

PATHOMIQ

Survival Starts with Early Action: Diagnosing Prostate Cancer in Minutes

MANTRA LABS



Client

PathomIQ Inc., headquartered in Silicon Valley, California, is a **computational pathology and multi-omics platform** to assist Pharmaceutical and Healthcare Industries with faster, cost-effective drug development and scalable personalized therapy design.

The company is founded by the veterans of biomarker research, data scientists and clinical pathology.







Problem **Statement**

- PathomIQ required a mechanism to detect different patterns of **prostate cancer** for a given slide.
- Cancer grading is a daunting task because of the enormous data size and very subtle differences between cancer and benign glands. For example, 1 WSI (Whole Slide Image) contains over 6 billion pixels and the probability of the presence of high-grade cancerous cells (GP5) is < 0.005%.







Solution Components

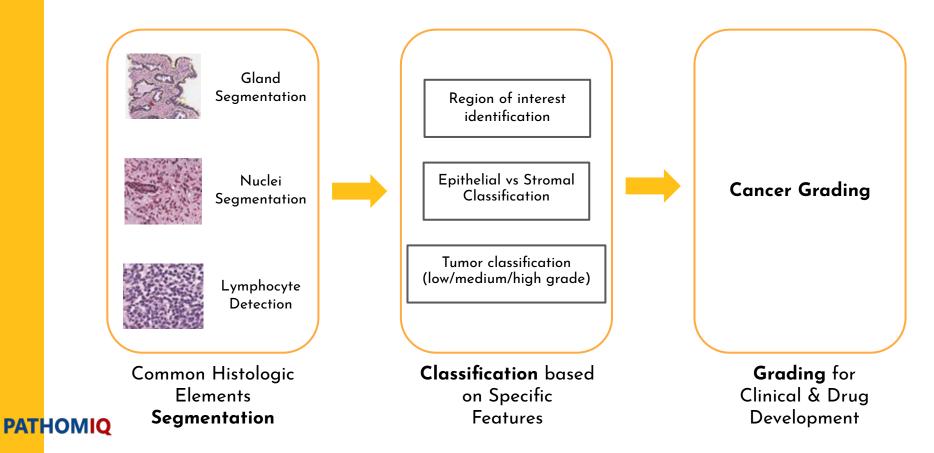
PATHOMIO

 Hybrid Deep Learning Architecture for Cancer Grading. (Combination of Classification & Segmentation Neural Networks)

- Multi-scale model to capture nuclear detail as well as glandular context.
- Fine-tuning model to make the algorithm sensitive to the minuscule amount of high-grade cancer cells.



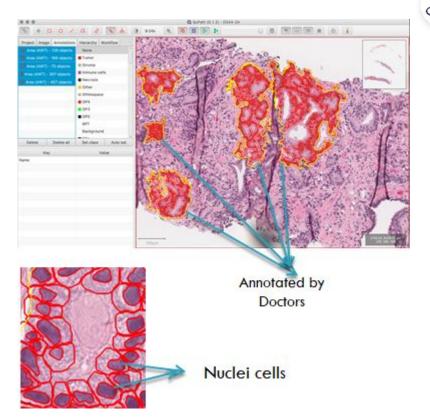
System Architecture



Data **Preparation**

The grading models are trained by extracting nuclei indices of different cancer patterns **annotated by pathologists**.

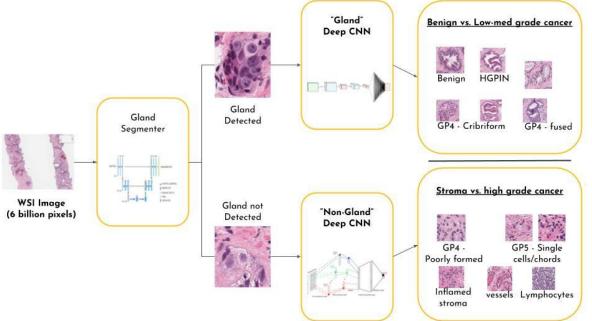
- Loading the annotated XML files on the QuPath.
- Drawing the annotation.
- Extracting the centroid X,Y coordinates of the nuclei cells and storing them into the file.



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Segmentation & Classification Models

The shape of the cells is important for determining the severity of cancer. Segmentation helps in identifying cancerous cell patterns in a more granular manner and classification models help in automated grading.

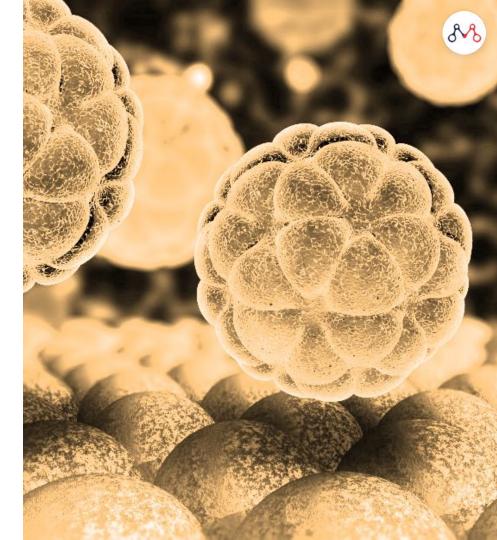


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Project Highlight

The platform has been trained to predict **5 different patterns** of prostate cancer.

- Stroma Normal cells
- **Benign or BPT** Early stage of cancer cells
- **GP3** Gleason Pattern 3 cancer cells
- **GP4** Gleason Pattern 4 cancer cells
- **GP5** Gleason Pattern 5 cancer cells (High-grade cancer)



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Technology **Stack**



Software: QuPath

QuPath is an open-source software for whole slide image (WSI) analysis and digital pathology.



Libraries

Primary: Theano & Lasagne

Other: Cv2, openslide, numpy Scipy, matplotlib



Outcomes

- Speed: High-speed processing and image viewing system.
- Automation: Created a predictive annotation system & pipelined multiple model predictions.
- Accuracy: Pathologists only need to review less than 5% of data for annotations.





Other Applications of the **Model**

Similar AI models can be used for **Leaf-disease detection** & classification for a sustainable and scalable agriculture.







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