QUANTIFICATION ANALYSIS OF MOLECULAR IMAGES USING AFFINITY PROPAGATION

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ABSTRACT

Molecular imaging techniques depend upon molecular mechanisms and cellular mechanisms. This imaging technique encompasses the visualization, characterization and measurement of biological processes at the molecular and cellular levels in humans and other living system. The techniques used include Positron Emission Tomography – Computed Tomography (PET-CT). The advantages and disadvantages of imaging techniques are Positron Emission Tomography (PET) has high sensitivity, shorter time scan, enables quantitative analysis but PET cyclotron or generator needed, also has relatively low spatial resolution. Single photon emission computed tomography (SPECT) has many molecular probes available, can image multiple probes simultaneously, may be adapted to clinical imaging system. CT has Unlimited depth penetration high spatial resolution whole body imaging of animals and humans short acquisition times (minutes) anatomical imaging and radiation exposure poor soft tissue contrast moderately expensive. These molecular imaging techniques are used as an accurate tool in localizing abnormal metabolic alteration and serve as a potential role as an invasive surrogate biomarker for various disease entities. These approached Molecular imaging techniques providing the more robustness and accurate qualitative metrics, and determining the optimal histology and slice localization.

Keywords: Affinity Propagation, Interpolation, Molecular Imaging Techniques, Quantification Rendering, Segmentation, Visualization.

I. INTRODUCTION

Today, there is almost no area of technical endeavor that is not impacted in some way or the other by digital image processing[5].With the sophistication in automated computing systems Bio-Medical Image analysis is made simple. Today there is an increase in interest for setting up medical system that can screen a large number of people for Molecular Imaging[5]-[10].Molecular Imaging is a new discipline which allows the biological processes takes place in the body to be viewed at a cellular and molecular level. This breakthrough enables doctor's early detection of disease in nascent stage, often well before they would be seen on CT and MR images and would otherwise require invasive surgery or biopsy – the removal of tissue for examination under the microscope[1].

Molecular imaging methodology are utilized to diagnose and deal with the treatment of cerebrum and bone issue, tumor, and gastrointestinal issue, heart and kidney infections, lung and thyroid issue. The biochemical movement of the cells changes when illness happens and, as it advances, this anomalous action begins to influence the body and reason changes in bones and tissue that may not be perceived utilizing routine CT or MRI filters[6].

Molecular imaging is a sort of therapeutic imaging that gives itemized pictures of what is going on inside the body at the sub-atomic and cell level. Where other analytic imaging systems, for example, x-rays, computed tomography (CT) and ultrasound—dominatingly offer anatomical pictures, molecular imaging permits doctors to perceive how the body is working and to gauge its compound and natural methods. Molecular imaging offers one of a kind bits of knowledge into the human body that empower doctors to customize patient consideration

In terms of diagnosis, molecular imaging has the capacity to:

• Give data that is unattainable with other imaging advancements or that would require more obtrusive methodology, for example, biopsy or surgery

• Identify disease in its most punctual stages and focus the careful area of a tumor, frequently before symptoms occur or irregularities can be recognized with other analytic tests[4].

The primary clinical helpful manifestation of digital image analysis was created in the early 1970s. The launch division (the volumetric portion of blood pumped out of the left ventricle in one pulse) was processed from cardiac nuclear medicine images in a semi-mechanized way. [1]This was an early type of evaluation. At the point when measuring, you are occupied with examining structure and capacity utilizing peculiarities as a part of the pictures. It can for instance be blood stream, tissue shape, tissue composition and movement. These features are regularly separated after a segmentation process. An alternate imperative piece of medicinal picture examination is image enhancement . Medical images can be of terrible quality for some reasons; superimposition of the encompassing tissue and Poisson noise from the photon emission in nuclear imaging are two of them[3]. The image enhancement can for instance be , contrast enhancement, noise removal or sharpen details (e.g. edges) to make the analysis less demanding - both visually and in potential further image analysis. Contrast enhancement can be attained by e.g. histogram leveling or equalization where the intensities are distributed over the histogram. Registration of images from distinctive modalities was considered without precedent for the late 1980s. One of the first endeavors was matching the limit surface of the mind that was physically segmented in CT, PET and MRI. They utilized the Euclidean metric between historic points to guide the segmentations to one another. Registration between distinctive modalities helps, for instance, in the quest for tumors. Tumors are visible in e.g. PET pictures, however it can be hard to decipher the careful anatomical position in these images. CT images give a superior anatomical perspective and by matching a CT picture with a PET image, the area of the tumor can be distinguished[3],[4],[6].

Registration can likewise be utilized to register images procured at distinctive times from the same patient or images from diverse patients with a specific end goal to make correlations. Most Most registration methods comprise of some peculiarity discovery, feature matching, estimation of model parameters and finally image transformation. Positron emission tomography (PET) has demonstrated equipped for imaging atomic methodologies, for example, blood stream in the brain and different organs utilizing O-15 water, as right on time as the 1970s. Yet, molecular imaging has just as of late been characterized as a different field. This was most likely actuated by the fruition of the human genome extend in April 2003 and the distinguishment that numerous illnesses have sub-atomic and cell causes. It is now recognized that imaging of processes intrinsic to metabolism, cell signaling and gene expression is possible. The development of our insight into atomic systems of illness and the advancement of imaging innovation are occurring quickly and in parallel, cultivating their consolidated application in molecular imaging[1],[6].

II. METHODS

2.1 Kernel Density Estimation via Diffusion

Generally, the histogram had been utilized to give a visual hint to the general state of the probability density capacity (pdf). The observed histogram of any image is the summation of histograms from numerous hidden articles "covered up" in the obeserved histogram. Our proposed technique expect that a top in the histogram relates to a moderately more homogeneous area in the image, it is likely that a top includes stand out class. The justification behind this supposition is that the histogram of items, inmedical images, are ordinarily considered the summation of Gaussian curves, which infers a top compares to a homogeneous region in the image(s)[1].

Because of the way of medical images, histograms have a tendency to be extremely boisterous with vast variability. This makes the optimal threshold choice for differentiating objects of interest troublesome. In the first place, the histogram of the image needs to be assessed in a hearty manner such that an expected histogram is less delicate to neighborhood local peculiarities in the image information. Second, the assessed histogram ought to be more delicate to the clustering of test values such that data clumping in certain regions and data sparseness in others–particularly the tails of the histogram–should be locally smoothed. To avoid all these problems and provide reliable signatures about objects within the images, herein we propose a framework for smoothing the histogram of PET images through diffusion-based KDE. KDE via diffusion deals well with boundary bias and are much more robust for small sample sizes, as compared to traditional KDE. We detail the steps of the KDE as follows :

1) Traditional KDE utilizes the Gaussian kernel density estimator, however it needs nearby adjustment; subsequently, it is sensitive to exceptions. To enhance neighborhood adjustment, a versatile KDE was made in view of the smoothing properties of linear diffusion processes. The kernel was seen as the transition density of a diffusion process, henceforth named as KDE via diffusion. For KDE, given N independent realizations, Xu∈{1,...,N }, the Gaussian kernel density estimator is customarily characterized as

$$g(x,t) = \frac{1}{N}\sum_{u=1}^{N} \emptyset(x,X_u;t),\ x \in R; \ldots\ldots\ldots\ldots\ldots(1)$$

where

$$\emptyset(x,X_u;t) = \frac{1}{\sqrt{2\pi t}} e^{-(x-Xu)2/(2t)}$$

is a Gaussian pdf at scale *t*, usually referred to as the bandwidth. An improved kernel via diffusion process was constructed by solving the following diffusion equation with the Neumann boundary condition

$$g^{diff}(x,X_u;t) = \sum_{z=-\infty}^{\infty} (\emptyset(x, 2z + Xu; t) + \emptyset(x, 2z - Xu; t))\ \ x \in [0,1]\ldots\ldots\ldots\ldots\ldots\ldots(2)$$

After KDE via diffusion, an exponential smoothing was connected to further decrease the noise; the crucial state of the histogram was saved all through this methodology. Data clumping and sparseness in the first histogram were removed, and any noise staying after KDE via diffusion was diminished impressively while as yet safeguarding the state of the pdf. The resultant histogram can now serve as a capable stage for the segmentation of the objects, the length of a powerful clustering methodology can place the valleys in the histogram[1],[7].

2.2 Affinty Propagation

Clustering data by recognizing a subset of agent illustrations is essential for processing signals and identifying examples in data. Such "exemplars" can be found by arbitrarily picking a starting subset of information focuses and afterward iteratively refining it, however this functions admirably just if introductory decision is near to a

decent arrangement. We contrived a strategy called "affinity propagation," which takes as info measures of likeness between sets of data focuses. Real valued messages are traded between data points until a high-quality set of models and comparing clusters continuously rises[1]. AP is valuable on the grounds that it is effective, insensitive to initialization, and produces groups at a low cluster rate. Essentially, AP partition the data taking into account the augmentation of the aggregate of likenesses between data points such that each one part is connected with its model (in particular its most prototypical data point. Dissimilar to other model based grouping systems, for example, k-centers clustering and k-means, Hence execution of AP does not depend on a "good" initial cluster/group. Rather, AP acquires exact arrangements by approximating the NP-hard issues in a significantly more productive and precise way. AP can utilize arbitrarily complex affinity functions since it doesn't have to inquiry or incorporate over a parameter space[2].

2.2.1 Background on AP:

AP at first expect all data points(i.e., voxels) as models and refines them down iteratively by passing two "messages" between all focuses: ***responsibility*** and ***availability***. Messages are scalar values such that each one point makes an impression on all different focuses, showing to what degree each of alternate focuses is suitable to be its model. The primary message is called ***responsibility***, demonstrated by r(i, k), and is the way mindful point k is to be the model of point i. In ***availability***, indicated by a(i, k), each one point makes an impression on all different guides and demonstrates toward what degree the point itself is accessible for serving as a model. The ***responsibility*** and ***availability*** were defined in Frey and Dueck's original paper as

$$\mathbf{r(i,k)\leftarrow s(i,k) - \max_{k'\{k'\neq k\}}\{a(I,k') + s(I,k')\}}$$

$$\mathbf{a(i,k)\leftarrow \min\{0, r(k,k) + \sum_{i'\{i'\notin\{i,k\}} \max\{0, r(i',k)\}\}}$$

where s(i, k) is the likeness between point i and point k, and k is all different focuses aside from i and k. Point k is not mindful to be the model for point i if there is an alternate point that portrays i better than k; subsequently, the most extreme quality for responsibility is arrived at. The whole of availabilities and responsibilities at any emphasis gives the current models and orders. At first, all focuses are thought to be conceivable models, which ensure all inclusive ideal arrangements. AP uses max-product belief propagation to acquire great models through maximizing the objective function argmax_k $[a(i, k) + r(i, k)]$[1],[2].

2.2.2 Novel Affinity Metric Construction

We developed a novel affinity metric to model the relationship between all data points utilizing the precisely evaluated histogram with the principle supposition that closer force qualities are more prone to have a place with the same tissue class. As such, the information is made out of focuses lying on a few unique straight spaces, however this data is covered up in the image histogram, given that the histogram is deliberately evaluated in the past step. This segmentation processes recovers these subspaces and relegates data points to their individual subspaces. Simultaneously, likenesses among the voxels assume an indispensable part. Most clustering routines are centered around utilizing either Euclidean or Gaussian separation capacities to focus the likeness between data points. Such a separation is direct in execution; be that as it may, it drops the shape data of the hopeful circulation. Since both probability- and intensity-based differences of any two voxels convey profitable data on the determination of appropriate threshold determination, we propose to combine these two limitations inside with another affinity model. These constrains can basically be joined with weight parameters n and m as :

$$s(i,j) = -(|d_{ij}^{x}|^{n} + |d_{ij}^{G}|^{m})^{1/2}$$

where s is the closeness capacity, d_ij^G is the registered geodesic separation between point i and j along the pdf of the histogram, and d_ij^xis the Euclidean separation between point i and j along x-axis.

The geodesic separation or distance between the two information focuses in the image naturally reflects the similitude because of the gradient information (i.e., voxel intensity differences). It likewise fuses extra probabilistic data through upholding neighborhood groupings for specific locales to have the same mark

$$d_{ij}^{G} = \sum_{k=1}^{j-1} dE(k, k+1), \text{ where } j > i.$$

Once the similarity function is computed for all points, AP tries to maximize the energy function

$$E(c) = \sum_{i=1}^{N} s(i, c_i) + \sum_{k=1}^{N} \delta k(c) \ldots\ldots\ldots\ldots\ldots\ldots (3)$$

an exemplar-consistency constraint δk (**c**) can be defined as

$$\delta k(c) = \begin{cases} -\infty, \text{if } ck \neq k \text{ but } \exists i;\ ci = k \\ 0, \quad \text{otherwise} \end{cases} \quad \ldots\ldots\ldots\ldots (4)$$

This limitation authorizes substantial design by presenting a huge punishment if some information point i has picked k as its model without k having been effectively named as a model. In the wake of embeddings a novel affinity function definition into the vitality imperative to be expanded inside the AP calculation, we got the following objective function:

$$E(c) = -\sum_{i=1}^{N}(|d_{ic1}^{x}|n + |d_{ic1}^{G}|m)1/2 + \sum_{k=1}^{N} \delta k(\arg\max_{k}[a(i,k) + r(I,k)]) \ldots\ldots\ldots\ldots\ldots\ldots (5)$$

all voxels are marked in light of the advancement of the target capacity characterized previously. Since the upgrade rules for AP compare to altered point recursions for minimizing a Bethe free-energy approximation, AP is effectively inferred as an occurrence of the max-entirety calculation in a factor graph portraying the requirements on the marks and the energy function[1].

III. RESULT & ANALYSIS

In this project PET and CT lung images of a rabbit lung are considered as inputs for Quantification. A GUI framework called QAV-PET (Courtesy: QAV: PET by Foster and Bagci of NIH) is used.

QAV-PET analysis allows easy, intuitive and efficient visualization and quantification of multi modal medical images. This is carried out in different steps such as Visualization, Interpolation, segmentation, Rendering, auto-reporting and Quantification

The results for each step are given below:

3.1 Visualization

Functional (PET image) and Anatomical (CT image) images of rabbit are read into the framework. These images can be shown in three categories:

a) Fused image

b) Functional image

c) Anatomical image

The Figure 1(a) shows the fused image, which is formed by the fusion of both Functional and Anatomical images., figure 1(b)Shows Functional Image, the image representing here is PET image which is showing the clear view of lungs, figure 1(c) shows the Anatomical image, the image here is CT image representation of rabbit lung mask.

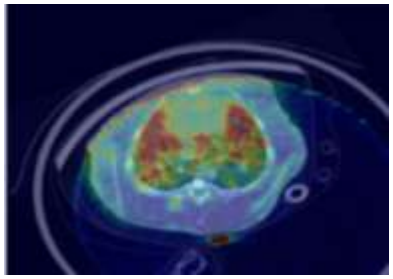

Fig 1(a): Fused Image

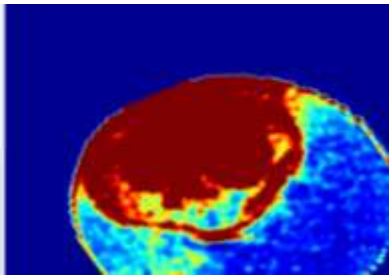

Fig 1(b): Functional Image

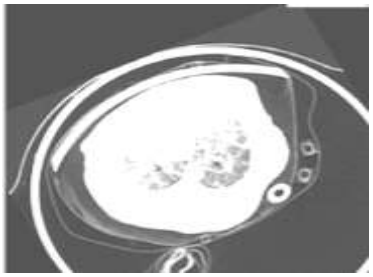

Fig1(c): Anatomical Image

3.2 ROI Definition

Region of Interest (ROI) is created to focus on specified area of lung mask to analyze the situation of image and quantify the image.

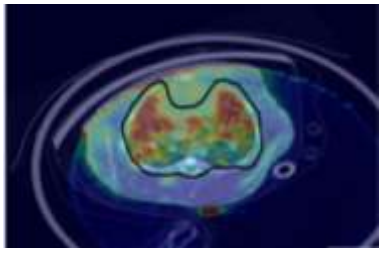

Fig 2: ROI Defined in Fused Image

3.3 Interpolation

Once the ROI is created, the image is subjected to interpolation. This is shown in below fig.3 Interpolation is used for the calculation of the value of a function between the values already known. Here Interpolation is used to measure the values of already created ROI regions and this gives us the accurate measure.

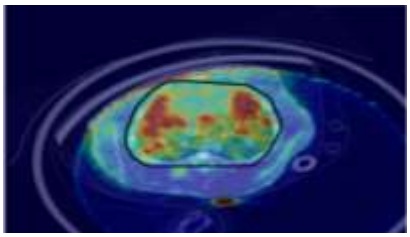

Fig 3: Interpolated Fused Image

3.4 Segmentation

Once the ROI is created, the segmentation process is carried out using Affinity Propagation Image segmentation. As a process the lesions formed due to Tuberculosis are segmented as shown in figure.4

Fig 4: AP Pet Image Segmentation

3.5 Opacity

The process shown below in figure is used for changing the opacity between Functional and Anatomical images. Threshold is adjusted in order to remove the background areas for improved visibility of underlying anatomical image.

Fig 4(a): 0 **Fig 4(b): 0.25** **Fig 4(c): 0.50** **Fig 4(d): 0.75** **Fig 4(e):1**

Figure 4(A), (B), (C), (D), (E): Representation of Varying The Opacity Between PET and CT on The Segmentations. The Opacity Ranges from 0, Fully Anatomical (CT) Information To 1, Fully Functional (PET) Information.

3.6 Rendering

The Rendering process is done in 3D-visualization. The Rendering is carried out for both lung mask and AP segmented Image. The figure 5 which have the lung mask rendering shows the affected area in red color indicated by a color bar adjacent to image. The color bar represents the intensity of damage happened to the lungs.

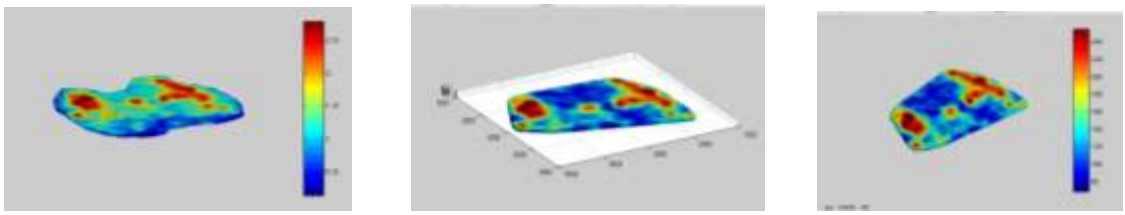

Fig 5(a) **Fig 5(b)** **Fig 5(c)**

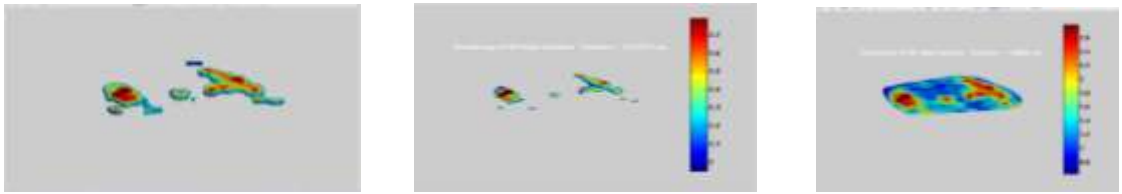

Fig 5(d) **Fig 5(e)** **Fig 5(f)**

Figure5 (a), (b), (c), (d), (e),(f) Shows Rendering Of Lung Mask, Lesion Rendering And Interpolated Image.

3.7 Auto-Reporting

It produces a report which includes the most important information needed for quantifying the disease and high uptake value regions. The report includes both Qualitative and Quantitative data. Quantitative data includes SUV_{mean}, SUV_{max} and volume of current label and the location of SUV_{max} on axial, sagittal and coronal view of PET Image.

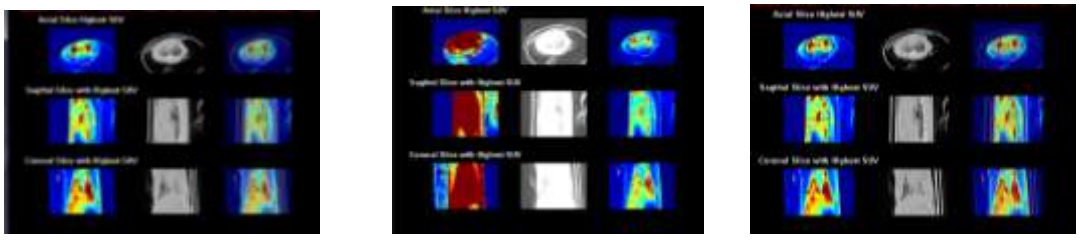

Figure: These Images Represent the Reporting for AP Segmented Images for Different Opacity Values.

- After the Reporting process, we acquire the Qualitative metrics and they are tabulated as :

3.8 Tabular Column

Table: Qualitative Metrics of Fused Images

VOLUME	SUV_{max}	SUV_{mean}
0.2740	2.7930	2.2540
0.2770	2.7930	2.2510
1.6460	2.7930	1.2930
1.6860	2.7930	1.2810
1.6560	2.7930	1.2945
1.6830	2.7930	1.2821

- These values represent the uptake values of lesions.

The report includes both quantitative and qualitative data. The quantitative data includes the SUVmax, SUVmean, and the volume of the current label, and, additionally, it provides the location of the SUVmax on the axial, sagittal, and coronal view of the PET image, the CT image and the PET-CT fused image All of this information allows the user to get a quick view of the highest uptake lesion, which is important for disease severity quantification.

IV. CONCLUSION

This can be used for quantification and visualization of abnormalities on PET-CT images of small animal infectious disease studies. The segmentation algorithm that is implemented has been shown to be particularly well-suited for the segmentation of diffuse, multi-focal PET radiotracer uptakes that are commonly seen with infectious diseases. It is used for visualization of the pathologies in three dimensions with the PET functional information overlaid for determining the optimal histology and slice localization. When taking histology slices from a diseased organ, this three dimensional view of the distribution of the disease will aid researchers in determining the best location to take the histology slices from for the best characterization. It includes a framework for quantification which can be easily manipulated and tuned to fit any medical imaging application.

V. ACKNOWLEDGEMENT

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REFERENCES

[1]. B. Foster, U. Bagci, Z. Xu, B. Dey, B. Luna, W. Bishai, S. Jain, and D. J.Mollura, \Segmentation of pet images for computer-aided functional quantification of tuberculosis in small animal models," IEEE Transactions on Biomedical Engineering, vol. 61, pp. 711{724, 2013.

[2.] B. Frey and D. Dueck, \Clustering by passing messages between data points," Science, vol. 315, no. 5814, pp. 972{976, 2007.

[3]. U. Bagci, J. K. Udupa, N. Mendhiratta, B. Foster, Z. Xu, J. Yao, X. Chen, and D. J. Mollura, \Joint segmentation of anatomical and functional images: Applications in quantification of lesions from pet, pet-ct, mri-pet, and mri- pet-ct images," Medical image analysis, vol. 17, no. 8, pp. 929{945, 2013.

[4]. Elsa Angelini[1] Yinpeng Jin[1] and Andrew Laine[1], "State of the Art of Level Set Methods in Segmentation and Registration of Medical Imaging Modalities".

[5]Fahimuddin.Shaik, R.Ravindraiah, Dr.M.N.Giriprasad - "Qualitative and Quantitative Analysis of Segmentation of Human Retinal Images" IEEE International Conference (ICCET- 2011), Published by IEEE Press and in IEEE Explorer, pp 76 - 80. T.N., India, Mar 2011(ISBN 978-1-4244-9391-3).

[6]. U.Bagci, J. Yao, K. Miller-Jaster, X. Chen, and D. J.Mollura,"Predicting future morphological changes of lesions from radiotracer uptake in 18FFDG- PET images." PlosOne, vol. 8, no. 2, p. e57105, 2013.

[7] B. Foster, U. Bagci, B. Luna, B. Dey, W. Bishai, S. Jain, Z. Xu, and D. J. Mollura, \Robust segmentation and accurate target definition for positron emission tomography images using affinity propagation," in 2013 IEEE 10th International Symposium on Biomedical Imaging (ISBI), 2013, pp. 1461{1464}.

[8] Z. Botev, J. Grotowski, and D. Kroese, \Kernel density estimation via diffusion," The Annals of Statistics, vol. 38, no. 5, pp. 2916{2957, 2010.

[9] U. Bagci, B. Foster, K. Miller-Jaster, B. Luna, B. Dey, W. R. Bishai, C. B.Jonsson, S. Jain, and D. J. Mollura, \A computational pipeline for quantification of pulmonary infections in small animal models using serial pet-ctimaging," EJNMMI research, vol. 3, no. 1, pp. 1{20, 2013}.

[10] Fahimuddin.Shaik, Dr.M.N.GiriPrasad, Dr.B.JayabhaskarRao, B.Abdul Rahim, Somasekhar - " Medical Image analysis of Electron Micrographs in Diabetic Patients using Contrast Enhancement" International Conference on Mechanical & Electrical Technology(ICMET 2010), Published by IEEE Press and in IEEE Explorer, Singapore, Sep'10-12th 2010(ISBN 978-1-4244-8100-2)