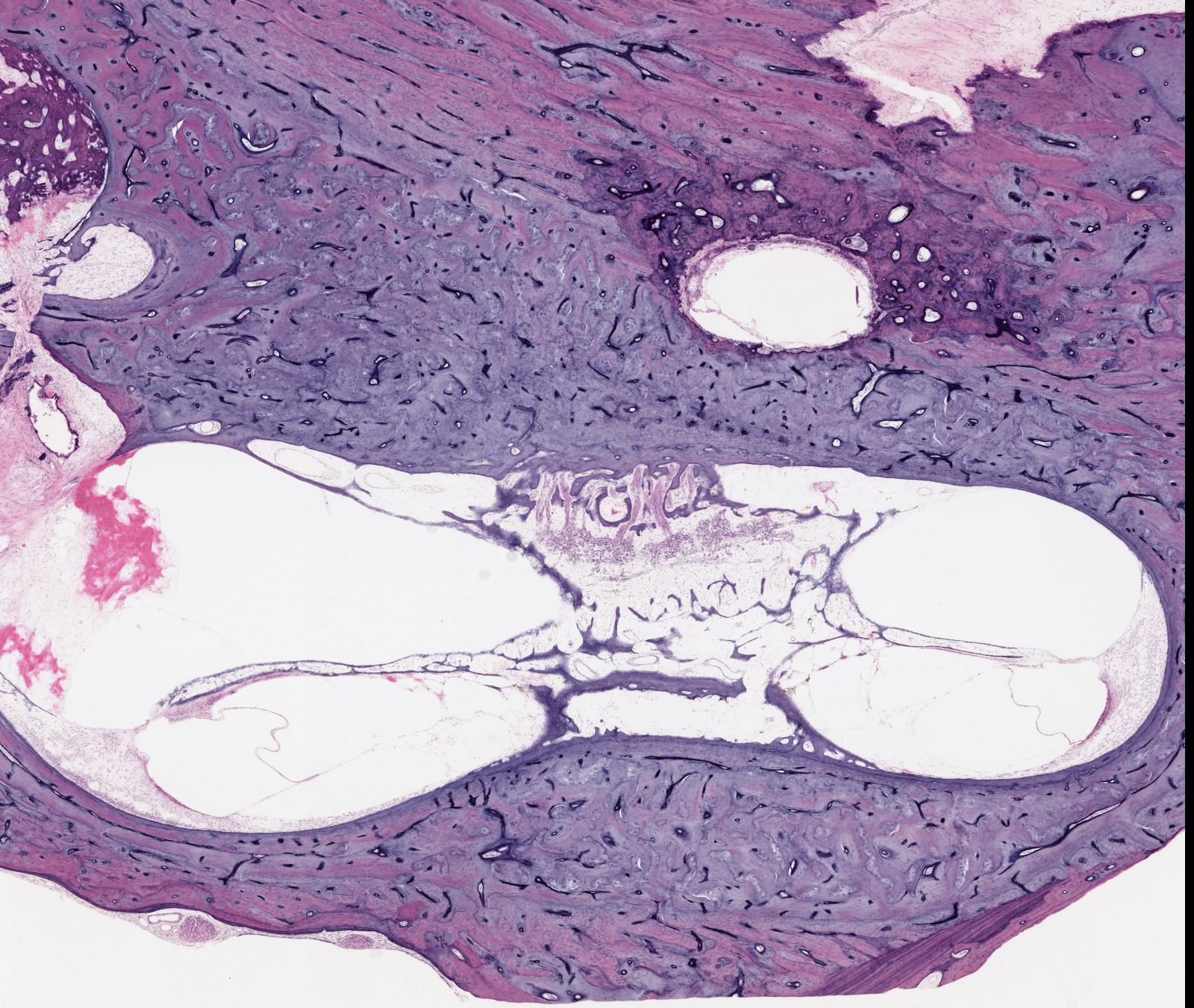


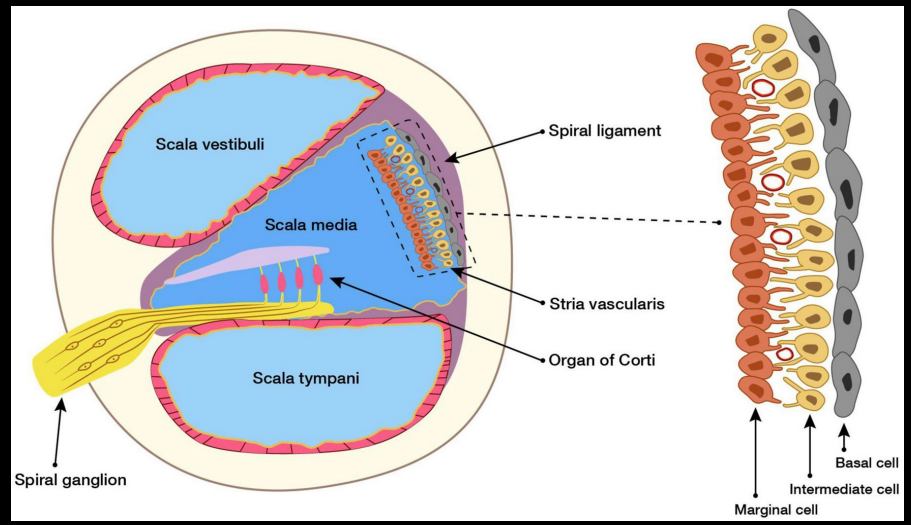
Automatic Segmentation and 3D Reconstruction of the Inner Ear from Histology slides

Group 6: Aseem Jain

Mentors: Dr. Lauer, Dr. Ward, Dr. Creighton

Project Overview

- Problem
  - Understanding structures from histology is critical for determining pathophysiology
  - Currently this is done manually and with 2D
- Goal
  - To automatically segment structure from the inner ear histology slides
  - To use segmentations to generate 3D models



Paper

- **Title**: Spatial analysis of histology in 3D: quantification and visualization of organ and tumor level tissue environment
- **Authors**: Ruusuvuori P, Valkonen M, Kartasalo K, Valkonen M, Visakorpi T, Nykter M, Latonen L.
- **Journal**: Heliyon, Vol 8, No 1, Jan 2022
- **Rationale**
  - Outlines pipeline for registration/alignment of histology slides and creation of 3D model
  - Demonstrates proof of concept for analysis of 3D tumor reconstruction

Paper: Summary and Key Takeaways

- Summary
  - Successfully align and reconstruct the prostate gland from histology sections across 6 mice with tumors
  - Perform volumetric analysis to cluster cancers
- Key Results
  - Proposed pipeline could extract volumetric data from high resolution prostate gland
  - Shape features extracted from tumors can be used to separate tumors of various genotypes

Paper: Background

- Advent of digital microscopy has allowed for creation of whole slide image(WSI)
- WSI typically analyzed in 2D space → value of 3D representation
- Goals
  - Previous work focused on determining best alignment techniques [2]
  - Extend pipeline to analyze volumetric data prostate gland tumors

Paper: Method

- 6 prostate tumors sectioned at 5 micrometer thickness; with 3 gene clusters
- Manual labeling of tumor
- Alignment Method
  - Separate background from gland
  - Down sample images
  - Register using Elastix Stack Alignment (ESA) in Fiji/ImageJ
- ESA
  - Extracts SIFT features(scale invariant feature transforms)
  - Perform rigid registration with SIFT features using RANSAC(Random Sample Consensus)

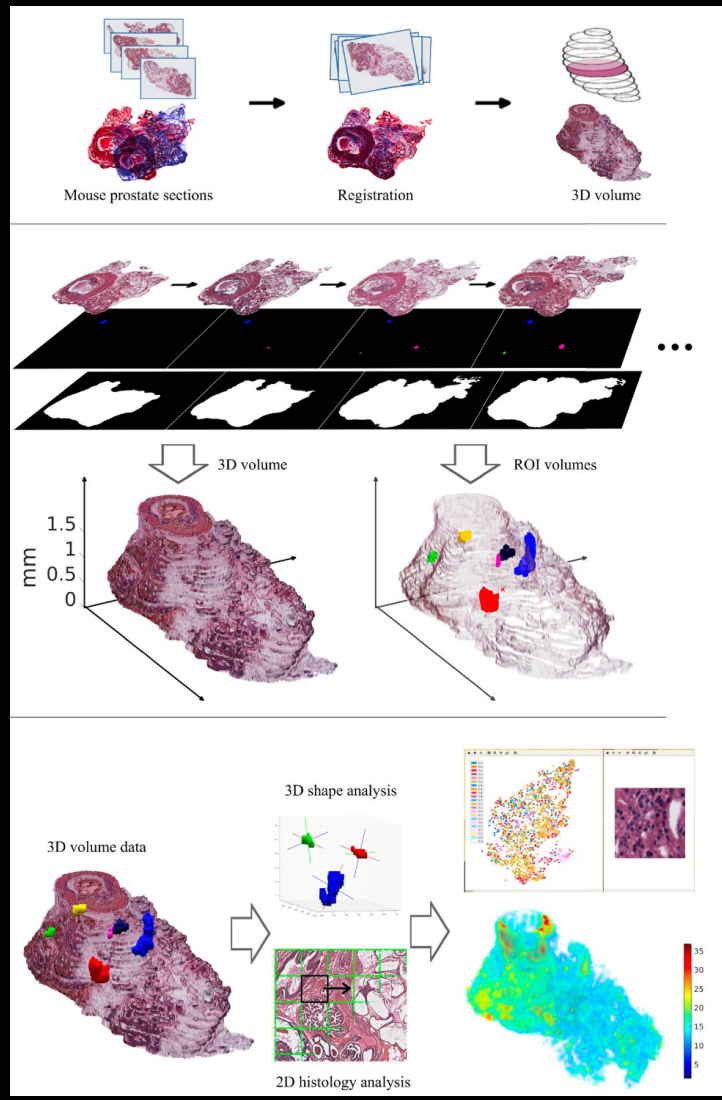
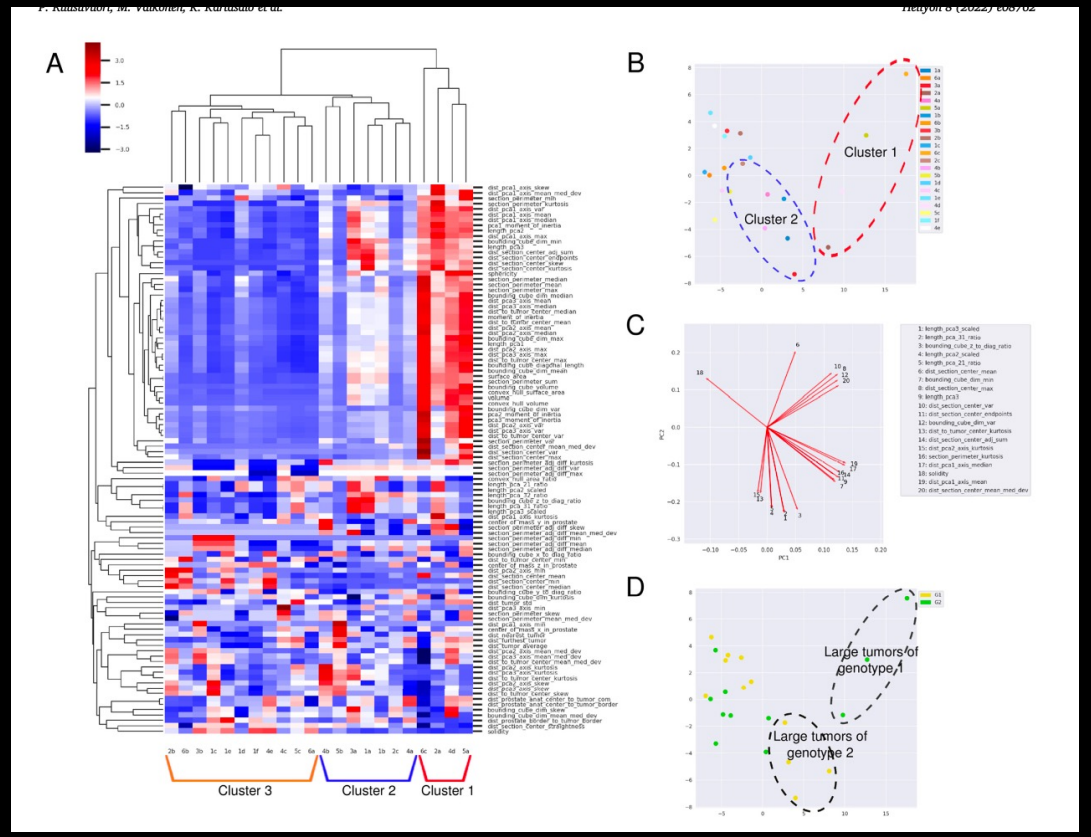


Fig 1: P. Ruusuvuori, M. Valkonen, K. Kartasalo et al.

Paper: Volumetric Analysis

- 22 tumors found expressing 6 genotypes
- Volumetric features extracted
  - Sphericity
  - Volume
  - Length along axis
- PCA to cluster tumors based on features extracted
- Distance to the edge of the prostate and average location within the prostate



Paper: Conclusion

- Demonstrated pipeline for generating and analyzing 3D features from histology sections
- Features extracted from 3D analysis of tumors can be used in ML platforms to create predictive models based on the genotype
- Could also be used for preoperative surgical decision making

Paper: Critical Review

- Pros
  - Accurately generate 3D models from histology slides
  - Analysis can serve as a framework for understanding tumor volume data
- Cons
  - Limited data size leads to poor generalizability
  - Manual segmentation of tumors with no interrater reliability

Relevance to project

- Can use similar pipeline for image alignment
- Analysis offers useful applications
  - Disease vs Normal
  - Volumetric data can be used in ML model to predict various pathologies

References

1. Ruusuvuori P, Valkonen M, Kartasalo K, Valkonen M, Visakorpi T, Nykter M, Latonen L. Spatial analysis of histology in 3D: quantification and visualization of organ and tumor level tissue environment. Heliyon. 2022 Jan 14;8(1):e08762. doi:10.1016/j.heliyon.2022.e08762. PMID: 35128089; PMCID: PMC8800033.
2. K. Kartasalo, L. Latonen, J. Vihinen, T. Visakorpi, M. Nykter, P. Ruusuvuori, Com- parative analysis of tissue reconstruction algorithms for 3D histology, Bioinformatics 34 (17) (2018) 3013–3021.