Analyzing your data WITHOUT coding experience: CCR Bioinformatics Licensed Software

Center for Cancer Research

BTEP

Bioinformatics Training & Education Program

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Bioinformatics Training and Education Program

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Event Overview

Event Description

Analyzing your data WITHOUT coding experience: Bioinformatics Licensed Software is a two-hour event featuring four guest speakers from popular commercial software accessible by individuals affiliated with the Center for Cancer Research (CCR). Guest speakers will outline the types of analyses / workflows (e.g., Variant analysis, RNA-seq, CITE-seq, ATAC-seq, ChIP-seq, scRNA-seq, etc.) possible with featured software. Each presentation will be approximately 30 minutes and include a 5 minute question and answer session.

Presentation Schedule:

1. 1:00 - 1:30 PM Partek Flow
2. 1:30 - 2:00 PM QIAGEN CLC Genomics Workbench
3. 2:00 - 2:30 PM Qlucore Omics Explorer
4. 2:30 - 3:00 PM NIH Integrated Data Analysis Platform (NIDAP)

Questions

If your question(s) remain unanswered following the event, please email us at ncibtep@nih.gov *(mailto:ncibtep@nih.gov)* and we will submit your question to the appropriate speaker.

Recordings

The event will be recorded and made available on the BTEP Video Archive *(https:// bioinformatics.ccr.cancer.gov/btep/btep-video-archive-of-past-classes/)* 24 to 48 hours following the event.

Additional Software

Interested in additional licensed software? Check out the BTEP resource pages *(https:// bioinformatics.ccr.cancer.gov/docs/resources-for-bioinformatics/software/)* for more information.

NIDAP

NIH Integrated Data Analysis Platform (NIDAP)

NIDAP is an innovative, cloud-based, collaborative data aggregation and analysis platform that hosts user-friendly bioinformatics workflows and component analysis and visualization tools developed by the NCI developer community based on open source tools and makes them immediately available to biologist end-users across NIH.

> **Why NIDAP?**
>
> 1. **Expandability & Flexibility** Workflows can be rearranged or created bespoke for specific analysis needs.
> 2. **Reproducibility** Results are reproducible and portable by anyone once extracted to GitHub; Open Source Code.
> 3. **Education** Users can learn both the biology and the code behind an analysis to the depth they desire with trainings and access to CCBR expert collaboration.
>   --- Event Speaker, Josh Meyer, PhD (Bioinformatics Analyst (CCBR))

Access NIDAP

License type: NIH wide

To access NIDAP:

1. You must be on the NIH network or NIH VPN.
2. Navigate to nidap.nih.gov
3. Login with NIH credentials
4. Fill out initial form.
5. **Recommended:** Check out the NIDAP documentation *(https://nih.sharepoint.com/sites/ NCI-CCR-CCBR-NIDAP/SitePages/NIH-Integrated-Data-Analysis-Platform-(NIDAP).aspx? csf=1&web=1&e=f6xGsT&CID=70c092a1-9089-8000-7a4c-6275e0787aa8&cidOR=SPO)*, which includes detailed training videos before getting started.

Event Slides and Other Resources

1. Slides: NIH Integrated Data Analysis Platform (NIDAP)

Additional Information

Additional information on NIDAP workflows can be found on the CCBR *(https:// bioinformatics.ccr.cancer.gov/ccbr/education-training/nidap-training/)* and BTEP *(https:// bioinformatics.ccr.cancer.gov/btep/training/nidap-training/nidap-workflows/)* websites.

There is also a NIDAP Community GitHub page *(https://github.com/NIDAP-Community)*.

Partek

Partek Flow

Partek Flow is a graphical user interface (GUI) based bioinformatics software that is dedicated to the analysis of next generation sequencing (NGS) data.

> **Why Partek Flow?**
>
> 1. Partek Flow is compatible with all major genomic formats and assays (including integrating different assays) for your complete analysis needs. There is no need to navigate the command line but you still get the same level of control. Save time using the easy point and click interface while analyzing data from start to finish.
> 2. Partek has many tools, some specific to Partek, some industry standard 3rd party tools. The platform also welcomes user tools.
> 3. Partek Flow can also be used to create publication quality, interactive visualizations as well as rigorous statistics and comprehensive tools to help you make the most out of your data.
> 4. It's easy to share projects and data (with no limitations on the size of the data) with collaborators.
>   --- ** Event Speaker, Alex Rutkovsky, PhD (Field Application Scientist, Partek Flow)**

Access Partek Flow

Partek Flow licenses are available for NCI researchers. NIH-wide Partek Flow licenses accessible through the NIH library were terminated in April 2025.

To obtain a license:

1. Get an NIH HPC account *(https://hpc.nih.gov/docs/accounts.html)*
2. Ensure you have enough space in `/data/username` on Biowulf to hold Partek Flow files. You can request additional space here *(https://hpcnihapps.cit.nih.gov/auth/dashboard/storage_request.php)*.
3. Contact staff@hpc.nih.gov *(mailto:staff@hpc.nih.gov)* to get your Partek Flow account activated.
4. Navigate to https://partekflow.cit.nih.gov/flow *(https://partekflow.cit.nih.gov/flow)* to start using Partek Flow

> **Note**
>
> You must be on the NIH network or connected via VPN to use Partek Flow.

Event Slides and Other Resources

1. Slides: Introduction to Partek Flow

Additional Information

Check out additional information on Partek Flow, including useful links, in the BTEP Resource pages *(https://bioinformatics.ccr.cancer.gov/docs/resources-for-bioinformatics/software/ partek_flow/)*.

Qlucore

Qlucore Omics Explorer

Qlucore Omics Explorer (Qlucore) is a graphical user interface (GUI) based package used for -omics data anlaysis. Qlucore Omics Explorer can analyze many types of -omics data that are in tabular format (e.g., RNA seq count table, protein expression table, etc.).

> **Note**
>
> CCR does not have a license for the optional NGS module. Please contact us at ncibtep@nih.gov if you are interested in this module.

> **Why Qlucore?**
>
> 1. Designed for biologists to get up to speed and advance with data handling as quickly as possible (no coding + minimal wizards).
> 2. Truly visualization-driven analysis - fast, instant, interactive every step of the way, even including statistical analysis and Machine Learning!.
> 3. Intuitive and flexible GUI - different options for many operations to support your hypothesis testing and exploratory based analyses.
> 4. Flexible data import options for your data, and direct public access to TCGA and GEO. It is also easy to share analyses and save sessions.
>   --- Event Speaker, Yana Stackpole, PhD (Sales and Support Manager, Qlucore)

Access Qlucore Omics Explorer

License type: CCR wide

You must submit a request through service.cancer.gov *(https://service.cancer.gov/ncisp)* to obtain access to Qlucore Omics Explorer. This software requires access to a floating license server (OSTR has 5 licenses). Please be sure to close the application when you are finished so the license becomes available to others. To use Qlucore Omics Explorer, a connection to the NIH network or VPN is necessary.

Event Slides and Other Resources

1. Slides: Qlucore Omics Explorer
2. Qlucore Omics Explorer v3.8 Features Overview

Additional Information

Check out additional information on Qlucore Omics Explorer, including useful links, in the BTEP Resource pages *(https://bioinformatics.ccr.cancer.gov/docs/resources-for-bioinformatics/software/qlucore/).*

Techincal Support

Contact Yana Stackpole (Qlucore) *(mailto:yana.stackpole@qlucore.com)* for help with support and training.

If you need help with some aspect of your data analysis with Qlucore Omics Explorer, 30 minute training sessions can be booked directly with Yana via calendly *(https://calendly.com/yana-stackpole/30min?month=2023-06).*

QIAGEN CLC Genomics Workbench

QIAGEN CLC Genomics Workbench is a graphical user interface (GUI) based bioinformatics software. It houses tools for molecular biology and next generation sequencing (NGS) analysis.

CLC genomics workbench functionality includes: Analysis of your NGS data, including de novo assembly of whole genomes and transcriptomes, resequencing analysis (WGS, WES and targeted panel support), variant calling, RNA-seq, ChIP-seq and DNA methylation (bisulfite sequencing analysis), and access to plug-ins.

Premium Modules

NCI licenses do not include access to premium modules such as the Microbial Genomics Module and the Single Cell Analysis Module. If you are interested in these modules, please contact us at ncibtep@nih.gov *(mailto:ncibtep@nih.gov)*.

Why QIAGEN CLC Genomics Workbench?

CLC is a single toolkit for all NGS analysis applications. Some key features are integrated analytics, ready-to-use workflows, custom workflow capability, and accurate performance. CLC is wizard driven to assist beginners through advanced users.
--- Event Contributor, Kristina Pinardo (Customer Solutions Manager, QIAGEN)

Access CLC Genomics Workbench

License type: NCI wide

You must submit a request through service.cancer.gov *(https://service.cancer.gov/ncisp)* to obtain access to CLC Genomics Workbench. This software requires access to a floating license server (three simultaneous users), and so care should be taken to return the license when the software is not actively being used (i.e. close the application). Working with CLC Genomics Workbench requires login to the NIH network or VPN connection if remote.

Event Slides and Other Resources

1. Slides: QIAGEN CLC Genomics Workbench

Additional Information

Check out additional information on QIAGEN CLC Genomics Workbench, including useful links, in the BTEP Resource pages *(https://bioinformatics.ccr.cancer.gov/docs/resources-for-bioinformatics/software/clc_genomic_workbench/)*.

For technical support questions, feel free to contact the Qiagen technical support team *(mailto:TS-Bioinformatics@qiagen.com)* directly.