

Gen3.2 - How to build a Gen3 data portal using the new frontend framework

Gen3 Community Forum
1 May 2024

- Introduction
- Gen3.2 Features and Capabilities - Craig Barnes, CTDS
- Migrating from Windmill to Gen3.2 - Matthew Peterkort, Oregon Health & Science University
- Q&A

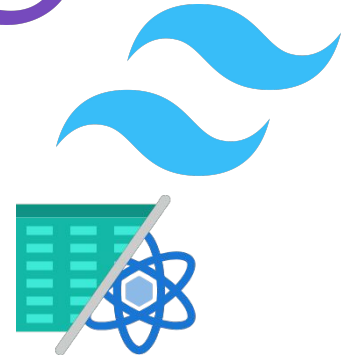
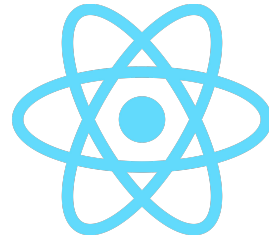
Gen3.2 Features and Capabilities

Craig Barnes
Center for Translational Data Science
University of Chicago

The Gen3 Frontend Framework provides:

- Integrated analysis tools
- Custom content
- Per commons codebase which enables a more flexible source code management and deployment
- Improved user, development, and administration experience
- Upgraded technology stack
- Extensibility and customization

- Core:
 - React 18
 - Typescript
 - Redux-toolkit
- Application Framework: Next.js 14
- Styling: Tailwind CSS
- UI Components:
 - Mantine.dev
 - mantine react table
- Gen3 Components
- Content:
 - HTML and MDX based static pages
 - Next.js custom page



- Styling and theming
- Data renderer customization for tables, charts
- Global selection feature: My Data Library
- Analysis tools
- Commons specific pages
- Update designs and improved UX

Existing:

- Explorer
- Discovery
- Workspaces
- Data Dictionary
- GraphQL query UI
- Profile
- Data Submission

New:

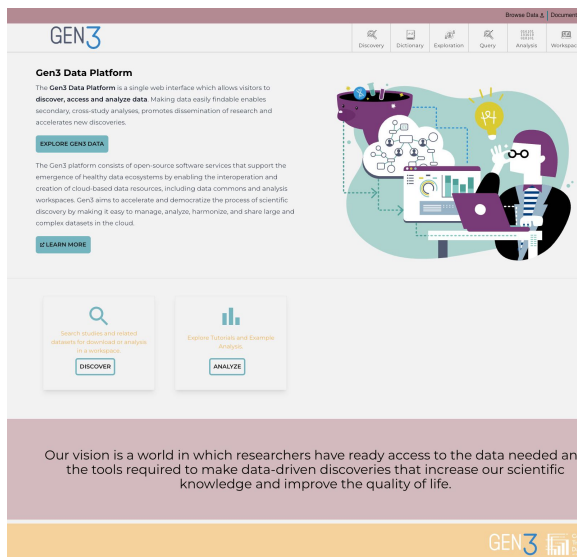
- Application Center
- My Data Library
- Administration UIs
- LLM Search
- Cohort Discovery
- 3rd party tools and applications

Styling and Theming

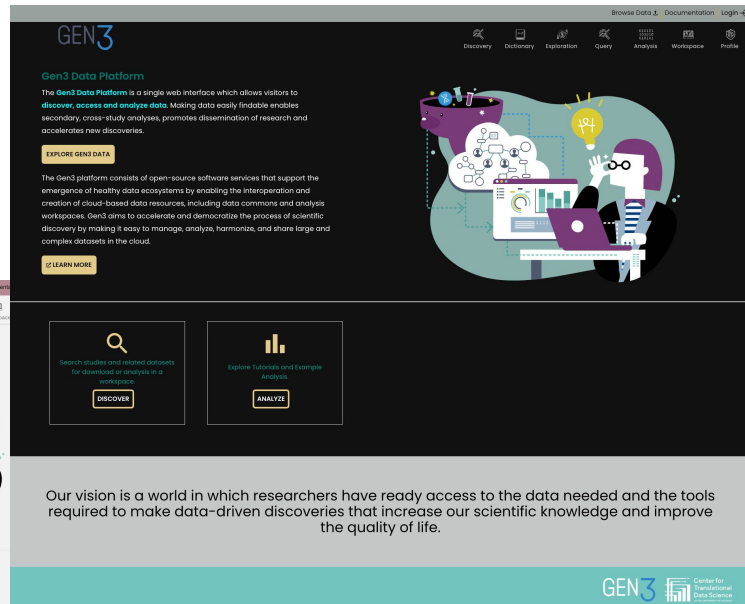
The portal's style can be customized by setting:

- Color theme
- Fonts
- Icons

Configuration tools
Style overrides



The screenshot shows the Gen3 Data Platform interface with a light theme. The header includes the Gen3 logo and navigation icons for Discovery, Dictionary, Exploration, Query, Analysis, and Workspace. The main content area features a large illustration of a person at a computer with a lightbulb idea, surrounded by data icons. Below the illustration is a 'DISCOVER' button and an 'ANALYZE' button. The footer contains the Gen3 logo and the text 'Center for Translational Data Science'.



The screenshot shows the Gen3 Data Platform interface with a dark theme. The header includes the Gen3 logo and navigation icons for Discovery, Dictionary, Exploration, Query, Analysis, Workspace, and Profile. The main content area features a large illustration of a person at a computer with a lightbulb idea, surrounded by data icons. Below the illustration is a 'DISCOVER' button and an 'ANALYZE' button. The footer contains the Gen3 logo and the text 'Center for Translational Data Science'.

Our vision is a world in which researchers have ready access to the data needed and the tools required to make data-driven discoveries that increase our scientific knowledge and improve the quality of life.

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Gen3.2's Color Theme is based on USWDS theme color token: primary/secondary/accent following the proportional 60/30/10 relationship

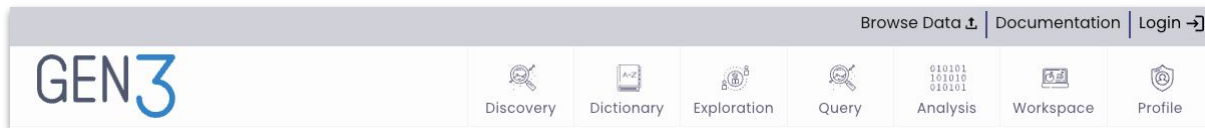
base	max	lightest	lighter	light	base	vivid	dark	darker	darkest	min
primary	max	lightest	lighter	light	primary	vivid	dark	darker	darkest	min
secondary	max	lightest	lighter	light	secondary	vivid	dark	darker	darkest	min
accent	max	lightest	lighter	light	accent	vivid	dark	darker	darkest	min
accent-warm	max	lightest	lighter	light	warm	vivid	dark	darker	darkest	min
accent-cool	max	lightest	lighter	light	cool	vivid	dark	darker	darkest	min
chart	max	lightest	lighter	light	chart	vivid	dark	darker	darkest	min
utility	link	success	warning	error	emergency	info	category1	category2	category3	category4

Configured like data-portal

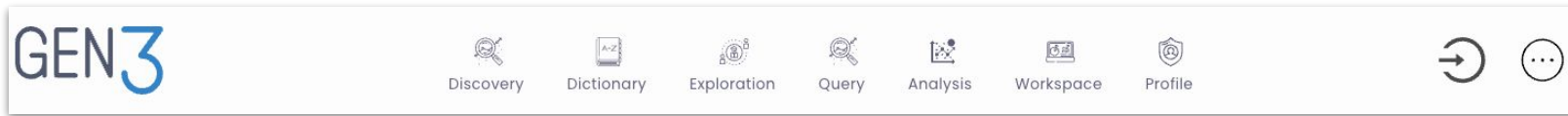
Customizable icons

3 layouts:

Classic:



Horizontal:





Discovery



Dictionary



Exploration



Query



Analysis



Workspace



Profile

Gen3 Data Platform

The **Gen3 Data Platform** is a single web interface which allows visitors to **discover, access and analyze data**. Making data easily findable enables secondary, cross-study analyses, promotes dissemination of research and accelerates new discoveries.

[EXPLORE GEN3 DATA](#)

The Gen3 platform consists of open-source software services that support the emergence of healthy data ecosystems by enabling the interoperability and creation of cloud-based data resources, including data commons and analysis workspaces. Gen3 aims to accelerate and democratize the process of scientific discovery by making it easy to manage, analyze, harmonize, and share large and complex datasets in the cloud.

[LEARN MORE](#)



- Striving to make developing commons as simple as possible.
- Initial set of documentation:
 - <https://github.com/uc-cdis/gen3-frontend-framework/tree/develop/docs>
- .env files for configuration
- Fine grain connection to remote Gen3 services
- Credentials based login
- Run Gen3.2 development outside of helm charts
- Local revproxy instruction
- Supported in **gen3-helm** charts
- Continuously refining development support

NextJS supports **.env** files for various deployments:

- .env.development
- .env.production

You can add more:

- .env.testing
- .env.staging

```
GEN3_COMMONS_NAME=gen3
```

```
NEXT_PUBLIC_GEN3_API=https://localhost:3010
```

Pending:

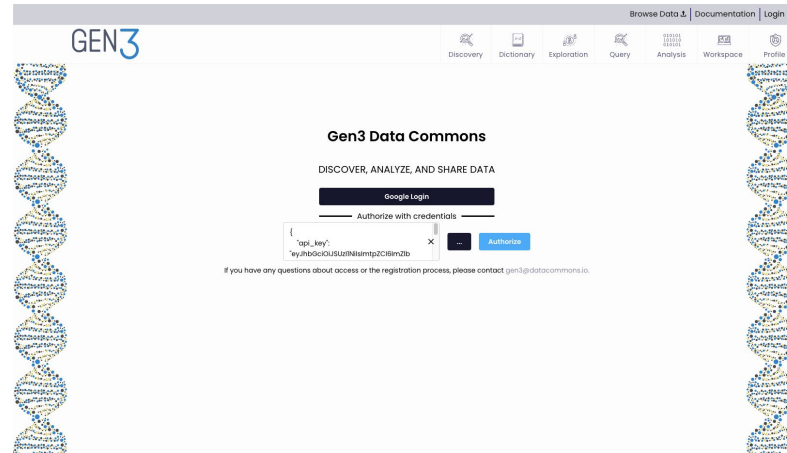
Set env variables/config in helm `values.yaml`

Override any Gen3 endpoint

```
NEXT_PUBLIC_GEN3_FENCE_API=https://localhost:3010
NEXT_PUBLIC_GEN3_DOMAIN=https://localhost:3010
NEXT_PUBLIC_GEN3_MDS_API=https://localhost:3010/mds
NEXT_PUBLIC_GEN3_AI_SEARCH_API=https://localhost:3010/ai
NEXT_PUBLIC_GEN3_GUPPY_API=https://localhost:3010/guppy
NEXT_PUBLIC_GEN3_FENCE_API=https://localhost:3010
NEXT_PUBLIC_GEN3_AUTHZ_API=https://localhost:3010/authz
NEXT_PUBLIC_GEN3_WORKSPACE_STATUS_API=https://localhost:3010/lw-workspace
NEXT_PUBLIC_GEN3_SUBMISSION_API=https://localhost:3010/api/v0/submission
```

Credentials based login

Mostly for development at CTDS:
Credentials based login



- Login with no fence redirect
- Connect FE to remote commons
- Only in development environment
- Scope restrictions on token

Extensible to custom data renderer for table cells and charts

Gen3.2 implementation of Guppy UI components

Pending work:

- Elimination of filter tabs
- Support for sharing selection with the same facet on other indexes
- Subtable in main table.
- Row details
- Authz based filtering



Exploration

Dictionary

Example Analysis

[Cases](#) |
 [Annotations](#) |
 [Measurements](#) |
 [Imaging Studies](#) |
 [Data Files](#)

Case Cohort

SEX ← Female × |
 RACE ← Black or African American × Asian × |
 ETHNICITY ← Hispanic or Latino × |
 INDEX EVENT ← First COVID Test × |
 ZIP ← US ×

Filters

[Collapse All](#)

[Download File Manifest for Cases \(193.35K\)](#)

70,314 CASES

Set the shared filters for all

Filter Set

Demographics

Case ID

Select Case ID

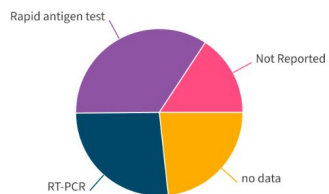
Sex

- Name Case
- Female 32,074
- Male 31,029
- no data 7,195
- Not Reported 16

Race

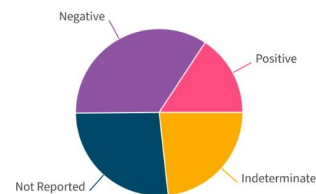
Name Case

Test Method



- RT-PCR 156,179 (90.2%)
- Rapid antigen test 12,155 (7%)
- Not Reported 323 (0.2%)
- no data 4,504 (2.6%)

COVID-19 Test Result




- Negative 132,770 (76.7%)
- Positive 39,254 (22.7%)
- Not Reported 1,105 (0.6%)
- Indeterminate 32 (0%)


[Download Table](#)

Case ID	Sex	Age At Index	Index Event	Race

Explorer in action: [imaging-hub](#)



MIDRC
BDF IMAGING HUB



Exploration

Series

Gender

Name Series

- F 4,816
- Female 290,229
- M 8,403
- Male 228,241
- No data 1,158
- Not Reported 267,253

1 more

Modality

Name Series

- CR 111,136
- CT 369,919
- DX 74,152
- FUSION 18
- KO 40
- MSD 2,328

19 more

Body Part Examined

Name Series

- ABD 2
- ABD PEL 29
- ABD PELV 4
- ABDOMEN 14,504
- ABDOMEN CAVIT 10
- ABDOMEN_PELVIS C 3

147 more

Primary Site

Name Series

- Abdomen 1,019
- Abdomen, Arm, Bladder, Ch... 566
- Abdomen, Mediastinum 342
- Abdomen, Pelvis 230
- Adrenal 151
- Adrenal Glands 662

39 more

Disease Type

Name Series

- Acute Myeloid Leukemia 123
- Adenocarcinoma 1,344
- Adenocarcinoma Colon 128
- Adenocarcinoma of colon, A... 1,203
- Adenocarcinoma Pancreas 804
- Adenocarcinoma Carcinoma 450

78 more

Commons

Name Series


- IDC 494,693
- MIDRC 304,597
- Stanford AIM 981

Default

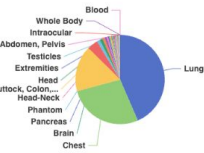
No filters currently applied.

800,271 Imaging Series

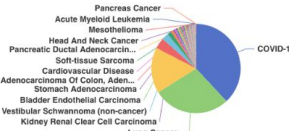
Platform



Primary Site



Disease Type



Study ID	Series Description	Body Part Examined	Primary Site	Disease Type	Platform	Series Images
13.6.14.114519.5.21.7695.4164.241925307562640520156786057201	ISPV2: VOLSER: uni-lateral cropped: original DCE	Breast	Breast	Breast Cancer	IDC	13.6.14.114519.5.21.7695.4164.21921025391523677931009446844
13.6.14.114519.5.21.148575914666371667824664303637931644021	ISPV2: PH1Av dyn mp 326 2.4 62 NO DELAY	Breast	Breast	Breast Cancer	IDC	13.6.14.114519.5.21.1304455037735569585531830064958637296030
216.840.1114274.1818.53461835389056699489659625913208967575	Lateral	CHEST	Lung	COVID-19	MIDRC	216.840.1114274.1818.554401999454926026218289419422485663633
216.840.1114274.1818.56845640510056939567275442370709537716	Lateral	CHEST	Lung	COVID-19	MIDRC	216.840.1114274.1818.5394386866525232953298480794078076821
12.826.0.13680043.10.474.232451.58164	CXR AP	CHEST	Lung	COVID-19	MIDRC	12.826.0.13680043.10.474.232451.58165
13.6.14.114519.5.21.7695.4164.60043108447748979436810741584	ISPV2: VOLSER: uni-lateral cropped: SER	Breast	Breast	Breast Cancer	IDC	13.6.14.114519.5.21.7695.4164.15062493327121430389561937373
216.840.1114274.1818.57556529350423146009897287611070846388		Chest	Lung	COVID-19	MIDRC	216.840.1114274.1818.48081260323237964134327068753514708641
13.6.14.114519.5.21.262515003865483086709704257818764943015	ISPV2: FAT IDEAL	Breast	Breast	Breast Cancer	IDC	13.6.14.114519.5.21.2454537963935081226838315635589593961
216.840.1114274.1818.545228284306237853214784614901252054148	Lateral	CHEST	Lung	COVID-19	MIDRC	216.840.1114274.1818.57528291821132132136335815560301269913
12.826.0.13680043.10.474.419639.25800447146683619699648154953	CHEST AP	CHEST	Lung	COVID-19	MIDRC	12.826.0.13680043.10.474.419639.430337098816615743129246630143

Rows per page: 10 | 1-10 of 800,271

Discovery Page for metadata browsing and searching

Support for custom renderers for table cells and rows

Once registered the cell renders can be added to the configuration

Define a data hook for retrieving and processing metadata from the Gen3 MDS

Basic functionality is working for all components

Todo:

- Advanced search
- Details page
- Selection
- Actions: export to workspace

Gen3.2 support extensibility using data renderers

Enables data to have visual representation in Tables and Charts

Overview of the process:

1. Write a function that takes a value and returns a ReactElement
2. Register function:

```
DiscoveryCellRendererFactory.registerCellRendererCatalog({...});
```

3. Add the function to the configuration:

```
"field": "__manifest",  
"contentType": "manifest",  
"cellRenderFunction": "inline",
```

Data Renderer Example

Inline chart renderer `__manifest` field Discovery Table

The screenshot displays the GEN3 Discovery Table interface. At the top, there are navigation links for 'Browse Data', 'Documentation', and 'Login'. Below this is a search bar and a table of studies. The table has columns for 'STUDY ID', 'STUDY NAME', 'STUDY TITLE', 'SOURCE', 'DATA FILES', and 'SUBJECTS'. Each row includes a checkbox, a study ID, a study name, a study title, a source, a data file visualization (a bar chart), and a subject count. Below each row is a brief description of the study and a button for more details (e.g., 'ALIGNED READS', 'IMAGING FILES', 'ARRAY').

<input type="checkbox"/>	STUDY ID	STUDY NAME	STUDY TITLE	SOURCE	DATA FILES	SUBJECTS
<input type="checkbox"/>	1000_Genomes_Project	1000 Genomes Project	1000 Genomes Project	1000 Genomes Project		0
<p>The 1000 Genomes Project is a collaboration among research groups in the US, UK, and China and Germany to produce an extensive catalog of human genetic variation that will support future medical research studies. It will extend the data from the International HapMap Project, which created a resource that has been used to find more than 100 regions of the genome that are associated with common human diseases such as coronary artery.</p> <p>ALIGNED READS</p>						
<input type="checkbox"/>	ACCOuNT_Clopidogrel_Arm	Discovery, Clopidogrel Arm	Discovery, Clopidogrel Arm	ACCOuNT consortium		167
<p>Pharmacogenomics is aimed at identifying genetic variation (SNPs) that influence inter-individual differences in drug response and adverse events and has widespread clinical relevance. Its application promises to enable targeted drug administration, improve therapeutic outcome, and inform drug development. Pharmacogenomic insights have improved our understanding of the underlying pathways and mechanisms behind adverse drug.</p>						
<input type="checkbox"/>	CCLC	CCLC (Cancer Cell Line Encyclopedia)	CCLC (Cancer Cell Line Encyclopedia)	Broad Institute		104
<p>The CCLC (Cancer Cell Line Encyclopedia) project is a collaboration between the Broad Institute, and the Novartis Institutes for Biomedical Research and its Genomics Institute of the Novartis Research Foundation to conduct a detailed genetic and pharmacologic characterization of a large panel of human cancer models, to develop integrated computational analyses that link distinct pharmacologic vulnerabilities to genomic patterns and to...</p> <p>ALIGNED READS</p>						
<input type="checkbox"/>	ds000030	UCLA Consortium for Neuropsychiatric Phenomics LA5c Study	UCLA Consortium for Neuropsychiatric Phenomics LA5c Study	OpenNeuro		272
<p>The Consortium for Neuropsychiatric Phenomics (CNP) is a large study funded by the NIH Roadmap Initiative that aims to facilitate discovery of the genetic and environmental bases of variation in psychological and neural system phenotypes, to elucidate the mechanisms that link the human genome to complex psychological syndromes, and to foster breakthroughs in the development of novel treatments for neuropsychiatric disorders. The...</p> <p>IMAGING FILES</p>						
<input type="checkbox"/>	GSE63878	Gene Networks Specific for Innate Immunity Define Post-traumatic Stress Disorder [Atymetrix]	Gene Networks Specific for Innate Immunity Define Post-traumatic Stress Disorder [Atymetrix]	Ichan School of Medicine at Mount Sinai		48
<p>The molecular factors involved in the development of Post-traumatic Stress Disorder (PTSD) remain poorly understood. Previous transcriptomic studies investigating the mechanisms of PTSD apply targeted approaches to identify individual genes under a cross-sectional framework lack a holistic view of the behaviours and properties of these genes at the system-level. Here we sought to apply an unsupervised gene-network-based approach.</p> <p>ARRAY</p>						

Rows per page: 10 | 1-5 of 5

Data Renderer Example

Popup chart renderer manifest field Discovery Table

The screenshot displays the GEN3 Discovery Table interface. At the top, there is a search bar and navigation links for Discovery, Dictionary, Exploration, Query, Analysis, Workspace, and Profile. The main table lists studies with columns for Study ID, Study Name, Study Title, Source, Data Files, and Subjects. A popup chart is visible for the 1000 Genomes Project, showing a bar chart with four segments: gt (25%), ts (25%), tv (25%), and pe (25%).

STUDY ID	STUDY NAME	STUDY TITLE	SOURCE	DATA FILES	SUBJECTS
1000_Genomes_Project	1000 Genomes Project	1000 Genomes Project		4	0
ACCOuNT_Clopidogrel_Arm	Discovery, Clopidogrel Arm	Discovery, Clopidogrel Arm	ACCOuNT consortium	763	167
CCLE	CCLE (Cancer Cell Line Encyclopedia)	CCLE (Cancer Cell Line Encyclopedia)	Broad Institute	932	104
ds000030	UCLA Consortium for Neuropsychiatric Phenomics LA5c Study	UCLA Consortium for Neuropsychiatric Phenomics LA5c Study	OpenNeuro	528	272
GSE63878	Gene Networks Specific for Innate Immunity Define Post-traumatic Stress Disorder [Aflymetrix]	Gene Networks Specific for Innate Immunity Define Post-traumatic Stress Disorder [Aflymetrix]	Ichsan School of Medicine at Mount Sinai	101	48

Rows per page: 10 | 1-5 of 5

The application framework of Gen3.2 is NextJS (vers 14.1)
Adding new pages is a matter of adding a tsk file to `src/pages`:
There is a template in `pages/SamplePage.tsx`

```
const SamplePage = ({ headerProps, footerProps }: NavPageLayoutProps) => {
  return (
    <NavPageLayout {...{ headerProps, footerProps }}>
      <div className="w-full m-10">
        <Center>
          <Paper shadow="md" p="xl" withBorder>
            <Text>This is a example custom page in Gen3</ Text>
            <Text>
              You can add your own content here, and add a link to this page in
              the navigation bar by editing the config file in
              navigation.json
            </Text>
          </Paper>
        </Center>
      </div>
    </NavPageLayout >
  );
};
```

Search in Analysis Center

Applications



Application

OmniGenome Commons

Login required

Lorem ipsum dolor sit amet consectetur. Viverra in vel natoque at quam euismod sagittis. Leo leo eget trincidunt senectus magna a odio. Dignissim blandit placerat risus arcu.

[Run App](#) [Demo](#)



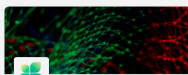
Application

DNAData Collaboratory

Login required

Lorem ipsum dolor sit amet consectetur. Viverra in vel natoque at quam euismod sagittis. Leo leo eget trincidunt senectus magna a odio. Dignissim blandit placerat risus arcu.

[Run App](#)



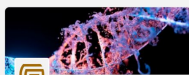
Application

NucleoNet Exchange

Login required

Lorem ipsum dolor sit amet consectetur. Viverra in vel natoque at quam euismod sagittis. Leo leo eget trincidunt senectus magna a odio. Dignissim blandit placerat risus arcu.

[Run App](#) [Demo](#)



Application

GeneSphere Hub

Login required

Lorem ipsum dolor sit amet consectetur. Viverra in vel natoque at quam euismod sagittis.

[Run App](#) [Demo](#)

Notebooks



Jupyter Notebook

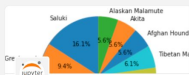
A Live View of COVID-19's Global Presence

Login required

In this notebook, we track COVID-19 local (US) and global cases with active, confirmed, recovered and death toll on the map at the latest time point. The interactive maps ...

[Extend text](#)

[View Notebook](#)

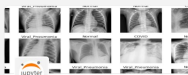


Jupyter Notebook

Canine Data Commons Data Visualization Notebook

Download node files, show/select data, and plot with this notebook using data hosted on the Canine Data Commons (<https://caninedc.org/>) stored under the NHGRI project.

[View Notebook](#)



Jupyter Notebook

COVID-19 X-ray images classification

This notebook replicates the DarkCovidNet model and performs transfer learning with the GoogLeNet model to classify radiological images as indicative of either 'COVID-19', ...

[Extend text](#)

[View Notebook](#)

COVID-19 X-ray images classification

Author: Yilin Xu • Date: Mar.12.2021

Introduction:

- "The novel coronavirus 2019 (COVID-19), which first appeared in Wuhan, China in December 2019, spread rapidly around the world and became a global pandemic. This resulted in a devastating effect on both daily lives, public health, and the global economy. It is critical to detect the positive cases as early as possible to prevent the further spread of this epidemic and to quickly treat infected patients. The need for auxiliary diagnostic tools has increased as there are no accurate automated toolkits available. Recent findings obtained using radiology imaging techniques suggest that such images contain salient information about the COVID-19 virus. Application of advanced artificial intelligence (AI) techniques coupled with radiological imaging can be helpful for the accurate detection of this disease, and can also be assistive to overcome the problem of a lack of specialized physicians in remote villages."
- This notebook is a replication of the DarkCovidNet model¹ and transfer learning of GoogLeNet model to classify radiological images as indicative of either "COVID-19", "No Finding" and "Pneumonia" to assist in the diagnosis of COVID-19. This is an extension of the notebook published along with the paper in GitHub <https://github.com/muhammedtalal/COVID-19/blob/master/DarkCovidNet%20%20for%20binary%20classes.ipynb>. We use data available in Kaggle <https://www.kaggle.com/tawisfurrhan/covid19-radiography-database>

1. Ozturk et. al. 2020. Automated detection of COVID-19 cases using deep neural networks with X-ray. Comput Biol Med. 2020 Jun; 121: 103792. (doi: 10.1016/j.complmed.2020.103792) [\[2\]](#)

Set up notebook

```
In [1]: %reload_ext autoreload
%autoreload 2
%matplotlib inline
import warnings
warnings.filterwarnings('ignore')
```

The Vision module in fastai package contains the classification methods we will use. Uncomment to install python package.

```
In [2]: # !pip install fastai==1.0.61 --user --no-use-pep517
# !pip install gitpython
# !pip install kaggle
from fastai.vision import *
import torchvision.models as TorchModels
import numpy as np
import shutil
from pathlib import Path
from sklearn.model_selection import StratifiedKFold
from sklearn.metrics import confusion_matrix
from sklearn.metrics import classification_report
from sklearn.metrics import roc_curve
from sklearn.metrics import auc
import os
```

DarkCovidNet for image classification

Download X-RAY images from Kaggle API

Possible to run data-portal simultaneously with Gen3.2

In helm charts (currently on a gen3-helm branch)

- Add configuration for frontend-framework and data-portal in value.yaml
- Add `frontendRoot: gen3ff`

Gen3.2 will be on `/` and data-portal will be on `/portal`

`frontendRoot: portal`

data-portal will be on `/` Gen3.2 will be on `/ff`

May 2024

- Workspaces
- Update explorer UI
- Discovery page improvements

June 2024:

- Analysis Center
- My Data Library
- Data Dictionary

July 2024:

- New application
- Homepage layouts
- Data Submission

Remaining:

- Eliminate issues and flaws
- Testing framework
- Accessibility compliance
- Documentation
- Improved deployment configuration
- Modals
- Nextjs app router
- SSR components
- Simplify configuration:
 - admin UI
 - config validation
- ...

Migrating from Windmill to Gen3.2

Matthew Peterkort
Oregon Health & Science University

<https://github.com/uc-cdis/gen3-frontend-framework/blob/develop/docs/Local%20Development/QuickStart.md>

Gen3.2 Frontend Quickstart

This guide will get you up to speed on configuring a Gen3 Frontend Applications. There are other tutorial on running it locally (for example: (Local Development)[]).

🔗 Getting Started

Gen3 Data Commons using the Gen3 Frontend Framework is a matter of the following:

- create a clone of [Gen3 Data Commons Application](#)
- Configure the commons by editing the configuration files in the `config` directory.
- Add your pages and content
- Deploy via helm charts or Docker.

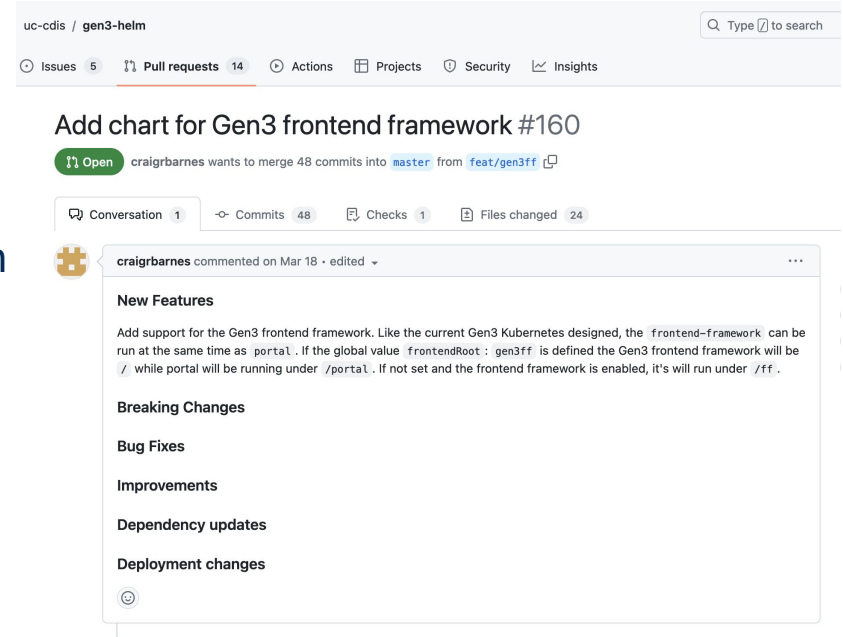
Changes to the Gen3 Data Commons Application can be pulled from the Common Frontend Repository. You need configure git to pull from the Common Frontend Repository.

```
git remote add upstream https://github.com/uc-cdis/commons-frontend-app.git
```



- [NVM](#) is a painless way of managing Node versions
- Gen3 helm kubernetes instance required
- It is important to understand that the local development setup passes portal requests to your local helm nginx setup
- If strictly following the docs using example revproxy config make sure you change your values.yaml hostname to be localhost
- If you wish to customize and add to gen3-frontend-framework fork from:
<https://github.com/uc-cdis/commons-frontend-app>
- If you wish to develop and make contributions to frontend framework fork from:
<https://github.com/uc-cdis/gen3-frontend-framework/tree/develop>
- See [gen3-frontend/framework/docs/Local Development/Using Helm Charts/ Local Development with Helm Charts](#) on the develop branch for setup docs.

- Gen3 Helm supports frontend framework deployments with minimal changes to existing helm gen3 deployments:
<https://github.com/uc-cdis/gen3-helm/pull/160>
- Make sure that “npm run build” and “npm run start” work as expected before building a custom image.
- Separate production and development environment variables are defined in the sample Commons. Make sure that the production hostname matches environment defined in helm and in the frontend-framework.



The screenshot shows a GitHub pull request interface for the repository 'uc-cdis / gen3-helm'. The title of the pull request is 'Add chart for Gen3 frontend framework #160'. It is currently open and shows 48 commits from the 'feat/gen3ff' branch into the 'master' branch. The pull request is categorized as 'New Features' and includes a detailed description of the changes. The description states that the pull request adds support for the Gen3 frontend framework, allowing it to be run alongside the current Gen3 Kubernetes design. It also mentions that the framework will be run under the '/portal' path if the global value 'frontendRoot: gen3ff' is defined, or under '/ff' if not set and the framework is enabled. The pull request also lists sections for 'Breaking Changes', 'Bug Fixes', 'Improvements', 'Dependency updates', and 'Deployment changes'.

Sample Commons Directory Layout

- src - Top level source code pages imported from @gen3/frontend
- public - The actual custom content files
- Config - Highly customizable settings files that control the look and feel of the website

```
src
├── lib
│   ├── CohortBuilder
│   │   └── CustomCellRenderers.tsx
│   ├── Discovery
│   │   ├── CustomCellRenderers.tsx
│   │   └── CustomRowRenderers.tsx
│   └── plugins
│       └── index.js
├── pages
│   ├── 404.tsx
│   ├── AISearch.tsx
│   ├── Colors.tsx
│   ├── DEMOGRIP.tsx
│   ├── DataDictionary.tsx
│   ├── Discovery.tsx
│   ├── Explorer.tsx
│   ├── GRIPREF.tsx
│   ├── Login.tsx
│   ├── Profile.tsx
│   ├── Query.tsx
│   ├── SamplePage.tsx
│   ├── Workspaces.tsx
│   ├── _app.tsx
│   └── _document.tsx
├── api
│   └── auth
│       ├── credentialsLogin.ts
│       ├── credentialsLogout.ts
│       ├── sessionLogout.ts
│       └── sessionToken.ts
├── index.tsx
└── styles
    └── globals.css
```

```
public
├── fonts
│   └── FranklinGothic.ttf
├── icons
│   ├── ACED_PARTNERS.jpg
│   ├── createdBy.png
│   ├── gen3-dark.png
│   ├── gen3-dark.svg
│   ├── gen3.png
│   ├── logo.png
│   ├── logo_small_2.png
│   └── midrc-logo.png
├── rolesPages
│   ├── analyze-local.png
│   ├── analyze-workspace.png
│   ├── behavior.png
│   ├── brain.png
│   ├── browse.png
│   ├── chronic.png
│   ├── database.png
│   ├── diagnose.png
│   ├── download.png
│   ├── effectiveness.png
│   ├── group.png
│   ├── intervention.png
│   ├── medication.png
│   ├── mental.png
│   ├── model.png
│   ├── new.png
│   ├── pain.png
│   ├── repository.png
│   ├── share.png
│   ├── state.png
│   └── therapy.png
├── images
│   ├── brh
│   │   ├── gene_bggy.svg
│   │   └── logo.png
│   ├── gene.svg
│   └── sideTexture.png
```

```
config
├── brh
│   ├── colors.json
│   ├── discovery.json
│   ├── footer.json
│   ├── landingPage.json
│   ├── login.json
│   ├── modals.json
│   ├── navigation.json
│   ├── profile.json
│   ├── query.json
│   └── workspaces.json
├── drsHostnames.json
├── gen3
│   ├── colors.json
│   ├── discovery.json
│   ├── explorer.json
│   ├── footer.json
│   ├── landingPage.json
│   ├── login.json
│   ├── navigation.json
│   ├── profile.json
│   └── query.json
├── icons
│   ├── aiSearch.svg
│   ├── analysis.svg
│   ├── bar-chart.svg
│   ├── chevron-down.svg
│   ├── datafile.svg
│   ├── dictionary.svg
│   ├── download.svg
│   ├── exploration.svg
│   ├── gen3-dark.svg
│   ├── gen3.json
│   ├── gen3.svg
│   ├── loginCircle.svg
│   ├── profile.svg
│   ├── query.svg
│   ├── upload.svg
│   ├── user.svg
│   └── workspace.svg
├── modals.json
├── session.json
├── siteConfig.json
├── themeColors.json
└── themeFonts.json
```

Config Directory – Global Configurations

```
config
├── brh
│   ├── colors.json
│   ├── discovery.json
│   ├── footer.json
│   ├── landingPage.json
│   ├── login.json
│   ├── modals.json
│   ├── navigation.json
│   ├── profile.json
│   ├── query.json
│   └── workspaces.json
├── drsHostnames.json
├── gen3
│   ├── colors.json
│   ├── discovery.json
│   ├── explorer.json
│   ├── footer.json
│   ├── landingPage.json
│   ├── login.json
│   ├── navigation.json
│   ├── profile.json
│   └── query.json
├── icons
│   ├── aiSearch.svg
│   ├── analysis.svg
│   ├── bar-chart.svg
│   ├── chevron-down.svg
│   ├── datafile.svg
│   ├── dictionary.svg
│   ├── download.svg
│   ├── exploration.svg
│   ├── gen3-dark.svg
│   ├── gen3.json
│   ├── gen3.svg
│   ├── loginCircle.svg
│   ├── profile.svg
│   ├── query.svg
│   ├── upload.svg
│   ├── user.svg
│   └── workspace.svg
├── modals.json
├── session.json
├── siteConfig.json
├── themeColors.json
└── themeFonts.json
```

```
packages > sampleCommons > config > {} session.json > ...
1   {
2     "sessionConfig" : {
3       "updateSessionTime": 5,
4       "inactiveTimeLimit": 20,
5       "logoutInactiveUsers": false
6     }
7   }
```

```
packages > sampleCommons > config > {} siteConfig.json > ...
1   {
2     "commons": "gen3"
3   }
4   |
```

```
packages > sampleCommons > config > {} themeFonts.json > ...
1   {
2     "heading": ["FranklinGothic", "Montserrat", "sans-serif"],
3     "content": ["FranklinGothic", "Noto Sans", "sans-serif"],
4     "fontFamily": "FranklinGothic"
5   }
6   |
```

```
packages > sampleCommons > config > g
1   {
2     "primary": "#00b6ed",
3     "secondary": "#BF7E06",
4     "accent": "#2e008b",
5     "base": "#CCCCCC",
6     "accentWarm": "#594B04",
7     "accentCool": "#908719",
8     "chart": "#0d95A1"
9   }
10  |
```


Page Level Configurations

```
packages > sampleCommons > config > gen3 > {} login.json > [ ] topContent
```

```
1  {
2  "topContent": [
3  {
4  "text": "ACED",
5  "className": "text-center text-3xl font-bold"
6  },
7  {
8  "text": "DISCOVER, ANALYZE, AND SHARE DATA",
9  "className": "text-center text-xl font-medium"
10 },
11 {
12 "text": "We are uniting world leading researchers to tackle the
13 "className": "text-center text-xl font-medium"
14 }
15 ],
16 "bottomContent": [
17 {
18 "text": "If you have any questions about access or the registra
19 "className": "text-center text-sm"
20 }
21 ],
22 "image": "images/gene.svg",
23 "showCredentialsLogin" : true
24 }
25
```

The screenshot shows a web browser displaying the ACED (Alliance for Cancer Early Detection) website. The page features a blue header with the ACED logo and navigation links for Exploration, DEMO, CRIPREF, Query, and Profile. The main content area includes the ACED logo, the tagline "DISCOVER, ANALYZE, AND SHARE DATA", a paragraph of text about uniting researchers, a "Login from Microsoft" button, and a "Authorize with credentials" section with an input field and an "Authorize" button. A footer note mentions a link for questions about access or registration. Green arrows point from the code on the left to these specific elements on the page.

```
{
  "body": [
    {
      "title": {
        "text": "ACED",
        "level": 2
      },
    },
    {
      "splitarea": {
        "left": [
          {
            "text": "We are <strong>uniting</strong> world leading re",
          },
          {
            "link": {
              "href": "/Explorer",
              "linkType": "portal",
              "text": "Explore Gen3 Data"
            },
          },
          {
            "text": "Lorem ipsum dolor sit amet, consectetur adipisci",
          },
          {
            "link": {
              "href": "https://gen3.datacommons.io",
              "text": "Learn More"
            },
          }
        ]
      }
    }
  ]
}
```



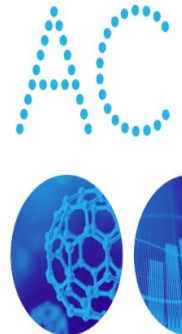
ACED

We are **uniting** world leading researchers to tackle the biggest challenges in early detection, an important area of unmet clinical need. Scientists in the Alliance are working together at the forefront of technological innovation to translate research into realistic ways to improve cancer diagnosis, which can be implemented into health systems and meaningfully benefit people with cancer.

[EXPLORE GEN3 DATA](#)

Lorem ipsum dolor sit amet, consectetur adipiscing elit. Etiam elit dui, commodo a tortor ut, vestibulum consectetur tellus. Aliquam erat volutpat. Aenean sodales lacus quis venenatis fermentum. Phasellus varius tempor odio a elementum. Aliquam sed diam molestie, ornare neque in, portitor mi. Aliquam hendrerit libero volutpat, bibendum ante at, auctor velit. Nulla eget augue a turpis facilisis dictum. Nulla vulputate accumsan aliquam. Fusce imperdiet arcu nibh, nec vehicula nisi placerat at. Phasellus eget magna elementum, tincidunt urna at, venenatis nulla. Cras ullamcorper ante sed ex portitor, at elementum ligula dapibus. Sed malesuada mi turpis, eu venenatis lorem convallis in.

[LEARN MORE](#)



- Backwards compatible config files
- Migration from gitops to FF is as simple as a couple of copy and pastes
- Expanded configurations for landing page, colors, profile and others.
- Many configs map straight across to the expected json file in `sampleCommons/config/gen3`

```
Users > peterkor > Desktop > {} brh.json > ...
1   {
2     "gaTrackingId": "UA-119127212-5",
3   >   "graphql": { ...
32  },
33   "components": {
34     "appName": "Biomedical Research Hub",
35  >   "index": { ...
81  },
82  >   "navigation": { ...
121 },
122 >   "topBar": { ...
134 },
135 >   "login": { ...
144 },
145 >   "footerLogos": [ ...
161 ],
162 >   "footer": { ...
197 },
198 >   "categorical9Colors": [ ...
208 ],
209 >   "categorical2Colors": [ ...
212 ]
213 },
214 "requiredCerts": [],
215 > "featureFlags": { ...
219 },
220 > "dataExplorerConfig": { ...
537 },
538 > "fileExplorerConfig": { ...
644 },
645 > "discoveryConfig": { ...
833 },
834 "useArboristUI": true,
835 > "terraExportWarning": { ...
839 }
840 }
```



Adding a New Font

- Add font file to public/fonts
- Add path to font file to globals.css
- Add font name to config/themeFonts.json for corresponding text types

```
packages > sampleCommons > src > styles > # globals.css > ...  
80  
81   @font-face {  
82     font-family: 'FranklinGothic';  
83     src: url('/fonts/FranklinGothic.ttf')  
84     format('truetype');  
85   }  
86
```

```
packages > sampleCommons > config > {} themeFonts.json > ...  
1   {  
2     "heading": ["FranklinGothic", "Montserrat", "sans-serif"],  
3     "content": ["FranklinGothic", "Noto Sans", "sans-serif"],  
4     "fontFamily": "FranklinGothic"  
5   }  
6
```

```
public  
├── fonts  
│   └── FranklinGothic.ttf  
├── icons  
│   ├── ACED_PARTNERS.jpg  
│   ├── createdby.png  
│   ├── gen3-dark.png  
│   ├── gen3-dark.svg  
│   ├── gen3.png  
│   ├── logo.png  
│   ├── logo_small_2.png  
│   └── midrc-logo.png  
├── rolesPages  
│   ├── analyze-local.png  
│   ├── analyze-workspace.png  
│   ├── behavior.png  
│   ├── brain.png  
│   ├── browse.png  
│   ├── chronic.png  
│   ├── database.png  
│   ├── diagnose.png  
│   ├── download.png  
│   ├── effectiveness.png  
│   ├── group.png  
│   ├── intervention.png  
│   ├── medication.png  
│   ├── mental.png  
│   ├── model.png  
│   ├── new.png  
│   ├── pain.png  
│   ├── repository.png  
│   ├── share.png  
│   ├── state.png  
│   └── therapy.png  
└── images  
    ├── brh  
    │   ├── gene_bggy.svg  
    │   └── logo.png  
    ├── gene.svg  
    └── sideTexture.png
```

Before / After

localhost:3010
Not Secure https://localhost:3010

Browse Data | Documentation | Login

GEN³

Discovery Dictionary Exploration Query Analysis Workspace Profile

Gen3 Data Platform

The **Gen3 Data Platform** is a single web interface which allows visitors to **discover, access and analyze data**. Making data easily findable enables secondary, cross-study analyses, promotes dissemination of research and accelerates new discoveries.

[EXPLORE GEN3 DATA](#)

The Gen3 platform consists of open-source software services that support the emergence of healthy data ecosystems by enabling the interoperation and analysis workspaces. Gen3 aims to accelerate and democratize the process of scientific discovery by making it easy to manage, analyze, harmonize, and share large and complex datasets in the cloud.

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ACED | Login

ACED

INTERNATIONAL ALLIANCE FOR CANCER EARLY DETECTION

Exploration DEMO GRIPREF Query Profile

ACED

We are **uniting** world leading researchers to tackle the biggest challenges in early detection, an important area of unmet clinical need. Scientists in the Alliance are working together at the forefront of technological innovation to translate research into realistic ways to improve cancer diagnosis, which can be implemented into health systems and meaningfully benefit people with cancer.

[EXPLORE GEN3 DATA](#)

Lorem ipsum dolor sit amet, consectetur adipiscing elit. Etiam elit dui, commodo a tortor ut, vestibulum consectetur tellus. Aliquam erat volutpat. Aenean sodales lacus quis venenatis fermentum. Phasellus varius tempor odio a elementum. Aliquam sed diam molestie, omare neque in, porttitor mi. Aliquam hendrerit libero volutpat, bibendum ante at, auctor velit. Nulla eget augue a turpis facilisis dictum. Nulla vulputate accumsan aliquam. Fusce imperdiet arcu nibh, nec vehicula nisi placerat in. Phasellus eget magna elementum, tincidunt urna at, venenatis nulla. Cras ullamcorper ante sed ex porttitor, at elementum ligula dapibus. Sed malesuada mi turpis, eu venenatis lorem convallis in.

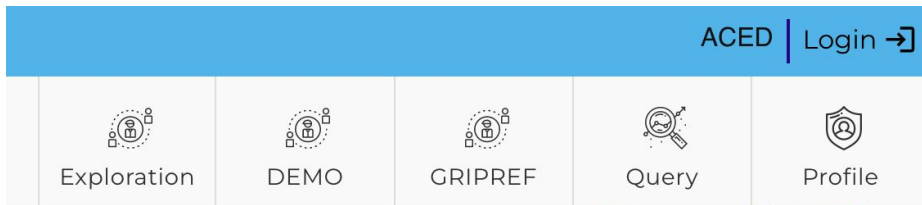
[LEARN MORE](#)

Search studies and related datasets by metadata
DISCOVER

Explore populated studies
ANALYZE

Adding a New Page

- Add a new .tsx file to gen3-frontend-framework/packages/sampleCommons/src/pages.
- SamplePage.tsx is given as a template for adding new pages
- <NavPageLayout> component and props serve as boilerplate, ex:



```
packages > sampleCommons > src > pages > SamplePage.tsx > SamplePage
1  import React from 'react';
2  import { Text, Paper } from '@mantine/core';
3  import {
4    NavPageLayout,
5    NavPageLayoutProps,
6    getNavPageLayoutPropsFromConfig,
7  } from '@gen3/frontend';
8  import { GetServerSideProps } from 'next';
9
10 const SamplePage = ({ headerProps, footerProps }: NavPageLayoutProps) => {
11   return (
12     <NavPageLayout {...{ headerProps, footerProps }}>
13       <div className="w-96 m-10">
14         <Paper shadow="md" p="xl" withBorder>
15           <Text>This is a example custom page in Gen3</Text>
16           <Text>
17             You can add your own content here, and add a link to this page in
18             the navigation bar by editing the config file in{' '}
19             <em>COMMONSNAME</em>/navigation.json
20           </Text>
21         </Paper>
22       </div>
23     </NavPageLayout>
24   );
25 };
26
27 export const getServerSideProps: GetServerSideProps<
28   NavPageLayoutProps
29 > = async () => {
30   return {
31     props: {
32       ...(await getNavPageLayoutPropsFromConfig()),
33     },
34   };
35 };
36
37 export default SamplePage;
```

- Add a link to SamplePage.tsx to sampleCommons/config/gen3/navigation.json, or anywhere else that allows linking pages
- To do this add a dict entry to “items” list as shown in right-hand image
- Supports full customization of icon, Name, and tooltip
- SamplePage is attached to the “DEMO” button in right-hand example

```
packages > sampleCommons > config > gen3 > {} navigation.js
1  {
2    "navigation": {
3      "logo": {
4        "src": "/icons/logo_small_2.png",
5        "height": 220,
6        "href": "/"
7      },
8      "items": [
9        {
10         "icon": "gen3:exploration",
11         "href": "/Explorer",
12         "name": "Exploration",
13         "tooltip": "The Exploration Page enable
14       },
15       {
16         "icon": "gen3:exploration",
17         "href": "/SamplePage",
18         "name": "DEMO",
19         "tooltip": "The Exploration Page enable
20     }
21   ]
22 }
```

- Guppy API fetching function part of the @gen3/core library
- More advanced fetching techniques are used in the cohort builder.
- Api endpoints fetching techniques are also supported in the core library

```
50  /**
51   * Similar to graphQLAPI except this
52   * guppyAPIFetch function is a branch of guppy core API defined below and
53   * graphQLAPI is a branch of gen3Services API.
54   */
55  ✓ export const guppyAPIFetch = async <T>(  
56    query: guppyApiSliceRequest,  
57  ): Promise<guppyApiResponse<T>> => {  
58    const res = await fetch(`${GEN3_GUPPY_API}/graphql`, {  
59      headers: {  
60        Accept: 'application/json',  
61        'Content-Type': 'application/json',  
62        'Access-Control-Allow-Origin': '*',  
63      },  
64      method: 'POST',  
65      body: JSON.stringify(query),  
66    });  
67  
68    if (res.ok) return res.json();  
69  
70    throw await buildGuppyFetchError(res, query);  
71  };  
72
```


Fetching Data from Guppy with FF

- Uses a basic useEffect hook to fetch data and use data in visualization
- Guppy expects query format

```
export interface guppyApiSliceRequest {  
  readonly query: string;  
  readonly variables?: Record<string, unknown>;  
}  
  
export interface guppyApiResponse<H = JSONObject> {  
  readonly data: H;  
  readonly errors: Record<string, string>;  
}
```

```
55 const query =  
56   `query($filter: JSON){  
57     file(filter: $filter first: 10000){  
58       subject  
59     }  
60   }`;  
61  
62 const variables = {  
63   filter: {  
64     AND: [{ IN: { project_id: ['synthea-test'] } } ]},  
65 },  
66 };  
67  
const SamplePage = ({ headerProps, footerProps }: SamplePageProps) => {  
  const [items, setItems] = useState<Item[]>([]);  
  const [isLoading, setLoading] = useState<boolean>(true);  
  
  useEffect(() => {  
    const fetchData = async () => {  
      try {  
        const result: GuppyAPIFetchResult = await guppyAPIFetch({  
          query: query,  
          variables: variables,  
        });  
        setItems(result.data.file);  
        setLoading(false);  
      } catch (error) {  
        console.error('Error fetching data:', error);  
      }  
    }  
  });  
  
  fetchData();  
}, []);  
85  
86  
87  
88
```

- Data Component used for processing and mapping data into a grid of “reference” entries.
- Essentially a grid of guppy results where each result is a “reference” to a patient

```
interface Item {
  id: string;
  subject: string;
}

interface DataComponentProps {
  data: Item[];
}

const DataComponent = ({ data }: DataComponentProps) => {
  return (
    <Grid>
      {data.map((item) => (
        <Grid.Col key={item.id} span={4} style={{ marginBottom: 5, marginTop: 5 }}>
          <Paper style={{ padding: 'lg', boxShadow: 'xs' }}>
            <div style={{ display: 'flex', alignItems: 'center' }}>
              <Text style={{ margin: 10 }}> ✓ </Text>
              <div>
                <div>Subject: {item.subject}</div>
              </div>
            </div>
          </Paper>
        </Grid.Col>
      ))}
    </Grid>
  );
};
```

Putting it all together

- Code demonstrates using basic JS hooks, fetching functions, and Mantine components to fetch data from Guppy
- Guppy data is displayed as a grid of entries
- Header and footer props are maintained to keep look and feel consistent with the rest of the site

```
packages > sampleCommons > src > pages > SamplePage.tsx > DataComponentProps
69 const SamplePage = ({ headerProps, footerProps }: SamplePageProps) => {
70   const [items, setItems] = useState<Item[]>([]);
71   const [isLoading, setLoading] = useState<boolean>(true);
72
73   useEffect(() => {
74     const fetchData = async () => {
75       try {
76         const result: GuppyAPIFetchResult = await guppyAPIFetch({
77           query: query,
78           variables: variables,
79         });
80         setItems(result.data.file);
81         setLoading(false);
82       } catch (error) {
83         console.error('Error fetching data:', error);
84       }
85     };
86
87     fetchData();
88   }, []);
89
90   return (
91     <NavPageLayout headerProps={headerProps} footerProps={footerProps}>
92       {isLoading ? (
93         <p>Loading data...</p>
94       ) : (
95         <Group style={{ margin: 20 }}>
96           <Title> Synthetic Data FHIR references </Title>
97           <DataComponent data={items} />
98         </Group>
99       )}
100     </NavPageLayout>
101   );
102 };
```

Putting it all together

The screenshot shows a web browser window with the URL `https://localhost:3010/SamplePage`. The page header includes the ACED logo (International Alliance for Cancer Early Detection) and a navigation menu with links for Exploration, DEMO, GRIPREF, Query, and Profile. The user is logged in as peterkor@ohsu.edu. The main content area is titled "Synthetic Data FHIR references" and displays a grid of 24 entries, each consisting of a green checkmark and a FHIR reference string.

✓ Subject: ResearchStudy/ 484de0fa-8fdb-5111-9ab7-9f173f7c8378	✓ Subject: Patient/45c11dad-2b38-4c8e-822e-7abff8a1ee1d	✓ Subject: Patient/45c11dad-2b38-4c8e-822e-7abff8a1ee1d
✓ Subject: Patient/45c11dad-2b38-4c8e-822e-7abff8a1ee1d	✓ Subject: Patient/b09d2e55-2754-448f-b058-85e15d8820ea	✓ Subject: Patient/b09d2e55-2754-448f-b058-85e15d8820ea
✓ Subject: Patient/b09d2e55-2754-448f-b058-85e15d8820ea	✓ Subject: Patient/b09d2e55-2754-448f-b058-85e15d8820ea	✓ Subject: Patient/b09d2e55-2754-448f-b058-85e15d8820ea
✓ Subject: Patient/bd88a6cc-26a4-46e0-94aa-f4dd49e39f7	✓ Subject: Patient/16c1d9e4-f8ab-4490-b48a-3101033c76a6	✓ Subject: Patient/16c1d9e4-f8ab-4490-b48a-3101033c76a6
✓ Subject: Patient/16c1d9e4-f8ab-4490-b48a-3101033c76a6	✓ Subject: Patient/16c1d9e4-f8ab-4490-b48a-3101033c76a6	✓ Subject: Patient/16c1d9e4-f8ab-4490-b48a-3101033c76a6
✓ Subject: Patient/6c41377e-1b05-4402-b95d-973ee35b2c48	✓ Subject: Patient/74af22f2-a67d-4aa6-b932-30383fec846b	✓ Subject: Patient/498fa911-aa03-4ed6-aaad-61ee425fc4df
✓ Subject: Patient/c6e3328e-34b8-4b4d-8e60-b96764ce5b99	✓ Subject: Patient/c6e3328e-34b8-4b4d-8e60-b96764ce5b99	✓ Subject: Patient/c6e3328e-34b8-4b4d-8e60-b96764ce5b99
✓ Subject: Patient/38a48a72-d2b2-4c92-aa70-42185c77b4a1	✓ Subject: Patient/38a48a72-d2b2-4c92-aa70-42185c77b4a1	✓ Subject: Patient/38a48a72-d2b2-4c92-aa70-42185c77b4a1
✓ Subject: Patient/38a48a72-d2b2-4c92-aa70-42185c77b4a1	✓ Subject: Patient/38a48a72-d2b2-4c92-aa70-42185c77b4a1	✓ Subject: Patient/73d39580-7a20-4716-ab13-5c21386bfdbc

- **Speakers**

- Craig Barnes - Center for Translational Data Science, University of Chicago
- Matthew Peterkort - Oregon Health & Science University

- **Gen3 Forum Steering Committee**

- Robert Grossman - Center for Translational Data Science, University of Chicago
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