Pan-Cancer Nuclei Segmentation in Hematoxylin and Eosin Whole Slide Images

Poster # 165

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Disclosures: All authors are employees of and stockholders in Tempus AI, Inc., a for-profit company.

INTRODUCTION

Nuclei segmentation is a critical stage in characterizing the morphology of cells in Hematoxylin and Eosin (H&E) stained whole slide images (WSIs).

Extensive research has been conducted on the application of deep learning models for nuclei segmentation.

While individual models have shown promising performance in segmenting nuclei for specific cancer types, a gap remains in the availability of a single model to segment nuclei across cancer types.

Here, we created a comprehensive training and validation dataset encompassing a broad spectrum of cancer types and histological subtypes to address this need.

METHODS

A cohort of WSIs was generated including 14 cancer types, with each having up to three histological subtypes (N=410, **Table 1.**).

From these WSIs, we randomly selected two fields of view (FOV) from the tissue area for annotation at 40x magnification.

During the training phase, we acquired one annotation per image, while for the validation phase, we gathered four annotations per image.

We trained a HoverNet model initializing using weights from a model previously trained on the CoNSeP dataset.

To assess the model performance, we conducted a comparative analysis between the trained model, the initial CoNSeP-trained model, and consensus evaluations of pathologists.

To determine consensus among pathologists, we computed majority votes for all possible permutations of three pathologists, with one annotator being excluded for each permutation.

We compared the consensus annotations with the model's output and the annotations of the held-out pathologists. As a result, we obtained four data points for the box plots presented in **Figure 1** and **2**. Statistical testing was performed using a t-test for independent samples and Bonferroni correction.

SUMMARY

In this study, we established an annotation dataset tailored explicitly to pan-cancer nuclei segmentation and have demonstrated that by utilizing the HoverNet architecture, this dataset can achieve near-human-level performance.

RESULTS

Figure 1. Performance: all cancers

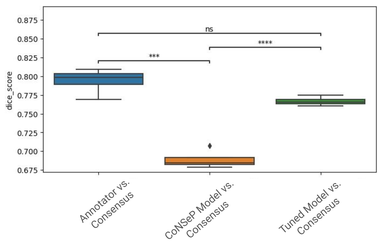

Figure 2. Performance by cancer type

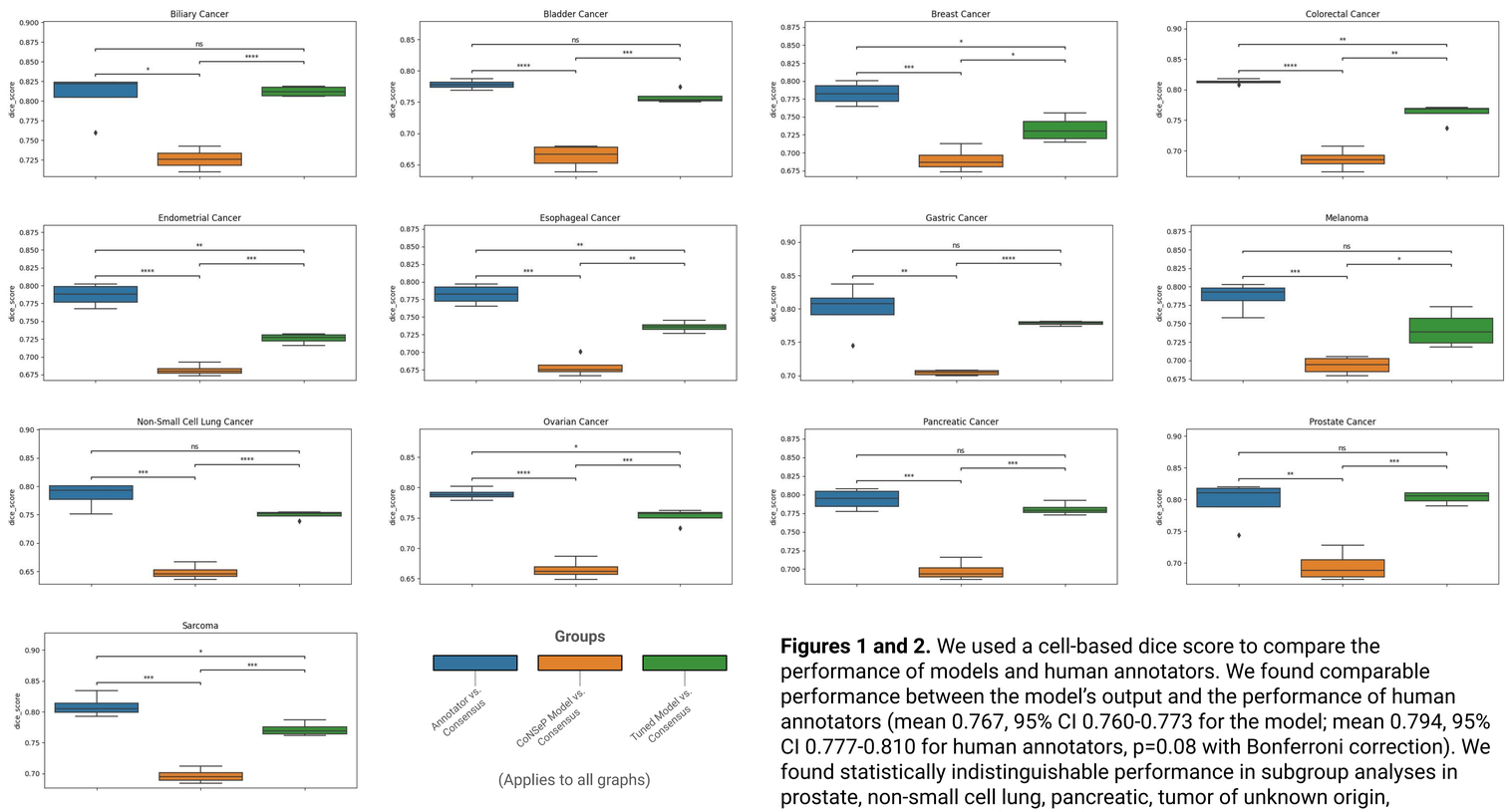

Table 1. Cohort

Cancer Type	Histology subtypes	Number of images in training	Number of images in validation
Biliary Cancer	cholangiocarcinoma	12	12
Bladder Cancer	urothelial carcinoma	12	12
Breast Cancer	breast carcinoma	10	11
Colorectal Cancer	colorectal adenocarcinoma	12	12
Endometrial Cancer	carcinosarcoma	12	12
	endometrial serous carcinoma	12	12
	endometrioid carcinoma	11	12
Esophageal Cancer	gastroesophageal adenocarcinoma	12	12
	gastroesophageal squamous cell carcinoma	12	12
	gastroesophageal adenocarcinoma	12	12
Melanoma	melanoma	12	12
NSCLC	lung adenocarcinoma	12	12
	lung squamous cell carcinoma	12	12
Ovarian Cancer	ovarian serous carcinoma	12	11
Pancreatic Cancer	pancreatic adenocarcinoma	12	12
	pancreatic neuroendocrine tumor	10	12
Prostate Cancer	prostatic adenocarcinoma	12	12
Sarcoma	fibrous sarcoma	11	12
	leiomyosarcoma	12	12
Tumor of Unknown Origin	NA	36	36

Figures 1 and 2. We used a cell-based dice score to compare the performance of models and human annotators. We found comparable performance between the model's output and the performance of human annotators (mean 0.767, 95% CI 0.760-0.773 for the model; mean 0.794, 95% CI 0.777-0.810 for human annotators, p=0.08 with Bonferroni correction). We found statistically indistinguishable performance in subgroup analyses in prostate, non-small cell lung, pancreatic, tumor of unknown origin, melanoma, gastric, bladder, and biliary cancers.

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