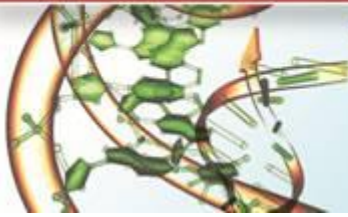




National Cancer Institute



The Cancer Genome Atlas and AACR 2012

April 1 | 2:30 - 3:30 pm | Room W194

The session will report The Cancer Genome Atlas' progress toward the 20 tumor type project goal. By the time of the AACR meeting, TCGA will have generated comprehensive genomic characterizations on more than 6,000 cases across those 20 subtypes of cancer. A major challenge has been the dissemination of TCGA data in ways to maximize their utility to multiple types of users. Speakers will discuss the plans and progress toward integrating and visualizing these complex data and innovative approaches for the generation of "bioinformatic and analysis pipelines." In addition, data from specific tumor projects will be used to provide examples of how high-quality, multi-dimensional data sets from robust numbers of high-quality samples can be interrogated by the cancer research community to generate novel insights.

Chairperson: Kenna Shaw, National Cancer Institute, Bethesda, MD

- TCGA – Strategy, Goals and Data Availability: Kenna Shaw, National Cancer Institute, Bethesda, Md.
- Applying for Access to Controlled Databases: Brad Ozenberger, National Human Genome Research Institute, Bethesda, Md.
- Resources for Users from Genome Data Analysis Centers: Greg Eley, National Cancer Institute, Bethesda, Md.
- Integrative Analysis Examples from TCGA Tumor Projects: Raju Kucherlapti, Harvard Medical School, Boston, Mass.
- Integrative Analysis Examples from TCGA Tumor Projects: Josh Stuart, University of California at Santa Cruz, Santa Cruz, Calif.
- Summary and Q&A: Kenna Shaw, National Cancer Inst., Bethesda, Md. and Brad Ozenberger. National Human Genome Research Institute, Bethesda, Md.

For more information about TCGA, visit cancergenome.nih.gov.