

TABLE 2. Results of MC-DC SVM cross-validation on dataset 1.

Sigma	TPs	FPs	PPV%	TPR% ^a	TPR% ^b
1.0	91	18	83.5	46.9	34.2
1.1	111	24	82.2	57.2	41.7
1.2	124	28	81.6	63.9	46.6
1.3	134	35	79.3	69.0	50.4
1.4	148	41	78.3	76.3	55.6
1.5	154	49	75.9	79.4	57.9
2.0	166	79	67.8	85.6	62.4

^aTotal of 371 chromosomes with both centromeres correctly detected by Centromere SVM.
^bTotal of 531 chromosomes with all known DCs scored, regardless of results of Centromere SVM.

TABLE 3. Results of MC-DC SVM test on dataset 2.

σ Value	No. TPs	No. FPs	PPV%	TPR% ^a	TPR% ^b
0.9	173	65	72.6	46.6	32.6
1.0	210	96	68.6	56.6	39.6
1.1	240	149	61.7	64.7	45.2
1.2	264	186	58.7	71.2	49.7
1.3	279	234	54.4	75.2	52.5
1.4	286	264	52.0	77.1	53.9
1.5	294	302	49.3	79.3	55.4

^aTotal of 194 with both centromeres correctly detected by Centromere SVM.
^bTotal of 266 with all known DCs scored, regardless of results of Centromere SVM.

TABLE 4. Performance of MC-DC SVM on dataset 3 at different exposure levels: Comparison with expert scoring.

Source of dicentric chromosome data		SVM σ value							HC ^b	CNL ^b	UWO ^a
		Performanc criteria									
High-Dose chromosome data, commonly scored ^b	TPs	71	79	90	98	102	108	110	175	176	179
	FPs	13	17	33	39	46	54	66	4	3	0
	PPV%	84.5	82.3	73.2	71.5	68.9	66.7	62.5	97.8	98.3	100
	TPR%	39.7	44.1	50.3	54.8	57.0	60.3	61.5	97.8	98.3	100
All High-Dose chromosome data ^c	TPs	214	250	280	301	314	327	333	N/A	N/A	476
	FPs	43	53	81	104	125	148	172			0
	PPV%	83.3	82.5	77.6	74.3	71.5	68.8	65.9			100
	TPR%	45.0	52.5	58.8	63.2	66.0	68.7	70.0			100
Low-Dose chromosome data ^c	TPs	13	18	18	20	20	20	20	N/A	N/A	27
	FPs	37	51	67	90	120	136	156			0
	PPV%	26.0	26.1	21.2	18.2	14.3	12.8	11.4			100
	TPR%	48.2	66.7	66.7	74.1	74.1	74.1	74.1			100

^aResults scored by University of Western Ontario (UWO/JHMK). DCs scored by UWO are treated as ground truth. Calculation of TPs and FPS based on comparing scoring by SVMs, by HC, and by CNL with ground truth.
^bThe DC chromosome subset commonly scored by UWO, Health Canada (HC), and Canadian Nuclear Laboratories (CNL) and by the software was exposed to high dose radiation.
^cAll data in the high-dose subset, scored by UWO and the software. This includes images that were not scored by all three experts. N/A, not applicable; TPs, true positives; FPS, false positive DCs; PPV, positive predictive value; TPR, true positive rate.

1)
Li Y, Knoll JHM, Wilkins R, Flegal FN, and Rogan PK. Automated Discrimination of Dicentric and Monocentric Chromosomes by Machine Learning-based Image Processing. Microscopy Research & Technique 79:393-402 (2016).