table	OHDSI attribute	Correction
12_4	Date of start of radiation therapy	PROCEDURE OCCURRENCE	procedure_concept_id, procedure_source_value	mapping into right values
13_2	Date of end of radiation therapy			

There is also FHIR extra conversion:

Source Text	Code	Display
6th	444256004	American Joint Commission on Cancer, Cancer Staging Manual, 6th edition neoplasm staging system (tumor staging)
7th	443830009	American Joint Commission on Cancer, Cancer Staging Manual, 7th edition neoplasm staging system (tumor staging)
8th	897275008	American Joint Commission on Cancer, Cancer Staging Manual, 8th edition neoplasm staging system (tumor staging)
9th	1269566009	American Joint Commission on Cancer, Cancer Staging Manual, 9th edition neoplasm staging system (tumor staging)

Source Text	Code	Display
X	okk	Stage X
0	0	Stage 0
0a	0a	Stage 0a
0is	0is	Stage 0is
I	I	Stage I
IA1	IA1	Stage IA1
IA2	IA2	Stage IA2
IA3	IA3	Stage IA3
IB	IB	Stage IB
IB1	IB1	Stage IB1
IB2	IB2	Stage IB2
IC	IC	Stage IC
IS	IS	Stage IS
II	II	Stage II
IIA	IIA	Stage IIA
IIA1	IIA1	Stage IIA1
IIA2	IIA2	Stage IIA2
IIB	IIB	Stage IIB
IIC	IIC	Stage IIC

Source Text	Code	Display
III	III	Stage III
IIIA	IIIA	Stage IIIA
IIIA1	IIIA1	Stage IIIA1
IIIA2	IIIA2	Stage IIIA2
IIIB	IIIB	Stage IIIB
IIIC	IIIC	Stage IIIC
IIIC1	IIIC1	Stage IIIC1
IIIC2	IIIC2	Stage IIIC2
IV	IV	Stage IV
IVA	IVA	Stage IVA
IVB	IVB	Stage IVB
IVC	IVC	Stage IVC

Source Text	Code	Display			
TX	TX	TX			
T0	T0	T0	Source Text	Code	Display
Ta	Ta	Ta			
Tis	Tis	Tis			
Tis(LAMN)	Tis(LAMN)	Tis(LAMN)	M0	M0	M0
Tis(DCIS)	Tis(DCIS)	Tis(DCIS)			
Tis(LCIS)	Tis(LCIS)	Tis(LCIS)			
Tis(Paget)	Tis(Paget)	Tis(Paget)	M1	M1	M1
Tis(pu)	Tis(pu)	Tis(pu)			
Tis(pd)	Tis(pd)	Tis(pd)			
T1	T1	T1			
T1mi	T1mi	T1mi			
T1a	T1a	T1a	M1a	M1a	M1a
T1a1	T1a1	T1a1			
T1a2	T1a2	T1a2			
T1b	T1b	T1b	M1b	M1b	M1b
T1b1	T1b1	T1b1			
T1b2	T1b2	T1b2	M1c	M1c	M1c
T1c	T1c	T1c	M1d	M1d	M1d
T1c2	T1c2	T1c2			
T1c3	T1c3	T1c3	MX	MX	MX
T1d	T1d	T1d			
Source Text	Code	Display			
T2	T2	T2			
T2a	T2a	T2a			
T2a1	T2a1	T2a1			
T2a2	T2a2	T2a2	Source Text	Code	Display
T2b	T2b	T2b	Nx	Nx	Nx
T2c	T2c	T2c	N0	N0	N0
T2d	T2d	T2d	N1	N1	N1
T3	T3	T3	N1(mi)	N1(mi)	N1mi
T3a	T3a	T3a	N1a	N1a	N1a
T3b	T3b	T3b	N1b	N1b	N1b
T3c	T3c	T3c	N1c	N1c	N1c
T3d	T3d	T3d	N2	N2	N2
T3e	T3e	T3e	N2a	N2a	N2a
T4	T4	T4	N2b	N2b	N2b
T4a	T4a	T4a	N2c	N2c	N2c
T4b	T4b	T4b	N3	N3	N3
T4c	T4c	T4c	N3a	N3a	N3a
T4d	T4d	T4d	N3b	N3b	N3b
T4e	T4e	T4e	N3c	N3c	N3c

Source Text	Code	Display	Source Text	Code	Display
Adenocarcinoma	1187332001	Adenocarcinoma (morphologic abnormality)	GX	12619005	GX grade (finding)
Mucinous carcinoma	72495009	Mucinous adenocarcinoma (morphologic abnormality)	G1	54102005	G1 grade (finding)
Signet-ring cell carcinoma	87737001	Signet ring cell carcinoma (morphologic abnormality)	G2	1663004	G2 grade (finding)
Medullary carcinoma	32913002	Medullary carcinoma (morphologic abnormality)	G3	61026006	G3 grade (finding)
Other	0	Other			

Surgery type mapping		
Original value	Code	Display
Abdomino-perineal resection	265414003	Abdominoperineal resection of rectum
Anterior resection of rectum	4558008	Anterior resection of rectum
Endo-rectal tumor resection	Missing	Missing
Left hemicolectomy	315324009	Left hemicolectomy with anastomosis
Low anteroir colon resection	Missing	Missing
Pan-procto colectomy	Missing	Missing
Right hemicolectomy	235326000	Right hemicolectomy
Sigmoid colectomy	84604002	Sigmoid colectomy
Total colectomy	26390003	total colectomy
Transverse colectomy	26925005	Transverse colectomy

bodySite mapping		
Original value	New value code	New value display
C18.0	32713005	Cecum structure
C18.1	Missing	Missing
C18.2	9040008	Ascending colon structure
C18.3	48338005	Structure of right colic flexur
C18.4	485005	Transverse colon structure
C18.5	72592005	Structure of left colic flexure
C18.6	32622004	Descending colon structure
C18.7	60184004	Sigmoid colon structure
C18.8	Missing	Missing
C18.9	Missing	Missing
C19	49832006	Structure of rectosigmoid junction
C20	34402009	Rectum structur

outcome mapping		
Value in openEHR	Code	Display
R0	258254000	Residual tumor stage R0 (finding)
R1	278271003	Residual tumor stage R1 (finding)
R2	278272005	Residual tumor stage R2 (finding)

Specific response FHIR		
Source text	Code	Display
Complete response	371001000	Patient cured (finding)
Stable disease	359746009	Patient's condition stable (finding)
Partial response	268910001	Patient's condition improved (finding)
Progressive disease	271299001	Patient's condition worsened (finding)

Vital status	
Source text	deceasedBoolean value
ALIVE	false
DEATH_COLON_CANCER	true
DEATH_OTHER	true
DEATH_UNKNOWN_REASON	true

FHIR field name	Node name	Note
Patient.identifier[0].value	Patient pseudonym (XSD label: Identifier)	
Patient.gender	Biological sex (XSD label: Dataelement_85_1)	
Patient.birthDate		Current version: during the ETL, the year of birth is calculated as: year of diagnosis (XSD label: Dataelement_51_3) - age at diagnosis (XSD label: Dataelement_3_1)
Patient.deceasedBoolean	XSD label: Dataelement_5_2	mapping table N
patient.deceasedDateTime	XSD label: Dataelement_6_3	only if deceasedBoolean == true

FHIR field name	Node name	Note
Procedure.code.coding[0].system		"http://snomed.info/sct"
Procedure.code.coding[0].code		"108290001"
Procedure.code.coding[0].display		"Radiation therapy"
Procedure.subject.reference		reference on patient
Procedure.performedPeriod.start	XSD Label: Dataelement_35_3	converted into date
Procedure.performedPeriod.end	XSD Label: Dataelement_36_1	converted into date

FHIR field name	Node name	Note
Observation.code.coding[0].system		"http://loinc.org"
Observation.code.coding[0].code		"21983-2"
Observation.code.coding[0].display		"Recurrence type first episode Cancer"
Object.subject.reference		reference on patient
Observation.valueQuantity.value	XSD Label: Dataelement_4_3	
Observation.valueQuantity.unit		"wk"
Observation.valueQuantity.system		"http://unitsofmeasure.org"
Observation.valueQuantity.code		"wk"

FHIR field name	Node name	Note
Observation.category.coding.system		"http://terminology.hl7.org/CodeSystem/observation-category"
Observation.category.coding.code		"therapy"
Observation.category.coding.display		"Therapy"
Observation.code.coding.system		"http://loinc.org"
Observation.code.coding.code		"100633-7"
Observation.code.coding.display		"Rapid response team Hospital Progress note"
Observation.subject.reference		reference on patient
Observation.effectiveDateTime	XSD Label: Dataelement_34_1	converted into date
Observation.valueCodeableConcept.coding[0].system		"http://snomed.info/sct"
Observation.valueCodeableConcept.coding[0].code		mapping table M - second column
Observation.valueCodeableConcept.coding[0].display	XSD Label: Dataelement_33_1	mapping table M - third column



FHIR field name	Node name	Note
Procedure.code.coding.system		"http://snomed.info/sct"
Procedure.code.coding.code	XSD Label: Dataelement_49_1 or Dataelement_67_1	mapping table J - second column
Procedure.code.coding.display		mapping table J - third column
Procedure.subject.reference		reference on patient
Procedure.performedPeriod.start	XSD Label: Dataelement_8_3	converted into date
Procedure.bodySite[0].coding.system		"http://snomed.info/sct"
Procedure.bodySite[0].coding.code	XSD Label: Dataelement_93_1	mapping table K - second column
Procedure.bodySite[0].coding.display		mapping table K - third column
Procedure.outcome.coding[0].system		"http://snomed.info/sct"
Procedure.outcome.coding[0].code	XSD Label: Dataelement_9_2	mapping table L - second column
Procedure.outcome.coding[0].display		mapping table L - third column
Procedure.note[0].text	XSD Label: Dataelement_67_1	

FHIR field name	Node name	Note
Procedure.code.coding[0].system		"http://hl7.org/fhir/uv/ichom-breast-cancer/CodeSystem/TreatmentTypesCodeSystem"
Procedure.code.coding[0].code		"targeted-therapy"
Procedure.code.coding[0].display		"Targeted therapy"
Procedure.subject.reference		reference on patient
Procedure.performedPeriod.start	XSD Label: Dataelement_35_3	converted into date
Procedure.performedPeriod.end	XSD Label: Dataelement_36_1	converted into date

FHIR field name	Node name	Note
Observation.code.coding[0].system		"http://snomed.info/sct"
Observation.code.coding[0].code		"445320007"
Observation.code.coding[0].display		"Survival time (observable entity)"
Object.subject.reference		reference on patient
Observation.effectiveDateTime	XSD Label: Dataelement_6_3	converted into date
Observation.valueQuantity.value	XSD Label: Dataelement_7_2	
Observation.valueQuantity.unit		"wk"
Observation.valueQuantity.system		"http://unitsofmeasure.org"
Observation.valueQuantity.code		"wk"

FHIR field name	Node name	Note
Observation.subject.reference		reference on patient
Observation.method.coding.system		"http://snomed.info/sct"
Observation.method.coding.code	XSD Label: Dataelement_73_3	mapping table C - second column
Observation.method.coding.display		mapping table C - third column
Observation.valueCodeableConcept.coding.system		"urn:oid:2.16.840.1.113883.15.16"
Observation.valueCodeableConcept.coding.code	XSD Label: Dataelement_70_2	mapping table D - second column
Observation.valueCodeableConcept.coding.display		mapping table D - third column
Observation.component[0].code.coding.system		"http://loinc.org"
Observation.component[0].code.coding.code		"21905-5"
Observation.component[0].code.coding.display		"Primary tumor.clinical [Class] Cancer"
Observation.component[0].valueCodeableConcept.coding.system		"urn:oid:2.16.840.1.113883.15.16"
Observation.component[0].valueCodeableConcept.coding.code	XSD Label: Dataelement_71_1	mapping table E - second column
Observation.component[0].valueCodeableConcept.coding.display		mapping table E - third column

FHIR field name	Node name	Note
Observation.component[1].code.coding.system		"http://loinc.org"
Observation.component[1].code.coding.code		"21900-6"
Observation.component[1].code.coding.display		"Regional lymph nodes.pathology [Class] Cancer"
Observation.component[1].valueCodeableConcept.coding.system		"urn:oid:2.16.840.1.113883.15.16"
Observation.component[1].valueCodeableConcept.coding.code	XSD Label: Dataelement_77_1	mapping table F - second column
Observation.component[1].valueCodeableConcept.coding.display		mapping table F - third column
Observation.component[2].code.coding.system		"http://loinc.org"
Observation.component[2].code.coding.code		"21900-6"
Observation.component[2].code.coding.display		"Regional lymph nodes.pathology [Class] Cancer"
Observation.component[2].valueCodeableConcept.coding.system		"urn:oid:2.16.840.1.113883.15.16"
Observation.component[2].valueCodeableConcept.coding.code	XSD Label: Dataelement_75_1	mapping table G - second column
Observation.component[2].valueCodeableConcept.coding.display		mapping table G - third column

FHIR field name	Node name	Note
Observation.component[3].code.coding.system		"http://snomed.info/sct"
Observation.component[3].code.coding.code		"1284862009"
Observation.component[3].code.coding.display		"Histologic type of primary malignant neoplasm of cecum and/or colon and/or rectum (observable entity)"
Observation.component[3].valueCodeableConcept.coding.system		"http://snomed.info/sct"
Observation.component[3].valueCodeableConcept.coding.code		mapping table H - second column
Observation.component[3].valueCodeableConcept.coding.display	XSD Label: Dataelement_91_1	mapping table H - third column
Observation.component[4].code.coding.system		"http://snomed.info/sct"
Observation.component[4].code.coding.code		"395557000"
Observation.component[4].code.coding.display		"Tumor finding (finding)"
Observation.component[4].valueCodeableConcept.coding.system		"http://snomed.info/sct"
Observation.component[4].valueCodeableConcept.coding.code		mapping table I - second column
Observation.component[4].valueCodeableConcept.coding.display	XSD Label: Dataelement_83_1	mapping table I - third column

## Quality checks

Here is the list of quality checks provided by the tool. At the end, there is a comparison with the original R script running on the original input data.

## Quality checks documentation

- 1. Warning: Vital check date precedes initial diagnosis date**  
**Description:** Subtract 'Timestamp of last update of vital status' from 'Date of diagnosis', if the result is negative, then 'Timestamp of last update of vital status' precedes 'Date of diagnosis', which is suspicious.  
**Dataelements:**
  - Name:**Timestamp of last update of vital status  
**dataelement\_id:** Dataelement\_6\_3
  - Name:**Date of diagnosis

**dataelement\_id:** Dataelement\_51\_3

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Values are compared, not subtracted.

**Implementation in extra OMOP:** Equivalent

- **2. Warning: Vital check date is equal to initial diagnosis date**

**Description:** Subtract 'Timestamp of last update of vital status' from 'Date of diagnosis', if the result is equal to zero, then 'Timestamp of last update of vital status' equals 'Date of diagnosis', which is suspicious.

**Dataelements:**

- **Name:**Timestamp of last update of vital status  
**dataelement\_id:** Dataelement\_6\_3
- **Name:**Date of diagnosis  
**dataelement\_id:** Dataelement\_51\_3

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Values are compared, not subtracted.

**Implementation in extra OMOP:** Equivalent

- **3. Warning: Suspicious survival information**

**Description:** Check if 'Timestamp of last update of vital status' and 'Date of diagnosis', are in correct order. Then 'Overall survival status' is divided by weeks between those two dates and result larger than 3 is suspicious.

**Dataelements:**

- **Name:**Timestamp of last update of vital status  
**dataelement\_id:** Dataelement\_6\_3
- **Name:**Date of diagnosis  
**dataelement\_id:** Dataelement\_51\_3
- **Name:**Overall survival status  
**dataelement\_id:** Dataelement\_7\_2

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Equivalent

**Implementation in extra OMOP:** Missing

- **4. Warning: Suspiciously young patient**

**Description:** Filter patients younger than 15. Compare 'Age at diagnosis (rounded to years)' to 15.

**Dataelements:**

- **Name:**Age at diagnosis (rounded to years)  
**dataelement\_id:** Dataelement\_3\_1

**Implementation in FHIR:** The 'Age at diagnosis (rounded to years)' is not directly mapped to FHIR, so it works with 'onsetDateTime' (originally 'Date of diagnosis') and 'birth\_date'. Other functionality stays the same.

**Implementation in extra FHIR:** Implemented in FHIR.

**Implementation in extra OMOP:** Similarly, as in FHIR, age is computed from 'condition\_start\_date' and 'year\_of\_birth'. Other functionality stays the same.

- **5. Warning: Suspiciously long survival**

**Description:** Filter patients with 'Overall survival status' larger than 4000 or patient was diagnosed under age of 95 and lived 100 years and more.

**Dataelements:**

- **Name:**Age at diagnosis (rounded to years)  
**dataelement\_id:** Dataelement\_3\_1
- **Name:**Overall survival status  
**dataelement\_id:** Dataelement\_7\_2

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Equivalent

**Implementation in extra OMOP:** Missing

- **6. Warning: Vital status timestamp missing**

**Description:** Filter 'Vital status' with 'UNKNOWN' value and 'Timestamp of last update of vital status' with null value.

**Dataelements:**

- **Name:**Vital status  
**dataelement\_id:** Dataelement\_5\_2
- **Name:**Timestamp of last update of vital status  
**dataelement\_id:** Dataelement\_6\_3

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Equivalent

**Implementation in extra OMOP:** Missing

- **7. Warning: Vital status timestamp is in the future**

**Description:** Filter null values 'Timestamp of last update of vital status', then filter future dates.

**Dataelements:**

- **Name:**Timestamp of last update of vital status  
**dataelement\_id:** Dataelement\_6\_3

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Equivalent

**Implementation in extra OMOP:** Equivalent

- **8. Warning: Initial diagnosis date is in the future**

**Description:** Filter null values 'Timestamp of last update of vital status', then filter future dates.

**Dataelements:**

- **Name:**Date of diagnosis  
**dataelement\_id:** Dataelement\_51\_3

**Implementation in FHIR:** Equivalent

**Implementation in extra FHIR:** Implemented in FHIR.

**Implementation in extra OMOP:** Equivalent

- **9. Warning: Pharmacotherapy scheme description is missing while pharmacotherapy scheme is Other**

**Description:** Filter pharmacotherapies where 'Scheme of pharmacotherapy' is equal to 'Other' and 'Other pharmacotherapy scheme' is missing.

**Dataelements:**

- **Name:**Scheme of pharmacotherapy  
**dataelement\_id:** Dataelement\_59\_5
- **Name:**Other pharmacotherapy scheme  
**dataelement\_id:** Dataelement\_81\_3

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Missing

**Implementation in extra OMOP:** Equivalent

- **10. Warning: Suspicious description of pharmacotherapy**

**Description:** Filter pharmacotherapies where 'Scheme of pharmacotherapy' is equal to 'Other' and 'Other pharmacotherapy scheme' is equal to one of the following values: 'No pharmacotherapy', 'other', 'unknown', 'NULL'.

**Dataelements:**

- **Name:**Scheme of pharmacotherapy  
**dataelement\_id:** Dataelement\_59\_5
- **Name:**Other pharmacotherapy scheme  
**dataelement\_id:** Dataelement\_81\_3

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Missing

**Implementation in extra OMOP:** Equivalent, but also check the values from warning #11

- **11. Warning: Missing specification of used substances in pharmacotherapy description**

**Description:** Filter pharmacotherapies where 'Scheme of pharmacotherapy' is equal to 'Other' and 'Other pharmacotherapy scheme' is equal to one of the following values: 'neoadjuvante Radiochemo', 'Substances: unbekannt'.

**Dataelements:**

- **Name:**Scheme of pharmacotherapy  
**dataelement\_id:** Dataelement\_59\_5
- **Name:**Other pharmacotherapy scheme  
**dataelement\_id:** Dataelement\_81\_3

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Missing

**Implementation in extra OMOP:** Equivalent, but also check the values from warning #10



- 12. Warning: Suspicious characters or words in description of pharmacotherapy**

**Description:** Filter pharmacotherapies where 'Scheme of pharmacotherapy' is equal to 'Other' and 'Other pharmacotherapy scheme' is equal to one of the following values: '%-FU', 'andLeucovorin'.

**Dataelements:**

  - Name:**Scheme of pharmacotherapy  
**dataelement\_id:** Dataelement\_59\_5
  - Name:**Other pharmacotherapy scheme  
**dataelement\_id:** Dataelement\_81\_3

**Implementation in FHIR:** Missing  
**Implementation in extra FHIR:** Missing  
**Implementation in extra OMOP:** Equivalent
- 13. Warning: Surgery and histological location do not match**

**Description:** Filter patients with only one surgery and check if surgery location and histopathology location match.

**Dataelements:**

  - Name:**Location of the tumor  
**dataelement\_id:** Dataelement\_93\_1
  - Name:**Localization of primary tumor  
**dataelement\_id:** Dataelement\_92\_1

**Implementation in FHIR:** Missing  
**Implementation in extra FHIR:** Equivalent  
**Implementation in extra OMOP:** Missing
- 14. Warning: Surgery and histological location do not match (but multiple surgeries per patient)**

**Description:** Filter patients with multiple surgeries and check if surgery location and histopathology location match.

**Dataelements:**

  - Name:**Location of the tumor  
**dataelement\_id:** Dataelement\_93\_1
  - Name:**Localization of primary tumor  
**dataelement\_id:** Dataelement\_92\_1

**Implementation in FHIR:** Missing  
**Implementation in extra FHIR:** Equivalent  
**Implementation in extra OMOP:** Missing
- 15. Warning: Mismatch between surgery location and surgery type**

**Description:** Check if surgery type match location of the tumor and filter suspicious records.

**Dataelements:**

  - Name:**Surgery type

- dataelement\_id:** Dataelement\_49\_1
  - Name:**Location of the tumor
  - dataelement\_id:** Dataelement\_93\_1

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Equivalent

**Implementation in extra OMOP:** Missing

- 16. Warning: Negative event (treatment/response) duration: end time is before start time**

**Description:** In radiation therapy, targeted therapy and pharmacotherapy filter rows where end of therapy precedes start.

**Dataelements:**

- Name:**Date of start of radiation therapy
  - dataelement\_id:** Dataelement\_12\_4
  - Name:**Date of end of radiation therapy
  - dataelement\_id:** Dataelement\_13\_2
  - Name:**Date of start of targeted therapy
  - dataelement\_id:** Dataelement\_35\_3
  - Name:**Date of end of targeted therapy
  - dataelement\_id:** Dataelement\_36\_1
  - Name:**Date of start of pharmacotherapy
  - dataelement\_id:** Dataelement\_10\_2
  - Name:**Date of end of pharmacotherapy
  - dataelement\_id:** Dataelement\_11\_2

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Implemented equivalent for Radiation Therapy and Targeted Therapy

**Implementation in extra OMOP:** Implemented equivalent for Pharmacotherapy

- 17. Warning: Event (treatment/response) starts or ends after survival of patient**

**Description:** Check if dataelement representing number of weeks since initial diagnosis is lower than calculated adjusted\_overall\_survival (= overall\_survival + first treatment for patient if there is any, otherwise only overall\_survival).

**Dataelements:**

- Name:**Time difference between initial diagnosis and surgery
  - dataelement\_id:** Dataelement\_8\_3
  - Name:**Date of start of radiation therapy
  - dataelement\_id:** Dataelement\_12\_4
  - Name:**Date of start of targeted therapy
  - dataelement\_id:** Dataelement\_35\_3
  - Name:**Date of start of pharmacotherapy
  - dataelement\_id:** Dataelement\_10\_2
  - Name:**Date of end of radiation therapy
  - dataelement\_id:** Dataelement\_13\_2

- **Name:**Date of end of targeted therapy  
**dataelement\_id:** Dataelement\_36\_1
- **Name:**Date of end of pharmacotherapy  
**dataelement\_id:** Dataelement\_11\_2
- **Name:**Date response was obtained in weeks since initial diagnosis  
**dataelement\_id:** Dataelement\_34\_1

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Missing pharmacotherapy. Changed, overall\_survival is saved as float, so dates are converted on number of weeks since diagnosis.

**Implementation in extra OMOP:** Missing

- **18. Warning: Start of response to therapy is before diagnosis**

**Description:** Check if dataelement representing number of weeks since initial diagnosis is negative.

**Dataelements:**

- **Name:**Date response was obtained in weeks since initial diagnosis  
**dataelement\_id:** Dataelement\_34\_1

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Changed, response start is saved as date and must be compared with date of diagnosis.

**Implementation in extra OMOP:** Missing

- **19. Warning: Suspect incomplete followup: patient died of colon cancer while last response to therapy is 'Complete response'**

**Description:** Filter last responses for each patient. Filter patients with 'Vital status' equals to 'DEATH\_COLON\_CANCER' and response equals to 'Complete response'.

**Dataelements:**

- **Name:**Specific response  
**dataelement\_id:** Dataelement\_33\_1
- **Name:**Vital status  
**dataelement\_id:** Dataelement\_5\_2

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Partial. Since the information, what was the cause of death, is missing, all death patients are checking on 'Complete response'.

**Implementation in extra OMOP:** Missing

- **20. Warning: Start of response to therapy is in the future**

**Description:** Start of response is represented as number of weeks since initial diagnosis. So date of diagnosis is added to start of response and result is compared with today.

**Dataelements:**

- **Name:**Date response was obtained in weeks since initial diagnosis  
**dataelement\_id:** Dataelement\_34\_1

- **Name:**Date of diagnosis  
**dataelement\_id:** Dataelement\_51\_3

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Changed, start is saved as date and must be compared with date of diagnosis.

**Implementation in extra OMOP:** Missing

- **21. Warning: Start of therapy is before diagnosis**

**Description:** In surgery, radiation therapy, targeted therapy and pharmacotherapy filter rows where start of therapy, represented by number of weeks since initial diagnosis, is negative.

**Dataelements:**

- **Name:**Time difference between initial diagnosis and surgery  
**dataelement\_id:** Dataelement\_8\_3
- **Name:**Date of start of radiation therapy  
**dataelement\_id:** Dataelement\_12\_4
- **Name:**Date of start of targeted therapy  
**dataelement\_id:** Dataelement\_35\_3
- **Name:**Date of start of pharmacotherapy  
**dataelement\_id:** Dataelement\_10\_2

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Only for Dataelement\_8\_3, Dataelement\_12\_4, Dataelement\_35\_3. Changed, start is saved as date and must be compared with date of diagnosis.

**Implementation in extra OMOP:** Only for Dataelement\_8\_3, Dataelement\_12\_4, Dataelement\_10\_2. Changed, start is saved as date and must be compared with date of diagnosis.

- **22. Warning: Start of treatment is in the future**

**Description:** Start of treatment is represented as number of weeks since initial diagnosis. So date of diagnosis is added to start of treatment and result is compared with today.

**Dataelements:**

- **Name:**Time difference between initial diagnosis and surgery  
**dataelement\_id:** Dataelement\_8\_3
- **Name:**Date of start of radiation therapy  
**dataelement\_id:** Dataelement\_12\_4
- **Name:**Date of start of targeted therapy  
**dataelement\_id:** Dataelement\_35\_3
- **Name:**Date of start of pharmacotherapy  
**dataelement\_id:** Dataelement\_10\_2

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Changed, start is saved as date and must be compared directly. Only for Dataelement\_8\_3, Dataelement\_12\_4, Dataelement\_35\_3.

**Implementation in extra OMOP:** Changed, start is saved as date and must be compared directly. Only for Dataelement\_8\_3, Dataelement\_12\_4, Dataelement\_10\_2.

- **23. Warning: End of treatment is in the future**

**Description:** End of treatment is represented as number of weeks since initial diagnosis. So date of diagnosis is added to end of treatment and result is compared with today.

**Dataelements:**

- **Name:**Date of end of radiation therapy  
**dataelement\_id:** Dataelement\_13\_2
- **Name:**Date of end of targeted therapy  
**dataelement\_id:** Dataelement\_36\_1
- **Name:**Date of end of pharmacotherapy  
**dataelement\_id:** Dataelement\_11\_2

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Changed, end is saved as date and must be compared directly. Only for Dataelement\_13\_2, Dataelement\_36\_1.

**Implementation in extra OMOP:** Changed, start is saved as date and must be compared directly. Only for Dataelement\_11\_2.

- **24. Warning: Non-surgery therapy starts and ends in week 0 since initial diagnosis (maybe false positive)**

**Description:** Filter therapies when start and end equal 0.

**Dataelements:**

- **Name:**Date of start of radiation therapy  
**dataelement\_id:** Dataelement\_12\_4
- **Name:**Date of end of radiation therapy  
**dataelement\_id:** Dataelement\_13\_2
- **Name:**Date of start of targeted therapy  
**dataelement\_id:** Dataelement\_35\_3
- **Name:**Date of end of targeted therapy  
**dataelement\_id:** Dataelement\_36\_1
- **Name:**Date of start of pharmacotherapy  
**dataelement\_id:** Dataelement\_10\_2
- **Name:**Date of end of pharmacotherapy  
**dataelement\_id:** Dataelement\_11\_2

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Changed, starts and ends are saved as date and must be compared with date of diagnosis. Only for targeted therapy and radiation therapy.

**Implementation in extra OMOP:** Changed, starts and ends are saved as date and must be compared with date of diagnosis. Only for pharmacotherapy.

- **25. Warning: Suspiciously short pharma therapy - less than 1 week (may be false positive)**

**Description:** Check if the duration of pharmacotherapy is less than 1 week by subtracting the end and start dates of pharmacotherapy.

**Dataelements:**

- **Name:**Date of start of pharmacotherapy  
**dataelement\_id:** Dataelement\_10\_2
- **Name:**Date of end of pharmacotherapy  
**dataelement\_id:** Dataelement\_11\_2

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Missing

**Implementation in extra OMOP:** Equivalent

- **26. Warning: Mismatch between provided and computed stage value**

**Description:** Filter null values and then check if the provided UICC stage equals the computed UICC stage.

**Dataelements:**

- **Name:**Primary Tumor  
**dataelement\_id:** Dataelement\_71\_1
- **Name:**Regional lymph nodes  
**dataelement\_id:** Dataelement\_77\_1
- **Name:**Distant metastasis  
**dataelement\_id:** Dataelement\_75\_1
- **Name:**Stage  
**dataelement\_id:** Dataelement\_70\_2

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Equivalent

**Implementation in extra OMOP:** Missing

- **27. Warning: Suspicious TNM value combination for given UICC version (e.g., N2a for UICC version 6) or uncomputable UICC stage**

**Description:** Check if the UICC stage is computable.

**Dataelements:**

- **Name:**Primary Tumor  
**dataelement\_id:** Dataelement\_71\_1
- **Name:**Regional lymph nodes  
**dataelement\_id:** Dataelement\_77\_1
- **Name:**Distant metastasis  
**dataelement\_id:** Dataelement\_75\_1
- **Name:**Stage  
**dataelement\_id:** Dataelement\_70\_2

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Equivalent

**Implementation in extra OMOP:** Missing

- **28. Warning: pNX provided in TNM values, while UICC stage is determined (how?)**

**Description:** Filter null values and then check if 'Primary Tumor' = NX while 'Stage' is not null or 'IV', 'IVA', 'IVB'.

**Dataelements:**

- **Name:**Primary Tumor  
**dataelement\_id:** Dataelement\_71\_1
- **Name:**Regional lymph nodes  
**dataelement\_id:** Dataelement\_77\_1
- **Name:**Distant metastasis  
**dataelement\_id:** Dataelement\_75\_1
- **Name:**Stage  
**dataelement\_id:** Dataelement\_70\_2

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Equivalent

**Implementation in extra OMOP:** Missing

- **1. Report: createPlotWithSampleYears**

**Description:** Filter patients with sample year value.

**Dataelements:**

- **Name:**Year of sample collection  
**dataelement\_id:** Dataelement\_89\_3

**Implementation in FHIR:** Partial. Implemented in missing\_collection\_collectedDateTime.

**Implementation in extra FHIR:** Missing

**Implementation in extra OMOP:** Partial. Implemented in missing\_specimen\_date.

- **2. Report: createPlotWithoutSampleYears**

**Description:** Filter patients without sample year value.

**Dataelements:**

- **Name:**Year of sample collection  
**dataelement\_id:** Dataelement\_89\_3

**Implementation in FHIR:** Equivalent. Implemented in missing\_collection\_collectedDateTime.

**Implementation in extra FHIR:** Missing

**Implementation in extra OMOP:** Equivalent. Implemented in missing\_specimen\_date.

- **3. Report: createPlotWithoutSampleID**

**Description:** Filter patients without sample ID value.

**Dataelements:**

- **Name:**Sample ID  
**dataelement\_id:** Dataelement\_56\_2

**Implementation in FHIR:** Equivalent. Implemented in patients\_without\_specimen\_type\_text.

**Implementation in extra FHIR:** Missing

**Implementation in extra OMOP:** Equivalent. Implemented in patients\_without\_specimen\_source\_id.

- **4. Report: createPlotWithoutPreservationMode**

**Description:** Filter patients without Preservation Mode value.

**Dataelements:**

- **Name:**Preservation mode  
**dataelement\_id:** Dataelement\_55\_2

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Equivalent. Implemented in create\_plot\_without\_preservation\_mode, with report # 14.

**Implementation in extra OMOP:** Missing

- **5. Report: createPlotWithoutMaterialType**

**Description:** Filter patients without Material Type value.

**Dataelements:**

- **Name:**Material type  
**dataelement\_id:** Dataelement\_54\_2

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Missing

**Implementation in extra OMOP:** Equivalent. Implemented in patients\_without\_specimen\_source\_value\_concept\_id.

- **6. Report: createPlotsWithoutHistoValues**

**Description:** Create plots with missing Histopathology values.

**Dataelements:**

- **Name:**Localization of metastasis  
**dataelement\_id:** Dataelement\_68\_2
- **Name:**Localization of primary tumor  
**dataelement\_id:** Dataelement\_92\_1
- **Name:**Morphology  
**dataelement\_id:** Dataelement\_91\_1
- **Name:**Grade  
**dataelement\_id:** Dataelement\_83\_1
- **Name:**Regional lymph nodes  
**dataelement\_id:** Dataelement\_77\_1
- **Name:**Primary Tumor  
**dataelement\_id:** Dataelement\_71\_1
- **Name:**Distant metastasis



- dataelement\_id:** Dataelement\_75\_1
  - **Name:**UICC version
  - dataelement\_id:** Dataelement\_73\_3
  - **Name:**Stage
  - dataelement\_id:** Dataelement\_70\_2

**Implementation in FHIR:** Partially. Implemented in patients\_without\_condition\_values, only for Dataelement\_92\_1.

**Implementation in extra FHIR:** Missing

**Implementation in extra OMOP:** Partially. Implemented in patients\_without\_condition\_values, only for Dataelement\_92\_1 and Dataelement\_51\_3 (name Date of diagnosis).

- **7. Report: createPlotsWithoutSurgeryValues**

**Description:** Create plots with missing Surgery values.

**Dataelements:**

- **Name:**Time difference between initial diagnosis and surgery
  - dataelement\_id:** Dataelement\_8\_3
  - **Name:**Surgery radicality
  - dataelement\_id:** Dataelement\_9\_2
  - **Name:**Location of the tumor
  - dataelement\_id:** Dataelement\_93\_1
  - **Name:**Surgery type
  - dataelement\_id:** Dataelement\_49\_1

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Missing

**Implementation in extra OMOP:** Partially. Implemented in patients\_without\_surgery\_values, only for Dataelement\_8\_3, Dataelement\_49\_1.

- **8. Report: createPlotsWithoutPatientValues**

**Description:** Create plots with missing Patient values.

**Dataelements:**

- **Name:**Age at diagnosis (rounded to years)
  - dataelement\_id:** Dataelement\_3\_1
  - **Name:**Biological sex
  - dataelement\_id:** Dataelement\_85\_1
  - **Name:**Vital status
  - dataelement\_id:** Dataelement\_5\_2
  - **Name:**Overall survival status
  - dataelement\_id:** Dataelement\_7\_2
  - **Name:**Colonoscopy
  - dataelement\_id:** Dataelement\_88\_1
  - **Name:**CT
  - dataelement\_id:** Dataelement\_31\_3
  - **Name:**Liver imaging

- dataelement\_id:** Dataelement\_61\_5
  - **Name:**Lung imaging
  - dataelement\_id:** Dataelement\_63\_4
  - **Name:**MRI
  - dataelement\_id:** Dataelement\_30\_3
  - **Name:**Mismatch repair gene expression
  - dataelement\_id:** Dataelement\_15\_2
  - **Name:**Microsatellite instability
  - dataelement\_id:** Dataelement\_14\_3
  - **Name:**KRAS exon 2 (codons 12 or 13)
  - dataelement\_id:** Dataelement\_20\_3
  - **Name:**KRAS exon 3 (codons 59 or 61)
  - dataelement\_id:** Dataelement\_21\_5
  - **Name:**NRAS exon 4 (codons 117 or 146)
  - dataelement\_id:** Dataelement\_25\_3

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Missing

**Implementation in extra OMOP:** Partially. Implemented in createPlotsWithoutPatientValues, only for Dataelement\_3\_1, Dataelement\_85\_1, Dataelement\_88\_1, Dataelement\_31\_3, Dataelement\_61\_5, Dataelement\_63\_4, Dataelement\_30\_3.

- **9. Report: createPlotsWithoutTargetedTherapy**

**Description:** Create plots with missing Targeted therapy values.

**Dataelements:**

- **Name:**Date of start of targeted therapy
- dataelement\_id:** Dataelement\_35\_3
- **Name:**Date of end of targeted therapy
- dataelement\_id:** Dataelement\_36\_1

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Missing

**Implementation in extra OMOP:** Partially. Implemented in createPlotsWithoutTargetedTherapy, only for Dataelement\_35\_3.

- **10. Report: createPlotsWithoutPharmacotherapy**

**Description:** Create plots with missing Pharmacotherapy values.

**Dataelements:**

- **Name:**Date of end of pharmacotherapy
- dataelement\_id:** Dataelement\_11\_2
- **Name:**Date of start of targeted therapy
- dataelement\_id:** Dataelement\_10\_2
- **Name:**Scheme of pharmacotherapy
- dataelement\_id:** Dataelement\_59\_5

**Implementation in FHIR:** Missing.

**Implementation in extra FHIR:** Missing.  
**Implementation in extra OMOP:** Equivalent.

- **11. Report: createPlotsWithoutRadiationTherapy**

**Description:** Create plots with missing Radiation Therapy values.

**Dataelements:**

- **Name:**Date of start of radiation therapy  
**dataelement\_id:** Dataelement\_12\_4
- **Name:**Date of end of radiation therapy  
**dataelement\_id:** Dataelement\_13\_2

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Missing

**Implementation in extra OMOP:** Partially. Implemented in createPlotsWithoutRadiationTherapy, only for Dataelement\_12\_4.

- **12. Report: createPlotsWithoutResponseToTherapy**

**Description:** Create plots with missing Response to therapy values.

**Dataelements:**

- **Name:**Specific response  
**dataelement\_id:** Dataelement\_33\_1
- **Name:**Date response was obtained in weeks since initial diagnosis  
**dataelement\_id:** Dataelement\_34\_1

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Equivalent. Implemented in create\_plots\_without\_response\_to\_therapy.

**Implementation in extra OMOP:** Missing

- **13. Report: createPlotForAllMissedValues**

**Description:** Create plot for all missing values.

**Dataelements:**

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Missing

**Implementation in extra OMOP:** Equivalent. Implemented in completeness for all values.

- **14. Report: getMissingSampleWithoutPreservationMode**

**Description:** Filter patients without Preservation Mode value.

**Dataelements:**

- **Name:**Preservation mode  
**dataelement\_id:** Dataelement\_55\_2

**Implementation in FHIR:** Missing

**Implementation in extra FHIR:** Equivalent

**Implementation in extra OMOP:** Missing

- 15-22. Report: getMissing\_\_\_RecordSet**  
**Description:** Create tibble with missing values in form (Sample, Histopathology, Surgery, Patient, Targeted therapy, Pharmacotherapy, Radiation therapy, Response to therapy)  
**Dataelements:**  
**Implementation in FHIR:** Missing  
**Implementation in extra FHIR:** Missing  
**Implementation in extra OMOP:** Equivalent. Implemented in completeness.
- 23-34. Report: getAll\_\_\_RecordSet**  
**Description:** Helper functions. Not implemented. Create tibble with values in form (Sample, Histopathology, Surgery, Patient, Targeted therapy, Pharmacotherapy, Radiation therapy, Response to therapy, Samples with FFPE, Patients with locations, Patients with TNM, All therapy and responses together)  
**Dataelements:**  
**Implementation in FHIR:** Missing  
**Implementation in extra FHIR:** Missing  
**Implementation in extra OMOP:** Missing
- 35-39. Report: getListOfDataFramesWithCountsOfAll\_\_\_Values, getCountFormsWith\_\_\_PerBiobank**  
**Description:** Helper functions. Create list with tibbles from getAll\_\_\_RecordSet  
**Dataelements:**  
**Implementation in FHIR:** Missing  
**Implementation in extra FHIR:** Missing  
**Implementation in extra OMOP:** Partially. 35 implemented as counts\_of\_records, the rest is in the completeness.
- 40. Report: getPatientsWithPreservationModeBUTWithoutFFPE**  
**Description:** Filter patients with other Preservation Mode then FFPE.  
**Dataelements:**
  - Name:**Preservation mode  
**dataelement\_id:** Dataelement\_55\_2**Implementation in FHIR:** Missing  
**Implementation in extra FHIR:** Equivalent. Implemented in get\_patients\_with\_preservation\_mode\_but\_without\_ffpe.  
**Implementation in extra OMOP:** Missing
- 41. Report: getPatientsWithoutSurgery**  
**Description:** Filter patients without Surgery form.  
**Dataelements:**  
**Implementation in FHIR:** Missing  
**Implementation in extra FHIR:** Missing  
**Implementation in extra OMOP:** Equivalent

- **42. Report:**  
**getPatientsWhereNewTreatmentAfterCompleteResponseButNoProgressiveDiseaseOrTimeofRecurrenceAfterIt**  
**Description:** Patient with new treatment after CompleteResponse, but no ProgressiveDisease or TimeofRecurrence after it - Note could include false-positive cases  
**Dataelements:**
  - **Name:**Time of recurrence (metastasis diagnosis)  
**dataelement\_id:** Dataelement\_4\_3
  - **Name:**Date of start of radiation therapy  
**dataelement\_id:** Dataelement\_12\_4
  - **Name:**Date of end of radiation therapy  
**dataelement\_id:** Dataelement\_13\_2
  - **Name:**Date of start of targeted therapy  
**dataelement\_id:** Dataelement\_35\_3
  - **Name:**Date of end of targeted therapy  
**dataelement\_id:** Dataelement\_36\_1
  - **Name:**Date of start of pharmacotherapy  
**dataelement\_id:** Dataelement\_10\_2
  - **Name:**Date of end of pharmacotherapy  
**dataelement\_id:** Dataelement\_11\_2
  - **Name:**Specific response  
**dataelement\_id:** Dataelement\_33\_1
  - **Name:**Date response was obtained in weeks since initial diagnosis  
**dataelement\_id:** Dataelement\_34\_1**Implementation in FHIR:** Missing  
**Implementation in extra FHIR:** Partially. Implemented in treatment\_after\_complete\_response\_without\_recurrence\_diagnosis. Works only with responses data frame, because all treatment are not mapped.  
**Implementation in extra OMOP:** Missing

## Dashboard and export

In the dashboard, the user can see the visualization of quality checks. Then, there are tables with failed rows. Users can download the graphs and failures in the zip files if needed later.

## Conclusion and further resources

I hope you find this tool helpful and valuable, and there are resources for more information:

<https://www.ohdsi.org/software-tools/>

<https://hakkoda.io/resources/fhir-to-omop/>

<https://medblocks.com/blog/which-health-it-standard-to-pick-fhir-openehr-or-omop>

[https://confluence.hl7.org/download/attachments/81018297/FHIR%20to%20OMOP%20Cookbook\\_v04.pdf?version=1&modificationDate=1707852008416&api=v2](https://confluence.hl7.org/download/attachments/81018297/FHIR%20to%20OMOP%20Cookbook_v04.pdf?version=1&modificationDate=1707852008416&api=v2)