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A Novel Analytical Model of Brain Tumor Based on Swarm Robotics

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Abstract: A tumor is referred to as "intracranial hard neoplasm" if it grows near the brain or central spinal vessel (neoplasm). In certain cases, it is possible that the responsible cells are neurons situated deep inside the brain's structure. This article discusses a strategy for halting the progression of brain tumor. A precise and accurate analytical model of brain tumors is the foundation of this strategy. It is based on an algorithm known as kill chain interior point (KCIP), which is the result of a merger of kill chain and interior point algorithms, as well as a precise and accurate analytical model of brain tumors. The inability to obtain a clear picture of tumor cell activity is the biggest challenge in this endeavor. Based on the motion of swarm robots, which are considered a subset of artificial intelligence, this article proposes a new notion of this kind of behavior, which may be used in various situations. The KCIP algorithm that follows is used in the analytical model to limit the development of certain cell types. According to the findings, it seems that different KCIP speed ratios are beneficial in preventing the development of brain tumors. It is hoped that this study will help researchers better understand the behavior of brain tumors, so as to develop a new drug that is effective in eliminating the tumor cells.

Keywords: Swarm robots; Brain tumor; Analytical computation; Kill chain; Interior point algorithm

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1. Introduction

The neurological symptoms and indications of brain tumors have no clear connection with the type of tumor; instead, they are related to the tumor's location within the central nervous system (CNS). Compression or invasion by a tumor may damage or shift neural tissues, resulting in localized pain. Edema increases the mass effect, which further compresses the brain in the surrounding region [1]. Patients with brain tumors are unable to make use of brain segmentation software tools. Three-dimensional (3D) imagery and augmented reality are now being utilized in healthcare settings where augmented reality and virtual reality are present [2]. **Figure 1** shows how brain tumors compress and displace normal brain tissues.

Aberrant mechanical stresses in the brain must be considered due to the physical limitations of the skull. Intravital imaging studies in mice use conventional transparent cranial windows with an adjustable screw for controlled acute or chronic compression and decompression in the brain [3]. Magnetic resonance imaging (MRI) was used to gather textural characteristics from the brains of patients with tumors. Following that, the feature space was processed using the correlation-based feature selection (CFS) technique and the partial least squares regression (PLSR) method [4]. The convolutional neural network (CNN) is a machine-learning technique that has shown impressive results in image segmentation and classification. Three different types of brain tumors may be classified using the novel CNN architecture. As compared to current

pre-trained networks, the newly created network is simpler. It was evaluated using T1-weighted contrast-enhanced MRI images [5]. Since the system utilizes a cubic model to minimize vascular input error, it is superior to existing best practices when it comes to treating brain tumors [6]. Dynamic contrast-enhanced magnetic resonance imaging (DCE-MRI) for brain tumor analysis is now possible with a fully automated system that handles everything from beginning to end. Using five different selection methods and six different classification algorithms, thirty diagnostic models were created; several criteria, including sensitivity, specificity, accuracy, and area under the curve (AUC), were considered in determining which model was the most effective area under curve [7].

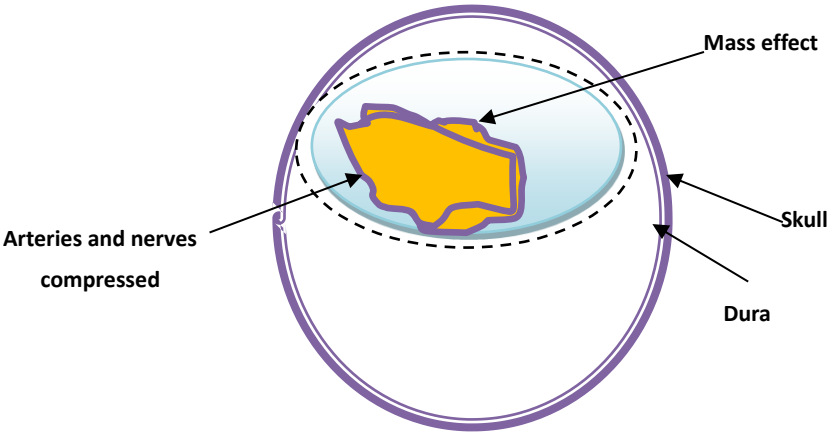

Figure 1. Compression and displacement of normal brain tissues by brain tumor

Preprocessing procedures, image segmentation, feature extraction, and image classification using neural network methods are all part of a computer-based approach for identifying tumors in the brain [8]. For medical image segmentation and classification, the fuzzy brain-storm optimization method combines fuzzy and brain-storm optimization techniques. The study's findings show that it outperforms its competition [9]. Radiologists use genetic algorithms because it is a simple idea and is well-understood by them. Omitted brain tumors can be displayed as segmented regions of interests (SROIs) using a content-based active contour (CBAC) model with content-based segmentation. Intensity and texture-based features for feature extraction genetic algorithms are used to reduce the number of available features [10]. Artificial intelligence has been used in attempt to gauge the severity of brain tumor malignancy. Fuzzy c-means clustering was used to isolate the brain areas suspected of having abnormal growths by radiologists. When it comes to precisely identifying the tumor's boundaries, Fourier descriptors come in handy. There are many Fourier descriptors that introduce a problem with overlearning and the possibility of misclassifications. The proposed diagnosis system efficiently searches for significant boundary features by genetic algorithm and feeds them to an adaptive neuro-fuzzy classifier that is built on these features [11]. An algorithm developed to automatically identify tumor segmentation and outline threshold was applied to MRI brain scans to segment tumor images in a study. MRI brain images and radiology records were used to create two databases for the experiment [12]. Healthcare practitioners may benefit from a MRI method that detects brain tumors shared via the internet. While other techniques sacrifice some visual information to take smaller images, this one does not. In another study, a modified K-means clustering method was utilized to identify the tumor's position before conducting the initial segmentation using mean shift segmentation. Following that, a threshold setting was used to transform the image to black and white, and an erode process was carried out to eliminate noise. The tumors in the images were then located using a watershed technique [13]. A patch-based technique and an inception module were used to extract two concentric patches of different sizes from the input images before training the deep network, which employed dropout regularization to

address the over-fitting problem caused by a lack of data [14]. The MR slices from three distinct axes of the brain include heterogeneous tumor kinds and tissue features that may be accurately segregated for improved visibility by oncologists [15]. Using another method, aberrant and normal brain tissues may be better detected with less gray-level intensity separation, and human brain malignancies may be detected much faster than with previous algorithms, in seconds as opposed to minutes [16].

The aim of this paper is to investigate the relationship between brain tumors and delimited cells to better understand the behaviors of these cells during the invasion process. This information is useful in early-stage cancers because it gives an idea of the degree of risk. The study of brain tumors was modeled in this paper using swarm robots. Following that, KCIP, an integrated version of the kill chain and interior point algorithm, was used to slow down tumor growth. Swarm robot behaviors are determined by probabilistic, automata, differential, and dynamical equations. In this model, a swarm of robots attempts to kill individual robots by injecting brain tumors into their bodies. The research on swarm robotics is concerned with the design of robots, their physical bodies, and their calculating behaviors. It is based on swarm intelligence but is not constrained by it. Individual rules that are simple and easy to follow can lead to a highly complex composite swarming behavior. The constant feedback generated by group communication is a critical component. Individuals changing with the group and group actions are described by swarm behaviors.

2. A proposed analytical model of brain tumor behavior

This section introduces an analytical methodology to simulate brain tumors using an equation set of swarm robots describing their behaviors. In addition, this section introduces an analytical model of a drug that can revive the damaged cells in the brain. Swarm robotics is an innovative approach to the harmonization of multi-robot systems, which consist of hefty numbers of regularly undemanding, substantial robots. It is theoretical that a preferred communal performance emerges from the relationship linking the robots and the relation between the robots and the environment. The equation set should contain the Langevin equation, transition rate, cohesive swarms, integro-differential, Fokker-Plank equation, dynamics of random walk, and Markov chain process.

In this proposed model, these equations are used to describe the behavior of these swarm robots during their spread as comparable to the spread of a brain tumor. **Figure 2** illustrates the general framework of the proposed analytical model using swarm robots. The swarm robots depend on the equation set in their spread to invade the victim cells. Brain tumors begin, as most cancers do, in some other place within the body and unfold to affect the mind. They form when most cancer cells travel through the bloodstream to the brain.

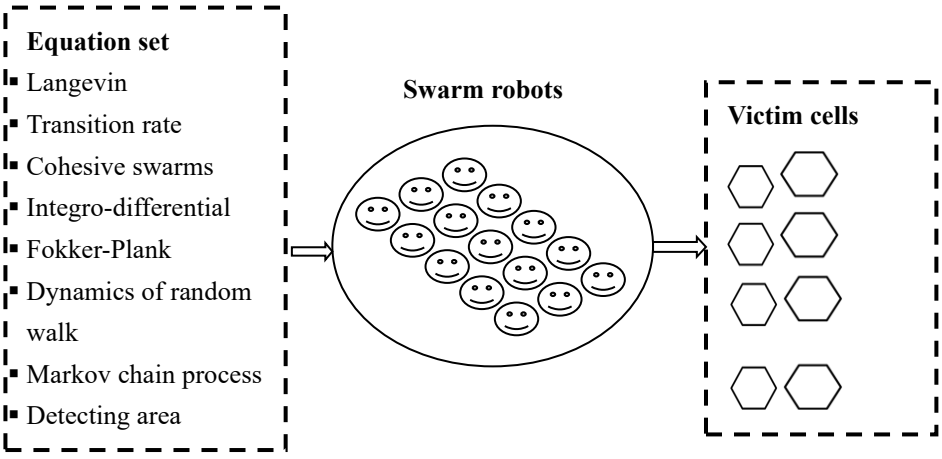

Figure 2. General framework of the planned analytical model using swarm robots

The most common not-unusual cancers that spread to the brain are lung and breast cancers. The brain is unable to make space for an upward accumulation. Some brain tumors may cause a blockage of cerebrospinal fluid, which flows around and through the organ. This blockage will cause an increase in intracranial pressure and enlarge the ventricles. Some brain tumors may also cause edema. A variety of symptoms may occur due to the mass effect produced by pressure, swelling, and even the size of the tumor itself. The following equations describe the glioma type, its conversion, cell migratory response, diffraction, and a model of glioma vessels. Glioma is one of the most prevalent brain tumors that originates from the support cells of the brain, called glial cells. Glial cells are the majority of the brain's universal cellular constituents. There are five to 10 times more glial cells than neurons. Glioma cells migrate more efficiently in the white matter than in the grey matter.

3. Kill chain interior point (KCIP) algorithm for overcoming brain tumor

In order to overcome brain tumors, a proposed algorithm is introduced. It is an integrated version of the kill chain and interior point algorithm. It measures the gap between two superellipsoids. The term kill chain was used as an armed idea linked to the construction of an assault, consisting of target detection, the delivery to the target, the result and arrangement to assault the target, and lastly, the damage to the target. The methodology of this paper depends on measuring the minimum gap between two swarm robots using the interior point algorithm, and then applying the kill chain algorithm to overcome the growth of brain tumor, depending on the analytical analysis of its growth. The proposed methodology assumes that the kill chain algorithm adversaries are familiar with the capabilities and structure of the target system. It employs different methods to deliver loads to their destination. A malware is installed, and the adversaries establish a hidden control channel with compromised entities. Within the victim system, the attack campaign and adversaries now perform actions on their own objectives. The proposed KCIP begins by recognizing an entity of probable concern, while precisely and continuously finding targets, and then compares a call of concern with the preferred entity. The minimum distance between the two swarm robots is calculated.

Suppose r is the first vertex, n-1 paths have to leave r. For any other vertex, the number of paths entering the vertex must be exactly one larger than the number of paths leaving the vertex.

The primary problem with using Newton's technique is making sure s zero, which might cause very small step lengths that result in convergence issues. Interior point techniques, in essence, approximately solve a sequence of structures of nonlinear equations.

The center of the concerned objects is the instantaneous preference for the initial bet. The outer loop determines the range of instances μ has to be up to date, that is the number of times needed to be approximately solved for the collection of μ values. At the same time, the inner loop is a version of Newton's method used for approximately solving a set price of μ. Instead of selecting the next node with the lowest price, the selection is based on the cost of the initial node plus an estimate of the immediacy of the destination. The proposed approach would remedy the hassle of finding the most desirable path. Within this context, the cost of node V might be calculated as follows:

f(V) = distance from S to V + estimate of the distance to D
f(V) = d(V) + h(V,D), $f(v) = d(V) + \sqrt{(x(V) - x(D))^2 + (y(V) - y(D))^2}$;

where x(V), y(D) and x(V), y(D) are the coordinates for node V and destination node D. Affirmation employs an extremely complicated broadcasting network. Advanced ability presumably provides support immediately and mechanically; nonetheless, this is a simple estimate of certainty. Stages that were previously sociable perceive the objective, classify it as the preferred objective, and obtain approval to free a bat. A stage may then initiate its sky-to-land arms. It is called the "start" stage. In the "manage" stage,

after a stage starts a bat, the bat may need extra in-journey objective data revision. A few bats do not need maintenance. The management stage ends with bat impact. To conclude the achievement of an assault, responsive stages must execute a fight-harm evaluation. This is known as the "assess" stage. This occasion's conclusion brings the kill chain for this target to a close. The KCIP algorithm is indicated in algorithm (A), as shown below [14].

ALGORITHM (A): KILL CHAIN INTERIOR POINT (KCIP)

```
Start
for each step sp do
for each objective O, compute space(p,t)
calculate speedRatio(p,t)
for each objective O do
task(t,0)=ON , task(t,8)=OFF, completion(t,0)=ON, existinginstance, time_stepCounter=0
total_specified, total_finished=OFF
do while total_finished=OFF
partially_specified=OFF
for each objective O and function f do
if existing_instance=completionTime(t, f) and, existing_instance<>0    then p=laststep(t,f)
if f<>launch then increment step function
for each step p do
calculate closest_objective(p); nearby_specified_objective(p)
if f<=assess then find a nearby
    strictly feasible x0, i
    barrier parameter μ0,
    Output: Closest points solution
        Solve system of linear equations for Newton direction
        Determine step length αk by line search
        xk + 1 ← xk + αk Δxk, sk + 1 ← sk + αk Δsk, λk + 1 ← λk + αk Δλk
        k ← k + 1
if nearby>0 then
     set current task possessions
     add current task to gantt (nearby)
     partially_specified=ON
if nearby=0 then nearby_specified_objective(closest step)=t
       for each objective O and function f, determine total_specified, total_finished
            if total_specified=OFF and total_finished=OFF then
            if partially_specified=ON then nextTime = the earliest completion time of
            the tasks assigned on this iteration
            if secondobjective>1 then nextTime=existing_instance+1
            if partially_specified=OFF then nextTime=existing_instance+0.1
            if total_specified=ON and total_finished=OFF then
            nextTime=the earliest completion time of the tasks that are
            if total_finished=ON then
                for each step p and objective O do
                compute space from last position; time_step=secondobjective
if time_step>0 then for each step do update step position
for every objective O do
compute space(p, t), calculate speedRatio(p, t); time_stepCounter=time_stepCounter+1
if time_stepCounter>500 then state is infeasible; exit sub
End
```

4. Discussion and results

A network with a limited number of nodes is assumed in the proposed method, which is a reasonable assumption. There are degrees assigned to each of the network's nodes, with the lowest being level 1 and the highest being stage okay. m represents the number of nodes in level 1 of the warned graph, and it represents the number of nodes in level 2 of the cautious graph. As indicated by the symbol n, the entire range of nodes in all degrees of the counseled graph, from the smallest to the biggest, are represented. The number of nodes between stage 1 and level k is equal to the number of stages (n-m). It is possible to use the heuristic method with many nodes that have less than (n-m). The suggested approach is based on the idea of initiating a seek operation from the start node to find the nodes that are closest to the start node and are in stage 1 of the search process. In this phase, any further search operations should begin from each node in order to discover the quickest route to the destination using a brand-new heuristic approach, which is implemented in a brand-new heuristic method, starting from each node in the previous step. Using a mathematical formula, the distance between each node in stage 1 and the target node in the second stage is calculated. While these calculations are taking place, the hints are keeping track of which nodes are on which routes. The shortest distance between two points is calculated, as is the position of the pointer. In this case, the shortest path to the destination node is the one that has the least distance; thus, the route with the shortest distance is chosen. The new heuristic technique is implemented as part of a suggested set of recommendations, which includes other heuristic methods.

The accessibility of glioma cells to their surrounding environment is shown in **Figure 3**. According to the diagram, tumor cells are progressively penetrated until they reach a level of vulnerability, which is apparent from the convergence of points A, B, C, and D. Once they reach this state of vulnerability, the tumor cells are destroyed. In **Figure 4**, the development of neomusculature can be appreciated with the use of swarm robots. The convergence of points A, C, and D shows that evolution is only moving in one direction and accelerating at a specific area inside these cells. A swarm of robots perform the bifurcation process as shown in **Figure 5**. The diagram shows that this process is both, resilient and effective in the case of tumor cell development, as shown by the close convergence of points A, C, and D.

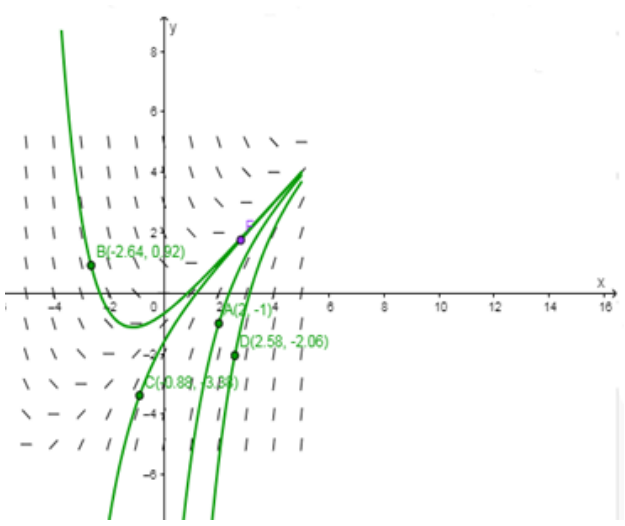

Figure 3. Accessibility of the dissemination of glioma cells

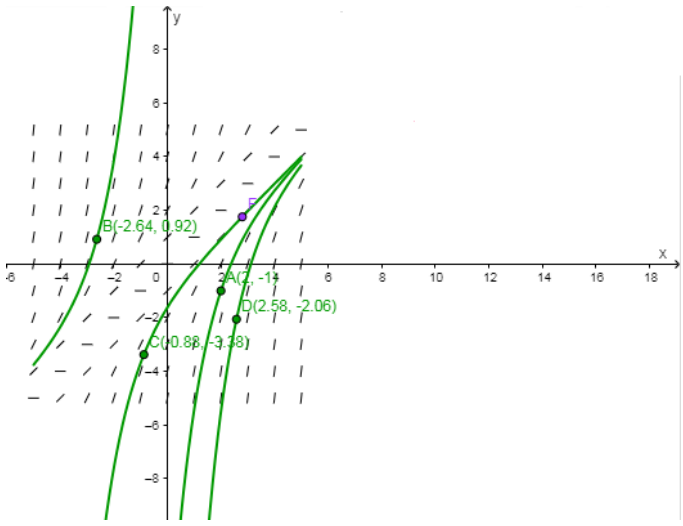

Figure 4. Evolving neomusculature using swarm robots

As demonstrated in **Figure 6**, the rate of cell development is increasing. Based on the diagram, tumor cell proliferation is progressing, but not in a random way; it may be described as a regular growth, as shown by the consistent distances between points A, C, and D. In conducting an examination of the proposed

method, superellipsoids are utilized in this research. This is accomplished by measuring the distance between two superellipsoids in a variety of unique cases.

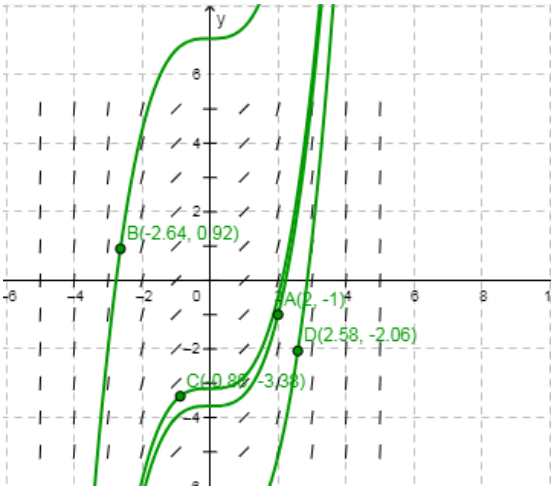

Figure 5. Bifurcation equation using swarm robots

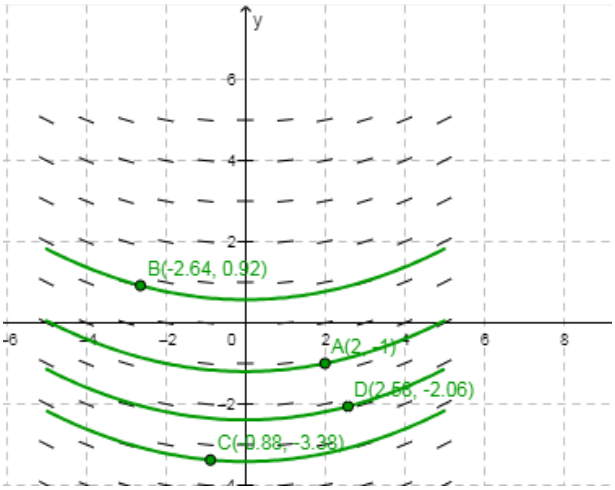

Figure 6. Growth rate of cells

This section includes several case studies, which are denoted by the Roman numerals I to VIII. Taking Case Study I as a reference point, the shortest distance between the two sites is 0.128959 nm, as shown in **Figure 7**. **Figure 8** is an illustration of Case Study II, in which there is a minimum distance of 6.338194 meters between the two sites. **Figure 9** is an illustration of Case Study III with a minimum distance of 3.169937 nm between the two sites. **Figure 10** depicts Case Study IV, which has a minimum distance of 2.490361 nm between the two points in the center of the two-point line.

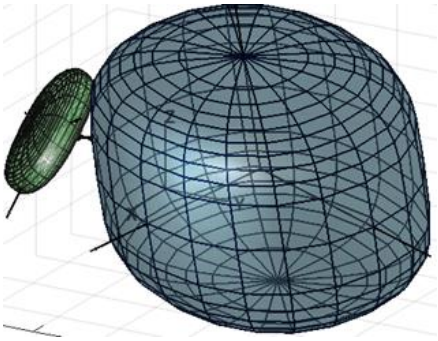

Figure 7. Case Study I (minimum distance 0.128959 nm)

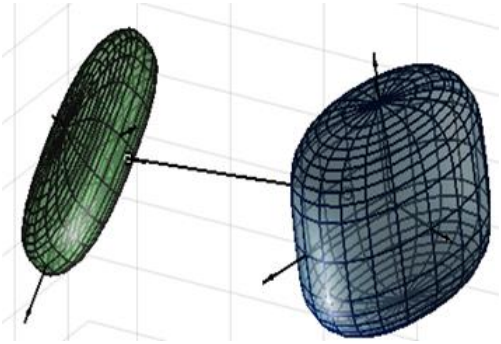

Figure 8. Case Study II (minimum distance 6.338194 nm)

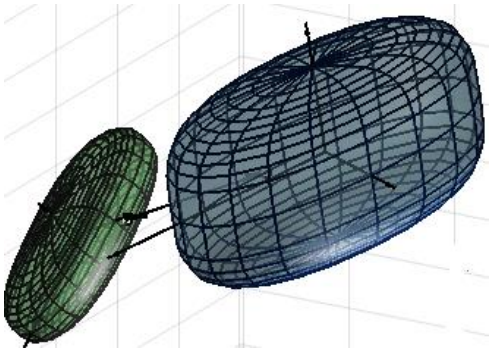

Figure 9. Case Study III (minimum distance 3.169937 nm)

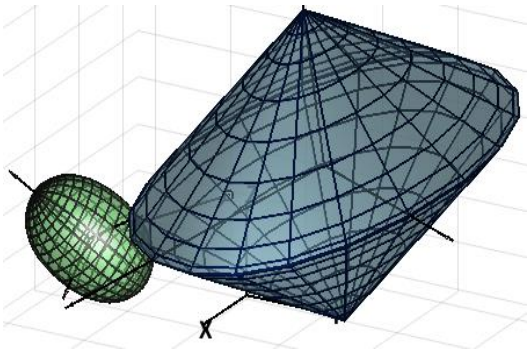

Figure 10. Case Study IV (minimum distance 2.490361 nm)

Figure 11 is an illustration of Case Study V, which has a minimum distance of 1.704994 nm between the two sites. The findings of Case Study VI, which was carried out at a minimum distance of 7.932791 nm and yielded the following results, are shown in **Figure 12**. Case study VII is shown in **Figure 13** with a minimum distance of 1.193461 nm between the two sites, which is the shortest distance feasible. **Figure 14** depicts Case Study VIII, with a minimum distance of 1.464478 nm between the two points. Taking all case studies into consideration, the shortest distance between various characteristic distributions can be estimated based on their shifting locations using the suggested approach.

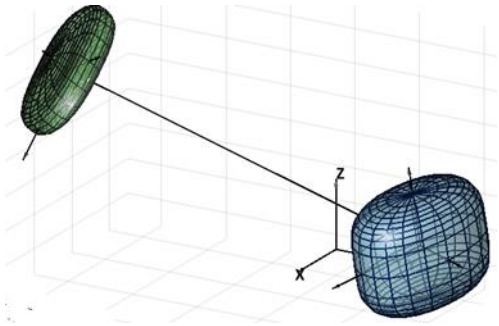

Figure 11. Case study V (minimum distance 1.704994 nm)

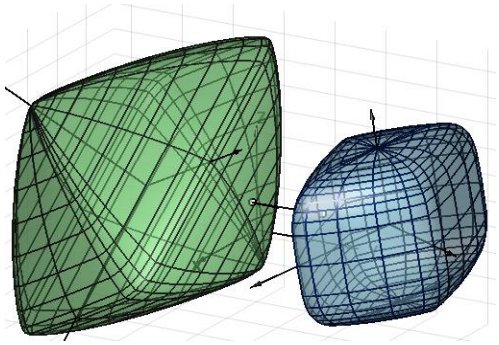

Figure 12. Case study VI (minimum distance 7.932791 nm)

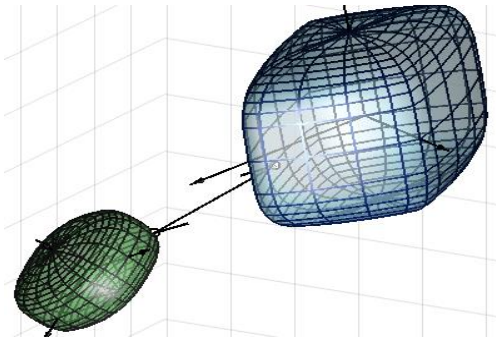

Figure 13. Case Study VII (minimum distance 1.193461 nm)

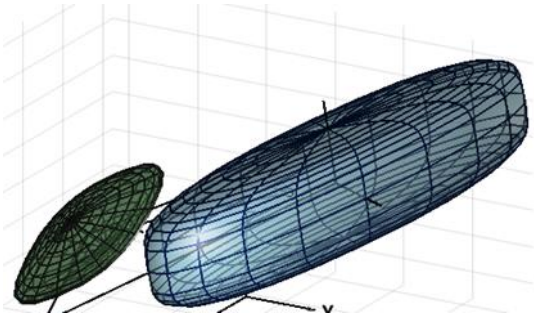

Figure 14. Case Study VIII (minimum distance 1.464478 nm)

5. Conclusion

A brain tumor is a collection, or mass, of abnormal cells in the brain. The skull, which encloses the brain, is very rigid. Any growth inside such a confined space can cause a problem. Brain tumors may be cancerous or non-cancerous. The purpose of this research is to analyze the performance of brain tumors by simulating tumor performance through the motion of swarm robots. The KCIP algorithm, a new logarithm, is proposed by combining the properties of both, the kill chain and the interior point algorithm. This algorithm measures the shortest distance between two robots and then destroys the cancer cells, which are represented by one of these robots. The results have shown how the tumor enters these cells, showing that it does so gradually until the cells reach a stage where they are vulnerable to invasion. The evolving process accelerates at a specific part of these cells, and evolution continues in one direction only. Swarm robots are used in the bifurcation process. In the case of tumor cell proliferation, this process is effective and robust. The tumor cell proliferation process gradually increases but not in a random manner; it may be described as a consistent increase, which is evident from the regular distances.

Disclosure statement

The authors declare no conflict of interest.

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