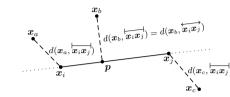
A CHEAPER RECTIFIED-NEAREST-FEATURE-LINE-SEGMENT CLASSIFIER BASED ON SAFE POINTS

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Rectified-Nearest-Feature-Line-Segment (RNFLS) classifier



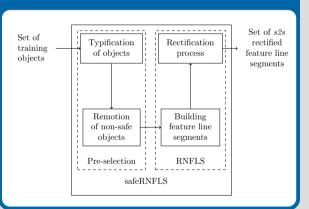
- RNFLS [1] **improves** over NFL [2] by solving two drawbacks of the latter: *interpolation* and *extrapolation* inaccuracies.
- Segmentation: Distances on the extrapolating part of the feature line are replaced with the distance to the nearest endpoint.
- Rectification: Remove feature lines segments crossing the territory of other classes. Very costly!
 - Degenerated lines are also considered. So, RNFLS includes 1-NN as a special case.

Typification according to the 5-nearest neighbors

According to the proportion $\{Same \ class\}: \{Different \ class\}$ among its 5-nearest neighbors, a point \boldsymbol{x} is categorized as [3]:

- **safe** (*s*) if 5:0 or 4:1;
- **borderline** (b) if 3:2 or 2:3;
- **rare** (*r*) if 1:4 but, only if its nearest neighbor from the same class has, in turn, a proportion or either 0:5 or 1:4. Otherwise, *x* is *b* [4];
- outlier (o) if 0:5.

safeRNFLS: the cheaper proposal



Classification accuracies (20 rep., 50-50 random train-test)

Proposed typification of feature line segments

• We propose to categorize each feature line segment according to the types

of its endpoints: s2s, s2b, s2r, s2o, b2b, b2r, b2o, r2r, r2o, o2o.

• The most preserved category after the rectification process is s2s. In

• Hypothesis: removing of all non-safe examples, prior the building of the

feature line segments, allows to avoid computations without significantly deteriorating the classification performance of the original RNFLS.

addition, most of the class labels are assigned by s2s feature line segments.

	(a) 1-NN [·]	vs. safeNN	(b) RNFLS	vs. safeRNFLS	(c) NFL vs. safeNFL		
Dataset	1-NN	safeNN	RNFLS	safeRNFLS	NFL	safeNFL	
Hepatitis	92.25 ± 0.95	87.75 ± 1.16	91.50 ± 0.99	$91.38 {\pm} 0.99$	93.62 ± 0.86	$93.00 {\pm} 0.90$	
Iris	93.40 ± 0.64	$93.67 {\pm} 0.63$	94.87 ± 0.57	$94.80 {\pm} 0.57$	87.07±0.87	$87.47 {\pm} 0.85$	
Pima	70.29 ± 0.52	72.93 ± 0.51	74.14±0.50	$74.44 {\pm} 0.50$	68.05 ± 0.53	$68.31 {\pm} 0.53$	
Wine	94.33 ± 0.55	$94.27 {\pm} 0.55$	95.45 ± 0.49	$95.34 {\pm} 0.50$	95.73 ± 0.48	$95.62 {\pm} 0.49$	
Liver	59.83 ± 0.83	$58.32 {\pm} 0.84$	63.67 ± 0.82	$62.86 {\pm} 0.82$	61.16 ± 0.83	$61.04 {\pm} 0.83$	
Ionosphere	84.49 ± 0.61	$77.50 {\pm} 0.70$	90.43 ± 0.50	$89.38 {\pm} 0.52$	83.89 ± 0.62	$83.38 {\pm} 0.63$	
WDBC	94.88 ± 0.29	95.61 ± 0.27	96.47 ± 0.24	$96.53 {\pm} 0.24$	94.77 ± 0.29	$94.88 {\pm} 0.29$	
WPBC	65.46 ± 1.08	$75.36 {\pm} 0.98$	72.99 ± 1.01	74.33 ± 0.99	72.16 ± 1.02	$71.75 {\pm} 1.02$	
Glass	66.40 ± 1.02	58.41 ± 1.07	68.36 ± 1.01	67.10 ± 1.02	62.90 ± 1.04	$60.28 {\pm} 1.06$	
Gastro	52.11 ± 1.81	$49.08 {\pm} 1.81$	55.66 ± 1.8	45.53 ± 1.81	58.55 ± 1.79	$51.97 {\pm} 1.81$	

Execution times (in seconds) and percentage of savings

				(1)			()		
	(a) 1-NN vs. safeNN			(b) RNFLS vs. safeRNFLS			(c) NFL vs. safeNFL		
Dataset	1-NN	safeNN	Saving	RNFLS	safeRNFLS	Saving	NFL	safeNFL	Saving
Hepatitis	0.03	0.02	7.27%	0.44	0.40	8.53%	0.49	0.46	6.78%
Iris	0.14	0.10	26.20%	1.56	1.38	11.56%	1.41	1.26	10.56%
Pima	2.03	0.91	55.11%	127.74	96.19	24.70%	334.62	134.60	59.78%
Wine	0.11	0.08	21.17%	1.74	1.69	2.90%	2.59	2.08	19.85%
Liver	0.34	0.11	69.49%	4.71	1.72	63.54%	28.85	2.82	90.22%
Ionosphere	0.35	0.27	21.35%	17.62	14.77	16.12%	33.67	27.08	19.59%
WDBC	0.91	0.87	4.21%	101.81	98.03	3.71%	135.29	117.02	13.51%
WPBC	0.11	0.06	45.63%	2.64	1.78	32.54%	6.24	1.21	80.53%
Glass	0.13	0.05	61.60%	1.08	0.42	61.12%	3.55	0.88	75.31%
Gastro	0.02	0.005	78.90%	0.06	0.01	81.14%	0.34	0.004	98.89%

Conclusions

- *s2s* feature line segments are typically the ones providing the class label assignments for the RNFLS classifier; see the exhaustive study in our conference paper.
- **safeRNFLS** is, in general, **not significantly different** from RNFLS but **cheaper** (saved computations and excecution times, in most cases, are outstanding).
- Safe variants of 1-NN and NFL were also studied; see results for **safeNN** and **safeNFL** respectively.
- safeRNFLS is not recommended for complicated compositions along with very sparse representations (few examples in very high-dimensional feature spaces); c.f. Gastro.

References

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