A PARALLEL COMPUTING TEST BED FOR PERFORMING AN UNSUPERVISED FLUOROSCOPIC ANALYSIS OF KNEE JOINT KINEMATICS

by

Renu Ramanatha

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Renu Ramanatha

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The following individuals read and discussed the thesis submitted by student Renu Ramanatha, and they evaluated her presentation and response to questions during the final oral examination. They found that the student passed the final oral examination.

Amit Jain, Ph.D.	Chair, Supervisory Committee
Elisa H. Barney Smith, Ph.D.	Co-Chair, Supervisory Committee
Timothy Andersen, Ph.D.	Member, Supervisory Committee

The final reading approval of the thesis was granted by Amit Jain, Ph.D., Chair of the Supervisory Committee and Elisa H. Barney Smith, Ph.D., Co-Chair of the Supervisory Committee. The thesis was approved for the Graduate College by John R. Pelton, Ph.D., Dean of the Graduate College.

dedicated to my husband, Prashant and my parents, Geetha and Ramanatha

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ABSTRACT

Fluoroscopic analysis of knee joint kinematics involves accurately determining the position and orientation of bones in the knee joint. This data can be derived using the static 3-D CT scan images and 2-D video fluoroscopy images together. This involves generating hypothetical digitally reconstructed radiographs (DRR) from the CT scan image with known position and orientation and comparing them to the original fluoroscopic frame. This represents a search problem in which, among all the DRRs possible from a CT image, the image that most closely matches the target fluoroscopy frame of the knee joint has to be found.

Each image in the search space differs from another by the set of position and orientation values. Position is defined by the x, y and z co-ordinates in the Cartesian coordinate system. Orientation is defined by the values of *azimuth*, *elevation* and *rotation*. Therefore, this constitutes a six dimensional search problem, and using a brute force method to search for the target image can take a tremendous amount of time. The fact that it is difficult to order or categorize the set of six values adds the complexity of the search. Further, previous research conducted by Scott et al. [1] suggests that even good sequential search algorithms such as the sequential Monte Carlo method can be very time-consuming. Therefore, a better search solution suitable for this kind of 6-D search that provides a significant speedup has to be found. This thesis explores using Swarm Intelligence (SI) techniques in a parallel computing environment to create a test bed for fluoroscopic analysis and increase the speed of the process. Parallel programs are developed using two SI techniques: Bees Algorithm and Particle Swarm Optimization technique.

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LIST OF ABBREVIATIONS

CT – Computer Tomography

DRR – Digital Reconstructed Radiograph

SI – Swarm Intelligence

PSO – Particle Swarm Optimization

ACO – Ant Colony Optimization

SDS – Stochastic Diffusion Search

CHAPTER 1

INTRODUCTION

1.1 Fluoroscopic Analysis

A good understanding of knee joint kinematics is essential for evaluating and researching the problems associated with the joint. To understand knee joint kinematics, determination of the position of the bones in the joint during motion in three dimensions is required. Fluoroscopy is a medical imaging technique that produces real-time, two dimensional images of an object, whereas, computer tomography (CT) is an imaging technique that produces static three dimensional image of the scanned object. The two dimensional fluoroscopy frames and the three dimensional CT scan images are not individually sufficient to provide complete information about the position of the bones in the joint in motion as a function of time. However, three dimensional position data over time can be derived using the static CT scan images and real-time information from video fluoroscopy images together.

A digitally reconstructed radiograph (DRR) is a simulation of a conventional 2-D X-ray image or a fluoroscopy frame created from CT data. Once the CT scan and a fluoroscopic video of the joint are generated, a DRR image can be generated using the CT scan image. This requires a simulation of the fluoroscope with the X-ray source or camera and the X-ray film or screen placed at equal radial distances on opposite sides of the origin. The CT cube is placed at the origin in between the X-ray source and the film. The distance between the X-ray source and the film is fixed and known. The cube in the center can translate in three dimensions: *x*, *y*, and *z*. The film can rotate while the X-ray source can move in azimuth and elevation dimensions. This simulation is illustrated in Figure 1.1. The projection of the X-rays from the simulated source onto the film through the CT cube produces a DRR image. Different values of the X-ray source's *azimuth* and *elevation*, the film's *rotation* and the cube's *x*, *y*, and *z* co-ordinates generate different DRR images. If a generated DRR image matches the fluoroscopy frame, the position of the cube, and the orientation of the X-ray source and the film are known. Using this information, a three dimensional rendering of the joint in motion can be constructed.

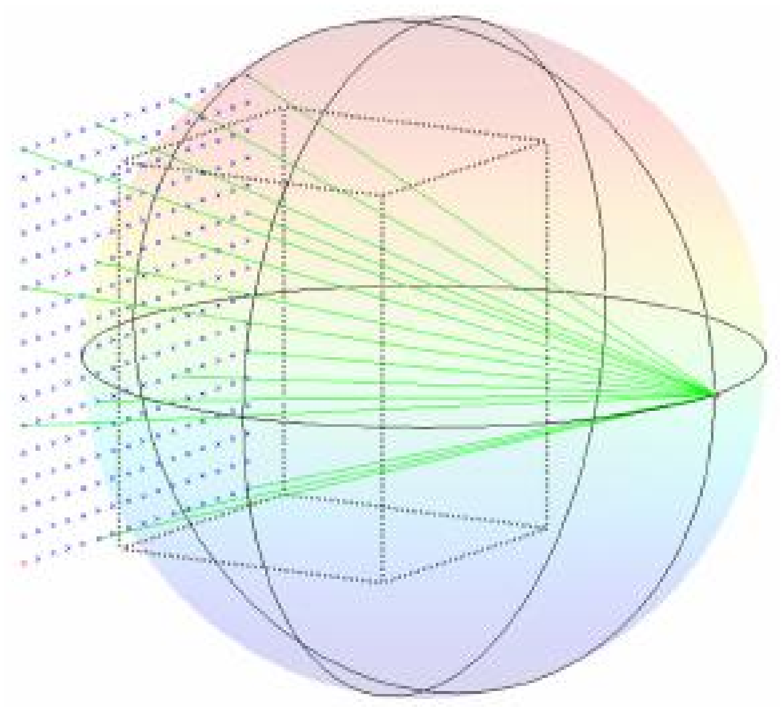


Figure 1.1: Geometric configuration of the simulated fluoroscope [1]

In order to accomplish this, several algorithms are used for different operations including generating DRR images, extracting the edges of DRR images, and comparing the edge images. These algorithms are based on the work of several researchers [2, 3]. Previous experiments used a Monte Carlo search technique to search for the matching DRR image, given an X-ray fluoroscopy image [1]. These experiments were conducted to search for azimuth and elevation of the camera and the rotation of the film. They have demonstrated that this can be achieved to an accuracy of 0.5 degree *rotation*, *azimuth* and *elevation*. The process, however, is very time consuming and calls for advanced search algorithms to reduce the time taken for finding the orientation of the X-ray source, the X-ray film and the position of the bones. This thesis uses swarm intelligence techniques in a parallel computing environment to achieve faster results.

1.2 Swarm Intelligence in a Parallel Computing Environment

Swarm intelligence is a branch of artificial intelligence based on the behavior of a group of entities working together to solve a common problem. "It is based on the collective behavior of decentralized, self-organized systems" [15, 26]." Swarms move through the search space and their collective intelligence leads the to the solution. Ant colony optimization (ACO), bees algorithm, particle swarm optimization (PSO), and stochastic diffusion search (SDS) are some of the techniques that exhibit swarm intelligence [5, 9, 11, 13]. These techniques have been used in many optimization problems like the traveling salesman problem, telecommunications routing, factory scheduling, etc. Swarm intelligence techniques are known to be robust and easy to implement.

Based on a review of some of the swarm intelligence techniques, bees algorithm and particle swarm optimization have been chosen to solve the search problem in fluoroscopic analysis of knee joint kinematics [5, 9]. The bees algorithm is a "biologically inspired" technique based on the food foraging behavior of a swarm of honey bees [29, 30]. The bees in the group are divided into scout bees and worker bees. Scout bees go on a random search for flower patches and come back to the bee hive to report their findings. The quality and distance of each of the flower patches found is evaluated. Finally, the best ones are chosen and worker bees are sent to them to collect nectar. The second algorithm used in this thesis, the particle swarm optimization technique, is influenced by the flocking behavior in birds [33]. It consists of several particles organized into close knit groups or neighborhoods. The particles move in the search space searching for the destination by interacting with one another and they collectively arrive at the destination. It is based on the communication and interaction among particles which re-calculate their position and velocity values accordingly and move through the search space to find the solution [32].

Bees algorithm and particle swarm optimization are suitable methods to solve the six dimensional search problem because the entities in the system can begin the search independently and with periodic communication, they can guide each other to go in the right direction toward the destination. They can be easily mapped to the search problem discussed in Section 1.1. It is also easy to implement them in parallel. Each entity, a bee or a particle, can map to a process in the parallel computing system. Both these methods depend on random number generators just like the Monte Carlo method. But they are more easily parallelizable than the Monte Carlo method which assumes a very sequential approach. This thesis entails implementing the solution using both these techniques in a parallel computing environment.

1.3 Prior Research

This thesis is an extension to the research done by Scott et al. [1]. The goal of the research conducted by Scott et al. was to develop a method for collecting accurate, real time three dimensional kinematic data of bones and joints using two dimensional X-ray images resulting from a video fluoroscopy technique combined with the static three dimensional Computer Tomography data [1]. The process used in their research involved creating virtual X-rays from the CT image through the digitally reconstructed radiograph projections. Traditional methods used to achieve kinematic data of the joints require human intervention to initialize the starting position. The method they proposed was minimally invasive and used a Monte Carlo search technique with a variable search range. The search range decreased as matching between the target image and the image created with known position values improved. This was an optimization search. This is a very efficient method for small ranges of postion values.

Considering the extent of the allowed movement of the knee joint within the fluoroscope and the allowed width of the angular movements of the X-ray source and the X-ray film, the potential range of the position values is enormous. Therefore, this calls for an efficient search algorithm that is very fast in finding the values required. The purpose of the research in this undertaking is to find suitable parallelized search mechanisms to speed up the process of determining the three dimensional position data of the bones and joints using the same image processing techniques that were used by Scott et al.

1.4 Thesis Statement

The objective of this thesis is to create a test bed or a framework for fluoroscopic analysis process. The framework will include implementation for all the components of the fluoroscopic analysis in a parallel computing environment. This implementation is aimed at increasing the speed of the search process involved in fluoroscopic analysis. Swarm intelligence algorithms, namely, the bees algorithm and the particle swarm optimization are used for implementing the search component. The test bed is implemented in such a way that it is easy to use alternative algorithms for each component and also to test the framework with different input images.

CHAPTER 2

ALGORITHMS USED FOR FLUOROSCOPIC ANALYSIS

In this chapter, the meaning of fluoroscopic analysis and the algorithms used in the analysis are discussed.

2.1 Fluoroscopy

Fluoroscopy is an imaging technique that uses a fluoroscope to obtain real-time X-ray images of a moving body part such as bones, muscles, and organs such as the heart. “A fluoroscope consists of an X-ray source and a fluorescent screen between which a patient is placed” [21]. Figure 2.1 shows a modern day fluoroscope. “Modern fluoroscopes couple the screen to an x-ray image intensifier and video camera allowing the images to be recorded and played on a monitor” [21]. Thus it is possible to view an X-ray movie of the body part being analyzed. The X-ray video is displayed using a continuous series of images produced in quick succession, similar to a television video transmission. The fluoroscopic technique has been used in several medical procedures such as diagnosing problems in the organs in the human body, analyzing functioning of the heart and other moving organs and guiding several kinds of surgeries, procedures and placements of artificial implants.

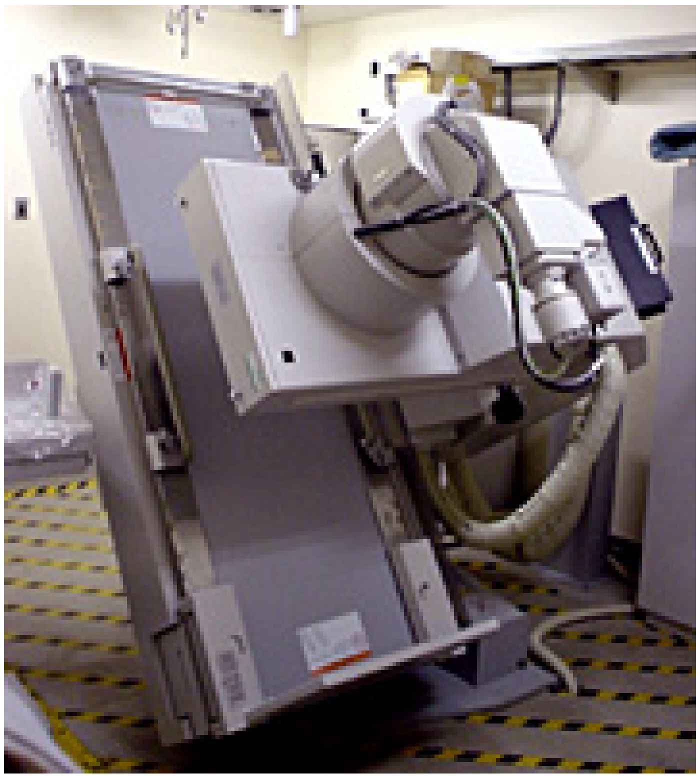


Figure 2.1: Fluoroscope [16]

2.2 Computer Tomography

Computer Tomography (CT) is a medical imaging technique that uses X-rays. It is based on the concept of tomography. “The word ’tomography’ is derived from the Greek tomos (slice) and graphein (to write)” [22]. This means a series of slices or cross sectional images are stacked together to construct a three dimensional model of the object being scanned. These images are processed using a computer and several individual images for each slice are created. After completing all the required processing of these images, a detailed three dimensional picture of the internal structure of the body part that was scanned can be obtained. Figure 2.2 shows a modern CT scanning equipment. The patient is placed on the horizontal surface and the scanner takes cross sectional images and computes a CT scan image of the required body part [17].

A CT scan can be used to study many organs and parts of the human body [18]. A CT scan image of knee joint can be helpful in diagnosing the problems in the kinematics of the knee joint and can be useful in the placement of an artificial implant. An example of a CT scan is shown in Figure 2.3, which is a CT scan image of a knee joint.

2.3 Knee Joint Kinematics

A knee joint connects the thigh with the leg. It joins the two bones: *femur*, the thigh bone, and *tibia*, the leg bone. Figure 2.4 shows the anatomy of a knee [19]. A knee joint is one of the largest and most complicated joint in the human body. The knee joint allows different kinds of movements between the bones. The types of movements that are possible with the knee are flexion, extension, medial and lateral rotation. The knee joint is the key to the movement of human beings from one place to another.

Figure 2.2: CT Scanner [17]

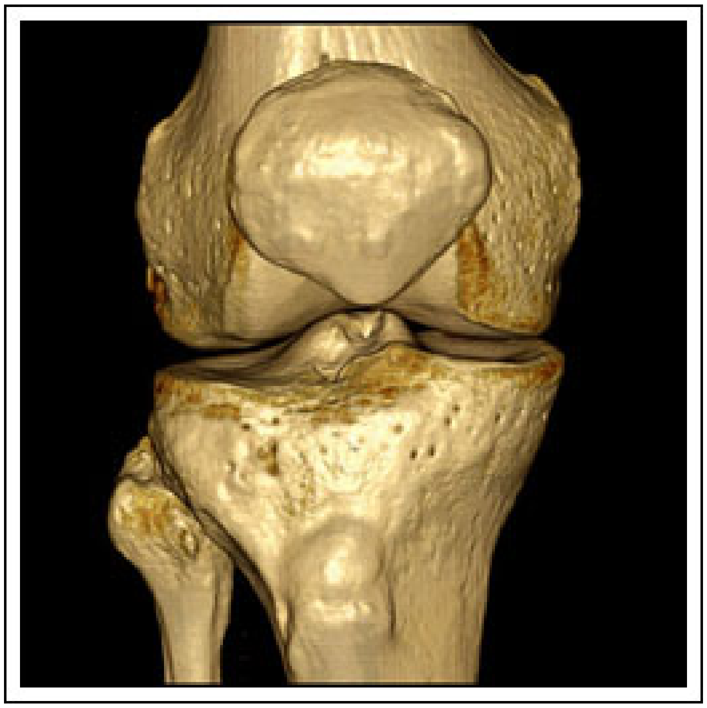


Figure 2.3: CT scan of a knee joint [20]

Knee disorders or injuries can make the movement of the knee very difficult and painful. Surgery or any kind of knee treatments require accurate diagnosis and measurements. X-rays and CT scans are used to study the structure of the knee and take appropriate measurements. However, sometimes, diagnosis requires more than just static images and measurement of the joint structure. The different kinds of movements possible with the knee joint, the friction between bones connected during motion, the impact of the surrounding ligaments and the knee cap and other biological factors increases the complexity of diagnosis. Therefore, the structure of the knee joint has to be studied in vivo. Study of the knee joint kinematics is crucial to diagnosing knee problems. The positions of the bones and the joint in motion have to be determined. In addition, to diagnosing knee joint conditions, this kind of information can assist in the diagnosis of other joint problems.

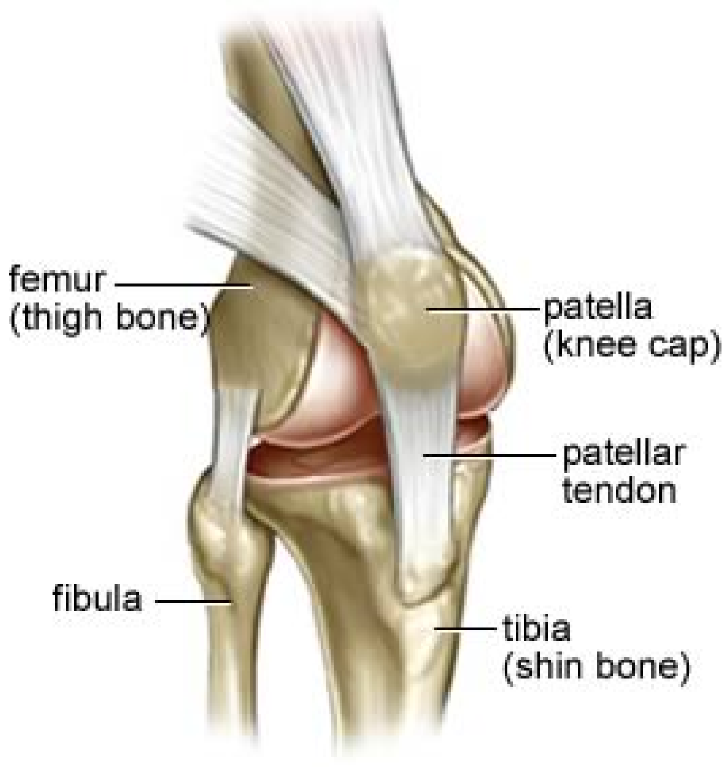


Figure 2.4: Anatomy of a knee [19]

A CT scan and an X-ray are sufficient to determine the position of the bones in a stationary postion. However, doing the same while the joint is in motion is a very difficult task. In the past, invasive position capture techniques were used. Research conducted by Scott et al. developed a method to determine three dimensional real-time kinematic data of the knee joint without using invasive methods [1]. The subsequent sections in this chapter will describe how this was achieved. The focus of the research involved in this thesis is to decrease the time taken to conduct this operation.

2.4 Fluoroscopic Analysis

The process of determining three dimensional position data over time can be achieved using 3-D CT data and 2-D fluoroscopy images. This process is called fluoroscopic analysis. There are several steps required in this process. Figure 2.5 provides a block diagram of the major steps involved.

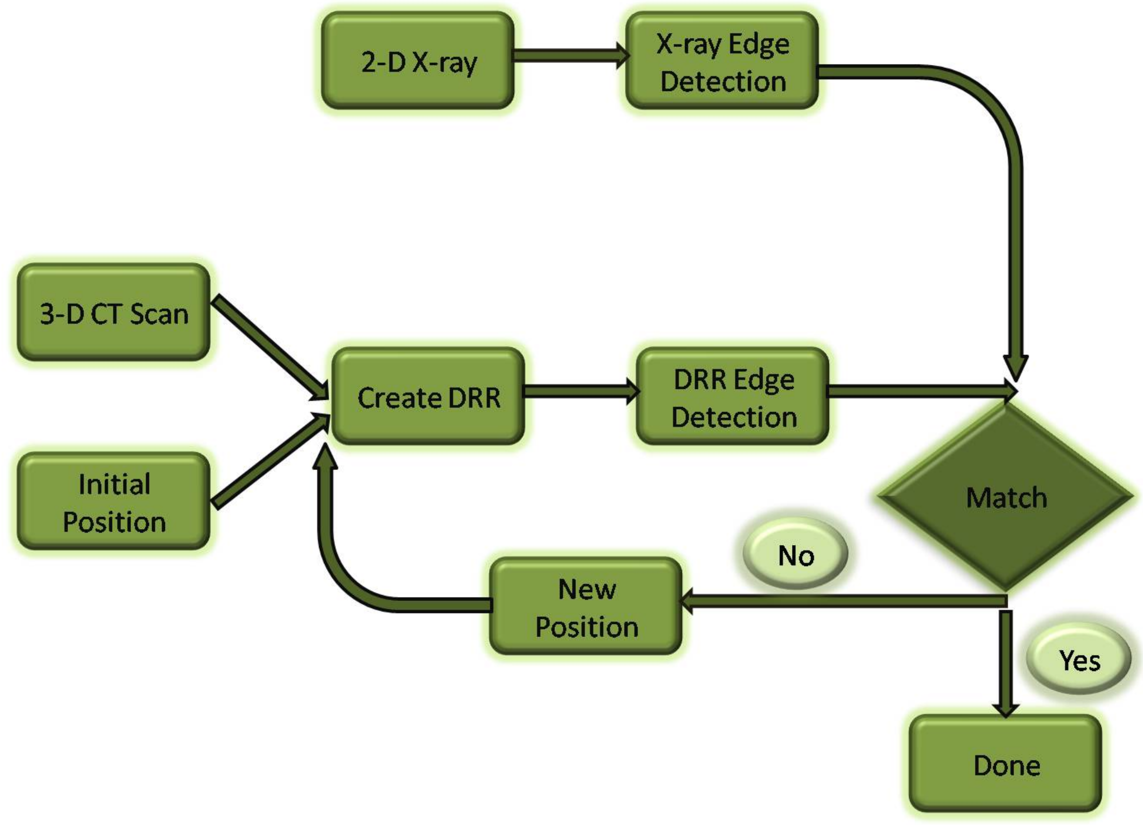


Figure 2.5: Procedure for fluoroscopic analysis

Consider a fluoroscopy environment in which the knee joint is placed. Refer to Figure 1.1 in Chapter 1. The knee joint is placed in between the X-ray source and the X-ray film. The position of the knee joint is affected by the lateral movements of the joint in any of the three directions (x, y, and z) about the origin. Secondly, the position is influenced by the *azimuth* and *elevation* of the X-ray source and thirdly, by the *rotation* of the X-ray film about a central axis. The knee joint can also change its azimuth, elevation and rotation values, but in this experiment, those values for the joint are kept constant, while the film and the X-ray source are rotated instead. Thus, values of the six dimensions have to be measured over time in order to obtain the real-time positional information of the knee joint.

Using the static CT scan image as input, the 3-D real time position data of the knee joint is constructed. In the first step, virtual X-ray images of the joint at different positions are created using the CT data. Then, the essential features of the image which are useful to determine the position are extracted. The essential features of the target X-ray frame from the fluoroscopy video images are also extracted. In the next step, the virtual image is compared with the target image. This process continues until there is a match. A match indicates the position of the joint for the first target fluoroscopy image. The whole process must be repeated for each fluoroscopy image in the video.

This process provides a rendering of the 3-D positional data over time. Sections 2.4.1 to 2.4.4 provided details for each of the above steps.

2.4.1 DRR Image Creation

A Digitally Reconstructed Radiograph (DRR) is a simulation of a 2D X-ray image, created from CT data. Ray tracing involves constructing a DRR from a CT image by calculating the radiological path through a three-dimensional CT array. Siddon's algorithm [2] is used for this purpose. This method considers the CT data as consisting of the intersection volumes of three orthogonal sets of equally spaced, parallel planes. The intersection of the ray with the volume elements (voxels) are obtained as a subset of the intersections of the ray with the planes. For each voxel intersection length, the corresponding voxel indices are obtained and the products of the intersected length and voxel density summed over all the intersections yields the radiological path and attenuation. The ray tracing mechanism employed here is similar to the ray tracing used in computer graphics to generate 3-D images. But in computer graphics, the reflection or the path of the light rays off the pixels is used to generate the image, whereas, in fluoroscopic analysis, the transmittance of the X-rays to the film is used to generate the DRR image.

2.4.2 Edge Detection

Edge detection of an image is used to "identify points in the image at which the image brightness changes sharply or more formally has discontinuities" [23]. By applying an edge detector to an image, the amount of information contained in the image can be significantly reduced by filtering out the less relevant information and retaining only the structural properties of the object in the image. Using edges for comparison increases the probability of finding a match between a DRR image and a fluoroscopy image, as opposed to the comparison of the images themselves whose X-ray intensities may not match. This also decreases the amount of data to be processed and thus significantly simplifies the computations that involve interpreting the information contained in the image. In our implementation, Sobel's edge detection method is used [4, 24]. This method finds the edges in an image using the gradient filter method.

In Sobel's edge detection method, a pixel location is declared an edge location if the value of the gradient exceeds some threshold. Edges will have a higher intensity gradient than uniform regions. Whenever the gradient value exceeds the threshold value, an edge is detected. Sobel's edge detector uses two 3x3 convolution masks. The two masks are applied to each pixel, one with a horizontal trend and one with a vertical trend. The convolution mask, which is much smaller than the actual image, is slid over the image, manipulating a square of pixels at a time. The Sobel masks *Gx* and *Gy* for the two gradients

-1	0	+1
-2	0	+2
-1	0	+1

+1	+2	+1
0	0	0
-1	-2	-1

Figure 2.6: Sobel Gx and Gy masks

are shown in Figure 2.6. The *Gx* mask highlights the edges in the horizontal direction and the *Gy* mask in the vertical direction. After taking the magnitude of both, the resulting output detects the edges in both directions.

The magnitude of the gradient is calculated using

$$|G| = \sqrt{Gx^2 + Gy^2}. \tag{2.1}$$

An approximate magnitude can be calculated using

$$|G| = |Gx| + |Gy|. \tag{2.2}$$

2.4.3 Image Matching

The target X-ray fluoroscopic frame has to be compared with a DRR image generated using arbitrary camera and film orientation, and cube displacement values. Both the images are converted to edge images using the Sobel filter and then compared. Our implementations involve several such comparisons with images generated using different camera and film orientation and cube displacement values. A contour matching algorithm is used to evaluate the overlap of two edge images [3]. The matching score resulting from a comparison is a value between 0 and 1. A value of 1 indicates a perfect match. The matching score is obtained by multiplying the two images together pixel by pixel and summing the result and then normalizing by the sum of the predicted image. If *J(x,y)* is the input contour image and *K(x,y)* is the predicted contour image, then contour match score (*CMS*) is calculated using

$$CMS = \frac{\Sigma_{(x,y)} J(x,y) K(x,y)}{\Sigma_{(x,y)} K(x,y)}. \tag{2.3}$$

2.4.4 Searching

The position of the knee joint is defined by six values, viz., the x, y, and z co-ordinate values and the *azimuth*, *elevation* and *rotation* values. Since each of these values has a large range, a simple brute force method of searching is highly inefficient. Each iteration of the search is a time-consuming process, because it involves creating a virtual image with known position values using ray tracing, extracting the edges and comparing it to the target image. Therefore, the goal should be to reduce the number of iterations of the search as well as the range of search with each iteration.

The measurement of the actual fluoroscope gives the range of values possible for each of the six positional parameters. The azimuth values of the X-ray source can range from -180 to +180 degrees and the elevation can be anywhere between -90 to +90 degrees. The film can rotate from -90 to +90 degrees. The knee joint or the hypothetical CT cube that is used in our experiments has a wide range of translation possible. Typically the object being scanned is placed close to the center and hence, for the tests conducted in this project, -5cm to +5cm translations from the center, on each axis, are considered.

Efficient search algorithms, like binary search, cannot be effectively applied to a six dimensional problem of this proportion. With a binary search algorithm, we can only divide the values for one of the six dimensions into half. Even though this can potentially cut down the number of permutations of the six values to half of them, the number of remaining permutations is still dramatically large. And moreover, there is simply no way to sort the values for any of the six parameters due to the nature of the comparisons performed in the search. All search algorithms involve comparisons of the elements being searched for in one way or another. In this case, we compare two images and the matching algorithm used for this comparison produces a match score between 0 and 1 for each comparison. The values of the six positional parameters are known when the score is 1. The images are being compared and not the six values. There is no easy way to sort the images in any manner. Thus, this indicates that the usage of any search algorithm that depends on sorted elements is ruled out.

Some search algorithms that use hashing methods require that the elements are organizable into some form of groups. The search problem presented in this project does not fit well into this category either. Monte Carlo search methods that depend on random sampling and a few swarm intelligence algorithms are useful for this kind of search problems. The details for the Monte Carlo and the swarm intelligence algorithms are presented in Chapter 3.

CHAPTER 3

SEARCH ALGORITHMS

In Chapter 2, the necessity of an efficient search algorithm in fluoroscopic analysis was explained. This chapter provides details of the algorithms adopted in this thesis. In addition to the Monte Carlo method that was used in prior research, the two SI techniques used in this thesis, the bees algorithm and particle swarm optimization, are presented here.

3.1 Monte Carlo Search Technique

The Monte Carlo search method is a non-deterministic method that depends on random sampling. The Monte Carlo method is generally used to solve problems that are difficult to solve using deterministic methods [14, 25]. This method solves problems by generating random numbers in each try. After evaluating each of these trials, it can be predicted if the solution has been reached or not, or if the system is getting closer to the solution. Monte Carlo methods have been heavily used in a wide variety of fields ranging from economics to nuclear physics.

In the research conducted by Scott et al., the Monte Carlo method is used to search for the DRR image that matches the target image [1]. In order to search, a DRR image must be created with different values of camera's azimuth and elevation, and the film's rotation angles in each iteration. The DRR image thus created is compared to the target frame to find a match. Initially, the camera azimuth, elevation, and film rotation angles are set to

```
1. Initialize the current parameter value to zero.
   // This current value is evaluated based on the expected
   // target value in each iteration.
2. While (stopping criterion not met)
3.   Generate random values and add it to the initial value.
4.   Evaluate the fitness of the value obtained in step 3.
5.   Negate the random values and add it to the current value.
6.   Evaluate the fitness of the value obtained in step 5.
7.   Select the better of the two values.
     (This becomes the current value)
8. End While.
```

Figure 3.1: The pseudocode for the Monte Carlo search algorithm

arbitrary values generated using a random number generator. Random step values with a range of 0 to 10^o are generated for each iteration of the search. Two sets of orientation values are obtained by adding and subtracting the step values to the initial values. DRR images are then generated using both these sets. A contour match score is calculated for the comparison of each of these images with the edge image of the target fluoroscopy frame. The parameter values that produce a better score is retained and the path that is more promising is chosen. Figure 3.1 gives the pseudocode for the Monte Carlo search algorithm.

The search continues by producing two new sets of random steps, which are added and subtracted to the current values obtained from the previous iteration. This cycle is repeated until a match is found and the score of the match is greater than 0.8. Thus, in each iteration of the search, the search space decreases and the search gets closer to the solution. This results in values that are approximately equal to the desired values.

Once the preliminary search is completed, a fine search is performed with smaller step values. The fine search is used to search closer to the parameter values obtained from the previous round of search. It is assumed that the first stage of the search results in a value that is close to the solution and hence the next stage of the search is expected to obtain a more accurate solution by searching in smaller steps. After both the stages are completed, the resulting parameter values should be fairly accurate. The sequential implementation of this method has been able to generate values within 0.5^o of the desired parameter values.

3.2 Swarm Intelligence

The word *Swarm* means a group of insects that are close to one another and engaged in a common activity. In general, *swarm* is a term used to describe the behavior of a group of animals that are similar to one another. Swarming behavior can be observed in many animals such as bees, ants, other insects, fish, bacteria and even people. This phenomenon can be called by different names such as flocking in birds, schooling in fishes, societal behavior in human beings and growth of colonies in bacteria.

Swarm intelligence is a phenomenon, based on self-organization, in which the group of insects or other beings solve complex problems together. The swarm arrives at the solution collectively. Constant and consistent communication and feedback among the group, and adherence to common rules are essential to the success of the swarm. Errors and randomness are the pillars of this system. Even if a few individuals fail to achieve their objective, the group as a whole can succeed. Examples of this behavior can be observed in the food foraging behavior in ants and bees, and migration in birds and fishes. Chances of foraging food, finding mates, avoiding predators, overcoming obstacles, migrating to a better place are made faster and easier by swarm intelligence. Swarm intelligence has a strongly noticeable benefit for all the members of the swarm.

The swarm intelligence concept, when applied to computing, can help solve many computing problems. This is a branch of artificial intelligence in which interaction and co-operation among entities in a system is the key to solving a problem. The expression *Swarm intelligence (SI)* was introduced by Gerardo Beni and Jing Wang in 1989 in the context of cellular robotic systems [15]. There are several SI techniques such as the ant optimization algorithm, bees algorithm, particle swarm optimization, and stochastic diffusion search. SI techniques can be applied in problems involving finding the shortest path, swarm-based data analysis, robotics, financial forecasting, search, network management, Internet server optimization, etc. SI methods generally have simple rules and are easy to implement.

Though the Monte Carlo method is suited for the search problem in fluoroscopic analysis, it is very sequential in nature. It is difficult to implement it in parallel and hence not chosen for implementation in this thesis. SI techniques were explored and it was found that some of them are either not easy to map to the search problem in the fluoroscopic analysis process or to implement in a parallel computing environment. Ant colony optimization algorithm [27], which is very useful in the shortest path problems, is based on the concept of leaving behind clues in the path and the strength of the clue determines whether the path is desirable or not. Ants leave behind a substance called 'pheromone' on the paths they travel, both on the way to the destination and back. If the path is long, the pheromone evaporates and its strength reduces. If the path is short, the ant reinforces the pheromone by depositing on the same spot again on its way back, without too much of a time-gap and thus strengthens it in the process. When other ants visit the same path, if the strength of the pheromone is high then they are encouraged to take that path. If it is weak, the path is abandoned. This is not as easy to map to the search problem in fluoroscopic analysis as some other SI algorithms. Stochastic diffusion search [28] is another SI algorithms that is used to solve search and optimization problems. They expect that the objective function can be broken down into independent components that can be worked on by individual entities in the population. An entity is expected to communicate with every other entity in the system. This leads to significant communication overhead and is therefore not very suitable for parallel implementation.

The two SI techniques chosen to solve the search problem in fluoroscopic analysis are bees algorithm and particle swarm optimization. The group of entities in both methods can be easily mapped to processes in a parallel computing system. In addition to being easily parallelizable, they are also easy to implement. Sections 3.2.1 and 3.2.2 describe these two methods in depth.

3.2.1 Bees Algorithm

The bees algorithm [5, 29] is inspired by the behavior of a honey bees working together to find the sources of nectar, collecting it and storing it back in their hives. It is a population-based search algorithm [5]. This approach has been used to solve many optimization problems.

A honey bee colony has many worker bees with specific roles. The main functions of the colony are to identify food sources and collect and store nectar in the bee hives. Scout bees are given the task of finding nectar sources. The scout bees begin searching in random directions. When they come back to the hive, they communicate about their findings to all other bees by performing a dance known as the *Waggle Dance*. *Waggle Dance* [7, 31] is the "figure-eight dance" performed by the scout bees to share the information about the distance, direction and quality of the flower patch. While dancing the bees move in the form of a figure-eight. If a line passing through the sun and the designated dance area is considered as a reference line, the angle between that line and the direction of the waggle dance indicates the direction of the food source. It could be in the direction of the sun, to the right or left of the sun. The duration of the waggle dance indicates the distance of the flower patch. Figure 3.2 depicts the bee waggle dance. All the scout bees perform the waggle dance after returning from the flower patches. After learning about the distance and quality of all the flower patches through the waggle dances, the flower patches are evaluated based on some criteria. A few best sites are chosen from these if their fitness value is above a certain threshold. A large number of worker bees are recruited to collect nectar from the most promising sites and the remaining worker bees are sent to the other flower patches. Sites that are very far and those that have very few flowers with nectar and pollen are discarded. The scout bees are sent again in search of new flower patches for the next round.

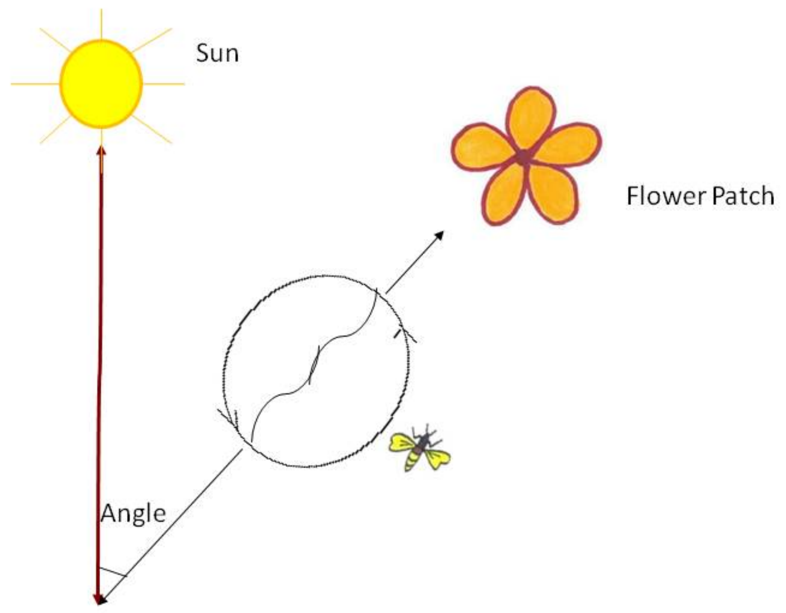


Figure 3.2: Waggle Dance [31]

```
1. Initialize the population with random solutions.
2. Evaluate fitness of the population.
3. While (stopping criterion not met)
   //Forming new population.
4.    Select sites for neighborhoods search.
5.    Recruit bees for selected sites
      (more bees for best e sites)
      and evaluate fitnesses.
6.    Select the fittest bee from each patch.
7.    Assign remaining bees to search randomly
      and evaluate their fitnesses.
8. End While.
```

Figure 3.3: The pseudocode for the bees algorithm in its simplest form [6]

The bees algorithm in its simplest form requires a number of parameters [6], namely:

1. number of scout bees (*n*)
2. number of sites selected out of *n* visited sites (*m*)
3. number of best sites out of *m* selected sites (*e*)
4. number of bees recruited for best *e* sites (*nep*)
5. number of bees recruited for the other (*m-e*) selected sites (*nsp*)
6. initial size of the patches (*ngh*)
7. stopping criterion

The pseudocode is presented in Figure 3.3.

The bees algorithm is illustrated using Figures 3.4 and 3.5. In Figure 3.4, the scout bees set out in random directions away from the main bee hive. Some flower patches are big while some are small. Some are very far from the hive while some are very close. There can also be more than one way to reach a flower patch. In Figure 3.5, the returning scout bees perform the waggle dance in the bee hive and as a result of this the majority of the worker bees fly to the larger and closer sites via the shortest route. Scout bees go in search of new sites.

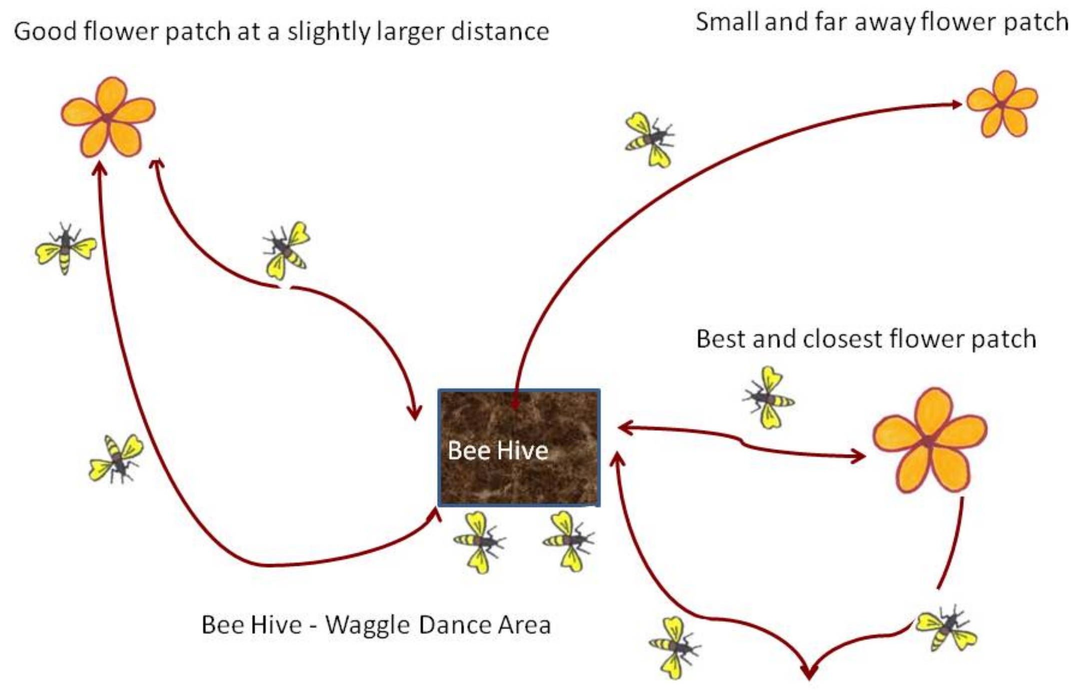

Good flower patch at a slightly larger distance
Small and far away flower patch
Best and closest flower patch
Bee Hive
Bee Hive - Waggle Dance Area

Figure 3.4: Food foraging in bees - scout bees are going in search of flower patches

3.2.2 Particle Swarm Optimization

“Particle swarm optimization (PSO) is a population based stochastic optimization technique developed by Dr. Eberhart and Dr. Kennedy in 1995, inspired by social behavior of bird flocking or fish schooling” [8–10, 33]. A particle swarm system is similar to a social

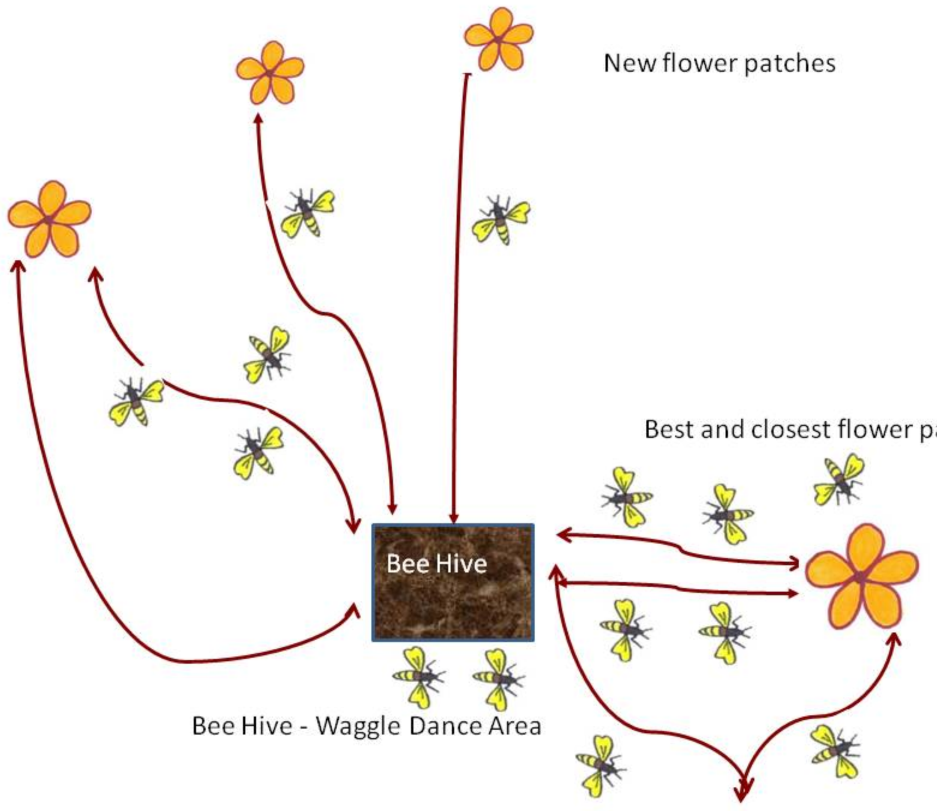


Figure 3.5: Food foraging in bees - worker bees are going to the best flower patches

network and depends on a communication structure in the network. Just as a person benefits from his interaction with society, a particle in the swarm enhances its position in the system due to its interaction with other particles. People in a society talk to other people to find out their experiences, and try to solve their problems using the inputs given by others. Other people's views and attitudes might affect an individual's own opinions and future decisions. Some people are more influential than the others. There are various factors that can affect the social dynamics such as who the neighbors are, how they influence the direction an individual takes in his journey to a destination and his own progress at any moment.

Particle swarms are used to simulate social networks as well as several engineering applications. Particle swarm optimization techniques can be used in search problems, where the particles in the swarm communicate with one another and reach the solution faster than they would have if they were on their own. This technique has also been used to address other complex optimization problems, pattern recognition, data mining and image processing.

The particle swarm can be modeled as a population of particles in a multi-dimensional space [32]. Each particle has a position and a velocity with which it moves. All particles have a starting point and they move randomly in the search space. As the particles move from one position to another, they have to evaluate the fitness of that postion based on some criteria, which determines how close they are to the solution. Navigation of the particles in the correct direction depends significantly on the accuracy of the fitness evaluation function. Periodically, a particle finds the best position it has held among the previous set of positions. It resets its position to the best position and continues the search. Each particle has a set of designated neighbors with which it should interact at regular intervals. The particles should not only keep track of the local best value, but also find out the best value in the neighborhood by communicating with other particles in the neighborhood. There is

```
1. Initialize the particle positions and velocities.
2. While (global best value does not match solution)
3.    Move particle to a random position from the current
      position within a certain threshold from the
      current position.
4.    Store the local best value.
5.    Talk to neighbors and exchange neighborhood
      search information.
6.    Store neighborhood best value.
7.    Store global best value.
8.    Update position and velocity to the neighborhood best.
9. End While.
```

Figure 3.6: The pseudocode for the general PSO [32]

a particle designated in every neighborhood to keep track of the best global value. The particles adjust their postions at regular intervals based on the best local, neighborhood and global values. Thus they move towards those particles in their neighborhood, that have the best fitness values. Over time they converge toward good positions and move about in the search space in close proximity to the best global value and stop exploring the rest of search space. The rest of the search space, which has a very low likelihood of containing the solution, is discarded. The pseuodocode that explains this technique is given in Figure 3.6.

Figures 3.7, 3.8 and 3.9 illustrate this concept. Figure 3.7 shows a swarm of fifteen particles organized into three groups of five particles. The particles in the three groups are denoted by circles, squares and triangles, respectively. In this figure, all the particles are initialized to some random values. In Figure 3.8, after fitness evaluation is conducted by all the particles, they are communicated to all particles in the neighborhood. These values help the particles to decide if they can continue from their current position or if they should follow a neighbor. This communication results in the movement of the particles toward the neighbor with the best fitness value. In ideal cases, after several iterations of this exercise, the particles converge toward the best global fitness value and thus converge to the solution. This stage looks similar to what is shown in Figure 3.9. All the particles then begin to search intensively around the best value until they find the solution.

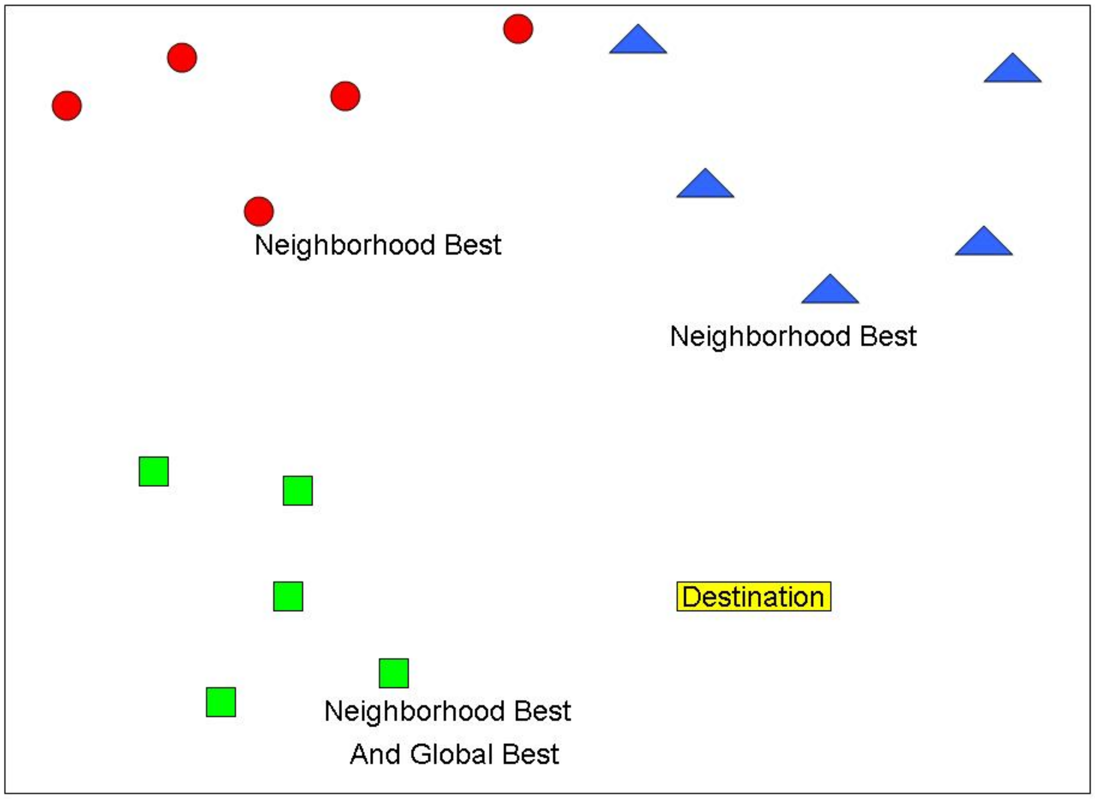


Figure 3.7: Particles in the swarm are moving randomly toward their destination

The application of the bees algorithm and the particle swarm optimization to the image search part of fluoroscopic analysis is described in detail in Chapter 4.

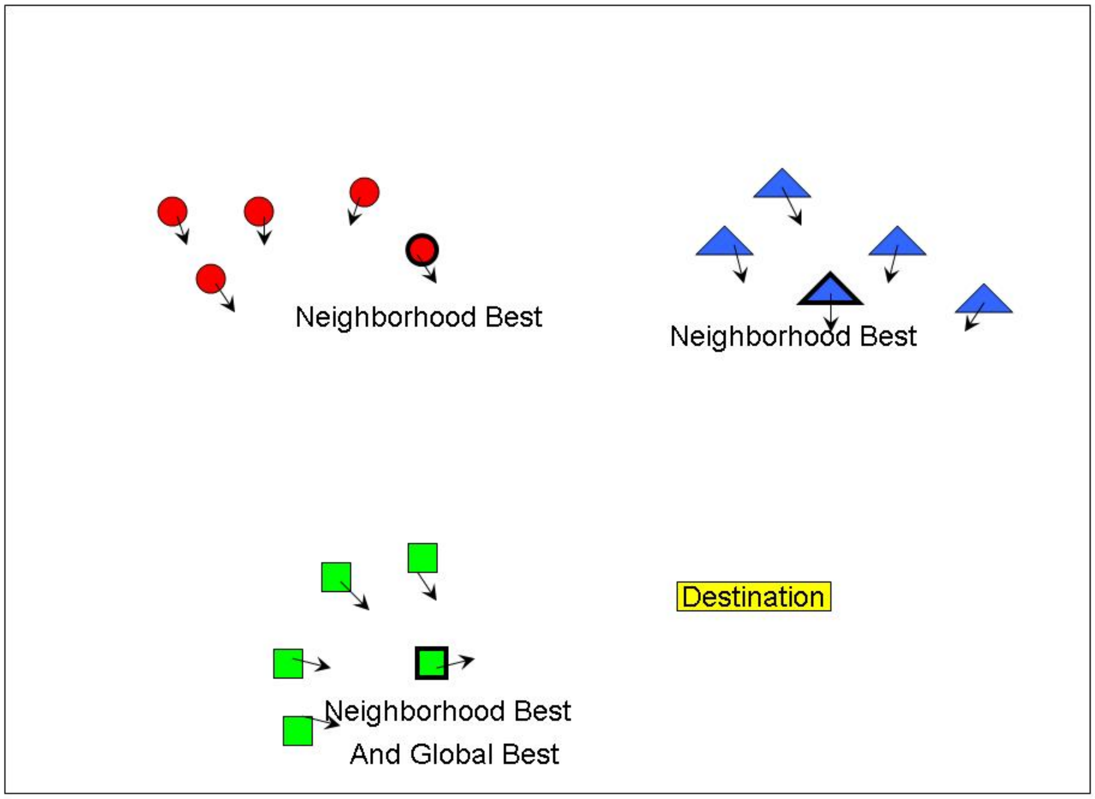


Figure 3.8: Particles are getting closer to the best position of the neighborhood

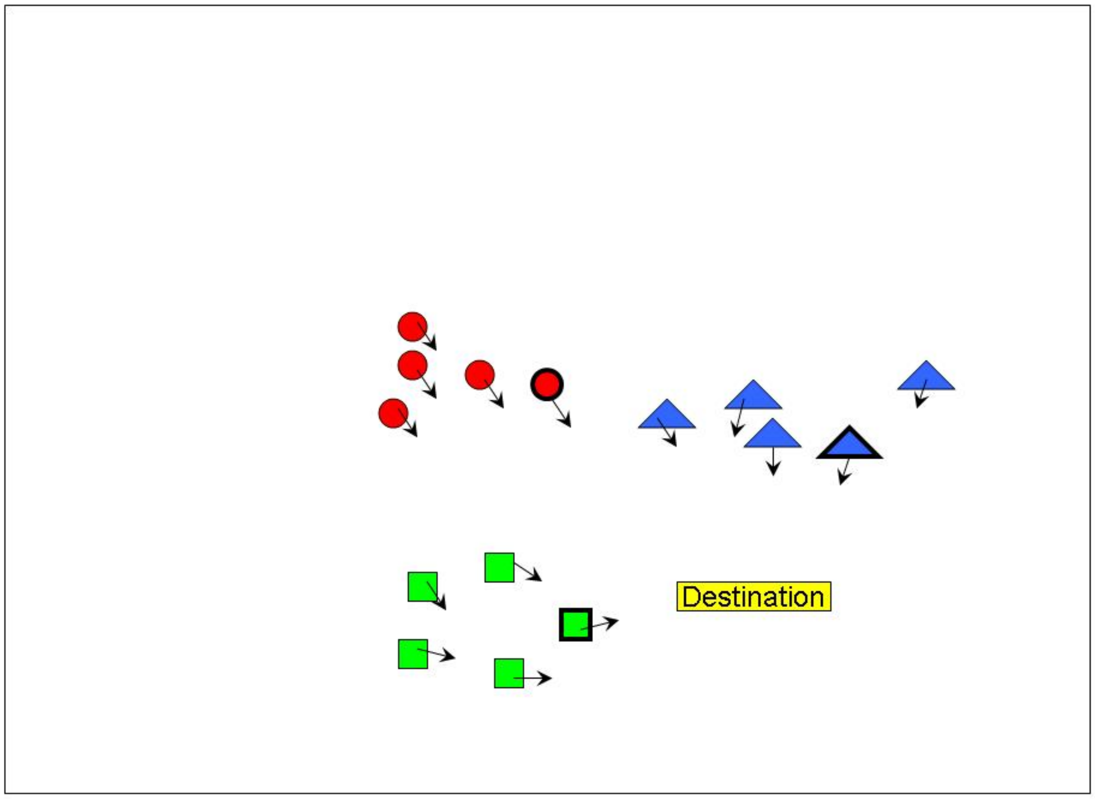


Figure 3.9: Particles are getting closer to the best global position

CHAPTER 4

DESIGN AND IMPLEMENTATION

The search problem involved in the fluoroscopic analysis process has been decribed in Chapter 1. While Chapter 2 provided an introduction to the world of fluoroscopic analysis and presented the computing problems associated with the process, Chapter 3 presented different methods to solve the search problem in fluoroscopic analysis. In this chapter, the design and implementation details as well as the pseudocode for the bees algorithm and particle swarm optimization method used for this thesis are provided.

4.1 Design Approach

This thesis consists of providing solutions to a search problem in a parallel computing environment. After finding the suitable algorithms for the search problem, a pseudocode for implementing it in the parallel environment was developed. Additionally, pseudocode for the sequential version of the algorithm was also developed. In order to measure the speed and effectiveness of the parallel implementation, comparison with its sequential counterpart is required. After a detailed analysis of the fluoroscopic analysis application, and exploration of different search strategies, two swarm intelligence algorithms, Bees and PSO were chosen. Developing pseudocode for these two algorithms for parallel and sequential implementation was the first step toward the design of this project.

The second step consisted of developing a good organization structure and an activity flow-chart, which are very essential to a good design. All the steps involved in the process were studied. Each step required an separate component. For fluoroscopic analysis, different components are required for specific tasks, such as, generating DRR images from a given postion and a CT scan image, image filtering for extracting the edges of an X-ray or DRR image, image matching, and fluoroscopic searching. Figure 2.5 in Chapter 2 provides an activity flow-chart for fluoroscopic analysis that illustrates the different stages in the fluoroscopic analysis and the steps to transition from one stage to another.

The third step involved identifying the different entities in the system and designing data structures for each of them. The main entities are:

1. CT Volume - used to represent a CT scan image.
2. DRR Image - used to represent a DRR X-ray image.
3. Bee - used to represent a bee in bees algorithm.
4. Particle - used to represent a particle in PSO method.
5. Sobel filter kernels - used in the Filtering method to extract edges of an X-ray image

These data structures are presented in Appendix B.

Figure 4.1 provides the pseudocode for the general fluoroscopic analysis. Figures 4.2, 4.3 and 4.4 provide the pseudocode for the sequential bees algorithm and particle swarm optimization method respectively. The pseudocode for the parallel bees algorithm is shown in Figures 4.5 and 4.6, while Figures 4.7 and 4.8 provide the pseudocode for the parallel particle swarm optimization method.

```
Fluoroscopic Analysis(CTCube, TargetXrayImage)

1. TargetEdges = SobelFilter(TargetXrayImage)
2. score = 0
3. While(score < GOOD_MATCH_SCORE)
4.      x = Random()
5.      y = Random()
6.      z = Random()
7.      azimuth = Random()
8.      elevation = Random()
9.      rotation = Random()
10.     TestDRRImage =
        GenerateDRR(CTCube,x,y,z,azimuth,elevation,rotation)
11.     TestEdges = SobelFilter(TestDRRImage)
12.     score = ContourMatching(TestEdges, TargetEdges)
13. Match found.
    Position values are x, y, and z.
    Orientation values are azimuth, elevation, and rotation
```

Figure 4.1: Pseudocode for fluoroscopic analysis in the simplest form

4.2 Build Infrastructure

Build infrastructure provides the capability to add new code to the project, compile and maintain the code. The project files are organized in such a manner that it facilitates the ease of compiling and executing the application. All the code and the input files are placed in a repository controlled by a version control system called Subversion. The main makefile is placed in the main directory of the project. This makefile facilitates all the build actions required for the project. The makefile targets and the functions performed by them are given in Appendix A.

The directories are organized in such a way that it becomes convenient to maintain different libraries, input images, results, and configuration individually without affecting other parts of the project. The directory structure of the project files is provided in Appendix

```
Sequential_Bees(CTCube, TargetXrayImage)

n = Number of bees
m = Number of best sites
p = Number of bees chosen for the best sites (best bees)
q = n-p = Number of bees chosen as scout bees for the next
          iteration
r = Number of individual bee iterations

1. TargetEdges = EdgeFilter(TargetXrayImage)
2. While(BestScore < GOOD_MATCH_SCORE):
3.     Foreach Bee:
4.         For i = 0  to p:
5.             if(scout bee)
                   //In the first iteration of #1, all bees are
                   //scout bees
6.                 Generate random values for position(x,y,z)
                   and orientation(az,el,rt)
7.              else if(worker bee)
8.                 Generate random step values and
                   add them to the previous values.
9.              TestDRRImage = GenerateDRR(x,y,z,az,el,rt, CTCube)
10.             TestEdges = EdgeFilter(TestDRRImage)
11.             BeeScore = ContourMatching(TestEdges,TargetEdges)
12.     BeeScore = Calculate best of all the p scores

//Waggle dance section
13.     Rank the BeeScore of all the individual bees
14.     Choose the m best sites from the list based on scores.
15.     Assign p bees to m sites equally (worker bees)
16.     Assign q bees for random search (scout bees)
17.     Save the BestScore and the values associated with it
18. End While
19. [x,y,z,az,el,rt] associated with BestScore
    are the required position and orientation values.
20. End
```

Figure 4.2: Pseudocode for sequential bees algorithm

```
Sequential_PSO(CTCube, TargetXrayImage)

n = Number of particles
m = Number of neighborhoods
p = Number of particles in a neighborhood
r = Number of individual particle iterations

1. TargetEdges = EdgeFilter(TargetXrayImage)
2. Foreach neighborhood m:
3.      NeighborhoodBest = 0.0
4. GlobalBest = 0.0
5. While(BestScore < GOOD_MATCH_SCORE):
6.    Foreach Neighborhood m:
7.       if NeighborhoodBest < 0.1:
            //This means, search randomly
8.          RANDOMSTEP = 0
9.       else if NeighborhoodBest < 0.4
            //Add large random steps to previous value
10.         RANDOMSTEP =  LARGESTEP
11.      else if NeighborhoodBest < 0.6
            //Add medium random steps to previous value
12.         RANDOMSTEP =  MEDIUMSTEP
13.      else if NeighborhoodBest < 0.8
            //Add small random steps to previous value
14.         RANDOMSTEP =  SMALLSTEP
```

Figure 4.3: Pseudocode for sequential PSO

```
15.         Foreach neighbor p:
16.             For i = 0  to r:
17.            if(RANDOMSTEP == 0):
                  //In the 1st iteration all particles
                  //search randomly
18.               Generate random values for position(x,y,z)
                  and orientation(az,el,rt)
19.            else:
20.               Generate random step values and
                  add them to the previous neighborhood best
                  values.
21.               TestDRRImage =
                  GenerateDRR(x,y,z,az,el,rt, CTCube)
22.               TestEdges = EdgeFilter(TestDRRImage)
23.               ParticleScore =
                  ContourMatching(TestEdges,TargetEdges)
24.               ParticleBestScore =
                  the best of all the r particle scores
25.        NeighborhoodBest =
               the best of all scores in the neighborhood
26.     GlobalBest = the best of all scores
27. End While
28. [x,y,z,az,el,rt] associated with GlobalBest
    are the required position and orientation values.
29. End
```

Figure 4.4: Pseudocode for sequential PSO, ctd

```
Parallel_Bees(CTCube, TargetXrayImage)

n = Number of bees/processes
m = Number of best sites
p = Number of bees chosen for the best sites (best bees)
q = n-p = Number of bees chosen as scout bees for the
          next iteration
r = Number of individual bee iterations

1. TargetEdges = EdgeFilter(TargetXrayImage)
2. Barrier()  //Wait for all processes to arrive at this point
3. While(BestScore < GOOD_MATCH_SCORE):
4.    Foreach Bee:
5.       For i = 0  to p:
6.          if(scout bee)
            //In the first iteration of #1, all bees are
            //scout bees
7.             Generate random values for position(x,y,z)
               and orientation(az,el,rt)
8.          else if(worker bee)
9.             Generate random step values and
               add them to the previous values.
10.         TestDRRImage = GenerateDRR(x,y,z,az,el,rt,CTCube)
11.         TestEdges = EdgeFilter(TestDRRImage)
12.         BeeScore = ContourMatching(TestEdges,TargetEdges)
13.   BeeScore = Calculate best of all the p scores
```

Figure 4.5: Pseudocode for parallel bees algorithm

```
      //Waggle Dance section
14.   if( process_id != 0):
      //All processes other than process 0,
      //send their scores and 6 value to process 0
15.       Send(BeeScore,x,y,z,az,el,rt) to Process 0
16.   else if(process_id == 0):
17.       for(i =1 to n):
18.          Recv(BeeScore,x,y,z,az,el,rt)
             from Process i

19.       Rank the BeeScore of all the individual bees
20.       Choose the m best sites from the list based on
          scores.
21.       Save the BestScore and the values associated
          with it

22.       for(i=1 to n):
             //Send information about best sites to the
             // best bees. Make some bees random.
23.          Send(BeeScore, x,y,z,az,el,rt,ScoutOrWorkerFlag)
             to Process i.
24.   if(process_id != 0)
25.       Recv(BeeScore, x,y,z,az,el,rt,ScoutOrWorkerFlag)
          from Process 0
26. End While
27. [x,y,z,az,el,rt] associated with BestScore
    are the required position and orientation values.
28. End
```

Figure 4.6: Pseudocode for parallel bees algorithm, Ctd

```
Parallel_PSO(CTCube, TargetXrayImage)

n = Number of particles/processes
    Every particle in the system has a particle_id
m = Number of neighborhoods/process groups
p = Number of particles in a neighborhood
    Every neighbor in a neighborhood has a neighbor_id
r = Number of individual particle iterations

1. TargetEdges = EdgeFilter(TargetXrayImage)
2. Create m ProcessGroups //Neighborhoods
3. Initialize all neighbors in a group/neighborhood
4. GlobalBest = 0.0
5. Barrier() //Wait for all particles to get initialized
6. While(BestScore < GOOD_MATCH_SCORE):
      //This is done by all neighborhoods.
7.    if NeighborhoodBest < 0.1:
8.       RANDOMSTEP = 0 //This means, search randomly
9.    else if NeighborhoodBest < 0.4
10.      RANDOMSTEP =  LARGESTEP
         //Add large random steps to previous value
11.   else if NeighborhoodBest < 0.6
12.      RANDOMSTEP =  MEDIUMSTEP
         //Add medium random steps to previous value
13.   else if NeighborhoodBest < 0.8
14.      RANDOMSTEP =  SMALLSTEP
         //Add small random steps to previous value
15.   For i = 0  to r:
16.      if(RANDOMSTEP == 0):
            //In the 1st iteration all particles search randomly
17.         Generate random values for position(x,y,z)
            and orientation(az,el,rt)
18.      else:
19          Generate random step values and
            add them to the previous neighborhood best values
20.      TestDRRImage = GenerateDRR(x,y,z,az,el,rt, CTCube)
21.      TestEdges = EdgeFilter(TestDRRImage)
22.      ParticleScore= ContourMatching(TestEdges,TargetEdges)
23.      ParticleBestScore= the best of all the r particle scores
```

Figure 4.7: Pseudocode for parallel PSO

```
24.    if(neighbor_id != 0):
          //All neighbors send their score
          //and values to neighbor with id=0
25.       Send(ParticleBestScore, x,y,z,az,el,rt)
          to neighbor 0
26.    else:
          //neighbor 0 receives all the scores
27.       for( i=1 to p):
28.          Recv(ParticleBestScore, x,y,z,az,el,rt)
             from neighbor i
29.          Store the NeighborhoodBest score
             //Send the neighborhood best score and
             //values back to others
30.          for( i=1 to p):
31.             Send(NeighborhoodBest, x,y,z,az,el,rt)
                to neighbor i

32.    if(neighbor_id !=0):
33.       Recv(NeighborhoodBest, x,y,z,az,el,rt)
          from neighbor 0

34.    if(particle_id != 0):
35.       Send(NeighborhoodBest, x,y,z,az,el,rt)
          to particle 0
36.    else:
37.       for( i=1 to n):
38.          Recv(NeighborhoodBest, x,y,z,az,el,rt)
             from particle i
39.          Store the GlobalBest score
40. End While
41. [x,y,z,az,el,rt] associated with GlobalBest
    are the required position and orientation values.
42. End
```

Figure 4.8: Pseudocode for parallel PSO, Ctd

A.

4.3 Implementation Details

Implementation of this application consists of several files of C code that implement all the algorithms required for each step in fluoroscopic analysis. The inputs to this application are DRR images of pre-determined postions and orientation or an actual 2-D X-ray fluoroscopic frame as the target images, CT scan image, and configuration files that describe the parameters required to define the algorithms. The program outputs the position and orientation of the best matching score. By configuring the makefile to generate the debug version of the program, the program can be made to print out more information about each iteration of the search.

The algorithms are implemented as library plugins that can be dynamically linked to the main program. The main program performs all the main steps of extracting the CT volume information from the input CT image, and making dynamic calls to the required libraries for each of the other functions such as searching, generating DRR, etc. By implementing the algorithms as dynamically linked plugins, the flexibility for using any algorithm for a specific task is provided. This makes it possible to implement a new algorithm for any step and compile it independently. No changes are needed to any other part of the project to use the new plugin. The new plugin has to only be specified as a parameter while executing the application. This is done to allow further research and experimentation for the fluoroscopic analysis and to make it easy to explore different possibilities of solving this problem.

The environment details required to develop and execute this project is provided in Table 4.1. The instructions to execute this project are provided in Figure 4.9.

Operating System	Linux - CentOS release 5.2
Version Control System	Subversion 1.4.2
Programming Language	C
Libraries	mpich2, nrutils
Sequential Compiler	gcc
Parallel Compiler	mpicc
Parallel Computing platform	Beowulf cluster
Scripting Language	Korn Shell
Debugger	gdb
Memory Profiler	Valgrind

Table 4.1: Environment details

```
Execution of sequential program:
    fluoro_s
       <path to search plugin(.so lib file)>
       <path to the input config file>

Execution of parallel program:
    mpiexec -l -n <num of processes> fluoro_p
       <path to search plugin(.so lib file)>
       <path to the input config file>
```

Figure 4.9: Program execution

An example config files for the bees algorithm and the particle swarm optimization method is provided in Figures 4.10 and 4.11, respectively.

4.4 Test Infrastructure

The configuration driven program execution adopted in this project makes it very easy to set up tests for this project. In this project, the specification of a particular algorithm and a set of parameters constitute a test case. By varying the choice of algorithm and the parameters required to define it, plenty of test cases can be generated. To generate a test case, the creation of a config file with the required details is necessary. This can be given

```
#Input CT image
CT_IMAGE=<path>/images/really_small_cube.txt
#Target DRR with known postion values
DRR_IMAGE=<path>/images/drr_image10_10_10_8_8_8.txt
GENERATE_DRR_LIB=<path>/lib/libp_generate_drr_raytracing.so
FILTER_LIB=<path>/lib/libp_filter_sobel_bw.so
MATCH_LIB=<path>/lib/libp_match_contour_bw.so
MAX_ITER=3
BEE_ITER=1
NUM_BEES=8
NUM_BEST_BEES=6
NUM_BEST_SITES=3
RANDOM_SEED=123
AZIMUTH_RANGE=180  #In degrees
ELEVATION_RANGE=90 #In degrees
ROTATION_RANGE=90  #In degrees
TRANSLATION_RANGE=20 #In pixels
TRANSLATION_FINE_STEP=3 #In pixels
ORIENTATION_FINE_STEP=5 #In degrees
```

Figure 4.10: Config file for bees algorithm

```
#Input CT image
CT_IMAGE=<path>/images/really_small_cube.txt
#Target DRR with known postion values
DRR_IMAGE=<path>/images/drr_image10_10_10_8_8_8.txt
GENERATE_DRR_LIB=<path>/lib/libp_generate_drr_raytracing.so
FILTER_LIB=<path>/lib/libp_filter_sobel_bw.so
MATCH_LIB=<path>/lib/libp_match_contour_bw.so
MAX_ITER=3
PARTICLE_ITER=1
NUM_PARTICLES=8
NUM_NEIGHBORHOODS=4
RANDOM_SEED=123
AZIMUTH_RANGE=180  #In degrees
ELEVATION_RANGE=90 #In degrees
ROTATION_RANGE=90  #In degrees
TRANSLATION_RANGE=20  #In pixels
TRANSLATION_FINE_STEP_LEVEL1=10  #In pixels
TRANSLATION_FINE_STEP_LEVEL2=5   #In pixels
TRANSLATION_FINE_STEP_LEVEL3=3   #In pixels
ORIENTATION_FINE_STEP_LEVEL1=10  #In degrees
ORIENTATION_FINE_STEP_LEVEL2=5   #In degrees
ORIENTATION_FINE_STEP_LEVEL3=1   #In degrees
```

Figure 4.11: Config file for PSO

as an input to the program executable to run the test case. This structure makes it easy to write different configuration files and write a script to run the application with each config file and thus easily automate the test execution process. The output from each application can be redirected to a results folder and used to compare with subsequent test executions for the same test case in regression testing.

CHAPTER 5

TESTING AND RESULTS

The implementation details for the fluoroscopic analysis process and the test infrastructure developed are provided in Chapter 4. This chapter lists the efforts to test this implementation.

5.1 Test Cases

Software implementations require thorough testing for verifying the code and also validating the results obtained for the given inputs. Testing the implementation of fluoroscopic analysis process is required for the following purposes:

- To check the correctness of code by running it against various inputs and checking if the program runs to completion successfully.
- To verify if the parallel implementation does generate the required output in shorter time compared to the sequential implementation.
- To find the better of the two SI methods, bees algorithm and particle swarm optimization, for solving the search problem in fluoroscopic analysis.

The implementation for both the sequential and parallel versions provide the time taken for the search operation. This helps in comparing the differences in the time taken for the two versions. Several test cases are designed to test the implementation to enable the verification of all the the points mentioned above.

The implementation for the bees algorithm and the particle swarm optimization algorithm require several parameters to be set to successfully initialize the system. The bees algorithm requires values for the number of bees, number of best sites to choose, the number of bees to allocate to each best site, etc. In the case of particle swarm optimization, the set of parameters include the number of particles, number of neighborhoods and number of members in a neighborhood. These parameter values are placed in a configuration file and given as input to the main program. Examples of the configuration files for the Bees and particle swarm optimization algorithms are provided in Figures 4.10 and 4.11 respectively. In this project, different test cases are derived by specifying different parameters for each algorithm. Therefore, by creating several configuration files, one for each set of test configurations, many test cases are constructed.

An attempt has been made to diversify the parameters in such a way that the program will be tested for different sizes of the groups (bees or particles), different sizes of the sub-groups, different position and orientation values of the target image, and so on. This would help in the determination of an optimized combination of parameters. For example, a particle population consisting of 36 particles grouped into 6 neighborhoods of 6 members each, might give faster results than a population grouped into 12 neighborhoods of 3 members each. In the case of bees algorithm, if 3 best sites are chosen and 10 bees are selected for each of the 3 sites from a population of 36 bees, while allowing the remaining 6 bees to search randomly, the grouping might provide better results than any other grouping of the bees.

Bees algorithm and particle swarm optimization method are both swarm intelligence algorithms that use different mechanisms of grouping and sharing information among one another within their colony. Which method is more suitable for fluoroscopic analysis? How many entities are required for the search to provide optimal results without costing any severe communication overhead? What is an ideal grouping of the entities involved? Do smaller number of groups with large sizes work better than larger numbers of groups with small sizes? What kind of target images result in good solutions? Does the implementation provide good results only for a small subset of the target images or does it hold for any range? The execution of tests attempts to answer these question that help determine the limitations and strengths of each algorithm by configuring several permutations and combinations of the parameter values. Tables 5.1 and 5.2 provide some of the test cases for the bees algorithm and the particle swarm optimization method respectively. Additionally, these combinations are executed multiple times with different target DRR images and for several number of maximum iterations.

Configuration/ Testcase	1	2	3	4	5	6
Number of Bees	12	24	24	24	36	36
Number of Best Bees	9	20	18	16	27	30
Number of Scout Bees	3	4	6	8	9	6
Number of Best Sites	3	2	6	4	9	6

Table 5.1: Test Cases for bees algorithm

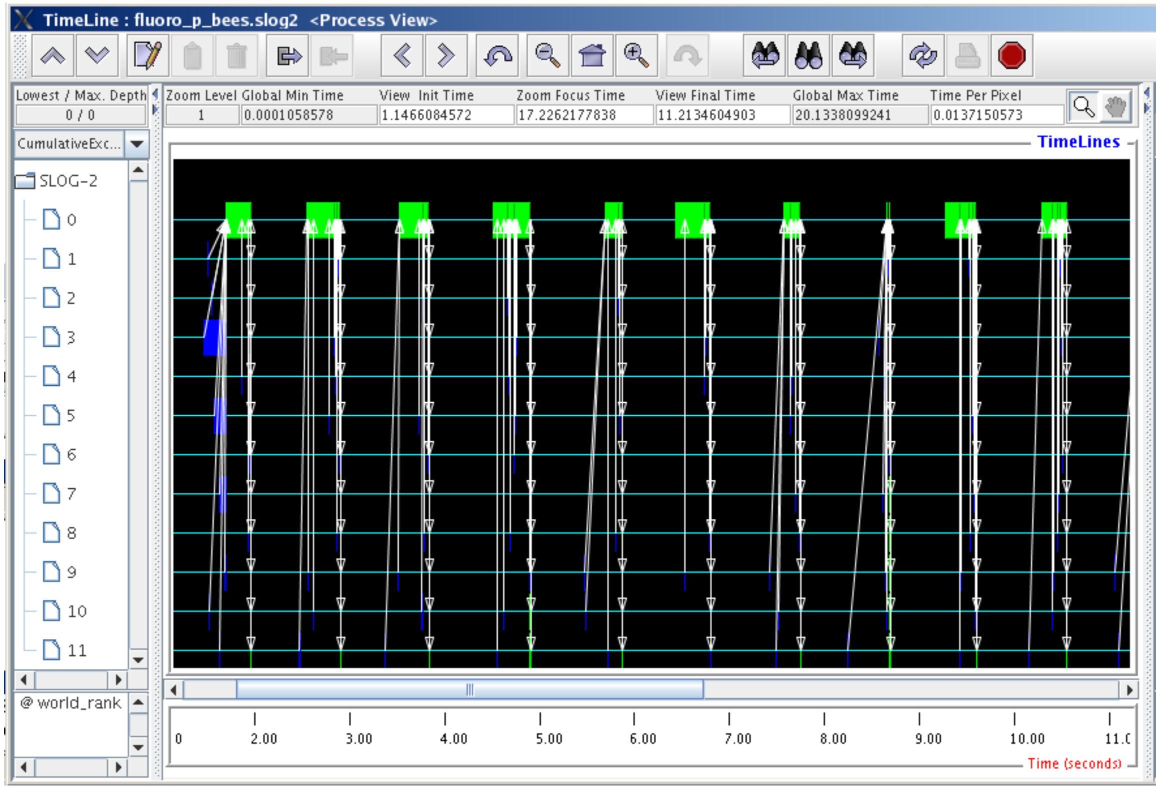
Configuration/ Testcase	1	2	3	4	5	6
Number of Particles	12	24	24	24	36	36
Number of Neighbors	4	6	4	3	4	6
Number of Neighborhoods	3	4	6	8	9	6

Table 5.2: Test Cases for PSO

In order to study the communication overhead caused in the parallel implementations of the two SI algorithms, a snapshot of the inter-process communication has been taken by adding extra logging to the program and Jumpshot 4.0 software has been used to visualize the communication in terms of send and receive operations between the processes by reading those logs. Figure 5.1 provides the visualization of the inter-process communication during the execution of bees algorithm. The left pane of the picture lists the 12 processes with id 0 to 11. The timeline is seen at the bottom pane. It can be noted that for each iteration, all the bees or processes send their values to the master process (id = 0) and the master process sends a value after comparison and evaluation of all sent values, back to all the bees. This cycle repeats for every iteration of the search. The inter-process communication for particle swarm optimization algorithm is quite different from this. Figure 5.2 provides the visualization for this communication. In this, it can be seen that in each iteration, subgroups communicate among themselves first, where all the subgroup members send message to and receive from the subgroup leader. The leaders then communicate with the master process. The communication overhead load on the master process is much lesser in the case of particle swarm optimization than bees algorithm. Considering the time taken for each iteration in generating a DRR image and comparing that to a target DRR image, the communication overhead caused by sending and receiving matching score values at the end of each iteration is not very significant.

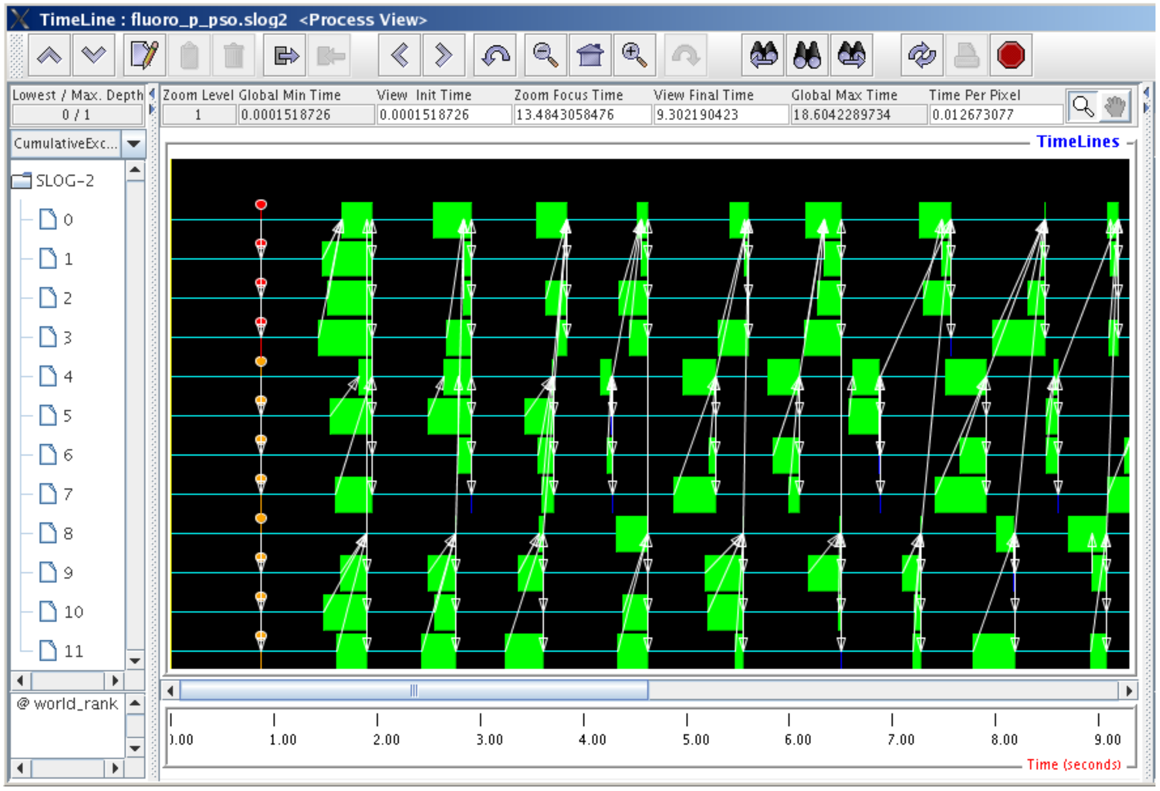
5.2 Results

Search algorithm implementations require several iterations of DRR image generation and their comparison to target image before finding the required position and orientation values. In sequential execution, each iteration of the search is conducted sequentially and hence takes roughly $n.x$ amount of time for n iterations, if x is the amount of time taken for one operation of DRR image generation and comparison. In both the parallel implementations, the parallel processes share the number of iterations of the search. In ideal cases, if p is


TimeLine : fluoro_p_bees.slog2 <Process View>

Lowest / Max. Depth	Zoom Level	Global Min Time	View Init Time	Zoom Focus Time	View Final Time	Global Max Time	Time Per Pixel
0 / 0	1	0.0001058578	1.1466084572	17.2262177838	11.2134604903	20.1338099241	0.0137150573

Figure 5.1: Communication visualization for the parallel bees algorithm


TimeLine : fluoro_p_pso.slog2 <Process View>

Lowest / Max. Depth	Zoom Level	Global Min Time	View Init Time	Zoom Focus Time	View Final Time	Global Max Time	Time Per Pixel
0 / 1	1	0.0001518726	0.0001518726	13.4843058476	9.302190423	18.6042289734	0.012673077

Figure 5.2: Communication visualization for the parallel PSO method

the number of processes, then the time taken for *n* iterations reduces by a factor of *n/p*. Of course, the actual value will be less than this if we account for the process communication overhead.

Mode of Execution	Algorithm	Max Iteration	Number of Entities	Time Taken (in secs)	Speed Up
Sequential	Bees	100	12	1161.554	
Parallel	Bees	100	12	104.893	11.07
Sequential	PSO	100	12	1183.173	
Parallel	PSO	100	12	104.777	11.29

Table 5.3: Timing results

All the experiments confirmed that the the time taken by the parallel programs were less than the time taken by their sequential counterparts by a significant amount. One such instance is provided in Table 5.3.

These results help in verifying the first test objective and part of the second objective. The sequential and parallel programs have run without any crashes or execution errors for all the configuration values for large number of iterations. In addition, for the same number of iterations, the parallel programs are considerably faster than the sequential programs.

In order to get the results, each component of the fluoroscopic analysis process have to function accurately. One of the most crucial roles in affecting the results is played by the DRR X-ray image matching algorithm. The image matching algorithm chosen in this project provided unexpected matching score values in some cases. This has made it very difficult to obtain the expected position and orientation values from the search operation. Hence, this prevents us from effectively comparing the sequential and parallel implementations and also comparing different methods of searching to find out which method takes us to the result in the shortest amount of time.

Owing to the difficulties in extracting the essential information from the complex X-ray images, and inaccuracy of the matching operation due to the presence of unsuitable information given by prior steps, the second and the third test objectives cannot be fully analyzed. The other reason could also be that the random position and orientation values used to generate the reference DRR images might not represent valid X-ray images. Due to this, all the subsequent processes of filtering and matching are bound to go wrong. There is scope for further research to improve the results and this is discussed in Chapter 6.

CHAPTER 6

CONCLUSIONS

6.1 Swarm Intelligence for Solving the Search Problem

Fluoroscopic analysis of knee joint kinematics consists of determining the position and orientation of the bones in the knee joint. In the experiments conducted in this thesis, a hypothetical fluoroscope with a CT cube placed between an X-ray camera and an X-ray film, is used. The objective of the thesis is to find the position of the CT cube and azimuth and elevation angles of the camera and the rotation of the film for a given CT scan image and a target fluoroscopy X-ray frame.

The focus of this thesis has been to develop faster search algorithms for finding the position and orientation information. This is done by implementing the two swarm intelligence techniques, the bees algorithm and the particle swarm optimization method, for sequential and parallel execution. Both these methods are biologically inspired algorithms. While the bees algorithm mimics the food foraging behavior of the bees, particle swarm optimization method is inspired by the social behavior of a flock of birds or a school of fish. By adopting the communication and collaboration among a population of entities to solve a common problem, it is easier to reach a better solution faster.

Parallel computing is a suitable method for solving problems that are enormously time consuming. Fluoroscopic analysis is one such problem and the usage of parallel computing for solving this is well warranted. The bees algorithm and the particle swarm optimization method are easily parallelizable and are easy to apply to a problem of this nature. The experiments conducted to test the implementation provide sufficient information to indicate that parallel computing can significantly decrease the time required to search the position and orientation values in the fluoroscopic process. Several configurations of the bees and the particle swarm optimization algorithms have been successfully executed.

6.2 Future Scope

There is scope for further research in several components of the fluoroscopic analysis process. In order to derive accurate results, it is essential to have very efficient and effective methods for each of the analysis operations such as the DRR image generation, filtering of essential information from DRR or X-ray images, matching two DRR or X-ray images as well as searching for the position and orientation values from a given CT image and a target X-ray image. While the bees and particle swarm optimization algorithms appear to be promising solutions to the search problem, more analysis has to be carried out to find the best configuration to get optimum results out of these two methods, and this would be possible with accurate results from the other steps in the fluoroscopic process.

The intent of this fluoroscopic analysis process is to provide dynamic real-time information of the knee joint to assist in several diagnostic or surgical processes. This research can be extended to include Magnetic Resonance Imaging (MRI) process to find alternate solutions. Additionally, the fluoroscopic analysis process can be applied to any joint in the human body to help diagnose and treat ailments of the joints. There is a huge potential for this process to truly help the medical community in the treatment of joint-related problems.

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APPENDIX A

README FILE

```
-------------------------------------------------------
                      Readme file
                   Fluoroscopy Project
-------------------------------------------------------

Sections:
    1.  Description
    2.  Steps Invloved in Executing the Project.
    3.  How to Compile the Project.
    4.  Makefile Features.
    5.  How to Run the Project.
    6.  Directory Structure of the Project.
    7.  How to Add a Plugin.
    8.  Code Documentation.
    9.  Naming Conventions.
    10. Scripts.
    11. Config Files.
    12. Results.
    13. Examples for Compiling and Executing the Project.

--------------------------------------------------------
1. Description
--------------------------------------------------------
This project performs an unsupervized fluoroscopic
analysis of knee-joint kinematics. The operations
involved include
    1. reading a CT scan image,
    2. generating DRR images,
    3. filtering the edges from a DRR image,
    4. matching the edges of two different DRR images
       and having a score associated with it,
    5. and searching for the right DRR image for a CT
       image, by using different combinations of the
       film and camera orientation and CT cube offsets.

--------------------------------------------------------
2. Steps Involved in Executing the Project
--------------------------------------------------------
The main program of this project relies on the
availability of shared libraries for the following
operations : generating DRR, filtering, matching and
searching. Below are a list of steps required to execute
this project. Refer to relevant sections for details in
each step. In order to use the Makefile provided as is,
please follow the directory structure and the other
requirements as mentioned for each step. Deviation from
them would require custom makefiles or modification to
paths in the makefile or whatever is required for the
specific change.

    1. Place the CT image file in the 'images' directory.
    2. Place a DRR image for that CT image in the 'images'
       directory.  The DRR image file for a CT image,
       can also be created by running the program
       create_target_drr with the required camera and
       film orientation and cube offsets. Refer to section
       3.A and 5.A.
    3. Create an input config file which lists all the
       parameters required for running the program, such
       as number of iterations to run the search, path
       to the CT image, path to the DRR image, and any
       other parameters required for the algorithm chosen.
       Place this file in the 'config' directory.  Refer
       to section 3.E
    4. Compile all the plugins required for the instance
       of the program.  Each plugin should be in a
       separate directory in the 'plugins' directory.
       Place libraries (*.so files) in the lib directory
       and turn off the selinux security restrictions
       for those libraries. Refer to section 3.B and 3.C.
    5. Compile the main program by specifying the
       compiler. Refer to section 3.D.
    6. Run the program by providing the input config
       file. Refer to section 5.B.

--------------------------------------------------------
3. How to Compile the Project
--------------------------------------------------------
$(FLUOROSCOPY) represents the path to the fluoroscopy
project source, the outermost directory of the trunk,
which consists of main makefile and all other
directories.

    A. To compile the create_drr_image program:
       cd /$(FLUOROSCOPY)
       make clean_create_drr
       make create_drr

    B. To compile all the plugins in the 'plugins'
       directory:
       cd /$(FLUOROSCOPY)
       make clean_plugins
       make plugins

       Note: This creates a .so file for sequential
       and parallel, for DOF=3 and 6, and all the
       permutations required.
       DOF = Degrees of Freedom

    C. To compile a single plugin:
       For any plugin, you can run 'make clean' followed
       by 'make all' to make all libraries that are possible
       for that plugin.  To only make a particular library,
       run make with required parameters.

    D. To compile the main program:
       cd /$(FLUOROSCOPY)
       make clean
       make main CC=<compiler>

       NOTE: Compiler should be 'gcc' or 'mpicc'.
    E. To create input config files:
       Run the relevant scripts from the 'scripts'
       directory or run the makefile with the right
       target to create the config files.

       make configure_bees #For Bees
       make configure_pso #For PSO
       make configure_montecarlo #For MonteCarlo


    F. To create lib config file[obsolete]:
       make configure_libs

       NOTE: This feature is preserved for any future
       use that might necessitate the need for a lib
       config file.

--------------------------------------------------------
4. Makefile Features
--------------------------------------------------------
The Makefile present in the main directory of the
project trunk, facilitates many operations.  Below is a
list of all the targets accepted by the makefile.
    make clean_all
        executes clean, clean_create_drr, clean_libs,
        clean_plugins, and clean_swapfiles
    make clean
        cleans the current directory and source directory
    make clean_create_drr
        cleans files associated with create_target_drr
        program from the source directory
    make clean_libs
        deletes all the libraries (*.so) files from the
        'lib' directory
    make clean_plugins
        cleans all the plugin directories
    make clean_swapfiles
        cleans all the swap files (*~) from all the
        directories in the project recursively.
    make create_drr
```

```
        compiles the create-target_drr program
    make plugins
        compiles all the plugins in the 'plugins'
        directory and copies all the libs to the lib
        folder
    make main CC=<compiler>
        compiles the main program. CC= <gcc|mpicc>
    make help
        prints all the targets accepted by make
    make configure_bees
        runs a script that creates an input config file
        for the Bees algorithm by taking user inputs and
        copies it to the config folder
    make configure_pso
        runs a script that creates an input config file
        for the PSO algorithm by taking user inputs and
        copies it to the config folder
    make configure_montecarlo
        runs a script that creates an input config file
        for the MonteCarlo algorithm by taking user
        inputs and copies it to the config folder
    make configure_libs
        runs a script that creates an lib config file
        and copies it to the config folder
    make documentation
        compiles and creates the code documentation
        and copies them to the doc folder.

Makefile for the main program:
The makefile for the main program is named Makefile_main and is
present in the 'source' directory.

Makefile for the create_target_drr program:
The makefile for the create_target_drr program is named
Makefile_drr and is present in the 'source' directory.

Makefiles for plugins:
Each plugin has a directory associated with it in the 'plugins'
directory. Each plugin has its own makefile named 'Makefile'.

--------------------------------------------------------
```

```
5. How to Run the project
--------------------------------------------------------
    A. To run the create_target_drr program:
       create_target_drr
       <path to generate_drr plugin(.so lib file)>
       <CT image file>
       <resolution>
       <path to output drr file>
       [<azimuth> <elevation> <rotation>
       [<x offset> <y offset> <z offset>] ]

       NOTE: Example for resolution is 128, 256, 512 etc.
       Resolution for really_small_cube.txt is 128.

    B. To run the main program
       Sequential:
       fluoro_s
       <path to search plugin(.so lib file)>
       <path to the input config file>

       Parallel:
       mpiexec -l -n <num of processes> fluoro_p
       <path to search plugin(.so lib file)>
       <path to the input config file>

--------------------------------------------------------
6. Directory Structure of the Project
--------------------------------------------------------
$(FLUOROSCOPY) represents the main truck directory of
the project.

Create an environment variable for this as follows:
export FLUOROSCOPY=<fluoroscopy trunk absolute path>

$(FLUOROSCOPY)
        |
        |__matlab
        |
        |__config
        |
        |__doc
        |
        |__include
        |
        |__images
        |
        |__lib
        |
        |__results
        |
        |__scripts
        |
        |__source
        |        |__util
        |
        |__plugins
                |__filter_sobel_bw
                |__filter_sobel_gs
                |__match_contour_bw
                |__match_contour_gs
                |__search_parallel_bees
                |__search_parallel_pso
                |__search_sequential_bees
                |__search_sequential_pso
                |__search_sequential_montecarlo
                |__generate_drr_raytracing
                        |__sort_insertion
                        |__sort_qsort
                        |__sort_quick

Place the files in the relevant directories.  The
directory names are self-explanatory and clearly
indicate what kind of files are expected to be
present within them.

NOTE: The Makefile in the trunk directory does
not compile the source in 'matlab' directory.
'matlab' directory contains the source for
fluoroscopy in matlab language. All the other
folders and files are associated with the C
implementation for fluoroscopy.
```

```
---------------------------------------------------------
7. How to Add a Plugin
---------------------------------------------------------
Following are the steps to create a new plugin:
    1. Create a folder in the 'plugins' directory.
       Follow the naming conventions provided in section
       9.
    2. Place all the source files in the created
       directory.
    3. If the plugin depends on other libraries or other
       set of source files, or different sort techniques
       etc, make separate directories for each of them
       within the directory for the plugin. For example,
       generate_drr_raytracing has 3 directories for the
       sort function. One of them is used to compile the
       library.
    4. Create a makefile for the plugin.
    5. In the makefile, create a target 'all' which
       generates multiple libraries files for all the
       required combinations.
       Refer to other plugin makefiles as examples.
    6. Create an input config file, as required for your
       libraries and execute the main program with the
       appropriate parameters.

---------------------------------------------------------
8. Code Documentation
---------------------------------------------------------
The open source tool Doxygen is used for generating the
code reference manual.  The configuration file Doxyfile
is present in the main truck directory. Currently, it is
configured to provide html, latex-pdf and perlmod-pdf
documentations. Edit this file to customize the
documentation to your needs. Please refer to the Doxygen
tutorial for details on installing, configuring and
running the tool.  Some basic steps are:

    To generate documentation, run the commands:
        make documentation

    To view the documentation, run any of the following
    commands:
        firefox docs/index.html
        acroread docs/CodeDocumentation.pdf
        acroread docs/CodeReferenceManual.pdf

    Alternate way to generate documentation:
        doxygen Doxyfile

    Alternate way to view documentation:
        cd html; firefox index.html
        cd latex; make; acroread refman.pdf
        cd perlmod; make; acroread doxylatex.pdf

Currently, the documentation includes all the plugins.
If desired, separate documentation can be created for
each plugin, by providing a Doxygen config file for
each plugin and following the steps similar to the
above instructions.

--------------------------------------------------------
9. Naming Conventions
--------------------------------------------------------
The names chosen for files or directories should be
self-explanatory and easy to understand.

The names of the plugin directories should have a first
name that indicates the operation performed or the
interface implemented, e.g., filter, match, search etc.
The second name should indicate if it is parallel or
sequential if applicable. The next name should indicate
the algorithm used, e.g., sobel, contour, bees etc.  Any
other variations should be next, e.g., bw for black and
white, or gs for grayscale,  etc. Separate the names by
underscores.

The lib names should begin with 'lib', followed by 's'
or 'p' to indicate if they are sequential or parallel.
After this, separate each name with an underscore and
follow a pattern as mentioned above.

--------------------------------------------------------
```

```
10. Scripts
--------------------------------------------------------
Below is the list of existing script files and its
functions:
    configure_libs.sh
        Used to create a lib config file [obsolete]
    configure_input_bees.sh
        Used to create an input config file for Bees
        algorithm
    configure_input_montecarlo.sh
        Used to create an input config file for Monte
        Carlo algorithm
    configure_input_pso.sh
        Used to create an input config file for PSO
        algorithm
    run_s_sanity.sh
        Used to run all the sequential programs for
        sanity checking. Basically to check if the
        program does not crash for the minimum number
        of iterations.
    run_s_limited.sh
        Used to run all sequential programs for
        testing the limited range for search parameters
    run_s_full.sh
        Used to run all sequential programs for
        testing the full range for search parameters
    run_p_sanity.pbs
        Used to run all the parallel programs for
        sanity checking. Basically to check if the
        program does not crash for the minimum
        number of iterations.
    run_p_limited.pbs
        Used to run all parallel programs for testing
        the limited range for search parameters
    run_p_full.pbs
        Used to run all parallel programs for testing
        the full range for search parameters
    run_s.sh
        Used by the run_s_* scripts internally.
    run_p.sh
        Used by the run_p_* scripts internally.
    helper_s.sh
        Used by the run_s.sh script internally.
    helper_p.sh
        Used by the run_p.sh script internally.

    NOTE: Check to see if any paths need to be changed
    in the scripts.  In some places, the path is set
    to the current user's working directory.

--------------------------------------------------------
11. Config Files
--------------------------------------------------------
    Input configuration files can be created using the
    steps specified in 3E.  The main program requires a
    config file as an input. It consists of all the
    algorithm parameters and also the target DRR image.
    In this project, a naming convention is used to name
    the config files for ease of use.

    $(FLUOROSCOPY)/config directory consists of all the
    config files.  The config files required for
    sequential tests are placed in 's_tests' folder, and
    files required for parallel tests are placed in
    'p_tests' folder.  Within these two folders, there
    can be many folders with separate config files, one
    for each test case.

    Note: Naming convention for config and result
    directories:

    Directory used for tests to just check if the
    programs run without error:
    Name = sanity

    Directory used for tests that limit the search
    space:
    Underscore delimited name contains:
    1. "limited"
    2. num of processors
    3. [num of neighbors]-[num of neighborhoods]  (for PSO)
       Use the second number for [num of best sites] (for Bees)
    5. num_bee_iter(for Bees) or num_particle_iter (for PSO)
    6. drr_image : "img" followed by az,el,rt
                    orientation
    and x,y,z translation values

    Directory used for tests that search the entire
    search space also follow the above naming
    convention except that the name starts with "full"
    instead of "limited".

--------------------------------------------------------
12. Results
--------------------------------------------------------
    $(FLUOROSCOPY)/results directory is created to
    contain all the output redirected from test
    executions.  The result files required for
    sequential tests are placed in 's_tests' folder, and
    files required for parallel tests are placed in
    'p_tests' folder.  Within these two folders, there
    can be many folders, one for each test case.

    The same naming convention used for naming config
    files may also be used for result files for easier
    maintenance and management of tests.

--------------------------------------------------------
13. Examples for Compiling and Executing the Project
--------------------------------------------------------
    A. Steps for the sequential program:
        1.  cd $(FLUOROSCOPY)
        2.  make clean_all
        3.  make plugins
        4.  make create_drr
        5.  cd $(FLUOROSCOPY)/source
        6.  ./create_target_drr
            $(FLUOROSCOPY)/lib/libs_generate_drr_raytracing.so
            $(FLUOROSCOPY)/images/really_small_cube.txt
            128
            $(FLUOROSCOPY)/images/drr_image.txt
            60 30 45 8 17 22
        7.  cd $(FLUOROSCOPY)
        8.  make clean_create_drr
        9.  make main CC=gcc
        10. fluoro_s $(FLUOROSCOPY)/lib/libs_search_bees_6d.so
            $(FLUOROSCOPY)/config/<config file>

    B. Steps for the parallel program:
        1. make clean_all
        2. make plugins
        3. make create_drr
        4. cd $(FLUOROSCOPY)/source
        5. ./create_target_drr
            $(FLUOROSCOPY)/lib/libp_generate_drr_raytracing.so
            $(FLUOROSCOPY)/images/really_small_cube.txt
            128
            $(FLUOROSCOPY)/images/drr_image.txt
            60 30 45 8 17 22
        6. cd $(FLUOROSCOPY)
        7. make clean_create_drr
        8. make main CC=mpicc
        9. fluoro_p $(FLUOROSCOPY)/lib/libp_search_bees_6d.so
            $(FLUOROSCOPY)/config/<config file>

    Note: The main differences between sequential and
    parallel executions are in the .so library names
    and the executable names.
--------------------------------------------------------
```

APPENDIX B

CODE DOCUMENTATION

This appendix chapter consists of the source code documentation for the essential components of the code. This documentation is extracted from the code with the help of a tool called *Doxygen*.

B.1 Data Structure Documentation

The following sections from Section B.2 to B.9 provide the main data structures used in the implementation of this thesis. Sections B.2 to B.6 are used in the fluoroscopic analysis process, Section B.7 is used in the configuration file reader program, and Section B.8 and B.9 are used in the SI search algorithms namely Bees algorithm and PSO method respectively.

B.2 _ctVolume Struct Reference

B.2.1 Detailed Description

This struct represents a 3-D Computer Tomography volume information used in the experimental fluoroscope.

Data Fields

- **double * volume**
- **int size**
- **double width**
- **double height**
- **double length**
- **float cam_to_table**
- **double cube_adjust [3]**
- **double cube_offset [3]**
- **int origin [3]**
- **double far_corner [3]**
- **double dimension [3]**

B.2.2 Field Documentation

B.2.2.1 float _ctVolume::cam_to_table

Distance between the camera and the fluoroscope table

B.2.2.2 double _ctVolume::cube_adjust[3]

CT cube adjustment buffer

B.2.2.3 double _ctVolume::cube_offset[3]

CT cube offset (x,y,z translations from the origin)

B.2.2.4 double _ctVolume::dimension[3]

CT volume dimensions

B.2.2.5 double _ctVolume::far_corner[3]

Coordinates of far corner of the CT cube

B.2.2.6 double _ctVolume::height

CT volume height in cm

B.2.2.7 double _ctVolume::length

CT volume length in cm

B.2.2.8 int _ctVolume::origin[3]

CT cube origin coordinates(x,y,z), in pixels

B.2.2.9 int _ctVolume::size

number of elements in volume

B.2.2.10 double* _ctVolume::volume

3-D CT volume data

B.2.2.11 double _ctVolume::width

CT volume width in cm

The documentation for this struct was generated from the following file:

- **fluoro.h**

B.3 _drrImage Struct Reference

B.3.1 Detailed Description

This struct represents the DRR image.

Data Fields

- **int n**
- **int m**
- **double $**$ image**

B.3.2 Field Documentation

B.3.2.1 double$**$ _drrImage::image

2-D image

B.3.2.2 int _drrImage::m

Number of rows

B.3.2.3 int _drrImage::n

Number of columns

The documentation for this struct was generated from the following file:

- **fluoro.h**

B.4 _film Struct Reference

B.4.1 Detailed Description

This struct represents the film in the experimental fluoroscope.

Data Fields

- **double size**
- **double resolution**
- **double dist**
- **double table_to_film**
- **double pixel_size**
- **double offset [3]**
- **double center [3]**
- **double rotation**
- **double azimuth**
- **double elevation**
- **double distance**

B.4.2 Field Documentation

B.4.2.1 double _film::azimuth

Film azimuth

B.4.2.2 double _film::center[3]

B.4.2.3 double _film::dist

Distance

B.4.2.4 double _film::distance

Distance

B.4.2.5 double _film::elevation

Film elevation

B.4.2.6 double _film::offset[3]

Film offset (x,y,z)

B.4.2.7 double _film::pixel_size

Pixel size

B.4.2.8 double _film::resolution

Pixel resolutions

B.4.2.9 double _film::rotation

Film rotation

B.4.2.10 double _film::size

Size of the film

B.4.2.11 double _film::table_to_film

Distance between the film and the fluoroscopic table

The documentation for this struct was generated from the following file:

- **fluoro.h**

B.5 _camera Struct Reference

B.5.1 Detailed Description

This struct represents the X-ray camera in the experimental fluoroscope.

Data Fields

- **int camera_to_table**
- **double azimuth**
- **double elevation**
- **double dist**
- **double offset [3]**
- **double coord [3]**

B.5.2 Field Documentation

B.5.2.1 double _camera::azimuth

Camera azimuth

B.5.2.2 int _camera::camera_to_table

Distance between the camera and the fluoroscopic table

B.5.2.3 double _camera::coord[3]

Camera coordinates

B.5.2.4 double _camera::dist

Camera distance

B.5.2.5 double _camera::elevation

Camera elevation

B.5.2.6 double _camera::offset[3]

Camera offset

The documentation for this struct was generated from the following file:

- **fluoro.h**

B.6 _edges Struct Reference

B.6.1 Detailed Description

This struct represents the filtered DRR image that consists of edges of the image.

Data Fields

- **int n**
- **int m**
- **double** ∗∗ **image**

B.6.2 Field Documentation

B.6.2.1 double∗∗ _edges::image

2-D image

B.6.2.2 int _edges::m

Number of rows

B.6.2.3 int _edges::n

Number of columns

The documentation for this struct was generated from the following file:

- **fluoro.h**

B.7 _dict Struct Reference

B.7.1 Detailed Description

This struct defines a dictionary to hold the key-value pairs of a configuration item present in a config file.

Data Fields

- **char key [MAX_VALUE_LEN]**
- **char value [MAX_VALUE_LEN]**

B.7.2 Field Documentation

B.7.2.1 char _dict::key[MAX_VALUE_LEN]

Configuration item key

B.7.2.2 char _dict::value[MAX_VALUE_LEN]

Configuration item value

The documentation for this struct was generated from the following file:

- **config_reader.h**

B.8 _bee Struct Reference

B.8.1 Detailed Description

This data structure represent a Bee in the Bees Algorithm. Each bee that is involved in the search for the right drr image, is associated with the values for orientation of camera and film, offset of the cube and score of the resulting DRR image, at a given time.

Data Fields

- **double orientation [3]**
- **double offset [3]**
- **double score**
- **int finesearch**
- **int rank**

B.8.2 Field Documentation

B.8.2.1 double _bee::orientation

Represents the orientation of the camera (az and el) and the film (rt)

B.8.2.2 int _bee::finesearch

Indicates whether the bee will next search around the previous values or in random. Value is either 1 or 0

B.8.2.3 double _bee::offset

Represents the cube offset values

B.8.2.4 int _bee::rank

Represents the ranking of the bee based on the score value

B.8.2.5 double _bee::score

Represents the score of the resulting DRR image

The documentation for this struct was generated from the following files:

- **search_parallel_bees.c**
- **search_sequential_bees.c**

B.9 _particle Struct Reference

B.9.1 Detailed Description

This data structure represent a particle in the Particle Swarm Optimization methos. Each particle that is involved in the search for the right DRR image, is associated with the values for orientation of camera and film, offset of the cube and score of the resulting DRR image, at a given time.

Data Fields

- **double orientation [3]**
- **double offset [3]**
- **double score**

B.9.2 Field Documentation

B.9.2.1 double _particle::orientation

Represents the orientation of the camera(az and el) and film(rt)

B.9.2.2 double _particle::offset

Represents the cube offset values

B.9.2.3 double _particle::score

Represents the score of the resulting DRR image

The documentation for this struct was generated from the following files:

- **search_parallel_pso.c**

- **search_sequential_pso.c**

B.10 Plugin Interface Documentation

The following sections from Section B.11 to B.13 provide the details of the header files used as interfaces to the plugins to the fluoroscopic project. Implementation of fluoroscopic analysis requires algorithms to be implemented using these interfaces. The algorithm implementation will define all the functions declared in the corresponding header file. This makes it possible for any algorithm that implements this interface to fit into main fluoroscopic analysis program. Provisions have been made to specify which algorithm to use during run time of the main program.

B.11 generate_drr.h File Reference

B.11.1 Detailed Description

This header file provides an interface for implementing an algorithm for generating Digitally Reconstructed Radiograph images from a given CT image.

Typedefs

- **typedef void ∗ CT_Volume_Ptr**
- **typedef void ∗ Drr_Image**

Functions

- **void generate_drr (double camera_azimuth, double camera_elevation, double film_rotation, double cube_offset[ ], CT_Volume_Ptr cube, Drr_Image out_drr_-image)**

B.11.2 Typedef Documentation

B.11.2.1 typedef void ∗ CT_Volume_Ptr

This typedef is used to define a CT volume.

B.11.2.2 typedef void ∗ Drr_Image

This typedef is used to define a DRR image.

B.11.3 Function Documentation

B.11.3.1 void generate_drr (double *azimuth*, double *elevation*, double *rotation*, double *offset*[ ], void ∗ *_cube*, void ∗ *_drr_image*)

This function creates a DRR model.

Parameters:

azimuth Azimuth angle of the camera

elevation Elevation angle of the camera

rotation Rotation angle of the film

offset x,y,z offsets of the CT cube

_cube 3-D CT volume data

_drr_image Pointer to the generated output DRR image [output parameter]

Returns:

Void

B.12 filter.h File Reference

B.12.1 Detailed Description

This header file provides an interface for implementing an algorithm for filtering X-ray images to extract required information from an image.

Typedefs

- **typedef void $*$ Filter_Image**

Functions

- **Filter_Image filter (Filter_Image image)**

B.12.2 Typedef Documentation

B.12.2.1 typedef void $*$ Filter_Image

This typedef is used to define an image.

B.12.3 Function Documentation

B.12.3.1 Filter_Image filter (void $*$ *image*)

Filters the input image and provides an image with only the requires features of the input image.

Parameters:

image Image to be filtered

Returns:

Filtered image

B.13 match.h File Reference

B.13.1 Detailed Description

This header file provides an interface for implementing an algorithm for matching or comparing two images.

Typedefs

- **typedef void $*$ Match_Image**

Functions

- **double match (Match_Image ref_image, Match_Image target_image)**

B.13.2 Typedef Documentation

B.13.2.1 typedef void $*$ Match_Image

This typedef is used to define an image.

B.13.3 Function Documentation

B.13.3.1 double match (void $*$ *ref_image*, void $*$ *target_image*)

Computes the score of an image. This routine is intended to be used after an image has been filtered using a sobel operator for black and white images.

Parameters:

ref_image	Reference Contour image
target_image	Target Contour image

Returns:

Score value between 0 and 1

B.14 search.h File Reference

B.14.1 Detailed Description

This header file provides an interface for implementing a search algorithm for searching the position and orientation information with a given CT image and configuration information required for the algorithm.

Typedefs

- **typedef void ∗ Search_CT_Volume_Ptr**

Functions

- **void search (Search_CT_Volume_Ptr cube, FILE ∗search_config_filename)**

B.14.2 Typedef Documentation

B.14.2.1 typedef void∗ Search_CT_Volume_Ptr

B.14.3 Function Documentation

B.14.3.1 void search (void ∗ *_cube*, FILE ∗ *config_file*)

This function attempts to search for an fluoroscopy image. The search algorithm is based on a Bees algorithm, where random camera positions are tried until a close match is found.

Parameters:

_cube Pointer to the CT_VOLUME

config_file Pointer to the open file containing all the configuration values required for this algorithm

Returns:

Void

B.15 Source File Documentation

The following sections from Section B.16 to B.31 provide the details of the source files included in this thesis.

Section B.16 contains information about the program that is used to create a DRR image from a given CT image along with position and orientation data. This program is kept separate from the rest of the fluoroscopic analysis code, so that, required DRR images can be created beforehand and used as input to the main fluoroscopy program. Images once created and stored, need not be recreated during each program execution.

Section B.17 contains information about the program which is the main entry point to the entire fluoroscopic analysis process. Sections B.21 to B.31 provide information about the plugins that implement the interfaces defined in Sections B.11 to B.13

B.16 create_target_drr.c File Reference

B.16.1 Detailed Description

This program is used to generate a DRR image from the specified orientation and offset configuration inputs for a given CT image. USAGE: <ProgramName> <PathToGenerate-DrrPlugin> <PathToCTImageFile> <Resolution> <PathToOutputFile> [<Azimuth> <Elevation> <Rotation> [<X_Offset> <Y_Offset> <Z_Offset>]]

Functions

- **static void print_usage (const char ∗appname)**
- **int main (int argc, char ∗argv[ ])**

Variables

- **void ∗ handle**
- **void(∗) generate_drr_function (double azimuth, double elevation, double rotation, double offset[ ], void ∗_cube, void ∗_drr_image)**
- **const char ∗ dlError**

B.16.2 Function Documentation

B.16.2.1 int main (int *argc*, char ∗ *argv*[ ])

This is the main function for creating DRR images from a given CT image. It is responsible for creating a drr image file from the specified orientation and position offset configuration inputs for a given CT image.

Parameters:

argc Number of command line parameters

argv Array of command line parameters

Returns:

0 on success, 1 on failure

B.16.2.2 static void print_usage (const char ∗ *appname*) `[static]`

Displays the command line parameters required for this program

Parameters:

appname Name of the program

Returns:

Void

B.16.3 Variable Documentation

B.16.3.1 const char∗ dlError

B.16.3.2 void(∗) generate_drr_function(double azimuth, double elevation, double rotation, double offset[ ], void ∗_cube, void ∗_drr_image)

B.16.3.3 void∗ handle

B.17 main.c File Reference

B.17.1 Detailed Description

This is the main entry point for the fluoroscopy program. This program is dependent on shared libraries for filtering and searching DRR images USAGE: <ProgramName> <PathToSearchPlugin> <PathToInputConfigFile>.

Functions

- **static void print_usage_exit (const char ∗appname)**
- **int main (int argc, char ∗argv[ ])**

Variables

- **void ∗ search_handle**
- **void(∗) search_function (void ∗, FILE ∗)**
- **const char ∗ dlError**

B.17.2 Function Documentation

B.17.2.1 int main (int *argc*, char ∗ *argv*[ ])

This is the main function for the fluoroscopy program.

- The input configuration file is parsed to extract the CT image file and the DRR image file.
- CT volume and DRR image are constructed from these two files.
- Following this the edges of the drr image are extracted.

- Using this as a target, a search for the orientation and the offset of the CT cube is begun.
- This function relies on shared libraries for filtering and searching which have to be provided while compiling this program.

Parameters:

argc Number of command line parameters

argv Array of command line parameters

Returns:

0 on success, 1 on failure

B.17.2.2 static void print_usage_exit (const char ∗ *appname*) `[static]`

Displays the command line parameters required for this program

Parameters:

appname Name of the program

Returns:

Void

B.17.3 Variable Documentation

B.17.3.1 const char∗ dlError

B.17.3.2 void(∗) search_function(void ∗, FILE ∗)

B.17.3.3 void∗ search_handle

B.18 write_image.c File Reference

B.18.1 Detailed Description

This file contains routines for writing matrices representing a CT cube and a DRR image to a text file.

Functions

- **void write_image (double ∗∗image, int m, int n, const char ∗filename)**
- **void write_array (double ∗array, int n, const char ∗filename)**
- **void write_drr (DRR_IMAGE ∗drr_image, const char ∗filename)**

B.18.2 Function Documentation

B.18.2.1 void write_array (double ∗ *array*, int *n*, const char ∗ *filename*)

Writes an array to a text file. Each value is delimited by a space

Parameters:

array Array of doubles

n Number of elements

filename File name to create and write into

Returns:

Void

B.18.2.2 void write_drr (DRR_IMAGE $*$ *drr_image*, const char $*$ *filename*)

Writes a DRR image to a text file. First two lines contain the number of rows and number of columns respectively. The image values are inserted from the third line. Each value is delimited by a space.

Parameters:

drr_image DRR image

filename File name to create and write into

Returns:

Void

B.18.2.3 void write_image (double $**$ *image*, int *m*, int *n*, const char $*$ *filename*)

Writes an image array to a text file. Each value is delimited by a space

Parameters:

image Image array (output parameter)

m Number of rows

n Number of columns

filename File name to create and write into

Returns:

Void

B.19 util.c File Reference

B.19.1 Detailed Description

This file contains general application utility functions.

Functions

- **static void set_volume_defaults (CT_VOLUME ∗volume)**
- **FILM ∗ create_film ()**
- **void free_film (FILM ∗film)**
- **CAMERA ∗ create_camera ()**
- **void free_camera (CAMERA ∗cam)**
- **DRR_IMAGE ∗ alloc_drr (int m, int n)**
- **DRR_IMAGE ∗ create_drr (const char ∗filename)**
- **void free_drr (DRR_IMAGE ∗drr)**
- **CT_VOLUME ∗ create_volume (const char ∗filename)**
- **void free_volume (CT_VOLUME ∗volume)**
- **double ∗∗∗ alloc_dcube (int m, int n, int p)**
- **void free_dcube (double ∗∗∗cube)**
- **double ∗∗ alloc_dmat (int m, int n)**
- **void free_dmat (double ∗∗dmat)**
- **void ∗ xmalloc (size_t bytes)**
- **double xrandom ()**
- **double yrandom ()**
- **int zrandom (double limit)**

- **double d_abs (double val)**

B.19.2 Function Documentation

B.19.2.1 double $***$ alloc_dcube (int *m*, int *n*, int *p*)

Allocates memory for a 3 dimensional array of doubles as a contiguous block of memory.

Parameters:

m Number of rows

n Number of columns

p Number of planes

Returns:

A 3-D array of doubles

B.19.2.2 double $**$ alloc_dmat (int *m*, int *n*)

Allocates memory for a 2 dimensional array of doubles as a contiguous block of memory.

ARGS: Number of rows Number of columns

Returns:

Data array(double)

B.19.2.3 DRR_IMAGE $*$ alloc_drr (int *m*, int *n*)

Allocates memory for a DRR image.

Parameters:

m Number of rows

n Number of columns

Returns:

Pointer to a DRR_IMAGE object

B.19.2.4 CAMERA $*$ create_camera ()

Creates a new CAMERA object.

Returns:

Pointer to a new CAMERA object

B.19.2.5 DRR_IMAGE $*$ create_drr (const char $*$ *filename*)

Creates an DRR image initialized by the data contained in the specified file.

Parameters:

filename Name of the file containing the DRR_IMAGE data

Returns:

Pointer to a DRR_IMAGE object

B.19.2.6 FILM $*$ create_film ()

Creates a FILM object.

Returns:

Pointer to a new FILM object

B.19.2.7 CT_VOLUME $*$ create_volume (const char $*$ *filename*)

Creates an volume object initialized by the data contained in the specified file.

Parameters:

filename Name of the file containing the CT volume data

Returns:

Pointer to a CT_VOLUME object

B.19.2.8 double d_abs (double *val*)

Returns the absolute value.

Parameters:

val Input value

Returns:

Absolute value

B.19.2.9 void free_camera (CAMERA $*$ *cam*)

Frees up the CAMERA object.

Parameters:

cam Pointer to a CAMERA object

Returns:

Void

B.19.2.10 void free_dcube (double $***$ *cube*)

Frees a dcube object.

Parameters:

cube Pointer to a dcube

Returns:

Void

B.19.2.11 void free_dmat (double $**$ *dmat*)

Frees a dmat object.

Parameters:

dmat Pointer to a dmat object to free

Returns:

Void

B.19.2.12 void free_drr (DRR_IMAGE $*$ *drr*)

Frees memory allocated for a DRR_IMAGE object.

Parameters:

drr Pointer to a DRR_IMAGE

Returns:

Void

B.19.2.13 void free_film (FILM ∗ *film*)

Frees a FILM object.

Parameters:

film Pointer to a FILM object

Returns:

void

B.19.2.14 void free_volume (CT_VOLUME ∗ *volume*)

Frees memory for a CT_VOLUME object.

Parameters:

volume Pointer to a CT_VOLUME object

Returns:

Void

B.19.2.15 static void set_volume_defaults (CT_VOLUME ∗ *volume*) `[static]`

Initializes the default values for the volume object.

Parameters:

volume Pointer to the CT volume

Returns:

void

B.19.2.16 void $*$ xmalloc (size_t *bytes*)

Allocates memory. If memory allocation fails, the application will abort.

Parameters:

bytes Number of bytes to allocate

Returns:

Pointer to a chunk of memory

B.19.2.17 double xrandom ()

Generates a random number (double) between 0 and 1. It is always positive

Returns:

Random number (double)

B.19.2.18 double yrandom ()

Generates a random number (double) between 0 and 1. It can be a positive or a negative number. The positiveness or negativeness is also generated randomly.

Returns:

Random number (double)

B.19.2.19 int zrandom (double *limit*)

Generates a random number (int) that lies within the specified limit. It can be a positive or a negative number. The positiveness or negativeness is also generated randomly.

Returns:

Random number (int)

B.20 config_reader.c File Reference

B.20.1 Detailed Description

This file contains functions to extract the configuration information from a file consisting of key-value pairs in a suitable format. Example for a configuration item: 'MAX_ITER=500', where MAX_ITER is the key and 500 is the value.

Functions

- **void read_config (FILE ∗config)**
- **void print_dict ()**
- **int get_config_value (char ∗key, char ∗∗value)**

B.20.2 Function Documentation

B.20.2.1 void get_config_value (char ∗ *key*, char ∗∗ *value*)

Searches for the given key in the dictionary of configuration items and returns 1 or 0 to indicate the success of the search. It also returns the value through the output parameter.

Parameters:

key String that denotes the key to be searched for in the configuration.

value This will hold the value associated with the key as a result of this operation.

Returns:

1 if key-value pair is found, 0 otherwise.

B.20.2.2 void print_dict ()

Prints the configuration dictionary contents in the form of key-value pairs.

Returns:

void

B.20.2.3 void read_config (FILE $*$ *config*)

Reads the configuration file and constructs a dictionary of key-value pairs for each configuration item.

Parameters:

config FilePointer to the configuration file

Returns:

void

B.21 generate_drr.c File Reference

B.21.1 Detailed Description

This file implements the interface **generate_drr.h** (p. 91). This file contains utility routines for creating Digitally Reconstructed Radiograph (DRR) images. It contains the routine for creating a DRR model which includes setting up the point on a film array and uses ray tracing to create a DRR image for the given orientation and offset values.

Functions

- **static void sph2cart (double theta, double phi, double rho, double cart[ ])**
- **void generate_drr_helper (CAMERA ∗cam, CT_VOLUME ∗cube, double ∗∗∗film_array, int m, int n, int p, DRR_IMAGE ∗drr_image)**
- **void generate_drr (double azimuth, double elevation, double rotation, double offset[ ], void ∗_cube, void ∗_drr_image)**

B.21.2 Function Documentation

B.21.2.1 void generate_drr (double *azimuth*, double *elevation*, double *rotation*, double *offset*[ ], void ∗ *_cube*, void ∗ *_drr_image*)

This function creates a DRR model.

Parameters:

azimuth Azimuth angle of the camera

elevation Elevation angle of the camera

rotation Rotation angle of the film

offset x,y,z offsets of the CT cube

_cube 3-D CT volume data

_drr_image Pointer to the generated output DRR image [output parameter]

Returns:

Void

B.21.2.2 void generate_drr_helper (CAMERA $*$ *cam*, CT_VOLUME $*$ *cube*, double $***$ *film_array*, int *m*, int *n*, int *p*, DRR_IMAGE $*$ *drr_image*)

This is a helper function that calls the ray tracing routine to create a DRR image from the given information.

Parameters:

cam Pointer to camera orientation

cube Pointer to a CT volume

film_array Pointer to a 3D array containing points on a film

m Number of rows

n Number of columns

p Depth of the array

drr_image Pointer to the DRR image [output parameter]

Returns:

Void

B.21.2.3 static void sph2cart (double *theta*, double *phi*, double *rho*, double *cart*[ ]) `[static]`

This function converts spherical coordinates to Cartesian coordinates.

Parameters:

theta Value of theta

phi Value of phi

rho Value of rho

cart Array for 3-D Cartesian coordinates [output parameter]

Returns:

Void

B.22 ray_tracing.c File Reference

B.22.1 Detailed Description

This file implements Siddon's ray tracing algorithm". Ray tracing involves constructing a DRR from a CT image by calculating the radiological path through a three-dimensional CT array.

Functions

- **void trace_CT (double ∗cam_pt, double ∗film_array, int ∗film_dims, double ∗CT_image, double ∗N_vox, double ∗CT_size, int ∗CT_orig, double ∗DRR_out_-im)**

Variables

- **const int ∗ film_dims**

B.22.2 Function Documentation

B.22.2.1 void trace_CT (double ∗ *cam_pt*, double ∗ *film_array*, int ∗ *film_dims*, double ∗ *CT_image*, double ∗ *N_vox*, double ∗ *CT_size*, int ∗ *CT_orig*, double ∗ *DRR_out_im*)

B.22.3 Variable Documentation

B.22.3.1 const int∗ film_dims

B.23 filter_sobel_bw.c File Reference

B.23.1 Detailed Description

This file implements the interface "filter.h". It is the plugin for filtering using Sobel algorithm for black and white values.

Functions

- **static int $**$ conv2d (double $**$image, int num_rows, int num_cols, const int filter_kernal[ ][3], int fk_row, int fk_col)**
- **void $*$ filter (void $*$image)**

Variables

- **static const int x_filt [ ][3]**
- **static const int y_filt [ ][3]**
- **static const int d1_filt [ ][3]**
- **static const int d2_filt [ ][3]**

B.23.2 Function Documentation

B.23.2.1 static int $**$ conv2d (double $**$ *image*, int *num_rows*, int *num_cols*, const int *filter_kernal*[ ][3], int *fk_row*, int *fk_col*) `[static]`

Function for two dimensional convolution: g(x,y) = SUM{ SUM{ w(s,t)f(x+s,y+t), t=-b..b}, s=-a..a}

Parameters:

image 2-D image array

num_rows Number of rows in image array

num_cols Number of cols in image array

filter_kernal 2-D filter kernal

fk_row Number of rows in filter kernal

fk_col Number of cols in filter kernal

Returns:

Weighted average value

B.23.2.2 Filter_Image filter (void * *image*)

Filters the input image and provides an image with only the requires features of the input image.

Parameters:

image Image to be filtered

Returns:

Filtered image

B.23.3 Variable Documentation

B.23.3.1 const int d1_filt[ ][3] `[static]`

B.24 filter_sobel_gs.c File Reference

B.24.1 Detailed Description

This file implements the interface "filter.h". It is the plugin for filtering using Sobel algorithm for grayscale values.

Functions

- **static int $**$ conv2d (double $**$image, int num_rows, int num_cols, const int filter_kernal[ ][3], int fk_row, int fk_col)**
- **void $*$ filter (void $*$image)**

Variables

- **static const int x_filt [ ][3]**
- **static const int y_filt [ ][3]**
- **static const int d1_filt [ ][3]**
- **static const int d2_filt [ ][3]**

B.24.2 Function Documentation

B.24.2.1 static int $**$ conv2d (double $**$ *image*, int *num_rows*, int *num_cols*, const int *filter_kernal*[ ][3], int *fk_row*, int *fk_col*) `[static]`

Function for two dimensional convolution: g(x,y) = SUM{ SUM{ w(s,t)f(x+s,y+t), t=-b..b}, s=-a..a}

Parameters:

image 2-D image array

num_rows Number of rows in image array

num_cols Number of cols in image array

filter_kernal 2-D filter kernal

fk_row Number of rows in filter kernal

fk_col Number of cols in filter kernal

Returns:

Weighted average value

B.24.2.2 void∗ filter (void ∗ *image*)

Filters the input image and provides an image with only the requires features of the input image.

Parameters:

image Image to be filtered

Returns:

Filtered image

B.24.3 Variable Documentation

B.24.3.1 const int d1_filt[ ][3] `[static]`

B.25 match_contour_bw.c File Reference

B.25.1 Detailed Description

Provides contour matching for black and white images. This file implements the interface ”match.h”. It uses contour matching algorithm for comparing two black and white contour images.

Functions

- **double match (void ∗image, void ∗target_image)**

B.25.2 Function Documentation

B.25.2.1 double match (void ∗ *image*, void ∗ *target_image*)

Computes the score of an image. This routine is intended to be used after an image has been filtered using a sobel operator for black and white images.

Parameters:

image Reference Contour image

target_image Target Contour image

Returns:

Score value between 0 and 1

B.26 match_contour_gs.c File Reference

B.26.1 Detailed Description

Provides contour matching for grayscale images. This file implements the interface ”match.h”. It uses contour matching algorithm for comparing two grayscale contour images.

Functions

- **double match (void ∗image, void ∗target_image)**

B.26.2 Function Documentation

B.26.2.1 double match (void ∗ *image*, void ∗ *target_image*)

Computes the score of an image. This routine is intended to be used after an image has been filtered using a sobel operator for black and white images.

Parameters:

image Reference Contour image

target_image Target Contour image

Returns:

Score value between 0 and 1

B.27 search_sequential_montecarlo.c File Reference

B.27.1 Detailed Description

This file implements the interface 'search.h using Monte Carlo search technique. This is a sequential program that contains routines for attempting to find a fluoroscopy image frame by deriving a matching DRR image from a CT volume. Monte Carlo method is used to achieve this. This program depends on libraries for filtering and matching a DRR image.

Functions

- **static double get_score (double cam[ ], double offset[ ], double step[ ], EDGES ∗t_edges, CT_VOLUME ∗cube)**
- **void search (void ∗_cube, FILE ∗config_file)**

Variables

- **void ∗ generate_drr_handle**
- **void ∗ filter_handle**
- **void ∗ match_handle**
- **void(∗) generate_drr_function (double, double, double, double[ ], void ∗, void ∗)**
- **void ∗(∗) filter_function (void ∗)**
- **double(∗) match_function (void ∗, void ∗)**
- **const char ∗ dlError**
- **double offset [3] = {0,0,0}**

B.27.2 Function Documentation

B.27.2.1 static double get_score (double *cam*[ ], double *offset*[ ], double *step*[ ], EDGES ∗ *t_edges*, CT_VOLUME ∗ *cube*) `[static]`

Creates a DRR image for the given orientation and offset and returns its score as compared to the target DRR image.

Parameters:

cam Camera coordinates for the required DRR image

offset Cube offsets for the required DRR image

step Camera offset step values for the required DRR image

t_edges Pointer to the edges of the target DRR image

cube Pointer to the CT volume data

Returns:

Image score

B.27.2.2 void search (void ∗ *_cube*, FILE ∗ *config_file*)

This function attempts to search for an fluoroscopy image. The search algorithm is based on a Bees algorithm, where random camera positions are tried until a close match is found.

Parameters:

_cube Pointer to the CT_VOLUME

config_file Pointer to the open file containing all the configuration values required for this algorithm

Returns:

Void

B.27.3 Variable Documentation

B.27.3.1 const char$*$ dlError

B.27.3.2 void$*$($*$) filter_function(void $*$)

B.27.3.3 void $*$ filter_handle

B.27.3.4 void($*$) generate_drr_function(double, double, double, double[ ], void $*$, void $*$)

B.27.3.5 void$*$ generate_drr_handle

B.27.3.6 double($*$) match_function(void $*$, void $*$)

B.27.3.7 void $*$ match_handle

B.27.3.8 double offset[3] = {0,0,0}

B.28 search_sequential_bees.c File Reference

B.28.1 Detailed Description

This file implements the interface 'search.h' using Bees Algorithm. This is a sequential program that contains routines for attempting to find a fluoroscopy image frame by deriving a matching DRR image from a CT volume. Bees algorithm is used to achieve this. This program depends on libraries for filtering and matching a DRR image.

Data Structures

- **struct _bee**

Typedefs

- **typedef _bee bee**
- **typedef _bee * BeePtr**

Functions

- **static BeePtr create_bee ()**
- **static void copy_bee (BeePtr from_bee, BeePtr to_bee)**
- **static void free_bee (BeePtr the_bee)**
- **static double get_score (BeePtr the_bee, EDGES *t_edges, CT_VOLUME *cube)**
- **static void print_info (long iteration, int bee_id, BeePtr the_bee, char *msg)**
- **void search (void *_cube, FILE *config_file)**

Variables

- **void ∗ generate_drr_handle**
- **void ∗ filter_handle**
- **void ∗ match_handle**
- **void(∗) generate_drr_function (double, double, double, double[ ], void ∗, void ∗)**
- **void ∗(∗) filter_function (void ∗)**
- **double(∗) match_function (void ∗, void ∗)**
- **const char ∗ dlError**

B.28.2 Typedef Documentation

B.28.2.1 typedef struct _bee bee

B.28.2.2 typedef struct _bee∗ BeePtr

B.28.3 Function Documentation

B.28.3.1 static void copy_bee (BeePtr *from_bee*, BeePtr *to_bee*) `[static]`

Copies the values of one bee to another bee.

Parameters:

from_bee Pointer to the bee whose values are to be copied

to_bee Pointer to the bee whose values should be copied from the from_bee

Returns:

Void

B.28.3.2 static BeePtr create_bee () `[static]`

Creates a new bee and allocates memory to it. It also initializes all its members to 0.

Returns:

Pointer to a bee

B.28.3.3 static void free_bee (BeePtr *the_bee*) `[static]`

Deallocate the memory allocated to the bee.

Parameters:

the_bee Pointer to the bee

Returns:

Void

B.28.3.4 static double get_score (BeePtr *the_bee*, EDGES $*$ *t_edges*, CT_VOLUME $*$ *cube*) `[static]`

Creates a DRR image for the given orientation and offset and returns its score as compared to the target DRR image.

Parameters:

the_bee Pointer to the bee which contains the values of camera and film orientation, cube position offsets and score

t_edges Pointer to the edges of the target DRR image

cube Pointer to the CT volume data

Returns:

Image score

B.28.3.5 void print_info (long *iteration*, int *bee_id*, BeePtr *the_bee*, char ∗ *msg*) `[static]`

This function is used to print debug information. It is not a general purpose logger, but very specific to printing orientation and offset values for a specific bee at a specific iteration.

Parameters:

iteration Iteration of the search

bee_id Id of the bee whose info is to be printed

msg String that displays the message associated with the information

B.28.3.6 void search (void ∗ *_cube*, FILE ∗ *config_file*)

This function attempts to search for an fluoroscopy image. The search algorithm is based on a Bees algorithm, where random camera and film orientation and CT cube positions are tried until a close match is found.

Parameters:

_cube Pointer to the CT_VOLUME

config_file Pointer to the open file containing all the configuration values required for this algorithm

Returns:

Void

B.28.4 Variable Documentation

B.28.4.1 const char∗ dlError

B.28.4.2 void∗(∗) filter_function(void ∗)

B.28.4.3 void ∗ filter_handle

B.28.4.4 void(∗) generate_drr_function(double, double, double, double[ ], void ∗, void ∗)

B.28.4.5 void∗ generate_drr_handle

B.28.4.6 double(∗) match_function(void ∗, void ∗)

B.28.4.7 void ∗ match_handle

B.29 search_sequential_pso.c File Reference

B.29.1 Detailed Description

This file implements the interface 'search.h' using Particle Swarm Optimization method. This is a sequential program that contains routines for attempting to find a fluoroscopy image frame by deriving a matching DRR image from a CT volume. Particle Swarm Optimization algorithm is used to achieve this. This program depends on libraries for filtering and matching a DRR image.

Data Structures

- **struct _particle**

Typedefs

- **typedef _particle particle**
- **typedef _particle $*$ ParticlePtr**

Functions

- **static ParticlePtr create_particle ()**
- **static void copy_particle (ParticlePtr from_particle, ParticlePtr to_particle)**
- **static void free_particle (ParticlePtr the_particle)**
- **static double get_score (ParticlePtr the_particle, EDGES $*$t_edges, CT_-VOLUME $*$cube)**
- **static void print_info (long iteration, int neighborhood_id, int particle_id, ParticlePtr the_particle, char $*$msg)**
- **void search (void $*$_cube, FILE $*$config_file)**

Variables

- **void $*$ generate_drr_handle**
- **void $*$ filter_handle**
- **void $*$ match_handle**
- **void($*$) generate_drr_function (double, double, double, double[ ], void $*$, void $*$)**
- **void $*$($*$) filter_function (void $*$)**
- **double($*$) match_function (void $*$, void $*$)**
- **const char $*$ dlError**

B.29.2 Typedef Documentation

B.29.2.1 typedef struct _particle particle

B.29.2.2 typedef struct _particle$*$ ParticlePtr

B.29.3 Function Documentation

B.29.3.1 static void copy_particle (ParticlePtr *from_particle*, ParticlePtr *to_particle*) `[static]`

Copies the values of one particle to another particle.

Parameters:

from_particle Pointer to the particle whose values are to be copied

to_particle Pointer to the particle whose values should be copied from the from_-particle

Returns:

Void

B.29.3.2 static ParticlePtr create_particle () `[static]`

Creates a new particle and allocates memory to it. It also initializes all its members to 0.

Returns:

Pointer to a particle

B.29.3.3 static void free_particle (ParticlePtr *the_particle*) `[static]`

Deallocate the memory allocated to the particle.

Parameters:

the_particle Pointer to the particle

Returns:

Void

B.29.3.4 static double get_score (ParticlePtr *the_particle*, EDGES ∗ *t_edges*, CT_VOLUME ∗ *cube*) `[static]`

Creates a DRR image for the given orientation and offset and returns its score as compared to the target DRR image.

Parameters:

the_particle Pointer to the particle which contains the values of camera and film orientation,cube position offsets and score

t_edges Pointer to the edges of the target DRR image

cube Pointer to the CT volume data

Returns:

Image score

B.29.3.5 void print_info (long *iteration*, int *neighborhood_id*, int *particle_id*, ParticlePtr *the_particle*, char ∗ *msg*) `[static]`

This function is used to print debug information. It is not a general purpose logger, but very specific to printing orientation and offset values for a specific bee at a specific iteration.

Parameters:

iteration Iteration of the search

neighborhood_id ID of the particle's neighborhood

particle_id ID of the particle whose info is to be printed

the_particle Pointer to the particle

msg String that displays the message associated with the information

B.29.3.6 void search (void ∗ *_cube*, FILE ∗ *config_file*)

This function attempts to search for an fluoroscopy image. The search algorithm is based on a Bees algorithm, where random camera and film orientation and CT cube positions are tried until a close match is found.

Parameters:

_cube Pointer to the CT_VOLUME

config_file Pointer to the open file containing all the configuration values required for this algorithm

Returns:

Void

B.29.4 Variable Documentation

B.29.4.1 const char∗ dlError

B.29.4.2 void∗(∗) filter_function(void ∗)

B.29.4.3 void ∗ filter_handle

B.29.4.4 void(∗) generate_drr_function(double, double, double, double[ ], void ∗, void ∗)

B.29.4.5 void∗ generate_drr_handle

B.29.4.6 double(∗) match_function(void ∗, void ∗)

B.29.4.7 void ∗ match_handle

B.30 search_parallel_bees.c File Reference

B.30.1 Detailed Description

This file implements the interface ’search.h’ using Bees Algorithm. This is parallel program that contains routines for attempting to find a fluoroscopy image frame by deriving a matching DRR image from a CT volume. Bees algorithm is used to achieve this. This program depends on libraries for filtering and matching a DRR image.

Data Structures

- **struct _bee**

Typedefs

- **typedef _bee bee**
- **typedef _bee * BeePtr**

Functions

- **static BeePtr create_bee ()**
- **static void copy_bee (BeePtr from_bee, BeePtr to_bee)**
- **static void free_bee (BeePtr the_bee)**
- **static double get_score (BeePtr the_bee, EDGES *t_edges, CT_VOLUME *cube)**
- **static void print_info (long iteration, int bee_id, BeePtr the_bee, char *msg)**
- **void search (void *_cube, FILE *config_file)**

Variables

- **void * generate_drr_handle**
- **void * filter_handle**
- **void * match_handle**
- **void(*) generate_drr_function (double, double, double, double[ ], void *, void *)**
- **void *(*) filter_function (void *)**
- **double(*) match_function (void *, void *)**
- **const char * dlError**

B.30.2 Typedef Documentation

B.30.2.1 typedef struct _bee bee

B.30.2.2 typedef struct _bee* BeePtr

B.30.3 Function Documentation

B.30.3.1 static void copy_bee (BeePtr *from_bee*, BeePtr *to_bee*) `[static]`

Copies the values of one bee to another bee.

Parameters:

from_bee Pointer to the bee whose values are to be copied

to_bee Pointer to the bee whose values should be copied from the from_bee

Returns:

Void

B.30.3.2 static BeePtr create_bee () `[static]`

Creates a new bee and allocates memory to it. It also initializes all its members to 0.

Returns:

Pointer to a bee

B.30.3.3 static void free_bee (BeePtr *the_bee*) `[static]`

Deallocate the memory allocated to the bee.

Parameters:

the_bee Pointer to the bee

Returns:

Void

B.30.3.4 static double get_score (BeePtr *the_bee*, EDGES ∗ *t_edges*, CT_VOLUME ∗ *cube*) `[static]`

Creates a DRR image for the given orientation and offset and returns its score as compared to the target DRR image.

Parameters:

the_bee Pointer to the bee which contains the values of camera and film orientation,cube position offsets and score

t_edges Pointer to the edges of the target DRR image

cube Pointer to the CT volume data

Returns:

Image score

B.30.3.5 void print_info (long *iteration*, int *bee_id*, BeePtr *the_bee*, char ∗ *msg*) `[static]`

This function is used to print debug information. It is not a general purpose logger, but very specific to printing orientation and offset values for a specific bee at a specific iteration.

Parameters:

iteration Iteration of the search

bee_id Id of the bee whose info is to be printed

msg String that displays the message associated with the information

B.30.3.6 void search (void ∗ *_cube*, FILE ∗ *config_file*)

This function attempts to search for an fluoroscopy image. The search algorithm is based on a Bees algorithm, where random camera and film orientation and CT cube positions are tried until a close match is found.

Parameters:

_cube Pointer to the CT_VOLUME

config_file Pointer to the open file containing all the configuration values required for this algorithm

Returns:

Void

B.30.4 Variable Documentation

B.30.4.1 const char$*$ dlError

B.30.4.2 void$*$($*$) filter_function(void $*$)

B.30.4.3 void $*$ filter_handle

B.30.4.4 void($*$) generate_drr_function(double, double, double, double[ ], void $*$, void $*$)

B.30.4.5 void$*$ generate_drr_handle

B.30.4.6 double($*$) match_function(void $*$, void $*$)

B.30.4.7 void $*$ match_handle

B.31 search_parallel_pso.c File Reference

B.31.1 Detailed Description

This file implements the interface 'search.h' using Particle Swarm Optimization method. This is a parallel program that contains routines for attempting to find a fluoroscopy image frame by deriving a matching DRR image from a CT volume. Particle Swarm Optimization algorithm is used to achieve this. This program depends on libraries for filtering and matching a DRR image.

Data Structures

- **struct _particle**

Typedefs

- **typedef _particle particle**
- **typedef _particle * ParticlePtr**

Functions

- **static ParticlePtr create_particle ()**
- **static void copy_particle (ParticlePtr from_particle, ParticlePtr to_particle)**
- **static void free_particle (ParticlePtr the_particle)**
- **static double get_score (ParticlePtr the_particle, EDGES *t_edges, CT_-VOLUME *cube)**
- **static void print_info (long iteration, int neighborhood_id, int particle_id, ParticlePtr the_particle, char *msg)**
- **void search (void *_cube, FILE *config_file)**

Variables

- **void ∗ generate_drr_handle**
- **void ∗ filter_handle**
- **void ∗ match_handle**
- **void(∗) generate_drr_function (double, double, double, double[ ], void ∗, void ∗)**
- **void ∗(∗) filter_function (void ∗)**
- **double(∗) match_function (void ∗, void ∗)**
- **const char ∗ dlError**

B.31.2 Typedef Documentation

B.31.2.1 typedef struct _particle particle

B.31.2.2 typedef struct _particle∗ ParticlePtr

B.31.3 Function Documentation

B.31.3.1 static void copy_particle (ParticlePtr *from_particle*, ParticlePtr *to_particle*) `[static]`

Copies the values of one particle to another particle.

Parameters:

from_particle Pointer to the particle whose values are to be copied

to_particle Pointer to the particle whose values should be copied from the from_-particle

Returns:

Void

B.31.3.2 static ParticlePtr create_particle () `[static]`

Creates a new particle and allocates memory to it. It also initializes all its members to 0.

Returns:

Pointer to a particle

B.31.3.3 static void free_particle (ParticlePtr *the_particle*) `[static]`

Deallocate the memory allocated to the particle.

Parameters:

the_particle Pointer to the particle

Returns:

Void

B.31.3.4 static double get_score (ParticlePtr *the_particle*, EDGES ∗ *t_edges*, CT_VOLUME ∗ *cube*) `[static]`

Creates a DRR image for the given orientation and offset and returns its score as compared to the target DRR image.

Parameters:

the_particle Pointer to the particle which contains the values of camera and film orientation, cube position offsets and score

t_edges Pointer to the edges of the target DRR image

cube Pointer to the CT volume data

Returns:

Image score

B.31.3.5 void print_info (long *iteration*, int *neighborhood_id*, int *particle_id*, ParticlePtr *the_particle*, char ∗ *msg*) [static]

This function is used to print debug information. It is not a general purpose logger, but very specific to printing camera and film orientation and CT cube offset values for a specific bee at a specific iteration.

Parameters:

iteration Iteration of the search

neighborhood_id ID of the particle's neighborhood

particle_id ID of the particle whose info is to be printed

the_particle Pointer to the particle

msg String that displays the message associated with the information

B.31.3.6 void search (void ∗ *_cube*, FILE ∗ *config_file*)

This function attempts to search for an fluoroscopy image. The search algorithm is based on a Bees algorithm, where random camera and film orientation and CT cube positions are tried until a close match is found.

Parameters:

_cube Pointer to the CT_VOLUME

config_file Pointer to the open file containing all the configuration values required for this algorithm

Returns:

Void

B.31.4 Variable Documentation

B.31.4.1 const char$*$ dlError

B.31.4.2 void$*$($*$) filter_function(void $*$)

B.31.4.3 void $*$ filter_handle

B.31.4.4 void($*$) generate_drr_function(double, double, double, double[ ], void $*$, void $*$)

B.31.4.5 void$*$ generate_drr_handle

B.31.4.6 double($*$) match_function(void $*$, void $*$)

B.31.4.7 void $*$ match_handle