

ProstNFound: Integrating Medical Foundation Models with Ultrasound and Clinical Domain Knowledge for Robust Prostate Cancer Detection

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1 Materials

1.1 Dataset

Table 1. Summary of our five-center dataset, with the number of patients and cores originating from each center, and the breakdown of number of benign cores and the number of cancer cores by Gleason Score (GS).

Center	Location	Patients	Cores	Benign	GS7	GS8	GS9	GS10
JH	Baltimore, USA	60	616	568	32	10	6	0
UVA	Virginia Beach, USA	236	2335	2018	221	57	28	11
PCC	Calgary, Canada	171	1599	1400	162	23	14	0
PMCC	Toronto, Canada	71	588	486	90	12	0	0
CRCEO	Quebec City, Canada	155	1469	1255	170	32	12	0
Total	-	693	6607	5727	675	134	60	11

2 Method

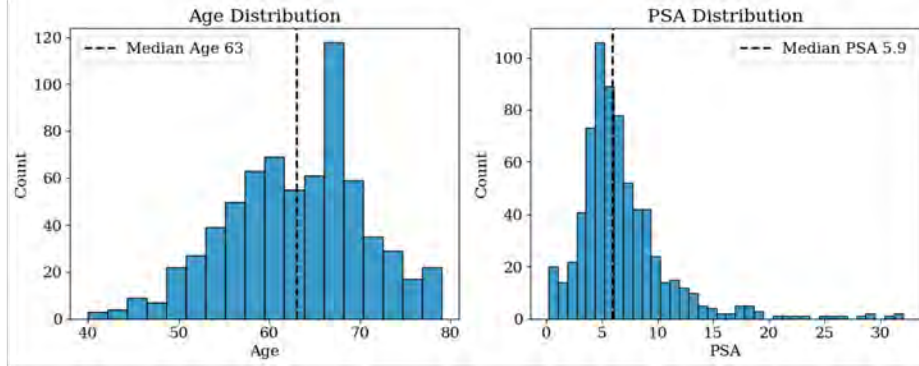


Fig. 1. Distribution of Age and PSA values in dataset

Table 2. Hyper-parameter tuning

Hyper-parameters	Value Range	Best
Self-supervised Learning		
Epochs	1, 5, 10, 20	5
Optimizer	Adam	Adam
Batch size	64, 256, 1024	64
Learning rate	1e-3, 1e-4	1e-4
Main Training		
Epochs	15, 25, 35	35
Optimizer	AdamW, SGD+momentum	AdamW
Batch size	1, 4, 8, 16	8
Data augmentation	none, random resized crop, random translation	random translation
Learning rate scheduler	none, cosine annealing, linear warmup+cosine annealing	linear warmup+cosine annealing
Learning rate	1e-6, 1e-5, 1e-4	1e-5
Learning rate (Image encoder)	1e-6, 1e-5, 1e-4	1e-5
Learning rate (Patch encoder)	0, 1e-6, 3e-6, 1e-5	1e-6
Weight decay	0, 1e-4, 1e-3	0
Pooling method (for patch-embeddings)	max, mean, none	max