On the Use of Local and Global Search Paradigms for Computer-Aided Diagnosis of Breast Cancer

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Abstract: Cancer is one of the most dangerous diseases around the world and the most common cancer among women is breast cancer. Although not all the cancer types are curable upon diagnosis, breast cancer can be cured if it is diagnosed early. The most reliable way of diagnosing breast cancer is mammographic screening which can diagnose the disease 1.5 to 4 years before it is clinically diagnosed. Double Reading is the important diagnostic process in which two experts/radiologists should read the same mammogram image to make an accurate diagnosis. But this process is not a cost-effective approach for early detection of breast cancer. Computer-Aided Diagnosis (CAD) can act as the second expert and therefore one expert would be enough for breast cancer diagnosis. In this study, we use the data extracted from low-resolution as well as high resolution mammography images. The attributes extracted from mammographic images are imported into Support Vector Machine (SVM) to classify the patients. An important point about the attributes is that sometimes there may be some irrelevant or even noisy attributes that have negative effect on the classification accuracy. Therefore, the main objective of this study is to apply local and global search paradigms in order to find the best subset of attributes to construct the most accurate CAD system that can effectively distinguish between benign and healthy patients. Artificial Bee Colony (ABC) is a population-based swarm intelligence algorithm with good global exploration ability, and Simulated Annealing (SA) is a robust local-search algorithm. Thus, we utilize a hybrid global and local search algorithm (named ABCSA) to simultaneously benefit from the advantages of both ABC and SA. In this approach, ABC is firstly performed for the global exploration in the search space. Then, SA is utilized to search locally in the vicinity of the best solution found via ABC, in order to improve the quality of the final solution. Obtained simulation results over four different mammographic datasets show that the proposed algorithm outperforms the existing metaheuristic feature selection approaches in terms of minimizing the number of features, while maximizing the detection accuracy.

Keywords: *Early detection of breast cancer, mammographic data, Support Vector Machine (SVM), feature selection, Artificial Bee Colony (ABC), Simulated Annealing (SA)*

1. INTRODUCTION

Breast cancer is the most common cancer among women, with around 1.7 million and 52000 estimated diagnosed cases and deaths in 2012, respectively (Torre et al., 2015). The patient can be survived if the disease is diagnosed early. Mammography, which is a low-dose X-ray image, is currently the most common way to early diagnosis of breast cancer. There are two kinds of mammography image: Screen-Film Mammography (SFM) and Full-Field digital Mammography (FFDM). In the first type, the image takes a form of photographic film, while in the latter, an electronic image is recorded directly on a computer (Faridah, 2008). Due to SFM drawbacks, such as X-ray exposure range, image contrast, and slow processing, FFDM with advantages, such as wider range, better contrast, less noise, higher quality of image, and lower dose of X-ray, has become more popular. Although it has been reported that there is little difference between overall accuracy of SFM and FFDM (Pisano et al., 2005), FFDM outperforms in particular cases (Spurgeon, 2005). As a case in point, it has been shown that FFDM is able to detect more lesions than SFM, particularly for microcalcifications (Spurgeon, 2005). It has been also found that FFDM has better accuracy for premenopausal/perimenopausal women (under 50 years old) who have denser breasts (Pisano et al., 2008).

In order to increase the reliability of mammography-based diagnosis, two radiologists are usually asked to check the mammogram images (this process is called double reading). Besides the possibility of failure in identifying lesions by radiologists, the double reading process is costly. Thus, Computer-Aided Detection (CAD) systems, which utilize computer-based algorithms to detect lesions in mammographic images and then classify patients as benign or malignant, can replace one of the radiologists to overcome the aforementioned issues (Sampat et al., 2005). Therefore, CAD system is considered as a second opinion. It has been reported that the detection sensitivity can be improved by more than 20% if a radiologist uses CAD system for breast cancer diagnosis (Brem et al., 2003). A typical CAD system extracts attributes from mammography images (through image processing techniques), and selects the most important features (through attribute selection methods), and finally classifies patients using a classification algorithm.

Four different types of attributes can be extracted from mammography images. The first group comprises clinical attributes, such as breast density, microcalcification, architectural distortion, etc. The second and third groups are calculated from the pixel grey-level intensity of the patch using statistical calculations. The second group is intensity-based descriptors (such as Mean, standard deviation, Skewness, etc.) while the third group is texture-based descriptors (such as energy, contrast, entropy, etc.). The last type of attributes includes location and shape-based features, such as area, centre of mass, solidity, etc. Using all the aforementioned attributes may not result in the most accurate CAD system because there may be some irrelevant or noisy attributes that hinder the system's ability to distinguish between healthy and cancer patients correctly. Therefore, it is crucial to adopt an appropriate attribute selection strategy in order to select the most important subset of attributes that can be later used to classify patients accurately (Abroudi et al., 2013). Numerous CAD systems for early detection of breast cancer have been presented and they have used different data as well as different metrics to measure the system classification performance (Table 1). One of the most common measures is the area under the Receiver Operating Characteristics (ROC) curve which is mostly depicted as A_Z. The specificity (the ratio of true negatives to healthy cases), sensitivity (the ratio of true positives to cancer cases), and accuracy (the ratio of all true classified instances to all instances) are three other measures. A list of some CAD systems applied on different mammography-based datasets is presented in Table 1. It can be seen that the number of mammogram images varies between different studies (40 to 3369) and the applied classification algorithms are also different, such as various Artificial Neural Network (ANN) extensions, Linear Discriminant Analysis (LDA), Hybrid techniques, Support Vector Machine (SVM). Therefore, it is hard to make a fair comparison between performance of different CAD systems.

Table 1. Details of some current mammography-based CAD systems

Author(s)	Images	Method	Performance
(Chan et al., 1995)	168	Linear Discriminant Analysis (LDA)	A_Z: 0.82
(Sahiner et al., 1996)	168	Convolution Neural Network (CNN)	A_Z: 0.87
(Kinoshita et al., 1998)	92	Back Propagation Neural Network (BPNN)	Acc: 0.81
(Hadjiiski et al., 1999)	348	Hybrid (Art2 and LDA)	A_Z: 0.81
(Bruce & Adhami, 1999)	60	A simple Euclidian Metric	Acc: 0.83
(Mudigonda et al., 2001)	56	LDA	A_Z: 0.9
(Verma & Zakos, 2001)	58	BPNN	Acc: 0.889
(Baeg & Kehtarnavaz, 2002)	404	ANN-MLP	A_Z: 0.9
(De Santo et al., 2003)	102	ANN-MLP	A_Z: 0.79
(Campanini et al., 2004)	512	Support Vector Machine (SVM)	Sens: 0.80
(Guo et al., 2005)	40	Radial-Base Function (RBF) Neural Network, SVM	Acc: 0.725
(Bellotti et al., 2006)	3369	ANN-MLP	Sens: 0.80, A_Z: 0.783
(Timp et al., 2007)	465	SVM	A_Z: 0.77
(Al Mutaz et al., 2011)	120	Artificial Neural Network (ANN)–Multi-Layer Perceptron (MLP)	Sens: 0.916 Spec: 0.841
(Dinesh, 2011)	190	SVM	Sens: 0.96 Spec: 0.97

In this paper, using both SFM and FFDM data, we aim to enhance the CAD system performance for early detection of breast cancer through a combination of heuristic local and global search methods (to find the best subset of attributes) that can render the highest accuracy for SVM classifier. The rest of the paper is organized as follows: In Section 2, SFM and FFDM datasets are described. The proposed ABCSA feature selection algorithm is illustrated in detail in Section 3. Simulation results and comparison with existing algorithms are summarized in Section 4. Finally, concluding remarks are presented in Section 5.

2. SFM AND FFDM DATASETS

This study uses two SFM and two FFDM datasets retrieved from Breast Cancer Digital Repository (BCDR) database (http://bcdr.inegi.up.pt) (López et al., 2012). The details of these datasets can be seen in Table2.

Table 2. Details of SFM and FFDM datasets

Dataset Name	Dataset Type	# Women	# Lesions	# Segmentations
SFM1	SFM	190	200	362
SFM2	SFM	98	103	188
FFDM1	FFDM	64	79	143
FFDM2	FFDM	162	230	455

The list of attributes (including clinical, intensity-, Texture-, location and Shape-based features) and a short description of each are summarized in Table 3 (Moura & López, 2013; Moura et al., 2012).

Table 3. The list of attributes

	Attribute	Explanation
CLINICAL ATTRIBUTES	Age	The patient's age when he/she took the test
	Image View	Image view type which can be 1-RCC, 2-LCC, 3-RO, or 4-LO
	Breast Density	The breast density based on the Breast Image Reporting and Data System (BI-RADS) standard (D'orsi et al., 2003).
	Mammography Type	Whether abnormality is present or not
	Mammography Nodule	Whether there is a mass in the lesion or not
	Mammography Architectural	Whether an architectural-related distortion is present or not
	Mammography Microcalcification	Whether there are Microcalcifications in the lesion or not
	Mammography Stroma Distortion	Whether a stroma-related distortion is present or not
	Mammography Axillary Adenopathy	Whether axillary adenopathy is present or not
	Mammography Calcification	Whether there are calcifications in the lesion or not
	Classification	Category of the lesion based on the result of the biopsy
INTENSITY-BASED ATTRIBUTES	Mean	$M = \frac{1}{p}\sum_{k=1}^{p} y_k$, where p is the total number of pixels in patch and y_k is the intensity of kth pixel within the corresponding patch.
	Standard Deviation	$SD = \sqrt{\frac{1}{p-1}\sum_{k=1}^{p}(y_k - M)^2}$,
	Skewness	$SKW = \dfrac{\frac{1}{p}\sum_{k=1}^{p}(y_k-M)^3}{\left(\sqrt{\frac{1}{p}\sum_{k=1}^{p}(y_k-M)^2}\right)^3}$,
	Kurtosis	$KRT = \dfrac{\frac{1}{p}\sum_{k=1}^{p}(y_k-M)^4}{\left(\frac{1}{p}\sum_{k=1}^{p}(y_k-M)^2\right)^2} - 3$,
	Min	$MN = min(y_k)$, The lowest grey-level intensity found inside the patch.
	Max	$MX = max(y_k)$, The highest grey-level intensity found inside the patch.
TEXTURE-BASED ATTRIBUTES	Energy	$ENG = \sum_{m=1}^{G}\sum_{n=1}^{G} p(m,n)^2$, where p is co-occurrence matrix of grey-levels, G is different possible grey-levels, and $p(m,n)$ is the probability of co-occurrence of grey-levels m,n.
	Contrast	$CNT = \sum_{m=1}^{G}\sum_{n=1}^{G}(m-n)^2 \times p(m,n)$,
	Correlation	$CRL = \frac{\sum_{m=1}^{G}\sum_{n=1}^{G}(m \times n) \times p(m,n)-(\mu_x \times \mu_y)}{(\sigma_x \times \sigma_y)}$, where σ and μ are standard deviations and means of corresponding Partial Probability Distribution Function (PPDF), P_x or P_y.
	Variance	$VAR = \sum_{m=1}^{G}\sum_{n=1}^{G}(m-\mu)^2 \times p(m,n)$,
	Homogeneity	$HOM = \sum_{m=1}^{G}\sum_{n=1}^{G}\frac{1}{1+(m-n)^2} \times p(m,n)$,
	Sum Average	$SA = \sum_{m=2}^{2G} m \times p_{x+y}(m)$, where $m = x + y$, and $p_{x+y}(m)$ is co-occurrence matrix probability when the coordinates are summed.
	Sum Entropy	$SENT = -\sum_{m=2}^{2G} p_{x+y}(m) \times \log(p_{x+y}(m))$,
	Sum Variance	$SVAR = \sum_{m=2}^{2G}(m - SENT)^2 - p_{x+y}(m)$,
	Entropy	$ENT = -\sum_{m=1}^{G}\sum_{n=1}^{G} p(m,n) \times \log(p(m,n))$,
	Difference Variance	$DVAR = \sum_{m=0}^{G-1} m^2 \times p_{x-y}(m)$, where $m = |x - y|$, and $p_{x-y}(m)$ is co-occurrence matrix probability when the coordinates are subtracted.
	Difference Entropy	$DENT = -\sum_{m=0}^{G-1} p_{x-y}(m) \times \log(p_{x-y}(m))$,
	Information Measure of Correlation 1	$\dfrac{\sum_{m=1}^{G}\sum_{n=1}^{G} p(m,n) \times \log(p_x(m) \times p_y(n)) - \sum_{m=1}^{G}\sum_{n=1}^{G} p(m,n) \times \log(p(m,n))}{\max\left\{\sum_{m=1}^{G} p_x(m) \times \log(p_x(m)), \sum_{m=1}^{G} p_y(m) \times \log(p_y(m))\right\}}$

	Information Measure of Correlation 2	$\sqrt{1 - exp\left\{2 \times \left[\sum_{m=1}^{G}\sum_{n=1}^{G} p_x(m) \times p_y(n) \times \log(p_x(m) \times p_y(n)) - \sum_{m=1}^{G}\sum_{n=1}^{G} p(m,n) \times \log(p(m,n))\right]\right\}}$
LOCATION & SHAPE-BASED ATTRIBUTES	Area	$A = |pix|$, where pix indicates the segmented area's pixels
	Perimeter	$Per = lng(E)$, where $lng(E)$ indicates the length of edge pixels
	Centre of Mass	$COM = coordinates\ of\ the\ mass\ centre$,
	Solidity	$Sld = {}^{A}/_{|CH|}$, where CH is the set of convex hull pixels of the patch
	Extent	$Ext = {}^{A}/_{|BB|}$, where BB is the set of bounding box pixels of the patch
	Elongation	$Elg = {}^{mn}/_{mj}$, where mn and mj are minor and major axes of most similar ellipse to the patch (having the equal second central moments), respectively.
	Circularity	$Crl = 4\pi \times \frac{A}{Per^2}$,
	Form	$Form = \frac{Elg \times Per}{8 \times A}$,

Having these attributes, our aim is to select the most effective subset of attributes that renders the highest classification accuracy for early detection of breast cancer. This will be done through local and global search methods that are presented in the following section.

3. THE PROPOSED ABCSA ALGORITHM

Artificial Bee Colony (ABC) (Karaboga & Basturk, 2007) is a swarm intelligence algorithm with good global exploration ability. Also, Simulated Annealing (SA) is a metaheuristic single-solution optimization algorithm which has a very good local search mechanism (Shokouhifar & Jalali, 2015). Our motivation is to incorporate the advantages of both ABC and SA into a hybrid ABCSA algorithm. Generally, in the beginning of the optimization process, we search globally in the search space. On the other hand, local search can be very useful at the later iterations. In our approach, at first, ABC is performed, and then, SA is used to search in the vicinity of the best solution found by ABC, in order to improve the best solution of ABC. The overall flowchart of the proposed hybrid ABCSA algorithm can be seen in Fig. 1.
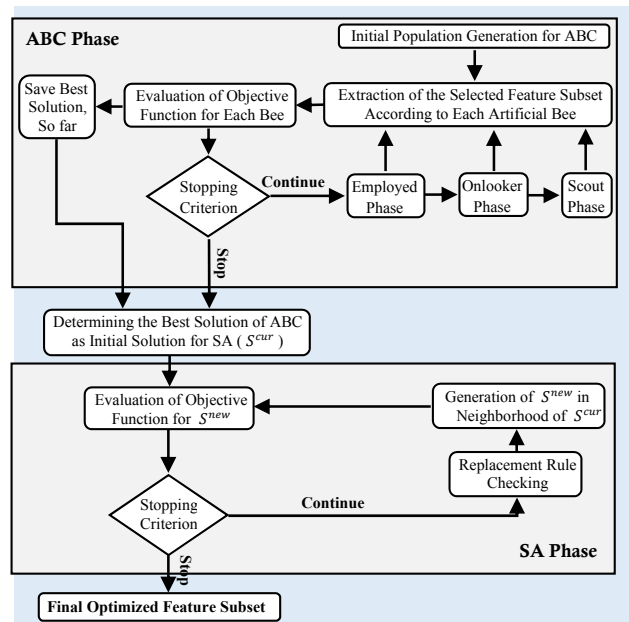

Figure 1. Overall flowchart of the ABCSA algorithm

3.1. Problem Representation

In both ABC and SA phases, as seen in Fig. 2, a feasible solution can be represented as a binary string of length L, where L is the total number of original features. The multi-objective cost function in both ABC and SA phases contains two objectives, both to be minimized. On the other hand, the first objective (the percent of the selected features) is in conflict with the second objective (the classification error), in such a way that as the first objective minimized (more discarded features), it would generate a greater classification error rate. In this case, the two objective functions can be combined into a single one by means of a weighted sum, as follows:

$$Minimize\ \left\{Cost = w_1 \times \left(\frac{1}{L}\sum_{i=1}^{L} S_i\right) + w_2 \times E\right\} \tag{1}$$

$$S_i = \begin{cases} 1 & if\ feature\ i\ has\ been\ selected \\ 0 & otherwise \end{cases} \tag{2}$$

where the left term is to minimize the number of features, and the right term is to minimize the classification error achieved via SVM on the test instance set. w_1 and w_2 are two constant weights to adjust the relative importance of the two terms within the objective function. Since the classification accuracy is more important than the selected feature subset size, we assume $w_2 \gg w_1$.
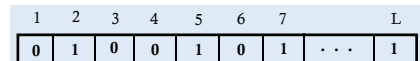

Figure 2. A feasible solution: "1" denotes that the corresponding feature is present, and "0" otherwise.

3.2. Global Search via ABC

In ABC, each feasible solution corresponds to a food source position in L-dimension area (see Fig. 2), where L is the number of optimization variables (number of original features). The nectar value of a feasible solution relates to the fitness of the solution. The nectar value (fitness) of kth bee is calculated as $Fitness_k = 1/Cost_k$, in which, $Cost_k$ is the cost of kth bee to be minimized. An artificial bee colony consists of three kinds of artificial bees: employed bees, onlooker bees and scout bees (Shokouhifar & Jalali, 2014). At first, the initial population is randomly generated. At the every iteration, each employed bee is moved onto her previously visited food source environment to explore a new food source in the vicinity of the present one. If the nectar amount of the new solution is higher, the bee forgets the previous one and memorizes the new one. The employed bee whose food source has been abandoned will become a scout bee. It is controlled by a parameter called *limit*. Scout bees carry out random searching to discover a new solution. Whenever all employed bees construct their solutions, they come back into the hive and share their information with onlookers. As seen in Eq. (3), the more nectar the employed contains, the more probability the onlooker to choose it, in which, n is the number of employed bees, and β is a constant parameter. Each onlooker goes onto the area of the selected employed bee, in order to explore a new food source within its vicinity.

$$P_k = \frac{(Fitness_k)^\beta}{\sum_{k=1}^{n}(Fitness_j)^\beta} \tag{3}$$

3.3. Local Search via SA

Generally, SA starts with a random initial solution. However, in this study, the final global best solution of ABC is selected as the initial solution for SA. The role of SA is to search in the vicinity of the final solution of ABC, with the aim to improve it. At every iteration, a new solution (S^{new}) is generated in the neighborhood of the current one (S^{cur}). If $Cost^{new} < Cost^{cur}$, the current solution is replaced with the new one. If $Cost^{new} > Cost^{cur}$, the new solution may be accepted with the probability of:

$$P_w = exp(-(Cost^{new} - Cost^{cur})/T) \tag{4}$$

where $Cost^{cur}$ and $Cost^{new}$ are the cost function for S^{cur} and S^{new}, respectively. Also, t_{SA} and max_iter_{SA} are the current iteration, and the defined number of iterations in SA, respectively. The temperature T is considered to decrease linearly from $T_{initial}$ (initial temperature) to T_{final} (final temperature), during algorithm execution, as follows:

$$T = T_{initial} + \frac{t_{SA}}{max\_iter_{SA}} \times (T_{final} - T_{initial}) \tag{5}$$

As demonstrated in Fig. 3, binary swap operator is utilized for the neighborhood search in both ABC and SA phases.
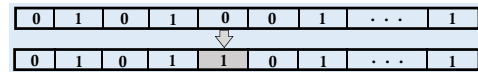

Figure 3. Binary swap operator for the neighborhood search in both ABC and SA

4. SIMULATION RESULTS

In order to adjust the controllable parameters of the proposed ABCSA algorithm, different values were evaluated and the best ones (in terms of objective function and convergence speed) were determined. Settings for the parameters of the proposed hybrid ABCSA algorithm can be summarized in Table 4. Different kernel functions for SVM classifier are evaluated, and the linear kernel achieved the best result among them. Thus, we use linear kernel for the SVM classifier in our experiments. The obtained results of the ABCSA algorithm and comparison with the original datasets (containing all original features) can be summarized in Table 5. Furthermore, we have compared the obtained results with other metaheuristic feature selection algorithms including Genetic Algorithm, Artificial Bee Colony, and Simulated Annealing.

Table 4. Settings for the parameters of the proposed ABCSA algorithm

Parameter	Value/Description
max_iter_{ABC}	L
Population size of ABC phase	20
Number of employed bees	25 (the half of colony)
Number of onlooker bees	25 (the half of colony)
Limit	2.5 order larger than the best cost
β in Eq. (3)	5
max_iter_{SA}	$2 \times L$
$T_{initial}$ in Eq. (5)	0.01
T_{final} in Eq. (5)	0
w_1 in Eq. (1)	0.01
w_2 in Eq. (1)	0.99

Table 5. Comparison of the results of the proposed ABCSA algorithm with original datasets

Dataset Name		# Features	Sens	Spec	Acc
SFM1	All Features	38	81.03 %	88.24 %	84.4 %
	Selected Features	29	87.93 %	86.27 %	87.16%
SFM2	All Features	38	64.29 %	82.14 %	73.21 %
	Selected Features	19	78.57 %	89.29 %	83.93 %
FFDM1	All Features	38	93.75 %	81.48 %	86.05 %
	Selected Features	8	93.75 %	96.3 %	95.35 %
FFDM2	All Features	38	93.33 %	99.17 %	98.53 %
	Selected Features	23	100 %	100 %	100 %

The simulation results can be seen in Table 6, in terms of the number of selected features and final accuracy. According to result of the simulations, the proposed ABCSA outperforms the other metaheuristic algorithms, in terms of the minimization of the selected features while maximizing the detection accuracy. From Table 6, it can be seen that the proposed ABCSA algorithm outperforms all compared algorithms for the two datasets SFM1 and FFDM1. In the case of SFM2 dataset, the ABCSA and ABC have achieved equal accuracy, and the both algorithms outperform GA and SA. However, ABCSA has 19 features (3 features lower than ABC). Finally, in the case of FFDM2 dataset, the proposed ABCSA, ABC and GA have achieved the maximum accuracy 100%. In this case, both ABCSA and ABC have 23 features. As seen, in SFM1 and FFDM1 ABCSA outperforms ABC, but in SFM2 and FFDM2, both ABCSA and ABC have equal accuracy. It is due to added local search exploration via SA. On the other hand, in SFM1 and FFDM1 datasets, the added local search mechanism (via SA) leads to improve the result of ABC.

Table 6. Comparison of the results of the ABCSA with other metaheuristic feature selection algorithms

Dataset Name	GA		SA		ABC		Proposed (ABCSA)	
	# Features	Accuracy	# Features	Accuracy	# Features	Accuracy	# Features	Accuracy
SFM1	27	86.32%	32	84.91%	24	85.54%	29	87.16%
SFM2	16	79.19%	26	80.6%	22	83.93%	19	83.93 %
FFDM1	15	92.26%	17	94.12%	13	93.33%	8	95.35 %
FFDM2	26	100%	19	99.24%	23	100%	23	100 %

5. DISCUSSION AND CONCLUSIONS

The best and most common way of breast cancer diagnosis is mammography which has been reported to be able to detect the cancer up to four years in advance. Therefore, in this paper, a hybrid feature selection algorithm based on both local and global search paradigms has been presented for the early detection of breast cancer based on two types of mammogram images. The central objective of this paper is to apply ABC (as global search method) and SA (as local search method) to find the best subset of features in order to accurately classify benign and healthy patients. The proposed hybrid algorithm is called ABCSA. We have used SVM as the classifier. Simulations show that the proposed ABCSA algorithm outperforms the existing metaheuristic feature selection algorithms in terms of maximizing the detection accuracy. As a future work, we plan to utilize the proposed methodology for genome-based breast cancer datasets. We also plan to propose other hybrid global and local search algorithms for effective feature selection in different problems.

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