

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

Gen3 Community Forum  
1 May 2024

# The Agenda

- 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

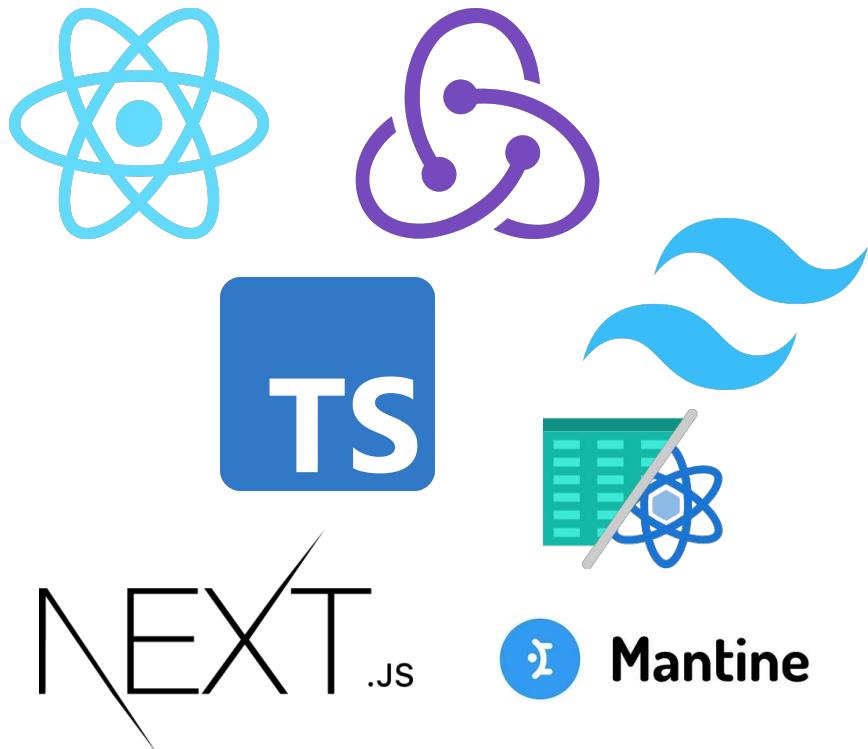
Craig Barnes  
Center for Translational Data Science  
University of Chicago

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 Technologies

- 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



# Gen3.2 Features



- 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

# Gen3.2 Applications



## Existing:

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

## New:

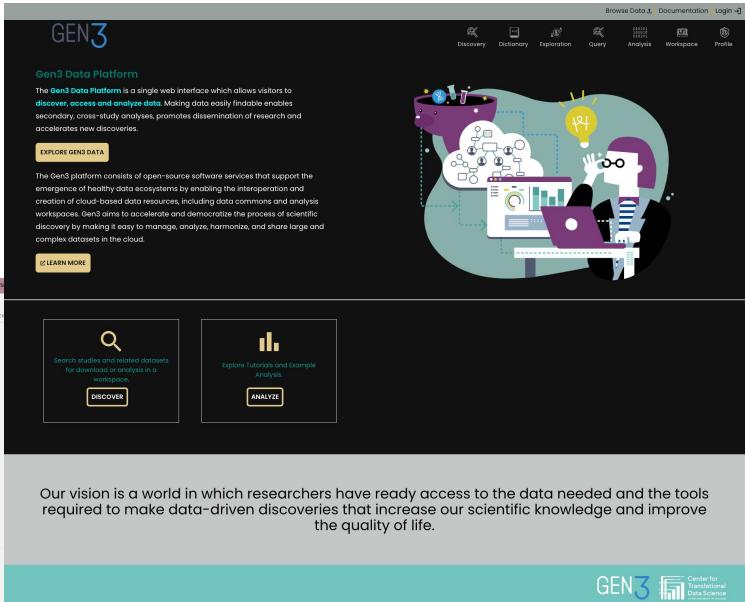
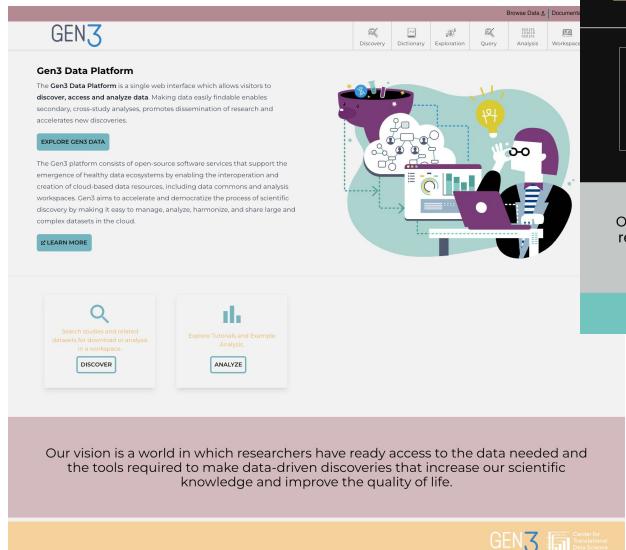
- Application Center
- My Data Library
- Administration UIs
- LLM Search
- Cohort Discovery
- 3rd party tools and applications

# Styling and Theming

The portal's style can be customized by setting:

- Color theme
- Fonts
- Icons

Configuration tools  
Style overrides



# Colors

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

# Navigation

Configured like data-portal

Customizable icons

3 layouts:

Classic:



Horizontal:



# Navigation: Vertical

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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 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](#)



# Development support

- 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

# Environment Files



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

# Environment Files

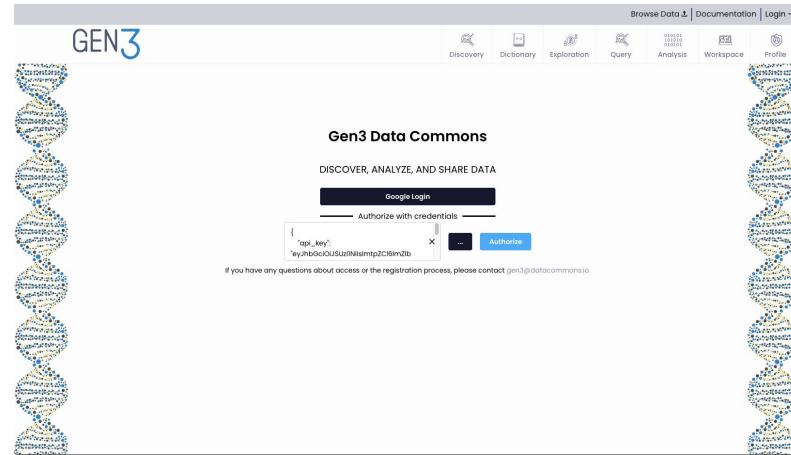


Override any Gen3 endpoint

```
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/submit
```

# 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

## New Explorer UI

About | Get Started | Cite MIDRC | DUA | Resources | Gen3 | Email Support | Login

**MIDRC**  
MEDICAL IMAGING AND DATA RESOURCE CENTER

Exploration      Dictionary      Example Analysis

Cases      Annotations      Measurements      Imaging Studies      Data Files

### Case Cohort

SEX: Female    RACE: Black or African American    ETHNICITY: Hispanic or Latino    INDEX EVENT: First COVID Test    ZIP: US

Filters      Collapse All      Download File Manifest for Cases (193.35K)      70,314 CASES

**Test Method**

Test Method	Count	Percentage
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**

Test Result	Count	Percentage
Negative	132,770	76.7%
Positive	39,254	22.7%
Indeterminate	32	0.6%
Not Reported	1,105	0%

Download Table

Case ID	Sex	Age At Index	Index Event	Race
1	Female	18-24	First COVID Test	Black or African American
2	Male	25-34	First COVID Test	Asian
3	Female	35-44	First COVID Test	Hispanic or Latino
4	Male	45-54	First COVID Test	White
5	Female	55-64	First COVID Test	Black or African American
6	Male	65-74	First COVID Test	Asian
7	Female	75-84	First COVID Test	Hispanic or Latino
8	Male	85+	First COVID Test	White

# Explorer in action: imaging-hub

**MIDRC BOF IMAGING HUB**

**Series**

Gender	
Name	Series
F	4,816
Female	296,226
M	4,403
Male	238,241
no data	1,158
Not Reported	267,253

**Modality**

Modality	
Name	Series
CR	111,136
CT	369,919
DX	74,152
FUSION	16
KO	49
MIDC	2,398

**Body Part Examined**

Body Part Examined	
Name	Series
ABD	2
ABD, PEL	26
ABD, PELV	4
ABDOMEN	14,504
ABDOMEN, CAVIT	10
ABDOMEN, PELVIS C	3

**Primary Site**

Primary Site	
Name	Series
Abdomen	1,019
Abdomen, Am, Bladder, Ch.	556
Abdomen, Mediastinum	342
Abdomen, Pelvis	230
Aben	191
Adrenal Glands	662

**Disease Type**

Disease Type	
Name	Series
Acute Myeloid Leukemia	123
Adenocarcinoma	1,344
Adenocarcinoma, Colon	128
Adenocarcinoma of colon, A.	1,203
Adenocarcinoma Pancreas	604
Adrenocortical Carcinoma	455

**Commons**

Commons	
Name	Series
IDC	494,693
MIDRC	304,597
Stanford AIMI	981

**Default**  
No filters currently applied.

**Platform**

**Primary Site**

**Disease Type**

**Study ID**

Study ID	Series Description	Body Part Examined	Primary Site	Disease Type	Platform	Series Images
13.6.1.4114519.5.21.7695.4164.24925307562640520156786057201	ISPY2: VOLSER: uni-lateral cropped: original DCE		Breast	Breast Cancer	IDC	13.6.1.4114519.5.21.7695.4164.219210253915236771931009446944
13.6.1.4114519.5.21.14857591466637166782466430363793644021	ISPY2: Phl/Ax dyn mp 326.2 4 62 NO DELAY		Breast	Breast Cancer	IDC	13.6.1.4114519.5.21.304455137355695853180064958637296030
216.840.1114274.1818.53401835389056699489659625913208967575	Lateral	CHEST	Lung	COVID-19	MIDRC	216.840.1114274.1818.554440199454926026218289419422485663633
216.840.1114274.1818.568456405100569395725442370709537716	Lateral	CHEST	Lung	COVID-19	MIDRC	216.840.1114274.1818.5394386866525323915329848074078076821
12.826.01368004310.474.23245158164	CXR AP	CHEST	Lung	COVID-19	MIDRC	12.826.01368004310.474.23245158165
13.6.1.4114519.5.21.7695.4164.600431084477489794368107141584	ISPY2: VOLSER: uni-lateral cropped: SER		Breast	Breast Cancer	IDC	13.6.1.4114519.5.21.7695.4164.15062493327211430389551937373
216.840.1114274.1818.5755652935042314600989728761070846388	Chest		Lung	COVID-19	MIDRC	216.840.1114274.1818.48081260322371961034327068753514708641
13.6.1.4114519.5.21.262515001865483086709704257518764943015	ISPY2: FAT/IDEAL		Breast	Breast Cancer	IDC	13.6.1.4114519.5.21.22454537935693508132268383156355895939360
216.840.1114274.1818.54522828430623785321478461490125054148	Lateral	CHEST	Lung	COVID-19	MIDRC	216.840.1114274.1818.5752829182113213213633581560301269913
12.826.01368004310.474.47639.258004471646836619699648154953	CHEST AP	CHEST	Lung	COVID-19	MIDRC	12.826.01368004310.474.47639.430337098816615743129246630143

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

# Discovery

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

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5 STUDIES

Search studies by keywords

Study ID Study Name Study Title Source Data Files Subjects

1000\_Genomes\_Project 1000 Genomes Project 1000 Genomes Project 1000 Genomes Project 0

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...

ALIGNED READS

ACCOuNT\_Clopidogrel\_Arm Discovery, Clopidogrel Arm Discovery, Clopidogrel Arm ACCOuNT consortium 167

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...

CCLE CCLE (Cancer Cell Line Encyclopedia) CCLE (Cancer Cell Line Encyclopedia) Broad Institute 104

The CCLE (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...

ALIGNED READS

ds000030 UCLA Consortium for Neuropsychiatric Phenomics UCLA Consortium for Neuropsychiatric Phenomics OpenNeuro 272

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...

IMAGING FILES

GSE63878 Gene Networks Specific for Innate Immunity Define Post-traumatic Stress Disorder [Affymetrix] Gene Networks Specific for Innate Immunity Define Post-traumatic Stress Disorder [Affymetrix] Ichan School of Medicine at Mount Sinai 48

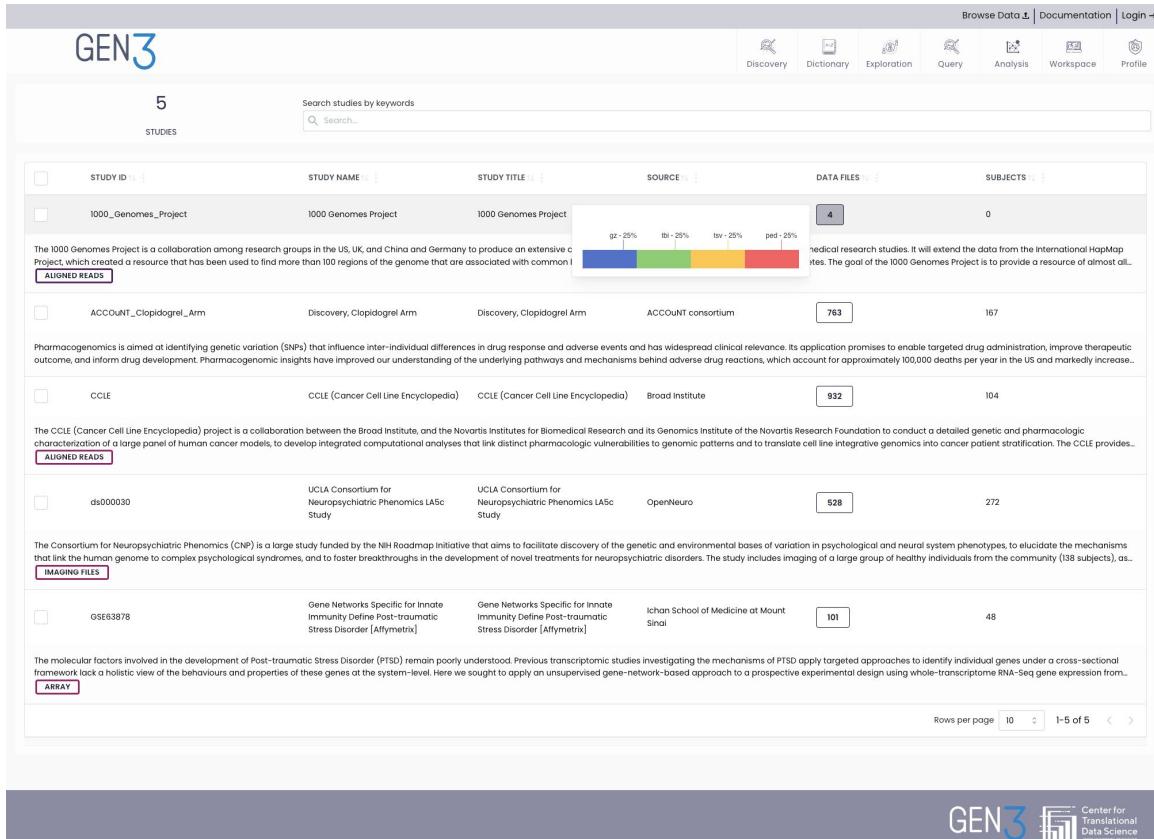
The molecular factors involved in the development of Post-traumatic Stress Disorder (PTSD) remain poorly understood. Previous transcriptomic studies investigating the mechanisms of PTSD apply targeted approaches to identify individual genes under a cross-sectional framework lack a holistic view of the behaviours and properties of these genes at the system-level. Here we sought to apply an unsupervised gene-network-based approach to...

ARRAY

Rows per page 10 1-5 of 5 < >

# Data Renderer Example

## Popup chart renderer manifest field Discovery Table



# Custom Pages

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>
  );
};
```

# Analysis Tool Center

Browse Data | Documentation | Login

Search in Analysis Center

GEN3

Analysis Center | Discovery | Dictionary | Exploration | Query | Network Browser | Profile

### Applications

OmniGenome Commons (Login required)  
Lorem ipsum dolor sit amet consectetur. Viverra in vel natoque at quam euismod sagittis. Leo leo egest tincidunt senectus magna a odio. Dignissim blandit placerat risus arcu.  
[Run App](#) [Demo](#)

DNAData Collaboratory (Login required)  
Lorem ipsum dolor sit amet consectetur. Viverra in vel natoque at quam euismod sagittis. Leo leo egest tincidunt senectus magna a odio. Dignissim blandit placerat risus arcu.  
[Run App](#) [Demo](#)

NucleoNet Exchange (Login required)  
Lorem ipsum dolor sit amet consectetur. Viverra in vel natoque at quam euismod sagittis. Leo leo egest tincidunt senectus magna a odio. Dignissim blandit placerat risus arcu.  
[Run App](#) [Demo](#)

GeneSphere Hub (Login required)  
Lorem ipsum dolor sit amet consectetur. Viverra in vel natoque at quam euismod sagittis.

### Notebooks

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](#)

Canine Data Commons Data Visualization Notebook (Login required)  
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](#)

COVID-19 X-ray images classification (Login required)  
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](#)

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Designed for the health community, the Open Access Data Commons is a scalable, cloud-based platform for computational discovery.  
Dictionary v0.3.0 | Submission v2023.04 | Portal v5.13.0

Browse Data | Documentation | Login

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Analysis Center | Discovery | Dictionary | Exploration | Query | Network Browser | Profile

### 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 model<sup>1</sup> 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/muhammedtal0/COVID-19/blob/master/DarkCovidNet%20for%20binary%20classes.ipynb>. We use data available in Kaggle <https://www.kaggle.com/tawsifurrahman/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.compbiomed.2020.103792). ↗

#### 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
# !pip install fastai
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

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GEN3  
Designed for the health community, the Open Access Data Commons is a scalable, cloud-based platform for computational discovery.  
Dictionary v0.3.0 | Submission v2023.04 | Portal v5.13.0

# Running with data-portal



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~~

# Roadmap

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
```

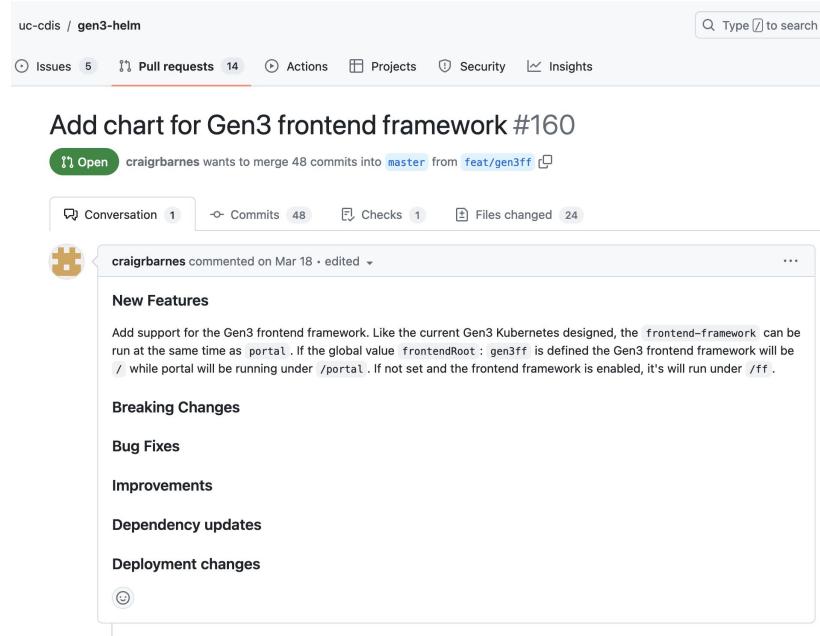


# Local Development Setup

- 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.

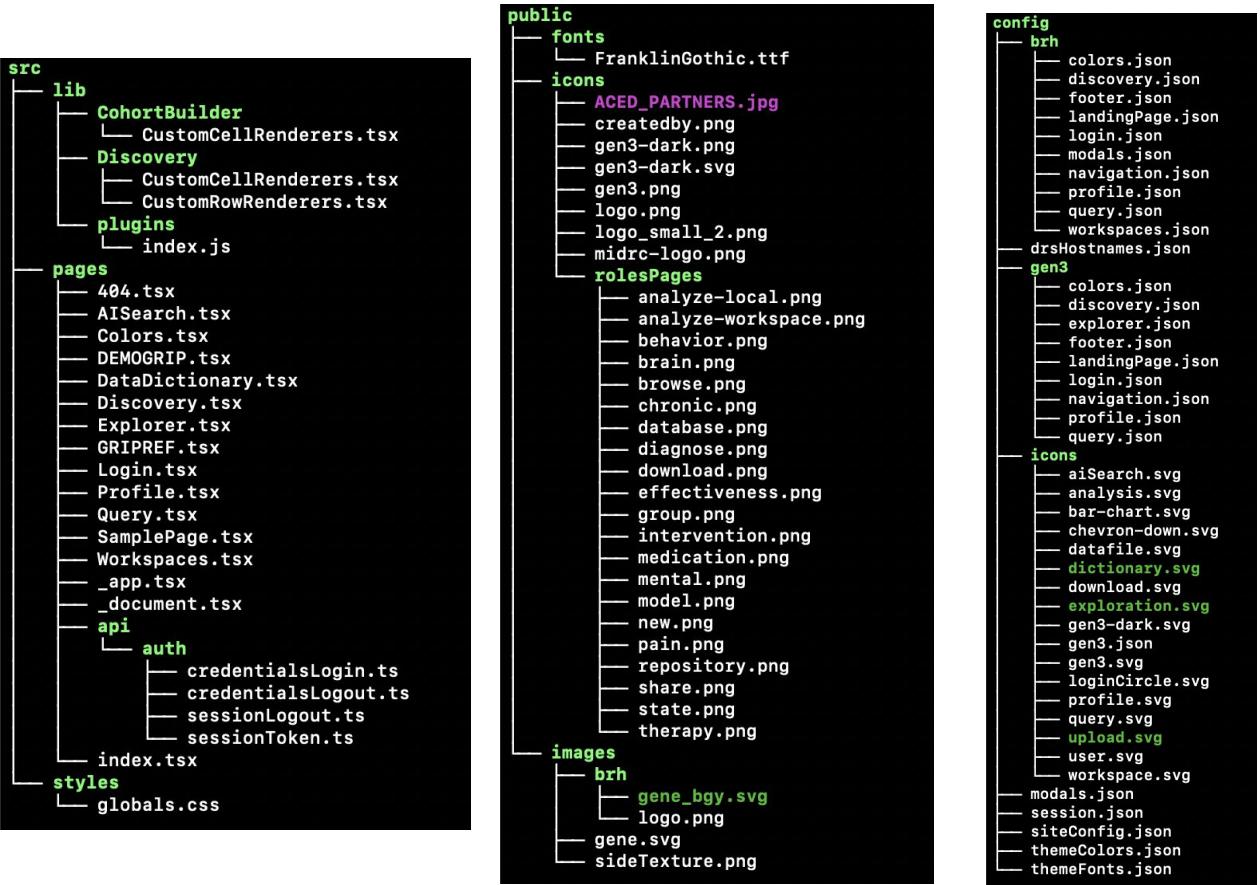
# Deployment Setup

- 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.



# 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



# 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 |
```

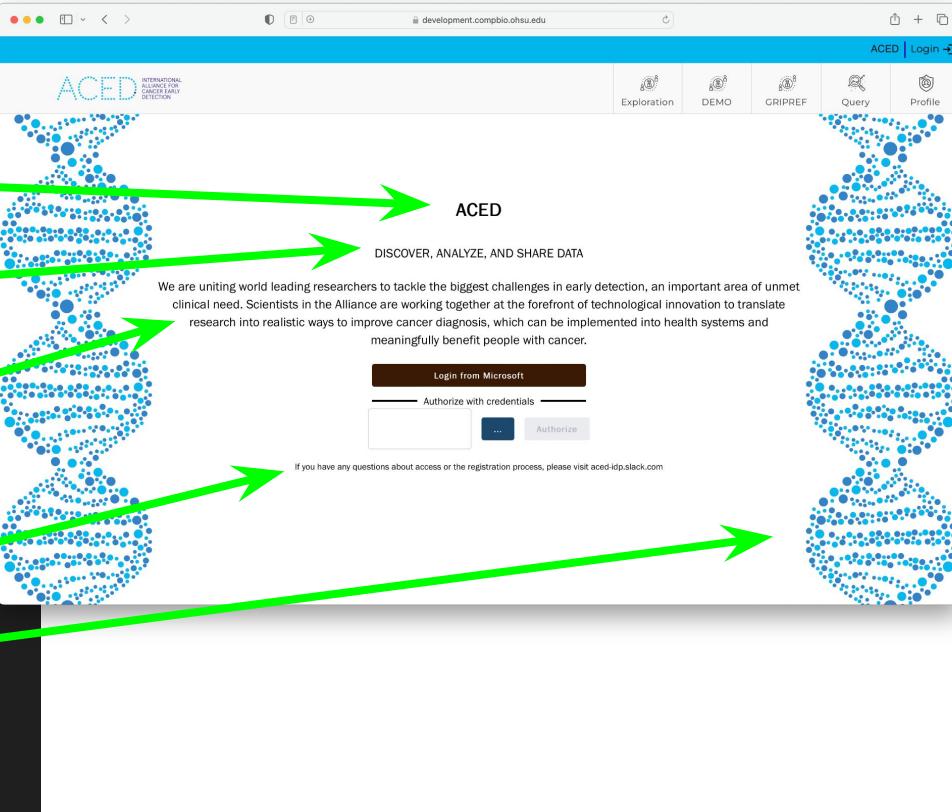
```
packages > sampleCommons > config > {} themeFonts.json > ...
1  {
2    "heading": ["FranklinGothic", "Montserrat", "sans-serif"],
3    "content": ["FranklinGothic", "Noto Sans", "sans-serif"],
4    "fontFamily": "FranklinGothic"
5  }
6 |
```

```
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 registration",
19       "className": "text-center text-sm"
20     }
21   ],
22   "image": "images/gene.svg",
23   "showCredentialsLogin" : true
24 }
25 }
```



# Page Level Configurations

```
[{"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, 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 at. 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](#)



# Gitops Migration

- 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

The screenshot shows a terminal window with two parts. On the left, a JSON configuration file named 'brh.json' is displayed with line numbers 1 through 840. The file contains various configuration objects like 'gaTrackingId', 'graphql', 'components', 'appName', 'index', 'navigation', 'topBar', 'login', 'footerLogos', 'footer', 'categorical9Colors', 'categorical2Colors', 'requiredCerts', 'featureFlags', 'dataExplorerConfig', 'fileExplorerConfig', 'discoveryConfig', and 'useArboristUI'. On the right, a list of generated JSON files is shown, each preceded by a white line and a green 'gen3' label. The files are: colors.json, discovery.json, explorer.json, footer.json, landingPage.json, login.json, navigation.json, profile.json, and query.json.

```
Users > peterkor > Desktop > {} brh.json > ...
1  {
2    "gaTrackingId": "UA-119127212-5",
3    "graphql": {...},
4    "components": {...},
5    "appName": "Biomedical Research Hub",
6    "index": {...},
7    "navigation": {...},
8    "topBar": {...},
9    "login": {...},
10   "footerLogos": [...],
11   "footer": {...},
12   "categorical9Colors": [...],
13   "categorical2Colors": [...],
14 },
15   "requiredCerts": [],
16   "featureFlags": {...},
17   "dataExplorerConfig": {...},
18   "fileExplorerConfig": {...},
19   "discoveryConfig": {...},
20   "useArboristUI": true,
21   "terraExportWarning": {...}
22 }
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gen3

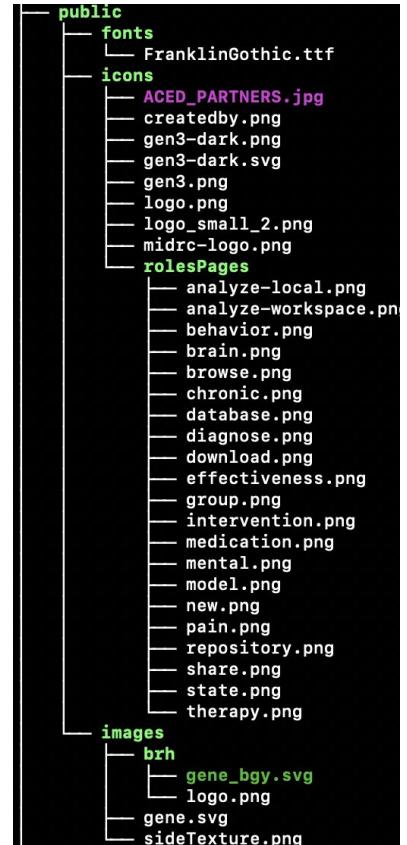
- colors.json
- discovery.json
- explorer.json
- footer.json
- landingPage.json
- login.json
- navigation.json
- profile.json
- query.json

# 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 }
```



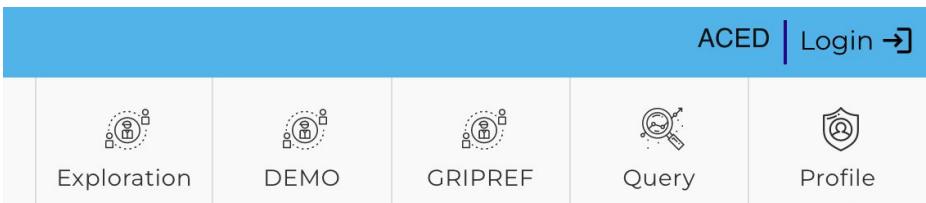
# Before / After

The screenshot shows the original GEN3 Data Platform interface. At the top, there's a navigation bar with links for 'Discovery', 'Dictionary', 'Exploration', 'Query', 'Analysis', 'Workspace', and 'Profile'. Below the navigation is a main content area titled 'GEN3 Data Platform' which describes the platform as a single web interface for discovery, access, and analysis. It highlights features like secondary, cross-study analyses and the democratization of scientific discovery. A large green arrow points from this interface to the ACED interface.

The screenshot shows the ACED interface. At the top, there's a navigation bar with links for 'Exploration', 'DEMO', 'GRIPREF', 'Query', and 'Profile'. The main content area features a large 'ACED' logo with the subtitle 'INTERNATIONAL ALLIANCE FOR CANCER EARLY DETECTION'. Below the logo is a paragraph of placeholder text (Lorem ipsum). At the bottom, there are two call-to-action buttons: 'DISCOVER' and 'ANALYZE', each accompanied by a small icon and a brief description.

# 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;
```

# Linking to Navigation Bar

- 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 enables"
14        },
15        {
16          "icon": "gen3:exploration",
17          "href": "/SamplePage",
18          "name": "DEMO",
19          "tooltip": "The Exploration Page enables"
20        }
21      ]
22    }
23  }
```

# Guppy Api Fetch

- 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
68  const SamplePage = ({ headerProps, footerProps }: SamplePageProps) => {
69    const [items, setItems] = useState<Item>([]);
70    const [isLoading, setLoading] = useState<boolean>(true);
71
72    useEffect(() => {
73      const fetchData = async () => {
74        try {
75          const result: GuppyAPIFetchResult = await guppyAPIFetch({
76            query: query,
77            variables: variables,
78          });
79          setItems(result.data.file);
80          setLoading(false);
81        } catch (error) {
82          console.error('Error fetching data:', error);
83        }
84      };
85
86      fetchData();
87    }, []);
88
```

# Guppy Output Processing

- 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,
78            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 for 'localhost:3010/SamplePage' with the URL 'https://localhost:3010/SamplePage'. The page title is 'ACED | peterkor@ohsu.edu Logout'. The main content area is titled 'Synthetic Data FHIR references' and lists 24 entries, each preceded by a green checkmark and the text 'Subject:'. The entries are organized into four columns:

Column 1	Column 2	Column 3	Column 4
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-f4dd494e39f7	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-ab13-5c21386fbdc	

# Acknowledgements



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  - Claire Rye - New Zealand eScience Infrastructure
  - Plamen Martinov - Open Commons Consortium
  - Michael Fitzsimons - Center for Translational Data Science, University of Chicago