

Supplementary Figures and Tables

1. Additional details on the cancer pathology report data used in our study

All the results presented in the manuscript are based on a study design which involves 2,923,291 samples across 7 different registries (LA, KY, UT, NJ, SA, CA, NM). Samples are effectively pathology reports, from which registrars manually annotate values. Specifically, tumor registrars abstract information from pathology reports by manually annotating information about each tumor. We refer to this information as the ground truth labels or classes in the Cancer/Tumor/Case (CTC) database. In the SEER Program Coding and Staging Manual 2023, these are referred to as *Topography Codes*; an example of the classes for primary anatomic subsite (324 CTC ground truth classes) is shown in [Figure 1](#). Such manually coded categorical information is used for our training labels.

Primary Site	Topography Codes
Head and Neck	C000-C148, C300-C329, C410, C411, C442
Colon, Rectosigmoid, Rectum	C180-C189, C199, C209
Lung	C340-C349
Cutaneous Melanoma	C440-C449 with Histology 8720-8780
Breast	C500-C506, C508-C509
Kidney	C649
Urinary Sites	C659, C669, C670-C679, C680-C681, C688-C689
Non-malignant CNS	C700, C701, C709, C710-C719, C720-C725, C728, C729, C751-C753
Malignant CNS and Peripheral Nerves	C470-C479, C700, C701, C709, C710-C719, C720-C725, C728, C729, C751-C753
Other Sites	Excludes Head and Neck, Colon, Rectosigmoid, Rectum, Lung, Cutaneous Melanoma, Breast, Kidney, Urinary Sites, Peripheral Nerves, CNS

Figure 1: Example of topography codes, i.e. CTC classes, for primary anatomic subsite.

In our manuscript we aim to show the performance of a multitask classifier for classifying the text pathology reports from the US National Cancer Institute SEER registries to partially automate a human workflow on four tasks: primary cancer site (70 CTC ground truth classes), primary anatomic subsite (324 CTC ground truth classes), laterality (7 CTC ground truth classes), and histological type (620 CTC ground truth classes). With the proposed AI-supporting strategies, human annotator tumor registrars would not have to review every single sample—only those samples that are not retained

at the threshold level of interest. Also, since the registries receive several million reports annually, the proposed strategies translate into significant savings in person-hours when the systems are deployed.

2. Additional details on the second experimental study to investigate how the retained predictions varies among classes

All the results presented in the manuscript are based on a study design which involves 2,923,291 samples, or pathology reports, across 7 different registries (LA, KY, UT, NJ, SA, CA, NM). [Figure 2](#) below shows the counts of samples, or pathology reports, for 7 randomly chosen ground truth CTC classes (out of 324 classes CTC ground truth classes) for primary anatomic subsite. The same could be shown for primary cancer site (70 CTC ground truth classes), laterality (7 CTC ground truth classes), and histological type (620 CTC ground truth classes).

CTC	Fixed 97% (correct/incorrect)	Delta 97% (correct/incorrect)	Entropy 97% (correct/incorrect)	Bayes-Beta 97% (correct/incorrect)	DAC 97% (correct/incorrect)
C750 -	11	1 (1/0)	1 (1/0)	1 (1/0)	1 (1/0)
C631 -	23	8 (7/1)	8 (7/1)	6 (6/0)	8 (7/1)
C060 -	235	91 (87/4)	100 (96/4)	77 (73/4)	91 (87/4)
C172 -	435	178 (161/17)	173 (156/17)	178 (159/19)	178 (161/17)
C209 -	6373	3235 (3040/195)	2930 (2761/169)	3409 (3200/209)	3234 (3040/194)
C341 -	16551	6577 (6250/327)	6658 (6317/341)	6488 (6170/318)	6562 (6235/327)
C421 -	20039	16971 (16676/295)	17068 (16762/306)	16628 (16369/259)	16971 (16676/295)
					17697 (17281/416)

Figure 2: Number of samples (i.e. pathology reports) for 7 classes of primary anatomic subsite (out of the 324 CTC ground truth classes). For example, we have 16,551 samples with ground truth CTC class C341 for primary anatomic subsite; based on the DAC targeting a 97% accuracy level (which is the arbitrary level used in our study), we predict 6,043 samples for class C341, of which 5,742 are predicted correctly, while 301 are predicted incorrectly. The same interpretation goes for the samples retained with the proposed a posteriori methods (Fixed, Delta, Entropy, Bayes-Beta). We are indeed retaining predictions for rare classes (≤ 500 ground truth CTC samples: C750, C631, C060, C172), common classes (1,000-10,000 ground truth CTC samples: C209), and most prevalent classes ($> 10,000$ ground truth CTC samples: C341, C421).

We note that with all the proposed a posteriori methods we retain a larger or equal rate of classes (number of retained predicted classes vs. ground truth CTC classes) compared to the DAC. A larger number of retained classes is encouraging, as the model

learned to classify examples while treating the classes with equal importance; nevertheless, classes do not have the same frequencies, so it is difficult to achieve the same accuracy in each class, and the DAC seems more oriented to increasing the number of correct predictions from the majority class than from the minority ones. In turn, the a posteriori methods better preserve the class distribution retained at the specified accuracy and corresponding rejection rate.

3. Additional Figures and Tables

Set	Task	Architecture	Model	Accuracy [95% CI]	Rejection rate (%)
Validation UTNJLAKYSA	Laterality	MTHiSAN - Sigmoid	Delta	0.974[0.974;0.975]	14.7
Validation UTNJLAKYSA	Histology	MTHiSAN - Softmax	Delta	0.974[0.973;0.975]	75.7
Validation UTNJLAKYSA	Site	MTHiSAN - Softmax	Delta	0.979[0.979;0.979]	14.4
Validation UTNJLAKYSA	Subsite	MTHiSAN - Softmax	Fixed	0.976[0.975;0.977]	67.2
Validation UTNJLAKYSA	Laterality	MTHiSAN - Sigmoid	DAC	0.974[0.974;0.975]	16.0
Validation UTNJLAKYSA	Histology	MTHiSAN - Softmax	DAC	0.974[0.973;0.975]	77.4
Validation UTNJLAKYSA	Site	MTHiSAN - Softmax	DAC	0.979[0.979;0.980]	16.2
Validation UTNJLAKYSA	Subsite	MTHiSAN - Softmax	DAC	0.976[0.975;0.977]	68.3
Test UTNJLAKYSA	Laterality	MTHiSAN - Sigmoid	Delta	0.977[0.976;0.977]	13.2
Test UTNJLAKYSA	Histology	MTHiSAN - Softmax	Bayes-Beta	0.979[0.978;0.980]	72.3
Test UTNJLAKYSA	Site	MTHiSAN - Softmax	Fixed	0.978[0.977;0.978]	12.2
Test UTNJLAKYSA	Subsite	MTHiSAN - Softmax	Entropy	0.980[0.979;0.981]	62.6
Test UTNJLAKYSA	Laterality	MTHiSAN - Sigmoid	DAC	0.977[0.976;0.977]	14.4
Test UTNJLAKYSA	Histology	MTHiSAN - Softmax	DAC	0.981[0.980;0.982]	74.2
Test UTNJLAKYSA	Site	MTHiSAN - Softmax	DAC	0.983[0.982;0.983]	14.5
Test UTNJLAKYSA	Subsite	MTHiSAN - Softmax	DAC	0.980[0.979;0.981]	63.9

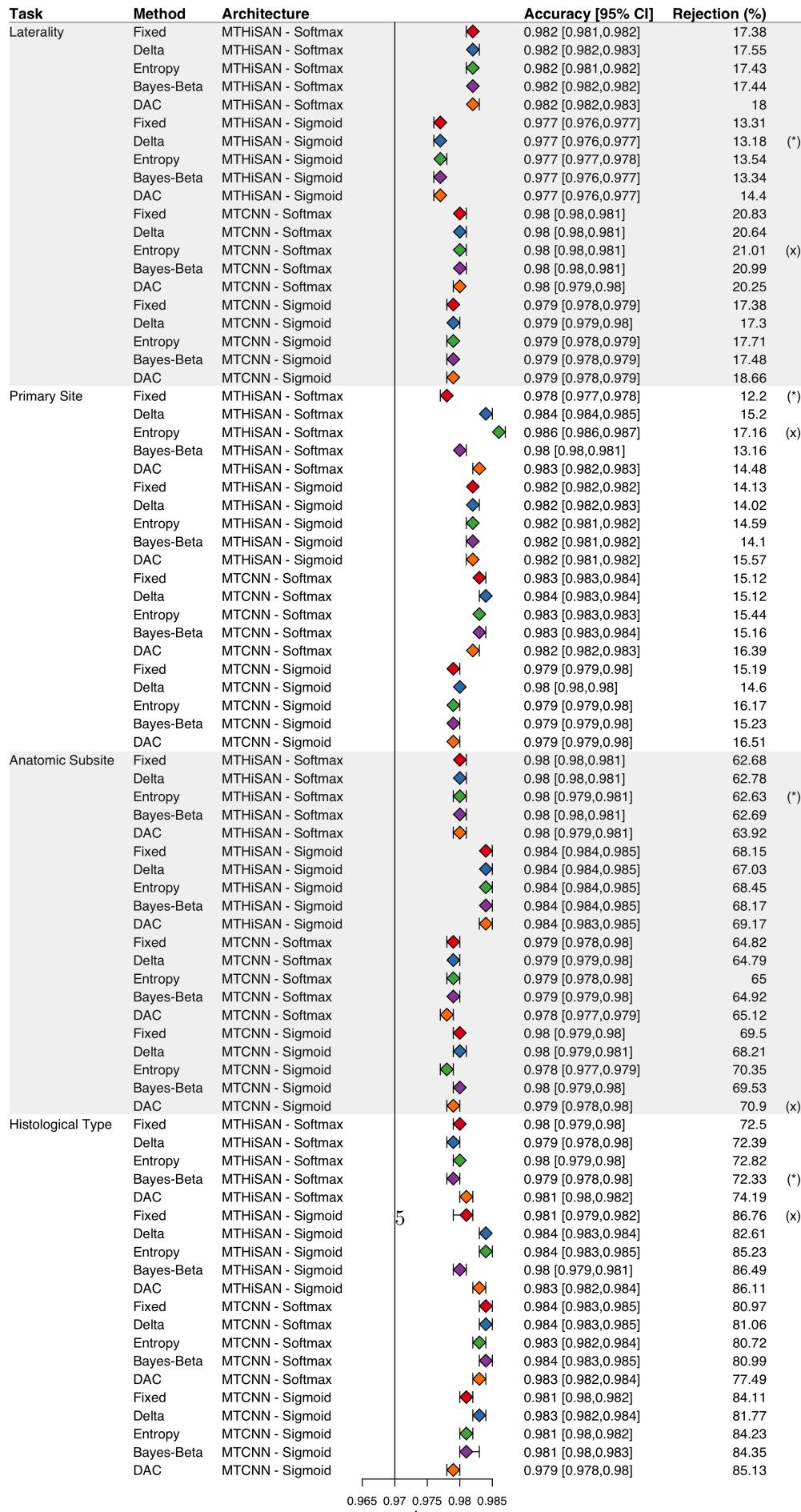
Table 1: *Experimental study 2*: validation (top) and test (bottom) set results as a combination of architecture and activation function achieving 97% accuracy or higher and the lowest rejection rate by task for the best among the proposed methods in a comparison analysis with the DAC.

Validation Set UTNJKYLASA - Support=398,266

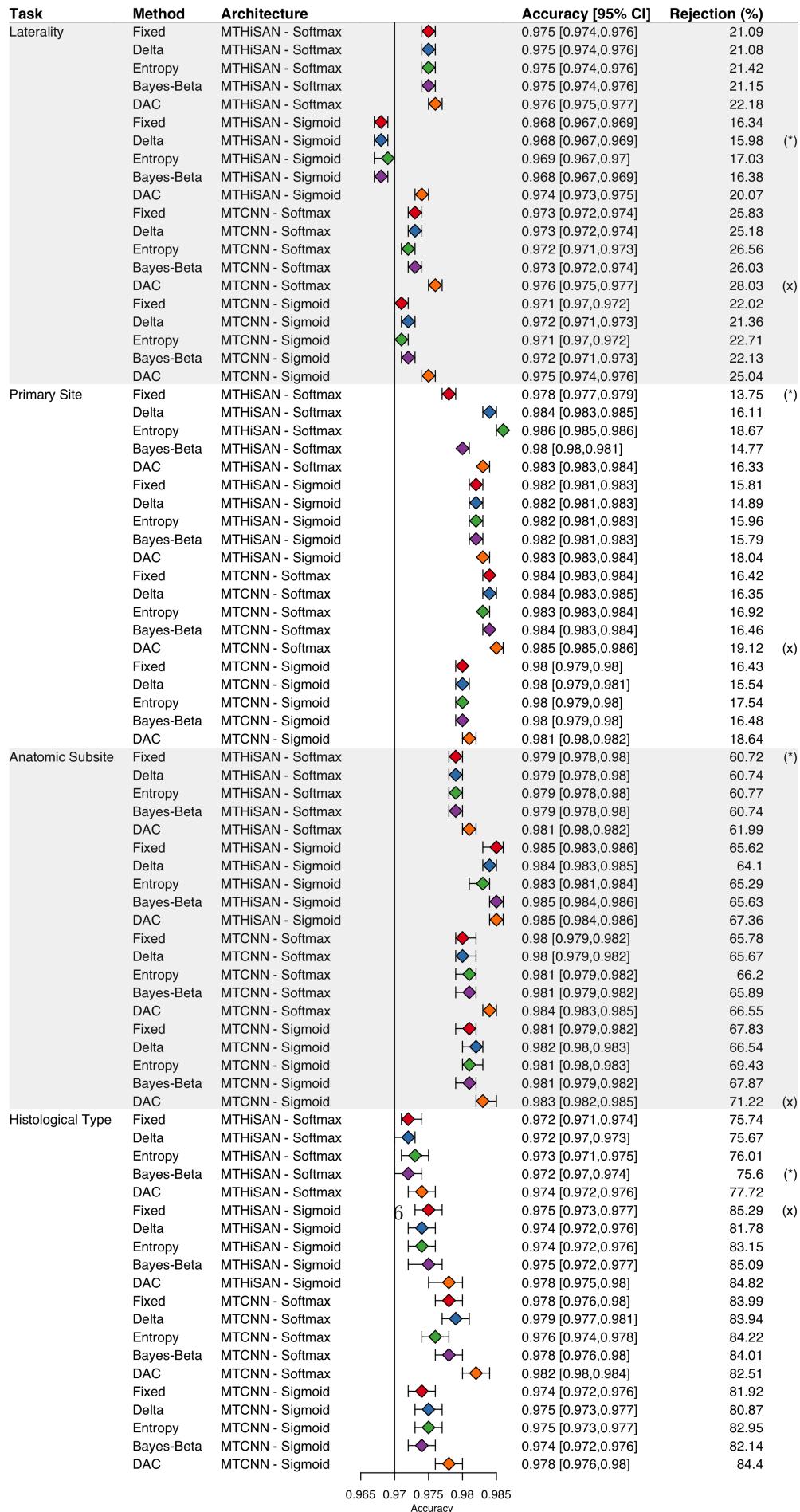
Task	Method	Architecture	Accuracy [95% CI]	Rejection (%)
Laterality	Fixed	MTHISAN - Softmax	0.98 [0.98,0.981]	19.29
	Delta	MTHISAN - Softmax	0.98 [0.98,0.981]	19.4
	Entropy	MTHISAN - Softmax	0.98 [0.98,0.98]	19.36
	Bayes-Beta	MTHISAN - Softmax	0.98 [0.98,0.981]	19.34
	DAC	MTHISAN - Softmax	0.98 [0.979,0.98]	19.74
	Fixed	MTHISAN - Sigmoid	0.974 [0.974,0.975]	14.91
	Delta	MTHISAN - Sigmoid	0.974 [0.974,0.975]	14.68 (*)
	Entropy	MTHISAN - Sigmoid	0.974 [0.973,0.975]	15.06
	Bayes-Beta	MTHISAN - Sigmoid	0.974 [0.974,0.975]	14.94
	DAC	MTHISAN - Sigmoid	0.974 [0.974,0.975]	15.96
	Fixed	MTCNN - Softmax	0.977 [0.977,0.978]	22.53
	Delta	MTCNN - Softmax	0.977 [0.976,0.978]	22.29
	Entropy	MTCNN - Softmax	0.977 [0.976,0.978]	22.79 (x)
	Bayes-Beta	MTCNN - Softmax	0.977 [0.977,0.978]	22.73
	DAC	MTCNN - Softmax	0.977 [0.976,0.977]	22.03
Primary Site	Fixed	MTCNN - Sigmoid	0.976 [0.975,0.977]	19.13
	Delta	MTCNN - Sigmoid	0.976 [0.976,0.977]	18.91
	Entropy	MTCNN - Sigmoid	0.976 [0.975,0.977]	19.55
	Bayes-Beta	MTCNN - Sigmoid	0.976 [0.976,0.977]	19.23
	DAC	MTCNN - Sigmoid	0.976 [0.975,0.976]	20.43
	Fixed	MTHISAN - Softmax	0.979 [0.979,0.98]	14.42
	Delta	MTHISAN - Softmax	0.979 [0.979,0.979]	14.4 (*)
	Entropy	MTHISAN - Softmax	0.979 [0.979,0.979]	14.53
	Bayes-Beta	MTHISAN - Softmax	0.979 [0.979,0.98]	14.46
	DAC	MTHISAN - Softmax	0.979 [0.979,0.98]	16.15
	Fixed	MTHISAN - Sigmoid	0.977 [0.977,0.978]	15.39
	Delta	MTHISAN - Sigmoid	0.977 [0.977,0.978]	14.94
	Entropy	MTHISAN - Sigmoid	0.977 [0.976,0.978]	15.88
	Bayes-Beta	MTHISAN - Sigmoid	0.977 [0.977,0.978]	15.35
	DAC	MTHISAN - Sigmoid	0.977 [0.977,0.978]	16.98
Anatomic Subsite	Fixed	MTCNN - Softmax	0.979 [0.979,0.98]	16.72
	Delta	MTCNN - Softmax	0.979 [0.979,0.98]	16.59
	Entropy	MTCNN - Softmax	0.979 [0.979,0.979]	17.21
	Bayes-Beta	MTCNN - Softmax	0.979 [0.979,0.98]	16.75
	DAC	MTCNN - Softmax	0.979 [0.979,0.98]	18.22 (x)
	Fixed	MTCNN - Sigmoid	0.975 [0.975,0.976]	16.62
	Delta	MTCNN - Sigmoid	0.975 [0.975,0.976]	15.82
	Entropy	MTCNN - Sigmoid	0.975 [0.974,0.976]	17.94
	Bayes-Beta	MTCNN - Sigmoid	0.975 [0.975,0.976]	16.65
	DAC	MTCNN - Sigmoid	0.975 [0.974,0.975]	18.09
	Fixed	MTHISAN - Softmax	0.976 [0.975,0.977]	67.24 (*)
	Delta	MTHISAN - Softmax	0.976 [0.975,0.977]	67.31
	Entropy	MTHISAN - Softmax	0.976 [0.975,0.977]	67.24
	Bayes-Beta	MTHISAN - Softmax	0.976 [0.975,0.977]	67.25
	DAC	MTHISAN - Softmax	0.976 [0.975,0.977]	68.29
Histological Type	Fixed	MTHISAN - Sigmoid	0.979 [0.978,0.98]	71.73
	Delta	MTHISAN - Sigmoid	0.979 [0.978,0.98]	70.68
	Entropy	MTHISAN - Sigmoid	0.979 [0.978,0.98]	71.82
	Bayes-Beta	MTHISAN - Sigmoid	0.979 [0.978,0.98]	71.74
	DAC	MTHISAN - Sigmoid	0.979 [0.978,0.98]	72.41
	Fixed	MTCNN - Softmax	0.975 [0.974,0.976]	69.6
	Delta	MTCNN - Softmax	0.975 [0.974,0.976]	69.54
	Entropy	MTCNN - Softmax	0.975 [0.974,0.976]	69.89
	Bayes-Beta	MTCNN - Softmax	0.975 [0.974,0.976]	69.7
	DAC	MTCNN - Softmax	0.975 [0.974,0.975]	69.38
	Fixed	MTCNN - Sigmoid	0.974 [0.973,0.975]	72.82
	Delta	MTCNN - Sigmoid	0.974 [0.973,0.975]	71.75
	Entropy	MTCNN - Sigmoid	0.974 [0.973,0.975]	74.39 (x)
	Bayes-Beta	MTCNN - Sigmoid	0.974 [0.973,0.975]	72.86
	DAC	MTCNN - Sigmoid	0.974 [0.973,0.975]	74.2
	Fixed	MTHISAN - Softmax	0.974 [0.973,0.975]	75.91
	Delta	MTHISAN - Softmax	0.974 [0.973,0.975]	75.73 (*)
	Entropy	MTHISAN - Softmax	0.974 [0.973,0.975]	76.28
	Bayes-Beta	MTHISAN - Softmax	0.974 [0.973,0.975]	75.77
	DAC	MTHISAN - Softmax	0.974 [0.973,0.975]	77.37
	Fixed	MTHISAN - Sigmoid	0.975 [0.973,0.976]	87.7 (x)
	Delta	MTHISAN - Sigmoid	0.974 [0.973,0.975]	84.27
	Entropy	MTHISAN - Sigmoid	0.974 [0.973,0.975]	86.73
	Bayes-Beta	MTHISAN - Sigmoid	0.974 [0.973,0.975]	87.48
	DAC	MTHISAN - Sigmoid	0.974 [0.972,0.975]	87.23
	Fixed	MTCNN - Softmax	0.979 [0.978,0.98]	85.27
	Delta	MTCNN - Softmax	0.978 [0.977,0.979]	85.16
	Entropy	MTCNN - Softmax	0.978 [0.977,0.979]	85.17
	Bayes-Beta	MTCNN - Softmax	0.979 [0.978,0.98]	85.28
	DAC	MTCNN - Softmax	0.978 [0.977,0.979]	81.53
	Fixed	MTCNN - Sigmoid	0.971 [0.97,0.973]	85.93
	Delta	MTCNN - Sigmoid	0.971 [0.97,0.973]	84.17
	Entropy	MTCNN - Sigmoid	0.971 [0.97,0.972]	87.24
	Bayes-Beta	MTCNN - Sigmoid	0.972 [0.97,0.973]	86.16
	DAC	MTCNN - Sigmoid	0.971 [0.97,0.973]	87.05

0.965 0.97 0.975 0.98 0.985
Accuracy

Test Set UTNJKYLASA - Support=371,820

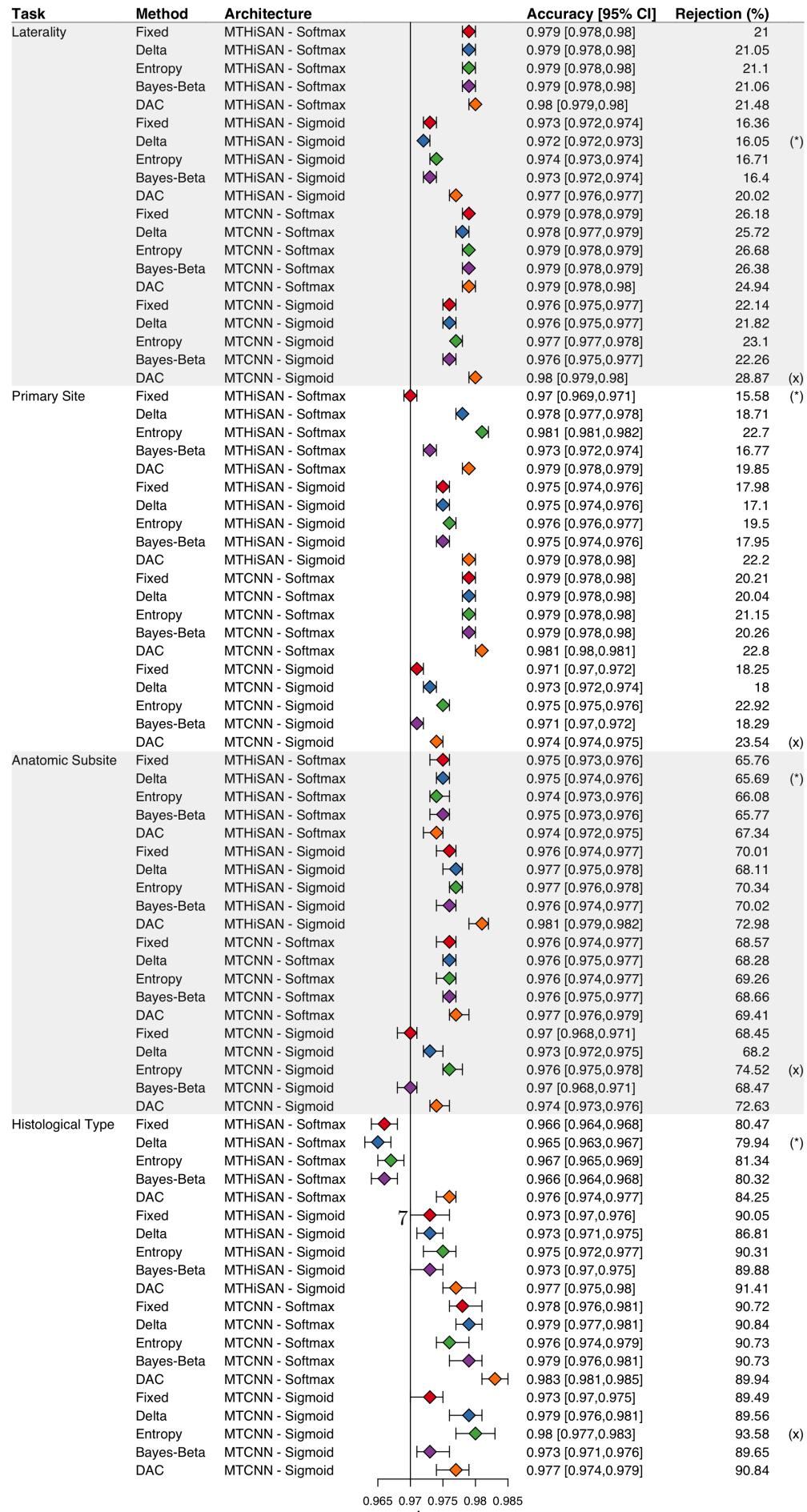


Test Set CA - Support=131,050



0.965 0.97 0.975 0.98 0.985
Accuracy

Test Set NM - Support=158,056



0.965 0.97 0.975 0.98 0.985
Accuracy

Set	Task	Architecture	Model	Accuracy [95% CI]	Rejection rate (%)
OOD Test CA	Laterality	MTHiSAN - Softmax	Delta	0.975[0.974;0.976]	21.1
OOD Test CA	Histology	MTHiSAN - Softmax	Bayes-Beta	0.972[0.970;0.974]	75.6
OOD Test CA	Site	MTHiSAN - Softmax	Fixed	0.978[0.977;0.979]	13.7
OOD Test CA	Subsite	MTHiSAN - Softmax	Fixed	0.979[0.978;0.980]	60.7
OOD Test CA	Laterality	MTHiSAN - Sigmoid	DAC	0.974[0.973;0.975]	20.1
OOD Test CA	Histology	MTHiSAN - Softmax	DAC	0.974[0.972;0.976]	77.7
OOD Test CA	Site	MTHiSAN - Softmax	DAC	0.983[0.983;0.984]	16.3
OOD Test CA	Subsite	MTHiSAN - Softmax	DAC	0.981[0.980;0.982]	62
OOD Test NM	Laterality	MTHiSAN - Sigmoid	Delta	0.972[0.972;0.973]	16
OOD Test NM	Histology	MTHiSAN - Sigmoid	Delta	0.973[0.971;0.975]	86.8
OOD Test NM	Site	MTHiSAN - Softmax	Fixed	0.970[0.969;0.971]	15.6
OOD Test NM	Subsite	MTHiSAN - Softmax	Delta	0.975[0.974;0.976]	65.7
OOD Test NM	Laterality	MTHiSAN - Sigmoid	DAC	0.977[0.976;0.977]	20
OOD Test NM	Histology	MTHiSAN - Softmax	DAC	0.976[0.974;0.977]	84.3
OOD Test NM	Site	MTHiSAN - Softmax	DAC	0.979[0.978;0.979]	19.8
OOD Test NM	Subsite	MTHiSAN - Softmax	DAC	0.974[0.972;0.975]	67.3

Table 2: *Experimental study 2*: out-of-distribution test set results for CA (top) and NM (bottom) as a combination of architecture achieving 97% accuracy or higher and the lowest rejection rate by task for the best among the proposed methods in a comparison analysis with the DAC.