Integrating Analysis Tools with GDC 2.0: Harnessing the Power of the GDC SDK

16 September 2024

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Agenda

- 1. Overview of GDC 2.0
- 2. The GDC SDK & API
- 3. GDC Analysis Tool Challenge
- 4. Resources for Support
- 5. Q&A



2

Overview of GDC 2.0

Cohorts and Analysis Tools



GDC 2.0 Workflow



Step 1: Build and Save Cohort in Cohort-Builder

| NATIONAL CANCER INSTITUTE GDC Data Portal Image: Context and the second sec | ▶ Video Gui ⓒ Cohort Builder 📄 Repo | des र्रेन् Send Feed sitory | lback 🕜 Browse Annotations | Manage Se Q e.g. BRAF | ts 📜 Cart o → Login , Breast, TCGA-BLCA, TCGA-A5-AC | GDC Apps ▼ | |
|---|--|--|----------------------------|--|--|-------------------------------------|--|
| D Brain Cohort Custom ・< | | | | | | | |
| Brain Cohort Custom Clear All GENDER PRIMARY SITE Program PROGRAM TCGA × × | | | | | | | |
| COHORT BUILDER | COHORT BUILDER | | | | | | |
| General | Program | ۹ () ک | Project | د ال | Disease Type | ୯ [] ୨ | |
| Demographic | Name CPTAC EXCEPTIONAL RESPONDERS | Cases \$ | Name ▲ | Cases \$ 1 (0.00%) 366 (0.82%) | Name | Cases 🗘 651 (1.46%) 1 (0.00%) | |
| General Diagnosis Disease Status and History | HCMI MATCH | 24 (0.05%) 7 (0.02%) 652 (1.46%) | TCGA-LGG | 285 (0.64%) | | . (0.00 %) | |

Step 2: Choose Analysis Tool in Analysis Center

Step 3: Cohort Applies to Analysis Tools Automatically

| Analysis Center 🔹 Projects 🚱 Cohort Builder 🥃 Repository | Q e.g. BRAF, Breast, TCGA-BLCA, TCGA-A5-A0G2 |
|---|--|
| Brain Cohort Custom | ✓ 652 CASES |
| | |
| MYC HMGA1 SFRP4 FBLN2 COL3A1 COL1A1 NDRG1 MAFB | |

The GDC SDK and API

Development tools

GDC 2.0 Analysis Tool Software Development Kit (SDK)

- The GDC 2.0 Portal is built on top of the <u>React</u> framework and uses the <u>Redux</u> library for state management
- UI Components are built using the React <u>Mantine</u> library, which provides a responsive design. Apps can use GDC UI Components
- UI Components and Apps interact with the GDC APIs via the SDK
 - Apps can access the core context and their own context using the SDK
 - Apps use *Hooks* to query for cohort information and fetch data from the GDC API
 - Selectors are used to access the state of the Portal's Redux store and get updates when a cohort changes
 - *Actions* are used to update the state of the App such as adding, removing, or clearing filters

App Structure

- Apps are higher-order components (HOC) that are rendered in the Analysis Center
- Each App handles a specific task and can be used to refine and analyze cohorts
- Local and Cohort filters are available to applications
 - Local filters are filters available from the GDC API that are specific to the application and are used to refine the data
 - Cohort filters are filters used to retrieve the active cohort, alter cohorts, or create new cohorts via the Cohort API
- Apps use *Hooks*, *Selectors*, and *Actions* for querying the GDC API and accessing and updating state, respectively
- A Component Library is provided for component re-use

Hooks, Selectors, & Actions

REST/GraphQL

Cohorts

- useGetGenesQuery
- useGetCasesQuery
- useGetSsmsQuery
- • •

onons

- selectCurrentCohort
- selectCurrentCohortFilters
- selectCurrentCohortCaseCount
- updateCohortFilter
- removeCohortFilter
- ...

Filters

- useEnumFacets
- selectRangeFacets
- fetchFacetContinuousAggregation
- fetchEnumFacets

• • •

Projects, Files, Cart

- *useGetProjectsQuery*
- useGetFilesQuery
- addFilesToCart
- removeFilesFromCart
- selectCart

Genomics

- useGenesSummaryData
- selectGenesSummaryDatauseSSMS
- selectSsmsSummaryData
 - ...

Cases

- useCaseSummary
- selectCaseSummaryData
- useAllCases

..

GDC Component Library

https://github.com/NCI-GDC/gdc-frontend-framework

Buttons

20 Save New Cohort Data Service Servic

Vertical Tables

| 0 | Cart | Slides | Case ID 🌲 | Project 🌐 | Primary Site 🗘 | Gender 🌐 | Files 🌲 | Annotations |
|---|------------|-----------|--------------------|-------------|----------------|----------|---------|-------------|
| | | 40 | STARGET-52-PAKHTL | TARGET-RT | Kidney | male | 19 | 0 |
| 0 | X • | 4 | S TARGET-52-PAUCGI | TARGET-RT | Kidney | female | 19 | 0 |
| | X • | 4.0 | S TARGET-52-PATEXW | S TARGET-RT | Kidney | male | 20 | 0 |
| 0 | H • | A | TARGET-52-PATENH | TARGET-RT | Kidney | female | 20 | 0 |
| | W • | (d III) | TARGET-52-PARUGK | TARGET-RT | Kidney | male | 20 | 0 |
| 0 | X • | (A) | S TARGET-52-PAINEZ | IARGET-RI | Kidney | male | 19 | 0 |
| | X • | | S TARGET-52-PASXGE | S TARGET-RI | Kidney | male | 12 | 0 |
| 0 | H • | 4 🖩 | TARGET-52-PAJLRA | TARGET-RT | Kidney | female | 18 | 0 |
| | X * | 40 | TARGET-52-PAVYKD | TARGET-RT | Kidney | female | 8 | 0 |
| 0 | H • | 1 III | TARGET-52-PARZRH | TARGET-RT | Kidney | male | 19 | 0 |

Facets

| | Da | ys | | Years | | |
|---------------------------------|----------------|-------|-------|---------------|--|--|
| | From | ≥ | > | eg90 years | | |
| • | То | 5 | < | eg. 90 years | | |
| | | | Apply | | | |
| Na | ame 🔻 | | | Cases 🛟 | | |
| 0 | ≥ 50 to < 60 y | /ears | | 8,569 (9.90% | | |
| $\bigcirc \ge 40$ to < 50 years | | | | 4,726 (5.46% | | |
| ○ ≥ 30 to < 40 years | | | | 2,259 (2.61%) | | |
| ○ ≥ 20 to < 30 years | | | | 973 (1.12%) | | |
| ○ ≥ 10 to < 20 years | | | | 2,107 (2.44%) | | |
| \bigcirc | ≥ 0 to < 10 ye | ears | | 4,109 (4.75% | | |
| | | | | | | |

- EnumFacet a facet that is used to filter on an enum field
- DateFacet a facet that is used to filter a date field
- NumericRangeFacet a facet that is used to filter on a range field
- PercentileFacet a facet that is used to filter on a percentile field
- AgeRangeFacet a facet that is used to filter on an age range field
- TextFacet a facet that is used to filter a text field
- BooleanFacet a facet that is used to filter on a boolean field

Developing an GDC Analysis Tool

- Clone GDC Portal repository
- Create a new directory in portal-proto/src/features.
- Incorporate hook/selectors/actions from gff/core
- Develop application specific hooks/selectors, app state, and UI components
- Add tests, documentation, and demo
- Register application by adding to the GDC app config:
 - Icon
 - Description
 - Cohort data count hook (if needed)
 - Metadata

Example: Mutation Frequency

Features:

- Local filtering of current cohort
- Interfaces to GDC API via SDK
- Add gene/ssm to current cohort
- Create new cohorts and sets
- Access Gene/SSM Summaries

Mutation Frequency File Structure

- TS types.ts
- TS utils.ts

Application local context/store

- If shared state information is needed this will require use of an Application State
- Enable creation of custom hooks based on redux-toolkit for custom data fetches
- SDK provides a functions to create application scoped redux objects

```
const persistConfig = {
   key: "MutationFrequency",
   version: 1,
   storage,
   whitelist: ["filters"],
};
```

```
const reducers = combineReducers({
  filters: geneFrequencyFiltersReducer,
});
```

```
export const { id, AppStore, AppContext,
useAppSelector, useAppDispatch } =
    createAppStore({
        reducers: persistReducer(persistConfig,
        reducers),
        name: "MutationFrequency",
        version: "0.0.1",
    });
```

export type AppState = ReturnType<typeof reducers>;

Application registration

- Apps need to be registered with the GDC portal in order to be launched from the analysis center
- SDK provides a call to register the app using the root component for the application

```
import { createGdcAppWithOwnStore } from "@gff/core";
import { AppContext, AppStore, id } from
"@/features/genomic/appApi";
import GenesAndMutationFrequencyAnalysisTool from
"@/features/genomic/GenesAndMutationFrequencyAnalysisTool"
;
```

```
export default createGdcAppWithOwnStore({
    App: GenesAndMutationFrequencyAnalysisTool,
    id: id,
    name: "Genes and MutationFrequency",
    version: "v1.0.0",
    requiredEntityTypes: ["gene","ssm"],
    store: AppStore,
    context: AppContext,
});
```

```
export const GenesAndMutationFrequencyAppId: string = id;
```

Anatomy of a Tool Card

Tool Card registration

Register the tool card by adding an entry in:

```
packages/portal-proto/src/features/userflow/workflow/registeredApps.tsx
```

```
name: "Mutation Frequency",
icon: (<MutationFrequencyIcon role="img"</pre>
aria-label="Mutation Frequency icon"
/>),
tags: ["variantAnalysis", "ssm"],
hasDemo: true,
       "MutationFrequencyApp",
id:
countsField: "ssmCaseCount",
description: "Visualize most frequently
mutated genes and somatic mutations.",
noDataTooltip:"Current cohort does not
have SSM data available for
visualization.",
```

}

Developer Resources

- Developers Guide
 - Overview, architecture, and application code walkthrough
- <u>Style Guide</u>
 - Guidelines for color, icons, typography
- API Documentation
 - Generated from the source code
 - Documents SDK functions and not smaller utility functions
- Code has a number of application to use as examples

What is the GDC API?

The GDC API is how we make harmonized clinical and genomic data available.

45,000 Cases

- 650 clinical properties
 - Demographics
 - Diagnosis
 - Treatments
- 200 biospecimen properties
 - Tissue Type (Tumor, Normal, etc.)
 - Tumor Descriptor (Primary, Metastatic, etc.)

1,000,000 Files

- 350 properties
- Experimental Strategy
 - WGS
 - WXS
- Data Category
 - Sequencing Reads
 - Simple Nucleotide Variation
 - Copy Number Variation

Getting Started with the GDC API

Documentation: https://docs.gdc.cancer.gov/API/Users_Guide/Getting_Started/

Basics

- Base URL: <u>https://api.gdc.cancer.gov</u>
- GraphQL endpoint
- RESTful endpoints
- Open-access data is available anonymously
- Controlled-access data requires authorization

Features

- Search and retrieval
- Analysis
- Download

Search and Retrieval

Query by any of the properties, and get properties you want.

- 45,000 cases
- 1,000,000 files
- 1,000 properties

Query Language

- Works with both GraphQL and RESTful endpoints
- Allows caller to define the search criteria

GraphQL

/graphql

RESTful

- /cases
- /files
- /projects

Filter Language

Syntax

```
"op": <OPERATOR>,
"content": {
    "field": <FIELD NAME>,
    "value": <VALUE>
}
```

Example

```
"op": "=",
"content": {
   "field": "demographic.gender",
   "value": "female"
```

Operators

- =, !=
- >, >=, <, <=

Data Analysis

Somatic Mutations

- /ssms
 - 2,900,000 ssms
- /ssm_occurrences
 - 3,300,000 occurrences

Copy Number Variations

- /cnvs
 - 38,000 cnvs
- /cnv_occurrences
 - 75,000,000 occurrences

Genes

/genes

Gene Expression

- /gene_expression/availability
- /gene_expression/gene_selection
- /gene_expression/values

Top Mutated Cases

/analysis/top_mutated_cases_by_gene

Survival Analysis

/analysis/survival

File Download

RESTful

/data

Params

One or more files ids

Single file download

- One file id is requested
- The response is an octet-stream of the file.

Multi-file download

- Multiple file ids are requested
- The response is a tarball of the files.

Example: Single file analysis

- Some files are small enough to fit in a browser
- Seurat analysis for scRNA-Seq

Example: BAM slicing

- /slicing
- Single file download
- Single part range request Range: bytes=1234-5678

GDC API Documentation

More information:

https://docs.gdc.cancer.gov/API/Users_Guide/Getting_Started/

GDC Analysis Tool Challenge

Add your tool to the GDC!

Challenge Goal

Provide the research community with a novel analysis tool to analyze data in the GDC in support of cancer research

Analysis Tool Requirements

- The Analysis Tool shall demonstrate scientific need and innovation beyond the existing GDC Analysis Tools made available in the Analysis Center
- The Analysis Tool must use
 GDC data and be able to
 integrate with the GDC
 using the GDC Analysis Tool
 Software Development Kit
- ✓ The Analysis Tool must be open-source
- **Mutation Signature** Analysis **Copy Number** Variation (CNV) Analysis Structural Variant Analysis **RNA Expression** Analysis **Regulatory Element** Exploration functional enrichment **Pathway & Network** Analysis **Phylogenetic Analysis Integration of Multi-Omics Data** cancer biology Longitudinal Data Visualization Machine Learning for Slide Images

Example Analysis Tool Types

•Tools to identify and interpret mutation signatures in cancer genomes, helping to understand the underlying mutational processes

•Tools for detecting and analyzing copy number variations in cancer genomes to identify amplifications or deletions

•Tools for detecting and characterizing structural variations such as translocations, inversions, and duplications in cancer genomes

•Tools for performing differential expression analysis, alternative splicing, alternative isoform analysis, and single cell RNA-Seq analysis

•Tools for exploring RNA expression profiles for gene regulatory elements, miRNA analysis, methylation data visualization, and functional enrichment

•Tools that analyze the impact of genetic alterations on biological pathways and gene networks relevant to cancer

•Tools to reconstruct the evolutionary history of cancer cells, helping researchers understand tumor heterogeneity and evolution

•Tools that integrate genomics data with other omics data (e.g., transcriptomics, proteomics) to provide a comprehensive view of cancer biology

•Tools that plot clinical, diagnostic images, and genomic data on a time continuum, patient treatments and outcomes over time, and variation and expression plots in relation to time of other events

 Machine Learning algorithms that use tissue or diagnostic slide images for predictive analysis (e.g., cancer prognosis, genomic correlations such as spatial transcriptomics)

Analysis Tool Data

| GDC Data Types | GDC Data Subtypes |
|--|---|
| Whole Exome and Targeted Sequencing | Alignments (BAM) Raw somatic variants (variant caller level; VCF) Annotated somatic variants (variant caller level; VCF + MAF) Ensembled somatic variants (all callers; MAF) Masked somatic variants (all callers; MAF) |
| Whole Genome Sequencing | Alignments (BAM) Raw somatic variants (indels + point mutations; VCF) Copy number segments (TXT) Copy number estimates (TSV) Structural variants (BEDPE + VCF) |
| RNA-Seq | Alignments (genomic, transcriptome, chimeric; BAM) Augmented gene expression counts (counts + normalization; TSV) Splice junctions (TSV) Transcript fusions (BEDPE + TSV) |
| Single cell RNA-Seq | Alignments (BAM) Counts (raw + filtered; MEX) Differential gene expression (TSV) Single cell analysis (PCA, tSNE, UMAP; TSV) Full analysis loom file (HDF5) |
| miRNA-Seq | Alignments (BAM) miRNA expression (TXT) Isoform expression (TXT) |
| Methylation Array | Masked methylation array (IDAT) Methylation beta values (TXT) |

| GDC Data Types | GDC Data Subtypes | | | |
|-----------------------|---|--|--|--|
| ATAC-Seq | Alignments (BAM) | | | |
| SNP6 Genotyping Array | Copy number segment (TXT) Copy number estimate (TXT/TSV) In addition, SNP6 raw array intensities (CEL) files and SNP6 birdseed genotype files (TXT) are not processed, but made available to researchers as is. | | | |
| Genomic Profile | Raw somatic variants (variant caller level; VCF) Annotated somatic variants (variant caller level; VCF + MAF) Copy number estimates (TXT) Structural variants (BEDPE) | | | |
| RPPA | Protein expression quantification (RPPA) (TSV) are not processed but provided to researchers as is | | | |
| Clinical data | Clinical supplement (XML, JSON, TSV, Biotab, XLSX) Pathology report (PDF) Clinical data as GDC node properties | | | |
| Biospecimen data | Biospecimen supplement (XML, JSON, TSV, Biotab, XLSX) Biospecimen data as GDC node properties | | | |
| Imaging data | Tissue slides (SVS) Diagnostic slides (SVS) | | | |

Whole Exome & Targeted Sequencing Analysis Tool Data

| Whole Exome and Targeted Alignments (BAM) Raw somatic variants (variant caller level; VCF) Annotated somatic variants (variant caller level; VCF + N Ensembled somatic variants (all callers; MAF) Masked somatic variants (all callers; MAF) |
|--|
|--|

RNA-Seq Analysis Tool Data

| Alignments (genomic, transcriptome, chimeric; BAM) Augmented gene expression counts (counts + normalization TSV) Splice junctions (TSV) Transcript fusions (BEDPE + TSV) | | |
|---|---------|--|
| | RNA-Seq | Alignments (genomic, transcriptome, chimeric; BAM) Augmented gene expression counts (counts + normalization; TSV) Splice junctions (TSV) Transcript fusions (BEDPE + TSV) |

Analysis Tool Evaluation

- Analysis tools will be evaluated based on the following criteria:
 - ✓ Scientific need
 - Innovation
 - Ability to integrate with the GDC Data Portal and use of GDC data
 - Requirements compliance (e.g., open source)

Winning Tool Integration with the GDC

 Winning tools will be integrated with the GDC Data Portal and will be made available in the <u>Analysis Center</u>

Challenge Timeline

- Phase 1: Challenge Registration
 - 9/1/2024 10/31/2024
- Phase 2: Finalists Tool Integration
 - 1/1/2025 6/30/2025
- Tool Awards & Recognition
 - 10/1/2025 12/31/2025
- How to Enter:

Register Now!

https://www.challenge.gov/?challenge=nci-gdc-analysis-toolchallenge&tab=how%20to%20enter

Resources for Support

Users Guides, Videos, and More!

Analysis Tool Integration

- GDC resources are available for analysis tool integration:
 - <u>GDC Developer's Guide</u> Provides detailed instructions on using the GDC Analysis Tool Software Development Kit (SDK)
 - <u>GDC Frontend Framework GitHub Repository</u> Allows developers to build a local instance of the GDC 2.0 Data Portal to test tool integration
 - ProteinPaint GitHub Repository An example of tool integration
 - <u>GDC API User's Guide</u> Provides examples of how to retrieve and analyze data from the GDC
 - <u>GDC Component Library</u> including a Style Guide Provides guidance for UI components

GDC Developer's Documentation: docs.gdc.cancer.gov

GDC API Search & Retrieval: docs.gdc.cancer.gov

| Home API Data Portal | Data Submission Data Transfer Tool Data Dictionary Data Encyclopedia | | | | |
|---|--|--|--|--|--|
| | | | | | |
| API | Search and Retrieval | | | | |
| Getting Started | | | | | |
| Search and Retrieval Downloading Files Data Analysis | Introducing Search and Retrieval Requests | | | | |
| BAM Slicing | The GDC API provides endpoints that search and retrieve information stored in the GDC | | | | |
| Submission | according to the GDC Data Model. The general format of requests to search & retrieval endpoints | | | | |
| Python Examples | is described below. | | | | |
| GraphQL Examples System Information Additional Examples Appendix A: Available Fields | Note: Queries described in this section work for datasets that have been released to the GDC Data Portal. Unreleased data that is in the process of being submitted to GDC cannot be queried using these methods. See Submission to learn how to query unreleased data using GraphQL. | | | | |
| Appendix B: Key Terms | | | | | |
| Appendix C: Format of Submission Queries and Responses | Components of a Request | | | | |
| Release Notes | A typical search and retrieval API request specifies the following parameters: | | | | |
| Download PDF | • a filters parameter, that specifies the search terms for the query | | | | |
| | several parameters that specify the API response, such as: | | | | |

GDC Website: gdc.cancer.gov

An official website of the United States government

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|--|---|---|
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| Training | Documentation | Get Support |
| GDC Webinars | GDC Data Portal User's Guide | Contact GDC Help Desk ⊠ |
| GDC Tutorial Videos | GDC Data Transfer Tool User's Guide | Join the GDC User Listserv |
| NCI GDC YouTube Playlist 🖻 | GDC Data Submission Portal User's Guide | X Follow us on @NCIGDC_Updates a |
| | GDC API User's Guide | in Subscribe to NCI Precision Oncology 🛚 🌅 |
| | GDC Application Developer Guide | |
| | GDC FAQs | |
| → More about Analyzing Data | | to therapy. |

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1-800-4-CANCER

Produced September 2024