A view of using Computing Model in Medical Data Analysis

Ravi S Malashetty1, Dr Sanjaypande 2

1:Research scholar, 2:Research supervisor

Abstract: Many researchers have already taken interest in classification algorithm for finding the better predication rate and reduced error rate. Classification is a process to assign an object into predefined classes by evaluating their membership into class according to attribute values for that objects. For making significant improvement in classification process many researchers have employed different approaches and adopt different learning methods which are better than previous traditional approaches but very few researchers have tried for classification process preceded by clustering approach.

Rapid computer applications in medical areas provide many advantages in health care applications. Some applications include: telemedicine, medical image analysis, and databases on medical information such as medical record or medical image. Medical image analysis is related to the specific purposes of medical image that is one of diagnostic tools. X-Ray image is one kind of medical images used as diagnostic tools

Keywords: Tuberculosis, Computing model, Medical Imaging.

— — — — — — — — ◆ — — — — — — — — —

2.1. Introduction:

Medical diagnosis of diseases is one of the most foremost important issues in the healthcare unit. The medical industry is one of the new fields, which requires engineering technologies to access uncertain information objectively. With recent developments in medical engineering and other control areas have been achieved by state-of-art intelligent computing techniques ranging from computer-aided diagnosis, computer aided recognition, pattern recognition, bioinformatics, text categorization and intensive care unit. Making use of artificial intelligence, information processing, and data mining hold new strategies for approximate inference.

Artificial intelligence has witnessed an intensive research interest towards integrated different computing paradigms together including fuzzy logic, artificial neural network, and genetic algorithms. All these methodologies work together and provide flexible information capabilities from one form to another to handle real life ambiguous situations *[02]*. An emerging class of intelligent machines that could aid in physicians diagnosis is the development of clinical diagnosis decision support system. This clinical system is defined as a computer program designed to assist physicians and health experts in making clinical decision tasks. Clinical decision support system is broadly

classified as Knowledge-based clinical decision support system; Non-knowledge based clinical decision support system *[31]*.

2.2 Medical Overview:

One-third of the world's population is having latent TB, and it is estimated that nine million new cases occur every year. According to World Health Organization report, among 8.6 million tuberculosis positive cases, 2.2(25%) million cases are from India, which shows India is the world's highest tuberculosis burden country. Globally the mortality rate for TB is over 1.3 million people. Moreover it is very dangerous because it can be easily transmitted through air medium, when the sufferers are coughing, sneezing and speaking. Hence, the Tuberculosis disease becomes major problem to Indian Government *[50]***.**

In India, screening of tuberculosis patients is practiced as following methods are commonly used, chest x-ray, Computed tomography scan, MRI scan, ultrasound scan, biological culture, Mantoux test (tuberculosis skin test), interferon-γ test, nucleic acid amplification test and sputum smear microscopy. Of these tests, two tests are most common and conventional method. They are Biological culture and Sputum smear microscopy. For Biological culture test, the result can be viewed

only after four weeks. Since the need for earlier diagnosis of this disease, Sputum smear microscopy is typically used for rapid examination. Two common methods for identifying the TB bacilli through sputum smear microscopy: Auramine and ZeihlNeelson (ZN) method. For auramine stained sputum smear, fluorescent microscope is required.

Fluorescent microscope is difficult to install, very expensive and it needs very high maintenance. For ZN stain method, bright-field microscope is required. For bright field microscope, the installation is easy, low cost equipment and ease maintenance. Moreover, the staining procedure for ZN is cost effective than auramine method *[29]*.For economic concern, ZN staining method is suitable for rural areas. Moreover, some of the rural places from India facing problem as insufficient equipment, shortage of senior Pathologist and higher caseload which may arise happening of higher error for predicting the TB positive and negative cases. Moreover, to examine single slide under microscopy it takes about 2-3 hours.

Detection of bacteria is very important in order to prevent diseases and maintain health of the world's population. There are various types of bacteria. Some bacteria are beneficial to humans and some are harmful. Mycobacterium tuberculosis is one of the harmful bacteria which can be fatal to human's life, children and also to animals. Tuberculosis is an infectious disease that is a leading cause of death throughout the world especially when it occurs in HIV-infected patients *[33,38]*. It is a catastrophe because lots of people suffer and died because of this infectious disease. The World Health Organization has declared tuberculosis as a global public health emergency. It is reported that approximately 9.4 million tuberculosis cases occur globally in 2009 *[04]*.

In an effort to reduce the burden of tuberculosis disease in India, automated bacilli detection is introduced using ZN image. By using automated tuberculosis screening systems in ZN image the TB positive patients can be identified easily even without pathologist. The examination time also reduced which reduce the pathologist work burden. Since ZN is most conventional and inexpensive method which is suitable for Indian Government hospitals.

Detection of Tuberculosis Bacilli using Image Processing Techniques*[45]*.Tuberculosis (TB) is one of the major diseases and TB detection is based on sputum examination microscopically by using Ziehl-Neelsen stain (ZN-stain) method. This method needs human expertise and intensive examination. The availability of expertise, time and cost are the constraints of the human intervention based examinations. Therefore, there is a need of automation of examination and detection of TB bacteria using digital image of ZN-stain sample. In this paper, an algorithm based on image processing was developed for identification of TB bacteria in sputum. The method is based on Otsu thresholding and k-means clustering approach. The performance of clustering and thresholding algorithms for segmenting TB bacilli in tissue sections was compared. The developed automated technique shows good accuracy and efficiency.

Modeling TB dynamics has a long history, including mathematical models and analytical techniques to describe and predict disease prevalence at the population level *[49, 37, 09]*. Analytical studies, however, are usually restricted by their simplifying assumptions regarding the population heterogeneity, network structure, and parameters uncertainty, and do not provide a realistic representation of transmission dynamics.

Simulation modeling of TB epidemics in human populations, on the other hand, has a shorter history. One group of studies uses system dynamics to model disease prevalence at the population level *[05,01]*. Following a top-down approach, these studies divide the population into different health states, and use transition rates to describe the disease's natural history. A system of differential equations is used to model disease prevalence through time. In comparison to the analytical approach, such studies apply a semi-Markov system in which transition rates can change with time, and are able to capture output uncertainty.

Other researchers have developed discrete-event simulation (DES) models of TB to evaluate the impact of new diagnostic tools or to study more complex structure as in the confection

of HIV/TB *[23,34]*. The DES studies use a schedule of events that are executed in chronological order, and model disease transmission using random generation of Poisson distributions in each mixing group. The aggregate (top-bottom) modeling nature of DES, however, offers low flexibility for direct modeling of contacts (and transmission events) at the individual level, and restricts application of such models to complex social networks.

ABS is an alternative approach that models the system at the individual level and offers high flexibility to incorporate various modeling assumptions. ABS models have wide application in the social sciences *[17, 35]*, and the models have been applied to study various infectious diseases such as influenza *[10]*, smallpox *[32]* and HIV/AIDS. The literature on application of ABS models in the study of TB, however, is quite limited. *[16]* use an ABS approach to study the emergence of drug-resistant TB due to treatment with antibiotics. They assume a lattice structure for spatial presentation of their population and model TB transmission through local and global interactions across the lattice. The lattice structure, however, does not provide a realistic representation of social settings and cannot be used to study transmission dynamics at the individual level.

Chest X-rays (CXR) can be used for automatic detection of TB. Previous methods related to this work are also considered in this study. The purpose of the segmentation is to find corresponding regions within the lung fields. Segmentation of lung fields on PA chest radiographs has received considerable attention in the literature. ASMs have been developed *[14]* and have been applied to various segmentation tasks in medical imaging *[07]*. An object is described by points, referred to as landmark points. The landmark points are (manually) determined in a set of training images. From these collections of landmark points, a point distribution model is constructed. This method make use of active shape mode segmentation method *[06]* for segmenting the lung field. Since the presence of cavities in the upper thoracic area often suggests typical TB, automatic segmentation and classification of these cavities taking spatial,

geometric and demographic information into consideration is useful for a CAD system.

Active contour (AC) models (or snakes) *[26,48]* are commonly used as segmentation techniques for medical images, though prior knowledge of the region of interest (ROI) is often needed in order to guide the execution and successful convergence of these algorithms. AC models can be categorized into two types: level set and parametric. The convergence of level set techniques is usually slower than parametric methods because the deformation of a higher dimensional function is required *[XM-08]*.Besides, level set is very sensitive to noise resulting in the extraction of too many false objects. Given an initial contour, the external and internal forces of parametric snakes drive the evolution and converge to the final contour much faster than level set snakes.

Mean shift *[12]*is a feature space analysis technique that clusters neighboring data points with similar characteristics using a neighborhood search procedure, which locates the local maxima in a probability density function (PDF), based on the kernel density estimation (or Parzen window method). The mean shift segmentation is based on a recursive mean shift procedure If a cavity appears near the clavicles, it is very likely that the cavity is partially occluded, which makes the visible part of the cavity violate the circularity criterion. In addition, the radio-dense clavicles make the intensity distribution of lung fields near them quite different from other portions of the lung fields which may require a different GICOV threshold. Therefore, if no cavity is confirmed in the clavicle regions in second stage, those regions go through segmentation and classification stage (third stage), using new GICOV and circularity thresholds calculated for them *[18]*. In the hybrid scheme, GICOV algorithm for inner boundary features and circular measure for shape feature together for classification are used.

A region based active contour method for x-ray lung segmentation *[19]* work, a level set energy for segmenting the lungs from digital Posterior-Anterior (PA) chest x-ray images is presented. Segmentation using combined lung mask*[44]* use an average of three different masks

for lung segmentation: the intensity mask, the lung model mask, and the Log Gabor mask. A method called segmentation using serial chest radiographs *[52]* used two kinds of shape statistics, the population based and the patient-specific shape statistics.

The mechanism by which M. tuberculosis crosses the BBB into the CNS is not well characterized. Some have postulated that free bacilli traverse across the endothelial barrier, while others suggested that bacilli enter via the passage of infected macrophages. One method of examining this question is to develop an in vitro model of the BBB and evaluate how M. tuberculosis interacts with this barrier. Adapting an in vitro model used for examining other bacteria that cause meningitis*[27]*, used an in vitro monolayer of human brain microvascular endothelial cells and infected them with several strains of mycobacteria. They reported that M.tuberculosis H37Rv and CDC1551 were able to invade and traverse the endothelial monolayer, thus supporting the notion that extra-cellular mycobacteria are capable of traversing these highly specialized endothelial cells. However, while their in vitro model utilized brain microvascular endothelial cells, cells that form the brain side of the BBB (mainly astrocytes) were not included in the model, and thus, it is unclear what role these cells play in defense against entry into the brain parenchyma. Despite this, the model proposed by Jain et al. will go a long way toward understanding the important interaction of myco-bacteria and endothelial cells.

Automatic Tuberculosis Screening Using Chest Radiographs *[11]*, Tuberculosis is a major health threat in many regions of the world. Standard diagnostics still rely on methods and are slow and often unreliable. This paper presents an automated approach for detecting tuberculosis in anterior chest radiographs. The lung region has extracted using graph cut segmentation method. For this lung region, a set of texture and shape features was computed, which enable the X-rays to be classified as normal or abnormal using a binary classifier. The performance of the system depends on two datasets: a set collected by the tuberculosis control program, and a set collected by Shenzhen Hospital, China. An area is estimated under the ROC curve (AUC) of 87% (78.3% accuracy) for the first set, and an AUC of 90% (84% accuracy) for the second set. The system performance of the first set was compared with the performance of radiologists.

Detecting tuberculosis in radiographs using combined lung masks *[30]* Tuberculosis (TB) is a major health threat in many regions of the world, while diagnosing tuberculosis still remains a challenge. This paper presents an automated approach for detecting TB on conventional postero-anterior chest radiographs. The idea is to provide developing countries, which have limited access to radiological services and radiological expertise, with an inexpensive detection system that allows screening of large parts of the population in rural areas. In this paper, the results produced by the TB screening system were presented. A lung shape model, a segmentation mask, and a simple intensity model were combined to achieve better segmentation mask for the lung. With the improved masks, an area was achieved under the ROC curve of more than 83%, measured on data compiled within a tuberculosis control program.

Automatic identification techniques of tuberculosis bacteria *[13]* Tuberculosisis a serious illness which control is based on early diagnosis. A technique commonly used consists of analyzing sputum images for detecting bacilli. However, the analysis of sputum is quite expensive, time consuming and requires highly trained personnel to avoid errors. Image processing techniques provide a good tool for improving the manual screening of samples. In this paper, a new bacilli detection technique was proposed with the aim to attain a high specificity rate and therefore reducing the time required to analyze such sputum samples. This technique is based on the heuristic acknowledge extracted from the bacilli shape contour.

Agent-based modeling has been recently recognized as a method to overcome the translational gap in systems biology *[22]*. Agent-based models(ABM) are direct computational representations of discrete dynamics systems where the system level behaviors emerge from the local interaction of constituent entities called

agents. On a computer, agent are represented as concurrent objects whose state transitions are governed by rules. Agent-based modeling is well suited to capture the multi-scale nature of biological systems. ABMs are well suited to capture stochasticity, het-erogeneity, and hierarchy that is present in biological systems. Agent rules can be explicitly derived from the description of biological functions obtained through bench re-search. Unlike equation based modeling, ABMs are descriptive and it is easier for biologists with limited mathematical background to relate to this modeling technique. It has been previously used to simulate inflammatory cell tracking [47], to model tumor growth to simulate intracellular processes bio-molecular reactions, wound healing.

There is several research efforts related to ABM simulation on the GPU. [24] developed an extension of Cellular Automata called Coupled Lattice Maps to simulate boiling, react-diffusion, and convection. [28] developed a particle simulator implemented almost entirely on the GPU. For spawning, they used a CPU-based allocator. However, this allocator can be prohibitively time consuming for large model sizes. [36] developed a system to simulate crowd behaviors on the GPU. However, their work did not incorporate agent replication and collision avoidance.

More recently [41] developed an extended cellular automata approach to simulate several canonical ABMs on the GPU. While their technique did include collision avoidance, it does not incorporate replication. In addition, mobile agents are bound to lattice sites with a maximum of one agent per site. [42] have recently developed techniques to simulated agents in a grid-free environment. Their method is similar to many particle systems developed previously. However, their agents are able to communicate with each other in a user-defined radius.

The authors previously developed techniques for simulating large-scale ABMs on GPUs[46].They demonstrated their techniques by implementing a large-scale version of the Sugar Scape ABM. Their incorporated in-corporated features such as environmental resource growth, agent replacement, agent movement, agent mating, pollution formation, and pollution diffusion. They

develop a randomized memory allocator that executed entirely on the GPU. In addition, they developed a collision resolution algorithm based on z-culling. This work has greatly expanded the size and complexity of models that can be handled by performing all computations entirely on the GPU.

2.3. Technical Overview:

Tuberculosis is an infectious disease and in case of an epidemic the only option of diagnosis remains is the sputum examination. To improve the diagnostic process, an automated method was proposed for the detection of tuberculosis bacilli in clinical specimens, preferably sputum smears. The proposed method makes use of image processing techniques and neural network classifiers for the automatic identification of TB bacilli using auramine stained specimens of sputum. The developed system shows 93.5% sensitivity for identifying individual bacilli. There are numerous TB bacilli with active pulmonary TB in the patient's sputum. The overall diagnostic accuracy of the patients with positive smear is expected to be very high. Some potential benefits of automated screening for TB are accurate and rapid diagnosis increased population screening and reduced health risk [25].

Automated Tuberculosis Diagnosis Using Fluorescence Images from a Mobile Microscope [39] the most common method of tuberculosis (TB) diagnosis is visual identification of rod-shaped TB bacilli in sputum smears by microscope. An algorithm was proposed for automated TB detection in smear images taken by digital microscopes such as Cell Scope [11], a novel low-cost, portable device capable of bright field and fluorescence microscopy. Automated processing on such platforms could save lives by bringing healthcare to rural areas with limited access to laboratory-based diagnostics.

This algorithm is applied to morphological operations and template matching with a Gaussian kernel to identify TB-object candidates. The geometric, photometric, and oriented gradient features were used to characterize these objects and perform discriminative, support vector machine

classification. The algorithm is tested on a large set of cellscope fluorescence images from sputum smears collected at clinics in Uganda (594 images corresponding to 290 patients). The object-level classification is highly accurate, with average precision of 89:2% -2:1%. For slide-level classification, the algorithm performs at the level of human readers, demonstrating the potential for making a significant impact on global healthcare.

The main benefit of data pre-clustering is that it decomposes the heterogeneous dataset into smaller homogenous datasets such that data in each dataset shows higher similarity. Classification algorithms works well in homogeneous datasets in comparison to heterogeneous dataset so clustering before classification improves results. So if clustering will be more accurate than results can show significant improvements. So motive of this paper is to bring classification and clustering together with certain improvement in k-mean clustering algorithm *[15]*.

There are several clustering algorithms exist in research but k-mean algorithm is popular because of its simplicity for implementation and capability to produce good results. It is a partitioning based approach which divides dataset into predefined k partition known as clusters which have minimum intra cluster Euclidean distance. Although it is a basic algorithm but it has some shortcomings such as the result of the algorithm mostly depends upon initial value of centroid chosen for each cluster the other drawback is in error function of k-mean where several minima is are possible and can easily fall to local minima *[43, 03].*The objective of this paper is to combine clustering and classification with some improvement in k-mean algorithm. This presents a novel method by modifying in initial centroid selection technique of k-mean algorithm and then applying some well known classifier on clustered data. Clustering algorithm produces better results as compared to simple k-mean by using tuberculosis dataset*[03].*

A thoracic X-Ray image commonly is used by physician as diagnostic tool to find some diseases related to human lung, such as lung TB. Tuberculosis is a disease caused by an infection of Myobacterium tuberculosis *[40]*. It is a systemic disease that can strike any part of human organs with lung as the primary infection. In 2009, World Health Organization reported that Indonesia was the world's fifth largest TB patients population. To make an X-Ray image, the patient will need several days before receiving the result. X-Ray image need to be examined, diagnosed, and notated by radiologist before given to the patient. In Indonesia, the number of radiologist expert doesn't match the number of patient *[20]*. This condition makes the waiting time for patient to receive X-Ray images result relatively longer than those in advanced countries, especially for patient from remote areas in India.

2.4. Summary:

The paper presents an application based on pattern recognition to identify lung TB using computer. Identification using computer in this research is conduct using thoracic X-ray image of the patient also this paper makes is clear foundation base for taking up new avenues for computing tool in multi-displinary areas of chemical understanding of disease which plays a vital role in image understanding.

We have presented modeling using Fuzzy-clustering of data, Digitizing the Images, Use of Data-Mining, Modeling based on Statistical analysis and a specific case of understanding Pulmonary Tuberculosis.

REFERENCES (SAMPLE)

[1] Atun, R. A., R. M. Lebcir, F. Drobniewski, M. McKee, and R. J. Coker. 2007. "High Coverage With HAART is Required to Substantially Reduce the Number of Deaths from Tuberculosis: System Dy-namics Simulation." International Journal of STD and AIDS 18: 267-273.

[2] F. Amato, A. Lopez, E.M Pena-mendez, P. Vanhara, A. Hampl, "Artificial neural networks in Medical diagnosis," Journal of applied biomedicine, doi: 10.2478/v10136-012-0031-x, ISSN 1214-0287, pp. 47-58, 2013.

[3] K.S. Al-Sultan, "A Tabu Search Approach to the Clustering Problem," Pattern Recognition, vol.28, no.9, pp. 1443-1451, 1995.

[4] D. F. L. Blanc, C. Fitzpatrick, K. Floyd, I. Garcia, C. Gilpin, P. Glaziou, T. Hiatt, D. Sculier, C. Sismanidis, H. Timimi and M. Uplekar, "Global Tuberculosis Control, WHO report," 2010.

[5] Brewer, T. F., S. J. Heymann, G. A. Colditz, M. E. Wilson, K. Auerbach, D Kane, and H. V. Fineberg. 1996. "Evaluation of Tuberculosis Control Policies Using Computer Simulation."

Journal of the American Medical Association 23: 1898-1903.

[6] Bram van Ginneken, Shigehiko Katsuragawa, Bart M. ter Haar Romeny, KunioDoi, and Max A. Viergever, Member, IEEE, Automatic Detection of Abnormalities in Chest RadiographsUsing Local Texture Analysis, 2002.

[7] G. Behiels, D. Vandermeulen, F. Maes, P. Suetens, and P. Dewaele, Active shape model based segmentation of digital X-ray images, in Lecture Notes in Computer Science. Berlin, Germany: Springer-Verlag,1999,

[8] Campbell, J.B. 1996. Introduction to Remote Sensing. Taylor & Francis, London. ERDAS MAGINE 8.4 Field Guide: ERDAS Inc.

[9] Castillo-Chavez, C, and B. Song. 2004. "Dynamical Models of Tuberculosis and Their Applications." Mathematical Bioscience and Engineering 1: 361-404.

[10] Chao, D. L., M. E. Halloran, V. J. Obenchain, and I. M. Longini. 2010. "FluTE, a Publicly Available Sto-chastic Influenza Epidemic Simulation Model." PLoS Computational Biology 6: e1000656.

[11] S. Candemir, S. Jaeger, K. Palaniappan, S. Antani, and G. Thoma, "Graph-cut based automatic lung boundary detection in chest radiographs," in Proc. IEEE Healthcare Technol. Conf.: Translate. Eng. Health Med., 2012, pp. 31–34.

[12] D. Comaniciu and P. Meer, Mean shift: A robust approach toward feature space analysis, IEEE Trans. Pattern Anal. Mach. Intell., vol. 24, no. 5, May 2002

[13] S. Candemir, K. Palaniappan, and Y. Akgul, "Multi-class regularization parameter learning for graph cut image segmentation," in International Symposium on Biomedical Imaging, 2013, pp. 1473–1476.

[14] T. F. Cootes, C. J. Taylor, D. Cooper, and J. Graham,Active shape models and their training and application, Comput. Vis. Image Understanding,1995.

[15] T. Divya, and A. Sonali, "A survey on Data Mining approaches for Healthcare", International Journal of Bio-Science and Bio-Technology, vol. 5, no. 5, pp. 241-266, 2013.

[16] Espíndola, A. L., C.T. Bauch, B. C. T. Cabella, and A. S. Martinez. 2011. "An Agent-Based Computa-tional Model of the Spread of Tuberculosis." Journal of Statistical Mechanics: Theory and Experi-ment 5: P05003.

[17] Epstein, J. M. 1999. "Agent-Based Computational Models And Generative Social Science." Complexity 4: 41-60.

[18] V. Ezhil Swanly, L. Selvam, P. Mohan Kumar, J. Arokia Renjith, M. Arunachalam, and K. L. Shunmuganathan,Smart Spotting of Pulmonary TB Cavities Using CT Images,Computational and Mathematical Methods in Medicine Volume 2013,

[19] P. Annangi, S. Thiruvenkadam, A. Raja, Hao Xu, Xiwen Sun, Ling Mao,A region based active contour method for x-ray lung segmentation using prior shape and low level features,IEEE International Symposium on Biomedical Imaging , pp. 892-895, 2010

[20] Faisal A., "Radiologi dapat Digunakan untuk Terapi Belum Semua RS Miliki Alat Radiologi," Pusat Data & Informasi PERSI, http://www.pdpersi.co.id, accesed October 17th , 2011.

[21] M. G. Forero, F. Sroubek, and G. Cristóbal, "Identification of tuberculosis bacteria based on shape and color," Real-Time Imaging, vol. 10, pp. 251-262, 2004.

[22] GAn. Agent-based computer simulation and sirs: build-ing a bridge between basic science and clinical trials. Shock, 16(4):266–273, 2001.

[23] Hughes, G. R., C. S. M. Currie, and E. L. Corbett. 2006. "Modeling Tuberculosis In Areas of High HIV Prevalence." In Proceedings of the 2006 Winter Simulation Conference, edited by F. P. Wieland, J. Liu, B. G. Lawson, D. M. Nicol, and R. M. Fujimoto, eds L. F. Perrone, 459-465. Piscataway, New Jersey: Institute of Electrical and Electronics Engineers, Inc.

[24] M Harris, G. Coombe, T Scgeuermann, and A Lastra. Physically-based visual simulation on graphics hard-ware. In Proceedings Eurographics/SIGGRAPH Work-shop on Graphics Hardware, 2002.

[25] S. Jaeger, A. Karargyris, S. Antani, and G. Thoma, "Detecting tuberculosis in radiographs using combined lung masks," in Int. Conf. IEEE Engineering in Medicine and Biology Society (EMBS), 2012, pp. 4978–4981.

[26] K. Sum and P. Cheung, Boundary vector field for parametric active contours, Pattern Recognition .,vol. 40, no. 6, pp. 16351645, 2007.

[27] Kim, K. S. 2003. Pathogenesis of bacterial meningitis: from bacteraemia to neuronal injury. Nat. Rev. Neurosci. 4:376–385.

[28] A Kolb, L Latta, and C Rezk-Salama. Hardware-based simulation and collision detection for large particle sys-tems. In Proceedings of the ACM 2004 Graphics Hard-ware Conference, Grenoble, France, 2004.

[29] Khutlang, Rethabile "Classification of Mycobacterium tuberculosis in images of ZN-stained sputum smears." Information Technology in Biomedicine, IEEE Transactions on 14.4(2010): 949-957

[30] C. Leung, "Re-examining the role of radiography in tuberculosis case finding," Int. J. Tuberculosis Lung Disease, vol. 15, no. 10, pp.1279–1279, 2011.

[31] C. Loganathan, K.V.Girija "Hybrid Learning For Adaptive Neuro Fuzzy Inference System," International Journal Of Engineering And Science, ISSN: 2278-4721, vol. 2, no. 11, pp. 6-13, 2013.

[32] Longini, I. M., M. E. Halloran, A. Nizam, Y. Yang, S. Xu, D. S. Burke, D. AT Cummings, and J. M. Ep-stein. 2006. "Containing a Large Bioterrorist Smallpox Attack: A Computer Simulation Approach." International Journal of Infectious Diseases 11: 98-108.

[33] M. Longmore, I. B. Wilkinson, and S. R. Rajagopalan, Oxford handbook of clinical medicine: Oxford University Press, USA, 2004.

[34] Mellor, G. R., C. S. M. Currie, and E. L. Corbett. 2011. "Incorporating Household Structure into a Dis-crete-Event Simulation Model of Tuberculosis and HIV." ACM Transactions on Modeling and Com-puter Simulation 21: 26.

[35] Macal, C. M., and M. J. North. 2010. "Tutorial on Agent-Based Modeling and Simulation." Journal of Simulation 4: 151-162.

[36] E Millan and I Rudomın. Impostors and pseudo instancing for gpu crowd rendering.   In GRAPHITE a06: Proceedings of the 4th international conference on Computer graphics and

interactive techniques in Aus-tralasia and Southeast Asia, pages 49–55, New York, NY, USA, 2006.

[37] Porco, T. C., and S. M. Blower. 1998. "Quantifying the Intrinsic Transmission Dynamics of Tuberculo-sis." Theoretical Population Biology 54: 117-132.

[38] M. Phillips, V. Basa-Dalay, G. Bothamley, R. N. Catateo, P. K. Lam, M. P. R. Natividad, P. Schmitt, and J. Wai, "Breath biomarkers of active pulmonary tuberculosis," Tuberculosis, vol. 90, pp. 145-151, 2010.

[39] C. Pangilinan, A. Divekar, G. Coetzee, D. Clark, B. Fourie, F. Lure, and S.Kennedy, "Application of stepwise binary decision classification for reduction of false positives in tuberculosis detection from smeared slides," presentedatthe Int.Conf.Image.SignalProcess.Healthcare Technol.,Washington, DC, 2011.

[40] Pusponegoro, Hardiono D., dkk, Standar Pelayanan Medis Kesehatan Anak, first ed., Badan Penerbit IDAI, 2005.

[41] K Perumalla and B Aaby. Data parallel execution challenges and runtime performance of agent simulations on the gpu. In Proceedings of the 2008 ACM Spring simulation multi conference. ACM, 2008

[42] P Richmond and R Daniela. A high performance frame-work for agent based pedestrian dynamics on gpu hard-ware. In Proceedings of EUROSIS ESM 2008, Univer-site du Havre, Le Havre, France, 2008.

[43] M. Sakthi, and Dr. Antony Selvadoss Thanamani, "An Effective Determination of Initial Centroids in K-Means Clustering Using Kernel PCA," International Journal of Computer Science and Information Technologies, vol. 2, no. 3, pp. 955-959, 2011.

[44] Stefan Jaeger, Alexandros Karargyris, Sameer Antani, and George Thoma,Detecting Tuberculosis in Radiographs Using Combined Lung Masks,International Conference of the IEEE EMBS,September, 2012

[45] M. Stegmann, and M. Loog, "Segmentation of anatomical structures in chest radiographs using supervised methods: A comparative study on a public database," Med. Image Anal., vol 10, no. 1, pp. 19–40, 2006.

[46] R M D'Souza, M Lysenko, and K Rahmani. Sugarscape on steroids: simulating over a million agents at interactive rates. In Proceedings of the Agent2007 Conference, 2007.

[47] J Tang. Simulating leukocyte-venule interactions–a novel agent-oriented approach. In Conf. Proc. IEEE Eng. Med. Biol. Soc., volume 7, pages 4978–4981, 2004.

[48] T. Wang, I. Cheng, and A. Basu, Fluid vector flow and applications in brain tumor segmentation, IEEE Trans. Biomed. Eng., vol. 56, no. 3, Mar. 2009.

[49] Waaler, H. T., A. Gese, and S. Anderson. 1962. "The Use of Mathematical Models in the Study of the Epidemiology of Tuberculosis." American Journal of Pubic Health 52: 1002-1003.

[50] World Health Organization,"Global tuberculosis report, "Rep. WHO/HTM/TB/2013.6, 2013.

[51] X. Xie and M. Mirmehdi, MAC: Magnetostatic active contour model, IEEE Trans. Pattern Anal. Mach. Intell., vol. 30, no. 4,May 2008.

[52] Yonghong Shi, Feihu Qi, Zhong Xue, Liya Chen, Kyoko Ito, Hidenori Matsuo, and Dinggang Shen,Segmenting Lung Fields in Serial Chest Radiographs Using Both Population-Based and Patient-Specific Shape Statistics,IEEE Transactions on medical imaging, vol. 27, no. 4, april 2008.