































































	Feat	ure Red	uction I	Results
-	Method	Minimum No. of Features for 80% Accuracy	Highest Accuracy (No. Features)	P-value of paired <i>t</i> test against the result from the original 84 features
	None	N/N	85% (all 84)	N/N
	PCA	17	83% (41)	N/N
	NLPCA	N/N	75% (64)	N/N
	KPCA	17	86% (117)	0.38
	ICA	22	83% (41)	N/N
	Informatio n Gain	11	87% (72)	0.08
	SDA	8	87% (39)	0.02
Annias tas Dia	FDR	18	86% (26)	0.16
Carnes	Genetic Algorithm	N/N	88% (43)	0.01







































	2D Classification											
	Results											
	True		Output of the Classifier								]	
	Clas s	DNA	ER	Gia	Gpp	Lam	Mit	Nuc	Act	TfR	Tub	1
	DNA	99	1	0	0	0	0	0	0	0	0	1
	ER	0	97	0	0	0	2	0	0	0	1	1
	Gia	0	0	91	7	0	0	0	0	2	0	1
	Gpp	0	0	14	82	0	0	2	0	1	0	1
	Lam	0	0	1	0	88	1	0	0	10	0	1
	Mit	0	3	0	0	0	92	0	0	3	3	1
	Nuc	0	0	0	0	0	0	99	0	1	0	1
	Act	0	0	0	0	0	0	0	100	0	0	1
	TfR	0	1	0	0	12	2	0	1	81	2	1
	Tub	and a	2	0	0	0	1	0	0	1	95	1
	n in sge to b	hoodedy	(	Dvera	all ac	cura	cy =	92%				
Carn	egie M	lellon					-					

	Human Classification Results									
True	Output of the Classifier									
s S	DNA	ER	Gia	Gpp	Lam	Mit	Nuc	Act	TfR	Tub
DNA	100	0	0	0	0	0	0	0	0	0
ER	0	90	0	0	3	6	0	0	0	0
Gia	0	0	56	36	3	3	0	0	0	0
Gpp	0	0	54	33	0	0	0	0	3	0
Lam	0	0	6	0	73	0	0	0	20	0
Mit	0	3	0	0	0	96	0	0	0	3
Nuc	0	0	0	0	0	0	100	0	0	0
Act	0	0	0	0	0	0	0	100	0	0
TfR	0	13	0	0	3	0	0	0	83	0
Tub	0	3	0	0	0	0	0	3	0	93















![](_page_10_Picture_4.jpeg)

![](_page_10_Picture_5.jpeg)

![](_page_11_Figure_0.jpeg)

![](_page_11_Figure_1.jpeg)

![](_page_11_Figure_2.jpeg)

![](_page_11_Picture_3.jpeg)

![](_page_11_Figure_4.jpeg)

![](_page_11_Figure_5.jpeg)

![](_page_12_Figure_0.jpeg)

![](_page_12_Figure_1.jpeg)

![](_page_12_Picture_2.jpeg)

![](_page_12_Figure_3.jpeg)

![](_page_12_Figure_4.jpeg)

![](_page_13_Picture_0.jpeg)

![](_page_13_Figure_1.jpeg)

![](_page_13_Picture_2.jpeg)

![](_page_13_Figure_3.jpeg)

![](_page_13_Figure_4.jpeg)

![](_page_13_Figure_5.jpeg)

![](_page_14_Figure_0.jpeg)

![](_page_14_Figure_1.jpeg)

![](_page_14_Picture_2.jpeg)

![](_page_14_Picture_3.jpeg)

![](_page_14_Figure_4.jpeg)

![](_page_14_Picture_5.jpeg)

![](_page_15_Figure_0.jpeg)

![](_page_15_Figure_1.jpeg)

![](_page_15_Figure_2.jpeg)

![](_page_15_Figure_3.jpeg)

![](_page_15_Figure_4.jpeg)

![](_page_15_Figure_5.jpeg)

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![](_page_16_Picture_15.jpeg)

![](_page_16_Picture_16.jpeg)

![](_page_16_Figure_17.jpeg)

![](_page_17_Figure_0.jpeg)

![](_page_17_Picture_1.jpeg)

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![](_page_17_Picture_4.jpeg)

![](_page_17_Picture_5.jpeg)

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K. Huang, J. Lin, J.A. Gajnak, and R.F. Murphy (2002). Image Content-based Retrieval and Automated Interpretation of Fluorescence Microscope Images via the Protein Subcellular Location Image Database. *Proceedings of the 2002 IEEE International Symposium on Biomedical Imaging (ISBI 2002)*, pp. 325-328.

![](_page_17_Picture_8.jpeg)

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