Spatial Analysis on Histological Images Using Spark

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Disclaimer

- This presentation is ...
 - − > NOT about computer vision / image processing
 - NOT about drug, biology, or biochemistry
 - − > NOT about new algorithm or infrastructure





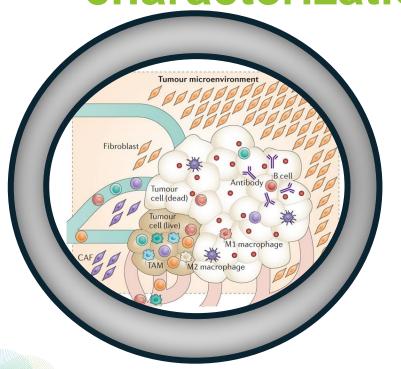
Disclaimer

- This presentation is ...
 - An application of Spark on spatial analysis on biomedical images
 - A proof of concept of a small module in a complex pipeline
 - A work in progress



Towards a systematic characterization of tumor context





Challenges:

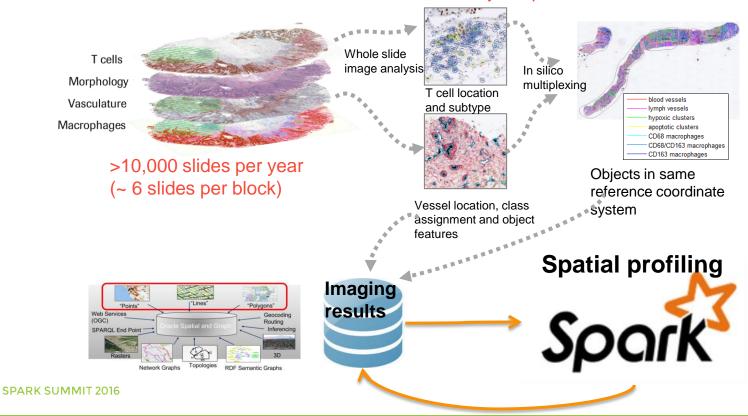
- Location and density of different immune cell populations are associated with patient prognosis and prediction outcome
- Huge variation in immune infiltrates across tumor entities and patients
- Inconsistent data in the literature



Nat Rev Drug Discov. 2015;14(9):603-22.

Roche pRED Tissue image analysis workflow

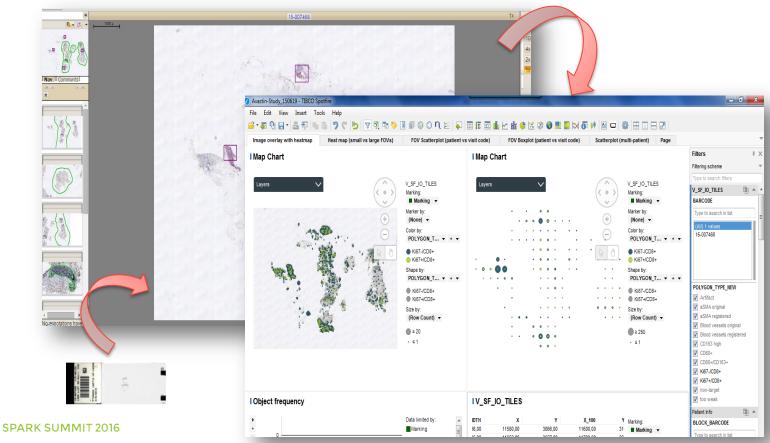
>100,000 objects per slide



Spark



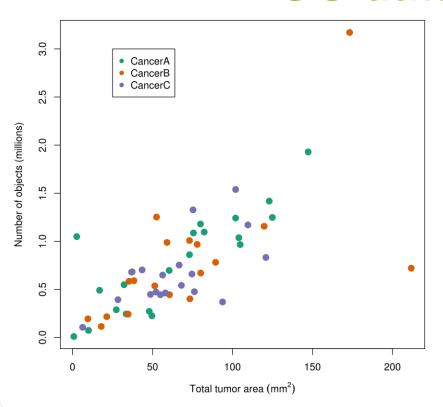
Goal: actionable data



Spark

POC data set





- 57 "blocks" of 3 cancer types
- Each block contains 6 or 7 slides
 - histology stain
 - cancer biomarker
 - microenvironment biomarker
- Each object annotated with object type (T cell, lymph vessels, etc.), shape (point / polygon), and coordinate





Distance calculation

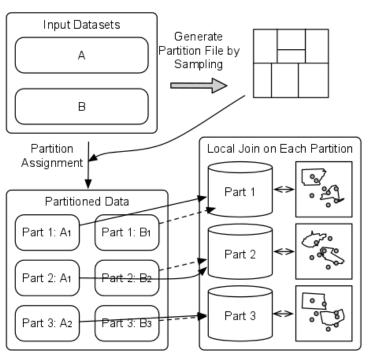
- Basic statistic for distribution, co-localization, spatial clustering, etc.
- Distance: shortest distance between two contours
- Total number of pairwise distances: 5.3 trillion (10¹²) pairs prohibitive
- Workaround: only calculate the distance between each object and its "neighbors" within a window *r*.





Spatial Spark





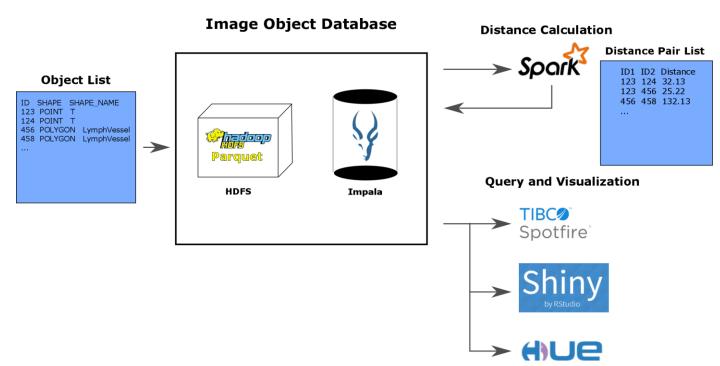
- An open source library developed by Dr. Simin You and Prof. Jianting Zhang from CUNY.
- Divide-and-conquer, following similar designs of HadoopGIS.
- Support multiple spatial partitioning methods: sort-tile partition, binary-split partition, fixed-grid partition

http://simin.me/projects/spatialspark/





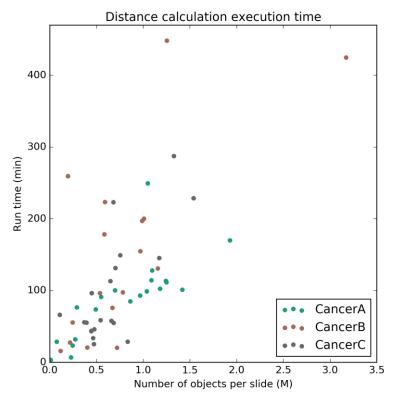
Spatial profiling workflow







Distance calculation: run time

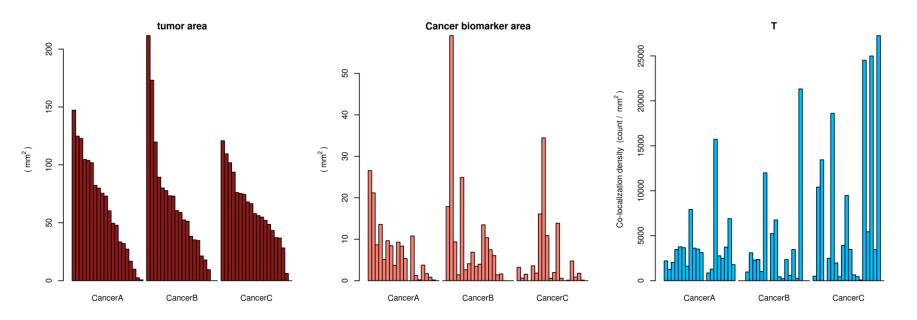


- Using 18 cores, 4 threads / core (72X parallelization).
- Radius = 232.5 μm
- Under shared test environment
- Execute time is roughly linear to number of object (theoretical time complexity).





Co-localization

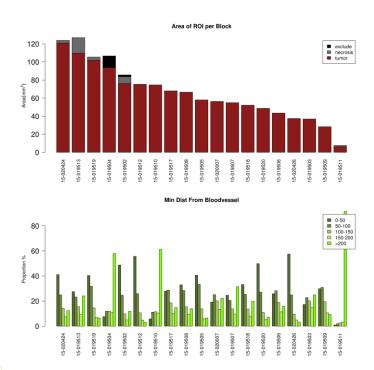


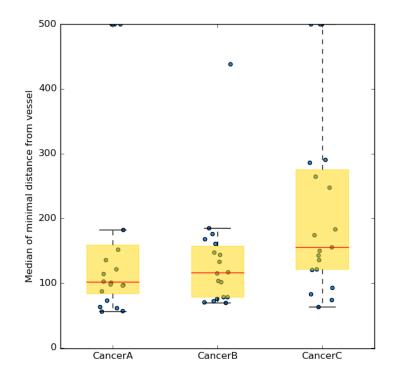
 Enables profiling of between-indication variation and between-tumor variation.



Distance distribution from immune cell to blood vessel





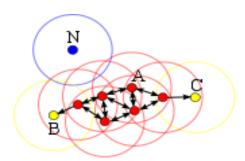






Spatial clustering of objects: DBSCAN

- Density-based spatial clustering of applications with noise (DBSCAN)
 clusters closely connected points into the same cluster, marking high-density
 regions.
- Parameters:
 - minPts: minimum number of neighbors
 - Eps: maximum distance to define a neighbor



minPts = 3
A: core point
B, C: reachable
N: outlier

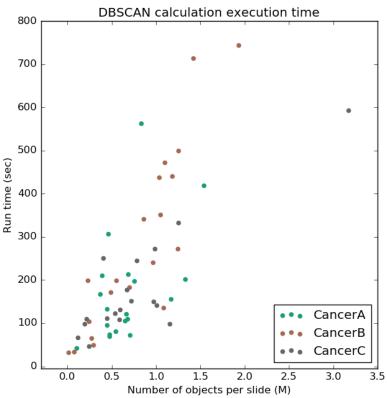








DBSCAN: run time



- Directly load distance from parquet.
- Run time is linear to the number of objects (given already calculated distances).





Future works

- Clinical information
- Genomic data
- Scale up and upstream integration
- UI integration



Acknowledgement



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Doing now what patients need next



THANK YOU.

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