After TCGA: Building Clinical Genomic Resources

New Pan-Cancer Atlas offers reference manual for cancer genome project.

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The last samples were collected long ago, the last plate labeled and sequenced, the last file uploaded and made public in the Genomic Data Commons (GDC). And last month, The Cancer Genome Atlas (TCGA) Research Network published the Pan-Cancer Atlas, a collection of papers serving as a cancer reference manual with overarching themes that have emerged from TCGA data. TCGA has formally come to a close. This large-scale program has changed cancer research and beyondExit Disclaimer, and as researchers continue to mine the data in different ways, we may see the impact go even further. The TCGA team takes a step back to appreciate the program's long and ambitious journey, the legacy it leaves behind, and what comes next.

"A Team Effort of the Most Wonderful Sort"

Dr. Francis Collins describes TCGA as "a team effort of the most wonderful sort." Indeed, there are thousands of people to thank for making TCGA a reality: Leaders who fought to create such an ambitious program of extraordinary breadth. Scientists, clinicians, and researchers who committed themselves to characterizing samples, improving technology, and refining their analyses. Perhaps most importantly, thousands of patients who selflessly agreed to contribute their samples to research when there was no clear benefit to themselves.

Together, these people have truly created a legacy with immeasurable impact. Without this team effort, cancer genomics, other entire fields of research, sequencing technology, computational techniques, and precision medicine would not be where it is today.

New Clinical Cancer Characterization Projects Already Underway

Though TCGA is complete, the instruments at the Genome Characterization Centers have continued to run non-stop. The Center for Cancer Genomics (CCG) at the National Cancer Institute has begun a new wave of projects with emphasis on collecting a rich profile of clinical features and outcomes. These are complementary to the molecular data and critical for answering clinically relevant questions and understanding the complex nuances of cancer.

CCG is molecularly characterizing thousands of samples derived from clinical trials in collaboration with groups within NCI and others worldwide. The projects are utilizing the Genomic

Characterization Pipeline, meaning whole genome and total RNA and microRNA sequencing, reverse phase protein array, and methylation data will be collected. As with TCGA, the new data will be open-access and available in the GDC.

With a renewed focus on clinical features and patient outcome, these projects will enable researchers to address questions that are relevant in the era of precision medicine. Why do some patients respond to a therapy when others do not? What are the mechanisms of resistance and how do we combat them? How does a cancer evolve as a patient progresses through treatment and what leads to relapse? By continuing to build our community resource of molecular and clinical data, we hope to help researchers achieve a deeper understanding of cancer and ultimately, improve diagnosis, treatment and care for patients.

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http://beta.docker.cancerhealth.com/blog/tcga-building-clinical-genomic-resources