



# **FHIR<sup>®</sup> for Immunization Information Systems (IIS)**

# FHIR in a Nutshell

- Fast Healthcare Interoperability Resources (FHIR)
- Next generation HL7 standard
- Set of Resources and a modern RESTful API for accessing them

# FHIR in a Nutshell

- **FHIR Bulk Data** – Export large amounts of data from a FHIR server
- **SMART on FHIR** – health app interface based on FHIR/open standards
- **CDS Hooks** – CDS services to be triggered within clinician workflow
- **Subscriptions** – allows clients to request notifications on events
- **FHIR Extended Operations** – supports additional use cases
- **Implementation Guides** – standards-based ways of using FHIR in specific domains

# Why FHIR for Immunization Data Access?

- More accessible to general purpose developers than HL7 v2
- Modern APIs, software, tools, resources, and support
- FHIR Bulk Query:
  - Efficiently access up-to-date immunization data
  - Reduce redundant queries
  - Easy to parse bulk data format
  - Modern authentication/authorization framework

# Immunization FHIR Example

## Patient Info

First Name: **TEST** Middle: **A** Last: **HIMSS-PATIENT**

Date of Birth: **04/20/2022**

Age: **10m 16d**

VALID DOSES					NEXT DUE
<b>COVID-19</b> 2 valid doses	10/20/2022 COV19 PF PFR 6m-5 6m 0d	11/20/2022 COV19 PF PFR 6m-5 7m 0d			<b>Due Now</b> (On or after 01/15/2023) Dose 3 <a href="#">Covid Record</a>
<b>Influenza</b>					<b>Due Now</b> (On or after 10/20/2022) Dose 1
<b>Hepatitis B</b> 3 valid doses	04/20/2022 HepB ped/adol 0m 0d	06/20/2022 VAXELIS 2m 0d	08/20/2022 VAXELIS 4m 0d [1]	10/20/2022 VAXELIS 6m 0d	<b>End of Series</b>
<b>DTaP/DT/Tdap/Td</b> 3 valid doses	06/20/2022 VAXELIS 2m 0d	08/20/2022 VAXELIS 4m 0d	10/20/2022 VAXELIS 6m 0d		<b>Due in the Future</b> (07/20/2023 - 12/17/2023) Dose 4
<b>Pneumo</b> 1 valid doses	06/20/2022 PCV15 2m 0d				<b>Past Due</b>
<b>Polio</b> 3 valid doses	06/20/2022 VAXELIS 2m 0d	08/20/2022 VAXELIS 4m 0d	10/20/2022 VAXELIS 6m 0d		<b>Due in the Future</b> (04/20/2026 - 05/17/2029) Dose 4
<b>Hib</b> 3 valid doses	06/20/2022 VAXELIS 2m 0d	08/20/2022 VAXELIS 4m 0d	10/20/2022 VAXELIS 6m 0d		<b>Due in the Future</b> (04/20/2023 - 09/16/2023) Dose 4
<b>Rotavirus</b> 0 valid doses					Maximum Age Reached

```

"name": [
  {
    "text": "TEST A HIMSS-PATIENT",
    "family": "HIMSS-PATIENT",
    "given": [
      "TEST",
      "A"
    ]
  }
],
"birthDate": "2022-04-20",

```

```

status": "completed",
"vaccineCode": {
  "coding": [
    {
      "system": "http://hl7.org/fhir/sid/cvx",
      "code": "215",
      "display": "PCV15"
    }
  ],
  "text": "Pneumococcal conjugate PCV15, polysaccharide CRM197 con;
},
"patient": {
  "reference": "11469529",
  "type": "Patient"
},
"occurrenceDateTime": "2022-06-20",
"recorded": "2023-01-01T07:10:39-05:00",
"primarySource": true,
"manufacturer": {
  "reference": "MSD",
  "type": "Organization",
  "display": "Merck & Co., Inc."
},
"lotNumber": "FK0101",
"expirationDate": "2024-01-01",
"site": {
  "coding": [
    {
      "system": "http://terminology.hl7.org/CodeSystem/v2-0163",
      "code": "LA",
      "display": "LEFT ARM"
    }
  ]
}

```

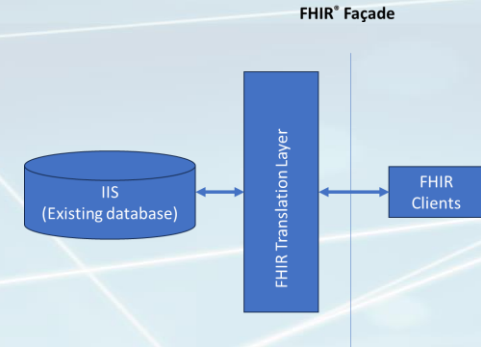
# FHIR Server Models

- **FHIR Façade**

- Data translation – translate FHIR REST calls to the underlying legacy database or service
- Intermediate FHIR server – synchronize native FHIR storage to underlying legacy database or service

- **Native FHIR server**

- FHIR storage is the operational data store



# Rhode Island IIS Implementation

- Rhode Island Child and Adult Immunization Registry (RICAIR)
- FHIR Façade Model using open source HAPI FHIR server and SMART Backend Services Authorization
- Bulk Query - Helios FHIR Accelerator for Public Health
  - Match and Bulk Match
  - Predefined Groups, or search and define custom groups
  - Query Patient, Immunization, ImmunizationRecommendation, and ImmunizationEvaluation resources
  - Download up to 100k patients or more in a fraction of the time of HL7 v2 QBP/RSP

# Rhode Island IIS Implementation

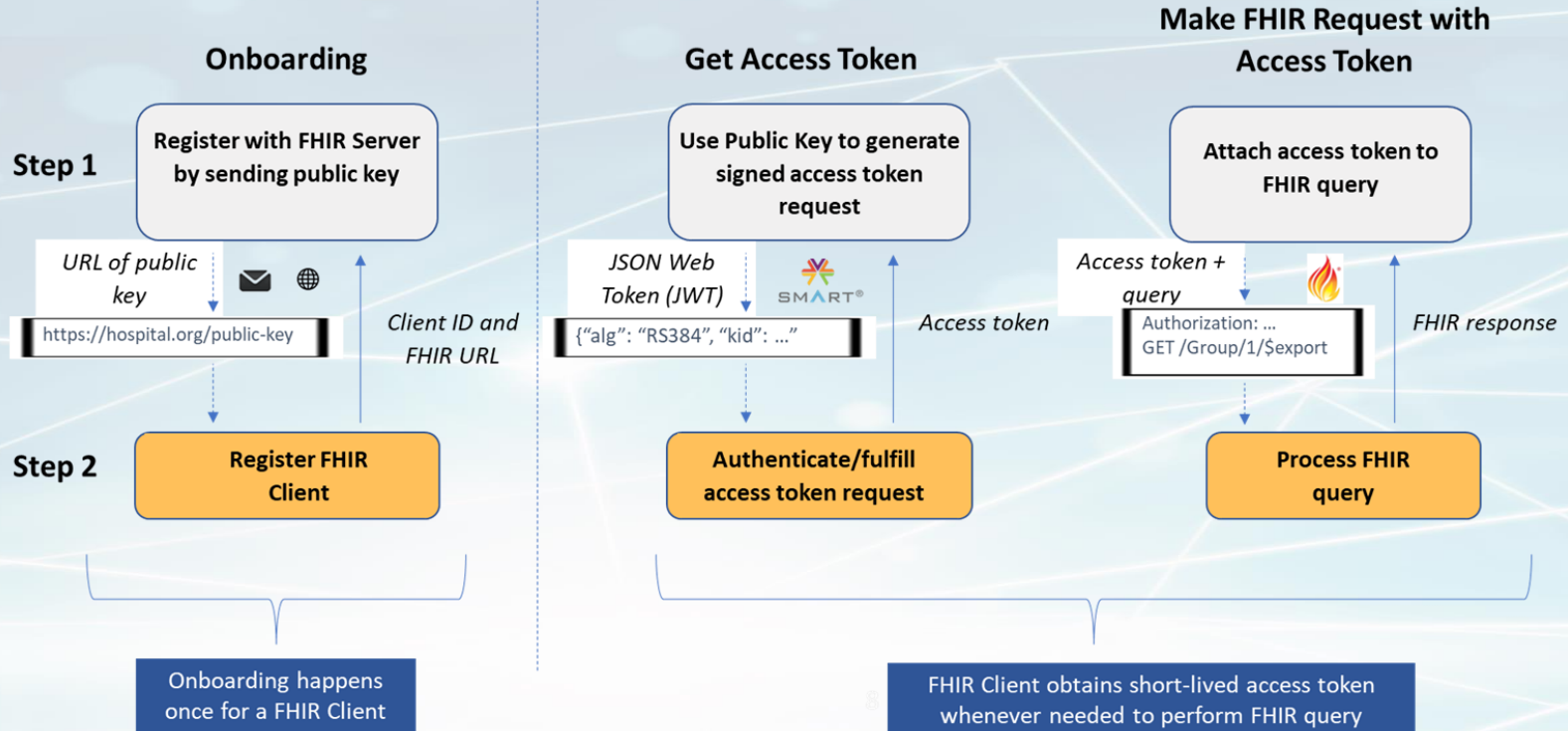
Functionality	FHIR functionality
Bulk Data Export	Group/[id]/\$export
Patient Match	Patient/\$match
Creation of Group resource	POST /Group {“member” [ ... ] }
Add Patient to Group	Group/[id]/\$member-add
Remove Patient from Group	Group/[id]/\$member-remove
Security/authentication – SMART Backend Services (OAuth/JWT)	/.well-known/smart-configuration POST /auth/token
Bulk Match	Patient/\$match with [1..*]
HL7 v2-Mediated Matching (Automatic Group Creation)	FHIR Group/[id] maintained based on HL7v2 messages



# FHIR IIS Authentication

- HL7 v2 Authentication
  - Typically involves username/password – tedious to share and can leak or be weak
  - Some use certificate authentication, but also tedious
- SMART Backend Services Authentication
  - Makes it possible to not have to share passwords with senders during onboarding
  - Partners provide IIS a URL containing their public key
  - Leverages public key authentication to securely provide FHIR access tokens

# FHIR IIS Authentication Workflow



# Using FHIR Bulk Data for App Modernization

- Replace legacy IIS web applications with modern front-ends that communicate with the FHIR back-end:
  - Immunization Data Entry/Update
  - Other potential uses:
    - Immunization Display, Patient Demographics, SMART Health Cards, School Forms, etc.
    - SMART on FHIR apps
    - Consumer apps

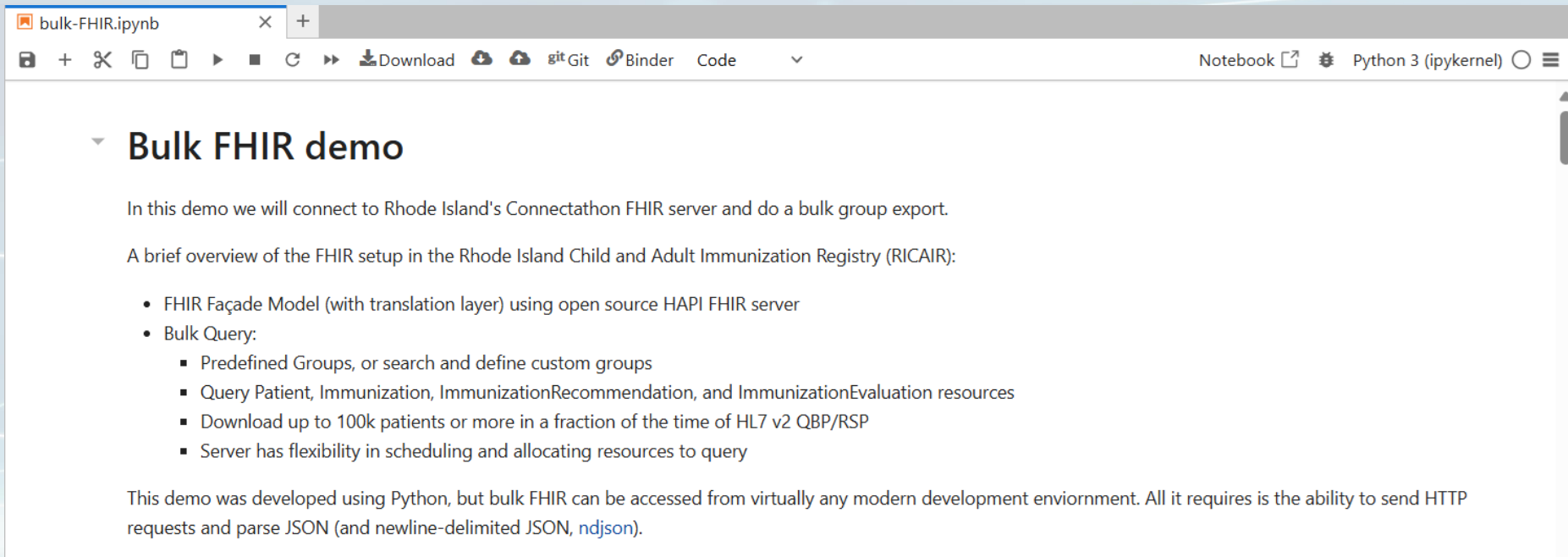
# FHIR IIS demonstration

## Python "Notebook"

Python Notebooks are interactive web applications that allow you to create and share documents containing live code, visualizations, and narrative text.

- Incredibly useful for HL7 Connectathons
- Participants can run and document their code in a readable and reproducible manner
- Excellent platform for collaboration

# Demonstration screenshots



bulk-FHIR.ipynb

Notebook Python 3 (ipykernel)

## Bulk FHIR demo

In this demo we will connect to Rhode Island's Connectathon FHIR server and do a bulk group export.

A brief overview of the FHIR setup in the Rhode Island Child and Adult Immunization Registry (RICAIR):

- FHIR Façade Model (with translation layer) using open source HAPI FHIR server
- Bulk Query:
  - Predefined Groups, or search and define custom groups
  - Query Patient, Immunization, ImmunizationRecommendation, and ImmunizationEvaluation resources
  - Download up to 100k patients or more in a fraction of the time of HL7 v2 QBP/RSP
  - Server has flexibility in scheduling and allocating resources to query

This demo was developed using Python, but bulk FHIR can be accessed from virtually any modern development environment. All it requires is the ability to send HTTP requests and parse JSON (and newline-delimited JSON, [ndjson](#)).

## Setup dependencies

First we need to do some setup in Python. We import our dependencies for HTTP requests, date and time parsing, logging, etc.:

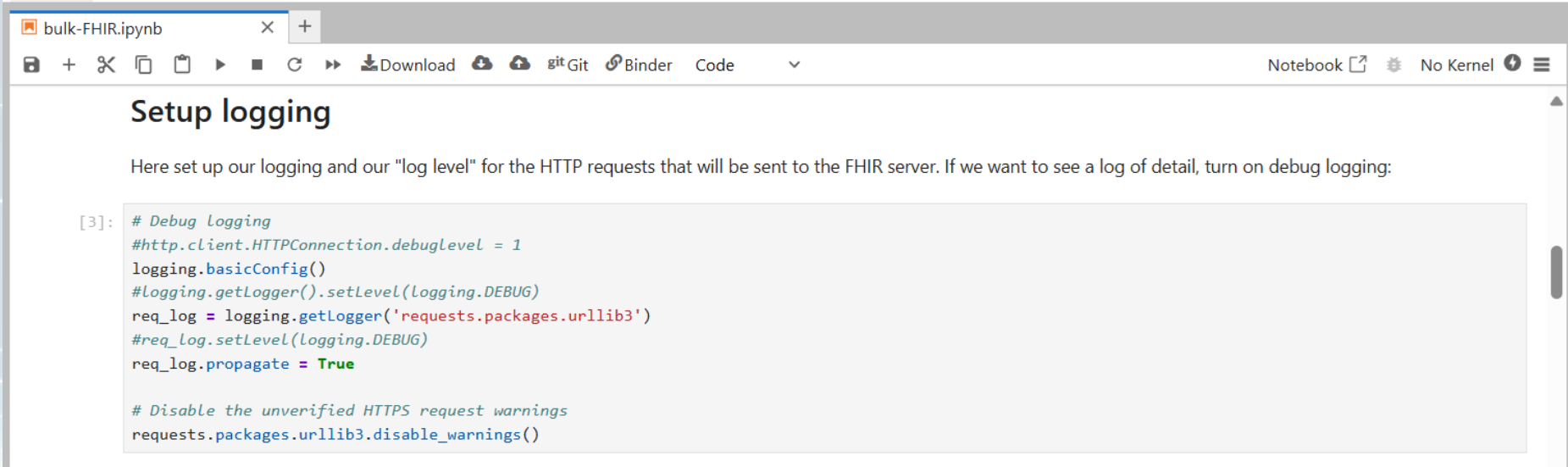
```
[1]: pip install -q -r requirements.txt
```

Note: you may need to restart the kernel to use updated packages.

```
[2]: #  
# for the FHIR operations  
#  
  
import os.path  
from datetime import datetime  
from time import sleep  
import requests as requests  
import logging  
import json  
from pyfhirclient.FhirClient import FhirClient  
  
#  
# for presenting the data  
#  
  
import pandas  
from IPython.display import JSON, HTML  
import plotly.express as plotly
```

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# Demonstration screenshots

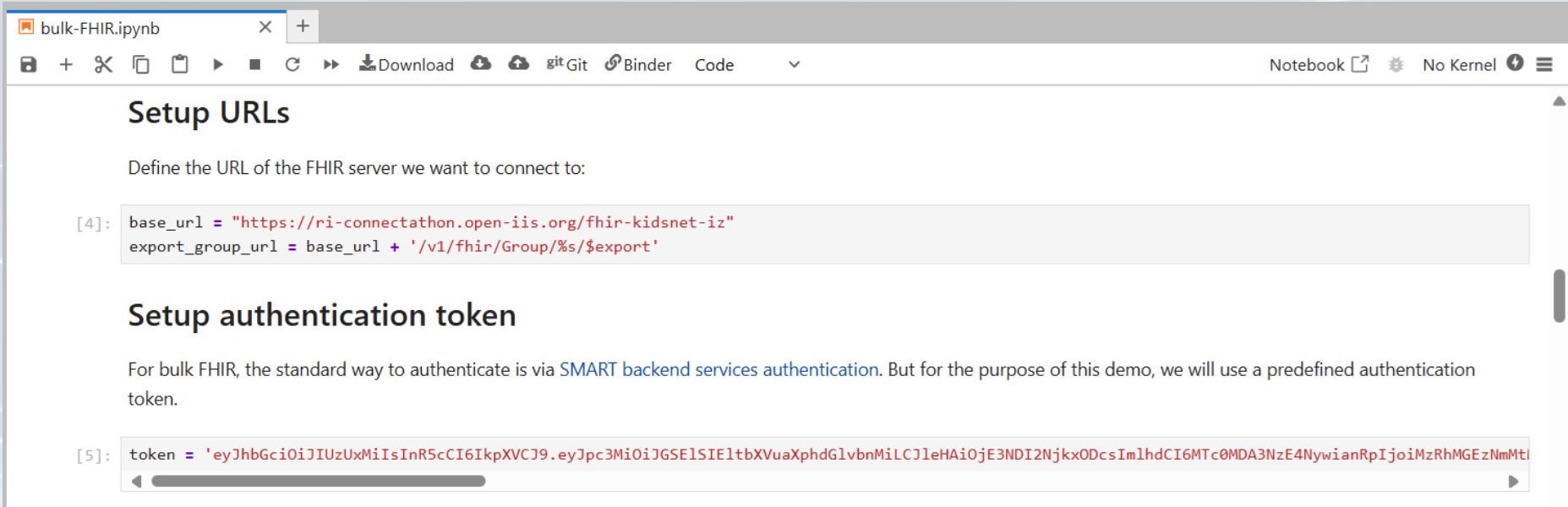


The screenshot shows a Jupyter Notebook window titled "bulk-FHIR.ipynb". The interface includes a toolbar with icons for file operations, a "Download" button, and links to "Git", "Binder", and "Code". The notebook content is titled "Setup logging" and contains a text block explaining the purpose of the code: "Here set up our logging and our 'log level' for the HTTP requests that will be sent to the FHIR server. If we want to see a log of detail, turn on debug logging:". Below this is a code cell with the following Python code:

```
[3]: # Debug Logging
#http.client.HTTPConnection.debugLevel = 1
logging.basicConfig()
#logging.getLogger().setLevel(logging.DEBUG)
req_log = logging.getLogger('requests.packages.urllib3')
#req_log.setLevel(logging.DEBUG)
req_log.propagate = True

# Disable the unverified HTTPS request warnings
requests.packages.urllib3.disable_warnings()
```

# Demonstration screenshots



The screenshot shows a Jupyter Notebook window titled "bulk-FHIR.ipynb". The interface includes a toolbar with icons for file operations, a "Download" button, and integration options for "git Git" and "Binder". The notebook content is divided into two sections:

## Setup URLs

Define the URL of the FHIR server we want to connect to:

```
[4]: base_url = "https://ri-connectathon.open-iis.org/fhir-kidsnet-iz"
      export_group_url = base_url + '/v1/fhir/Group/%s/$export'
```

## Setup authentication token

For bulk FHIR, the standard way to authenticate is via [SMART backend services authentication](#). But for the purpose of this demo, we will use a predefined authentication token.

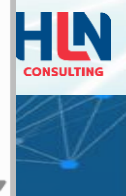
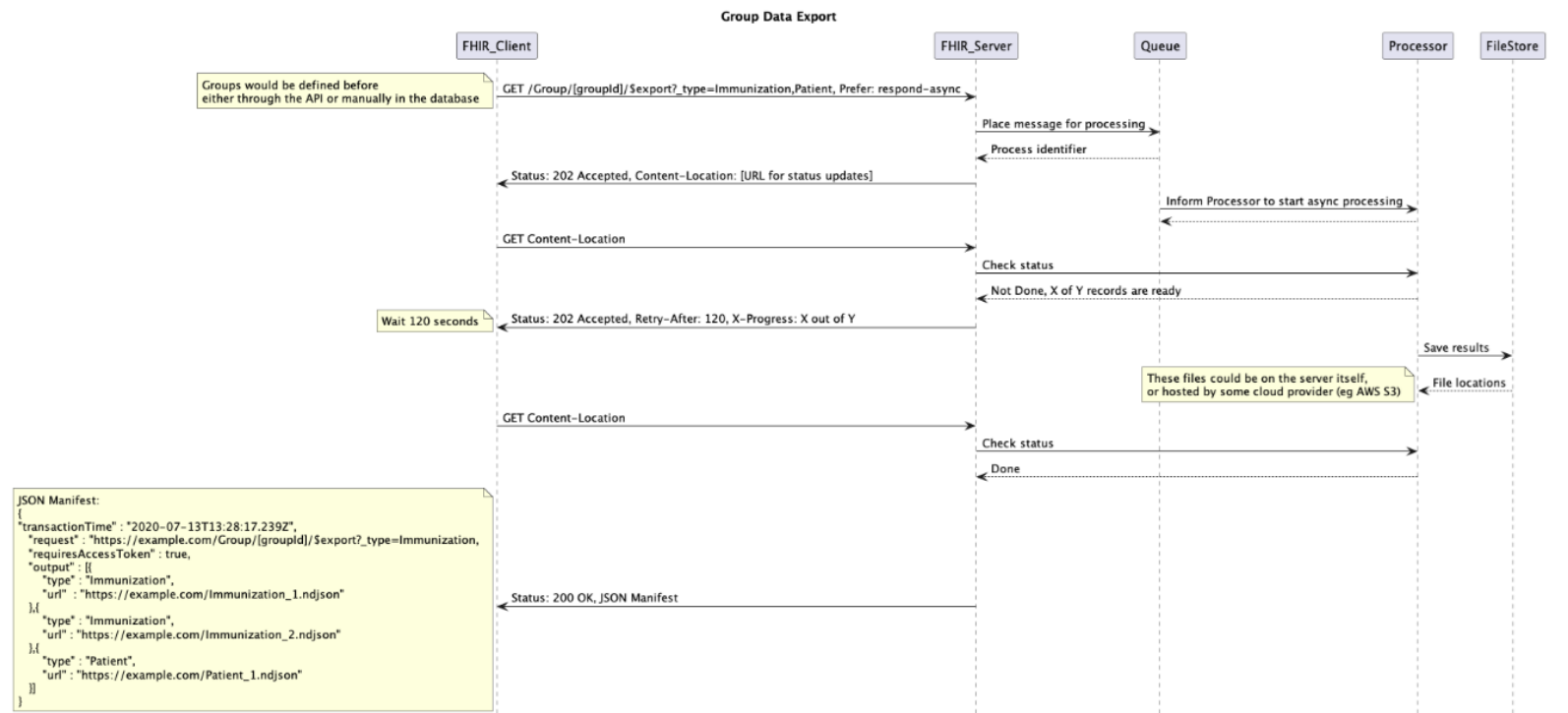
```
[5]: token = 'eyJhbGciOiJIUzUxMiIsInR5cCI6IkpXVCJ9.eyJpc3MiOiJGSE1SIEl1bXVuaXphdGlvbnMiLCJleHAiOjE3NDI2NjkxODcsIm1hdCI6MTc0MDA3NzE4NywiYW50IjoimzRhMGEzNmM0IiwiaWF0IjoiMj02MjA5MjYyLjYyLjYyInQ9'
```



# Group export, polling, and save output functionality

These functions actually do the work of the FHIR bulk export workflow:

1. Start Group Export
2. Poll
3. Save Output



```

JSON Manifest:
{
  "transactionTime": "2020-07-13T13:28:17.239Z",
  "request": "https://example.com/Group/{groupid}/$export?type=Immunization",
  "requiresAccessToken": true,
  "output": [
    {
      "type": "Immunization",
      "url": "https://example.com/Immunization_1.ndjson"
    },
    {
      "type": "Immunization",
      "url": "https://example.com/Immunization_2.ndjson"
    },
    {
      "type": "Patient",
      "url": "https://example.com/Patient_1.ndjson"
    }
  ]
}

```

```

{"resourceType":"Immunization","id":"..."}
{"resourceType":"Immunization","id":"..."}
{"resourceType":"Immunization","id":"..."}

```

```

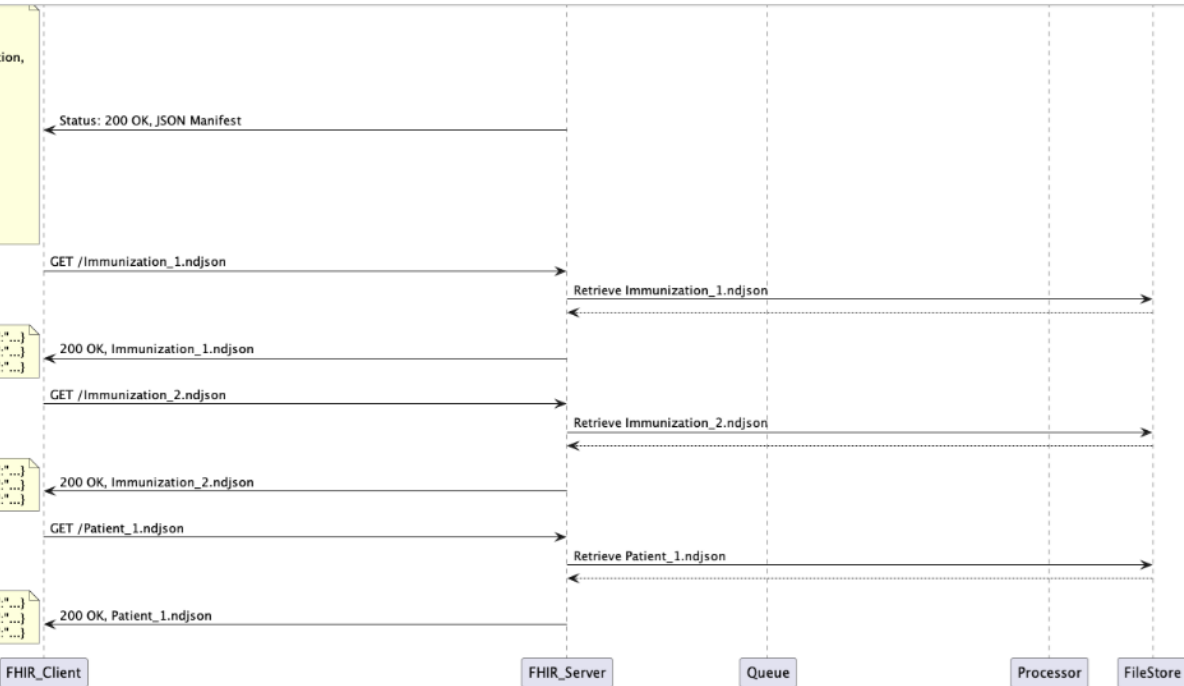
{"resourceType":"Immunization","id":"..."}
{"resourceType":"Immunization","id":"..."}
{"resourceType":"Immunization","id":"..."}

```

```

{"resourceType":"Patient","id":"..."}
{"resourceType":"Patient","id":"..."}
{"resourceType":"Patient","id":"..."}

```



## Start Group Export

This function actually sends the group export request and then gets the URL of the place that we should poll to check to see if the output is ready. The request contains:

1. An authorization header containing the authentication token
2. A "Prefer" header that tells the FHIR server that this is to be an asynchronous workflow where we will check back later on the status of the request
3. The Group ID we want

```
[6]: def start_group_export(token, group_id):
    headers = {
        "Authorization": "Bearer " + token,
        "Prefer": "respond-async"
    }

    response = requests.get(url=export_group_url % group_id, headers=headers, verify=False)
    if not response.ok:
        raise Exception("Unable to start export: " + str(response))

    print (f"Bulk group export started..")

    print (f"Sent request to: {export_group_url % group_id}")
    print (f"Server returned poll status URL: {response.headers['Content-Location']}")

    return response.headers['Content-Location']
```

## Poll

This function queries the URL provided by the FHIR server in the group export step in order to see if the ndjson files are ready.

For the purposes of the demo, when the server tells us to come back in 2 minutes (or at some later time) to check again, we override that and just wait 5 seconds.

Once the server is ready, it will provide URLs for downloading the ndjson (bulk) files for each FHIR resource that will be provided. By default, the RI FHIR server returns:

- Patient,
- Immunization,
- ImmunizationEvaluation, and
- ImmunizationRecommendation

```
[7]: def poll(token, poll_url):
      headers = {
          "Authorization": "Bearer " + token
      }

      while True:
          print (f"Checking poll status URL {poll_url}...")

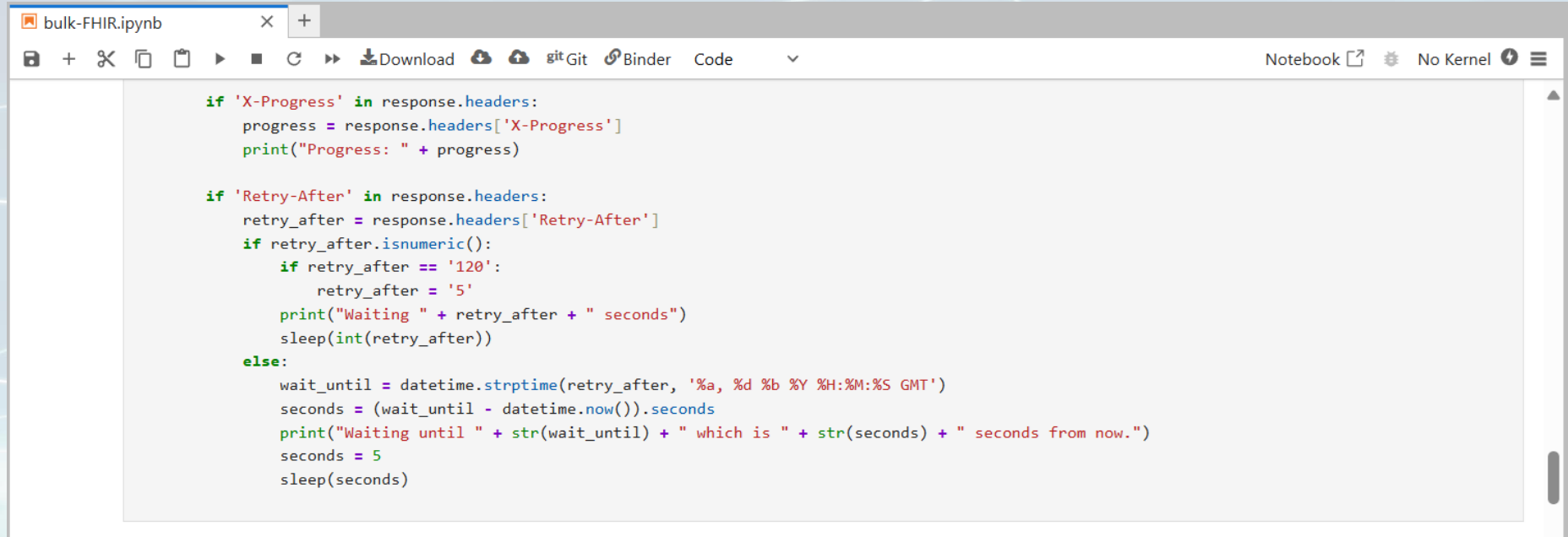
          response = requests.get(url=poll_url, headers=headers, verify=False)
          if not response.ok:
              raise Exception("Unable to poll status")

          if response.status_code == 200:
              print("Export is complete.")

              print ("Response: " + json.dumps(response.json()['output'], indent=4))
              return response.json()

          if 'X-Progress' in response.headers:
              progress = response.headers['X-Progress']
              print("Progress: " + progress)
```

# Demonstration screenshots



The screenshot shows a Jupyter Notebook window titled 'bulk-FHIR.ipynb'. The interface includes a toolbar with icons for saving, adding, deleting, and running code, as well as options for downloading, Git integration, Binder, and Code. The notebook content displays Python code that checks for 'X-Progress' and 'Retry-After' headers in a response. The 'Retry-After' logic includes a check for the value '120', which is replaced with '5', and a calculation of the wait time until the specified date and time.

```
if 'X-Progress' in response.headers:
    progress = response.headers['X-Progress']
    print("Progress: " + progress)

if 'Retry-After' in response.headers:
    retry_after = response.headers['Retry-After']
    if retry_after.isnumeric():
        if retry_after == '120':
            retry_after = '5'
        print("Waiting " + retry_after + " seconds")
        sleep(int(retry_after))
    else:
        wait_until = datetime.strptime(retry_after, '%a, %d %b %Y %H:%M:%S GMT')
        seconds = (wait_until - datetime.now()).seconds
        print("Waiting until " + str(wait_until) + " which is " + str(seconds) + " seconds from now.")
        seconds = 5
        sleep(seconds)
```

## Save Output

Once the FHIR server tells us that the ndjson files are ready, we take the URLs provided from that "ready" response and we get them, print them out, and save them.

*You can uncomment the "print" lines below in order to actually show the ndjson output and the pretty-printed JSON objects from the ndjson.*

## Reading the ndjson stream one line at-a-time

A typical way to read the ndjson response is to download it and load the entire ndjson file into memory.

An alternative that can be more suitable for large payloads is to read it one line at a time using the [stream option](#) and [iter\\_lines function](#) in the [Requests library](#).

```
[8]: def save_output_streaming(token, output):

    headers = {
        "Authorization": "Bearer " + token
    }

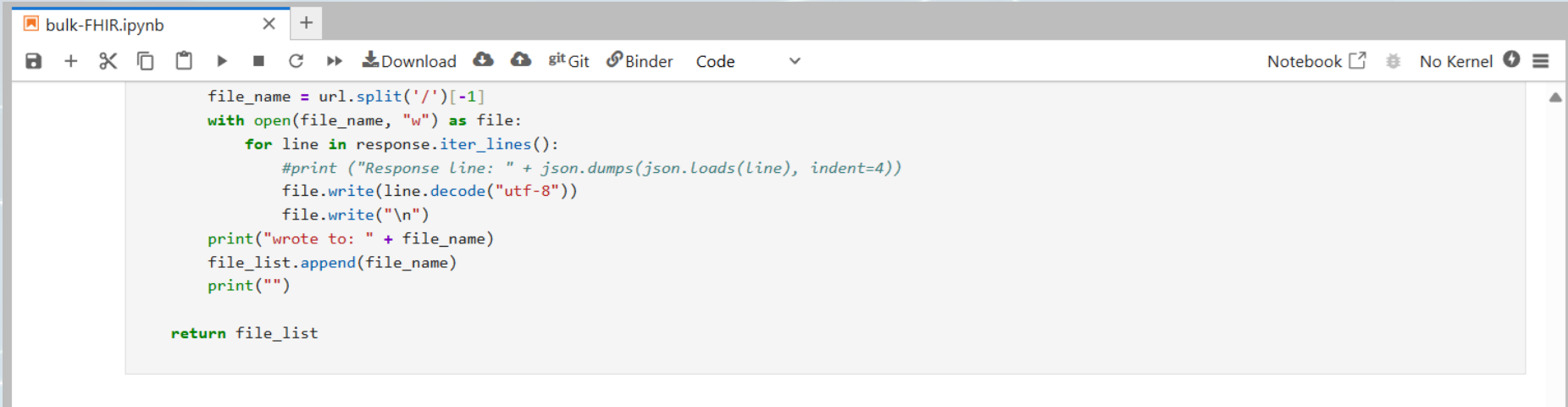
    file_list = []

    for entry in output['output']:
        type_ = entry['type']
        url: str = entry['url']
        print("type   : " + type_)
        print("url    : " + url)

        response = requests.get(url=url, headers=headers, stream=True, verify=False)
        if not response.ok:
            raise Exception("Unable to retrieve output: " + url)

        file_name = url.split('/')[-1]
        with open(file_name, "w") as file:
            for line in response.iter_lines():
                #print ("Response line: " + json.dumps(json.loads(line), indent=4))
                file.write(line.decode("utf-8"))
                file.write("\n")
```

# Demonstration screenshots



The screenshot shows a Jupyter Notebook window titled 'bulk-FHIR.ipynb'. The interface includes a toolbar with icons for save, copy, paste, and other actions, along with a 'Code' dropdown menu. The notebook content displays the following Python code:

```
file_name = url.split('/')[-1]
with open(file_name, "w") as file:
    for line in response.iter_lines():
        #print ("Response line: " + json.dumps(json.loads(line), indent=4))
        file.write(line.decode("utf-8"))
        file.write("\n")
print("wrote to: " + file_name)
file_list.append(file_name)
print("")

return file_list
```

bulk-FHIR.ipynb

Notebook No Kernel

## Initiate the group export

For the January 2023 Connectathon, participating servers configured pre-defined groups of patients based on test data fabricated by AIRA:

Number of patients	Group ID
10	1102356
100	1102357
1,000	1102358
10,000	1102359
100,000	1123654

```
[9]: group_id = 1102358
poll_url = start_group_export(token, group_id)

Bulk group export started...
Sent request to: https://ri-connectathon.open-iis.org/fhir-kidsnet-iz/v1/fhir/Group/1102358/$export
Server returned poll status URL: https://ri-connectathon.open-iis.org/fhir-kidsnet-iz/v1/fhir/$export-poll-status?jobId=573101c0-8d07-4fa0-b0fd-b3e8fb536b16
```



# Check the poll status URL to see if the bulk export is done

```
[10]: output = poll(token, poll_url)
print (f"Output from FHIR server includes {len(output['output'])} ndjson files:")
for file in output['output']:
    print(f" URL: {file['url']}")

print ('In an interactive demo, the JSON can be manipulated here:')
JSON(output)
```

Checking poll status URL [https://ri-connectathon.open-iis.org/fhir-kidsnet-iz/v1/fhir/\\$export-poll-status?jobId=573101c0-8d07-4fa0-b0fd-b3e8fb536b16...](https://ri-connectathon.open-iis.org/fhir-kidsnet-iz/v1/fhir/$export-poll-status?jobId=573101c0-8d07-4fa0-b0fd-b3e8fb536b16...)

Export is complete.

Response: [

```
{
  "type": "Immunization",
  "url": "https://ri-connectathon.open-iis.org/fhir-kidsnet-iz/v1/export/output/573101c0-8d07-4fa0-b0fd-b3e8fb536b16/Immunization_1.ndjson",
  "count": 2000
},
{
  "type": "ImmunizationEvaluation",
  "url": "https://ri-connectathon.open-iis.org/fhir-kidsnet-iz/v1/export/output/573101c0-8d07-4fa0-b0fd-b3e8fb536b16/ImmunizationEvaluation_1.ndjson",
  "count": 2000
},
{
  "type": "ImmunizationRecommendation",
  "url": "https://ri-connectathon.open-iis.org/fhir-kidsnet-iz/v1/export/output/573101c0-8d07-4fa0-b0fd-b3e8fb536b16/ImmunizationRecommendation_1.ndjson",
  "count": 16000
},
{
  "type": "Patient",
  "url": "https://ri-connectathon.open-iis.org/fhir-kidsnet-iz/v1/export/output/573101c0-8d07-4fa0-b0fd-b3e8fb536b16/Patient_1.ndjson",
  "count": 1000
}
]
```

Output from FHIR server includes 4 ndjson files:



```

]
Output from FHIR server includes 4 ndjson files:
URL: https://ri-connectathon.open-iis.org/fhir-kidsnet-iz/v1/export/output/573101c0-8d07-4fa0-b0fd-b3e8fb536b16/Immunization_1.ndjson
URL: https://ri-connectathon.open-iis.org/fhir-kidsnet-iz/v1/export/output/573101c0-8d07-4fa0-b0fd-b3e8fb536b16/ImmunizationEvaluation_1.ndjson
URL: https://ri-connectathon.open-iis.org/fhir-kidsnet-iz/v1/export/output/573101c0-8d07-4fa0-b0fd-b3e8fb536b16/ImmunizationRecommendation_1.ndjson
URL: https://ri-connectathon.open-iis.org/fhir-kidsnet-iz/v1/export/output/573101c0-8d07-4fa0-b0fd-b3e8fb536b16/Patient_1.ndjson
In an interactive demo, the JSON can be manipulated here:

```

```

[10]: root
  transactionTime "2025-03-04T14:28:30.820Z"
  request "https://ri-connectathon.open-iis.org/fhir-kidsnet-iz/v1/fhir/Group/1102358/$export"
  requiresAccessToken true
  output [ 4 items
    0
      type "Immunization"
      url "https://ri-connectathon.open-iis.org/fhir-kidsnet-iz/v1/export/output/573101c0-8d07-4fa0-b0fd-b3e8fb536b16/Immunization_1.ndjson"
      count 2000
    1
      type "ImmunizationEvaluation"
      url "https://ri-connectathon.open-iis.org/fhir-kidsnet-iz/v1/export/output/573101c0-8d07-4fa0-b0fd-b3e8fb536b16/ImmunizationEvaluation_1.ndjson"
      count 2000
    2
    3
  error [ 0 items

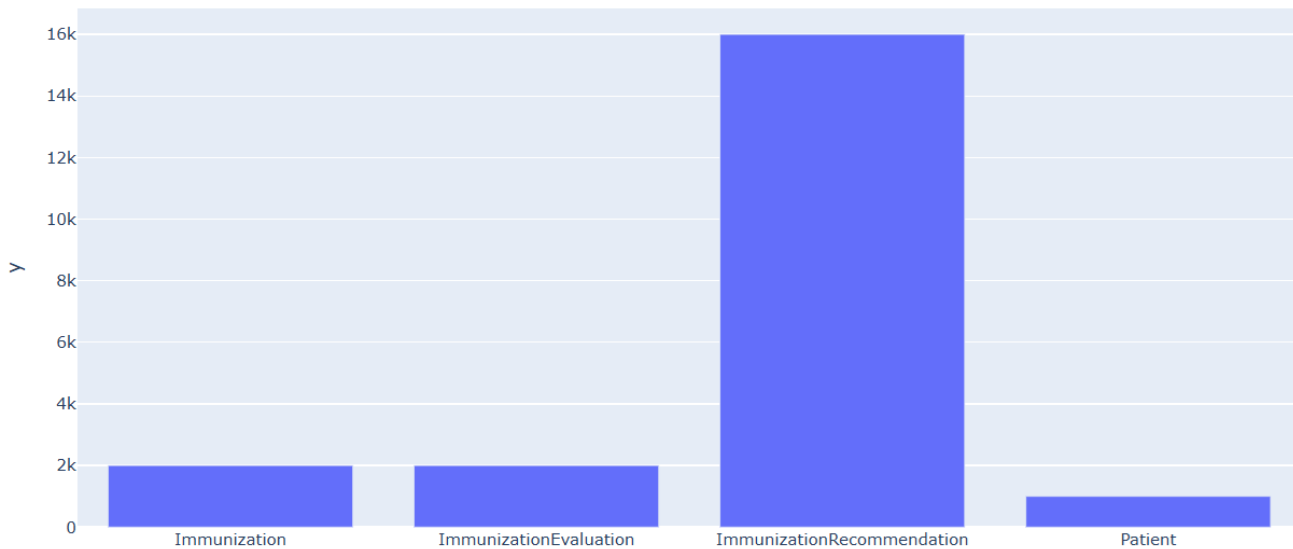
```

Find... 🔍

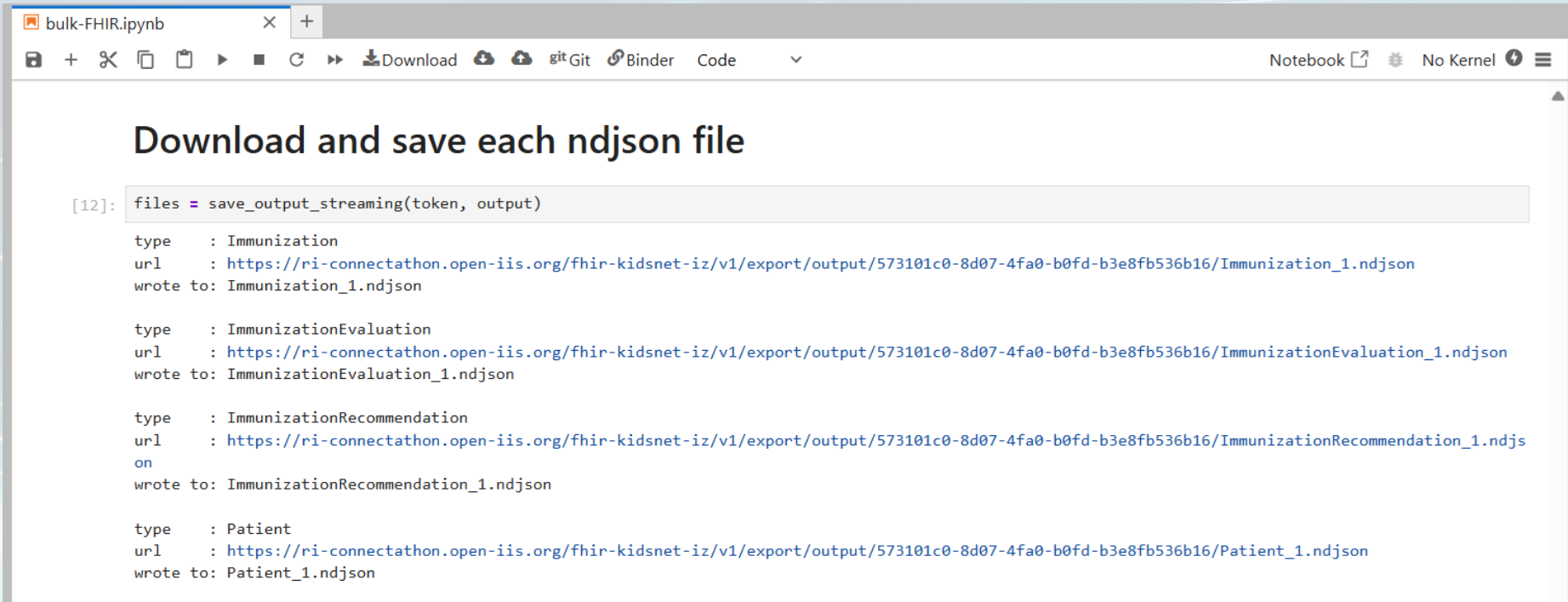


## Optionally, visualize the output in a bar chart

```
[11]: #  
# chart each FHIR resource with its number of records  
  
resources = []  
counts = []  
for resource in output['output']:  
    resources.append(resource['type'])  
    counts.append(resource['count'])  
fig = plotly.bar(x=resources, y=counts)  
fig.show()
```



# Demonstration screenshots



The screenshot shows a Jupyter Notebook window titled 'bulk-FHIR.ipynb'. The notebook contains a single code cell with the following content:

```
[12]: files = save_output_streaming(token, output)
```

The output of the cell is as follows:

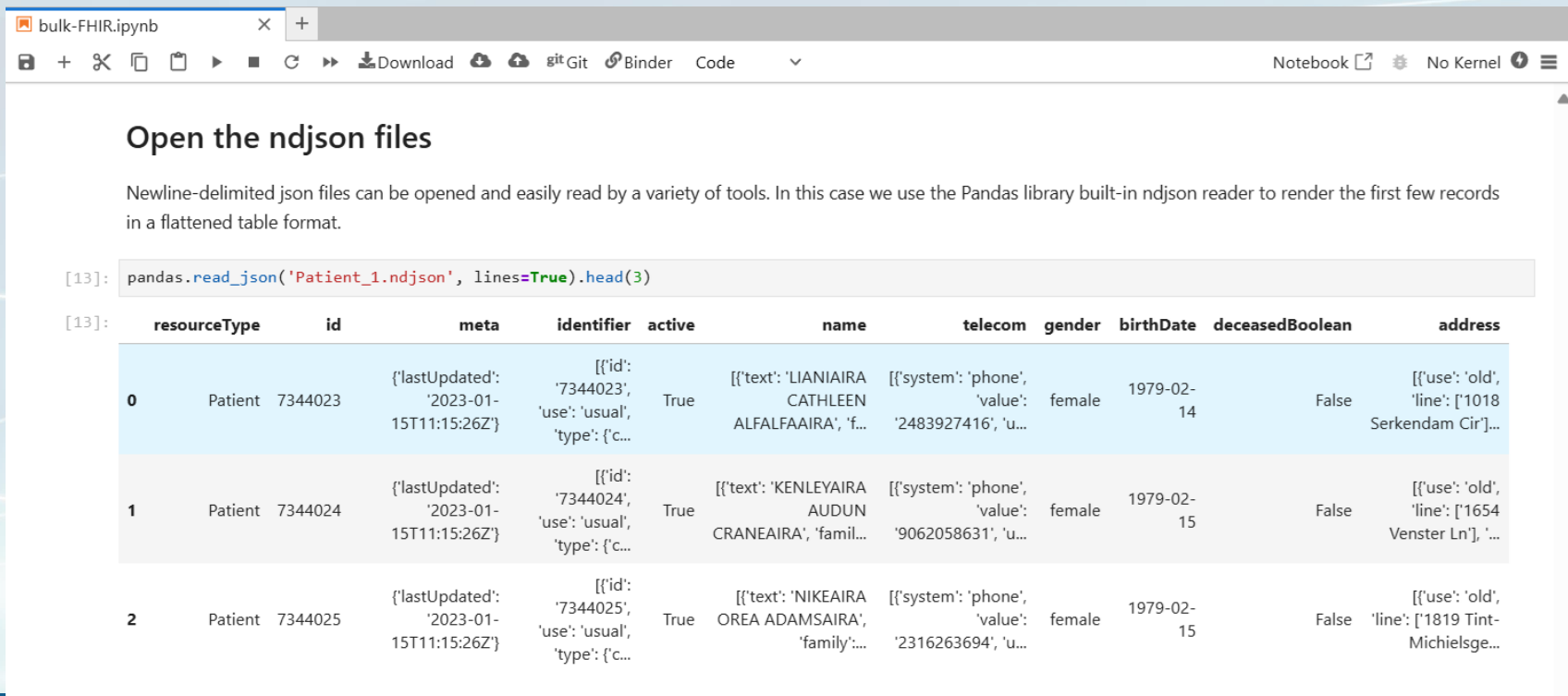
```
type      : Immunization
url       : https://ri-connectathon.open-iis.org/fhir-kidsnet-iz/v1/export/output/573101c0-8d07-4fa0-b0fd-b3e8fb536b16/Immunization_1.ndjson
wrote to: Immunization_1.ndjson

type      : ImmunizationEvaluation
url       : https://ri-connectathon.open-iis.org/fhir-kidsnet-iz/v1/export/output/573101c0-8d07-4fa0-b0fd-b3e8fb536b16/ImmunizationEvaluation_1.ndjson
wrote to: ImmunizationEvaluation_1.ndjson

type      : ImmunizationRecommendation
url       : https://ri-connectathon.open-iis.org/fhir-kidsnet-iz/v1/export/output/573101c0-8d07-4fa0-b0fd-b3e8fb536b16/ImmunizationRecommendation_1.ndjson
wrote to: ImmunizationRecommendation_1.ndjson

type      : Patient
url       : https://ri-connectathon.open-iis.org/fhir-kidsnet-iz/v1/export/output/573101c0-8d07-4fa0-b0fd-b3e8fb536b16/Patient_1.ndjson
wrote to: Patient_1.ndjson
```

# Demonstration screenshots



bulk-FHIR.ipynb

Download git Git Binder Code

Notebook No Kernel

## Open the ndjson files

Newline-delimited json files can be opened and easily read by a variety of tools. In this case we use the Pandas library built-in ndjson reader to render the first few records in a flattened table format.

```
[13]: pandas.read_json('Patient_1.ndjson', lines=True).head(3)
```

```
[13]:
```

	resourceType	id	meta	identifier	active	name	telecom	gender	birthDate	deceasedBoolean	address
0	Patient	7344023	{'lastUpdated': '2023-01-15T11:15:26Z'}	{'id': '7344023', 'use': 'usual', 'type': {'c...	True	{'text': 'LIANIAIRA CATHLEEN ALFALFAAIRA', 'f...	{'system': 'phone', 'value': '2483927416', 'u...	female	1979-02-14	False	{'use': 'old', 'line': ['1018 Serkendam Cir']...
1	Patient	7344024	{'lastUpdated': '2023-01-15T11:15:26Z'}	{'id': '7344024', 'use': 'usual', 'type': {'c...	True	{'text': 'KENLEYAIRA AUDUN CRANEAIRA', 'famil...	{'system': 'phone', 'value': '9062058631', 'u...	female	1979-02-15	False	{'use': 'old', 'line': ['1654 Venster Ln'], '...
2	Patient	7344025	{'lastUpdated': '2023-01-15T11:15:26Z'}	{'id': '7344025', 'use': 'usual', 'type': {'c...	True	{'text': 'NIKEAIRA OREA ADAMSAIRA', 'family':...	{'system': 'phone', 'value': '2316263694', 'u...	female	1979-02-15	False	{'use': 'old', 'line': ['1819 Tint-Michielsge...

# Demonstration screenshots

```
[14]: pandas.read_json('Immunization_1.ndjson', lines=True).head(3)
```

```
[14]:
```

	resourceType	id	meta	extension	identifier	status	vaccineCode	patient	occurrenceDateTime	recorde
0	Immunization	11159799	{'lastUpdated': '2023-01-14T11:43:09Z'}	{'url': 'https://health.ri.gov/vaccine-catego...'	{'use': 'usual', 'value': '11159799'}, {'use': ...	completed	{'coding': [{'system': 'http://hl7.org/fhir/si...	{'id': '7344023', 'reference': 'Patient/734402...	2021-01-19T00:00:00-04:00	2023-01-14T11:43:09.
1	Immunization	11159800	{'lastUpdated': '2023-01-14T11:43:09Z'}	{'url': 'https://health.ri.gov/vaccine-catego...'	{'use': 'usual', 'value': '11159800'}, {'use': ...	completed	{'coding': [{'system': 'http://hl7.org/fhir/si...	{'id': '7344023', 'reference': 'Patient/734402...	2021-03-04T00:00:00-04:00	2023-01-14T11:43:09.
2	Immunization	11159801	{'lastUpdated': '2023-01-14T11:43:09Z'}	{'url': 'https://health.ri.gov/vaccine-catego...'	{'use': 'usual', 'value': '11159801'}, {'use': ...	completed	{'coding': [{'system': 'http://hl7.org/fhir/si...	{'id': '7344024', 'reference': 'Patient/734402...	2021-01-19T00:00:00-04:00	2023-01-14T11:43:09.

# Demonstration screenshots

```
[15]: pandas.read_json('ImmunizationEvaluation_1.ndjson', lines=True).head(3)
```

```
[15]:
```

	resourceType	id	meta	status	patient	date	targetDisease	immunizationEvent	doseStatus
0	ImmunizationEvaluation	819120438	{'lastUpdated': '2023-01-15T11:15:26Z'}	completed	{'reference': 'Patient/7344024'}	2023-01-15 11:15:26+00:00	{'coding': [{'system': 'http://hl7.org/fhir/Va...']}	{'reference': 'Immunization/11159801', 'identi...']}	{'coding': [{'system': 'http://terminology.hl7..']}
1	ImmunizationEvaluation	819120439	{'lastUpdated': '2023-01-15T11:15:26Z'}	completed	{'reference': 'Patient/7344024'}	2023-01-15 11:15:26+00:00	{'coding': [{'system': 'http://hl7.org/fhir/Va...']}	{'reference': 'Immunization/11159802', 'identi...']}	{'coding': [{'system': 'http://terminology.hl7..']}
2	ImmunizationEvaluation	819120440	{'lastUpdated': '2023-01-15T11:15:26Z'}	completed	{'reference': 'Patient/7344025'}	2023-01-15 11:15:26+00:00	{'coding': [{'system': 'http://hl7.org/fhir/Va...']}	{'reference': 'Immunization/11159803', 'identi...']}	{'coding': [{'system': 'http://terminology.hl7..']}

# Demonstration screenshots

```
[16]: pandas.read_json('ImmunizationRecommendation_1.ndjson', lines=True).head(3)
```

```
[16]:
```

	resourceType	id	meta	patient	date	recommendation
0	ImmunizationRecommendation	410205242	{'lastUpdated': '2023-01-15T11:15:26Z'}	{'id': '7344025', 'reference': 'Patient/734402...}	2023-01-15 11:15:26+00:00	[{'vaccineCode': [{'coding': [{'system': 'urn:... }]}]}</td
1	ImmunizationRecommendation	410205243	{'lastUpdated': '2023-01-15T11:15:26Z'}	{'id': '7344025', 'reference': 'Patient/734402...}	2023-01-15 11:15:26+00:00	[{'vaccineCode': [{'coding': [{'system': 'urn:... }]}]}</td
2	ImmunizationRecommendation	410205244	{'lastUpdated': '2023-01-15T11:15:26Z'}	{'id': '7344025', 'reference': 'Patient/734402...}	2023-01-15 11:15:26+00:00	[{'vaccineCode': [{'coding': [{'system': 'urn:... }]}]}</td

```
[ ]:
```