The Cancer Genome Atlas

The Cancer Genome Atlas (TCGA) is an integrated network of hundreds of researchers across the United States and Canada. The diagram below provides a description of TCGA components and an explanation of how TCGA works.

Tissue Processing

- Cancer patients are asked to donate a portion of tumor tissue that has been removed as part of their cancer treatment along with a sample of normal tissue, usually blood. Tissue and fluid used for analysis are called biospecimens.

- Biospecimen samples used for genomic research need to meet a stringent set of criteria so that the genetic material (DNA and RNA) removed from them can be used by advanced genomic analysis and sequencing technologies.

- The TCGA Biospecimen Core Resources process samples to ensure they meet the TCGA biospecimen criteria and prepare them for analysis. Part of the process includes coding the biospecimens to remove any information that might connect a sample with a patient's private information.

Research and Discovery

- TCGA researchers analyze tumor and normal tissue from hundreds of patients for each cancer selected for study. This provides the statistical power needed to produce a complete genomic profile of each cancer, which is crucial to identifying those genomic changes that offer the greatest opportunities for therapeutic development.

- TCGA Genome Characterization Centers analyze many of the genetic changes involved in cancer including how the genome is rearranged or how gene expression changes in tumors compared to normal cells.

- High-throughput TCGA Genome Sequencing Centers identify the changes in DNA sequence associated with specific types of cancer. Newly developing sequencing technologies will be used to increase the scope of DNA sequencing efforts on TCGA samples.

- Thousands of cancer and normal tissues will be analyzed by these characterization and sequencing platforms and the data integrated within and across different tumor types. The TCGA Genome Data Analysis Centers will provide new information-processing, analysis and visualization tools to the entire research community to facilitate broader use of TCGA data.

Data Sharing

- The information that is generated by the TCGA Research Network is centrally managed at the TCGA Data Coordinating Center and entered into public databases as it becomes available, allowing scientists to continually access the information.

- Scientists search, download and analyze datasets generated by the TCGA Research Network through the TCGA Data Portal. Essentially, the Data Portal contains the genetic "fingerprints" of specific cancer types.

Community Research and Discovery

- TCGA's comprehensive and robust data is enabling research that could not be possible without it. TCGA data will continue to have a multiplier effect on the scope and quality of research from the broader cancer community.

- The ultimate goal of TCGA is to enable the cancer community to find new ways to better care for patients and significantly reduce the suffering and death due to cancer.