Deep Learning for Sub-Classification of Gleason Pattern 4 in Prostate Cancer

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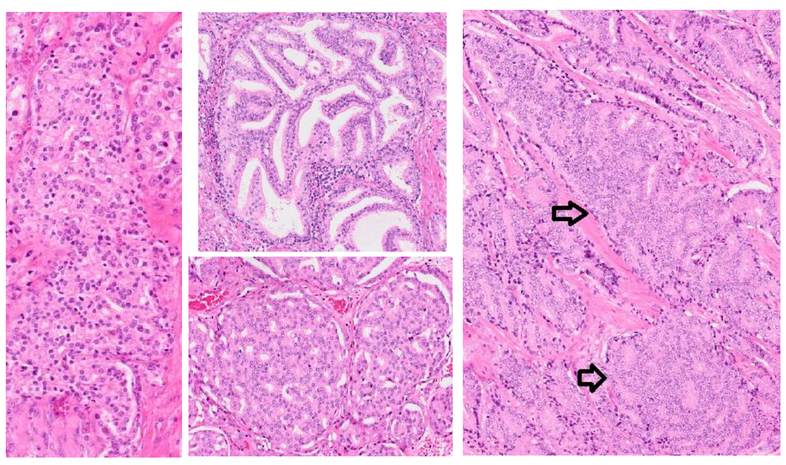
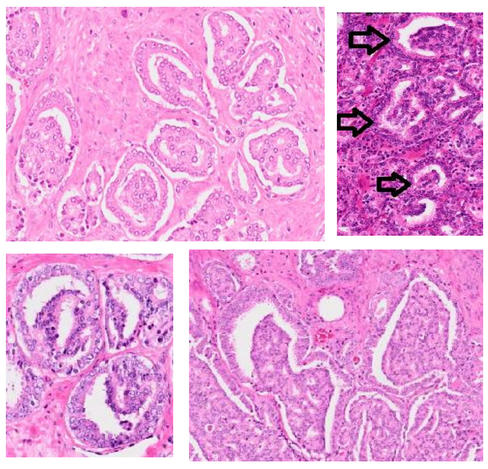
Introduction

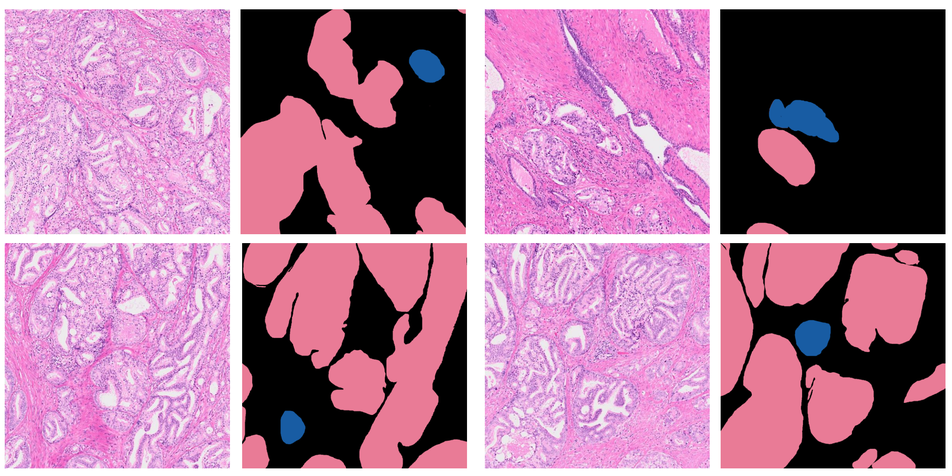
- Several studies provide compelling evidence on the relevance of reporting Gleason pattern 4 percentage in a tissue biopsy with a Gleason score (GS) 7. This impacts risk stratification and therapy planning and is crucial for making decisions on active surveillance (AS) or definitive therapy. The ISUP 2019 guidelines recommend reporting the Gleason pattern 4 proportion in all tissue samples. In addition, some studies have suggested the importance of recording the histologic pattern of Gleason pattern 4, due to a potential correlation with biochemical recurrence-free survival and metastasis-free survival.
- Poorly formed glands, glomeruloid structures, cribriform glands, and fused glands are all part of the GP4 morphology. The cribriform pattern is linked to a more aggressive clinical course and is a strong predictor of distant metastases and disease-specific mortality. Although glomeruloid pattern is regarded to represent an early stage of cribriform pattern, the impact on prognosis is debatable.
- We created a computational technique that uses Deep Learning to identify and quantify Cribriform and Glomeruloid patterns in whole mount images (WMI) of Robotic-Assisted Laparoscopic Prostatectomy (RALP) specimens.



Typical Cribriform Pattern



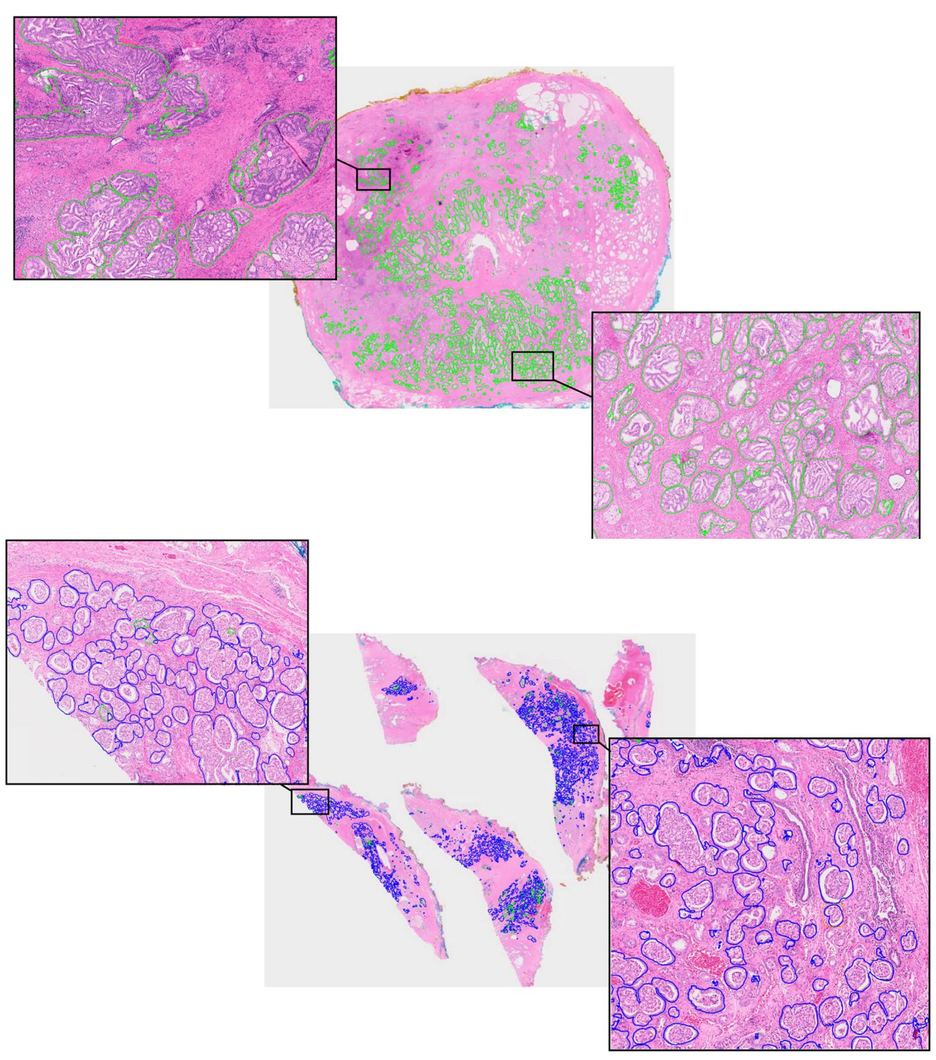
Typical Glomeruloid Pattern



Training Data Sample (Pink : Cribriform, Blue : Glomeruloid)

Materials and Methods

Using an Olympus VS200 scanner, FFPE whole-mount H&E-stained histopathological sections of RALP specimens displaying a combination of distinct GP4 subtypes were digitized at a magnification of 40x. To distinguish Cribriform and Glomeruloid patterns from benign glands, other tumour patterns, and stromal regions, a neural network based on U-Net++ with an EfficientNet backbone was trained. The model was trained using 13 RP images annotated by two pathologists. The model was put to the test with 42 RP images.



Inference result on Whole Mount Images of RP. (Green : Cribriform, Blue : Glomeruloid)

Results

The model scored well on the test dataset, with AUCs (Area Under Curve) of 0.87 for Cribriform pattern identification and 0.81 for Glomeruloid pattern identification. The segmentation model obtained an F1-score of 0.83 and 0.80 for the two patterns, respectively.

Conclusion

- Substantial research has been undertaken in the field of prostate cancer, for a better understanding of the pathology, risk stratification to improve therapy planning & resulting patient outcomes.
- Gleason grading has been established as an essential component in identifying optimal treatment options, with several studies stressing on the importance of assessing the quantity of Gleason 4 pattern in a tissue sample for risk assessment and predictive purposes.
- More recent expert recommendations have proposed that it is not only important to record the fraction of Gleason pattern 4 present in a sample, but also the histologic pattern, since it reflects severity and influences prognosis.
- A cribriform cellular arrangement appears to be linked to more aggressive clinical course and is a strong predictor of distant metastases and disease-specific mortality.
- However, studies done so far, rely on eyeball estimations of the amount of cribriform and glomeruloid patterns. This is particularly difficult in Radical Prostatectomy specimens in which different tumour morphologies & patterns maybe present in same or different sections.
- Using Deep Learning, we devised a method for automatically localizing Cribriform and Glomeruloid growth patterns in RALP images.
- This development would allow a more precise estimation of the amount of cribriform and/or glomeruloid morphology present in radical prostatectomy specimen.
- With this methodology, reliable estimation of the true impact of Gleason 4 cribriform/glomeruloid morphology can be assessed, with consequent informative translation to patient outcomes.
- We plan to conduct multi-centre trials on larger data sets for validation of this algorithm.

References

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