Investigating the Tumor Immune Microenvironment using Cancer Genomics and Computational Pathology

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Cancer Immunotherapy

Classification of current anticancer immunotherapies.

Checkpoint Inhibition


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Constitution of Tumor Microenvironment Correlates with Prognosis


Galon et al, ASCO 2016 *Validation of the Immunoscore (IM) as a prognostic marker in stage I/II/III colon cancer: Results of a worldwide consortium-based analysis of 1,336 patients.*

http://meetinglibrary.asco.org/record/123627/abstract
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TCGA: Tumor analysis on multiple platforms

33 types of cancer

- glioblastoma multiforme (brain)
- squamous carcinoma (lung)
- serous cystadenocarcinoma (ovarian)

Multiple data types

- Clinical diagnosis
- Treatment history
- Histologic diagnosis
- Pathologic report/images
- Tissue anatomic site
- Surgical history
- Gene Expression/RNaseq
- Chromosomal copy number
- DNA sequence
- DNA mutations
- Methylation patterns
- miRNA expression
- RPPA (protein)
- Loss of heterozygosity
Gastric Cancer - Platform-Specific Clusters

295 Tumor Samples
Research on Tumors of the Gastrointestinal Tract by the TCGA

Colorectal Cancer (Nature 2012)

Gastric Cancer (Nature 2014)

Esophageal Cancer (Nature 2017)
TCGA PanCancer Atlas

Cells-Of-Origin
- Squamous
- Stemness
- Gastro
- Kidney
- Gyn

Oncogenic Processes
- Mutation Signatures
- Germline

Pathways / Therapies
- MYC
- NOTCH
- HIPPO
- RAS
- Spliceosome
- TGFB
- SWI/SNF
- DDR
- PI3K

Immune
- Drivers / Essentials
- Aneuploidy
Expression deconvolution

OUTPUT


<table>
<thead>
<tr>
<th>Method</th>
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<th>Tissue</th>
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TCGA Immune Response Working Group
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Data Management and Integration

NCI Cloud Resources
Bringing data and computation together to create knowledge that accelerates cancer research and enables precision medicine

Broad Institute
Seven Bridges
Institute for Systems Biology

Sage
QuIP
caMicroscope

CANCER RESEARCH INSTITUTE
iATLAS
Harnessing bioinformatics to speed discovery in cancer immunotherapy.
Example Query: CTLA-4 Gene Expression

```
select * from [isb-cgc-01-0008:Filtered.EBpp_AdjustPANCAN_RNASeqV2_filtered] where Symbol="CTLA4"
```

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Can query directly from R using the 

`biarquery`

library, then do a plot
Thank you

**ISB Team** David Gibbs, Sheila M. Reynolds, Michael Miller, Ilya Shmulevich

**TCGA Gastroesophageal Cancer Working Group** Adam J. Bass (Dana Farber Cancer Institute), Peter W. Laird (Van Andel Research Institute), Ilya Shmulevich (ISB), Francisco Sánchez-Vega (MSKCC), Barbara G. Schneider (Vanderbilt), Toshinori Hinoue (Van Andel),...

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**CRI iAtlas Team** Justin Guinney, James Eddy (Sage Bionetworks), David Gibbs, Ilya Shmulevich (ISB)

TCGA Research Network, TCGA Patients and Families

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