# Molecular Imaging and Biomedical Process Modeling

**David Dagan Feng, Ph.D., FACS, FHKIE, FIEE, FIEEE**

Biomedical and Multimedia Information Technology (BMIT) Group,
School of Information Technologies, University of Sydney, Australia
and
Center for Multimedia Signal Processing (CSMP)
Dept of Electronic & Information Engineering, Hong Kong Polytechnic University, Hong Kong

feng@it.usyd.edu.au

## Abstract

This paper describes the core theories and enabling technologies developed for molecular imaging at the BMIT Group and the CMSP Center over the last 10 years, in the areas of dynamic image data acquisition, compression, storage, management, modeling, simulation, analysis, processing, registration, and visualization.

## 1 Introduction

Modern functional medical imaging with its unique capability of extracting molecular and quantitative physiological information from complex dynamic processes has opened a new window for scientific and biomedical research. Functional medical imaging techniques include single photon emission tomography (SPECT) and Positron Emission Tomography (PET). In each case, a radiotracer labelled compound which traces a specific physiological process is injected into the patient and imaged. The key requirements for quantitative functional imaging are illustrated in Fig. 1 for the case of PET imaging of $^{18}$*F-fluoro-deoxyglucose* (FDG). However, similar principles apply to SPECT quantitative functional imaging. The quantitative measurement of the dynamic uptake and clearance of the tracer in the organ of interest and the concentration of the tracer in the arterial plasma are applied to a mathematical model which describes the tracer behaviour and yields the physiological parameters of interest. Traditionally, the functional parameters were estimated for only specific regions in the organ of interest. However, much additional information and utility can be gained by providing images of the functional physiological parameters, called parametric images, and hence recent emphasis has been on this aspect, as well as many IT techniques for molecular imaging to provide a better understanding of the nature of the biological process in living systems.

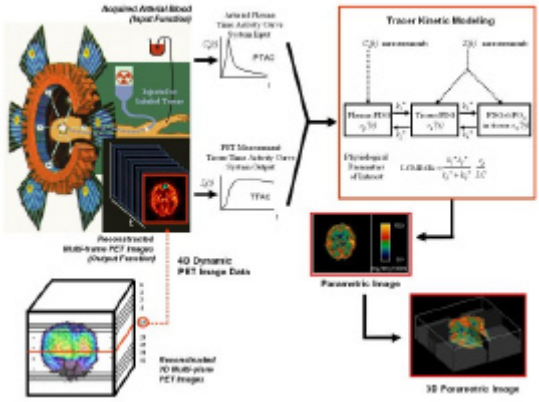


Fig. 1: Main requirements for quantitative physiological parameter estimation. The activity of the radio-tracer is measured quanti-tatively over time along with the activity in the plasma. The physiological parameters of interest, in this case local cerebral metabolic rate of glucose (LCMRGlc), are estimated by applying a mathemati-cal model (compartmental model) to the data. It is worth noting that 4 dimen-sional data (3 space and 1 time dimension) are re-quired to estimate the 3D parametic image set.

## 2 Data Acquisition [14, 18, 25, 28, 33, 39]

Over the last few decades, there has been an explosive growth in the use of digital media, including medical images and video. In addition to the recent advances in digital computing power, one of the most significant breakthroughs in science and technology to bring us into this digital age and digital world is probably the famous Shannon Sampling Theorem which provides the theoretical foundation on how to transform information originally stored in analog format into digital format without losing the representation accuracy of the information. This theory has developed into a new area of digital signal processing and is used to solve many problems in the natural world which involve analog signals. However although revolutionary, this Theorem is only applicable to a set of non-noisy signals and is only suitable for taking uniform samples. Nevertheless, in real life, non-uniform samples are often required and the signals may be significantly corrupted by strong noises. This is the situation for many practical problems, including nuclear medicine imaging systems for

---

quantitative studies where the non-uniform time accumulated counts samples are required.

Nuclear medicine function imaging is vital to modern biomedical research and clinical diagnosis and provides human internal biochemical information previously not available. However, for a routine dynamic study with a typical medical functional imaging system, such as Positron Emission Tomography (PET), it is easily to acquire over 1000 images (e.g., 31 planes x 35 time frames to sample/record the tissue time activities) for just one patient in one study. Such a large number of image frames has given a considerable burden for data storage, processing and transmission. Therefore, it is of great interest to find out what the minimum number of frames is absolutely required and how to record these frames. As the Shannon Sampling Theorem is not applicable to these situations, for decades many experimental trial and error studies were conducted. The resulting sampling protocols remained dubious and arguable until the Optimal Image Sampling Schedule (**OISS**) Theory was proposed [18, 39], for continuous non-uniform data acquisition of time accumulated counts measurements with/without existence of noise. Since then, OISS has become a standard data acquisition method for functional imaging and similar real life problems. OISS calculates the minimum number of frames required and where these image frames should be located. As a result of this theory, the number of the required PET image frames can be reduced by more than 80%, while the accuracy of information obtained remains unchanged. OISS is of significant benefit to molecular imaging research and clinical diagnosis, as the number of the images displayed on the screen is decreased by more than 80% while the quality of the images is at least 5 times more reliable than the previous ones. We have further successfully extended our OISS for both system input/output sampling schedule **(OISS-I/O)** [33], quantification of biomedical function with rotating camera systems (**OISS-RC**) [25, 28], which can be used for single head gamma camera imaging systems; and multi-bed imaging (**OISS-MB**) data acquisition [14], which can be used to conduct whole-body scanning with the regular 10cm wide camera head imaging systems.

## 3 Data Compression [16, 17, 19, 43]

Data compression is an extremely important topic in the "digital world", due to the explosive amount of information which we have to handle and need to store in digital format for digital videos, digital libraries, digital museums, as well as digital hospitals. Based on our OISS theory, we proposed the diagnostically lossless data compression (**DLLDC**) theory. This was a new concept and research direction which operated in parallel with the conventional lossless and lossy data compression. The lossless compression currently used for medical image systems has a relatively low compression ratio (less than 3:1), which is insufficient to efficiently realize a digital hospital and global telemedicine, and health-care network. The alternative lossy compression currently used for images can often achieve a 50:1 compression ratio while making no difference to human visual systems. But the current lossy compression is unacceptable to medical practitioners, as no significant difference for human subjective visual perception does not mean no significant difference for critical medical diagnosis. Our Diagnostically Lossless Data Compression (based on an objective quantification in line with diagnostic accuracy), which obtains a compression ratio of greater than 50:1 while maintaining diagnostic accuracy, is an important contribution. The main ideas behind our theory and algorithms are clustering all of the similar tissue time activities and labeling these clusters in a static reduced dimension index image, which removes all of the redundant representation of these similar tissue dynamic time activities, and uses minimum data to represent the 4-D time varying images in terms of a typical tissue time activity curves table + a single 3-D static cluster index image. It greatly reduces data storage space, and processing and transmission time, which makes real-time diagnosis, collaborative consultation and treatment of patients in remote locations possible.

## 4 Data Management [32, 34, 35, 36, 45, 46]

Our DLLDC theory not only reduces on-line data storage to less than 2% of the original size, but also classifies the typical tissue time activities and given the anatomic distribution of these activities which also facilitates content-based retrieval. We have, therefore, developed a novel content-based medical image retrieval (**CBMIR**) theory and standard, and developed the world's first CBMIR database management system. This system allows functional image retrieval based not only on text records (e.g., patients' names, ages, etc.), but also on image features (e.g., list all of the possible early brain tumour patients who have a raised metabolic rate of glucose in brain tissues). Such content-based retrieval is an important alternative and complement to traditional keyword-based searching for medical image data. This new search technique provides new opportunities for statistical and comparative analysis of patient functional image data. We have also proposed a new theory for content-based image retrieval using geometric signatures (**CBIR-GS**), which can be used for any type of images. Both **CBMIR** and **CBIR-GS** provide an important new option for data mining, critical information extraction, and new knowledge formation (and management) in this digital world.

## 5 Modelling & Simulation [3, 4, 5, 7, 10, 11, 13, 20, 22, 23, 24, 30, 40, 41]

We have investigated the Input Function Modelling (**IFM**) and proposed the Cascaded Modelling (**CCM**) Technique. The CCM method is particularly well suited to brain PET quantitative studies. In the past these studies have required invasive measurement of the tracer time-activity curve from arterial blood samples during the PET scanning period, which in some instances has involved continuously taking blood for up to 2 hours. The insertion of arterial lines and the subsequent collection and processing of arterial blood is a painful and risky practice. It limits patient throughput, requires extra personnel and processing time, exposes the patient to the unnecessary risks associated with the insertion of an arterial line and exposes personnel to the risks associated with the handling

of blood and radiation doses. The CCM method extracts previously ignored information which is embedded in the PET images. This obviates the need to take blood samples and has revolutionised the field. There is no longer a need to handle blood samples and patients no longer need to suffer the painful process of continuous collection of blood during the PET scanning. Our major contributions in this sub-area also include the double modeling approach (**DMA**) for dynamic cardiac-PET imaging studies using noise and spillover contaminated left ventricle measurements.

## 6 Analysis [1, 2, 9]

We Proposed the Compartmental Cut-Set Analysis (**CCSA**). CCSA allows complex models to be analysed and synthesised directly on a graph, avoiding more complicated mathematical equations. We also introduced the Model Decomposition and Coordination for Identifiability Analysis (**MDCIA**). MDCIA makes very large scale system experimental design possible. International researchers regularly use these two techniques to study complex metabolic, endocrine, pharmacokinetic and other biochemical processes in living systems. Research using CCSA has led to important discoveries in thyroid hormone secretion, distribution, metabolism and disposal at the University of California, Los Angeles (UCLA).

## 7 Processing [21, 37, 42, 44, 48]

Standard image processing techniques may not be suitable for many specific applications, e.g., medical image noise smoothing. If the standard image smoothing techniques are used, a new value will be assigned to each pixel based on the weighted average (using some filters) of its neighboring pixel values. This is unreasonable for medical images, e.g., a brain image, as the delicate structure of a brain has white matter, grey matter, vascular, all next to each other. It is not appropriate to average measured values from these different structures, as they are different tissues. Therefore, we developed a theory for Knowledge-based Image Processing (**KBIP**), taking full account of the physical structure of living systems into the image smoothing process. For this particular brain image case, our theory provides an algorithm to assign a new value to each pixel by using a weighted average (using some filters to process the values) of those pixels with a similar structure and property across the whole brain image, rather than neighbouring pixel values. Our KBIP theory has provided surprisingly satisfactory results and can be widely adopted in medical image processing and other image processing areas.

## 8 Registration [38, 47]

Image registration has been widely used to match multiple images obtained from different imaging modalities (e.g., to match the same patient images obtained from PET and MRI to identify an abnormal functional tissues physical location against the anatomic image obtained from MRI for pinpoint treatment) and at different times (e.g., to match the patients images obtained from the same imaging modality to monitor the progress after certain medical treatment, or to construct a single background image from a sequence of panoramic video shots, etc). Precision of registration is extremely important in clinical diagnosis and treatment, it is usually assessed by visual inspection or by referring to other methods that require special expertise and extensive experience. In addition to a number of significant contributions in proposing many new effective and accurate image registration algorithms, our greatest research contribution in this are is the novel automatic approach, based on statistical theory, to estimate confidence intervals of the registration parameters and allow the precision of registration results to be objectively assessed, which sets an objective assessment theory (**OAT**) in this area.

## 9 Visualisation [6, 8, 12, 15, 26, 27, 29, 31]

Medical parametric imaging requires modelling and parameter estimation for certain metabolic, pharmacokinetic, endocrine or other biochemical systems at voxel by voxel level. It is an important technique which provides image-wide quantifications of physiological and biochemical functions and allows the distributions of these functions corresponding to anatomic structures to be visualised. With the recent development of high spatial and temporal resolution functional imaging systems, e.g., PET, a variety of parametric imaging techniques have been developed. However, all of the techniques depend on various unrealistic assumptions or result in biased parameter estimation. We developed a general unbiased and statistically reliable fast algorithm (called **GLLS**) for *non-uniformly sampled* biomedical system identification. GLLS reduces computing time by more than 95% and makes unbiased image-wide parameter estimation for general biomedical systems possible. This can be used for accurately quantifying biochemical processes in the living human body, identifying cancer at an early stage, and assessing the progress of treatment for cancer patients, etc. It has been regarded as a major step forward in parametric imaging, as it: (1) can estimate continuous model parameters directly, (2) does not require the initial parameter values, (3) is generally applicable to a variety of models with different structures, (4) can estimate individual model parameters as well as physiological parameters, (5) requires very little computing time, and (6) can produce unbiased estimation. We have recently further improved our GLLS to bounded GLLS (**B-GLLS**), which can be robustly used for very noisy data, such as those obtained from Single Photon Computer Emission Tomography (SEPCT), and can ensure that the parameter estimated for every voxel can always be converged within the reasonable physiological or pathological range for every specific voxel.

## 10 Conclusion

Modern research in biology and medicine requires heavy involvement of information technology and Imaging techniques. The above mentioned areas are just a few examples and are just some starting points to facilitate a better understanding the complicated nature of biological processes in human living systems.

## 11 Acknowledgement

The author is very grateful to his colleagues and students for their outstanding research team work and the support from ARC, NH&MRC, RGC and CSMP grants.

## References

1. D. Feng & J. J. DiStefano, III, (Aug. 1991): Cut Set Analysis for Compartmental Models with Applications to Experiment Design, *American Journal of Physiology*, 261:E269-E284.
2. D. Feng & J. J. DiStefano, III, (June 1992): Decomposition-Based Qualitative Experiment Design Algorithms For a class of Compartmental Models, *Mathematical Biosciences*, 110/1, pp.27-43.
3. Z. Wang & D. Feng, (1992): Continuous-Time System Modeling by Using Weighted-Parabola-Overlapping Numerical Integration Method. *International Journal of System Sciences*, Vol. 23, No. 8, pp.1361-1369.
4. D. Feng, S. C. Huang & X. Wang, (1993): Models For Computer Simulation Studies of Input Functions for Tracer Kinetic Modelling With Positron Emission Tomography, *International Journal of Bio-Medical Computing*, 32:95-110.
5. D. Feng & X. Wang, (1993): A computer Simulation Study on the Effects of Input Function Measurement Noise in Tracer Kinetic Modelling with Positron Emission Tomography (PET), *Computers in Biology and Medicine*, Vol 23, No. 1, pp57-68.
6. D. Feng, Z. Wang & S. C. Huang, (1993): A study on Statistically Reliable and Computationally Efficient Algorithms for the Measurement of Local Cerebral Blood Flow with Positron Emission Tomography, *IEEE Transactions on Medical Imaging*, Vol. 12, No. 2, pp182-188.
7. D. Feng, X. Wang & H. Yan, (1994): A computer Simulation Study on the Effects of Input Function Sampling Schedules in Tracer Kinetic Modelling with Positron Emission Tomography (PET), *Computer Methods and Programs in Biomedicine*, Vol, 45, No. 3, pp175-86.
8. K. Chen, S. C. Huang & D. Feng, (1994): New Estimation Methods that Directly Use the Time Accumulated Counts in the Input Function in Quantitative Dynamic PET Studies, *Physics in Medicine and Biology*, 39:2073-2090.
9. *D. Feng & J. J. DiStefano, III, (1995): An Algorithm for the Identifiable Parameters and Parameter Bounds for a Class of Cascaded Mammillary Models," *Mathematical Biosciences*, 129:pp67-93.
10. D. Feng & X. Wang, (1995): A Method for Biomedical System Modeling and Physiological Parameter Estimation Using Indirectly Measured Input Functions", *International Journal of System Sciences*, Vol 26, No. 4, pp723-39.
11. K. Chen, E. Reiman, M. Lawson, D. Feng & S. C. Huang, (1995): Decay Correction Methods In Dynamic PET Studies", *IEEE Transactions on Nuclear Science*, Vol 42, No 6, p2173-9.
12. D. Feng, D. Ho, K. Chen, L. Wu, J. Wang, R. Liu & S. Yeh, (1995): An Evaluation of the Algorithms for Constructing Local Cerebral Metabolic Rates of Glucose Tomographical Maps Using Positron Emission Tomography Dynamic Date, *IEEE Transactions on Medical Imaging*, Vol 14, No 4, pp697-710.
13. D. Feng, X. Li & S. C. Huang, (1996): A New Double Modeling Approach for Dynamic Cardiac PET Studies Using Noise and Spillover Contaminated LV Measurements, *IEEE Transactions on Biomedical Engineering*, Vol. 43, No. 3, pp. 319-27.
14. K. Ho-Shon, D. Feng, R. Hawkins, S. Meikle, M. Fulham & X. Li, (1996): Optimized Sampling and Parameter Estimation for Quantification in Whole Body PET, *IEEE Transactions on Biomedical Engineering*, Vol. 43, No. 10, pp. 1021-1028.
15. D. Feng, S. C. Huang, Z. Wang & D. Ho, (1996): An Unbiased Parametric Imaging Algorithm for Non-uniformly Sampled Biomedical System Parameter Estimation", *IEEE Transactions on Medical Imaging*, Vol. 15, No. 4, pp. 512-18.
16. X. Li, D. Feng, & K, Chen, (1996): Optimal Image Sampling Schedule: A New Effective Way to Reduce Dynamic Image Storage Space and Functional Image Processing Time", *IEEE Transactions on Medical Imaging*, Vol. 15, No. 5, pp. 710-719.
17. X. Li & D. Feng, (1997): Towards the Reduction of Dynamic Image Data in PET Studies", *Computer Methods and Programs in Biomedicine*, Vol. 53, No. 2, pp. 71-80.
18. D. Feng, X. Li & W. C. Siu, (1997): Optimal Sampling Schedule Design for Positron Emission Tomography Data Acquisition", (Invited paper), *Control Engineering Practice*, Vol. 5, No. 12, pp. 1759-1766.
19. D. Ho, D. Feng & K. Chen, (1997): Dynamic Image Data Compression in Spatial and Temporal Domains: Theory and Algorithm", *IEEE Transactions on Information Technology in Biomedicine*, Vol. 1, No. 4, pp. 219-228, Dec.
20. D. Feng, K.P Wong, C.M. Wu & W.C. Siu, (1997): A Technique for Extracting Physiological Parameters and the Required Input Function Simultaneously from PET Image

Measurements: Theory and Simulation Study, *IEEE Transactions on Information Technology in Biomedicine*, Vol. 1, No. 4, pp. 243-254, Dec.

21. D. Feng, D. Ho, H. Iida & K. Chen, (1997): Techniques for Functional Imaging", an invited chapter contributing to "Medical Imaging Techniques and Applications", Edited by: C. T. Leondes, in 'Gordon and Breach International Series in Engineering, Technology and Applied Science, *Gordon and Breach Science Publishers*, pp85-145.
22. X. Li, D. Feng, K. Lin, and S. C. Huang, (January 1998): Estimation of Myocardial Glucose Utilization with PET Using the Left Ventricular Time-Activity Curve as a Noninvasive Input Function, *Medical & Biological Engineering & Computing*, Vol. 36, No. 1, pp. 112-117.
23. D. Ho, D. Feng & K. Chen, (January 1998): A New Method for the Analysis of Multiple Positron Emission Tomography Dynamic Datasets: An Example Applied to the Estimation of the Cerebral Metabolic Rate of Oxygen, *Medical & Biological Engineering & Computing*, Vol. 36, No. 1, pp. 83-90.
24. K Chen, E Reiman, D Bandy, SC Huang, M Lawson, LS Yun, K Sun, D Feng, L. Yun, & A. Palant, (July 1998): Non-invasive Quantification of the Cerebral Metabolic Rate for Glucose Using Positron Emission Tomography, $^{18}$F-Fluoro-2-deoxyglucose, the Patlak Method, and an Image-derived Input Function, *Journal of Cerebral Blood Flow & Metabolism*, Vol. 18, No. 7, pp. 716-723.
25. C. H. Lau, S. Eberl, D. Feng, H. Iida, D. Lun, W. C. Siu, Y. Tamura, G. Bautovich & Y. Ono, (1998): Minimum Dynamic SPECT Image Acquisition Time Required for T1-201 Tracer Kinetic Modeling, *IEEE Transactions on Medical Imaging*, Vol. 17, No. 3, pp. 334-43.
26. K. Chen, M. Lawson, E. Reiman, D. Feng, S. C. Huang, D. Bandy, D. Ho, L. Yun, & A. Palant, (1998): Generalized Linear Least Square Method for Fast Generation of Myocardial Blood Flow parametric Images with N-13 Ammonia PET, *IEEE Transactions on Medical Imaging*, Vol. 17, No. 2, pp. 236-243.
27. K. P. Wong, D. Feng & W. C. Siu, (Nov. 1998): Generalized Linear Least Squares Algorithms for Non-uniformly Sampled Biomedical System Identification with/without Repeated Eigenvalues, *Computer Methods and Programs in Biomedicine*, Vol. 57, Issue 3, pp. 167-177.
28. C. H. Lau, D. Feng, B. Hutton, D. Lun & W. C. Siu, (Dec 1998): Dynamic Imaging and Tracer Kinetic Modelling for Emission Tomography Using Rotating Detectors, *IEEE Transactions on Medical Imaging*, Vol. 17, No. 6, pp. 986-994.
29. D. Feng & W. Cai, (March 1999): The Studies on Functional Image Processing and Algorithms, (Invited paper) *Journal of Image and Graphic*, Vol. 4(A), No.3, pp.177-182.
30. D. Ho & D. Feng, (1999): Rapid Algorithms for the Construction of Cerebral Blood Flow and Oxygen Utilization Images with Oxygen-15 and Dynamic Positron Emission Tomography, *Computer Methods and Programs in Biomedicine*, Vol. 58, Issue 2, pp. 99-117.
31. D. Feng, D. Ho, K.K. Lau & W.C. Siu, (1999): GLLS for Optimally Sampled Continuous Dynamic System Modeling: Theory and Algorithm, *Computer Methods and Programs in Biomedicine*, Vol. 59, Issue 1, pp. 31-43.
32. D. Feng, (1999): Information Technology Applications In Biomedical Functional Imaging, *IEEE Transactions on Information Technology in Biomedicine*, Vol. 3, no. 3, pp. 221-230.
33. X. Li, D. Feng & K. Chen, (March 2000): Optimal Image Sampling Schedule for Both the Input and Output Functions In PET Cardiac Studies, *IEEE Transactions on Medical Imaging*, USA, Vol. 19, No. 3, pp233-242.
34. W. Cai, D. Feng & R. Fulton, (June 2000): Content-Based Retrieval of Dynamic PET Functional Images, *IEEE Transactions on Information Technology in Biomedicine*, Vol. 4, No. 2, pp. 152-158.
35. D. Feng, Guest Editor: (2000): Multimedia Information Technology in Biomedicine, *IEEE Transactions on Information Technology*, June Issue.
36. D. Feng, (Jan 2001): Content-Based Retrieval of Multimedia Information, *International Journal of Image and Graphics*, Vol. 1, No. 1, pp83-91.
37. W. Cai, D. Feng, & R. Fulton, (Jan/Feb 2001): Web-based Digital Medical Images, *IEEE Computer Graphics and Applications*, Vol. 21, No. 1, pp.44-47.
38. H. Wang, D. Feng, E. Yeh, S.C. Huang, (Feb 2001): Objective Assessment of Image Registration Results Using Statistical Confidence Intervals, *IEEE Transactions on Nuclear Science*, Vol. 48, No. 1, pp.106-110.
39. X. Li, D. Feng, KP, Wong, (2001): A General Algorithm for Optimal Sampling Schedule Design for Nuclear Medicine Imaging", *Computer Methods and Programs in Biomedicine*, Vol. 65, Issue 1, pp. 45-59.
40. K. P. Wong, D. Feng, S. R. Meikle & M. J. Fulham, (2001): Simultaneous Estimation of Physiological Parameters and the Input Function: In-vivo PET Data, *IEEE Transactions on Information Technology in Biomedicine*, Vol. 5, No. 1, pp67-76, Mar.

41. K. P. Wong, D. Feng, S. R. Meikle & M. J. Fulham, (2002): Segmentation of Dynamic PET Images Using Cluster Analysis, *IEEE Transactions on Nuclear Science*, vol. 49, no. 1, pp200-207.

42. W. Cai, D. Feng, R. Fulton and W.C. Siu, (2002): Generalized Linear Least Squares Algorithms for Modeling Glucose Metabolism in the Human Brain with Corrections for Vascular Effects, *Computer Methods and Programs in Biomedicine*, vol. 68, no. 1, pp1-14.

43. D. Feng, W. Cai and R. Fulton, (2002): Dynamic Image Data Compression in Spatial and Temporal Domains: Clinical Issues and Assessment", *IEEE Transactions on Information Technology in Biomedicine*. Vol. 6, No. 4, pp262-268.

44. K. P. Wong, S. R. Meikle, D. Feng & M. J. Fulham, (2002): Estimation of Input Function and Kinetic Parameters Using Simulated Annealing: Application in a Flow Model, *IEEE Transactions on Nuclear Science*, Vol. 49, No. 3, pp707-713.

45. David Dagan Feng, W. C. Siu & Hongjing Zhang, Editors: (January 2003): Multimedia Information Retrieval and Management – Technological Fundamentals and Applications, (476 pages), *Springer-Verlag*, Germany.

46. David Dagan Feng, Guest Editor: (Jan 2003): Special Issue on Multimedia Data Storage and Management, *International Journal of Images and Graphics*, Vol. 3, No 1, World Scientific.

47. X. Wang & D. Feng, "Automatic Elastic Medical Image Registration Based on Image Intensity", submitted to *International Journal of Image and Graphics*, accepted 6/2003, final version submitted 7/2003.

48. Sirong Chen, Chilai Ho, Dagan Feng, and Zheru Chi, "Tracer Kinetic Modeling of 11C-acetate Applied in the Liver with Positron Emission Tomography", *IEEE Transactions on Medical Imaging*, accepted, 10/2003, final version submitted 11/2003.

David Dagan Feng received his PhD degree in Computer Science from UCLA in 1988. After briefly working as assistant professor in USA, he joined the University of Sydney, Australia, as lecturer, senior lecturer, reader, and then professor. He is the former Head of Department of Computer Science/School of Information Technologies. He is currently Associate Dean of the Faculty of Science and Director of the Biomedical & Multimedia Information (BMIT) Research Group at the University of Sydney, and Chair-Professor of Information Technology, Center for Multimedia Signal Processing, Department of Electronic and Information Engineering, Hong Kong Polytechnic University. He has published over 300 scholarly research papers, pioneered several new research directions, made a number of landmark contributions in his field, and received the Crump Prize for Excellence in Medical Engineering. More important, however, is that many of his research results have been translated into solutions to real-life problems and have made tremendous improvements to the quality of life worldwide. He is a Fellow of ACS, HKIE, IEE and IEEE, and is currently chairman of IFAC-TC-BIOMED.