Data Analysis Centers (DACs)

A Data Analysis Center (DAC) is a tool or website which provides additional capabilities for downloading, visualizing or analyzing TCIA data by connecting to our TCIA Programmatic Interface (REST API) or by mirroring our Collections. If you have developed something which meets these criteria please contact the helpdesk so we can add it to this page. We will also work with you to ensure your site/tool provides adequate attributions and links back to TCIA to comply with our Data Usage Policies and Restrictions.

Resource	Description	Functionality	TCIA Data Access	Platform
3D Slicer TCIA Browser extension	3D Slicer (http://slicer.org) is a free and open source platform for medical image visualization and quantitative analysis. The **TCIA Browser extension** of 3D Slicer enables integration of the versatile visualization and computing tools of 3D Slicer with unique data resources of TCIA. Among other capabilities, 3D Slicer enables 2-, 3-, and 4-d visualization tools, DICOM interoperability for both images and image annotations, radiomics feature calculation, multi-modality fusion and deformable registration, a collection of segmentation tools, Matlab and python interface, and integration of such libraries as ITK, VTK, DCMTK and numpy.	Visualization and Analysis	API	Windows, Mac OS X, Linux
CancerImagingArchive.jl	Julia interface for exploring and downloading data on The Cancer Imaging Archive (TCIA)	Data access	API	Windows, Mac OS X, Linux
Clara Train for TCIA Datasets	Clara Train is NVIDIA's domain-optimized application-development framework for medical-imaging researchers and artificial intelligence (AI) developers. Clara Train SDK, which you deploy in a highly available (HA) configuration on the AWS Cloud, includes an AI Assisted Annotation developer toolkit that can be integrated into existing medical viewers, accelerating the creation of AI-ready, annotated medical-imaging datasets. Clara Train also provides a TensorFlow-based training framework with domain-specific pretrained models that accelerate AI development with techniques like transfer learning, federated learning, and automated machine learning. Models trained with Clara Train are packaged as Medical Model Archives (MMARs), which provide a standardized format for training workflows and collaborations. A sample notebook has been created in order to easily import and pre-process TCIA data for analysis with Clara Train.	Data access, Visualization, and Analysis	API	Linux
Community Code Share on Github	If you've developed open source code you'd like to share with the community you can use Github's topic feature to make it discoverable by tagging it with "tcia-dac". Please note these tools are not directly supported by TCIA or its helpdesk.	Data access, Visualization, and Analysis	API / Mirrored	Miscellaneous

DataScope	An open source data exploration and visual analytic tool that uses a declarative grammar to author interactive dashboards. Using a series of JSON files that describe the data, we are able to fuse clinical, radiology and digital pathology data. The TCIA CPTAC Pathology Portal is powered by DataScope.	Data access, Visualization	API	Web application
ePAD	ePAD is a freely available quantitative imaging informatics platform, developed by the Rubin Lab at Stanford Medicine Radiology at Stanford University. Its built-in connection to our REST API allows TCIA data to be seemlessly imported into ePAD for analysis.	Visualization and Analysis	API	Web application
G-DOC Plus	The Georgetown Database of Cancer Plus other diseases (G-DOC Plus) is a precision medicine platform containing molecular and clinical data from thousands of patients and cell lines, along with tools for analysis and data visualization. It contains mirrored data from the BREAST-DIAGNOSIS collection.	Visualization and Analysis	Mirrored	Web application
Google Cloud Healthcare API	The Cloud Healthcare API provides access to TCIA datasets via Google Cloud Platform (GCP) from Cloud Storage, BigQuery, or using the Cloud Healthcare API as described in GCP data access.	Data Access	Mirrored	Web application
MONAI	MONAI (https://monai.io) is a freely available, community-supported, PyTorch-based framework for deep learning in healthcare imaging. It provides deep learning capabilities tailored for healthcare imaging research, development, and deployment. MONAI is part of the larger Project MONAI effort, that includes MONAI Label for AI assisted annotation; MONAI Deploy for packaging, distributing, and deploying MONAI-based applications; and MONAI Tutorials which contains extensive educational and community building resources. MONAI's TCIA Dataset Tutorial describes how patient data (images, lab results, etc.) from NCI repositories such as the IDC and TCIA can be leveraged for MONAI model development and deployment. MONAI is available on cloud services such as Google CoLab and Amazon Sagemaker and across every major operating system and Python version via pip. MONAI Label is also available as a 3D Slicer Plugin.	Data access, Visualization, and Analysis	API	Windows, Mac OS X, Linux
NCI Imaging Data Commons	NCI Imaging Data Commons (IDC) is a cloud-based resource within NCI Cancer Research Data Commons (CRDC) that connects researchers with cancer imaging datasets, resources for exploring those datasets and identifying relevant cohorts, and other components of CRDC that will host additional data types and support computation on the defined cohorts.	Visualization and Analysis	Mirrored	Cloud-based platform
Oncora Medical TCIA boostrapper	Repository with minimal docker compose configuration and script to create a DICOM server with a TCIA collection locally. Can be extended modularly with additional docker images for deep learning experiments.	Data Access	API	Windows, Mac OS X, Linux

Orthanc TCIA Plugin	This plugin extends Orthanc with a Web interface that can be used to import open-data medical images from The Cancer Imaging Archive (TCIA), and serve them immediately using Orthanc. The plugin can be used to import so-called "cart spreadsheet" generated by the NBIA Search Client, or to browse the image collections of TCIA thanks to its REST API.	Data Access	API / Mirrored	Windows, Mac OS X, Linux
PRISM PathDB	PRISM Pathology Data Management Prototype for TCIA	Data access, Visualization, and Analysis	API	Web application
prostatecancer.ai	Tesseract-MedicalImaging (Tesseract-MI) is an open-source, web-based platform which enables deployment of AI models while simultaneously providing standard image viewing and reporting schemes. The goal of Tesseract-MI is to augment 3D medical imaging and provide a 4th dimension (AI) when requested by a user. As a case study, we demonstrate the utility of our platform and present **ProstateCancer.ai** (see also: https://github.com/Tesseract-MI/prostatecancer.ai), a web application which uses data from SPIE-AAPM-NCI PROSTATEx Challenges (PROSTATEx) for identification of clinically significant prostate cancer in MRI. The user can put the AI-assisted probe at any location on the images to see the result of the AI prediction for that specific location. For the reporting, the user can utilize the PI-RADS v2 interface which is provided. All the user's annotations will be saved in a database for further analysis.	Visualization and Analysis	Mirrored	Web application
pylidc	`pylidc` is a python library intended to improve workflow associated with the LIDC dataset.	Visualization and Analysis	N/A	Windows, Mac OS X, Linux
Seven Bridges Cancer Genomics Cloud (CGC)	An NCI-funded platform that is available to any non-commercial researcher for cloud-based data access and analysis. Through the CGC, users can access petabytes of public data, including select collections from TCIA, as well as hundreds of bioinformatic tools and workflows for scalable, cost-effective analysis in the cloud alongside their own data.	Data Access, Visualization, Analysis	Mirrored	Web application
tciaclient	This Python package uses the official TCIA REST API to enable downloads from www.cancerimagingarchive.net from within Python scripts and Jupyter Notebooks. The documentation can be found at https://moritzschwyzer.github.io/tciaclient/. This PyPI/Conda package is based on source code of the TCIA-API-SDK https://github.com/TCIA-Community/TCIA-API-SDK.	Data Access	API	Windows, Mac OS X, Linux
TCIApathfinder	A user-friendly R client for the TCIA REST API	Data access	API	Windows, Mac OS X, Linux

TCIA-Python3-Downloader	A python3 client designed to provide users of The Cancer Imaging Archive with the ability to easily interact and download data from the TCIA Programmatic Interface (REST API).	Data Access	API	Windows, Mac OS X, Linux
Zegami	Zegami helps easily find patterns, outliers and trends in large, curated image data sets, and uncover bias, overfitting and misclassifications in machine learning models, to assist with providing explainability of your Machine Learning models. Our scalable, cloud-based platform is powered by an image rendering engine and based on gaming technology. It can display tens of thousands of images (static or dynamic) over low bandwidth connections, and supports a wide variety of image and video formats . **Our solution helps with:** • Preparing high quality, unbiased and diverse training data sets • Reducing time-consuming data preparation and cleansing processes, enabling faster ROI • Un-blackboxing your ML models to achieve explainability • Benchmarking your model's predictive power vs. the gold standard • Validating your models to assist with achieving regulatory compliance • Lifecycle management of AI and monitoring of performance over time Check this publicly available demo using the CBIS-DDSM dataset sourced from TCIA: https://zegami.com/demo/dicom-mammograms/	Visualization, Analysis	Mirrored	Web application