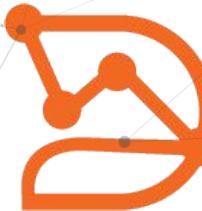


ADAPTATION OF HYBRID BINARY OPTIMIZATION SEARCH ALGORITHMS

Justice / Emmanuela



**DATA INTELLIGENCE
AND SWARM ANALYTICS LABORATORY**

Research Overview

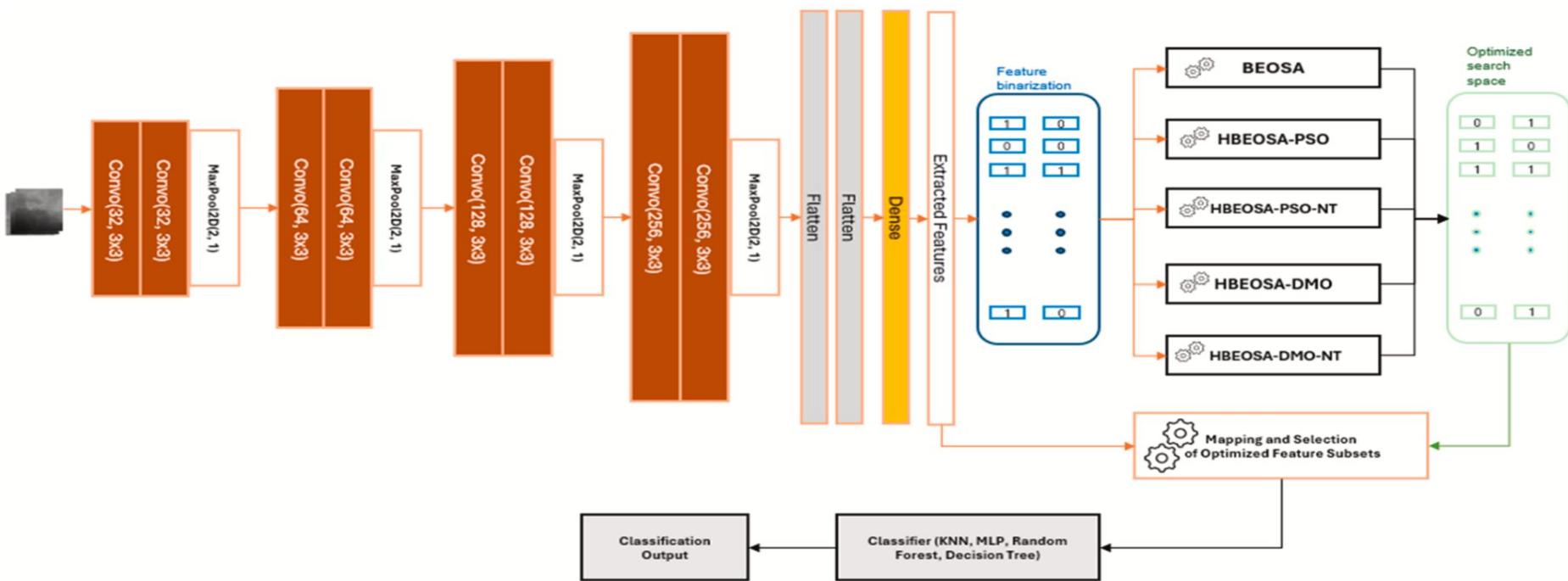
High-dimensional medical image data leads to heavy computation, overfitting, and poor interpretability, making traditional feature selection methods inadequate.

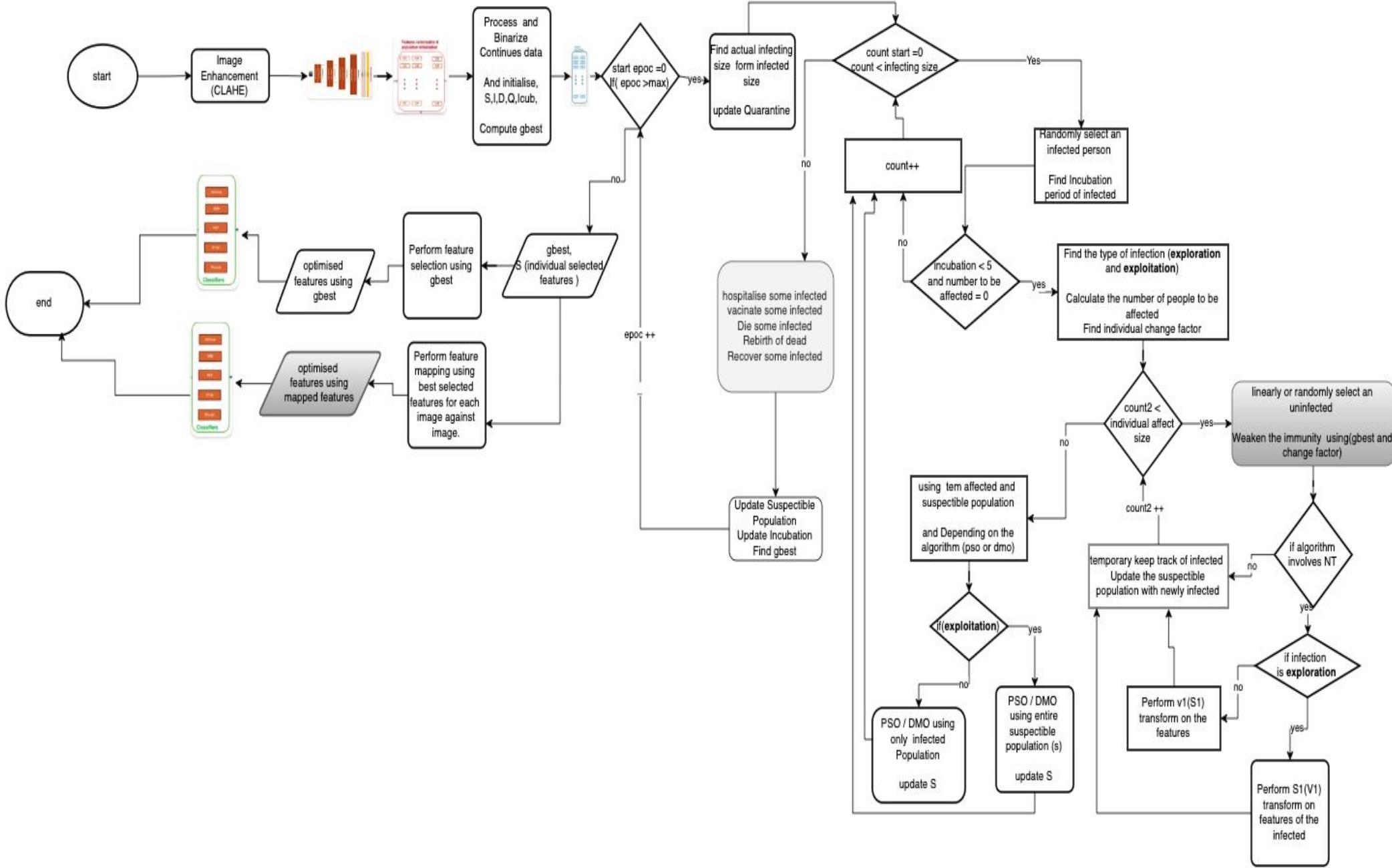
An optimized hybrid BEOSA variants (HBEOSA-DMO, HBEOSA-PSO, and NT-enhanced versions). In place of the Traditional Feature selection algorithms for Feature selection.



METHODOLOGY

FEATURE EXTRACTION, OPTIMIZATION AND CLASSIFICATION PIPELINE





Core Insight From the Research

Although the algorithm involved in the research used the adaptation of Hybrid Binary optimization algorithms. Thus HBEOSA-PSO, and HBEOSA-DMO. With Nested Functions

The success of this algorithm was the mimicking of the Ebola optimisation search algorithm as a compartmental Disease Model and of the Form (SIHV-D/Rb-RS) and utilizing the strength of PSO and DMO for its local or global optimization mechanism.



How to Determine the number of people to be moved to a particular compartment

With the use of Differential Equations the number of people to be moved to a particular compartment is computed using the following matrix.



EQUATIONS

- Susceptible individuals S

$$\frac{dS}{dt} = \pi - [(\beta_1 I + \beta_3 D + \beta_4 R + \beta_2 \eta PE)S] - (\delta S + d_r I)$$

- Infected individuals I

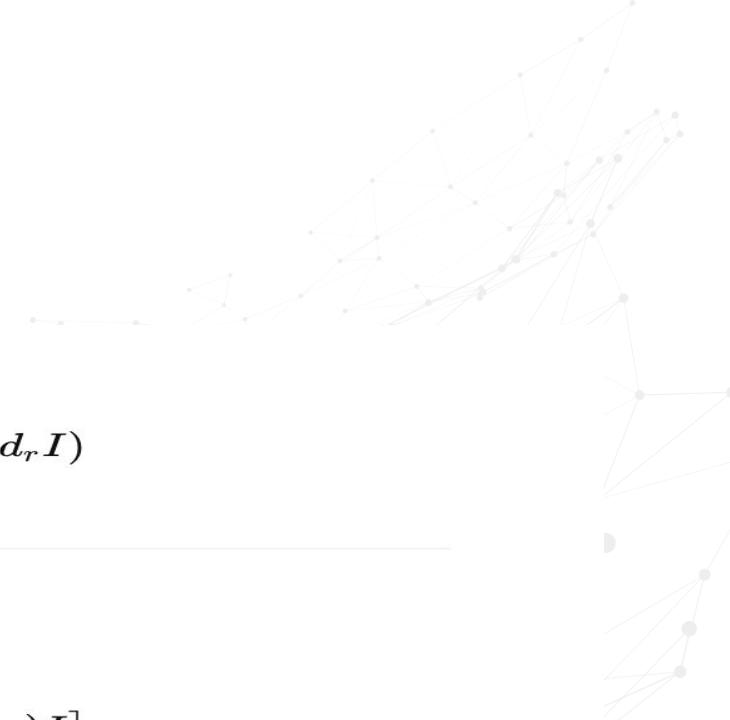
$$\frac{dI}{dt} = (\beta_1 I + \beta_3 D + \beta_4 R + \beta_2 \eta PE)S - [\delta S + (d_r + r_r)I]$$

- Hospitalized individuals H

$$\frac{dH}{dt} = \alpha I - (r_r + h_r)H$$

- Recovered individuals R

$$\frac{dR}{dt} = r_r I - \delta R$$



EQUATIONS

- Vaccinated individuals V

$$\frac{dV}{dt} = r_r I - (v_{rr} + v_r)V$$

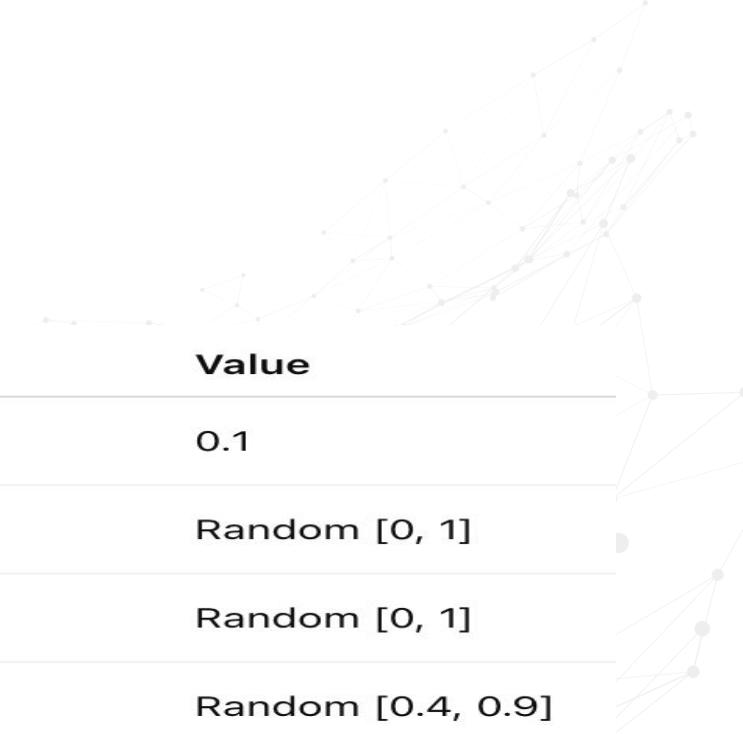
-
- Deceased individuals D

$$\frac{dD}{dt} = \delta I + d_r S - b_r D$$

-
- Quarantined individuals Q

$$\frac{dQ}{dt} = \pi I - (r_r R + \delta D) - q_{rr} Q$$

Symbols



Symbol	Meaning	Value
π	Recruitment rate of susceptible individuals	0.1
η	Decay rate of virus in environment	Random [0, 1]
α	Hospitalization rate	Random [0, 1]
δ	Disease-induced death rate	Random [0.4, 0.9]
β_1	Contact rate: infectious humans	0.1
β_2	Contact rate: environment	0.1
β_3	Contact rate: deceased humans	0.1
β_4	Contact rate: recovered humans	0.1
r_r	Recovery rate	Random [0, 1]
d_r	Natural death rate	Random [0, 1]
b_r	Burial rate	Random [0, 1]

Symbol

v_r

Vaccination rate

Random [0, 1]

h_r

Hospital treatment response rate

Random [0, 1]

v_{rr}

Vaccination response rate

Random [0, 1]

q_{rr}

Quarantine rate

Random [0, 1]



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Ro computation (How many can an infected individual affect.)

Total percentage of infected that affects its environment 25%.

The number of persons an infected person can infect is based a random number which is obtained on two nested piecewise functions.



Sub infection number calculation

$$R_0 = \begin{cases} \text{Random}\left(1, 0.1 \times (\text{infected} \times \text{epoch}) + 0.0001 + 0.01 \times \frac{\text{uninfected}}{2}\right), & \text{if } e^{-x} > 0.5 \\ & \text{if incubation} > 5 \\ \text{Random}\left(1, 0.7 \times (\text{infected} \times \text{epoch}) + 0.0001 + 0.01 \times \frac{\text{uninfected}}{2}\right), & \text{if } e^{-x} \leq 0.5 \\ 0, & \text{if incubation} \leq 5 \end{cases}$$

Immunity Change.

$$x_i^{\text{new}} = \Delta \times e^{rnd} \cos(2\pi rnd) \times (x_i - x_{\text{best}})$$

x_i^{new} The new mutated individual after applying the mutation step.

Δ Mutation factor that controls the strength or rate of mutation.

e^{rnd} Exponential scaling term introducing stochastic scaling.

rnd Random number drawn from a uniform distribution in $[-1, 1]$.

$\cos(2\pi rnd)$ Trigonometric modulation term introducing oscillatory behavior.

x_i Current individual in the population.

x_{best} The best individual in the current population based on fitness.

$x_i - x_{\text{best}}$ Directional difference vector guiding the mutation toward or away from the best solution.

Using Ant Colony Optimization for Feature Selection.

PSO (Particle Swarm Optimization) and **DMO** (Dwarf Mongoose Optimization) help balance:

- **Exploration** (searching new solutions).
- **Exploitation** (improving good solutions).

The ant colony is an alternative that also does this balance well.

Relation to PSO and DMO

Similar to PSO: uses a population that shares information (ants vs. particles).

Like DMO: balances **exploring new features** and **using good features more**.

ACO focuses on **paths (feature combinations)**, not positions.



The Ant Colony and How IT Works

What is Ant Colony Optimization (ACO)?

- Inspired by **real ants** finding food and marking trails.
- Ants build solutions step by step, using **pheromones** as a guide.
- Good paths get **more pheromone**, so other ants follow them more.

How does ACO work for feature selection?

- We think of each feature as a **decision point**: select (1) or skip (0).
- Each ant builds a subset of features based on pheromones.
- We evaluate each subset (e.g., using accuracy).
- We update pheromones to reward better subsets.

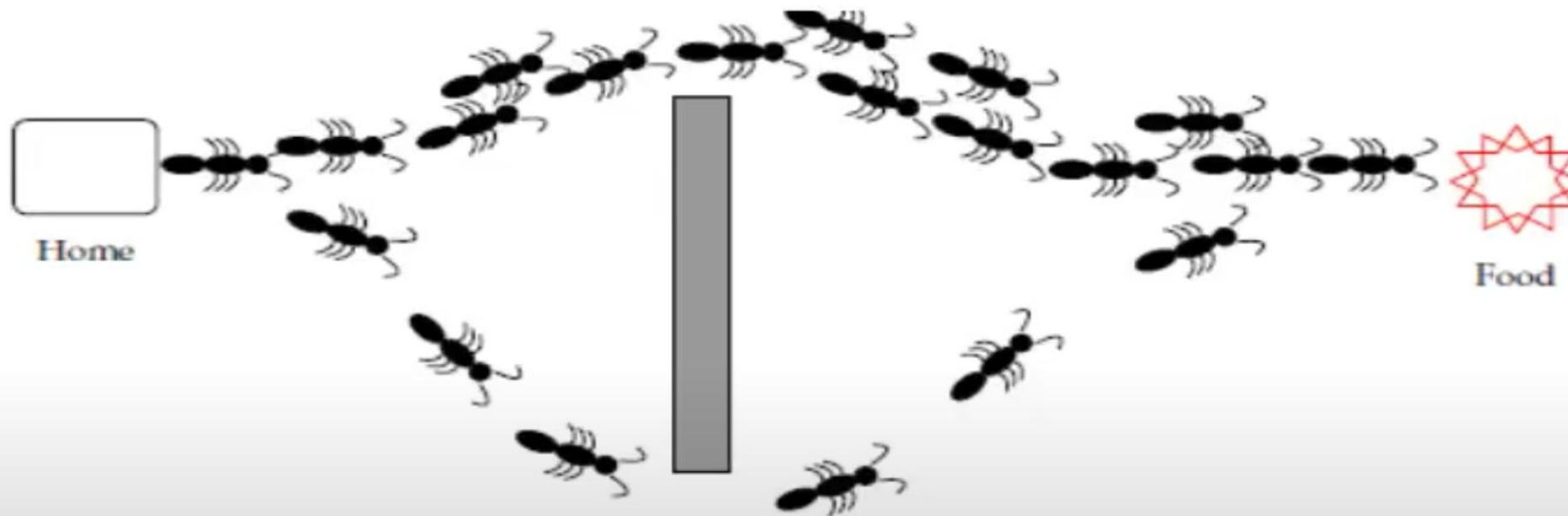


Benefits of using ACO

Works naturally for **binary problems** (0/1 selection).

Flexible and easy to adapt.

Reduces search space by learning good feature combinations.



What next?



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Results and Interpretation

Comparative analysis of the classification accuracy, precision, recall, F1-score, and AUC performances of features extracted when applied to KNN, RF, MLP and DTree algorithms for HBEOSA-DMO.

Stage	Classifier	Accuracy	Precision	Recall	F1-score	AUC
Pre-optimization	KNN	0.6623	0.85	0.94	0.89	0.7539
	RF	0.6731	0.73	0.67	0.84	0.7818
	MLP	0.6666	0.67	0.99	0.80	0.7918
	DTree	0.6147	0.72	0.92	0.81	0.7505
Post-optimization	KNN	0.7002	0.88	0.97	0.92	0.7954
	RF	0.8252	0.97	0.83	0.99	0.8291
	MLP	0.6743	0.76	0.69	0.81	0.7922
	DTree	0.6415	0.73	0.96	0.83	0.7591

Comparative analysis of the classification accuracy, precision, recall, F1-score, and AUC performances of features extracted when applied to KNN, RF, MLP and DTree algorithms for HBEOSA-DMO-NT.

Stage	Classifier	Accuracy	Precision	Recall	F1-score	AUC
Pre-optimization	KNN	0.6277	0.85	0.92	0.88	0.7656
	RF	0.6883	0.92	0.97	0.94	0.7888
	MLP	0.6731	0.68	0.67	0.81	0.7904
	DTree	0.6341	0.74	0.95	0.83	0.7506
Post-optimization	KNN	0.7002	0.88	0.97	0.92	0.7954
	RF	0.8286	0.97	1.00	0.98	0.8280
	MLP	0.6743	0.68	0.68	0.81	0.7922
	DTree	0.6415	0.73	0.96	0.83	0.7592

Results and Interpretation

Comparative analysis of the classification accuracy, precision, recall, F1-score, and AUC performances of features extracted when applied to KNN, RF, MLP and DTree algorithms for HBEOSA-PSO.

Stage	Classifier	Accuracy	Precision	Recall	F1-score	AUC
Pre-optimization	KNN	0.6277	0.85	0.92	0.88	0.7656
	RF	0.6905	0.92	0.97	0.94	0.7832
	MLP	0.6732	0.68	0.67	0.68	0.7905
	DTree	0.6342	0.74	0.95	0.83	0.7520
Post-optimization	KNN	0.7002	0.87	0.97	0.92	0.7954
	RF	0.8212	0.97	1.00	0.98	0.8284
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Stage	Classifier	Accuracy	Precision	Recall	F1-score	AUC
Pre-optimization	KNN	0.6536	0.86	0.93	0.89	0.7605
	RF	0.6731	0.72	0.67	0.83	0.7761
	MLP	0.6688	0.67	0.67	0.80	0.7932
	DTree	0.6342	0.69	0.95	0.80	0.7494
Post-optimization	KNN	0.7002	0.88	0.97	0.92	0.7954
	RF	0.825	0.96	1.00	0.98	0.8288
	MLP	0.6743	0.68	1.00	0.81	0.7922
	DTree	0.6415	0.73	0.96	0.83	0.7592

Main Insights From Research

Realised that BEOSA mimicked the a compartmental Modelling of the form S-I-Q-V-R-D-S in selecting the optimal features and Not just normal BEOSA as a **swarm based algorithm**

Compartment	Differential equation
S	$\frac{dS}{dt} = \pi - [\beta_1 I + \beta_3 R_b + \beta_4 R + \beta_2 PE \eta] S - (\text{dis} \cdot S + d_r \cdot I)$
I	$\frac{dI}{dt} = [\beta_1 I + \beta_3 R_b + \beta_4 R + \beta_2 PE \eta] S - (\text{dis} \cdot S + (d_r + r_r) \cdot I)$
H	$\frac{dH}{dt} = \alpha \cdot I - (r_r + h_r) \cdot H$
R	$\frac{dR}{dt} = r_r \cdot I - \text{dis} \cdot R$
V	$\frac{dV}{dt} = r_r \cdot I - (v_{rr} + v_r) \cdot V$
R_b	$\frac{dR_b}{dt} = \text{dis} \cdot I + d_r \cdot S - b_r \cdot R_b$
D	$\frac{dD}{dt} = \text{dis} \cdot R + b_r \cdot R_b$
Q	$\frac{dQ}{dt} = \pi \cdot I - (r_r \cdot R + \text{dis} \cdot R_b) - q_{rr} \cdot Q$

Possible Limitation of the paper

Potential Loss of Vital Data: Could impair the model's ability to detect subtle abnormalities or complex patterns.

Generalization Across Diverse Datasets: Limited evaluation on varied datasets and imaging modalities. Performance may vary with different data characteristics. Challenges in ensuring robust performance across different clinical settings.

Computational Cost: May limit real-time computation or large-scale applications.



Literature Review



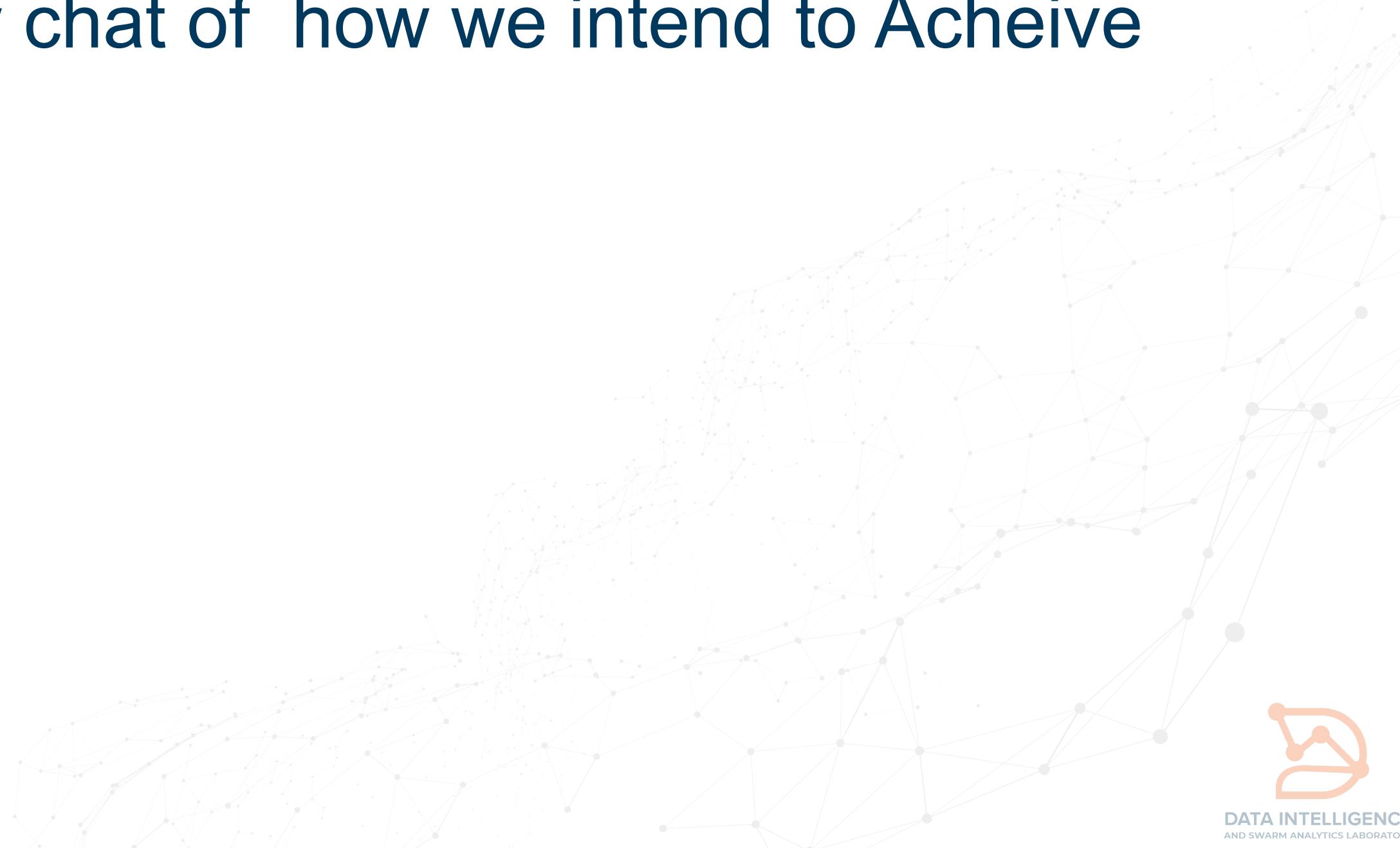
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Suggested Improvements



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Flow chat of how we intend to Acheive this



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What next



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INTRODUCTION

Medical images often come with high-dimensional datasets, which makes efficient analysis and feature selection a real challenge. Traditionally, these issues have been tackled using standard methods, but they don't always fully optimize classification performance.

In this project, a swarm intelligence-based machine learning protocol as an alternative to traditional computational numerical schemes for compartmental disease modeling in public health. These algorithms are enhanced with a novel nested transformation function, generating variants that effectively optimize binary search spaces while maintaining the relevance of important real-world features.

Tested on digital mammography datasets, the proposed methods show clearly improved classification accuracy compared to conventional techniques—highlighting their potential in advancing medical image analysis.



PROBLEM STATEMENT

High-dimensional datasets, especially in medical image analysis, pose major challenges for machine learning and classification tasks. These challenges include increased computational load, higher risk of overfitting, and decreased model interpretability. In the context of breast cancer detection using medical imaging data like mammograms, the sheer number of extracted features can significantly impact classification accuracy and overall model performance.

Conventional feature selection methods, while useful, often fall short in fully addressing the complexity and scale of such datasets—making it necessary to explore more adaptive and intelligent alternatives.



PROPOSED SOLUTION

This work presents an optimized swarm intelligence-based machine learning protocol as an alternative to traditional computational numerical schemes for compartmental disease modeling in public health. The protocol leverages the Binary Ebola Optimization Search Algorithm (BEOSA), a swarm-based metaheuristic, as the foundational framework.

To enhance its performance, BEOSA is hybridized with two other swarm intelligence algorithms—Binary Dwarf Mongoose Optimization (BDMO) and Binary Particle Swarm Optimization (BPSO)—resulting in two core variants: HBEOSA-DMO and HBEOSA-PSO. Further refinement is achieved through the integration of a nested transformation (NT) function, designed to improve search efficiency in high-dimensional binary spaces. This yields two additional enhanced variants: HBEOSA-DMO-NT and HBEOSA-PSO-NT.

This integrated approach not only improves classification accuracy and reduces dimensionality in complex datasets but also offers scalability and real-time decision-making support in public health applications—paving the way for more intelligent and efficient disease modeling.



DATASET

This study uses two types of datasets which are:

Text-based dataset(which are classified as high-dimensional, medium-dimensional and low-dimensional)

Image-based dataset(which are classified as Normal, Mass, Calcification, benign with calcification, and benign with mass).



METHODOLOGY

Overview of Approach

- Introduces a novel hybrid binary optimization algorithm for feature selection.
- Focused on identifying optimal feature subsets within a neural network architecture.

Methodology Breakdown

- **Stage 1:** Design of the **hybrid binary metaheuristic algorithm**, including:
 - Mathematical modeling
 - Algorithmic representation
- **Stage 2: Integration** of the optimizer into a **neural network (NN)**:
 - Seamless embedding into the neural network structure
 - Evaluation of performance impact



METHODOLOGY

Base Algorithms – BEOSA, BPSO, and BDMO

Foundational Algorithm:

The core binary optimizer is BEOSA.

Aims to enhance exploration and exploitation capabilities leads to the hybridization with BPSO and BDMO

Hybridization Strategy:

BPSO and BDMO selected for their effective optimization dynamics.

These are integrated with BEOSA to create: HBEOSA-PSO, HBEOSA-DMO

Innovative Enhancements:

Introduction of Nested Transfer (NT) functions to improve binary search space handling.
This leads to two additional variants: HBEOSA-PSO-NT , HBEOSA-DMO-NT



METHODOLOGY

Binary Ebola Optimization Search Algorithm (BEOSA)

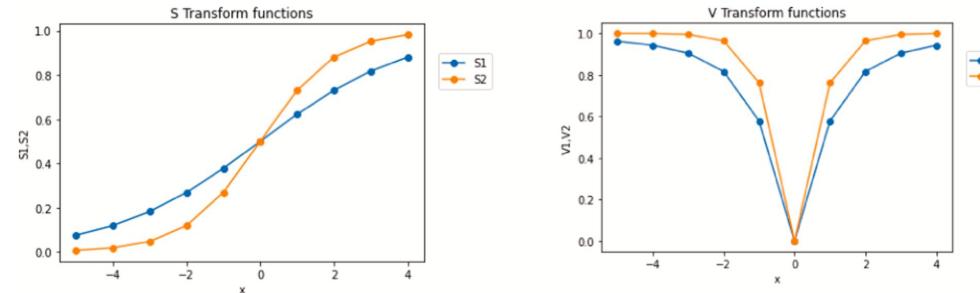
Origin & Binarization

Derived from the **continuous EOSA**;

Biological Inspiration

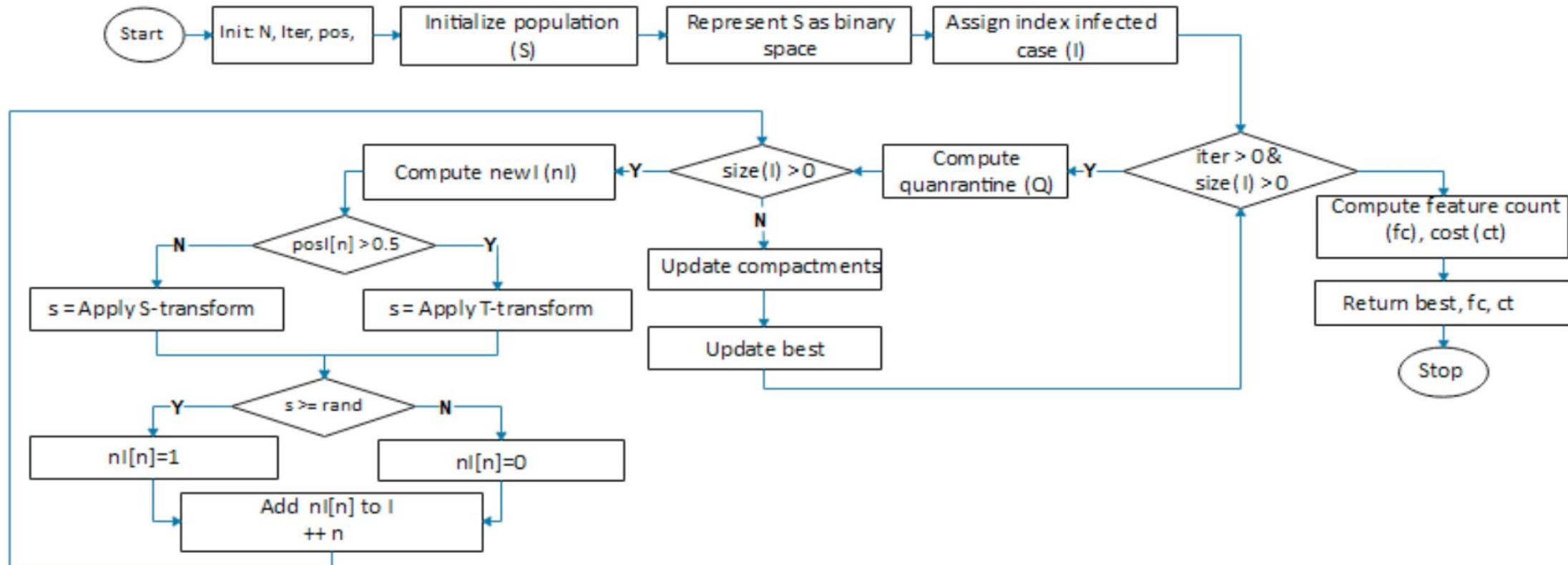
- Simulates **Ebola infection dynamics**:
 - Individuals in the search space represented as susceptible hosts.
 - Infection mimics **mutation** in feature representation, using fittest individual known, who infects the infected individual and some characteristics of Ebola diseases such as its circular nature, random nature etc.
 - Results in diverse **subpopulations** (e.g., infected, recovered, death, quarantine, rebirth).

Binarized using **S-shaped and V-shaped transfer functions** allows feature values to be **transformed into binary form (0s and 1s)** for optimization problems.



METHODOLOGY

Flow chart of BEOSA



METHODOLOGY

Hybridization Strategy – HBEOSA-PSO & HBEOSA-DMO

Why Hybridize BEOSA?

- BEOSA has limited local search refinement on its own.
- To enhance exploration (global search) and exploitation (local search), it's combined with stronger optimizers:
 - BPSO for swarm-based intelligence
 - BDMO for position-focused adaptation

Integration Logic

- Exploration phase:
 - When BEOSA attempts to explore new areas of the search space,
 - It delegates this to either BPSO or BDMO for wider population movement.
- Exploitation phase:
 - When intensifying the search locally around promising candidates,
 - BPSO or BDMO is activated for refinement

And this is done after a carrier has infected its environment. Based on the assumption that infected individuals interact with each other either locally or move out of their locality

Resulting In Hybrid Algorithms

- HBEOSA-PSO: BEOSA + BPSO collaboration → uses particle swarm behaviors to guide mutation and positioning.
- HBEOSA-DMO: BEOSA + BDMO integration → uses mongoose-style spatial adaptation for mutation and local selection



METHODOLOGY

Purpose of Nesting:

- Nesting (feature selection) helps reduce dimensionality and improve classifier accuracy by selecting only the most relevant features from medical images.

Why BPSO (Binary Particle Swarm Optimization)?

- Inspired by swarm behavior: Particles "fly" through solution space to find the best subset of features.
- Efficient global search: Good at escaping local optima early in optimization.
- Binary encoding: Naturally fits binary selection problems (feature selected = 1, not selected = 0).
- Fast convergence: Offers quicker exploration in the early search phase.

Why BDMO (Binary Dynamic Mongoose Optimization)?

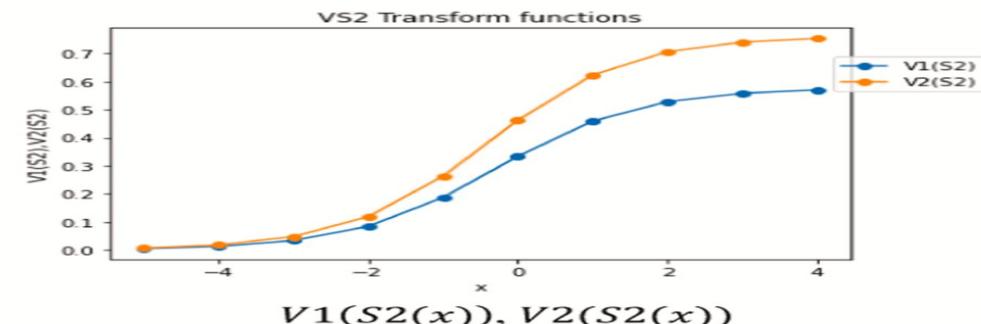
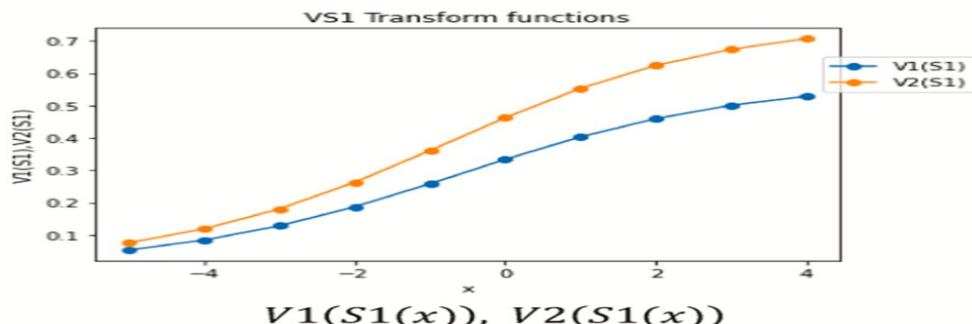
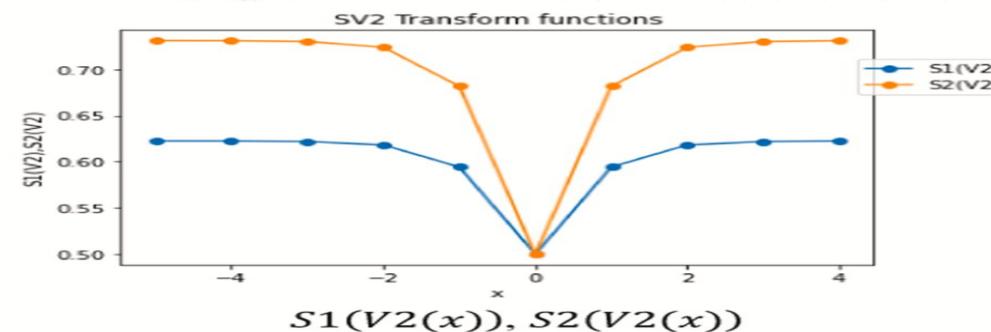
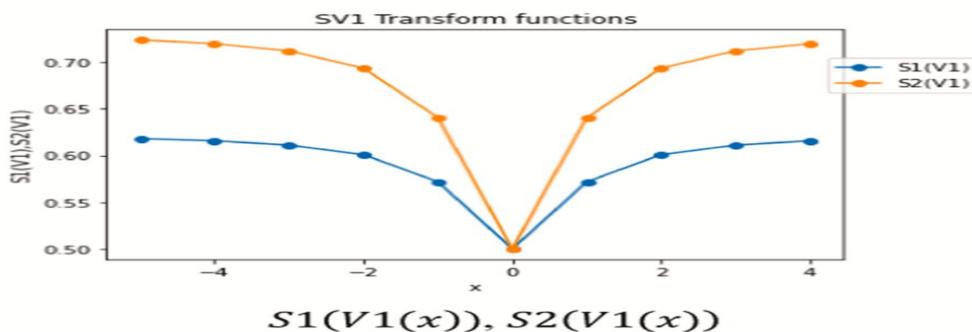
- Adaptive local search: Mimics mongoose foraging behavior with exploration–exploitation balance.
- Dynamic role-switching: Agents adapt their behavior (scout vs attacker) during search.
- Binary adaptation: Handles binary feature vectors effectively for selection.
- Improved refinement: Enhances local search



METHODOLOGY

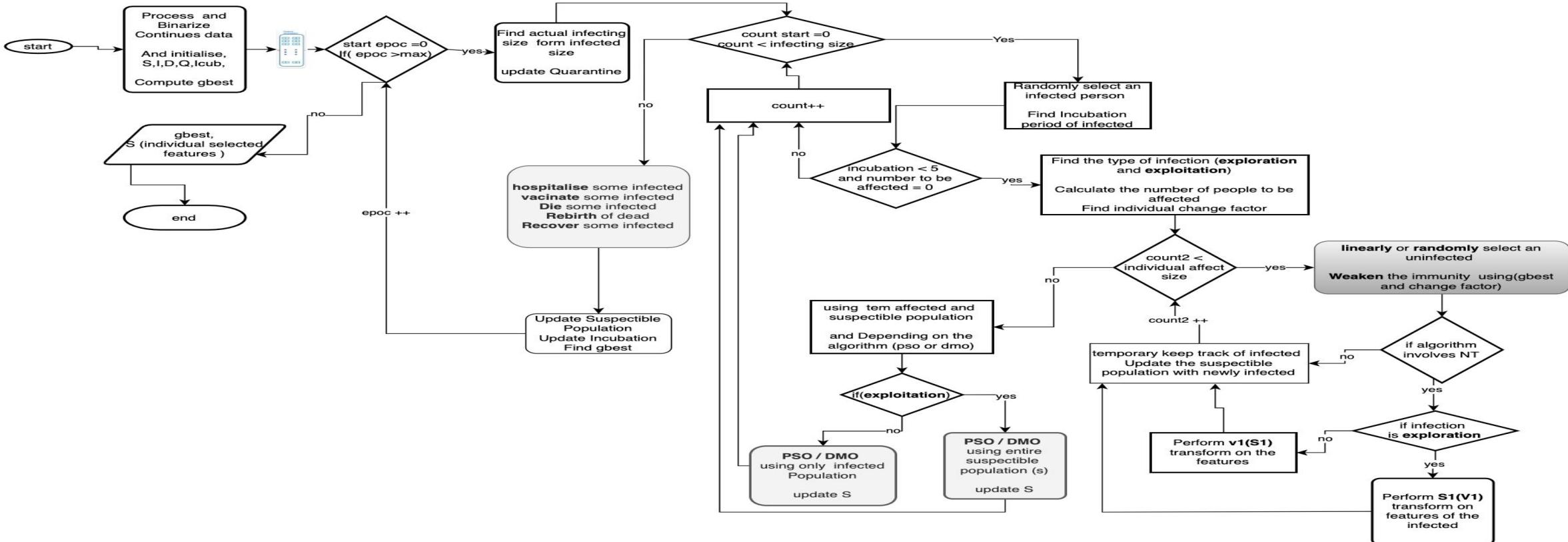
Hybridization Strategy – HBEOSA-PSO & HBEOSA-DMO with NT

Although HBEOSA-PSO and HBEOSA-DMO Performs very well further changes are made to the algorithm to generate more variants which involves the replacement of s_1, v_1, s_2, v_2 fuctions with nested the following Nested Transform function



METHODOLOGY

HYBRIDIZATION PROCESS FLOW CHART



METHODOLOGY

Integration of Algorithm into Neural Network

After the optimization process, selected features are mapped from the **binary search space** back to the **continuous feature domain** using two strategies:

1. Individual-Level Selection

- Each feature is represented as **0** or **1** in the binary solution.
- **0** = feature is ignored
- **1** = feature is selected
- Mapping is based on each agent's **personal best** solution.

2. Global-Level Selection

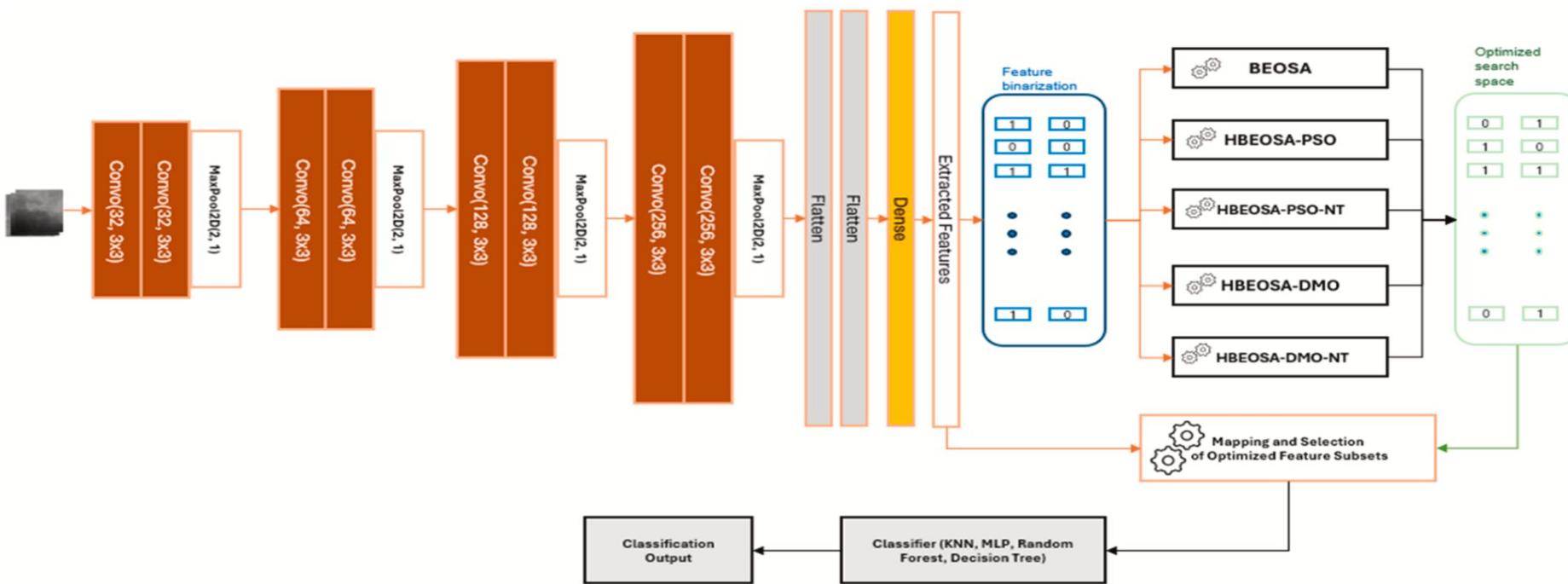
- Uses the **global best** binary solution from the final iteration.
- All features marked **1** are selected, representing the **overall optimal feature subset** across the population.

This results in **column reduction** of the dataset, retaining only the most relevant features—those marked **1**—for further classification or analysis, significantly reducing dimensionality and improving efficiency.



METHODOLOGY

FEATURE EXTRACTION, OPTIMIZATION AND CLASSIFICATION PIPELINE



RESEARCH OBJECTIVES

Designed a novel adaptation of the medical image feature representation in continuous space to a binary search space for the hybrid binary optimization strategies.

Proposed two hybrid binary optimization algorithms namely HBEOSA-DMO and HBEOSA-PSO.

Investigated the influence of the new nested function on the two proposed hybrid methods so that four variants were derived namely HBEOSA-DMO HBEOSA-DMO-NT HBEOSA-PSO and HBEOSA-PSO - NT.

Comparatively investigated the capability of the four binary optimizers with other recent binary methods.

Experimentally studied the impact of the new hybrid binary optimizers on improving classification accuracy of applying CNN to digital mammography



Results and Interpretation

Comparative analysis of the classification accuracy, precision, recall, F1-score, and AUC performances of features extracted when applied to KNN, RF, MLP and DTree algorithms for HBEOSA-DMO.

Stage	Classifier	Accuracy	Precision	Recall	F1-score	AUC
Pre-optimization	KNN	0.6623	0.85	0.94	0.89	0.7539
	RF	0.6731	0.73	0.67	0.84	0.7818
	MLP	0.6666	0.67	0.99	0.80	0.7918
	DTree	0.6147	0.72	0.92	0.81	0.7505
Post-optimization	KNN	0.7002	0.88	0.97	0.92	0.7954
	RF	0.8252	0.97	0.83	0.99	0.8291
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	DTree	0.6415	0.73	0.96	0.83	0.7591

Comparative analysis of the classification accuracy, precision, recall, F1-score, and AUC performances of features extracted when applied to KNN, RF, MLP and DTree algorithms for HBEOSA-DMO-NT.

Stage	Classifier	Accuracy	Precision	Recall	F1-score	AUC
Pre-optimization	KNN	0.6277	0.85	0.92	0.88	0.7656
	RF	0.6883	0.92	0.97	0.94	0.7888
	MLP	0.6731	0.68	0.67	0.81	0.7904
	DTree	0.6341	0.74	0.95	0.83	0.7506
Post-optimization	KNN	0.7002	0.88	0.97	0.92	0.7954
	RF	0.8286	0.97	1.00	0.98	0.8280
	MLP	0.6743	0.68	0.68	0.81	0.7922
	DTree	0.6415	0.73	0.96	0.83	0.7592

Results and Interpretation

Comparative analysis of the classification accuracy, precision, recall, F1-score, and AUC performances of features extracted when applied to KNN, RF, MLP and DTree algorithms for HBEOSA-PSO.

Stage	Classifier	Accuracy	Precision	Recall	F1-score	AUC
Pre-optimization	KNN	0.6277	0.85	0.92	0.88	0.7656
	RF	0.6905	0.92	0.97	0.94	0.7832
	MLP	0.6732	0.68	0.67	0.68	0.7905
	DTree	0.6342	0.74	0.95	0.83	0.7520
Post-optimization	KNN	0.7002	0.87	0.97	0.92	0.7954
	RF	0.8212	0.97	1.00	0.98	0.8284
	MLP	0.6743	0.68	1.00	0.81	0.7922
	DTree	0.6415	0.73	0.96	0.83	0.7591

Comparative analysis of the classification accuracy, precision, recall, F1-score, and AUC performances of features extracted when applied to KNN, RF, MLP and DTree algorithms for HBEOSA-PSO-NT.

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	MLP	0.6688	0.67	0.67	0.80	0.7932
	DTree	0.6342	0.69	0.95	0.80	0.7494
Post-optimization	KNN	0.7002	0.88	0.97	0.92	0.7954
	RF	0.825	0.96	1.00	0.98	0.8288
	MLP	0.6743	0.68	1.00	0.81	0.7922
	DTree	0.6415	0.73	0.96	0.83	0.7592

RESULT INTERPRETATION

accuracy for low dimension dataset

Dataset	Algorithm	Acc-50	Acc-100	Fit-50	Fit-100	Cost-50	Cost-100	FC	CT
Exactly	HBEOSA-DMO	0.760	0.652	0.168	0.301	0.832	0.699	6.000	934.955
	HBEOSA-DMO-NT	0.695	0.792	0.308	0.154	0.692	0.846	7.000	946.215
	HBEOSA-PSO	0.890	0.758	0.009	0.308	0.991	0.692	1.000	1027.426
	HBEOSA-PSO-NT	0.760	0.877	0.306	0.232	0.694	0.768	6.668	1151.243
	BEOSA	0.980	0.900	0.022	0.022	0.978	0.978	2.336	0.011
Exactly2	HBEOSA-DMO	0.700	0.722	0.237	0.238	0.763	0.762	1.000	1153.631
	HBEOSA-DMO-NT	0.770	0.760	0.238	0.238	0.762	0.762	3.500	820.203
	HBEOSA-PSO	0.740	0.650	0.025	0.235	0.975	0.765	2.000	855.708
	HBEOSA-PSO-NT	0.778	0.762	0.222	0.238	0.778	0.762	3.000	1091.790
	BEOSA	0.765	0.760	0.236	0.236	0.764	0.764	5.000	0.011
Iris	HBEOSA-DMO	0.953	0.967	0.071	0.054	0.929	0.946	2.000	2146.082
	HBEOSA-DMO-NT	0.973	0.973	0.036	0.070	0.965	0.920	1.600	2019.983
	HBEOSA-PSO	0.940	0.933	0.001	0.066	0.999	0.934	1.000	2187.545
	HBEOSA-PSO-NT	0.967	0.953	0.003	0.033	0.998	0.967	1.014	1884.631
	BEOSA	0.967	0.967	0.036	0.035	0.965	0.964	1.000	0.016
M-of-n	HBEOSA-DMO	0.810	0.797	0.326	0.217	0.674	0.783	6.000	874.501
	HBEOSA-DMO-NT	0.843	0.820	0.183	0.208	0.817	0.792	96.000	854.640
	HBEOSA-PSO	0.918	0.900	0.166	0.127	0.834	0.873	1.276	708.316
	HBEOSA-PSO-NT	0.837	0.910	0.152	0.027	0.848	0.973	4.550	757.834
	BEOSA	0.855	0.850	0.148	0.148	0.852	0.852	6.000	0.010
Tic-tac-toe	HBEOSA-DMO	0.742	0.719	0.179	0.252	0.921	0.748	1.000	1816.082
	HBEOSA-DMO-NT	0.776	0.773	0.209	0.224	0.791	0.776	6.000	1686.338
	HBEOSA-PSO	0.758	0.779	0.244	0.018	0.756	0.982	1.000	1804.136
	HBEOSA-PSO-NT	0.820	0.773	0.151	0.238	0.849	0.762	5.000	1778.422
	BEOSA	0.781	0.781	0.222	0.222	0.778	0.778	5.000	0.014
Wine	HBEOSA-DMO	0.903	0.903	0.030	0.059	0.970	0.941	5.000	1014.824
	HBEOSA-DMO-NT	0.972	1.000	0.032	0.004	0.968	0.996	4.500	762.768
	HBEOSA-PSO	0.986	0.889	0.003	0.025	0.997	0.975	2.137	840.244
	HBEOSA-PSO-NT	0.986	0.986	0.056	0.002	0.944	0.998	3.065	1090.850
	BEOSA	0.972	0.972	0.031	0.031	0.969	0.969	4.000	0.011

RESULT INTERPRETATION

Mid- Dimension Data set

Dataset	Algorithm	Acc-50	Acc-100	Fit-50	Fit-100	Cost-50	Cost-100	FC	CT
CongressEW	HBEOSA-DMO	0.954	0.931	0.036	0.046	0.964	0.954	1.000	477.454
	HBEOSA-DMO-NT	0.954	0.971	0.058	0.026	0.942	0.974	6.500	466.500
	HBEOSA-PSO	0.989	0.966	0.047	0.026	0.953	0.974	1.996	515.259
	HBEOSA-PSO-NT	0.966	0.954	0.037	0.036	0.963	0.964	4.000	531.094
	BEOSA	0.943	0.943	0.060	0.060	0.940	0.940	5.000	0.013
Lymphography	HBEOSA-DMO	0.833	0.000	0.136	0.165	0.864	0.835	6.000	718.970
	HBEOSA-DMO-NT	0.917	0.900	0.074	0.037	0.926	0.963	7.500	599.726
	HBEOSA-PSO	0.783	0.900	0.233	0.036	0.767	0.964	9.000	650.063
	HBEOSA-PSO-NT	0.900	0.917	0.103	0.067	0.897	0.933	4.124	636.246
	BEOSA	0.900	0.000	0.103	0.103	0.897	0.897	6.524	0.011
SpectEW	HBEOSA-DMO	0.843	0.870	0.170	0.150	0.830	0.850	7.000	617.395
	HBEOSA-DMO-NT	0.889	0.824	0.096	0.187	0.904	0.813	10.000	596.261
	HBEOSA-PSO	0.815	0.796	0.186	0.077	0.814	0.923	7.360	601.872
	HBEOSA-PSO-NT	0.870	0.870	0.130	0.132	0.870	0.868	7.632	608.789
	BEOSA	0.870	0.870	0.132	0.132	0.868	0.868	7.000	0.016
Vote	HBEOSA-DMO	0.975	0.942	0.004	0.051	0.996	0.949	4.500	465.388
	HBEOSA-DMO-NT	0.958	0.983	0.051	0.020	0.949	0.980	5.500	491.004
	HBEOSA-PSO	0.967	0.958	0.019	0.050	0.981	0.950	1.498	459.809
	HBEOSA-PSO-NT	0.967	0.967	0.019	0.035	0.981	0.965	3.410	459.633
	BEOSA	0.967	0.967	0.035	0.035	0.965	0.965	3.416	0.011
Zoo	HBEOSA-DMO	0.950	0.920	0.002	0.147	0.998	0.853	3.000	494.763
	HBEOSA-DMO-NT	0.925	0.900	0.104	0.053	0.896	0.947	6.000	477.552
	HBEOSA-PSO	1.000	0.900	0.092	0.053	0.908	0.947	1.641	454.429
	HBEOSA-PSO-NT	1.000	1.000	0.004	0.006	0.996	0.994	8.000	440.724
	BEOSA	1.000	1.000	0.006	0.006	0.994	0.994	8.000	0.011

Results and Interpretation

Dataset	Algorithm	Acc-50	Acc-100	Fit-50	Fit-100	Cost-50	Cost-100	FC	CT
BreastEW	HBEOSA-DMO	0.942	0.940	0.056	0.054	0.944	0.946	15.000	2540.629
	HBEOSA-DMO-NT	0.949	0.965	0.057	0.021	0.943	0.979	8.600	2766.993
	HBEOSA-PSO	0.963	0.953	0.072	0.035	0.928	0.965	7.000	2260.324
	HBEOSA-PSO-NT	0.965	0.946	0.016	0.053	0.984	0.947	6.381	3086.175
Colon	BEOSA	0.947	0.947	0.054	0.054	0.946	0.946	5.000	0.021
	HBEOSA-DMO	1.000	1.000	0.085	0.085	0.915	0.915	2.000	2413.129
	HBEOSA-DMO-NT	1.000	1.000	0.002	0.000	0.998	1.000	134.000	2088.655
	HBEOSA-PSO	1.000	1.000	0.089	0.157	0.911	0.843	76.077	2469.002
Ionosphere	HBEOSA-PSO-NT	1.000	1.000	0.002	0.000	0.998	1.000	45.315	2392.427
	BEOSA	1.000	1.000	0.0005	0.002	0.9995	0.9980	396.000	0.022
	HBEOSA-DMO	0.886	0.879	0.0849	0.085	0.9151	0.9146	2.000	708.539
	HBEOSA-DMO-NT	0.900	0.936	0.100	0.087	0.900	0.913	8.500	723.254
KrVsKpEW	HBEOSA-PSO	0.886	0.857	0.055	0.086	0.945	0.914	5.000	793.166
	HBEOSA-PSO-NT	0.914	0.936	0.114	0.073	0.886	0.927	4.500	786.935
	BEOSA	0.943	0.943	0.057	0.057	0.943	0.943	2.000	0.013
	HBEOSA-DMO	0.937	0.938	0.641	0.058	0.359	0.942	16.000	2943.689
Leukemia	HBEOSA-DMO-NT	0.931	0.947	0.057	0.072	0.943	0.928	15.000	2894.754
	HBEOSA-PSO	0.900	0.934	0.148	0.057	0.852	0.943	1057.872	2846.351
	HBEOSA-PSO-NT	0.966	0.961	0.037	0.028	0.963	0.972	10.257	3115.554
	BEOSA	0.948	0.948	0.055	0.055	0.945	0.945	12.899	0.012
PenglungEW	HBEOSA-DMO	1.000	1.000	0.0003	0.000	0.9997	1.000	145.000	3047.149
	HBEOSA-DMO-NT	0.987	1.000	0.00047	0.000358	0.9995	0.9996	213.000	2693.147
	HBEOSA-PSO	0.947	1.000	0.0001	0.0005	0.9999	0.9995	165.000	3301.407
	HBEOSA-PSO-NT	1.000	0.973	0.0004	0.0003	0.9996	0.9997	91.000	2799.496
Sonar	BEOSA	0.933	0.933	0.066	0.066	0.934	0.934	74.000	0.016
	HBEOSA-DMO	0.767	0.667	0.044	0.002	0.956	0.998	40.000	248.420
	HBEOSA-DMO-NT	0.867	0.733	0.068	0.067	0.932	0.933	17.500	250.196
	HBEOSA-PSO	0.800	0.767	0.069	0.023	0.931	0.977	49.000	256.531
WaveformEW	HBEOSA-PSO-NT	0.767	0.867	0.067	0.059	0.933	0.941	59.000	256.038
	BEOSA	0.933	0.933	0.000	0.000	1.000	1.000	9.732	0.018
	HBEOSA-DMO	0.929	0.810	0.096	0.120	0.904	0.880	17.000	646.479
	HBEOSA-DMO-NT	0.869	0.917	0.143	0.119	0.857	0.881	15.000	672.351
Wine	HBEOSA-PSO	0.857	0.821	0.095	0.072	0.905	0.928	9.407	513.774
	HBEOSA-PSO-NT	0.881	0.905	0.142	0.095	0.858	0.905	15.112	634.425
	BEOSA	0.905	0.905	0.099	0.099	0.901	0.901	25.000	0.013
	HBEOSA-DMO	0.811	0.780	0.200	0.197	0.800	0.803	20.000	4554.501
Yeast	HBEOSA-DMO-NT	0.813	0.820	0.177	0.189	0.823	0.811	24.500	4146.997
	HBEOSA-PSO	0.781	0.798	0.114	0.086	0.886	0.914	16.000	4549.970
	HBEOSA-PSO-NT	0.820	0.810	0.194	0.169	0.806	0.831	17.034	4685.436
	BEOSA	0.801	0.800	0.202	0.202	0.798	0.798	20.000	0.012

CONCLUSION

In conclusion, the proposed swarm intelligence-based machine learning protocol offers a promising alternative to traditional numerical schemes for compartmental disease modeling in public health.

The four developed algorithmic variants showed remarkable performance on text-based datasets, which inspired their integration into a neural network model.

This integration not only enhanced the classification accuracy of multiple classifiers but also contributed to dimensionality reduction and reduced computational resource demands—marking a significant step forward in efficient and intelligent disease modeling.





DATA INTELLIGENCE

AND SWARM ANALYTICS LABORATORY