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Explore cancer genomic databases to support immuno-oncology drug discovery

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Cancer genomic databases such as The Cancer Genome Atlas (TCGA) have become invaluable knowledgebases for cancer drug discover. Besides providing comprehensive genomic and genetic properties of cancer cells in a tumor, they also shed light on the profiles and distribution of tumor infiltriting lymphocytes (TILs) in the tumor micro-environment. Using markers uniqulely representing different lymphocytes such as cytotoxic and regulatory T cells, we have characterized the TIL districution of ~10,000 primary tumors from 30 different cancer types. The talk will provide concrete examples how we are using this anlaysis to identify novel targets, discover biomarkers and stratify patients.

Biography

Junping Jing has been a researching Scientist in GlaxoSmithKline (GSK) for 18 years. He joined GSK in 1998 and his research included bioinformatics analysis, biomarker discovery and translational medicine. He is currently senior scientific investigator in Department of Computational Biology, fucusing on bioinformatic analysis supporting cancer immune therapies. He received his PhD in Biochemistry from New York University in 1997 and was an early pioneer in developing array-based DNA analysis platform.

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