Application of Bio-inspired Krill Herd Algorithm for Breast Cancer Classification and Diagnosis

Sweta Kumari and Mohanapriya Arumugam*

¹Bioinformatics Division, School of Biosciences and Technology, Vellore Institute of Technology University, Vellore - 632 014, Tamil Nadu, India; sweta.kumari1231@gmail.com, mohanapriyaa@vit.ac.in

Abstract

Objectives: Our work presents a data mining approach, using Krill Herd optimization algorithm to generate more comprehensive classification of breast cancer dataset. Hybrid Krill Herd algorithm (HKH) is proposed which is suitable for generation of optimized classification rules. **Methods:** HKH algorithm has a very flexible encoding where each member of population (Krill Herd) corresponds to a classification rule. Each Krill Herd consist of many krills corresponding to antecedents of classification rule. For breast cancer classification, Wisconsin diagnostic breast cancer data set created from fine needle aspiration biopsy of breast mass was used. **Findings:** Using this optimization algorithm a very comprehensive and simple classification rule is obtained for breast cancer classification represented in form of If-Then rule. **Application:** The obtained rule can be used to further classify breast tissue specimens into malignant and benign classes, thus supporting the cancer diagnosis.

Keywords: Classification Rule, Krill Herd, Rule Mining, Swarm Optimization Algorithm, WDBC Dataset

Abbreviations

KH – Krill Herd
HKH – Hybrid Krill Herd
WDBC – Wisconsin Diagnostic Breast Cancer
FNA – Fine Needle Aspiration
GA – Genetic Algorithm
PSO – Particle Swarm Optimisation
ACO – Ant Colony Optimization
Se – Sensitivity
Sp – Specificity

1. Introduction

Optimization algorithms such as Genetic Algorithm (GA), Particle Swarm Optimisation (PSO), Ant Colony Optimization (ACO) etc. may be used to build classification models[1–9]. The obtained classification model can be further used for diagnostic purpose[10–14]. But, none of the available optimization algorithms are precise and leaves us with scope of improvement in classification sensitivity and specificity.

UC Irvine Machine Learning Repository provides open access to 301 datasets. Breast Cancer Wisconsin (diagnostic) dataset is chosen for our cancer classification study. Breast Cancer Wisconsin dataset consists of features computed from a digitized image of a Fine Needle Aspirate (FNA) of a breast mass[15]. Fine needle aspiration is a type of biopsy procedure which involves insertion of thin needle into abnormal appearing tissue area or body fluid[16]. In Wisconsin Diagnostic Breast Cancer (WDBC) dataset each record represents follow-up data for consecutive patients seen by Wolberg, et al. Each data entry consist of cell nuclei characteristics like radius,

texture, perimeter, area, smoothness, compactness, concavity, concave points, symmetry and fractal dimension. It includes only those cases which exhibit invasive breast cancer and no evidence of distant metastases during diagnosis[15–17]. The dependability of computer aided breast cancer diagnosis can be improved, when accurate classification model is built using information in this freely available dataset.

Classification model comprises one or more classification rules. Classification rules are generally denoted in the If-Then rules form. A rule contains two parts – antecedent (one or more) and consequent. Each antecedent contains the feature description, operator and value. Consequent is the second part of rule which contains description of class of the rule. Notation: IF (Feature$_1$, Operator, Value) AND IF (Feature$_2$, Operator, Value) . . .AND IF (Feature$_n$, Operator, Value), Then Class = "Class label". Decision tree can be constructed based on the classification rule which serves as a classification model[2,3].

Metaheuristic algorithms are popular for solving complex optimization problems. Bio-inspired algorithms are very efficient as it imitates the best features in nature[18]. Swarm optimization falls under category of bio-inspired algorithm. It imitates the ability of certain species like firefly, bat etc. to form a dense swarm and reach its goal. Many swarm optimization algorithms like ant colony optimization, bat algorithm, firefly algorithm, beehive algorithms have been widely used[19–21]. Krill Herd (KH) optimization algorithm has been proposed by Gandomi and Alvi in 2012[22]. It falls under category of swarm optimization algorithm as it is based on simulation of the herding behavior of krill individuals. For building the classification model, swarm optimization algorithm like KH optimization algorithm can be a powerful tool. KH method is based on the simulation of the herding of the krill swarms in response to any environmental and biological processes. On the basis of foraging activity, random diffusion and movement induced by surrounding Krill, time dependent position of individual krill is determined[22]. For classification model construction each attribute value of its corresponding record will contribute to one antecedent of classification rule and each antecedent will be considered as an individual krill. The values of each antecedent will be optimized to reach high classification accuracy. This approach has been discussed in methodology section.

2. Methods

2.1 Dataset

Wisconsin Diagnostic Breast Cancer (WDBC) dataset was retrieved from UCI machine learning repository (available at: https://archive.ics.uci.edu/ml/machine-learning-databases/breast-cancer-wisconsin/). The dataset contains 357 benign and 212 malignant class instances. Apart from patient's ID number and diagnosis class (benign or malignant), there are 30 features having real values which describe characteristics of the cell nuclei present in the sample. The feature values were computed from a digitized image of a fine needle aspirate (FNA) of a breast mass[15–17]. The characteristics described in dataset are radius, texture, perimeter, area, smoothness, compactness, concavity, concave points, symmetry and fractal dimension of cell nuclei. Mean, standard deviation and worst or largest value of these features constitute 30 real valued attributes of data set.

For measuring many characteristics of an individual nucleus the snake method was used. Radius measurement is done by taking average of the length of the radial line segments between individual snake points and the centroid of the snake. The variance of the grey scale intensities in the component pixels of digitized nuclei image is used to measure its texture. Perimeter of nucleus is the total distance between consecutive snake points. Area of nucleus is measured by the addition of the number of pixels on snake interior and one-half of the pixels on the perimeter. Difference between the length of a radial line and the mean length of the lines surrounding it determines the smoothness. For a perfect circle the difference between the radial line and mean of surrounding lines will be zero. Compactness of nucleus is given by (formula perimeter^2/area -1.0). For measuring concavity, chord is drawn between non-adjacent snake points. The extent of indentation of nuclear wall within the chord gives us concavity of nucleus. Concave points number of concave portions of the contour i.e. number of snake points lying on concave region of nuclear boundary. The difference in length of two perpendicular lines to the major axis through centre to the nuclear boundary in both directions gives the symmetry. The fractal dimension is given as ("coastline approximation" - 1)[15,17,23]. We intend to study the significance of cell nuclei characteristics in cancer diagnosis.

The dataset was divided into training set and test set, having 3:1 ratio, respectively. The training set contains 141 malignant class entries and 238 benign class entries.

The test dataset consists of 71 malignant class entries and 119 benign class entries. The training set data was used to construct classification rule. The efficiency of obtained classification rule was analysed through its application on test dataset.

2.2 Krill Herd Algorithm

KH is a biologically inspired algorithm proposed by Gandomi and Alavi in 2012 for optimization tasks. KH algorithm is based on the Lagrangian model of the Krill Herding[22]. It is based on the simulation of the herding of the KH in biological and environmental response. Initialization in KH algorithm imitates predation, in which individuals are removed, as a result of which average krill density falls and there is increase in distance of swarm from the food location. The fitness function of each krill individual is defined as its distances from food and highest density of the krill swarm. The time-dependent position of an individual krill is determined by following three essential actions: (1) movement induced by other krill individuals, (2) foraging activity and (3) random diffusion.

In order to make KH optimization algorithm capable of searching spaces of arbitrary dimensionality, Lagrangian model adopted by KH is generalized to a d dimensional search space. It is represented by following equation:

$$\frac{dx_i}{dt} = N_i + F_i + D_i \tag{1}$$

Where, N_i, F_i and D_i are the motion induced by other krill individuals, the foraging motion, and the physical diffusion of the ith krill individual, respectively.

The krill individual changes its position through defined motions at a specific position and thus krill approaches the best fitness. Using different effective parameters of the motion during the time, the position vector of a krill individual during the interval t to $(t + \Delta t)$ is given by the following equation.

$$X_i(t+\Delta t) = X_i(t) + \Delta t \, \frac{dX_i}{dt}$$

$d(2)$

where, is a constant which acts as scale factor for speed vector; dX_i is a complex motion variable determined through series of calculations explained later in this section. The speed scale factor is calculated through following formula.

$$\Delta t = Ct \sum_{j=1}^{NV}(UB_j + LB_j) \tag{3}$$

Here, NV is the total number of variables and LB_j and UB_j are lower and upper bounds of the jth variable. C_t is a constant which was originally proposed to be a constant number in range [0, 2]. Junpeng, Li, et al.[24] improvised the exploration and exploitation capacity of KH by proposing the following method for varying C_t calculation.

$$Ct \qquad Ct(t) = Ct_{max} - \frac{Ct_{max} - Ct_{min}}{t_{max}}.t \tag{4}$$

where, Ct_{max} and Ct_{min} is the maximum and the minimum values of Ct. t_{max} is the maximum number of iterations and t is the present number of iteration. Thus, a linear decrease is achieved in value of $Ct(t)$ from Ct_{max} to Ct_{min} with iterations. Low value of Ct allows krill individual to search the space more carefully.

Movement of an individual krill is defined in equation 1. First of its three major constituent *i.e.* movement induced by other krill is expressed as:

$$N_i^{new} = N^{max}\alpha_i + \omega_n N_i^{old} \tag{5}$$

Where,

$$\alpha_i = \alpha_i^{local} + \alpha_i^{target} \tag{6}$$

N^{max} is the maximum induced speed, ω_n is the inertia weight of the motion induced within the range [0,1]; N_i^{old} is the last motion induced α_i^{local}. is the local effect provided by the neighbours and α_i^{target} is the target direction effect provided by the best krill individual.

On the basis of food location and previous experience of food experience foraging movement is calculated. For ith krill individual the foraging motion is expressed as:

$$F_i = V_f\beta_i + \omega_f F_i^{old} \tag{7}$$

where,

$$\beta_i = \beta_i^{food} + \beta_i^{best} \tag{8}$$

and V_f is the foraging speed, ω_f is the inertia weight of the foraging motion in the range [0,1]; F_i^{old} is the last foraging motion, β_i^{food} is the food attractive β_i^{best} and is the effect of the best fitness of the ith krill.

The third component of individual Krill motion - is a random process. Physical diffusion is the product of maximum diffusion speed and a random directional vector[22].

The KH algorithm can be implemented through following steps:

KRILL$_1$			- - - - -			KRILL$_n$		
Value$_1$	Operator$_1$	Weight$_1$	- - - -	- - - -	- - - -	Value$_n$	Operator$_n$	Weight$_n$

Figure 1. Representation of a Krill Herd: encoding of each krill individual in a Krill Herd having 'n' number of krills.

(1) Random initialization of the population in the available search space. (2) Evaluation of fitness of each krill individual according to its position. (3) Calculation of motion: movement induced by the presence of other individuals; foraging motion; physical diffusion. (4) Application of genetic operators. (5) Update the krill individual position within the search space. (6) Repeat step 2–5 until a stop criterion is reached or a predefined number of iterations are completed.

2.3 KH Classification Algorithm

We have proposed a hybrid-KH algorithm to perform classification task of data mining. For a given dataset, initial set of k number of rules are generated which corresponds to krill population constituting k Krill Herds. Each KH consists of n number of krills (arity*n*as).

For our problem, we treat each antecedent as a krill. As in the original KH algorithm, here also initialization imitates the predation. As a result of predation, there is decrease in swarm density and increase in the distance from food. We have introduced competition among the krills in a herd so that the fittest krills attain the more core position in the swarm through the progression of generations. Fittest krills are less likely to be predated as they remain in the dense region of the krill swarm. All the KHs in a population together try to attain the highest density and least distance from food. The best KH corresponds to the generated classification rule. The fitness calculation has been discussed further in this section.

Individual encoding of a krill is shown in Figure 1. Each krill *i*th has three constituent: (1) value$_i$ which contains value of the antecedent (2) Operator$_i$ which can be <=, >=,== or !=(iii) weight$_i$ which is a binary variable. If weight is one then the antecedent is included in rule while its zero value denotes exclusion of antecedent from the rule. Value of ith krill is vigorously changing variable throughout the krill population propagation. The values are calculated using the KH method discussed in the previous section. In equation 1 *dXi* is the change in value of krill$_i$ of *k*th KH of population, *dt* is one iteration, *Ni* is the motion induced by *i*th krills of all Krill Herds,

Fi is foraging movement (high classification accuracy is deemed as food) and random diffusion *Di*. *Di* is the random diffusion of krills in KH. In equation 2, X_i corresponds to the value of *i*th krill, *t* is number of iteration, (*t* + Δt) symbolizes next iteration. Δt is calculated using equation 3, where UB_j and LB_j are upper and lower bounds of values in *j*th attribute of dataset, repectively. Weight and operator are almost constant throughout the iterations; however, the mutation operation is an exception. Consequent, the second part of the rule is constant for an individual run. Consequent may be user defined or chosen randomly.

For G generations, the motion calculation of each krill within every KH is carried out using the formula discussed in section 2.1. Motion calculation facilitates the optimization of krill value. But weight is also important for optimization of classification rule. Weight of each krill is subjected to mutation with low mutation probability.
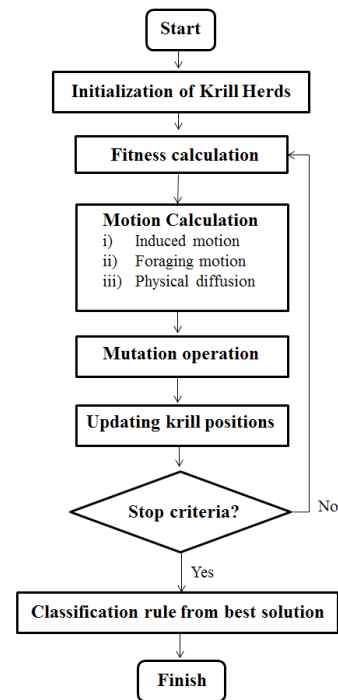

Figure 2. Flowchart: Hybrid Krill Herd (HKH) algorithm for classification rule mining.

To enhance the exploration and exploitation capacity of HKH, mutation operation is performed on krill individual values (Figure 2).

Elitism is also introduced to prevent the exploitation of best KH solution. Best *l* KH solutions are copied and replace worst *l* Krill Herds after completion of particular number of generation (*l* = elitism size). Thus it is ensured that exploration of best KH is also performed and best Krill Herds do not leave the krill population (Figure 3).

Algorithm : Hybrid Krill Herd algorithm for classification
1 Initialize Krill Herd Parameters
2 Initialize Krill Population with randomly generated *k* Krill Herds (*k* is population size)
3 Evaluate Krill Herds: Calculate fitness score of each krill herd in krill population.
4 **for** G generations **do**
5   Calculate position of each *krill_n* in each *krill herd_k*
i.   Calculate movement induced by other krill individual N_i
ii.   Calculate foraging motion F_i
iii. Calculate physical diffusion D_i
6   Perform Mutation
7   Re-evaluate Krill Herds
8   Perform Elitism
9 **end for**
10 Output: Krill herd with highest fitness score

Figure 3.   Algorithm 1.

2.4 Fitness Function

Fitness function is employed to evaluate the quality of each rule (individual KH). Fitness of a KH is defined by individual krill position, operator and weight. In HKH, competition exists amongst the krills. The krills with high weight are included in classification rule. So, the fitness score of KH (classification rule) follows the following relation.

$$Score\ (KH_i) \rightarrow f(Krill_1, Krill_2, \cdots \cdots, \cdots) \rightarrow f(Krill_1, Krill_2,)$$

Few basic concepts on classification rule evaluation are described here. When using a rule for classifying an example, depending on the true class of the example and on the class predicted by a rule, following four different types of results can be observed for the prediction: (1) TP (True Positives) is the number of cases covered by the rule that belong to the class predicted by the rule.(2) FP (False Positives) is the number of cases covered by the rule that belong to a class different from the class predicted by the rule.(3) FN (False Negatives) is the number of cases not covered by the rule but belong to the class predicted by the rule. (4) TN (True Negatives) is the number of cases that are not covered by the rule and do not belong to the class predicted by the rule.

The fitness function used by the optimization system is defined as the product of two indicators commonly used in medical domains, the sensitivity (Se) and specificity (Sp).

Fitness score = Se * Sp   (11)

Where, Se = TP / (TP + FN)

Sp = TN / (TN + FP)

The goal is to maximize both Se and Sp at the same time through optimization iterations and the product shown in above equation provides a good gradient for the function.

3. Result and Discussion

3.1 Dataset

Fine needle biopsy remains a widely practiced method as diagnostic tool, as it involves minor surgical procedure and gives reliable result with 'triple test' (combined cytological, clinical and radiologic findings)[25]. Decision tree based on classification rule can further strengthen the cancer diagnosis through computation assisted decision making. The WDBC dataset contains features which describes characteristics of cell nuclei. All characteristics are expressed as real numbers. The dataset not only contains the mean of the feature calculated from each image, but includes the standard error and largest value to ensure that even uncommon deviations are not ignored due to averaging process. For example, if we compare two images of elongated and circular nucleus through its feature values, they cannot be distinguished from each other on the basis of nucleus radius mean alone. But, features mean radius combined with feature largest radius value can easily distinguish them, as difference between mean and largest radius will be negligible in case of circular and there will be significant difference in mean and largest radius value[15–17]. Hence, standard error and largest (worst) value are important features for the study.

3.2 HKH Algorithm

HKH algorithm produced optimized solution for classification rule mining from WDBC dataset. Generation and fitness of the solutions generated followed a sigmoid curve. Initially the krills were more random and there was slow increase in classification accuracy during first 100 generations. Physical diffusion and mutation operation facilitated the exploration of krills. Elitism helped in

conservation of best krills and provided platform for their exploration. As number of features in the dataset is low, no heuristics was required. The HKH algorithm was able to mine rules from dataset without any heuristics. To ensure the comprehensibility and simplicity of rule the weight threshold for inclusion in rule was 0.9. In a KH (one solution), in case of absence of krill 0.9 or higher weight the largest weight krill was considered. In our work, mutation operation and optimization algorithm was not applied to weight of krills, as HKH algorithm is computationally expensive due to its dependence on several mathematical functions. Along the propagation of generations after initial 100 generations there was a significant increase in the classification accuracy of solutions. But after 350 generation there was a negligible increase in classification accuracy of best solution. After 500 generations (maximum number of iterations) the final classification rule solution was obtained.

3.3. Classification Rule

Application of HKH algorithm on WDBC training dataset lead to the derivation of a comprehensible classification rule with the accuracy of 93.13% (Table 1). The obtained classification rule contains two antecedents combined with AND operator, to predict the malignant class. The antecedent obtained suggests that if largest perimeter of nucleus is greater than 113.2 and largest area of nucleus is greater than 895.1, then the nucleus belongs to malignant cell class. The test set was classified with 87.9% accuracy, when the obtained rule was applied on it.

Table 1. Classification rule obtained and parameters to evaluate its efficiency

Classification rule	If (Worst/largest perimeter > 113.2) AND (Worst/largest area > 895.1) **Then** class = malignant	
	Accuracy Parameters	**Value**
Training dataset	Classification Accuracy	93.139 %
	Sensitivity	0.987
	Specificity	0.837
Test dataset	Classification Accuracy	87.89 %
	Sensitivity	0.975
	Specificity	0.718

Our result suggests that, through analysis of irregularity in shape of cell nucleus boundary and deviation in nuclear area malignant cancer cells can be distinguished from benign breast cell. If there is irregularity in nuclear shape, the worst/largest value of perimeter and area will vary to a greater extent from the mean value of the same parameter. If irregularity in nuclear shape is prominent in a cell, the doctor can proceed for further cancer diagnostic tests to confirm the diagnosis. Thus major biopsy can be avoided in most of the cases until there is prominent irregularity in cell nucleus. This will lead to cheaper and early diagnosis of breast cancer.

4. Conclusion

The work presented is an attempt to study cancer prediction through the cell nucleus of breast mass. We have used WDBC dataset, which illustrates the instances of malignant and benign breast cancer and the cell nucleus features associated with it. We have proposed a hybrid Krill Herd optimization algorithm (HKH), derived through Krill Herd optimization algorithm proposed by Gandomi and Alavi in 2012. The algorithm has been modified to be suitable to carry out classification rule mining. Through HKH application on WDBC dataset, we have derived classification rule (accuracy- 93.13% in training set, 87.89% in test set) which can be used in decision making process during breast cancer diagnosis. The rule derived emphasises that the malignant breast cells can be distinguished from benign cells, on the basis of irregularity in shape of the cell nucleus. This can help in early diagnosis and decision making process of cancer diagnosis. The proposed algorithm can be further applied on other biological and non-biological datasets for derivation of classification rules and construction of decision trees.

5. Acknowledgement

6. References

1. Nikumbh S, Ghosh S, Jayaraman VK. Biogeography-based informative gene selection and cancer classification using SVM and random forests. 2012 IEEE Congress on Evolutionary Computation (CEC). 2012 Jun; p. 1–6.

2. Kwedlo W, Krętowski M. Discovery of decision rules from databases: An evolutionary approach. Principles of Data Mining and Knowledge Discovery. Springer: Berlin Heidelberg. 1998; 1510:370–8.

3. Fidelis MV, Lopes HS, Freitas AA. Discovering comprehensible classification rules with a genetic algorithm. Proceedings of the 2000 Congress on Evolutionary Computation. La Jolla CA. 2000; 1. p. 805–10.

4. Bojarczuk CC, Setembro ASD, Lopes HS, Freitas AA, Conceio RI. Discovering comprehensible classification rules using Genetic Programming: a case study in a medical domain. 1999. p. 1–6.

5. Parpinelli RS, Lopes HS, Freitas AA. Data mining with an ant colony optimization algorithm. IEEE Transactions on Evolutionary Computation. 2002 Aug; 6(4):321–32.

6. Dorigo M, Birattari M. Ant Colony Optimization. In: Sammut C, Webb GI, editors. Encyclopedia of Machine Learning. Springer: US; 2011. p. 36–9.

7. Dorigo M, Birattari M, Blum C, Clerc M, Stützle T, Winfield AFT. Ant Colony Optimization and Swarm Intelligence. Springer: Berlin Heidelberg. 2008.

8. Falco ID, Cioppa AD, Tarantino E. Evaluation of particle swarm optimization effectiveness in classification. Fuzzy Logic and Applications. Springer: Berlin Heidelberg. 2006; 3849: p. 164–71.

9. Srimani PK, Koti MS. Knowledge discovery in medical data by using rough set rule induction algorithms. Indian Journal of Science and Technology. 2014 Jul; 7(7):905–15.

10. Delen D, Walker G, Kadam A. Predicting breast cancer survivability: a comparison of three data mining methods. Artificial Intelligence in Medicine. 2005; 34(2):113–27.

11. Kalaiselvi C, Nasira GM. Prediction of heart diseases and cancer in diabetic patients using data mining techniques. Indian Journal of Science and Technology. 2015 Jul; 8(14):1–7.

12. Abbass HA. An evolutionary artificial neural networks approach for breast cancer diagnosis. Artificial Intelligence in Medicine. 2002; 25(3):265–81.

13. Elter M, Schulz-Wendtland R, Wittenberg T. The prediction of breast cancer biopsy outcomes using two CAD approaches that both emphasize an intelligible decision process. Medical Physics. 2007 Nov; 34(11):4164–72.

14. Partridge AH, Elmore JG, Saslow D, McCaskill-Stevens W, Schnitt SJ. Challenges in DCIS Risk Communication and Decision-Making: Report from an American Cancer Society and National Cancer Institute Workshop. CA Cancer Journal Clinicians. 2012 May/Jun; 62(3):203–10.

15. Wolberg WH, Street WN, Mangasarian OL. Image analysis and machine learning applied to breast cancer diagnosis and prognosis. Analytical Quantitative Cytology and Histology. 1995 Apr; 17(2):77–87.

16. Ferrucci JT, Wittenberg J, Mueller PR, Simeone JF, Harbin WP, Kirkpatrick RH. Diagnosis of abdominal malignancy by radiologic fine-needle aspiration biopsy. American Journal Roentgenology. 1980 Feb; 134(2):323–30.

17. Wolberg WH, Street WN, Mangasarian OL. Machine learning techniques to diagnose breast cancer from image-processed nuclear features of fine needle aspirates. Cancer Letters. 1994; 77(2–3):163–71.

18. Simon D. Biogeography-based optimization. IEEE Transactions on Evolutionary Computation. 2008 Dec; 12(6):702–13.

19. Yang X-S. Nature-inspired metaheuristic algorithms: Second Edition. Luniver Press. 2010.

20. Yang X-S. Efficiency analysis of swarm intelligence and randomization techniques. Journal Computational and Theoretical Nanoscience. 2012; 9(2):189–98.

21. Yasodha P, Ananthanarayanan NR. Analysing big data to build knowledge based system for early detection of ovarian cancer. Indian Journal of Science and Technology. 2015 Jun; 8(14):1–7.

22. Gandomi AH, Alavi AH. Krill Herd: A new bio-inspired optimization algorithm. Communications in Nonlinear Science Numerical Simulation. 2012; 17(12):4831–45.

23. Li K, Lu Z, Liu W, Yin J. Cytoplasm and nucleus segmentation in cervical smear images using Radiating GVF Snake. Pattern Recognition. 2012 Apr; 45(4):1255–64.

24. Li J, Tang Y, Hua C, Guan X. An improved krill herd algorithm: Krill Herd with linear decreasing step. Applied Mathematics and Computation. 2014 May; 234:356–67.

25. Tasoulis M-K, Zacharioudakis KE, Dimopoulos NG, Hadjiminas DJ. Diagnostic accuracy of tactile imaging in selecting patients with palpable breast abnormalities: a prospective comparative study. Breast Cancer Research and Treatment. 2014 Oct; 147(3):589–98.