

Ensembles of selected classifiers and clusters

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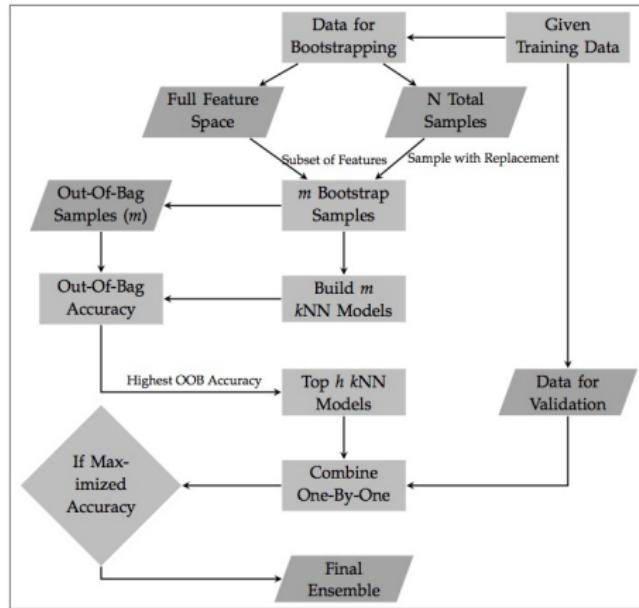
based on joint work on new methods with W Adler, PO Degens, A Gul, T Hothorn,
Z Khan, O Mahmoud, R Medellin, S Potapov and M Schumacher

Overview

- 1 Ensembles of selected classifiers
- 2 Optimal selection of cutpoints
- 3 Ensemble methods for cluster analysis

Ensemble of Subset of k -Nearest Neighbours Models

Gul et al. (ECDA2014, Springer 2016); R CRAN package ESKNN (2015)



Ensemble of Subset of k -Nearest Neighbours Models

Bench mark data sets

Data Sets	Sample size	Features	Feature Type (Continuous/Discrete/Catagorical)	Class Samples
Nki 70	144	76	(76/0/0)	48/96
SRBCT	54	2308	(2308/0/0)	25/29
Breast Cancer	77	4869	(4869/0/0)	33/44
DLBCL	77	5469	(5469/0/0)	19/58
Pomeroy	60	7128	(7128/0/0)	21/39
Golub Leukemia	72	7129	(7129/0/0)	25/47
West BC	49	7129	(7129/0/0)	24/25
Shipp	77	7129	(7129/0/0)	19/58

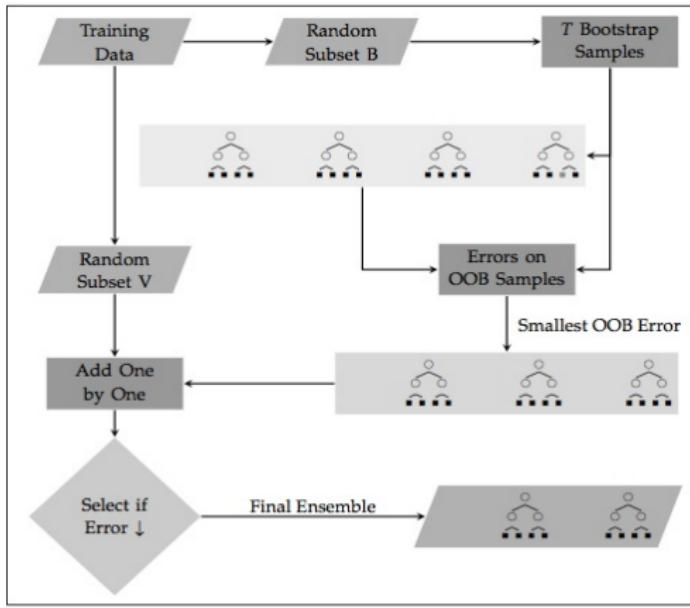
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Results

Data Sets	RF	SVM	ESkNN
Nki 70	0.141	0.266	0.147
SRBCT	0.002	0.035	0.049
Breast Cancer	0.379	0.399	0.371
DLBCL	0.104	0.083	0.069
Pomeroy	0.417	0.312	0.399
Golub Leukaemia	0.012	0.049	0.058
West BC	0.426	0.408	0.477
Shipp	0.095	0.097	0.092

Ensemble of Optimal Trees

Khan et al. (ECDA2014, Springer 2016); R CRAN package OTE (2015)



Data Set	<i>n</i>	<i>d</i>	FT (R/I/N)	kNN	Tree	RF	NH	SVM (Radial)	SVM (Linear)	SVM (Bessel)	SVM (Lapla.)	OTE
Mammogr.	830	5	(0/5/0)	0.141	0.123	0.129	0.121	0.134	0.125	0.131	0.135	0.137
Dystrophy	209	5	(2/3/0)	0.105	0.134	0.095	0.116	0.083	0.087	0.080	0.079	0.086
Monk3	122	6	(0/6/0)	0.089	0.069	0.066	0.182	0.070	0.157	0.066	0.094	0.061
Appendicitis	106	7	(6/0/0)	0.126	0.135	0.120	0.117	0.1360	0.1257	0.116	0.118	0.124
SAHeart	462	9	(5/3/1)	0.209	0.207	0.190	0.188	0.185	0.179	0.197	0.182	0.201
tic-tac-toe	958	9	(0/0/9)	0.228	0.147	0.041	0.120	0.148	0.219	0.120	0.197	0.044
Heart	303	13	(1/12/0)	0.222	0.168	0.123	0.144	0.144	0.128	0.123	0.125	0.129
House vote	232	16	(0/0/16)	0.066	0.032	0.029	0.066	0.030	0.035	0.158	0.039	0.029
Bands	365	19	(13/6/0)	0.223	0.255	0.188	0.224	0.199	0.203	0.223	0.211	0.181
Hepatitis	80	20	(2/18/0)	0.311	0.138	0.097	0.095	0.096	0.104	0.116	0.089	0.088
Parkinson	195	22	(22/0/0)	0.115	0.114	0.068	0.093	0.076	0.120	0.154	0.093	0.064
Body	507	23	(22/1/0)	0.019	0.073	0.031	0.055	0.012	0.012	0.238	0.022	0.030
Thyroid	9172	27	(3/2/22)	0.031	0.010	0.008	0.016	0.039	0.032	0.057	0.038	0.008
WDBC	569	29	(29/0/0)	0.054	0.064	0.031	0.043	0.027	0.021	0.203	0.028	0.031
WPBC	198	32	(30/2/0)	0.183	0.213	0.168	0.169	0.160	0.154	0.181	0.163	0.165
Oil-Spill	937	49	(40/9/0)	0.040	0.033	0.028	0.029	0.033	0.037	0.033	0.036	0.027
Spam base	4601	57	(55/2/0)	0.174	0.095	0.038	0.091	0.073	0.062	0.241	0.081	0.037
Glaucoma	196	62	(62/0/0)	0.137	0.110	0.089	0.092	0.094	0.124	0.219	0.119	0.090
Nki 70	144	76	(71/5/0)	0.146	0.141	0.147	0.147	0.168	0.202	0.235	0.183	0.133
Musk	476	166	(0/166/0)	0.142	0.188	0.096	0.175	0.096	0.110	0.247	0.189	0.087

Fair method: p -value adjusted classification trees

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- The set of objects is split into two subsets based on the factor \hat{k} and the corresponding cutpoint $\hat{\mu}$, if the adjusted p -value for K factors is smaller or equal to the prespecified value p_{stop} :

$$P_{H_0}(M(\mathbf{a}, \mathbf{X}, \varepsilon_1, \varepsilon_2) > b) \leq p_{stop} .$$

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$$P_{H_0}(M(\mathbf{a}, \mathbf{X}, \varepsilon_1, \varepsilon_2) > b) \leq p_{stop} .$$

- c) The partition procedure is stopped, if there exists no allowable split, or if $P_{H_0}(M(\mathbf{a}, \mathbf{X}, \varepsilon_1, \varepsilon_2) > b) > p_{stop}$ or because of the n_{min} criterion.

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- d) For each of the two subsets we repeat this procedure.

Clustering methods:

- Idea following Chen et al (2005) proposal 'Novel Hybrid Hierarchical-K-means Clustering Method (H-K-means) for Microarray Analysis'
- Improvement of algorithm; idea to estimate the number of clusters by hierarchical clustering
- R package work in progress

Cluster evaluation:

- Nonparametric bootstrap evaluation (Felsenstein 1985)
- Parametric bootstrap evaluation (Lausen and Degens 1988)
- Statistical model $d = d_u + e$; three-objects-variance estimation can be seen as an ensemble method; ...

Discussion

- Combination of POS and Ensemble of Subset of k -Nearest Neighbours Models demonstrate possible gains
- OTE may allow further gains
- Improvement of gene selection using Proportional Overlapping Score (POS)
- Features measured on different scales - p -value adjusted classification trees
- Ensemble methods and evaluation for cluster analysis
- (Ensemble) cluster methods for feature selection to improve predictive accuracy

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