Implementation and Application of a Particle Swarm Optimization Ontology to the Resolution of the Object Classification Problem: A Case Study to Classifying Cervical Cancer Cells Images

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Abstract: *We developed a Particle Swarm Optimization (PSO) inspired ontology to resolve the object classification problem, using cervical cancer cell images as a case study. Implemented in Protégé 5.5, the ontology was integrated with two datasets for cervical cancer images namely Herlev and SipakMed datasets to classify images into three categories: abnormal, normal, and benign. Python scripts were employed to extract key features from the two datasets and upload them into the ontology. Trained on SipakMed and tested on Herlev the model achieved a classification accuracy of 87.11%, with a precision of 96% and a recall of 96% for normal cells, and a precision of 95% and recall of 91% for abnormal cells. However, classification of benign cells still showed lower precision even when tested on each dataset independently or combined this could also be due to overlapping features with other classes and limited benign cell images. This study highlights the potential of PSO-inspired ontologies for effective object classification.*

Keywords: *Ontology, particle swarm optimization system, object classification problem.*

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1. Introduction

A scoping review on the application of swarm intelligence technologies to object classification was conducted Tsedura *et al*. [20], highlighting five prominent approaches [18]. Among these, Particle Swarm Optimization (PSO) emerged as the most prominent, motivating its selection for the development of a PSO-inspired swarm intelligence ontology [19].

This ontology comprises key components such as particles, swarm, search space, goal, environment, and fitness measures. Particles represent potential solutions to the optimization problem [14], while a swarm is a collection of these particles. Obstacles act as hindrances to particle movement. The goal defines the problem to be solved, and the environment encompasses all components. Fitness measures assess the quality of particle positions.

Each component was further decomposed into sub-entities, and their interrelationships were defined. The ontology design illustrated these relationships and data flows. A technology acceptance evaluation revealed that the designs are complete, reliable, usable, valid and scalable.

This article presents the implementation, application and evaluation of that ontology for object classification. Here, an ontology is a formalized representation of knowledge that defines concepts, categories [22, 24], their attributes, and the semantic relationships among them. Ontologies traditionally support data standardization and interoperability [6]. This ontology thus serves as a structured knowledge model to support object classification based on swarm intelligence principles.

1.1. The Problem

The object classification problem is an attempt to identify and separate entities into different categories [4]. Objects, in this case, are cancer cells images. Classification depends on the attributes of cells images. We believe that knowledge representation and formalization in the object classification domain involving cancer cells images is still ambiguous [20]. The explicit problem we address in this study is, the implementation of the PSO inspired swarm intelligence ontology for application to the object classification problem emphasizing “cancer cells images” objects. Hopefully, this ontology will systematically categorize and define the key concepts, relationships, and attributes related to cancer cells images.

1.2. Objectives

Implementing the PSO inspired swarm intelligence

ontology includes the use of particles, swarm, search space, goal, environment, and fitness measures in solving the object classification problem. The explicit objectives we seek to achieve are as follows:

- To implement a PSO inspired ontology.
- To enable the semantic representation of cancer cells images features in the PSO inspired ontology.
- To test the ontology in classifying cancer cells images into three classes; abnormal, benign, or normal cells.

Successful achievement of these objectives would trigger contributions of knowledge in the object classification domain. It would yield more robust and fault tolerant solutions to the object classification problem. The design of the ontology will bring about reusability and scalability. Also, the work sets a baseline upon which to build further research and advancement in the field.

1.3. Overview

The rest of the article proceeds as follows: section 2 provides a review of related work around the implementation and application of ontologies in object classification problem, elucidating the gap in this domain. Thereafter, section 3 presents the methods and materials we used, detailing the steps taken in implementing the ontology and how it was tested for validity in the cancer cells domain. In section 4 we share the results yielded from the evaluation of the ontology, along with the discussions and reflections thereof. We conclude the article in section 5, summarizing the key findings, contributions and proposing areas for future work.

2. Related Work

Ontologies have been implemented for knowledge representation [14, 24] data integration [22], information retrieval [22], decision support [4, 6] and knowledge sharing [22]. This section reviews the application of ontologies and the tools used to implement ontologies. The potential of combining ontologies with deep learning to improve interpretability in cancer detection was highlighted in a survey on deep learning tools for classification [15]. In that case, ontologies provided semantic knowledge to guide models towards better generalization [1]. However, despite deep learning models being powerful, they often lack the ability to provide reasoning capabilities that ontologies offer [15]. This limitation is due to the complexity of developing a robust ontology that can keep up with the continuous advancements in deep learning [15].

Support Vector Machines (SVM) and PSO have been integrated into an ontology for classification and feature selection of cervical cancer cells [10]. While the main features of the cancer cells were captured by the ontology, the PSO component improved the performance of the SVM arm through optimization. Nevertheless, the ontology's adaptability and scalability remained a challenge. In fact, the model struggled with new data to the ontology, where extensive domain knowledge was stored [15].

A claim that ontologies perform better than machine learning technologies has been raised [12]. As such, an ontological model grounded on the decision tree algorithm was implemented to predict breast cancer cells. Rules that differentiated malignant and benign breast cancer cells were extracted using the decision tree algorithm [10] to, subsequently, offer ontological reasoning for classification. In that case, the ontology classifier outperformed machine learning based classifiers with a prediction accuracy of 97.10%.

Ontological modelling was implemented using recursive recurrent neural network and crayfish optimization to attain a reliable prediction of breast cancer cells [11, 12]. Their work used the Semantic Web Rule Language (SWRL) to construct the ontology. The performance of the ontology model was evaluated based on F-score, accuracy, precision, and sensitivity. The models in [10, 12] both aimed at comparing the ontological models with machine learning techniques in detecting breast cancer cells. Our work is inspired by the views of these two ontological models towards demonstrating that ontologies are useful in predicting breast cancer cells with higher accuracy. In this demonstration, we differ from the use of ontologies to handle checks for childhood cancer cells using a modular approach and axioms [21]. In their case [11], automated reasoning processes were used but the size of the dataset limited the model's performance.

Continuous enrichment and advancement of ontology modelling is compelling. It brings on board relevancy and currency. Closely related to our views is a domain specific ontology for knowledge sharing and collaboration across various disciplines [21]. However, although ontologies are successful [3, 14, 16, 22], human validation is still apparent.

3. Methods and Materials

Methodologies have been proposed to direct the implementation of ontologies [5, 12, 13], including Methontology [9], Ontoclean [12], NeOn [12], Toronto Virtual Enterprise (TOVE) [2], Enterprise Model Approach [7] and IDEF5 [8]. However, lack of a unified approach is still apparent [2]. The difference between these methodologies is in the arrangement of the steps followed, without varying the methodological approach [9]. We follow a combination of steps from Methontology, Enterprise Model Approach and TOVE. We refer to our methodology as the PSOnto, comprising the following six steps; purpose identification, requirements elicitation, conceptualization, axiom specification, integration, implementation, evaluation,

and documentation. We elucidate on each step in subsequent sections.

3.1. Purpose Identification

The goal in PSOnto is to classify cervical cancer cells images. It seeks to provide a standardized and structured framework that systematizes knowledge associated with cervical cancer cells images, expediting accurate classification, and, hopefully, appropriate diagnosis and decision-making. Its primary purpose is to be able to classify annotated cervical cancer cell images into three classes namely, normal, abnormal and benign cancer cells images. In this context, normal cancer cells are healthy cells that maintain a uniform shape and size under microscopic examination [16]. On the other hand, abnormal cancer cells are cells that deviate from the structure and behavior of normal cells exhibiting irregularities like disparities in shape, size, or organization [3, 16]. Contrary, benign cancer cells are non-cancerous growths or tumors that have a different structure from normal cells [16].

3.2. Requirements Elicitation

Requirements elicitation for PSOnto focuses on functional and non-functional requirements to inform its conceptualization. The key functional requirement is to classify cervical cancer cell images by integrating PSO concepts such as particles, swarm and fitness functions with image features like nuclear size, texture, and color intensity.

The ontology supports reasoning, feature selection, and optimization processes, mapping optimized features to cancer stages or lesion types. Domain-specific requirements include preprocessing steps segmentation, normalization and linking optimized features to classification models like SVM and neural networks, evaluated using metrics such as accuracy and sensitivity.

Technically, PSOnto integrates with PSO libraries like Pyswarms and machine learning frameworks like TensorFlow, offering visualization capabilities to illustrate swarm behavior and relationships among features. It ensures computational efficiency for large-scale cervical cancer datasets, enabling real-time querying and reasoning. Non-functional requirements include scalability, performance optimization, user-friendliness, and interoperability with existing ontologies. The modular design allows independent updates without disruptions, ensuring reliability, consistency, and secure data handling.

3.3. Conceptualization and Ontology Visualization

PSOnto was developed in Protégé using the Web Ontology Language (OWL) and structured under the root class owl: Thing, combining biological, diagnostic and computational aspects which aid with cervical cancer cell classification as shown in Figure 1 below. Cell class is the base for representing all cervical cell instances. Corresponding to clinically relevant groupings each cell is then categorized into one of the three diagnostic classes namely NormalCell, BenignCell, and AbnormalCell in the CellCategory class. Herlev and SipakMed datasets were incorporated in the ontology under CellType class. Cell categories in this class are refined into two cytological types grouped into two HerlevCellType and SipakMedCellType mapping Herlev and SipakMed datasets respectively. SipakMedCellType has five groups of cervical cancer cells images namely DyskeratoticCell, KoilocytoticCell, MetaplasticCell, ParabasalCell, and SuperficialIntermediateCell. Superficial-Intermediate and Parabasal cells are subclasses of the normal cells while Koilocytotic and Dyskeratotic cells are subclasses of the abnormal cells and Metaplastic cells are a subclass of benign cells. HerlevCellType comprises of only abnormal and normal cells. The abnormal classes where various stages of cervical dysplasia are represented are CarcinomaInSitu, SevereDysplasia, ModerateDysplasia, and MildDysplasia. The normal epithelial cell types are represented in NormalIntermediate, NormalSuperficial, NormalColumnar. Cytoplasmic and nuclear cell features extracted for classification are stored in the class termed CellFeature. Cytoplasmic and nuclear features like area, shape and membrane irregularities are derived in this class.

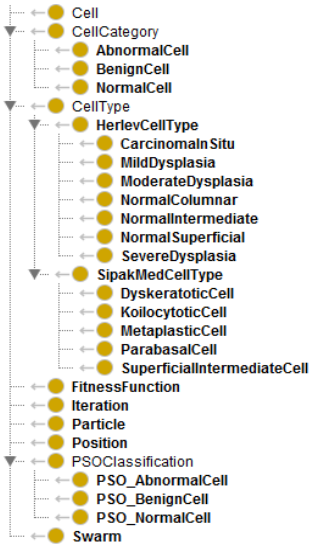

Figure 1. PSOnto Visualization from Protégé.

Restrictions were added to prevent a cell from belonging to more than one class. In the PSOClassification class the ontology incorporates components of the PSO algorithm. The Swarm class represents the population of candidate solutions, each modeled as a particle. Each particle holds a position, which represents its feature weights or decision thresholds, and evaluates its performance using a FitnessFunction. The iteration class tracks the

progression of the optimization process over time. The classification outcomes generated by the PSO model are captured under PSOClassification, which includes PSO_AbnormalCell, PSO_BenignCell and PSO_NormalCell representing PSOnto's predicted diagnostic classes.

3.4. Axiom Specification

In Protégé, an axiom represents basic statements or facts that define relationships or properties within an ontology [17]. It is a declarative statement that asserts something about the elements of the ontology. Thus, axioms define the structure and semantics of an ontology.

Protégé supports two types of relationships in ontology design. These are, namely, object properties and data properties [17]. Object properties represent relationships between classes or individuals while data properties link class elements with literal values or data types. Listed below as in Example 1 are some of the relationships between the classes and the data properties for the PSOnto.

Example 1: Sample ontology relationships among the classes and the object properties in PSOnto.

```
CellCategory SubClassOf Cell
HerlevCellType SubClassOf CellCategory
AbnormalCell SubClassOf CellCategory
PSO_Component hasObjective Ojective_Function
Particle optimizesFeature Feature
PSO_Component usesParticle Particle
```

In order to obtain ideal structures and patterns in the classification process, the hierarchy of cell types was also specified by defining the subclasses, their relations and restrictions. Precisely, axioms were implemented to enforce property constraints, by linking image data properties cyt and nuc features to specific cell types and ensuring the ontology remains logically consistent to support accurate automated classification and reasoning.

We also made use of the annotations within Protégé since they do not interfere with the reasoning engines. Annotations serve as the descriptive layer of the ontology with an aim to help with maintaining the ontology and making it more understandable and usable to other parties when the ontology evolves over time. The documentation process shall be ongoing as new changes and upgrades are made to the ontology.

3.5. Integration

Classes of cell images extracted from SipakMed and Herlev datasets are illustrated in Figures 2 and 3 respectively. Both datasets are publicly available and are primarily used in research for improving diagnostic accuracy in cervical cancer detection through the classification of normal and pathological cervical cells in Pap smear images.

SipakMed dataset includes about 4049 images distributed into five categories of cervical cell types, namely, superficial-intermediate (normal cells), Parabasal (potentially abnormal), Koilocytotic (indicative of HPV infection), Dyskeratotic (associated with dysplasia), and metaplastic (transitional changes in epithelial cells). The Herlev dataset has about 917 images in seven classes where each of these classes is either normal or abnormal. Normal cells category includes NormalIntermediate, NormalSuperficial, NormalColumnar while abnormal cells category includes CarcinomaInSitu, SevereDysplasia, ModerateDysplasia, and MildDysplasia. Unlike in SipakMed there are no benign cells in Herlev.

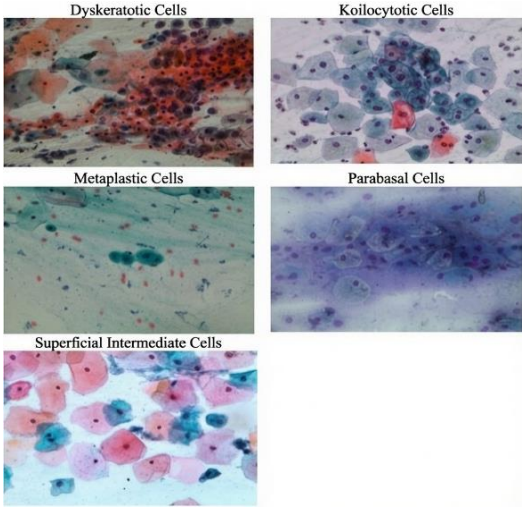

Figure 2. Sipakmed classes of cells.

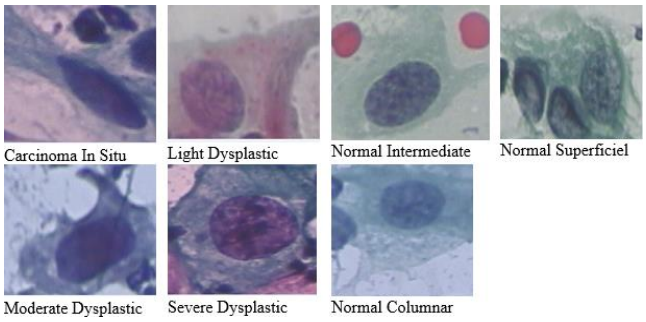

Figure 3. Herlev classes of cells.

These datasets support both traditional machine learning (such as SVM) and deep learning approaches, such as Convolutional Neural Networks (CNNs) [23]. Methods such as feature extraction, augmentation, and transfer learning are commonly applied to improve model performance. They have been instrumental in advancing automated diagnostics for cervical cancer screening. Because of the proximity of both datasets to our object classification problem, these datasets were adopted for testing the functionalities of our PSOnto. Patient information is excluded in the SipakMed dataset and that does not limit research endeavors aligned to the cell's classification problem. These two datasets were used together as a way of extending classification logic to handle images from multiple datasets with shared semantic categories.

3.6. Implementation

Table 1 shows the breakdown of the images and cells stored in the two datasets. Tabled classes represent different types of cells that are relevant for diagnosing cervical abnormalities. Each image focuses on either individual cells or small clusters. The images include clear manual delineation of regions of interest, such as the nucleus and cytoplasm, with associated feature data for these regions.

Table 1. SipakMed database.

Category	Classification	Dataset	Number of images
Superficial-intermediate	Normal	SipakMed	126
Parabasal	Benign	SipakMed	108
Koilocytotic	Abnormal	SipakMed	238
Dyskeratotic	Abnormal	SipakMed	271
Metaplastic	Abnormal	SipakMed	223
Normal intermediate	Normal	Herlev	74
Normal superficiel	Normal	Herlev	70
Normal columnar	Normal	Herlev	70
Light dysplastic	Abnormal	Herlev	78
Moderate dysplastic	Abnormal	Herlev	78
Severe dysplastic	Abnormal	Herlev	78
Carcinoma in situ	Abnormal	Herlev	80

The features of interest include the average intensity, texture, and shape. The features from the cells were extracted from hasNucleusCoordinates and hasCytoplasmCoordinates. All extracted features are stored in the ontology as data properties per individual as shown Figure 4 below.

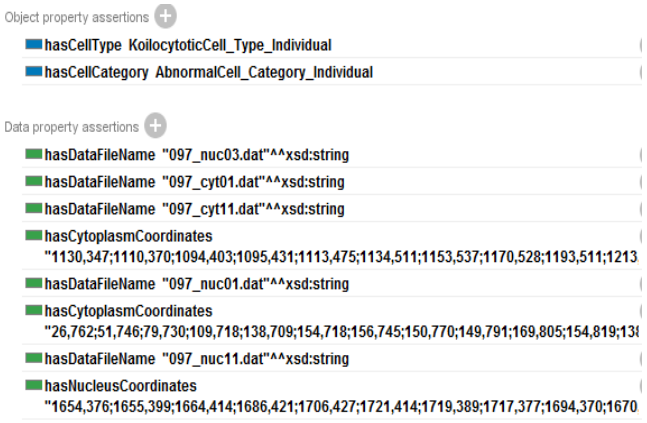

Figure 4. Extracted cell features from a cell.

Each cell image from the two datasets was added as an individual instance within the ontology, and corresponding features were linked using data properties. The cytoplasmic features and the nuclear features of each image are in the files with the .dat extension, where cyt and nuc indicate cytoplasmic and nuclear features respectively. Herlev dataset only has images without cytoplasm features so its features were extracted through hasActualClass and hasDataFileName. The baseline classification uses all valid individuals from the two datasets with the SipakMed as training and Herlev as test data.

LightGBM, a gradient boosting framework based on decision trees, was used to support classification within the ontology by learning from the feature data extracted from cervical cell images. After key features such as nucleus area, cytoplasm area, and the nucleus-to-cytoplasm ratio were extracted using Python scripts and stored as data properties within each Cell individual in the ontology, these features were exported into a structured dataset. LightGBM was then trained on this dataset, using the SipakMed labeled data as training input and Herlev as test data. The trained model learned to classify cells into NormalCell, BenignCell, or AbnormalCell based on the numeric patterns in their features. The predictions from the LightGBM model were then used to assign inferred classes like PSO_NormalCell, PSO_AbnormalCell to ontology individuals, enabling semantic reasoning and evaluation. This integration allowed the ontology to benefit from LightGBM's high accuracy and efficiency in handling large feature sets.

3.7. Evaluation

The experimental setup, outlined in Table 2, includes three categories namely the experiment phase, environment, and metrics evaluation. The experimental phase involves five steps to integrate extracted cell features from the labeled datasets into the ontology. The environment specifies software and hardware requirements. Finally, classification metrics such as precision, recall, F1-score, accuracy, completeness, consistency and usability evaluate the PSO-optimized ontology's effectiveness in classifying cervical cancer cells. The equations below show how these four aspects are calculated as follows:

Equation (1) calculates the *Accuracy* which is the sum of the True Positives (*TP*) and the True Negatives (*TN*) divided by the *Total Instances*.

$$Accuracy = \frac{TP + TN}{Total\ Instances} \quad (1)$$

Equation (2) calculates the precision by dividing the True Positives (TP) with the total of the *TP*s and the True Negatives (*TN*).

$$Precision = \frac{TP}{TP + FP} \quad (2)$$

Equation (3) computes the *Recall* metric which is the total of the relevant answers divided by the total of the relevant answers,

$$Recall = \frac{TP}{TP + FN} \quad (3)$$

Equation (4) calculates the *F1-score*, this calculation uses the *Recall* and *Precision*.

$$F1 - Score = \frac{2 * (Precision * Recall)}{Precision + Recall} \quad (4)$$

The ontology's reasoning capabilities were tested using SWRL rules to infer the cell type based on the optimized feature weights. The SWRL rules extend the automated reasoning capabilities of PSOnto. The SWRL rules

work in conjunction with the Pellet reasoner and the debugger. The reasoner was used to identify contradicting axioms and classes. The debugger indicated that PSOnto is coherent and consistent. Coherency denotes that class definitions are meaningful and usable for reasoning while consistency ensures the validity of data and results from reasoning. Both consistency and coherency would imply that PSOnto is logically sound and usable.

Table 2. Experimental setup.

Experiment Phases	
1. Ontology development	**Ontology tool:** Protégé 5.5. **Classes:** Define core classes such as Cell, CellType, CellFeature, PSO_Component, FeatureWeight, PSOClassification, ImageFeature, PSOParameters and PSO_Optimization. **Properties** • Object properties: Establish relationships. • Data properties: For numerical attributes like CytoplasmShapeWeight. **Axioms** • Specify equivalence, disjointness, and classification rules. • Define SWRL rules to aid in the classification process.
2. Dataset integration	**Dataset:** SipakMed and Herlev datasets. **Data Preprocessing** • Extract cytoplasmic and nuclear features like size, shape, and texture using python script. • Map feature values to corresponding ontology individuals. **Integration** • Import images as ontology individuals. • Assign features using data properties.
3. Feature Classification	**Automated reasoning**: Use SWRL rules to define classification logic.
4. PSO-inspired optimization	**Simulation** • Adjust feature weights iteratively using PSO logic. • Define particles representing candidate solutions (feature combinations) and evaluate using the classification rules of the ontology. **Outcome** • Update ontology with the best feature sets (GlobalBestFeatureSet).
5. Validation	**Tools**: Pellet Reasoner to validate consistency and infer classifications. **Testing** • Use cross-validation training the model with the SipakMed dataset and train with Herlev dataset. • Evaluate classification performance using precision, recall, F1-score, and accuracy.
Experiment Environment	
1. Hardware	• Processor: Intel i7 or equivalent. • RAM: 16 GB or more. • Storage: SSD with at least 500 GB for large datasets.
2. Software	• Protégé 5.5. (ontology editing). • Scikit-learn (classification). • Pyswarms (PSO). • Python 3.9/Spyder.
Metrics for Evaluation	
1. Classification performance	• Precision, Recall, F1-Score for cell categories. • Overall classification accuracy.
2. Ontology metrics	• Number of consistent inferences. • Ontology size (classes, properties, individuals).

3.8. Documentation

Documentation and clear visualizations to facilitate usability for non-technical users like medical professionals is availed. The ontology and its related programs were uploaded to a GitHub repository on the link: https://github.com/ntsedura/PSOnto with the intention of collaborating with other researchers for exploration and contribution towards improving the ontology.

4. Results and Discussions

A Python program was developed to evaluate the PSOnto's performance in four categories namely, cross-validation scores, accuracy, features, and classification. Cross-validation scores ranged from 0.713 to 0.929, indicating variability across folds due to data imbalances or noise. Accuracy, defined as the proportion of correctly classified instances, reached 87.11%. The scores also highlighted performance across cell types: abnormal, benign, and normal cells. Metrics such as precision, recall, F1-score, and accuracy collectively assessed the ontology's effectiveness.

Figure 5 illustrates the classification metrics indicating a strong overall performance, with an accuracy of 85% across the three classes. The abnormal class, which had the highest support (147 instances), achieved a high precision of 0.95 and a recall of 0.91, resulting in a strong F1-score of 0.91. PSOnto was effective in identifying abnormal cells correctly. Both precision and recall at were 0.96 for the normal class which reflects a balanced and an accurate classification. Contrary the benign class showed weaker performance, with a precision of 0.71 and a higher recall of 0.73, leading to an F1-score of 0.795.

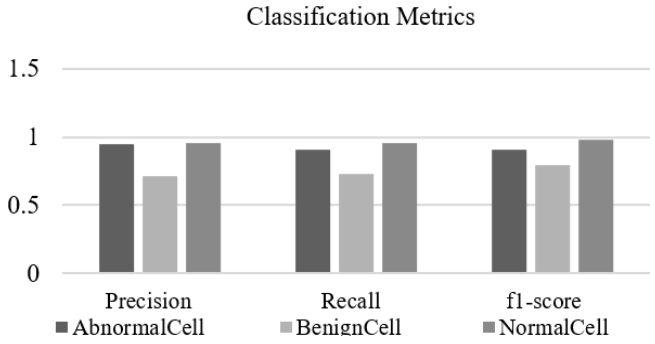

Figure 5. Classification metrics.

As illustrated in the confusion matrix see (Figure 6) the classifier demonstrated strong performance in distinguishing abnormal and normal cells, correctly identifying 134 out of 147 abnormal cases and 24 out of 25 normal cases. Although benign cells were correctly identified the model also mistakenly labeled non-benign cells as benign, indicating possible class overlap or feature insufficiency. Only 11 of the 22 benign instances were correctly classified, while the remaining 11 were misclassified as abnormal.

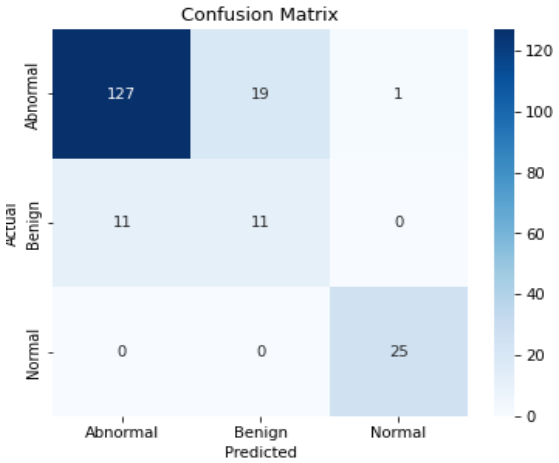

Figure 6. Confusion matrix.

The classification of cervical cancer cells relies on cytoplasmic and nuclear features, which differentiate cancerous from non-cancerous cells. Figure 7 highlights these five key features. The model heavily depends on cytoplasmic characteristics, with these features comprising over 50% of the total, emphasizing their importance in cell classification.

Other quality metrics that were also considered include completeness (class, property and instance coverage), consistency (incomplete classes and disjointness errors) and usability (annotation richness, avg. class depth, query success rate).

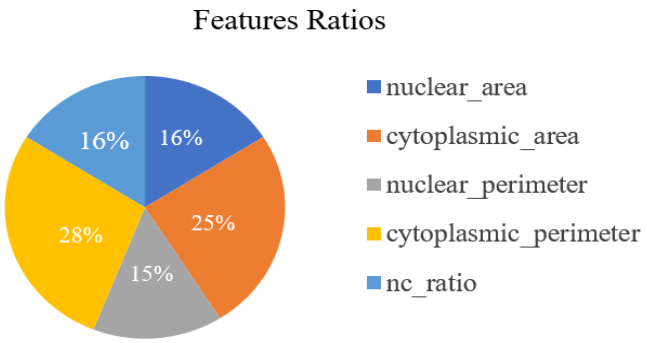

Figure 7. Features.

5. Conclusions and Future Work

This study reflects on its observations, gaps, contributions, and results. It successfully implemented PSOnto, a PSO-inspired ontology, to classify cervical cancer cells into three categories. This novel approach leverages ontology-driven frameworks for cancer cell classification, modeling key features like nuclear and cytoplasmic areas, perimeters, and nucleus-to-cytoplasm ratios for effective cell type differentiation.

By integrating the SipakMed and Herlev datasets and linking the image data to corresponding features, the ontology's application to real data was validated. The inclusion of cytoplasmic and nuclear coordinates, along with derived features, enabled accurate mapping to individual instances. Rule-based reasoning further facilitated classification into normal, benign, and abnormal cells.

Three main observations stand out from this study listed as follows:

1. Key components of a PSO system can be integrated with ontological reasoning in Protégé to enhance reasoning and decision-making for cervical cancer cell classification.
2. A PSO inspired ontology can be applied to classify cervical cancer cells.
3. Features of cervical cancer cells can be integrated in Protégé to automatically classify cervical cancer cells.

The visible contributions of this ontology are threefold:

1. A PSO inspired ontology structure for cervical cancer cells classification.
2. A semantic representation of the critical features of cervical cancer cells (cytoplasmic and nuclear)
3. A model that has a high accuracy score of cervical cancer cells classification.

Three apparent gaps can, consequently, be isolated from this study as follows:

1. The ability to link and integrate the PSO-inspired ontology with more than two biomedical datasets to yield a more diverse application in cervical cancer cells classification.
2. To produce an extensible and reusable ontology that can be shared for cervical cancer research and classification.
3. To diversify the ontology to accommodate other types of cancer and not just cervical cancer.

References

[1] Alduweib E., Alahmadi A., and Alromema W., "Enhancing Social Networks Services : An Ontology-based Approach," *The International Arab Journal of Information Technology*, vol. 23, no. 2, pp. 274-282, 2026. https://doi.org/10.34028/iajit/23/2/8

[2] Alfaifi Y., "Ontology Development Methodology: A Systematic Review and Case Study," *in Proceedings of the 2nd International Conference on Computing and Information Technology*, Tabuk, pp. 446-450, 2022. https://ieeexplore.ieee.org/document/9711664

[3] AlMohimeed A., Shehata M., El-Rashidy N., Mostafa S., and et al., "ViT-PSO-SVM: Cervical Cancer Predication Based on Integrating Vision Transformer with Particle Swarm Optimization and Support Vector Machine," *Bioengineering*, vol. 11, no. 7, pp. 1-21, 2024. https://doi.org/10.3390/bioengineering11070729

[4] Alqarqaz M., Younes M., and Qaddoura R., "An Object Classification Approach for Autonomous Vehicles Using Machine Learning Techniques," *World Electric Vehicle Journal*, vol. 14, no. 2, pp. 1-17, 2023. https://www.mdpi.com/2032-

6653/14/2/41

[5] Alrehaili N., Aslam M., Alharbi A., and Ashari R., "Find a Research Collaborator: An Ontology-based Solution to Find the Right Resources for Research Collaboration," *International Journal of Advanced Computer Science and Applications*, vol. 15, no. 5, pp. 38-48, 2024. http://dx.doi.org/10.14569/IJACSA.2024.0150505

[6] Anand S. and Kumar S., "Uncertainty Analysis in Ontology-based Knowledge Representation," *New Generation Computing*, vol. 40, pp. 339-376, 2022. https://doi.org/10.1007/s00354-022-00162-6

[7] Dar E. and Dorn J., "Ontology Based Classification System for Online Job Offers," *in Proceedings of the International Conference on Computing, Mathematics and Engineering Technologies*, Sukkur, pp. 1-8, 2018. https://ieeexplore.ieee.org/document/8346340

[8] Gokhale P., Deokattey S., and Bhanumurthy K., "Ontology Development Methods," *DESIDOC Journal of Library and Information Technology*, vol. 31, no. 2, pp. 77-83, 2011. https://doi.org/10.14429/djlit.31.2.860

[9] Haridy S., Ismail R., Badr N., and Hashem M., "An Ontology Development Methodology Based on Ontology-Driven Conceptual Modeling and Natural Language Processing: Tourism Case Study," *Big Data and Cognitive Computing*, vol. 7, pp. 1-23, 2023. https://doi.org/10.3390/bdcc7020101

[10] Horvat M., Krtalic A., Akagic A., and Mekterovic I., "Ontology-based Data Observatory for Formal Knowledge Representation of UXO Using Advanced Semantic," *Electronics*, vol. 13, no. 5, pp. 1-25, 2024. https://www.mdpi.com/2079-9292/13/5/814

[11] Hu J., Huang Z., Ge X., Shen Y., and et al., "Development and Application of Chinese Medical Ontology for Diabetes Mellitus," *BMC Medical Informatics and Decision Making*, vol. 24, pp. 1-14, 2024. DOI: 10.1186/s12911-023-02405-y

[12] Iglesias-Molina A., Cimmino A., Ruckhaus E., Chaves-Fraga D., and et al., "An Ontological Approach for Representing Declarative Mapping Languages," *Semantic Web*, vol. 15, pp. 191-221, 2024. DOI: 10.3233/SW-223224

[13] Li X., Martinez J., and Rubio G., "A New Fuzzy Ontology Development Methodology (FODM) Proposal," *IEEE Access*, vol. 4, pp. 7111-7124, 2016. DOI: 10.1109/ACCESS.2016.2621756

[14] Nayak J., Swapnarekha H., Naik B., Dhiman G., and Vimal S., "25 Years of Particle Swarm Optimization: Flourishing Voyage of Two Decades," *Archives of Computational Methods in Engineering*, vol. 30, no. 3, pp. 1663-1725, 2023. https://link.springer.com/article/10.1007/s11831-022-09849-x

[15] Niu S., Gao K., Ma P., Gao X., and et al., "Exploiting Sparse Self-Representation and Particle Swarm Optimization for CNN Compression," *IEEE Transactions on Neural Networks and Learning Systems*, vol. 34, no. 12, pp. 10266-10278, 2023. DOI: 10.1109/TNNLS.2022.3165530

[16] Rajeswari V. and Sakthi Priya K., "Ontological Modeling with Recursive Recurrent Neural Network and Crayfish Optimization for Reliable Breast Cancer Prediction," *Biomedical Signal Processing and Control*, vol. 99, pp. 106810, 2025. https://doi.org/10.1016/j.bspc.2024.106810

[17] Taye M. and Ghoul S., "An Approach Towards Goal-Oriented Requirements Ontology: Consistency and Completeness Based Requirements Analysis," *Journal of Software Engineering and Applications*, vol. 16, no. 2, pp. 31-49, 2023. DOI: 10.4236/jsea.2023.162003

[18] Tsedura N., Bhero E., and Chibaya C., "An Assessment of the Visibility of Particular Swarm Intelligence Technologies in the Resolution of the Object Classification Problem," *The Indonesian Journal of Computer Science*, vol. 13, no. 5, pp. 7145-7166, 2024. https://doi.org/10.33022/ijcs.v13i5.4275

[19] Tsedura N., Bhero E., and Chibaya C., "Towards the Design of a Particle Swarm Optimization Ontology for Object Classification," *Array*, vol. 27, pp. 1-12, 2025. https://doi.org/10.1016/j.array.2025.100449

[20] Tsedura N., Chibaya C., and Bhero E., "A Scoping Review of Literature on the Application of Swarm Intelligence in the Object Classification Domain," *International Journal of Research in Business and Social*, vol. 12, no. 5, pp. 463-473, 2023. https://doi.org/10.20525/ijrbs.v12i5.2586

[21] Wang L., "Mammography with Deep Learning for Breast Cancer Detection," *Frontiers in Oncology*, vol. 14, pp. 1-16, 2024. https://doi.org/10.3389/fonc.2024.1281922

[22] Wang Y., Yang J., and Yang G., "Ontology-based Decision-Making Support in Real-Time Strategy Game," *in Proceedings of the 4th International Conference on Consumer Electronics and Computer Engineering*, Guangzhou, pp. 255-259, 2024. https://ieeexplore.ieee.org/document/10504126

[23] Wubineh B., Rusiecki A., and Halawa K., "Classification of Cervical Cells from the Pap Smear Image Using the RES_DCGAN Data Augmentation and ResNet50V2 with Self-Attention Architecture," *Neural Computing and Applications*, vol. 36, no. 34, pp. 21801-21815, 2024. https://doi.org/10.1007/s00521-024-10404-x

[24] Yu C., Zong H., Chen Y., Zhou Y., and et al., "PCAO2: An Ontology for Integration of Prostate Cancer Associated Genotypic, Phenotypic and

Lifestyle Data," *Briefings in Bioinformatics*, vol. 25, no. 3, pp. 1-10, 2024. https://doi.org/10.1093/bib/bbae136

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