A COMPUTATIONAL FRAMEWORK FOR SYSTEMS PATHOLOGY OF PROSTATE CANCER

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NOVEL COMPUTATIONAL FRAMEWORK
- stratify prostate cancer into insignificant and aggressive
- identify genomic alteration profiles that enable the stratification
- integrate multi-omics datasets to strengthen the analysis

PROJECT OUTLINE

Molecular Dataset → Dictionary (D) → Dictionary Network → Phenotype - Genotype association network

 raw genomic datasets

molecular fingerprints of cancer

DATA: Copy Number Alteration (CNA) profiles from TCGA prostate tumor samples

Dictionary (D)

Sparse Coefficients (X)

Pathway Example: HALLMARK PI3K-AKT-MTOR SIGNALING

patient to gene specific mapping allows us to explore a more personalized molecular fingerprint of prostate cancer

DICTIONARY LEARNING WITH SPARSE CODING

\[ \min \| Y - D x \|^2, \quad s.t. \| x \|_1 \leq s, \| Y - D x \| \leq \epsilon \]


Acknowledgments
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PROSTATE CANCER

Incidence and Significance
- very high incidence
- but most cases are insignificant
- diagnostic screening is controversial
- overdiagnosis and overtreatment

Need for biomarker candidates
- stratify aggressive from insignificant PCa
- more accurate prognosis
- better than Gleason score (a histopathological grading of prostate tissue obtained by biopsy)

The 2016 WHO Classification of Tumors of the Urinary System and Male Genital Organs Part B: Prostate and Bladder Tumors

Grading:
- Grade group 1: Gleason score ≤ 6
- Grade group 2: Gleason score 3 + 4 = 7
- Grade group 3: Gleason score 4 + 3 = 7
- Grade group 4: Gleason score 8
- Grade group 5: Gleason score ≥ 9

these are signs that help us to stratify aggressive from insignificant PCa.

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