

CPTAC SIG Webinars

Join the [CPTAC Imaging Special Interest Group](#) to be notified of webinars & data releases, collaborate on common data wrangling tasks and seek out partners to explore research hypotheses! Announcements about upcoming webinars and artifacts from previous events can be found below.

Webinar schedule:

- [Proteogenomic analysis of Glioblastoma \(May 13, 2020\)](#)
- [NCI-OCCPR Webinar: The Cancer Imaging Archive \(March 18, 2020\)](#)
- [POSTPONED – Proteogenomic analysis of Lung Adenocarcinoma \(March 3, 2020\)](#)
- [Proteogenomic analysis of Clear Cell Renal Cell Carcinoma \(February 4, 2020\)](#)
- [Proteogenomic analysis of Uterine Corpus Endometrial Carcinoma \(January 14, 2020\)](#)
- [Imaging-Omic correlation studies utilizing CPTAC data \(September 9, 2019\)](#)
- [Accessing CPTAC data via Jupyter Notebooks \(August 6, 2019\)](#)
- [Program overview & data access tutorials \(July 1, 2019\)](#)

Proteogenomic analysis of Glioblastoma (May 13, 2020)

Please join us at 12pm Eastern on May 13, 2020 for presentations from Liang-Bo Wang and Runyu Hong about the consortium's proteogenomic analyses of the [CPTAC Glioblastoma \(GBM\)](#) cohort. This deep dive into the GBM genomic and proteomic datasets will help researchers better understand how these can be correlated with features derived from the imaging data.

Webex Details:

Wednesday, May 13, 2020 12:00 pm | 1 hour | (UTC-05:00) Eastern Time (US & Canada)

<https://cbit.webex.com/cbit/j.php?MTID=m77cd233a7120fda373fb1d21ba40681a>

Meeting number: 737 619 560

Password: CMCw32fZX*2

Phone: 1-650-479-3207 Call-in toll number (US/Canada)

Access code: 737 619 560

NCI-OCCPR Webinar: The Cancer Imaging Archive (March 18, 2020)

In collaboration with NCI's Office of Cancer Clinical Proteomics Research (OCCPR), Justin Kirby presents an overview of The Cancer Imaging Archive (TCIA) and its support for the Clinical Proteomics Tumor Analysis Consortium (CPTAC) imaging data. In this webinar he provides an overview of TCIA functionality and datasets with a special emphasis on the >1500 radiology and histology cases associated with the CPTAC patient cohorts. He also discusses how to access clinical, proteomic, and genomic data found in other CPTAC resources to facilitate correlation studies across multiple data types. ([Download the slides](#))

POSTPONED – Proteogenomic analysis of Lung Adenocarcinoma (March 3, 2020)

*** We regret to announce that Dr. Gillette has been pulled into emergency clinical duties today and will need to re-schedule this presentation. We will provide an update once a new date and time have been finalized. ***

Please join us at 12pm Eastern on March 3, 2020 for Dr. Michael Gillette's presentation about the consortium's proteogenomic analyses of the CPTAC Lung Adenocarcinoma (LUAD) cohort. This deep dive into the LUAD genomic and proteomic datasets will help researchers better understand how these can be correlated with features derived from the imaging data.

Proteogenomic analysis of Clear Cell Renal Cell Carcinoma (February 4, 2020)

Agenda & Slides

Dr. David Clarke presents the consortium's proteogenomic analyses of the [CPTAC](#) Clear Cell Renal Cell Carcinoma (CCRCC) cohort. This deep dive into the CCRCC genomic and proteomic datasets will help researchers better understand how these can be correlated with features derived from the imaging data. ([Download the slides](#))

Proteogenomic analysis of Uterine Corpus Endometrial Carcinoma (January 14, 2020)

Agenda & Slides

Emily Kawaler presents the consortium's proteogenomic analyses of the [Uterine Corpus Endometrial Carcinoma \(UCEC\)](#) cohort. This deep dive into the UCEC genomic and proteomic datasets will help researchers better understand how they can be correlated with features derived from the imaging data. ([Download the slides](#))

Imaging-Omic correlation studies utilizing CPTAC data (September 9, 2019)

Agenda & Slides

1) **Dr. Olivier Gevaert** is an assistant professor at Stanford University focused on developing machine-learning methods for biomedical decision support from multi-scale data. His lab develops machine learning methods including Bayesian, kernel methods, regularized regression and deep learning to integrate, clinical, molecular and biomedical image data. His presentation will show an example of how to process proteomic data from CPTAC Phase 2 projects (breast, ovarian and colorectal) with emphasis on how to use, preprocess and subsequently model proteomic data using bioinformatics algorithms. He will show an example of linking protein data to DNA methylation and mRNA gene expression data, and how proteomic data can be integrated with medical image data. ([Download the slides](#))

2) **Runyu Hong** is a computational biomedicine PhD student working in Dr. David Fenyö's lab of NYU School of Medicine's Institute for Systems Genetics. He will speak about their project which trained a deep learning model to distinguish STK11 mutated and wild type pathology slides from CPTAC-LUAD (lung adenocarcinoma) patients. The STK11 gene provides instructions for making a tumor suppressor, serine/threonine kinases 11. Multi-omics analyses of CPTAC non-small-cell lung cancer (LUAD) datasets have found that STK11-mutated patients showed less immune response than other patients. To visualize and validate this pattern in histopathology images, they trained an InceptionV3-architected convolutional neural network model that can achieve high performance (AUC=0.94444) in predicting STK11 mutations based on histopathology images. By extracting the model's last layer activation maps of a random-sampled tiled pieces of images from the test set, they clustered these tiles with dimensional reduction method for features' visualization. An experienced pathologist examined the tiles in the positively and negatively predicted clusters and was able to conclude that tiles in the STK11-positive clusters generally show plenty of cancer cells, but very few immune cells compared to the ones in STK11-negative clusters. This experiment supports the finding in multi-omics analyses and suggests that their model used immune cells as an important feature to distinguish STK11 mutated images. ([Download the slides](#))

Accessing CPTAC data via Jupyter Notebooks (August 6, 2019)

During this webinar you'll learn about a python-based open source tool (<https://github.com/PayneLab/CPTAC>) being developed by members of Sam Payne's lab at BYU which saves researchers the trouble of having to individually navigate the various websites where proteomic, genomic, and clinical data are stored. The slide deck is available here: [CPTAC SIG - 2019-08-06 - Easy Data Dissemination by Sam Payne.pptx](#)

Program overview & data access tutorials (July 1, 2019)

Agenda & Slides

- Welcome (Bob Nordstrom)
- [Clinical Proteomic Tumor Analysis Consortium \(CPTAC\) Project Overview](#) (Chris Kinsinger, 15min)
- CPTAC radiology & pathology image data at TCIA – live demo (Justin Kirby, 15min)
- [CPTAC Data Portal and the Proteomics Data Commons](#) (R. Rajesh Thangudu, 30min)
- [CPTAC genomic data at the Genomics Data Commons](#) (Ana Robles, 15min)
- Q&A (15min)