Introduction to Bioinformatics Resources at NIH

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Bioinformatics Training and Education Program

NIH NATIONAL CANCER INSTITUTE
Center for Cancer Research

The only thing you need to remember today:

ncibtep@nih.gov

What we're going to cover.

- The NCI Center for Cancer Research (CCR) Bioinformatics Training and Education Program (BTEP) and NIH Bioinformatics Calendar
- NIH High-Performance Compute Cluster (Biowulf)
- NCI – only Frederick based Compute Cluster (FRCE)
- NIH Library – Bioinformatics Workstations, Classes, Software, Expert Assistance
- Cloud – NIH STRIDES Program Cloud Lab, NCI CRDC (CGC, ISB-Gateway), HTAN, AnVIL (NHGRI), NIGMS Sandbox
- Production Workflows (NCI) – CCBR Github, NIDAP
- Software Licenses – Partek Flow, Qiagen Pathway Analysis, SnapGene, etc.
- Free NIH-wide Licenses – Anaconda, Coursera
- NCI CCR – Dataquest licenses
- NIH List Servs and Teams

Bioinformatics Training & Education Program

https://bioinformatics.ccr.cancer.gov/btep

NCI Center for Cancer Research Bioinformatics Training and Education Program (BTEP)

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AI in Biomedical Research at NIH Seminar Series	Bioinformatics Bulletin	Class Documentation & Resource Pages	Distinguished Speakers Seminar Series
Licenses to Online Learning Platforms	Monthly Coding Clubs	NIH Bioinformatics Calendar	Office Hours - in person and virtual
	Training	Video Archive	

Contact us ncibtep@nih.gov

bioinformatics.ccr.cancer.gov/btep

Our goal is to enable scientists to understand and analyze their own experimental data by providing instruction and training in bioinformatics software, databases, analyses techniques, and emerging technologies.

NCI CCR Bioinformatics Training and Education Program (BTEP)

Began in 2012 to provide training in bioinformatics software

In 2024, 80+ classes with over 2,000 attendees

NATIONAL CANCER INSTITUTE
Center for Cancer Research

Home | Seminar Series | Announcements | Training | Resources | Contacts | My Account

Bioinformatics Training and Education Program

ncibtep@nih.gov

Bioinformatics Training & Education Program

Enabling scientists to understand and analyze their own experimental data by providing instruction and training in bioinformatics software, databases, analyses techniques, and emerging technologies.

Upcoming Classes & Events →

Provide feedback

Classes & Events

Browse Classes, Special Events, and Series Webinars.

Browse Class Schedule

Bioinformatics Resources

Class Documentation, Core Facilities, and Software.

Resources & Software

Bioinformatics Forums

Ask Questions about Bioinformatics Topics.

Questions & Answers

Video Archive

Class and Webinar Recordings and Transcripts.

Watch Videos

bioinformatics.ccr.cancer.gov/btep

Upcoming Classes & Events

NIH Bioinformatics Calendar

bioinformatics.ccr.cancer.gov/btep

Although we are a NCI/CCR resource…

- Most of our events are open to all at NIH
- Our website is open to the world
- We answer questions within and outside of NIH
- Video Archive is open and available
- Class documentation and bioinformatics resources info are open
- We advertise our events throughout NIH

Where should I do my work?

LOCAL

HPC

CLOUD

What is Local?

Your NIH laptop or desktop

What can you do on your local machine?

- Run Data Analysis Software (CLC Genome Workbench, SnapGene, Qiagen Pathway Analysis)
- Connect to HPC (high-performance cluster) via SSH or GUI
- Learn at your own pace (programming, bioinformatics, data science, AI) on Coursera
- Access the cloud

What is HPC (High-Performance Cluster)?

Biowulf (NIH)

FRCE (Frederick)

hpc.nih.gov

Should I work on my local machine or Biowulf?

Working on Biowulf – Things to Know

- hpc.nih.gov
- Minimal, fixed monthly cost
- Thousands of scientific applications (software) available
- Reference Data (NCBI db, BLAST db, genomic alignment data)
- Login/head node
- Learn some beginner Unix (Command Line)
- Your home directory and your data directory
- Start an interactive node (sinteractive)
- Setting up swarm jobs (repetitive jobs)
- Running batch jobs (scripts/programs)
- Moving big data (Globus)
- https://bioinformatics.ccr.cancer.gov/docs/resources-for-bioinformatics/Biowulf/
- HPC on Demand GUI (RStudio, VSCode, JupyterNotebook, IGV, Matlab)

Frederick Research Computing Environment (FRCE)
NCI only

Available within NCI at no cost, optimized for Frederick researchers

250+ scientific applications installed

Next Gen Sequencing, structural biology, cryogenic electron microscopy, imaging and AI, text mining

Log in ssh or GUI, file transfers with Globus, batch and interactive jobs

https://ncifrederick.cancer.gov/staff/frce/

NIH Library

- Expert assistance (statistics, bioinformatics)
- Bioinformatics workstations
- Software (Partek Flow, CLC Genomics Workbench, Matlab)
- Classes in programming, statistics, and data analysis

NIH Library Training Classes: December 2024 and January 2025

Register now for NIH Library Training classes being offered in December and January!

nihlibrary.nih.gov

Cloud

- NCI Cloud Resources
- NIH STRIDES Initiative – NIH Cloud Lab
- NHGRI AnVIL

How is the Cloud different from HPC?

- Cost based on usage
- Flexible compute power
- Analyze publicly available data

How is Cloud similar to HPC?

- Large compute resources
- Pre-installed software and tools
- Bioinformatics and data science analyses
- Analyze your own data

Publicly Available NCI Cloud Resources

- Cancer Research Data Commons (CRDC)
- Cancer Genomics Cloud/7Bridges/Velsera
- ISB Gateway in the Cloud/CGC
- Human Tumor Atlas Network (HTAN)

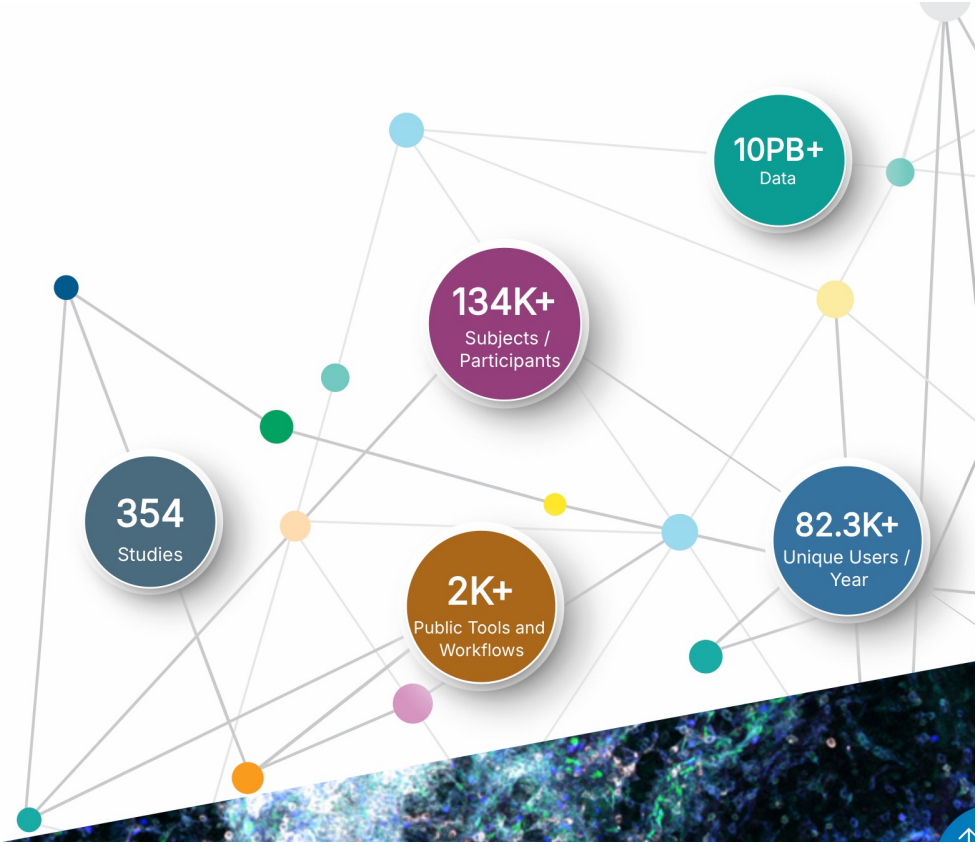
NCI Cancer Research Data Commons

Connecting Data to Accelerate Cancer Research

The NCI Cancer Research Data Commons (CRDC) is a cloud-based data science infrastructure that provides secure access to a large, comprehensive, and expanding collection of cancer research data. Users can explore and use analytical and visualization tools for data analysis in the cloud.

Watch CRDC Video

datacommons.cancer.gov



NCI Cancer Research Data Commons

Explore

DATA COMMONS

Genomic Data Commons (GDC)
Share, analyze, and visualize harmonized genomic data, including TCGA, TARGET, and CPTAC.

Proteomic Data Commons (PDC)
Share, analyze, and visualize proteomic data, such as CPTAC and The International Cancer Proteogenome Consortium (ICPC).

Imaging Data Commons (IDC)
Share, analyze, and visualize multi-modal imaging data from both clinical and basic cancer research studies.

Integrated Canine Data Commons (ICDC)
Share data from canine clinical trials, including the PRE-medical Cancer Immunotherapy Network Canine Trials (PRECINCT) and the Comparative Oncology Program.

Cancer Data Service (CDS)
Store and share NCI-funded data that are not hosted elsewhere to further advance scientific discovery across a broad range of research areas.

Clinical and Translational Data Commons (CTDC)
Store and share data from NCI-funded Clinical and Translational Studies.

CORE STANDARDS AND SERVICES

Cancer Data Aggregator (CDA)
Enables users to query and connect data distributed across the CRDC for integrative analysis.

Data Standards Services (DSS)
Provides services to facilitate interoperability of data across CRDC.

Data Commons Framework (DCF)
Provides secure user authentication and authorization and permanent digital object identifiers for data objects.

datacommons.cancer.gov

NCI Cancer Research Data Commons

CLOUD RESOURCES

Broad Institute FireCloud

Access NCI-funded datasets TARGET and TCGA along with a rich collection of other datasets and collaborative projects that are part of the biomedical ecosystem. Run analysis tools at scale and collaborate securely on a scalable cloud environment.

Seven Bridges Cancer Genomics Cloud developed by Velsera (SB-CGC)

Explore and analyze large datasets alongside secure and scalable analytical resources for large-scale computational research.

ISB Cancer Gateway in the Cloud (ISB-CGC)

Access data sets using fully interactive web-based applications, including BigQuery, which is hosted on Google Cloud Platform.

datacommons.cancer.gov

Seven Bridges Cancer Genomics Cloud/Velsera

cancergenomicscloud.org

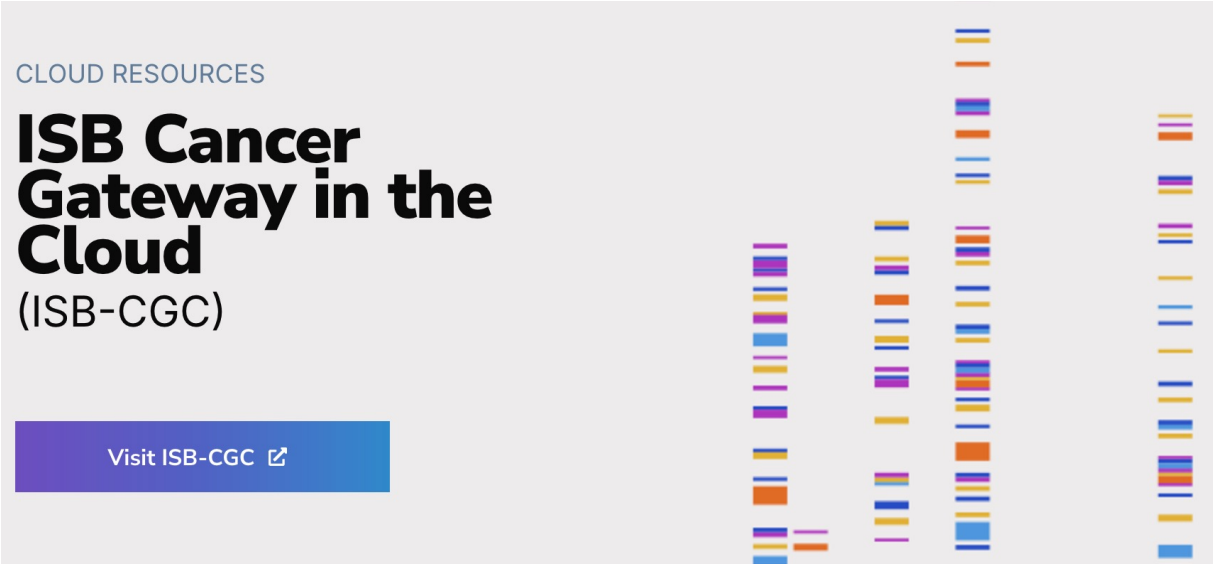
Cancer Genomics Cloud (CGC) SBR/Velsera

- Users can access:
  - Genomics data
  - Proteomics data
  - TCGA data
  - Data from multiple species
  - Their own data
  - Tool Library (850+)
  - Common Workflow Language (CWL)
  - Bring your own pipeline or tools
  - Jupyter Lab and Rstudio available

cancergenomicscloud.org

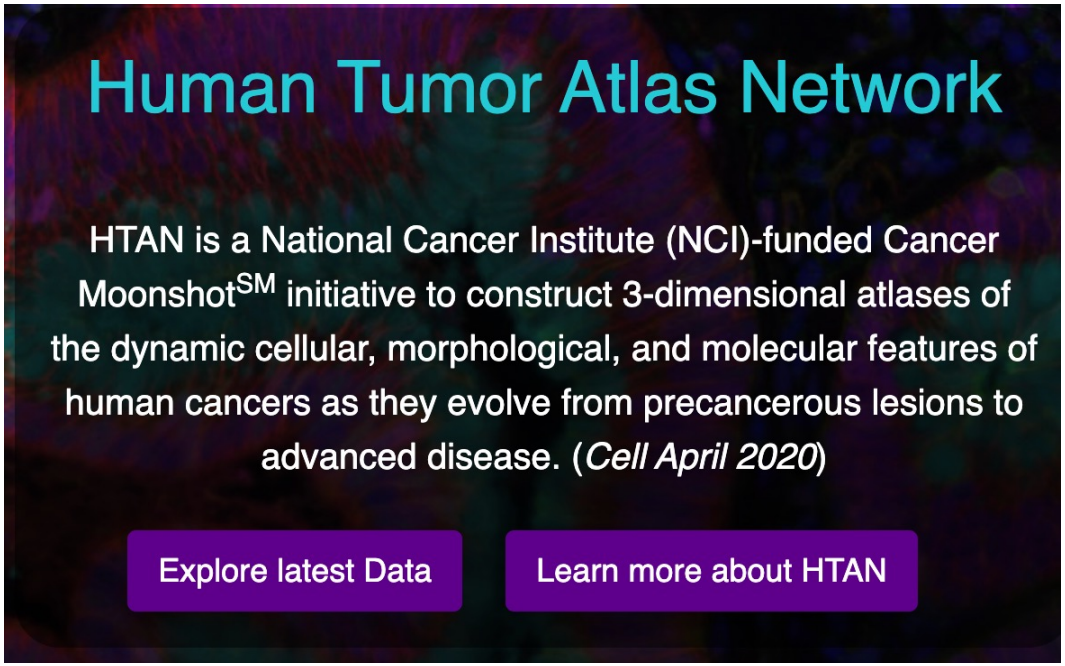
ISB Cancer Gateway in the Cloud (ISB-CGC)

- GoogleBigQuery – query across multiple data tables
- TCGA and TARGET data



https://datacommons.cancer.gov/analytical-resource/isb-cancer-gateway-cloud

Human Tumor Atlas Network

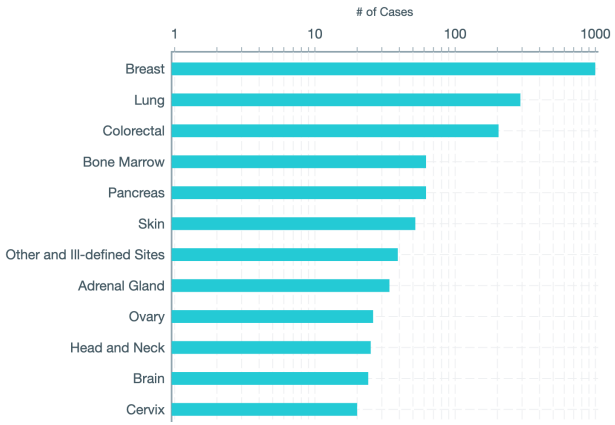


humantumoratlas.org

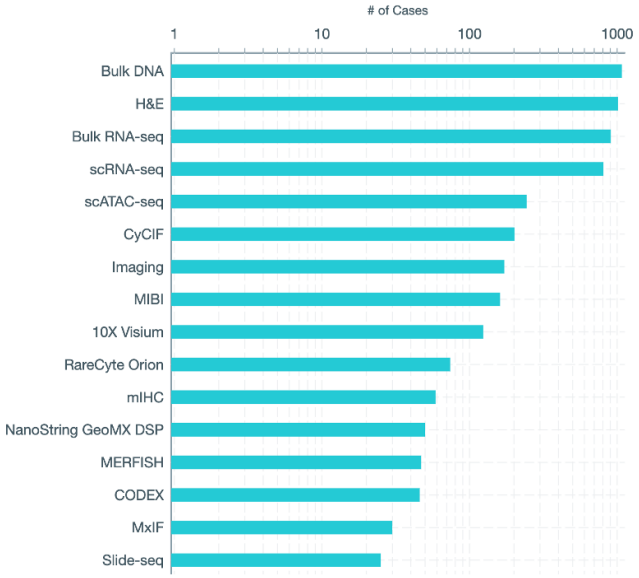
Human Tumor Atlas Network Organs and Assays

14	21	2147	9286
Atlases	Organs	Cases	Biospecimens

The latest HTAN data release includes tumors originating from **21** tumor sites:



The tumors were profiled with **30** different types of assays:



humantumoratlas.org

NIH STRIDES Iniative

- Accelerating Biomedical Research
- NIH Office of Data Science Strategy (ODSS)
- cloud.nih.gov
- NIH Cloud Lab

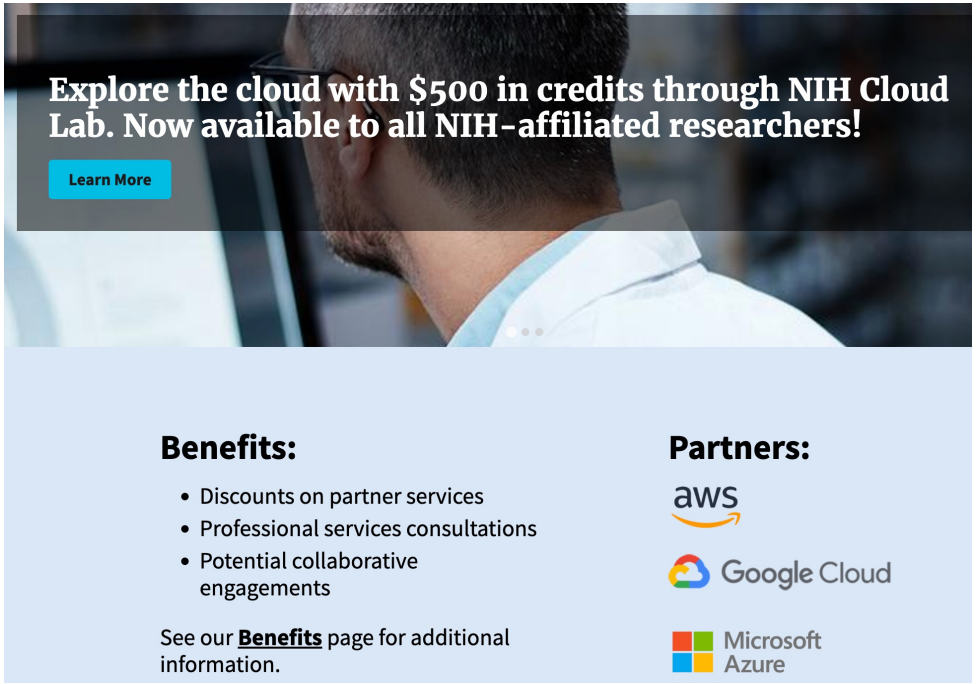
NIH STRIDES Initiative

The STRIDES Initiative aims to help NIH and its institutions accelerate biomedical research by reducing barriers in utilizing commercial cloud services. This initiative aims to harness the power of the cloud to accelerate biomedical discovery. NIH and NIH-funded researchers can take advantage of STRIDES benefits.

Enroll Now

cloud.nih.gov

NIH STRIDES Cloud Lab



cloud.nih.gov

NHGRI Analysis Visualization and Informatics Lab-space (AnVIL)

anvilproject.org

Free trials available

Tools

Dockstore – create and share docker-based workflows

NCPI – interoperate with other NIH data commons

Bioconductor

Galaxy

Jupyter (python, R)

Data sources

Telomere-to-telomere genome (T2T)

1000G thousand genomes

Genotype-tissue expersion project (GTEx)

Workflows (pipelines)

CCBR Workflows

bioinformatics.ccr.cancer.gov/ccbr

CCBR Pipelines and NIDAP (NIH Integrated Data Analysis Platform)

- CCBR pipelines (github/NIH)
- CCBR NIDAP (NIH)
- Free to use
- Consult CCBR in planning stage of experiment
- Don’t wait til you have data
- Submit help request for analysis project
- bioinformatics.ccr.cancer.gov/ccbr

Next Gen Seq Workflows/Pipelines
CCR Collaborative Bioinformatics Resource (CCBR)

github.com/ccbr

About Us

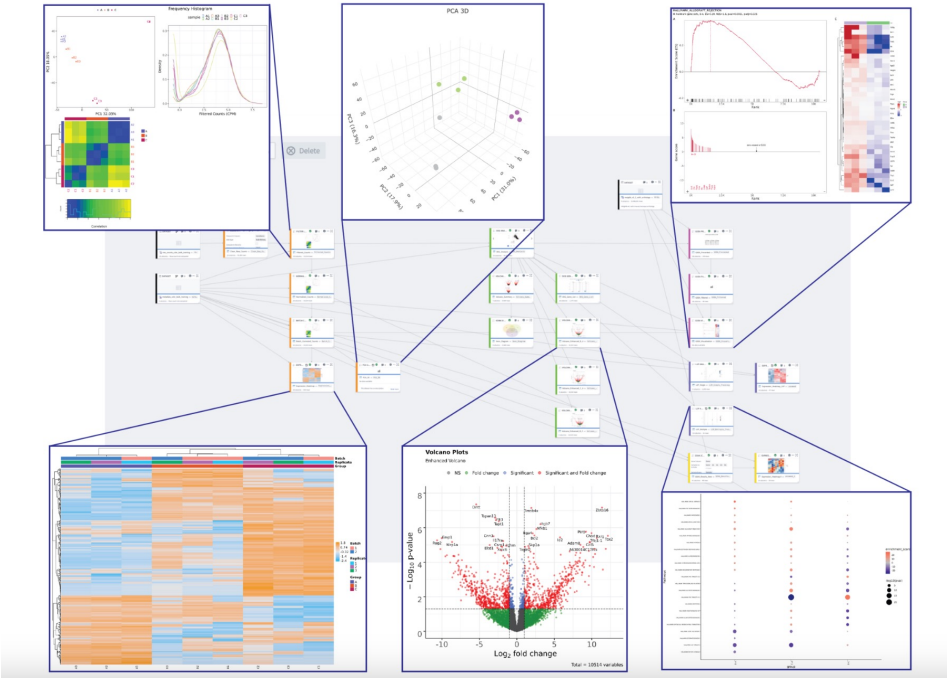
- 👋 Hi, we're the **@CCBR**, a group of bioinformatics analysts and engineers
- 📖 We build flexible, reproducible, workflows for next-generation sequencing data
- 💡 We collaborate with CCR PIs
- 📫 You can reach us at ccbr_pipeliner@mail.nih.gov
- 🏁 Check out our release history
- 🔗 Our Zenodo community

Available NGS Pipelines/Workflows

Here is a list of our prominent pipelines and their release schedule on BIOWULF:

Data Type	Pipeline Name	CLI* availability date	GUI* availability date
RNASeq[1]	RENEES snakemake	July 3rd 2023	July 14th 2023
WESSeq[2]	XAVIERS snakemake	July 21th 2023	Sep 1st 2023
ATACSeq[3]	ASPENS snakemake	November 30th 2023	TBD
ChIPSeq[4]	CHAMPAGNE nextflow	October 15th 2023	TBD
CRISPRSeq[5]	CRISPIN nextflow	September 31st 2023	TBD
CUT&RunSeq[6]	CARLISLES snakemake	October 31st 2023	TBD
EV-Seq[10]	ESCAPES snakemake	March 26th, 2024	TBD
circRNASeq[7]	CHARLIES snakemake	*Jul 31st 2024*	TBD
scRNASeq[8]	SINCLAIR nextflow	*Sep 30th 2024*	TBD
WGSSeq[9]	LOGAN nextflow	*Sep 30th 2024*	TBD
spatialSeq[11]	SPENCER nextflow	TBD	TBD

Bulk RNA-Seq Analysis on NIDAP (NIH Integrated Data Analyis Portal)



https://bioinformatics.ccr.cancer.gov/ccbr/education-training/nidap-training/

Commercial Software Available (NCI)

- Partek Flow – RNA-Seq, CITE-Seq, ATAC-Seq (also available to NIH via NIH Library)
- Qiagen Ingenuity Pathway Analysis (IPA) – from differential expression analysis (DEA) to pathways, biomarkers, drug targets (also available to NIH via NIH Library)
- CLC Genomics Workbench (also available to NIH via NIH Library)
- Qlucore Omics Explorer – RNA-Seq, visualizations, statistical analysis (NCI only)
- Request access at service.cancer.gov (NCI)
- SnapGene – molecular biology (alignment, PCR primers, cloning) (NCI only)

Free licenses for all at NIH

Anaconda - flexible python and R environment

Coursera - learning platform

Anaconda

What is Anaconda?

A distribution of the Python and R programming languages that aims to simplify package management and deployment (wiki)

”The operating system for AI”

The National Institutes of Health (NIH) offers a free Anaconda license to its employees and contractors. The license includes:

Technical support from the NIH Anaconda team

Access to secure, curated, and encrypted Python and R packages

Data science courses led by experts

Sample notebooks and extensions

Jupyter notebooks that are ready to code

Anaconda License Request Form

Training: Coursera licenses are available to all NIH, provided by NIH ODSS

- Free for everyone at NIH
- Video lectures
- Work at your own pace
- Large, worldwide, online classes (MOOCS)
- Courses, specializations, and guided projects
- Earn certificates for your resume/CV
- So many courses (thousands) available: Programming (R, Unix, Python), Genomics, Bioinformatics, Data Science, Language learning, AI
- https://bioinformatics.ccr.cancer.gov/btep/self-learning/

Dataquest (NCI CCR only)

- Dataquest.io
- Programming – Python, R, Unix/Bash, SQL, PowerBI, Excel, AI
- Provides interface for typing in code
- Free to NCI Center for Cancer Research only

list.nih.gov Interest Groups and Mailing Lists

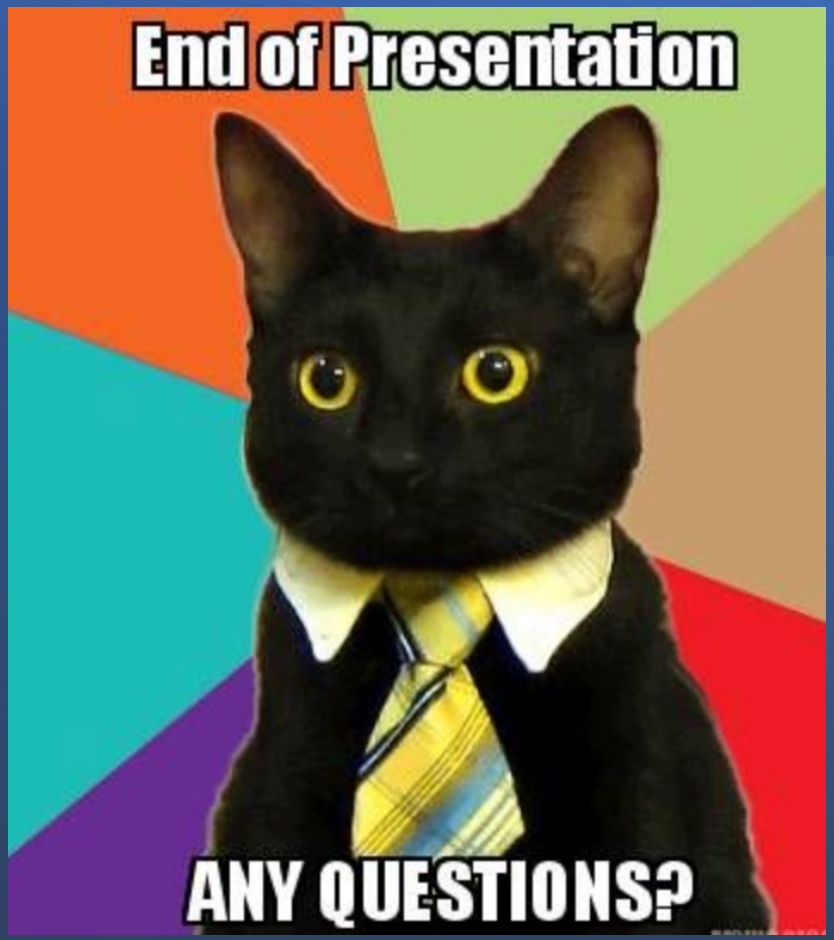
ARTIFICIAL-INTELLIGENCE

BIOINFORMATICS-SIG-L

DATA-SCI ICE

SINGLECELLGENOMICS (AND SPATIAL TRANSCRIPTOMICS)

SYSBIOSIG-L



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