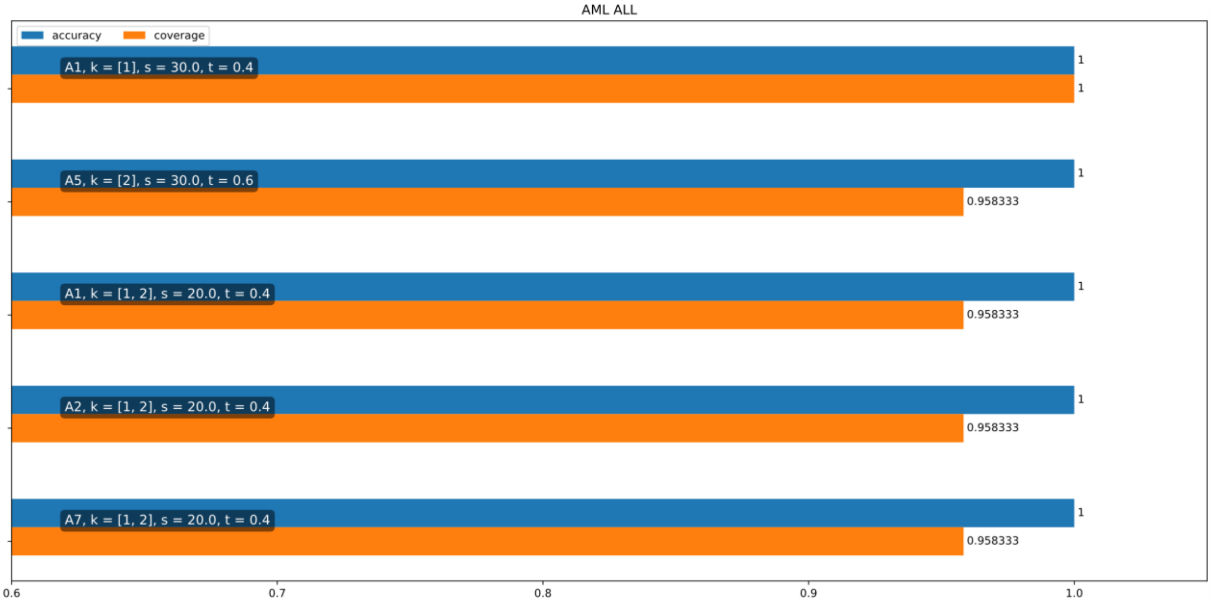
Supplementary materials for paper „An ensemble classifier based on kNN with an interval threshold strategy”.

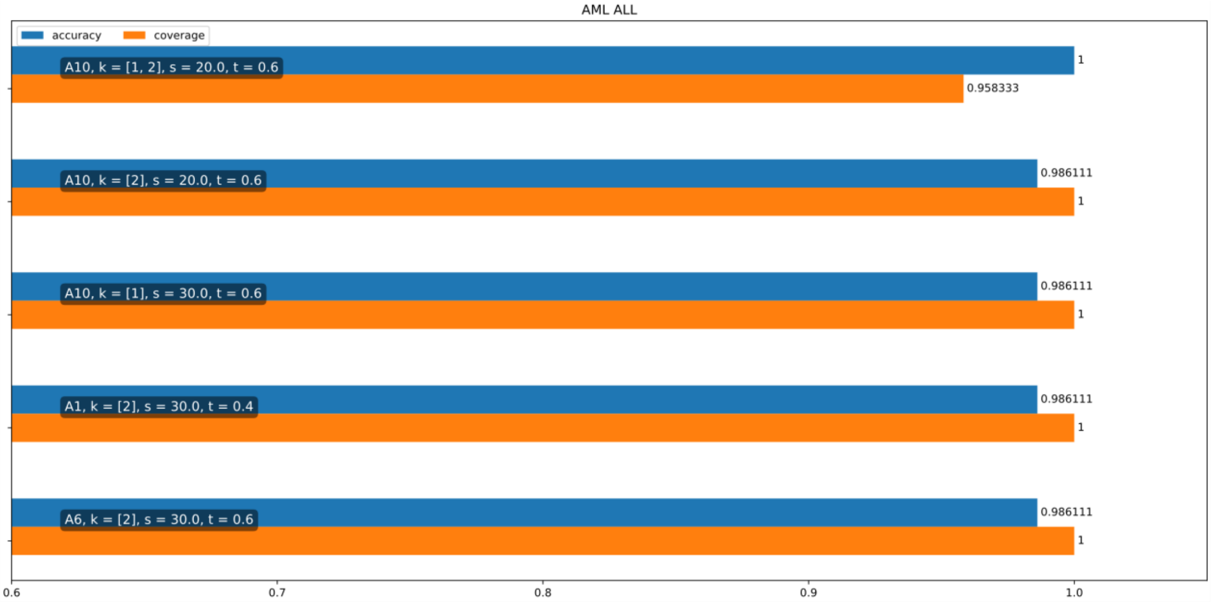
U. Bentkowska, M. Mrukowicz, W. Gałka, K. Lech

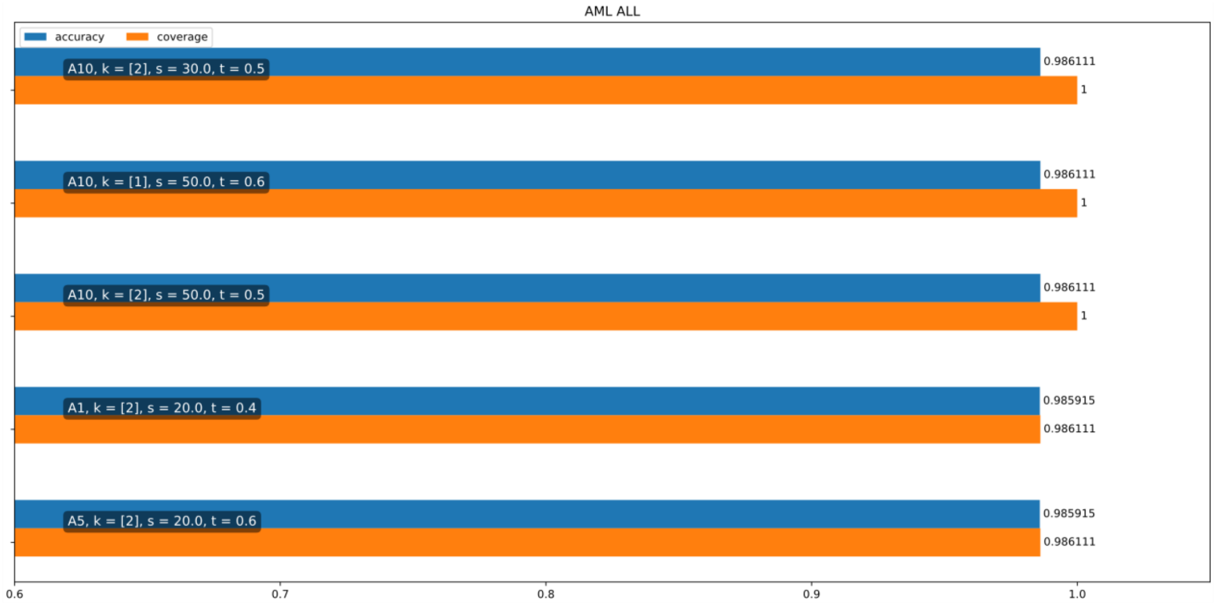
1. Figures

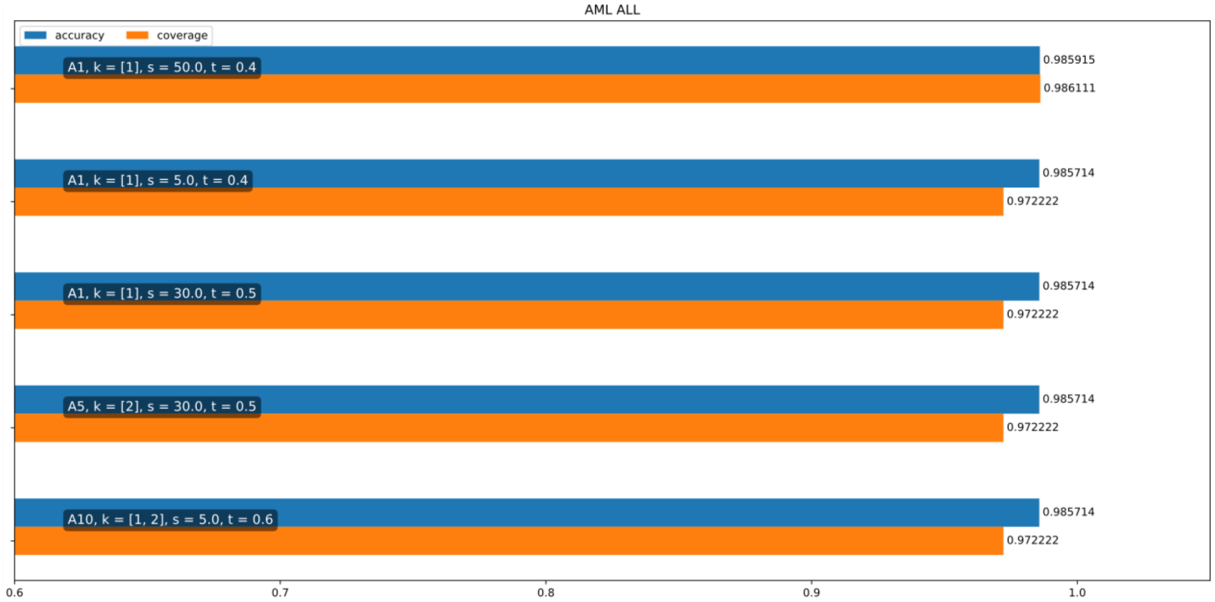
The results presented in Tables 2,4,6,8,10 are plotted here, respectively. The data in the figures are sorted by accuracy. Average values from folds in LOO are presented for both quality measures (accuracy and coverage) for the established hyperparameters: aggregation, k, s and t.

1.1. AML ALL (Lymphoma) dataset

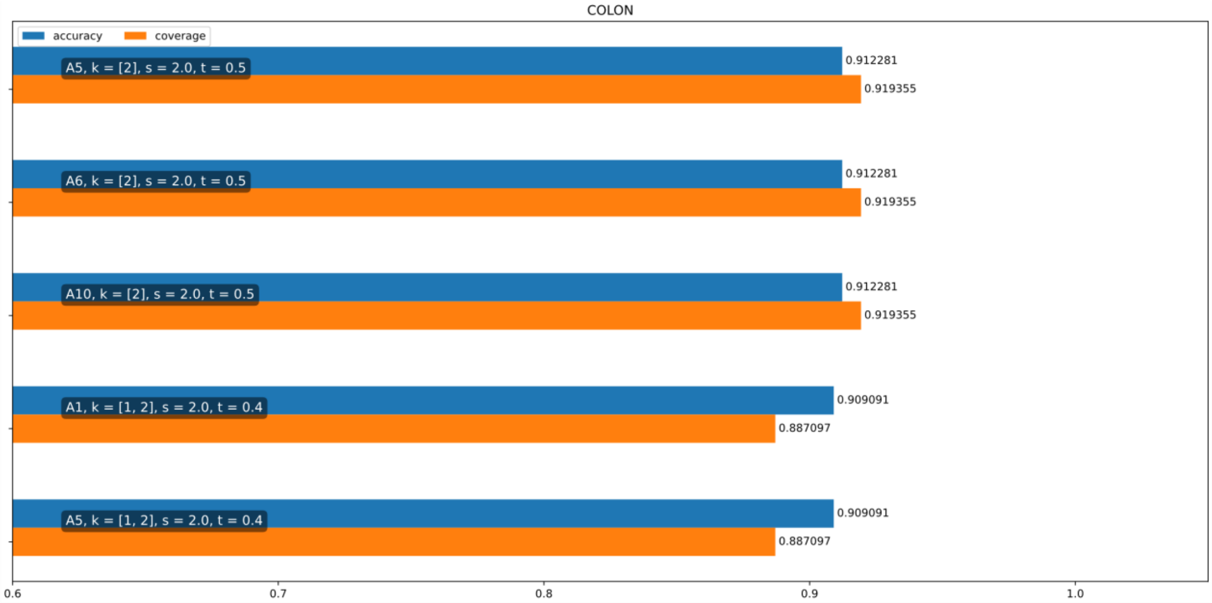


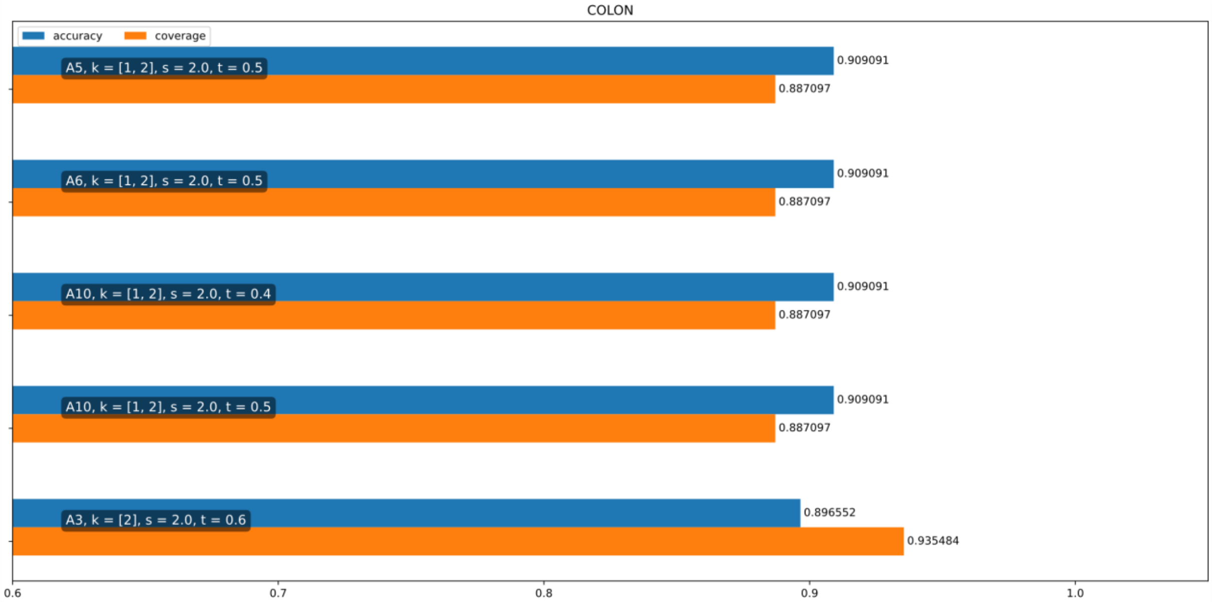


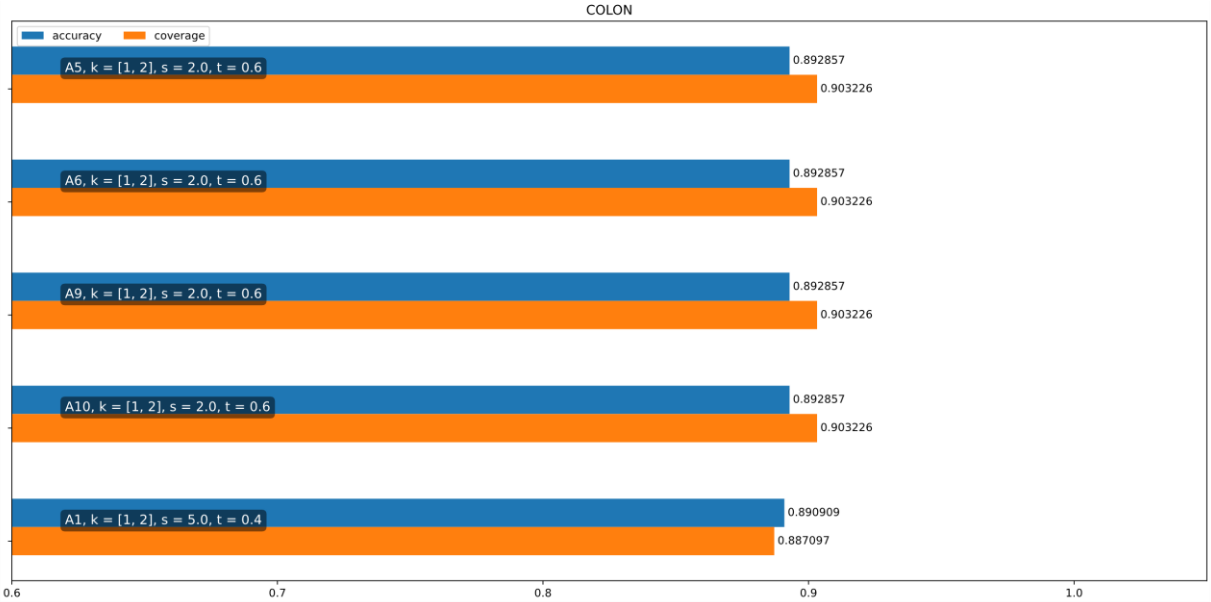

AML ALL
accuracy
coverage
A10, k = [2], s = 30.0, t = 0.5
0.986111
1
A10, k = [1], s = 50.0, t = 0.6
0.986111
1
A10, k = [2], s = 50.0, t = 0.5
0.986111
1
A1, k = [2], s = 20.0, t = 0.4
0.985915
0.986111
A5, k = [2], s = 20.0, t = 0.6
0.985915
0.986111
0.6
0.7
0.8
0.9
1.0

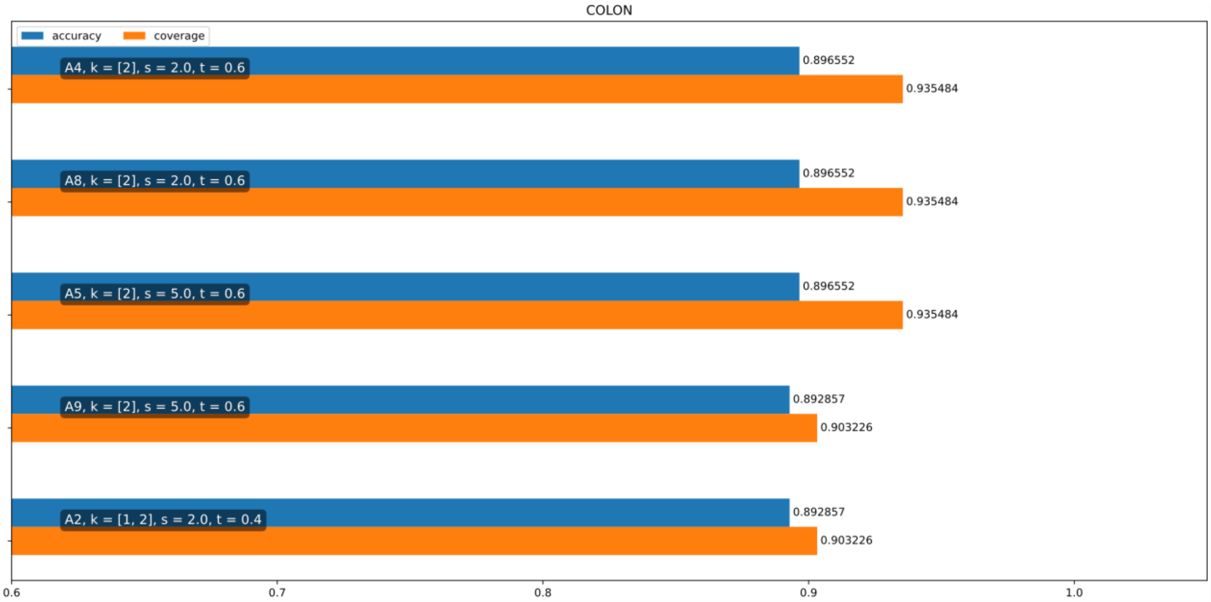

AML ALL
accuracy
coverage
A1, k = [1], s = 50.0, t = 0.4
0.985915
0.986111
A1, k = [1], s = 5.0, t = 0.4
0.985714
0.972222
A1, k = [1], s = 30.0, t = 0.5
0.985714
0.972222
A5, k = [2], s = 30.0, t = 0.5
0.985714
0.972222
A10, k = [1, 2], s = 5.0, t = 0.6
0.985714
0.972222
0.6
0.7
0.8
0.9
1.0

1.2. Colon

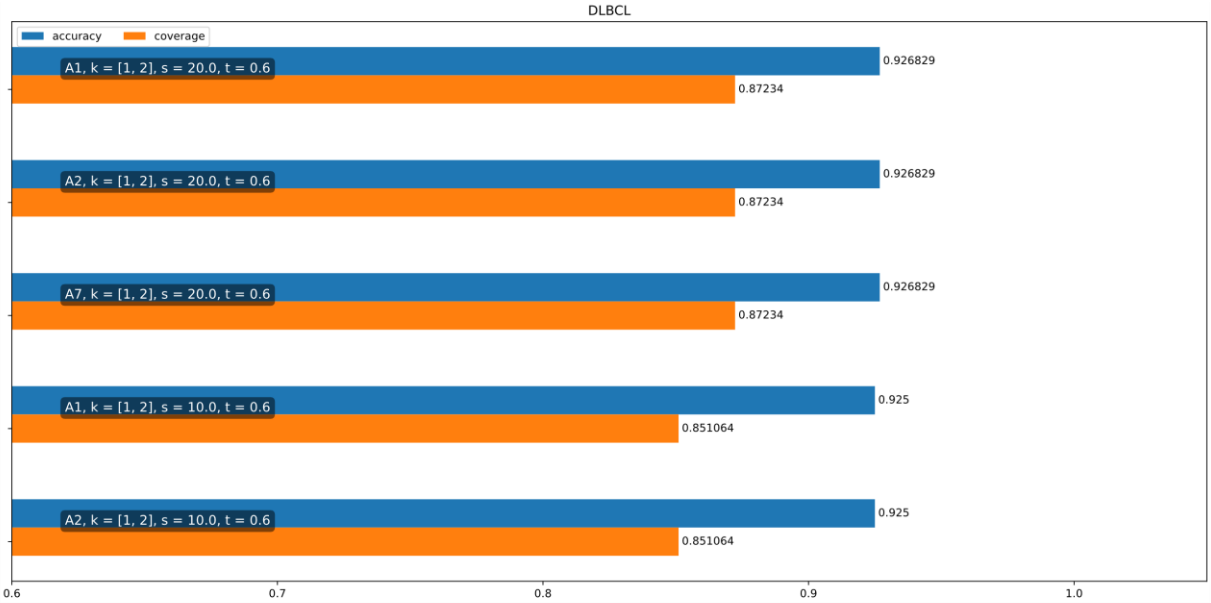

COLON
accuracy
coverage
A5, k = [2], s = 2.0, t = 0.5
0.912281
0.919355
A6, k = [2], s = 2.0, t = 0.5
0.912281
0.919355
A10, k = [2], s = 2.0, t = 0.5
0.912281
0.919355
A1, k = [1, 2], s = 2.0, t = 0.4
0.909091
0.887097
A5, k = [1, 2], s = 2.0, t = 0.4
0.909091
0.887097
0.6
0.7
0.8
0.9
1.0

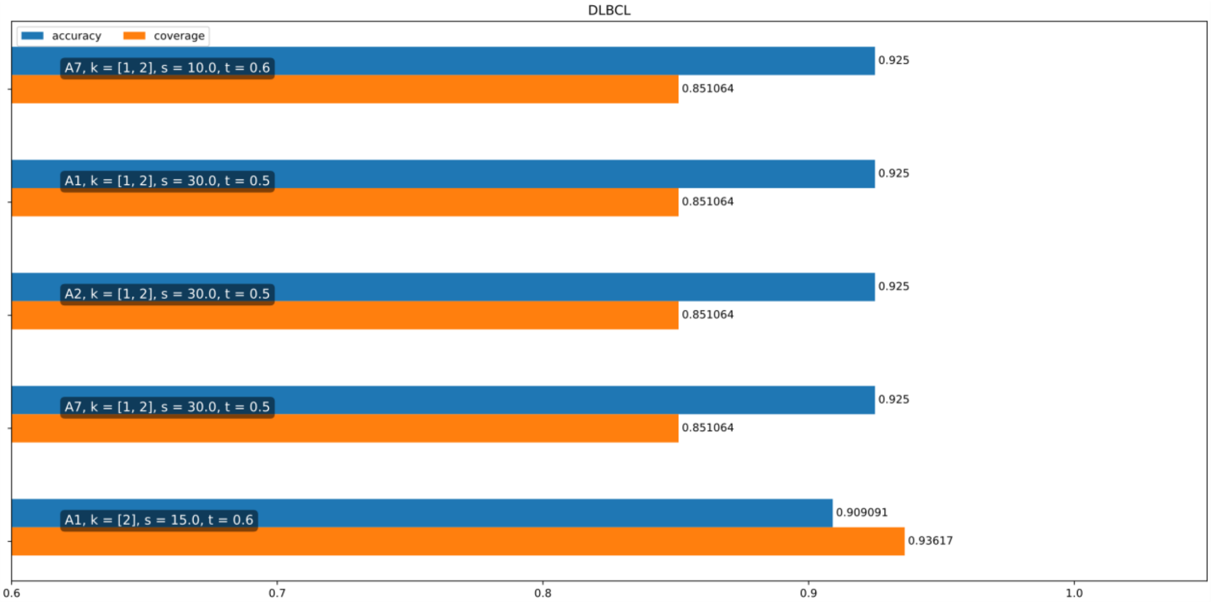

COLON
accuracy
coverage
A5, k = [1, 2], s = 2.0, t = 0.5
0.909091
0.887097
A6, k = [1, 2], s = 2.0, t = 0.5
0.909091
0.887097
A10, k = [1, 2], s = 2.0, t = 0.4
0.909091
0.887097
A10, k = [1, 2], s = 2.0, t = 0.5
0.909091
0.887097
A3, k = [2], s = 2.0, t = 0.6
0.896552
0.935484
0.6
0.7
0.8
0.9
1.0

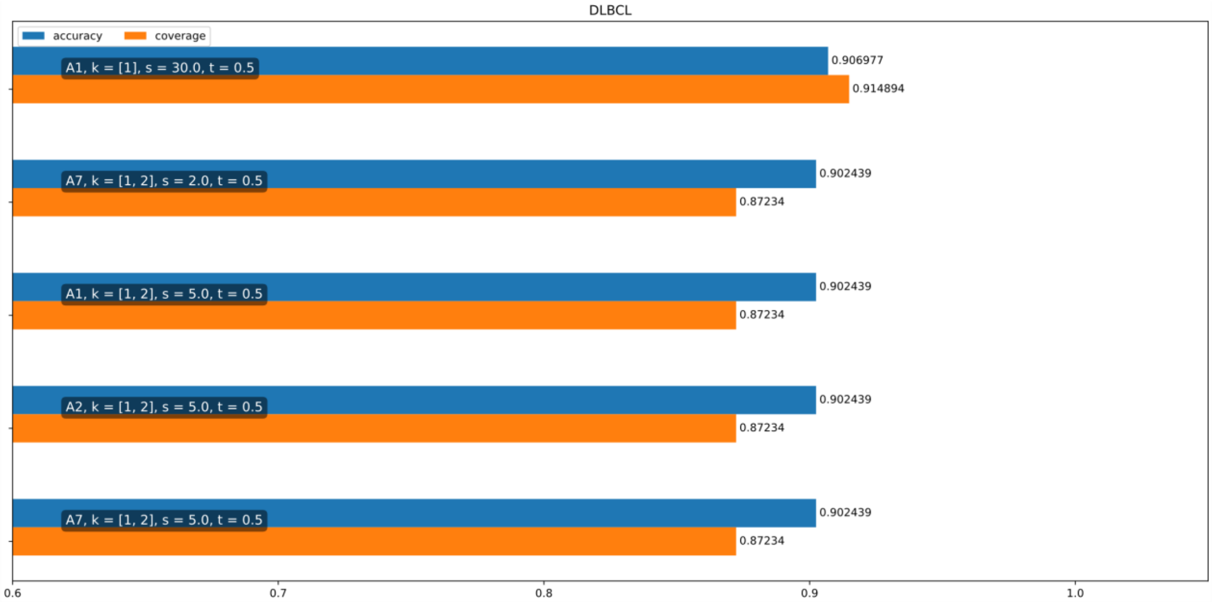

COLON
accuracy
coverage
A5, k = [1, 2], s = 2.0, t = 0.6
0.892857
0.903226
A6, k = [1, 2], s = 2.0, t = 0.6
0.892857
0.903226
A9, k = [1, 2], s = 2.0, t = 0.6
0.892857
0.903226
A10, k = [1, 2], s = 2.0, t = 0.6
0.892857
0.903226
A1, k = [1, 2], s = 5.0, t = 0.4
0.890909
0.887097
0.6
0.7
0.8
0.9
1.0

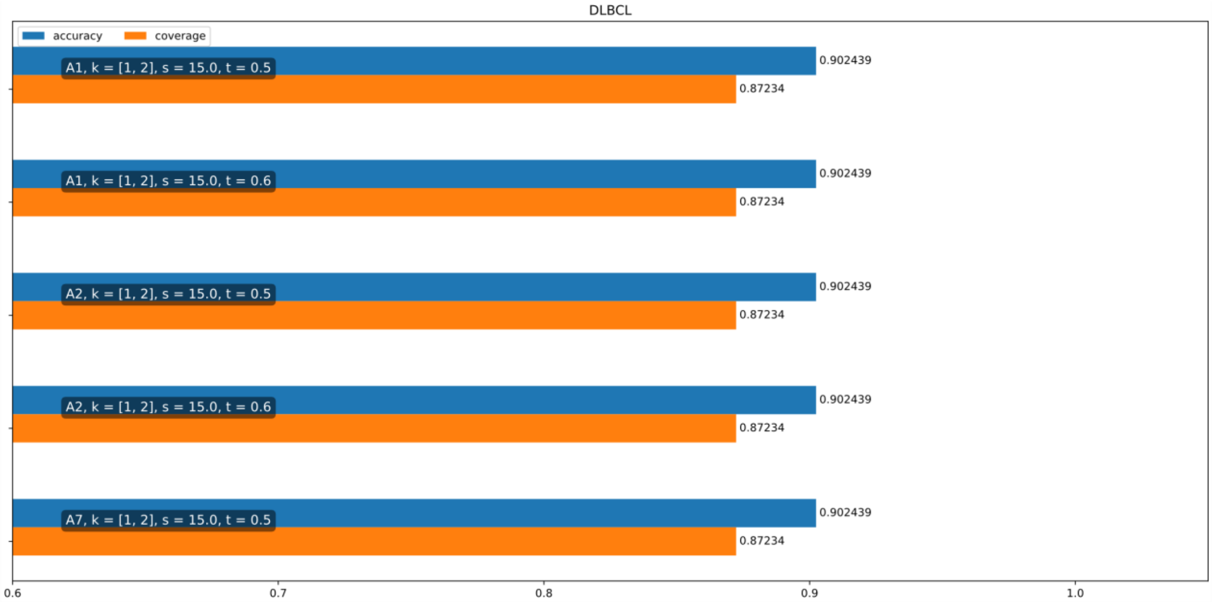

COLON
accuracy
coverage
A4, k = [2], s = 2.0, t = 0.6
0.896552
0.935484
A8, k = [2], s = 2.0, t = 0.6
0.896552
0.935484
A5, k = [2], s = 5.0, t = 0.6
0.896552
0.935484
A9, k = [2], s = 5.0, t = 0.6
0.892857
0.903226
A2, k = [1, 2], s = 2.0, t = 0.4
0.892857
0.903226
0.6
0.7
0.8
0.9
1.0

1.3. DLBCL

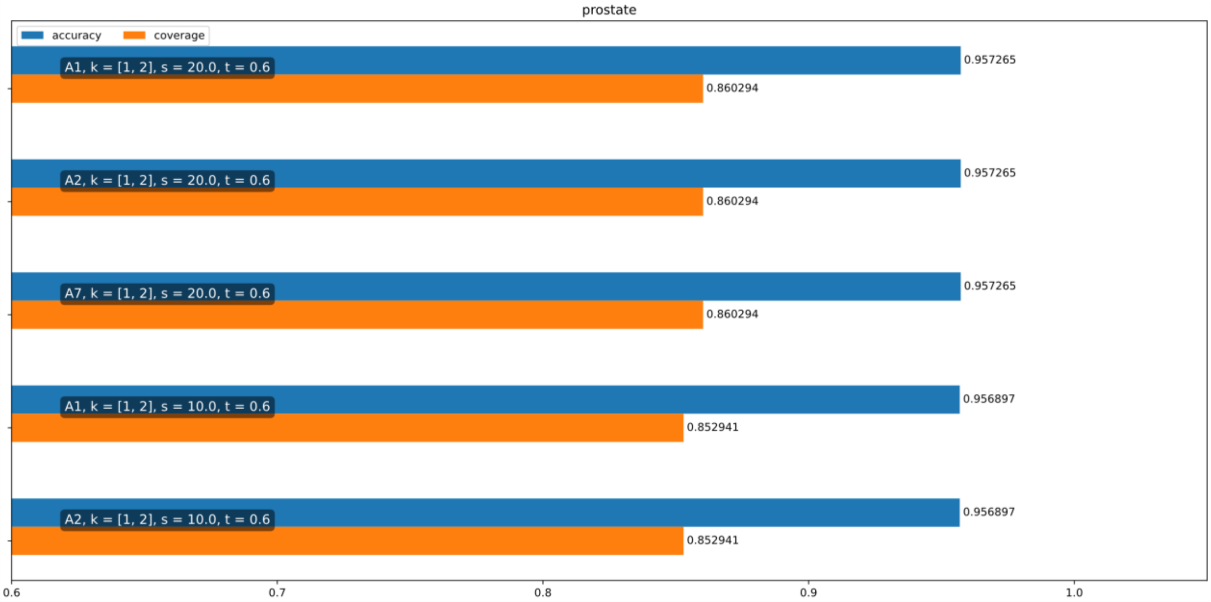

DLBCL
accuracy
coverage
A1, k = [1, 2], s = 20.0, t = 0.6
0.926829
0.87234
A2, k = [1, 2], s = 20.0, t = 0.6
0.926829
0.87234
A7, k = [1, 2], s = 20.0, t = 0.6
0.926829
0.87234
A1, k = [1, 2], s = 10.0, t = 0.6
0.925
0.851064
A2, k = [1, 2], s = 10.0, t = 0.6
0.925
0.851064
0.6
0.7
0.8
0.9
1.0

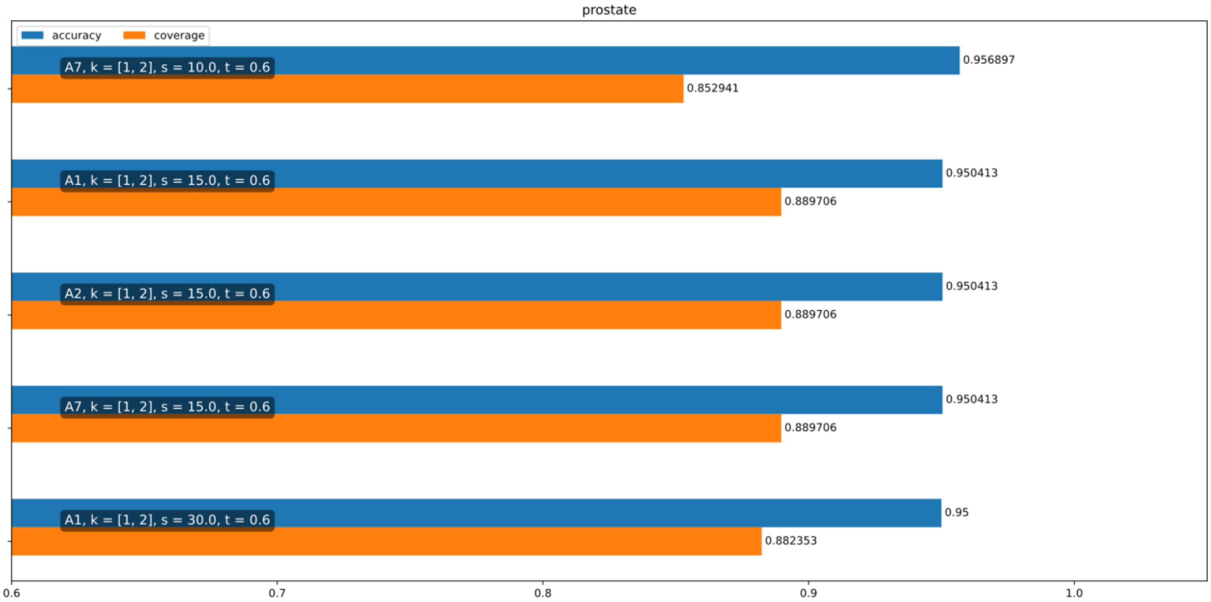

DLBCL
accuracy
coverage
A7, k = [1, 2], s = 10.0, t = 0.6
0.925
0.851064
A1, k = [1, 2], s = 30.0, t = 0.5
0.925
0.851064
A2, k = [1, 2], s = 30.0, t = 0.5
0.925
0.851064
A7, k = [1, 2], s = 30.0, t = 0.5
0.925
0.851064
A1, k = [2], s = 15.0, t = 0.6
0.909091
0.93617
0.6
0.7
0.8
0.9
1.0

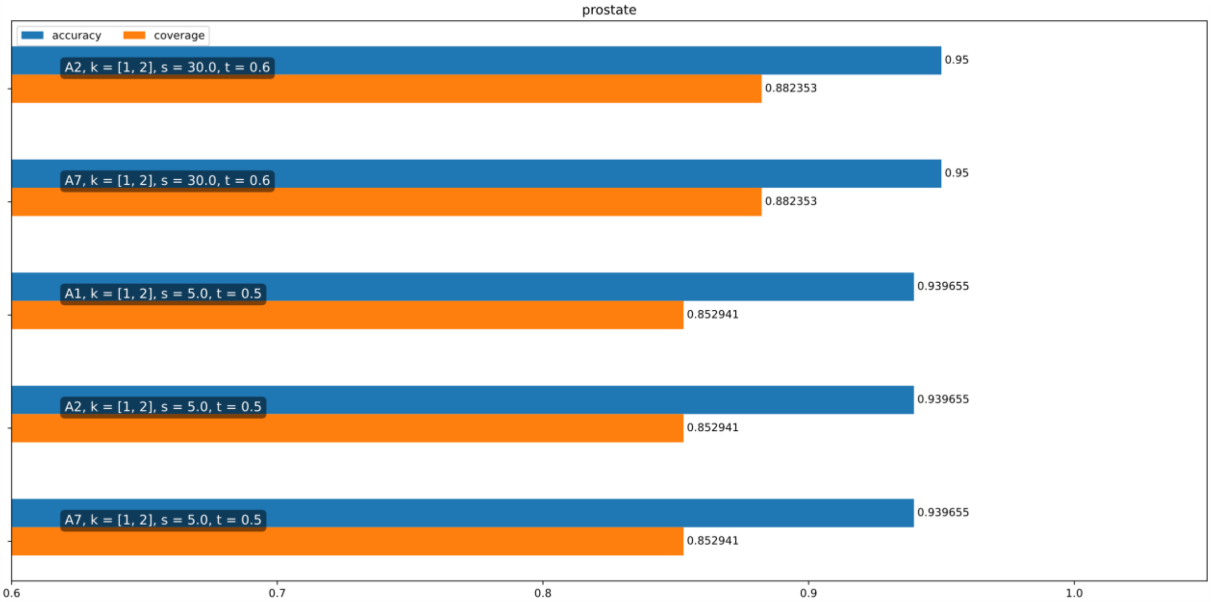

DLBCL
accuracy
coverage
A1, k = [1], s = 30.0, t = 0.5
0.906977
0.914894
A7, k = [1, 2], s = 2.0, t = 0.5
0.902439
0.87234
A1, k = [1, 2], s = 5.0, t = 0.5
0.902439
0.87234
A2, k = [1, 2], s = 5.0, t = 0.5
0.902439
0.87234
A7, k = [1, 2], s = 5.0, t = 0.5
0.902439
0.87234
0.6
0.7
0.8
0.9
1.0

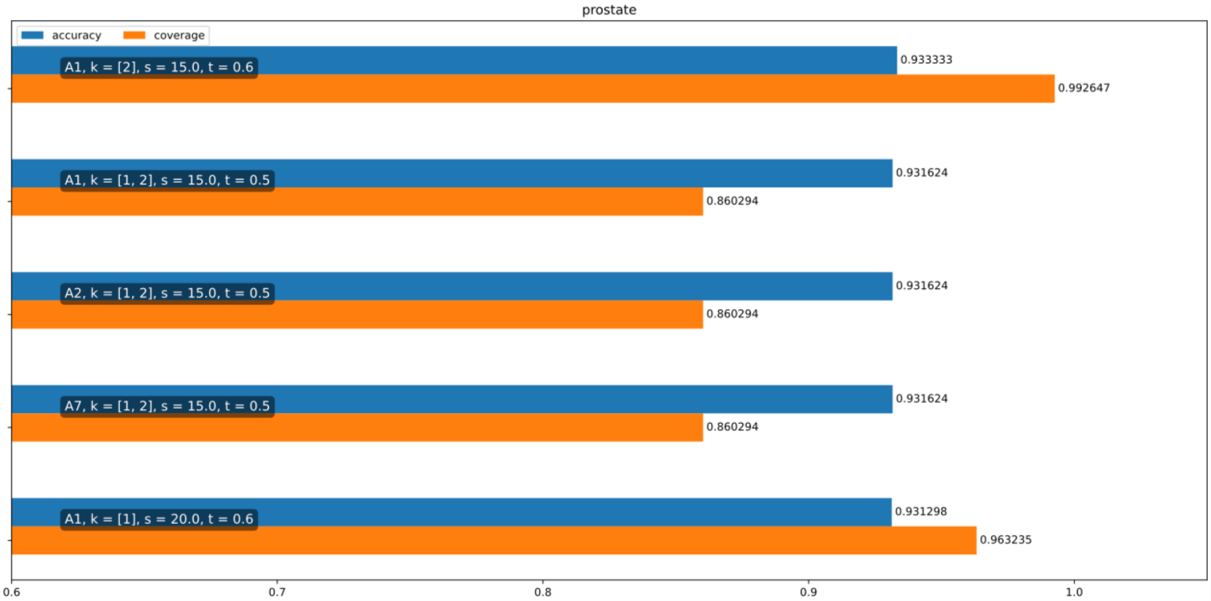

DLBCL
accuracy
coverage
A1, k = [1, 2], s = 15.0, t = 0.5
0.902439
0.87234
A1, k = [1, 2], s = 15.0, t = 0.6
0.902439
0.87234
A2, k = [1, 2], s = 15.0, t = 0.5
0.902439
0.87234
A2, k = [1, 2], s = 15.0, t = 0.6
0.902439
0.87234
A7, k = [1, 2], s = 15.0, t = 0.5
0.902439
0.87234
0.6
0.7
0.8
0.9
1.0

1.4. Prostate

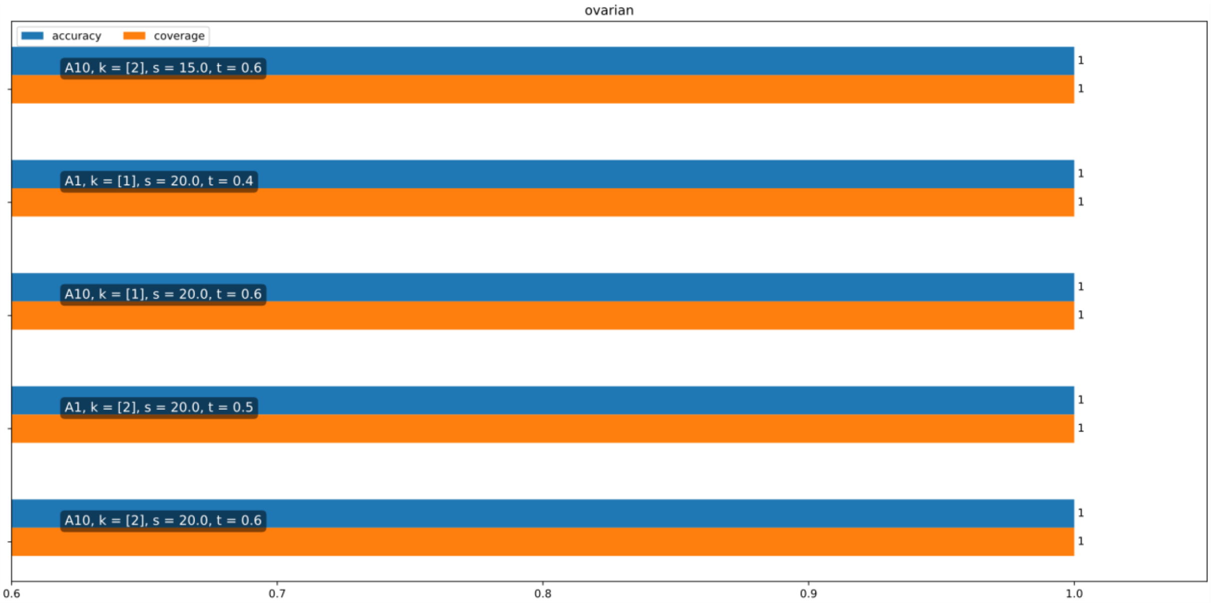

prostate
accuracy
coverage
A1, k = [1, 2], s = 20.0, t = 0.6
0.957265
0.860294
A2, k = [1, 2], s = 20.0, t = 0.6
0.957265
0.860294
A7, k = [1, 2], s = 20.0, t = 0.6
0.957265
0.860294
A1, k = [1, 2], s = 10.0, t = 0.6
0.956897
0.852941
A2, k = [1, 2], s = 10.0, t = 0.6
0.956897
0.852941
0.6
0.7
0.8
0.9
1.0

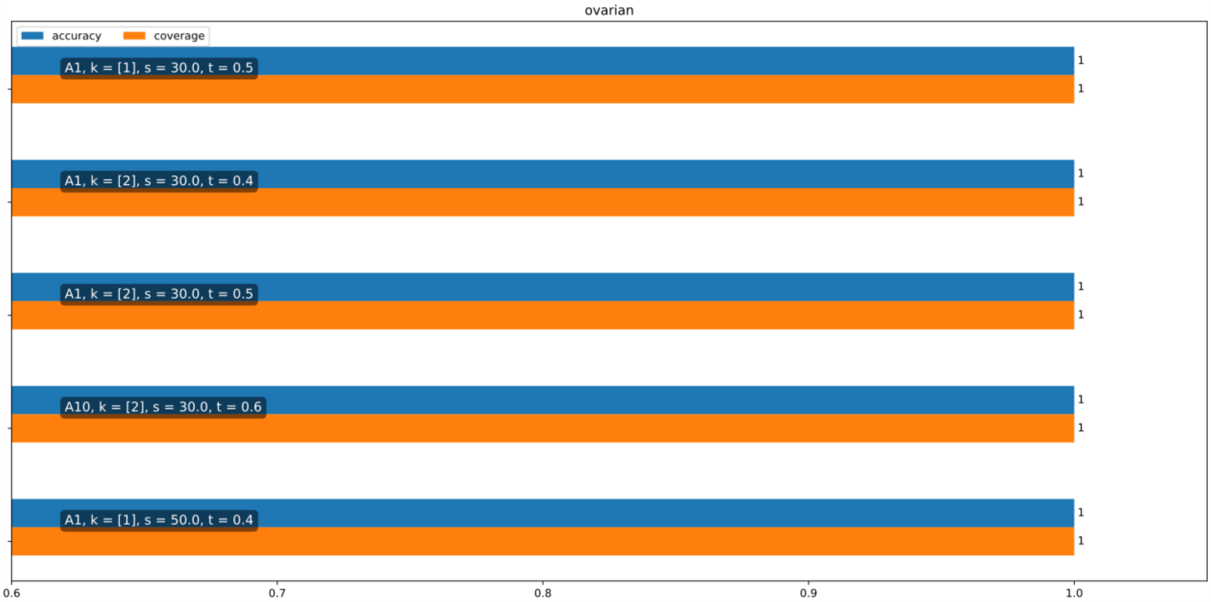

prostate
accuracy
coverage
A7, k = [1, 2], s = 10.0, t = 0.6
0.956897
0.852941
A1, k = [1, 2], s = 15.0, t = 0.6
0.950413
0.889706
A2, k = [1, 2], s = 15.0, t = 0.6
0.950413
0.889706
A7, k = [1, 2], s = 15.0, t = 0.6
0.950413
0.889706
A1, k = [1, 2], s = 30.0, t = 0.6
0.95
0.882353
0.6
0.7
0.8
0.9
1.0

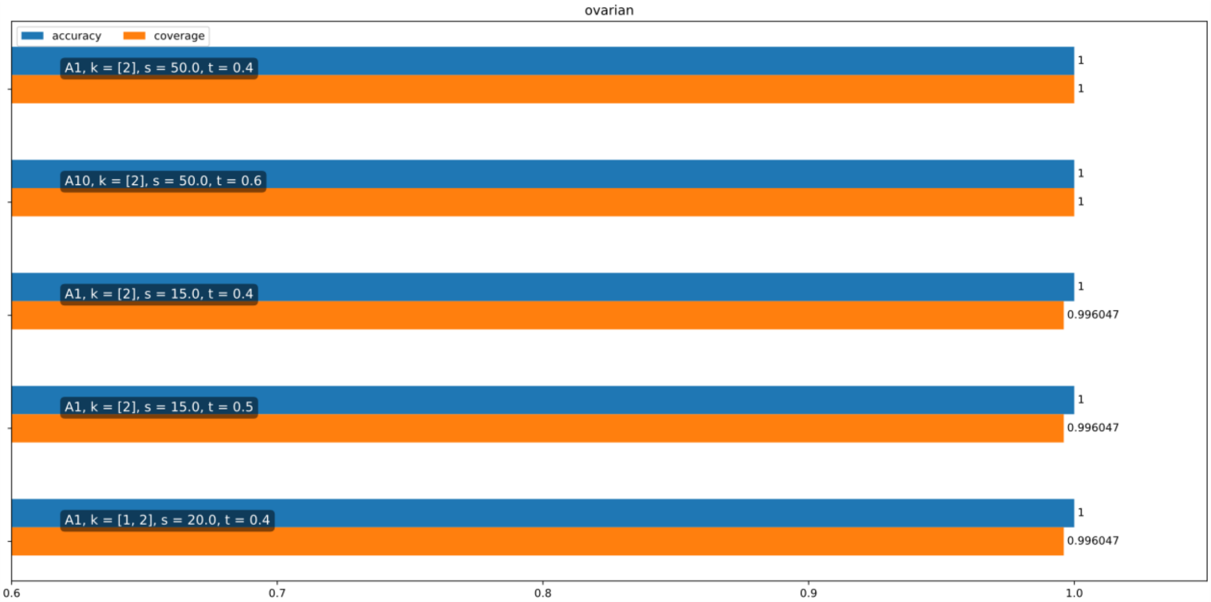

prostate
accuracy
coverage
A2, k = [1, 2], s = 30.0, t = 0.6
0.95
0.882353
A7, k = [1, 2], s = 30.0, t = 0.6
0.95
0.882353
A1, k = [1, 2], s = 5.0, t = 0.5
0.939655
0.852941
A2, k = [1, 2], s = 5.0, t = 0.5
0.939655
0.852941
A7, k = [1, 2], s = 5.0, t = 0.5
0.939655
0.852941
0.6
0.7
0.8
0.9
1.0

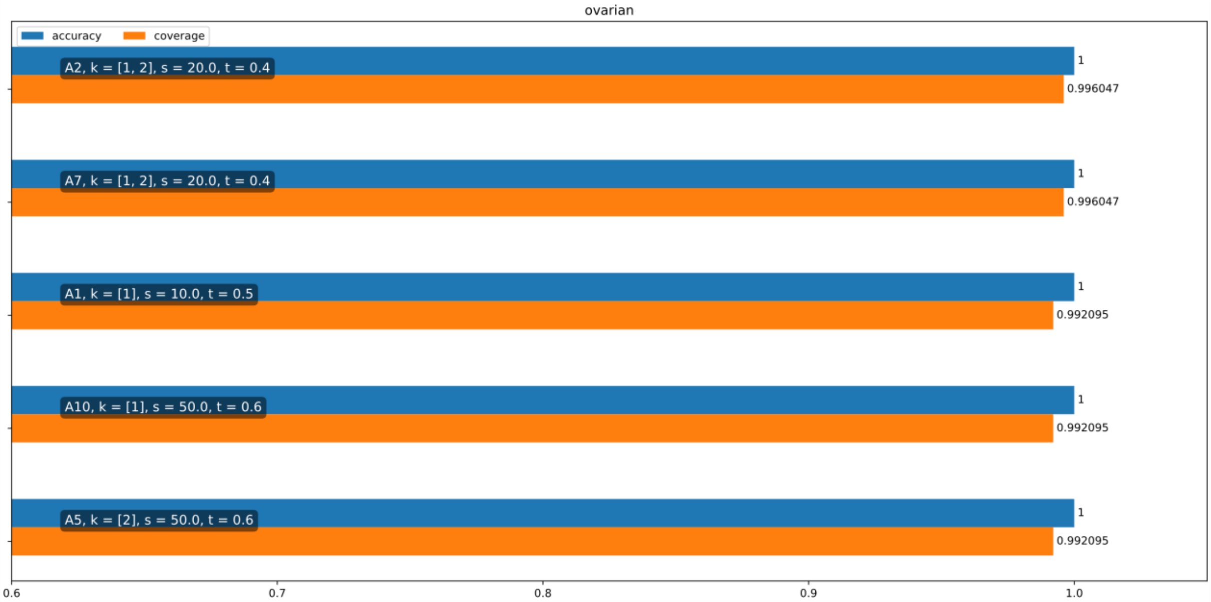

prostate
accuracy
coverage
A1, k = [2], s = 15.0, t = 0.6
0.933333
0.992647
A1, k = [1, 2], s = 15.0, t = 0.5
0.931624
0.860294
A2, k = [1, 2], s = 15.0, t = 0.5
0.931624
0.860294
A7, k = [1, 2], s = 15.0, t = 0.5
0.931624
0.860294
A1, k = [1], s = 20.0, t = 0.6
0.931298
0.963235
0.6
0.7
0.8
0.9
1.0

1.5. Ovarian


ovarian
accuracy
coverage
A10, k = [2], s = 15.0, t = 0.6
A1, k = [1], s = 20.0, t = 0.4
A10, k = [1], s = 20.0, t = 0.6
A1, k = [2], s = 20.0, t = 0.5
A10, k = [2], s = 20.0, t = 0.6
1
1
1
1
1
1
1
1
1
1
0.6
0.7
0.8
0.9
1.0


ovarian
accuracy
coverage
A1, k = [1], s = 30.0, t = 0.5
A1, k = [2], s = 30.0, t = 0.4
A1, k = [2], s = 30.0, t = 0.5
A10, k = [2], s = 30.0, t = 0.6
A1, k = [1], s = 50.0, t = 0.4
1
1
1
1
1
1
1
1
1
1
0.6
0.7
0.8
0.9
1.0





2. Statistical tests

2.1. Methodology

Based on the filtered results in Tables 3, 5, 7, 9, 11 there are obtained series of accuracy for fixed aggregation and interval-threshold but different s and t. However, only series with sufficient number of samples (above or equal to 10) and with mean accuracy comparable to the SOTA were considered.

To compare this series with SOTA models first, the Shapiro-Wilk test was performed to determine if one sample t-test is available (with additional check to not contain extreme outliers). If the series was not normally distributed, the Miao, Gel, and Gastwirth (MGG) symmetry test was performed and if the distribution was symmetric, the exact one sample Wilcoxon signed rank test was performed (due to the ties, sometimes present in data series). For some series of data neither t-test nor exact one sample Wilcoxon signed rank test was available. All tests were performed using a 0.05 significance level in R programming language.

Table 1. Shapiro-Wilk test. Bold font was used in the cases where the distribution is normal

series	W	p-value
AML ALL, A1 k=[1]	0,891843	0,024389

AML ALL, A1 k=[2]	0,862589	0,007054
AML ALL, A1 k=[1, 2]	0,739264	8,86E-05
AML ALL, A2 k=[1, 2]	0,739264	8,86E-05
AML ALL, A5 k=[1, 2]	0,854774	0,012692
AML ALL, A7 k=[1, 2]	0,744107	0,000103
AML ALL, A10 k=[1, 2]	0,905686	0,045165
COLON, A1 k=[1]	**0,912078**	**0,125704**
COLON, A1 k=[2]	**0,937927**	**0,324388**
COLON, A1 k=[1, 2]	**0,968286**	**0,852925**
COLON, A10 k=[2]	**0,932202**	**0,294286**
COLON, A10 k=[1, 2]	**0,917158**	**0,333862**
COLON, A2 k=[1, 2]	**0,948711**	**0,540873**
COLON, A5 k=[2]	**0,931437**	**0,319595**
COLON, A6 k=[2]	**0,953122**	**0,7055**
COLON, A7 k=[1, 2]	**0,949114**	**0,547042**
OVARIAN A1 k=[1]	0,775826	0,000287
OVARIAN A1 k=[2]	0,738545	8,67E-05
OVARIAN A1 k=[1, 2]	0,660697	9,26E-06
OVARIAN A2 k=[1, 2]	0,660356	9,18E-06
OVARIAN A5 k=[1]	0,794904	0,003165
OVARIAN A5 k=[2]	0,72897	8,99E-05
OVARIAN A5 k=[1, 2]	0,622027	0,000102
OVARIAN A6 k=[1]	0,820443	0,01748
OVARIAN A6 k=[2]	0,843133	0,010814
OVARIAN A6 k=[1, 2]	0,703955	0,000984
OVARIAN A7 k=[1, 2]v	0,660697	9,26E-06
OVARIAN A10 k=[1]	0,794389	0,000713
OVARIAN A10 k=[2]	0,754469	0,000143
OVARIAN A10 k=[1, 2]	0,77816	0,000415
prostate A1 k=[1, 2]	0,782761	0,001189
prostate A1 k=[1]	**0,945853**	**0,335122**
prostate A1 k=[2]	0,896272	0,029648
prostate A2 k=[1, 2]	0,804963	0,002375
prostate A5 k=[2]	**0,921433**	**0,298003**
prostate A7 k=[1, 2]	0,786981	0,001352
prostate A10 k=[2]	**0,925**	**0,29275**
DLBCL A1 k=[1, 2]	**0,906593**	**0,120066**
DLBCL A2 k=[1, 2]	**0,91151**	**0,142824**
DLBCL A7 k=[1, 2]	**0,904138**	**0,110106**

Table 2. MGG Symmetry Test. Bold font was used in the cases where the data are symmetric

series	statistic	p-value
AML ALL, A1 k=[1]	**-1,23555**	**0,216626**
AML ALL, A1 k=[2]	-2,57292	0,010084
AML ALL, A1 k=[1, 2]	**-0,91373**	**0,360856**
AML ALL, A2 k=[1, 2]	**-0,91373**	**0,360856**

AML ALL, A5 k=[1, 2]	**-1,92073**	**0,054766**
AML ALL, A7 k=[1, 2]	**-0,88522**	**0,376036**
AML ALL, A10 k=[1, 2]	-2,69147	0,007114
OVARIAN, A1 k=[1]	-3,56724	0,000361
OVARIAN, A1 k=[2]	-3,23553	0,001214
OVARIAN, A1 k=[1, 2]	-4,8396	1,3E-06
OVARIAN, A2 k=[1, 2]	-4,8396	1,3E-06
OVARIAN, A5 k=[1]	**-1,19308**	**0,232838**
OVARIAN, A5 k=[2]	-3,51416	0,000441
OVARIAN, A5 k=[1, 2]	**-0,85229**	**0,394055**
OVARIAN, A6 k=[1]	-2,36617	0,017973
OVARIAN, A6 k=[2]	-2,39562	0,016592
OVARIAN, A6 k=[1, 2]	-2,55678	0,010565
OVARIAN, A7 k=[1, 2]v	-4,8396	1,3E-06
OVARIAN, A10 k=[1]	**-1,91238**	**0,055827**
OVARIAN, A10 k=[2]	-3,87287	0,000108
OVARIAN, A10 k=[1, 2]	-2,96867	0,002991
prostate, A1 k=[1, 2]	-2,69562	0,007026
prostate, A1 k=[2]	-2,40168	0,01632
prostate, A2 k=[1, 2]	-2,74545	0,006043
prostate, A7 k=[1, 2]	-2,87105	0,004091

Table 3 Exact Wilcoxon signed rank test. Bold font was used in the cases of significant difference

series	V	p-value
AML ALL A1 k=[1] knn k=1	**204**	**0,001157**
AML ALL A1 k=[1] knn k=2	**231**	**9,54E-07**
AML ALL A1 k=[1] knn k=3	**224**	**1,72E-05**
AML ALL A1 k=[1] knn k=5	**231**	**9,54E-07**
AML ALL A1 k=[1] random forest	**50**	**0,021001**
AML ALL A1 k=[1, 2] knn k=1	**213**	**0,00023**
AML ALL A1 k=[1, 2] knn k=2	**230**	**1,91E-06**
AML ALL A1 k=[1, 2] knn k=3	**230**	**1,91E-06**
AML ALL A1 k=[1, 2] knn k=5	**230**	**1,91E-06**
AML ALL A1 k=[1, 2] random forest	101	0,626988
AML ALL A2 k=[1, 2] knn k=1	**213**	**0,00023**
AML ALL A2 k=[1, 2] knn k=2	**230**	**1,91E-06**
AML ALL A2 k=[1, 2] knn k=3	**230**	**1,91E-06**
AML ALL A2 k=[1, 2] knn k=5	**230**	**1,91E-06**
AML ALL A2 k=[1, 2] random forest	101	0,626988
AML ALL A5 k=[1, 2] knn k=1	**153**	**1,53E-05**
AML ALL A5 k=[1, 2] knn k=2	**153**	**1,53E-05**
AML ALL A5 k=[1, 2] knn k=3	**153**	**1,53E-05**
AML ALL A5 k=[1, 2] knn k=5	**153**	**1,53E-05**
AML ALL A5 k=[1, 2] random forest	90	0,538208
AML ALL A7 k=[1, 2] knn k=1	**213**	**0,00023**
AML ALL A7 k=[1, 2] knn k=2	**231**	**9,54E-07**

AML ALL A7 k=[1, 2] knn k=3	**230**	**1,91E-06**
AML ALL A7 k=[1, 2] knn k=5	**231**	**9,54E-07**
AML ALL A7 k=[1, 2] random forest	101	0,626988
OVARIAN A5 k=[1] knn k=1	91	0,080994
OVARIAN A5 k=[1] knn k=2	91	0,080994
OVARIAN A5 k=[1] knn k=3	87	0,131592
OVARIAN A5 k=[1] knn k=5	91	0,080994
OVARIAN A5 k=[1] random forest	**5**	**0,00061**
OVARIAN A5 k=[1, 2] knn k=1	**90**	**0,000488**
OVARIAN A5 k=[1, 2] knn k=2	**90**	**0,000488**
OVARIAN A5 k=[1, 2] knn k=3	**88**	**0,001221**
OVARIAN A5 k=[1, 2] knn k=5	**90**	**0,000488**
OVARIAN A5 k=[1, 2] random forest	**14**	**0,023682**
OVARIAN A10 k=[1] knn k=1	124	0,491716
OVARIAN A10 k=[1] knn k=2	113	0,776831
OVARIAN A10 k=[1] knn k=3	100	0,862623
OVARIAN A10 k=[1] knn k=5	113	0,776831
OVARIAN A10 k=[1] random forest	**8**	**4,39E-05**

Table 4 One sample t-test. Bold font was used in the cases of significant difference

series	statistic	p
COLON A1 k=[1] knn k=1	1,734633	0,103
COLON A1 k=[1] knn k=2	1,734633	0,103
COLON A1 k=[1] knn k=3	1,734633	0,103
COLON A1 k=[1] knn k=5	**7,314081**	**2,55E-06**
COLON A1 k=[1] random forest	**7,314081**	**2,55E-06**
COLON A1 k=[2] knn k=1	1,459003	0,165
COLON A1 k=[2] knn k=2	1,459003	0,165
COLON A1 k=[2] knn k=3	1,459003	0,165
COLON A1 k=[2] knn k=5	**6,053918**	**2,21E-05**
COLON A1 k=[2] random forest	**6,053918**	**2,21E-05**
COLON A1 k=[1, 2] knn k=1	**5,253814**	**0,000156**
COLON A1 k=[1, 2] knn k=2	**5,253814**	**0,000156**
COLON A1 k=[1, 2] knn k=3	**5,253814**	**0,000156**
COLON A1 k=[1, 2] knn k=5	**10,22664**	**1,39E-07**
COLON A1 k=[1, 2] random forest	**10,22664**	**1,39E-07**
COLON A10 k=[2] knn k=1	0,786319	0,445
COLON A10 k=[2] knn k=2	0,786319	0,445
COLON A10 k=[2] knn k=3	0,786319	0,445
COLON A10 k=[2] knn k=5	**4,855304**	**0,000255**
COLON A10 k=[2] random forest	**4,855304**	**0,000255**
COLON A10 k=[1, 2] knn k=1	**2,77546**	**0,0216**
COLON A10 k=[1, 2] knn k=2	**2,77546**	**0,0216**
COLON A10 k=[1, 2] knn k=3	**2,77546**	**0,0216**
COLON A10 k=[1, 2] knn k=5	**5,849461**	**0,000244**
COLON A10 k=[1, 2] random forest	**5,849461**	**0,000244**
COLON A2 k=[1, 2] knn k=1	**5,58961**	**8,78E-05**
COLON A2 k=[1, 2] knn k=2	**5,58961**	**8,78E-05**
COLON A2 k=[1, 2] knn k=3	**5,58961**	**8,78E-05**
COLON A2 k=[1, 2] knn k=5	**11,37143**	**3,97E-08**
COLON A2 k=[1, 2] random forest	**11,37143**	**3,97E-08**
COLON A5 k=[2] knn k=1	**2,404602**	**0,0318**
COLON A5 k=[2] knn k=2	**2,404602**	**0,0318**
COLON A5 k=[2] knn k=3	**2,404602**	**0,0318**
COLON A5 k=[2] knn k=5	**6,778901**	**0,000013**
COLON A5 k=[2] random forest	**6,778901**	**0,000013**
COLON A6 k=[2] knn k=1	1,081534	0,308
COLON A6 k=[2] knn k=2	1,081534	0,308
COLON A6 k=[2] knn k=3	1,081534	0,308
COLON A6 k=[2] knn k=5	**4,226342**	**0,00222**
COLON A6 k=[2] random forest	**4,226342**	**0,00222**
COLON A7 k=[1, 2] knn k=1	**5,212132**	**0,000168**
COLON A7 k=[1, 2] knn k=2	**5,212132**	**0,000168**
COLON A7 k=[1, 2] knn k=3	**5,212132**	**0,000168**
COLON A7 k=[1, 2] knn k=5	**10,64265**	**8,69E-08**

COLON A7 k=[1, 2] random forest	**10,64265**	**8,69E-08**
prostate A1 k=[1] knn k=1	**10,1644**	**6,94E-09**
prostate A1 k=[1] knn k=2	**10,1644**	**6,94E-09**
prostate A1 k=[1] knn k=3	**10,1644**	**6,94E-09**
prostate A1 k=[1] knn k=5	**11,89539**	**5,81E-10**
prostate A1 k=[1] random forest	**-8,13463**	**1,93E-07**
prostate A5 k=[2] knn k=1	**6,550198**	**4,13E-05**
prostate A5 k=[2] knn k=2	**6,550198**	**4,13E-05**
prostate A5 k=[2] knn k=3	**6,550198**	**4,13E-05**
prostate A5 k=[2] knn k=5	**8,024943**	**6,34E-06**
prostate A5 k=[2] random forest	**-9,03996**	**2,01E-06**
prostate A10 k=[2] knn k=1	**6,174766**	**4,76E-05**
prostate A10 k=[2] knn k=2	**6,174766**	**4,76E-05**
prostate A10 k=[2] knn k=3	**6,174766**	**4,76E-05**
prostate A10 k=[2] knn k=5	**7,667817**	**5,79E-06**
prostate A10 k=[2] random forest	**-9,60891**	**5,5E-07**
DLBCL A1 k=[1, 2] knn k=1	**6,043671**	**3,02E-05**
DLBCL A1 k=[1, 2] knn k=2	1,495912	0,157
DLBCL A1 k=[1, 2] knn k=3	**10,38471**	**5,84E-08**
DLBCL A1 k=[1, 2] knn k=5	**10,38471**	**5,84E-08**
DLBCL A1 k=[1, 2] random forest	**-7,18617**	**4,66E-06**
DLBCL A2 k=[1, 2] knn k=1	**4,04551**	**0,0012**
DLBCL A2 k=[1, 2] knn k=2	0,507355	0,62
DLBCL A2 k=[1, 2] knn k=3	**7,422839**	**3,24E-06**
DLBCL A2 k=[1, 2] knn k=5	**7,422839**	**3,24E-06**
DLBCL A2 k=[1, 2] random forest	**-6,2473**	**2,14E-05**
DLBCL A7 k=[1, 2] knn k=1	**6,358447**	**1,77E-05**
DLBCL A7 k=[1, 2] knn k=2	1,66072	0,119
DLBCL A7 k=[1, 2] knn k=3	**10,84264**	**3,4E-08**
DLBCL A7 k=[1, 2] knn k=5	**10,84264**	**3,4E-08**
DLBCL A7 k=[1, 2] random forest	**-7,30767**	**3,86E-06**

Table 5 The summary of statistical differences. Only the series when t-test or exact one sample Wilcoxon signed rank test was available are presented.

	kNN, k=1	KNN, k=2	kNN, k=3	kNN, k=5	Random Forest
AML ALL, A1, k=[1]	+	+	+	+	-
AML ALL, A1, k=[1, 2]	+	+	+	+	x
AML ALL, A2, k=[1, 2]	+	+	+	+	x
AML ALL, A5, k=[1, 2]	+	+	+	+	x
AML ALL, A7, k=[1, 2]	+	+	+	+	x
COLON, A1 k=[1]	x	x	x	+	+
COLON, A1 k=[2]	x	x	x	+	+
COLON, A1, k=[1, 2]	+	+	+	+	+
COLON, A2, k=[1, 2]	+	+	+	+	+
COLON, A5, k=[2]	+	+	+	+	+
COLON, A6, k=[2]	x	x	x	+	+

COLON, A7, k=[1, 2]	**+**	**+**	**+**	**+**	**+**
COLON, A10, k=[2]	x	x	x	**+**	**+**
COLON, A10, k=[1, 2]	**+**	**+**	**+**	**+**	**+**
OVARIAN, A5, k=[1]	x	x	x	x	-
OVARIAN, A5, k=[1, 2]	**+**	**+**	**+**	**+**	-
OVARIAN, A10, k=[1]	x	x	x	x	-
DLBCL, A1, k=[1, 2]	**+**	x	**+**	**+**	-
DLBCL, A2, k=[1, 2]	**+**	x	**+**	**+**	-
DLBCL, A7, k=[1, 2]	**+**	x	**+**	**+**	-
PROSTATE, A1, k=[1]	**+**	**+**	**+**	**+**	-
PROSTATE, A5, k=[2]	**+**	**+**	**+**	**+**	-
PROSTATE, A10, k=[2]	**+**	**+**	**+**	**+**	-

Legend:

-: statistically significant difference in favour of SOTA model

***+:* statistically significant difference in favour of the proposed model**

x: no statistically significant difference