

Supervised Infinite Feature Selection

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Abstract

In this paper, we present a new feature selection method that is suitable for both unsupervised and supervised problems. We build upon the recently proposed Infinite Feature Selection (IFS) method where feature subsets of all sizes (including infinity) are considered. We extend IFS in two ways. First, we propose a supervised version of it. Second, we propose new ways of forming the feature adjacency matrix that perform better for unsupervised problems. We extensively evaluate our methods on many benchmark datasets, including large image-classification datasets (PASCAL VOC), and show that our methods outperform both the IFS and the widely used “minimum-redundancy maximum-relevancy (mRMR)” feature selection algorithm.

1 Introduction and Related Work

In many practical machine learning and classification tasks, we encounter a very large feature space with thousands of irrelevant and/or redundant features. Presence of such features causes high computational complexity, poor generalization performance and decreased learning accuracy [14, 20]. The task of feature selection is to identify a small subset of most important, i.e. representative and discriminative, features. Many feature selection algorithms have been proposed in the last three decades (e.g. [20, 24, 33, 3]). Among them, *filters* have generated much interest, because they are simple, fast and not biased to any special learner. In these methods, each candidate feature subset is evaluated independent of the final learner, based on a diverse set of evaluation measures including mutual information [31, 4], consistency [11], significance [25, 39], etc.

Most filter methods rely on the concept of feature relevance [4, 25, 40]. For a given learning task, a feature can be in one of the following three disjoint categories: strongly relevant, weakly relevant and irrelevant. Strongly relevant features contain information that is not present in any subset of other features

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and therefore they are always necessary for the underlying task. Weakly relevant features contains information which is already present in a subset of strongly or irrelevant features. These features can be unnecessary (redundant) or necessary (non-redundant) with certain conditions. Irrelevant features contain no useful information and are not necessary at all. An ideal feature selection algorithm should eliminate all the irrelevant features and weakly redundant features. However, constructing such an algorithm is computationally infeasible, as it requires to check exponentially many combinations of features to ascertain weak relevancy. Therefore, several heuristics are proposed in the literature, which consider limited combination sizes [26, 2, 31, 17, 40, 29, 39].

Recently, an interesting filter method called "infinite feature selection" (IFS) was proposed by [32]. This method ranks features based on path integrals and the centrality concept on a feature adjacency graph. The most appealing characteristics of this approach are 1) all possible subsets of features are considered in evaluating the rank of a given feature and 2) it is extremely efficient, as it converts the feature ranking problem to simply calculating the geometric series of an adjacency matrix. Although it outperforms most of the state-of-the-art feature selection methods in image classification and gene expression problems, the algorithm suffers from two important deficiencies. Firstly, it is an unsupervised feature selection algorithm, i.e. it does not use the provided labels in a supervised learning problem. Secondly, its feature redundancy measure is not able to capture complex non-linear dependencies.

In this paper, we improve the IFS method in two ways. First, we propose a method to form the feature adjacency matrix for supervised problems. Second, we propose alternative ways of forming the adjacency matrix for unsupervised scenarios. In our experiments, we extensively compare our new methods with IFS and other popular feature selection methods. We show that our proposed methods outperform IFS on many different benchmark datasets and large image-classification datasets (PASCAL VOC 2007 and 2012) as well¹. Source code of our methods will be released upon acceptance of the paper.

The remainder of the paper is organized as follows: Section 2 presents the general idea behind IFS. Section 3 discusses the feature adjacency matrix along with our proposals for proper construction of this matrix in supervised and unsupervised feature selection. Section 4 reports experimental results and Section 5 concludes the paper.

2 Infinite Feature Selection

In this section, we review the general idea behind the IFS algorithm as proposed by [32], for completeness. Given a dataset with m features $\{f_1, f_2, \dots, f_m\}$, an undirected complete weighted graph $G = (V, E, e)$ can be constructed such that $V = \{f_i | f_i \in F\}$ represents the vertices, $E = \{\{f_i, f_j\} | f_i, f_j \in F \wedge i \neq j\}$ represents the edges and $e : E \rightarrow \mathbb{R}$ is a function calculating the pairwise energies between features. G can be represented using an adjacency matrix A , such that

¹Leaderboard snapshot taken in December 2016:

http://user.ceng.metu.edu.tr/~emre/resources/SIFS_PASCAL_result.png.
Our submission is named "SE." Anonymous results link:
<http://host.robots.ox.ac.uk:8080/anonymous/MV5IFE.html>. Live leaderboard:
<http://host.robots.ox.ac.uk:8080/leaderboard/displaylb.php?challengeid=11&compid=1>

$a_{ij} = e(\{f_i f_j\})$. Let $P_{i,j}^l$ be the set of all paths of length l (including paths with cycles) between nodes i and j , and let A^l denote the power iteration of matrix A . An initial idea for feature selection could be choosing an appropriate length l , then calculating energy scores, $s_l(i)$, for each feature f_i as:

$$s_l(i) = \sum_{j \in V} \sum_{p \in P_{i,j}^l} \prod_{k=0}^{l-1} a_{v_k, v_{k+1}} = \sum_{j \in V} A^l(i, j), \quad (1)$$

and finally taking a subset of features with maximum energy value. However, this idea has two major drawbacks; first, cycles can have high impact in calculating the scores and second, computation of A^l is of order $O(n^4)$, which is impractical when the number of features is large. The main contribution by [32] is to address the deficiencies by expanding the path length to infinity and summing over all path lengths. By extending the path length to infinity, the probability of being part of a cycle is uniform for all the features so the cycle effect is somewhat normalized. Therefore, a new energy score for each feature f_i , considering all path lengths including infinity, can be calculated as:

$$s(i) = \left[\left(\left(\sum_{l=0}^{\infty} A^l \right) - \mathbf{I} \right) \bar{\mathbf{1}} \right]_i \quad (2)$$

where \mathbf{I} is the identity matrix and $\bar{\mathbf{1}}$ is a column vector of ones.

In matrix algebra, $\sum_{k=0}^{\infty} X^k$ is called the geometric series of matrix X . This series converges to $(\mathbf{I} - X)^{-1}$ if and only if $\rho(X) < 1$, where $\rho(X)$ is the maximum magnitude of the eigenvalues of X . For any matrix X , it can be shown that $\rho(rX) < 1$ if and only if $0 < r < \frac{1}{\rho(X)}$. Using this property, the regularized energy score for each feature f_i can be defined as

$$\begin{aligned} s'(i) &= \left[\left(\left(\sum_{l=0}^{\infty} r^l A^l \right) - \mathbf{I} \right) \bar{\mathbf{1}} \right]_i \\ &= \left[\left((\mathbf{I} - rA)^{-1} - \mathbf{I} \right) \bar{\mathbf{1}} \right]_i. \end{aligned} \quad (3)$$

Therefore, the computation of power iterations of matrix A in Eq.1, is reduced to computing $\left((\mathbf{I} - rA)^{-1} - \mathbf{I} \right)$, with a complexity of $O(n^{2.37})$.

3 Forming the Adjacency Matrix

As explained in Section 2, the IFS algorithm uses the adjacency matrix A to compute ranking scores for given feature distributions. Therefore, the formation of the matrix can be considered as the most important task in the approach. In this section, we propose new ways of constructing the matrix A both for supervised and unsupervised feature selection scenarios.

3.1 Unsupervised Feature Selection (mIFS)

Defining feature relevance in unsupervised learning is a big challenge, because we do not know a-priori what type of patterns to look for or which error metric to

use. Furthermore, these two aspects often depend on the dataset used. However, one can analyse the features in terms of redundancy and dispersion.

If a certain feature has zero dispersion (i.e. variance) over the examples in the dataset, then that feature does not have any information and can be discarded. For a feature with non-zero dispersion, although we can not definitively relate its relevance to its dispersion magnitude, it has been shown that using dispersion measures improves the performance [32, 20]. Let STD_f be the standard deviation of feature f . Our experiments also show that keeping features that have large standard deviation, i.e. STD_f , improves the classification accuracy.

The other measure we use in unsupervised feature selection is redundancy. Unlike relevance, redundancy is a well-defined problem in unsupervised learning and can be expressed in terms of dependency. For example, when the dependency among two disjoint feature subsets is large, one of them could be considered as redundant. [32] used the Spearman’s rank correlation coefficient as a measure of redundancy of a feature. However, this measure is not able to individuate complex non-linear dependencies between features (e.g. non-monotonic non-linear dependencies). Our experiments show that using a mutual information-based measure for redundancy yields better results in terms of classification accuracy. This is probably due to the fact that mutual information takes into account any kind of dependency (both linear and non-linear) between random variables [13]. For a given feature set F and a feature $f \in F$, we define this measure as:

$$RDN_f = \frac{1}{|F| - 1} \sum_{f' \in F - \{f\}} \text{MI}(f', f) \quad (4)$$

where, $\text{MI}(X, Y)$ is the mutual information between two random variables X and Y , and is defined as

$$\text{MI}(X, Y) = \int_{\mathcal{X}} \int_{\mathcal{Y}} p(X = x, Y = y) \log \left(\frac{p(X = x, Y = y)}{p(X = x)p(Y = y)} \right). \quad (5)$$

Overall, we propose the following adjacency matrix to be used in unsupervised feature selection scenarios:

$$a_{ij} = \alpha (\max (STD_{f_i}, STD_{f_j})) + (1 - \alpha) (1 - \min (RDN_{f_i}, RDN_{f_j})), \quad (6)$$

where $\alpha \in [0, 1]$ is a loading coefficient that controls the relative importance of relevance vs. redundancy. We name this way of constructing A as the modified infinite feature selection or mIFS, for short.

3.2 Supervised Feature Selection (SIFS)

In supervised machine learning, the goal is to learn a general form of an unknown mapping from a feature vector f to a target variable Y . Therefore, the relevance of features can be expressed in terms of the Y -related information they have. Mutual information would be a proper measure to capture this relevance.

We augment the supervised relevancy measure with an unsupervised redundancy measure. Although mutual information based redundancy yields good accuracy for unsupervised scenarios, our experiments show that when it is combined with the same measure for relevance analysis, the accuracy deteriorates

Table 1: Summary of the high dimensional benchmark datasets together with their main challenges and the state of the art (SoA) performances. The star(*) in the last column indicates that our methods achieved a new SoA for the corresponding dataset.

dataset	#feat.	#classes	#samples	few train	noise	SoA
USPS [7]	241	2	1.5K			96.6% [28]
GINA [9]	970	2	3153			99.7% [19]
Gisette [8]	5K	2	7K			99.9% [21]
Colon [1]	2K	2	62	✓	✓	89.6% [27] *
Lung181 [18]	12533	2	181	✓	✓	99.8% [32] *
DLBCL [34]	7129	2	77	✓	✓	98.3% [32] *
Prostate [36]	6033	2	102	✓	✓	99.94% [12]
Arcene [8]	10K	2	200			99.93% [30]
REGED0 [10]	999	2	20.5K	✓		100% [6]
MARTIO [10]	999	2	20.5K	✓		99.94% [5]
Madelon [8]	500	2	2.6K			98.0% [21]
Sido0 [10]	4932	2	22678			94.7% [22]
VOC 2007 [15]	<i>not specified</i>	20	9963		✓	83.5% [32]
VOC 2012 [16]	<i>not specified</i>	20	22531		✓	85.4% [16]

significantly. Therefore, for supervised feature selection, we propose to use Spearman’s rank correlation based redundancy. Specifically, we propose the following adjacency matrix:

$$a_{ij} = \alpha (\max(\text{MI}(f_i, Y), \text{MI}(f_j, Y))) + (1 - \alpha) (1 - |\text{SPR}(f_i, f_j)|), \quad (7)$$

where $\text{SPR}(X, Y)$ is the Spearman’s rank correlation coefficient. We name this method as supervised infinite feature selection or SIFS, for short.

4 Experimental Results

We conducted three sets of experiments. First, as preliminary experiments, we explored the effects of different ways of constructing the adjacency matrix on the classification performance of IFS and SIFS. Next, we compared the classification performances of the IFS with original settings, IFS with the adjacency matrix proposed in Eq.6 (i.e. mIFS), SIFS with the adjacency matrix proposed in Eq.7 and the well-known minimum-redundancy maximum-relevancy (mRMR) algorithm proposed by [31]. Finally, we focused on the image classification problem where we used SIFS to select features from the state-of-the-art convolutional neural networks (CNN).

Table 1 summarizes the 14 high-dimensional benchmark datasets that we used in our experiments. These benchmarks include handwritten character recognition (USPS, GINA and Gisette), cancer classification and prediction on genetic data (Colon, Lung181, DLBCL, Prostate, Arcene, REGED0 and MARTIO), generic feature selection (Madelon), pharmacology (Sido0), and image classification (PASCAL VOC 2007-2012). We have chosen these datasets in order to present a diverse set of challenges to the feature selection algorithms. This table also reports – to the best of our knowledge – the state-of-the-art (SoA) for each dataset.

We use linear SVM to assess the classification performance of the feature selection algorithms. To set the parameters in our models, namely the tradeoff

Table 2: Effect of pre-processing method on unsupervised feature selection. AUC (%) on different datasets of SVM classification, averaging the performance obtained with the first 10, 50, 100, 150, and 200 features (unsupervised feature selection).

Dataset	Accuracy					
	Original Data		Normalized Data		Standardized Data	
	avg	max	avg	max	avg	max
Colon	79.79	82.68	87.12	90.51	79.85	89.98
USPS	90.81	95.66	90.66	95.65	87.70	91.83
Madelon	60.84	61.89	61.84	63.99	55.86	60.67
GINA	71.90	79.93	79.07	86.53	81.83	91.03
Prostate	93.39	96.46	87.51	95.87	87.10	93.84
Mean	79.34	83.32	81.24	86.51	78.46	85.47

parameter α and the C parameter of the linear SVM, we used 5-fold cross validation on training data.

4.1 Preliminary Experiments

Here, we study the effects of different ways of constructing the adjacency matrix and different data pre-processing schemes on the classification performances of IFS and SIFS algorithms. We report the results on five smaller datasets USPS, GINA, Colon, Prostate and Madelon.

We consider three pre-processing schemes: 1) no pre-processing (i.e. original data), 2) standardization where each feature is transformed to zero mean and unit variance, and 3) normalization where each feature is transformed into the interval $[0, 1]$. The standard deviation constitutes an important part of the pairwise energy term in generating the adjacency matrix in IFS algorithm [32]. Table 2 reports the effects of the three data pre-processing schemes on the classification accuracy of IFS.

The classification accuracy is reported in two ways: avg and max. First, the feature selector ranks all the features. Then, a linear SVM is trained and tested using the top N features, yielding classification accuracy (percent correct). Considering all such accuracies obtained for $N \in \{10, 50, 100, 150, 200\}$, “avg” refers to the average of them and “max” refers to the maximum. “avg” has been used by [32], so do we in order to be compatible, however, we also report “max” in all our experiments.

Considering the pre-processing methods, “normalization” yields better classification performance (than “no-preprocessing”) for IFS 2. However, standardization has a reverse effect, except for GINA. When using standardized data, all the features have the same standard deviation 1, and therefore, we expect smaller (near 0) α values, representing more importance of the Spearman’s correlation coefficient part. However, our experimental results are incompatible with this expectation. For all the five datasets, the returned best α value is 1. This means that the IFS algorithm does not really use SPR and ranks the features based on their order in the dataset. Moreover, these results show that the Spearman’s correlation coefficient alone is not a good feature ranking method and it should be used in combination with other measures.

Table 3: Effects of redundancy (as measured by Spearman’s rank correlation (SPR) or mutual information based redundancy (RDN)) and data pre-processing method, without using a relevance measure, on unsupervised feature selection.

Dataset	Accuracy											
	Original Data				Normalized Data				Standardized Data			
	SPR		RDN		SPR		RDN		SPR		RDN	
	avg	max	avg	max	avg	max	avg	max	avg	max	avg	max
Colon	59.92	75.90	79.91	87.16	65.46	80.48	81.34	86.21	58.06	67.22	80.48	84.14
USPS	84.89	93.74	86.75	95.69	85.11	94.84	88.84	95.91	83.31	91.44	83.42	91.05
Madelon	50.06	51.19	51.89	55.94	50.48	52.28	57.04	60.37	49.74	50.70	50.61	51.14
GINA	62.31	75.99	63.30	71.45	66.45	80.79	64.47	76.96	66.50	79.69	73.92	85.90
Prostate	77.99	88.95	89.42	97.76	80.41	91.32	94.13	96.25	80.39	92.51	92.06	97.50
Mean	67.03	77.15	74.25	81.60	69.58	79.94	77.16	83.14	67.60	76.31	76.09	81.94

Table 4: Effects of redundancy (as measured by SPR or RDN) and data pre-processing method, together with standard-deviation (STD) based relevance, on unsupervised feature selection.

Dataset	Accuracy											
	Original Data				Normalized Data				Standardized Data			
	SPR		RDN		SPR		RDN		SPR		RDN	
	avg	max	avg	max	avg	max	avg	max	avg	max	avg	max
Colon	79.79	82.68	85.54	91.97	87.12	90.51	88.51	89.88	79.85	89.98	88.86	91.46
USPS	90.81	95.66	90.60	95.64	90.66	95.65	90.86	95.89	87.70	91.83	87.87	92.78
Madelon	60.84	61.89	61.46	62.46	61.84	63.99	62.16	63.91	55.86	60.67	53.50	57.94
GINA	71.90	79.93	70.40	80.39	79.07	86.53	79.58	87.09	81.83	91.03	79.56	89.50
Prostate	93.39	96.46	94.28	98.16	87.51	95.87	94.67	98.02	87.10	93.84	93.11	97.51
Mean	79.34	83.32	80.45	85.72	81.24	86.51	83.15	86.95	78.46	85.47	80.58	85.83

Table 3 reports the effects of using SPR or RDN – which are two different choices to measure redundancy – alone in the construction of the adjacency matrix. As it can be seen, RDN is superior in most of the cases and shows increases of up to 8% for all the three data formats. SPR is not able to individuate non-monotonic dependencies between features and therefore more complex functional dependencies between features are not measured. On the other hand, RDN uses mutual information, which is able to individuate any kind of dependency (linear and non-linear) between features. Table 4 reports the effects of using SPR/RDN when they are used in combination with standard deviation (STD) based relevance. As it can be seen, RDN is superior again for this adjacency matrix setting. When we use the mutual information based relevance (Table 5), the results are slightly different and the SPR shows better classification performance. Moreover, we get the best classification performance for standardized data format, which is in contrast with the unsupervised matrix settings.

In summary, the following two important results can be derived from all these preliminary experiments:

1. For *unsupervised* feature selection, *normalizing* the data and then using *STD based relevance* in combination with *RDN based redundancy* yield the best classification performance. This corresponds to our ‘modified infinite feature selection’ method, mIFS.
2. For *supervised* feature selection, *standardizing* the data and then using

Table 5: Effects of redundancy (as measured by SPR or RDN) and data pre-processing method, together with mutual information (MI) based relevance, on supervised feature selection

Dataset	Accuracy											
	Original Data				Normalized Data				Standardized Data			
	SPR		RDN		SPR		RDN		SPR		RDN	
	avg	max	avg	max	avg	max	avg	max	avg	max	avg	max
Colon	93.31	97.00	93.07	97.85	90.46	92.14	91.98	95.66	94.67	97.71	93.06	95.79
USPS	92.18	95.64	92.28	96.06	90.06	95.71	91.39	95.89	89.42	93.21	89.33	93.05
Madelon	60.93	62.78	62.00	62.41	61.63	62.65	59.16	60.89	63.83	64.46	63.55	63.97
GINA	86.17	89.22	82.08	88.80	91.30	93.08	91.01	92.93	93.09	92.74	90.94	93.09
Prostate	97.85	98.39	97.71	98.80	96.24	98.57	93.12	96.38	98.31	98.84	98.09	98.78
Mean	86.08	88.60	85.42	88.78	85.93	88.43	85.33	88.35	87.86	89.39	86.99	88.93

Table 6: Classification accuracies obtained using different feature selectors, namely IFS [32], mRMR [31], mIFS (ours) and SIFS (ours). (See Section 4.1 for the explanations of ‘‘avg’’ and ‘‘max’’.)

Dataset	IFS		mIFS		mRMR		SIFS	
	avg	max	avg	max	avg	max	avg	max
USPS	90.66	95.65	90.86	95.89	91.11	93.28	89.42	93.21
GINA	79.07	86.53	79.58	87.09	91.98	92.86	92.74	93.09
Gisette	95.94	97.62	95.93	97.62	97.75	99.06	96.66	98.64
Colon	87.12	90.51	88.51	89.88	89.03	91.32	94.67	97.71
Lung181	99.14	100.00	99.51	100.00	99.87	100.00	100.00	100.00
DLBCL	99.50	100.00	99.63	100.00	96.90	99.23	99.10	100.00
Prostate	87.51	95.87	94.67	98.02	97.25	97.84	98.31	98.84
Arcene	74.09	82.18	86.23	88.55	76.35	83.28	80.12	82.67
REGED0	81.98	95.57	83.86	95.92	99.13	99.79	99.70	99.87
MARTI0	65.98	73.16	59.34	72.87	79.31	90.41	83.70	91.23
Madelon	59.54	61.79	61.00	62.55	58.82	61.13	60.70	63.03
Sido0	87.07	91.98	86.96	91.88	87.20	91.13	92.26	92.80
Average	83.97	89.23	85.75	90.02	88.72	91.13	90.61	92.59

mutual information based relevance in combination with *SPR based redundancy* gives the best classification performance. This corresponds to our ‘supervised infinite feature selection’ method, SIFS.

4.2 Comparison with IFS and mRMR

Here, we compare the performances of the proposed infinite feature selection algorithms with the state-of-the-art algorithms. For unsupervised feature selection, we compare the original IFS method [32] with mIFS, our proposed method for unsupervised problems. All features are normalized before feature selection. On 9 out of 12 datasets mIFS outperforms IFS (Table 6). Specifically, we report 12% improvement on *Arcene* and 7% on *Prostate* datasets.

For supervised feature selection, we compare mRMR [31] – arguably, the most well known information theoretic feature selection algorithm – with SIFS, our proposed method for supervised problems. All features are standardized before feature selection. On 10 out of 12 datasets, SIFS outperforms mRMR (Table 6) with an average improvement of 1.89% in classification accuracy.

Table 7: mAP (%) results obtained using different feature selectors on the PASCAL VOC object recognition datasets. The numbers in parentheses are the percentages of features kept by the approach after the cross-validation phase for ResNet, GoogleNet and VGG-VD, respectively.

Dataset	SoA	No feature selection	mRMR	SIFS
VOC 2007	83.5%	84.63%	84.95% (60,70,70)	85.90% (40,60,60)
VOC 2012	85.4%	85.78%	85.88% (50,70,70)	86.50% (40,60,60)

Finally, we compare IFS [32] with our SIFS. On average (over 12 datasets), SIFS outperforms IFS with a margin of about 6% in classification accuracy, which shows the impact of using supervision for feature selection.

4.3 Image classification experiments on PASCAL VOC datasets

The experiments here considers a combination of feature selection and linear SVM applied to convolutional neural network (CNN) based features. We extracted CNN features from the penultimate layers of the ResNet [23] (1000 features), GoogleNet [37] (1000 features), and VGG-VD [35] (4096 features) deep networks. We used the models, pre-trained on ILSVRC, from the MatConvNet distribution [38]. On each of the three feature sets, we applied normalization and our supervised infinite feature selection. Then, we trained a linear SVM per set and averaged the three SVM scores to obtain final classification scores. Table 7 shows the mean average-precision (mAP) results for the PASCAL VOC 2007 and 2012 datasets, using different feature selectors. Our method, SIFS, outperforms both IFS and mRMR on both datasets².

5 Conclusions

In this paper we present two new ways of constructing the feature adjacency matrix for the infinite feature selection method. For unsupervised feature selection, we propose the mIFS method which uses a combination of standard-deviation based relevance and mutual information based redundancy. For supervised feature selection, we propose the SIFS method which uses a combination of mutual information based relevance and spearman’s rank correlation based redundancy. We tested the accuracy of the proposed methods on 14 high dimensional benchmark datasets using linear SVM. Our proposed methods, mIFS and SIFS, gave top performances on most of the benchmark datasets beating both IFS [32] and mRMR [31]. Our source code is available at GitHub³ for the sake of reproducibility of our results.

²Leaderboard snapshot taken in December 2016:

http://user.ceng.metu.edu.tr/~emre/resources/SIFS_PASCAL_result.png.

Our submission is named "SE." Anonymous results link: <http://host.robots.ox.ac.uk:8080/anonymous/MV5IFE.html>. Live leaderboard: <http://host.robots.ox.ac.uk:8080/leaderboard/displaylb.php?challengeid=11&compid=1>

³ <https://github.com/Sadegh28/SIFS>

References

- [1] ALON, U., BARKAI, N., NOTTERMAN, D. A., GISH, K., YBARRA, S., MACK, D., AND LEVINE, A. J. Broad patterns of gene expression revealed by clustering analysis of tumor and normal colon tissues probed by oligonucleotide arrays. In *Proceedings of the National Academy of Sciences* (1999), pp. 6745–6750.
- [2] BATTITI, R. Using mutual information for selecting features in supervised neural net learning. *IEEE Transactions on Neural Networks* 5, 4 (1994), 537–550.
- [3] BOLÓN-CANEDO, V., SÁNCHEZ-MAROÑO, N., AND ALONSO-BETANZOS, A. A review of feature selection methods on synthetic data. *Knowledge and Information Systems* 34, 3 (2013), 483–519.
- [4] BROWN, G., POCOCK, A., ZHAO, M.-J., AND LUJÁN, M. Conditional likelihood maximisation: A unifying framework for information theoretic feature selection. *Journal of Machine Learning Research* 13 (2012), 27–66.
- [5] CAWLEY, G. C. Causal and non-causal feature selection for ridge regression. In *WCCI Causation and Prediction Challenge* (2008), pp. 107–128.
- [6] CHANG, Y.-W., AND LIN, C.-J. Feature ranking using linear svm. In *WCCI Causation and Prediction Challenge* (2008), pp. 53–64.
- [7] CHAPELLE, O., SCHÖLKOPF, B., AND ZIEN, A. *SemiSupervised Learning*. MIT press, 2006.
- [8] CLOPINET. Feature Selection Challenge, NIPS 2003. <http://clopinet.com/isabelle/Projects/NIPS2003/>, 2003. [Online; accessed 06-March-2015].
- [9] CLOPINET. Performance Prediction Challenge, WCCI 2006. <http://clopinet.com/isabelle/Projects/modelselect/>, 2006. [Online; accessed 06-March-2015].
- [10] CLOPINET. Causation and Prediction Challenge, WCCI 2008. <http://www.causality.inf.ethz.ch>, 2008. [Online; accessed 06-March-2015].
- [11] DASH, M., AND LIU, H. Consistency-based search in feature selection. *Artificial Intelligence* 151, 1 (2003), 155–176.
- [12] DÍAZ-URIARTE, R., AND DE ANDRES, S. A. Gene selection and classification of microarray data using random forest. *BMC bioinformatics* 7, 1 (2006), 1.
- [13] DIONISIO, A., MENEZES, R., AND MENDES, D. A. Mutual information: a measure of dependency for nonlinear time series. *Physica A: Statistical Mechanics and its Applications* 344, 1 (2004), 326–329.
- [14] ESKANDARI, S., AND JAVIDI, M. M. Online streaming feature selection using rough sets. *International Journal of Approximate Reasoning* 69, C (2016), 35–57.

- [15] EVERINGHAM, M., VAN GOOL, L., WILLIAMS, C. K. I., WINN, J., AND ZISSERMAN, A. The PASCAL Visual Object Classes Challenge 2007 (VOC2007) Results. <http://www.pascal-network.org/challenges/VOC/voc2007/workshop/index.html>, 2007.
- [16] EVERINGHAM, M., VAN GOOL, L., WILLIAMS, C. K. I., WINN, J., AND ZISSERMAN, A. The PASCAL Visual Object Classes Challenge 2012 (VOC2012) Results. <http://www.pascal-network.org/challenges/VOC/voc2012/workshop/index.html>, 2012.
- [17] FLEURET, F. Fast binary feature selection with conditional mutual information. *Journal of Machine Learning Research* 5 (2004), 1531–1555.
- [18] GORDON, G. J., JENSEN, R. V., HSIAO, L.-L., GULLANS, S. R., BLUMENSTOCK, J. E., RAMASWAMY, S., RICHARDS, W. G., SUGARBAKER, D. J., AND BUENO, R. Translation of microarray data into clinically relevant cancer diagnostic tests using gene expression ratios in lung cancer and mesothelioma. *Cancer Research* 62, 17 (2002), 4963–4967.
- [19] GUYON, I., ALIFERIS, C. F., COOPER, G. F., ELISSEEFF, A., PELLET, J.-P., SPIRITES, P., AND STATNIKOV, A. R. Design and analysis of the causation and prediction challenge. In *WCCI Causation and Prediction Challenge* (2008), pp. 1–33.
- [20] GUYON, I., AND ELLISEEFF, A. An Introduction to Variable and Feature Selection. *Journal of Machine Learning Research* 3 (2003), 1157–1182.
- [21] GUYON, I., LI, J., MADER, T., PLETSCHER, P. A., SCHNEIDER, G., AND UHR, M. Competitive baseline methods set new standards for the {NIPS} 2003 feature selection benchmark. *Pattern Recognition Letters* 28, 12 (2007), 1438 – 1444.
- [22] GUYON, I., SAFFARI, A., DROR, G., AND CAWLEY, G. Analysis of the {IJCNN} 2007 agnostic learning vs. prior knowledge challenge. *Neural Networks* 21, 2–3 (2008), 544 – 550.
- [23] HE, K., ZHANG, X., REN, S., AND SUN, J. Deep residual learning for image recognition. *arXiv preprint arXiv:1512.03385* (2015).
- [24] KOHAVI, R., AND JOHN, G. H. Wrappers for feature subset selection. *Artificial Intelligence* 97, 1–2 (1997), 273–324.
- [25] KOLLER, D., AND SAHAMI, M. Toward optimal feature selection. Tech. Rep. 1996-77, Stanford InfoLab, 1996.
- [26] LEWIS, D. D. Feature selection and feature extraction for text categorization. In *Proceedings of the Workshop on Speech and Natural Language* (Stroudsburg, PA, USA, 1992), HLT '91, pp. 212–217.
- [27] LOVATO, P., BICEGO, M., CRISTANI, M., JOJIC, N., AND PERINA, A. Feature selection using counting grids: Application to microarray data. In *Structural, Syntactic, and Statistical Pattern Recognition: Joint IAPR International Workshop, SSPR&SPR 2012, Hiroshima, Japan, November 7-9, 2012. Proceedings* (2012), G. Gimel'farb, E. Hancock, A. Imiya, A. Kuijper, M. Kudo, S. Omachi, T. Windeatt, and K. Yamada, Eds., pp. 629–637.

- [28] MAJI, S., AND MALIK, J. Fast and accurate digit classification. *EECS Department, University of California, Berkeley, Tech. Rep. UCB/EECS-2009-159* (2009).
- [29] MEYER, P. E., AND BONTEMPI, G. *On the Use of Variable Complementarity for Feature Selection in Cancer Classification*. Springer Berlin Heidelberg, Berlin, Heidelberg, 2006, pp. 91–102.
- [30] NEAL, R. M., AND ZHANG, J. *High Dimensional Classification with Bayesian Neural Networks and Dirichlet Diffusion Trees*. Springer Berlin Heidelberg, Berlin, Heidelberg, 2006, pp. 265–296.
- [31] PENG, H., LONG, F., AND DING, C. Feature selection based on mutual information criteria of max-dependency, max-relevance, and min-redundancy. *IEEE Transactions on Pattern Analysis and Machine Intelligence* 27, 8 (2005), 1226–1238.
- [32] ROFFO, G., MELZI, S., AND CRISTANI, M. Infinite feature selection. In *The IEEE International Conference on Computer Vision (ICCV)* (December 2015).
- [33] SAEYS, Y., INZA, I., AND LARRAÑAGA, P. A review of feature selection techniques in bioinformatics. *Bioinformatics* 23, 19 (2007), 2507–2517.
- [34] SHIPP, M. A., ROSS, K. N., TAMAYO, P., WENG, A. P., KUTOK, J. L., AGUIAR, R. C., GAASENBEEK, M., ANGELO, M., REICH, M., PINKUS, G. S., ET AL. Diffuse large b-cell lymphoma outcome prediction by gene-expression profiling and supervised machine learning. *Nature medicine* 8, 1 (2002), 68–74.
- [35] SIMONYAN, K., AND ZISSERMAN, A. Very deep convolutional networks for large-scale image recognition. *arXiv preprint arXiv:1409.1556* (2014).
- [36] SINGH, D., FEBBO, P. G., ROSS, K., JACKSON, D. G., MANOLA, J., LADD, C., TAMAYO, P., RENSHAW, A. A., D’AMICO, A. V., RICHIE, J. P., ET AL. Gene expression correlates of clinical prostate cancer behavior. *Cancer cell* 1, 2 (2002), 203–209.
- [37] SZEGEDY, C., LIU, W., JIA, Y., SERMANET, P., REED, S., ANGUELOV, D., ERHAN, D., VANHOUCHE, V., AND RABINOVICH, A. Going deeper with convolutions. In *The IEEE Conference on Computer Vision and Pattern Recognition (CVPR)* (June 2015).
- [38] VEDALDI, A., AND LENC, K. Matconvnet – convolutional neural networks for matlab. In *Proceeding of the ACM Int. Conf. on Multimedia* (2015).
- [39] WU, X., YU, K., DING, W., WANG, H., AND ZHU, X. Online feature selection with streaming features. *IEEE Transactions on Pattern Analysis and Machine Intelligence* 35, 5 (2013), 1178–1192.
- [40] YU, L., AND LIU, H. Efficient feature selection via analysis of relevance and redundancy. *Journal of Machine Learning Research* 5 (2004), 1205–1224.