

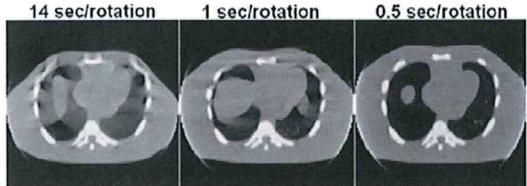
CT/SPECT 装置を使った吸収補正法の確立に向けて

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2008 年 12 月 9 日

背景

CT/SPECT 装置を使うと体内の吸収減弱係数マップが撮像でき、これを用いた正確な吸収補正が可能になると期待されてきた。また QSPECT 再構成法では散乱線補正までも実施可能であり、まさに PET に匹敵する定量評価が可能になると考えられる。一方、心筋領域の検査では、呼吸動に基づくエミッションデータと X 線 CT 画像との mismatch が存在し、未だ普遍的な補正法が成熟するには至っていない。特に呼吸を止めて高速撮像を行う方法では呼吸動に基づく吸収減弱補正のエラーが顕著とされる。一方、低い線量で比較的長時間（10 秒間程度）撮像する方法も試みられるが、十分に平滑化されるわけではなくアーチファクトが発生する場合がある。そのような中で、中期フェーズで呼吸を止めて高速撮像を行う方法が実用的であるとされるが、未だにその正当性や限界についての報告はない。心臓核医学の分野において、CT/SPECT 装置を用いた正確な画像の提供手法の確立に対する期待は大きく、早急に本課題を解決することが望まれている。

	<p>第 1 図 心筋部の X 線 CT 再構成画像の回転速度依存性。低速撮像では再構成アーチファクトが顕著である。図は Johns Hopkins 大学 B. Tsui 氏より。</p>																
<table border="1"> <thead> <tr> <th></th> <th>Attn. Map</th> <th>Polar Plot</th> <th>vs. no motion (% diff.)</th> </tr> </thead> <tbody> <tr> <td>Shallow (0.5 cm)</td> <td></td> <td></td> <td>2 -3 6 8</td> </tr> <tr> <td>Normal (1.5 cm)</td> <td></td> <td></td> <td>4 -19 7 2</td> </tr> <tr> <td>Deep (3 cm)</td> <td></td> <td></td> <td>18 -44 28 14</td> </tr> </tbody> </table>		Attn. Map	Polar Plot	vs. no motion (% diff.)	Shallow (0.5 cm)			2 -3 6 8	Normal (1.5 cm)			4 -19 7 2	Deep (3 cm)			18 -44 28 14	<p>第 2 図 X 線 CT 高速撮像時のエミッションポラマップ表示における、呼吸深度依存性。呼吸深度に依存してエミッション画像のアーチファクトは大きくなり、診断に重大な誤差をきたしてしまう。図は Johns Hopkins 大学 B. Tsui 氏より。</p>
	Attn. Map	Polar Plot	vs. no motion (% diff.)														
Shallow (0.5 cm)			2 -3 6 8														
Normal (1.5 cm)			4 -19 7 2														
Deep (3 cm)			18 -44 28 14														

目的

本研究の目的は、従来から行われてきた外部線源 (^{99m}Tc) を使ったトランスミッションスキャン法をゴールドスタンダードとし、中期フェーズで呼吸を止めて CT 撮像する方法の精度評価を行うことである。また、具体的なプロトコルにおける最適化を行い、当該 CT 撮像法の精度向上を目指すものである。

方法

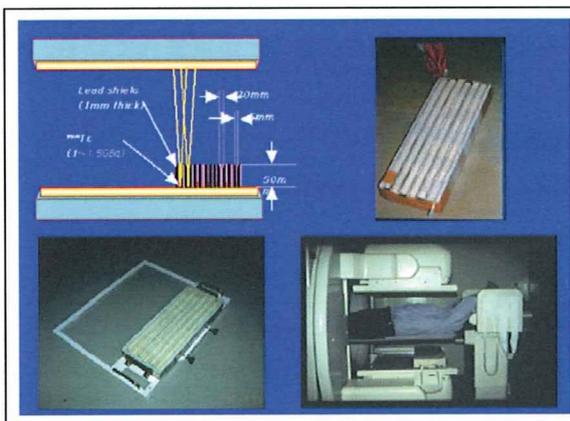
トランスミッションスキャンには、過去に性能評価を行った装置(文献 1)を利用する。第 3 図に示す構造

を有し、定量的な吸収減弱係数の計測が保障されている。タッチセンサー機構を有し安全面の配慮もなされている。対向型 SPECT 装置の一つの検出器表面に設置し、もう一つのカメラにて 360 度撮像を行う。ブランクスキャンに引き続き約 10 分間のトランスミッションスキャンを行い、吸収減弱係数マップを計算する（第 4 図）。

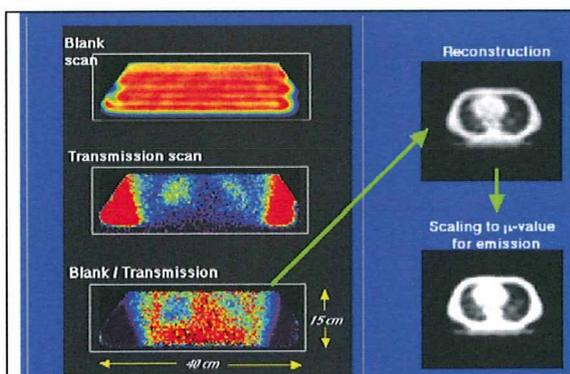
CT/SPECT 撮像においては、外部カメラを設置することで被験者自身が呼吸に基づく胸部の動きのモニターを可能にし、自身で中期フェーズでの呼吸停止を可能にする。この際の高速 X 線 CT 撮像を行い、セグメンテーション処理を行うことで、定量 SPECT 撮像に必要な吸収減弱係数マップを計算する。

エミッションスキャンとして、吸収減弱および散乱線の影響が大きいことが知られている ^{201}Tl 、および $^{99\text{m}}\text{Tc}$ 心筋血流製剤、および ^{123}I 標識製剤などの投与後の撮像を行い、上記二つの吸収減弱係数マップを利用したエミッション画像を再構成し、両者を比較する。両者が一致するような撮像プロトコルの最適化を試みる。

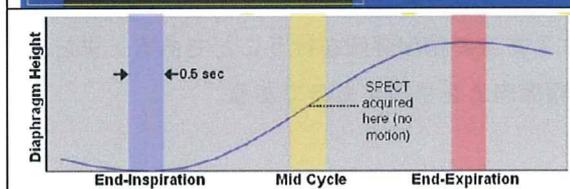
評価指標は、心筋領域における放射性薬剤の集積分布の視覚的比較、および放射能濃度の定量的比較、さらに ^{201}Tl においては心筋血流量（安静時および血管拡張時）の定量計測を行い、PET との一致を確認する。



第 3 図 当該研究で利用するトランスミッション線源の外観図。 $^{99\text{m}}\text{Tc}$ 線源を封入し、ブランクスキャンの後にトランスミッションスキャンを行う。計測における散乱線の影響を最小化し、かつ感度を最大化する設計仕様となっている。当該線源ブロックは対向型 SPECT 装置の一方のカメラ上面に設置し、もう一つのカメラにて撮像を行う。線源ブロックの表面にはタッチセンサーが装着されており、安全利用が図られている。



第 4 図 上記トランスミッション線源を利用して得たヒト胸部の吸収減弱係数マップの計算プロセス。ブランクスキャンの後にトランスミッションスキャンを行い、FBP 再構成法にて吸収減弱係数マップを得る。



第 5 図 呼吸動のフェーズ。中期フェーズにて撮像する、あるいはそれぞれの終端期にて撮像し平均化する、などの手法の妥当性を、TCT 線源データを参照に確認する。

対象

臨床診断を目的に CT/SPECT の検査を受けた患者殿最大で 20 名（最低 10 名）とする。健常ボランティアにおいても最大 20 名（最低 10 名）を対象とする。

予想される結果

当該検討によって、高速 X 線 CT 撮像に基づく CT/SPECT 画像再構成の最適なプロトコルが見出される。中期フェーズにて撮像する、あるいはそれぞれの呼吸終末期にて撮像し平均化するなどの手法の妥当性を、TCT 線源データを参照し確認する。現在の臨床核医学で大きな課題となっている CT を使った吸収減弱補正の最適化が確立することで、当該センターにおける日常診療の精度向上に貢献する。国際標準の樹立にも貢献する。

文献

1. Iida H, Shoji Y, Sugawara S, Kinoshita T, Tamura Y, Narita Y, Eberl S. Design and Experimental validation of a Quantitative myocardial ^{201}Tl SPECT System. *IEEE Trans Nucl Sci.* 46:720-26, 1999

QSPECT-Reconモード 使用手順マニュアル

How to handle SPECT - projection data
with X-CT mu map obtained from
Symbia-T6 (at NCVC, Osaka, Japan)
for QSPECT reconstruction?

Kenji Ishida/ Hidehiro Iida

November 28, 2008

March 24, 2010

How to handle SPECT-projection data for QSPECT reconstruction?

QSPECT Project

March 24, 2010

1

Test data information:

Materials

GCA7200 (Toshiba Medical Systems Corporation, Tochigi, Japan)
3D Brain Phantom (Molecular Imaging Labo inc., Osaka, Japan)
filled with 168.8 MBq Tc-99m solution in grey matter area,
including bone structure

Tc-99m SPECT

Energy center=140keV, Energy window=20%
Time per View=79.15sec/view, matrix=128x128, magnification=2.0
Start Angle=0, Step degree=4.0, Number of Views=90
Mode=continuous(return)

SPECT-projection data are exported to off-line Unix PC.
(Toshiba NEMA format)

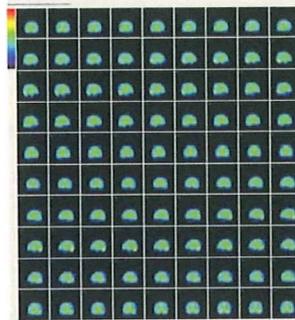
1. Emission_Projection

2

Test data included

- HowToUseQSPECTRecon.ppt
 - QSPECT_OUT
 - Raw Data
1. Emission Projection

1. Emission Projection



3

How to install QSPECT reconstruction program

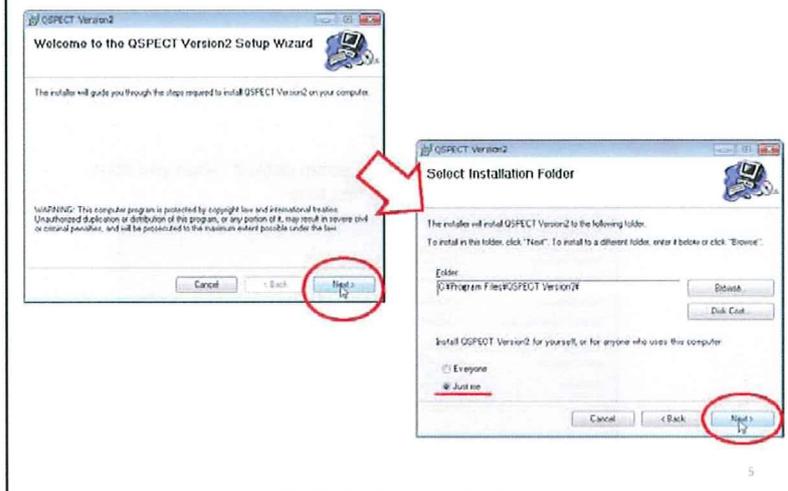
It can be downloaded from the following URL.

http://www2.invrad.com/qspect/attachment/wiki/QspectSetup/QSPECT_CD_Image_V2.6.1_20091222.zip

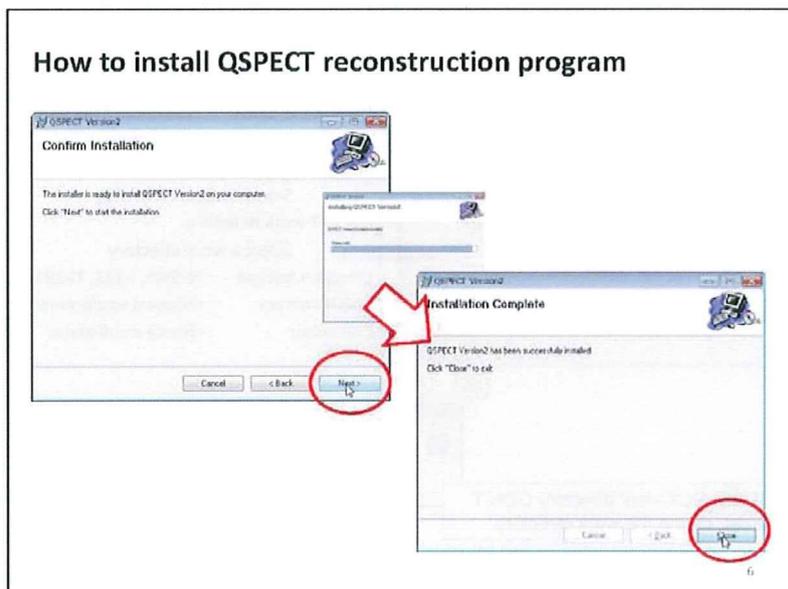
Should run the setup.exe in Fversion folder

<Warning>
Log on to the computer as an administrator,
and then install QSPECT package.

How to install QSPECT reconstruction program



How to install QSPECT reconstruction program



Set up QSPECT default



Run QSPECT-Recon program.

You have to set this "QSPECT setup default" when you start up QSPECT-Recon program first time.

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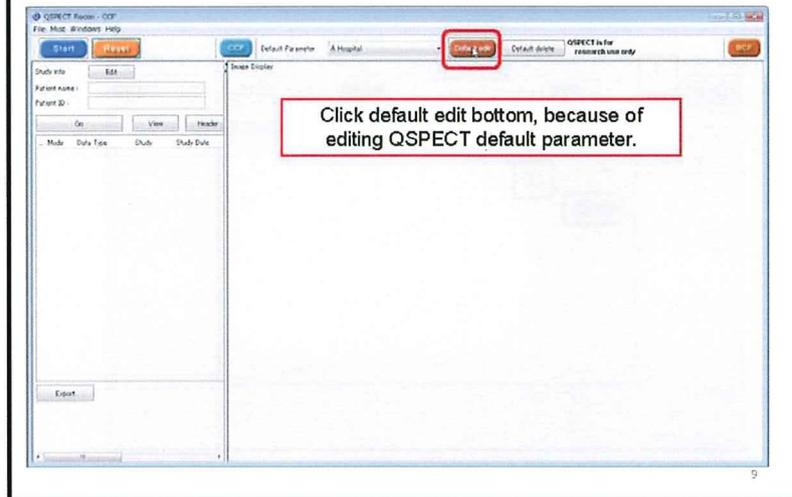
Set up QSPECT default

Default file name : Type default file name
 Hospital name : Type hospital name
 Import directory :
 Select a import directory
 QSPECT work directory :
 Select a work directory
 Emission isotope : Tc-99m, I-123, TI-201
 SPECT camera : choose a equipment
 Collimator : choose a collimator

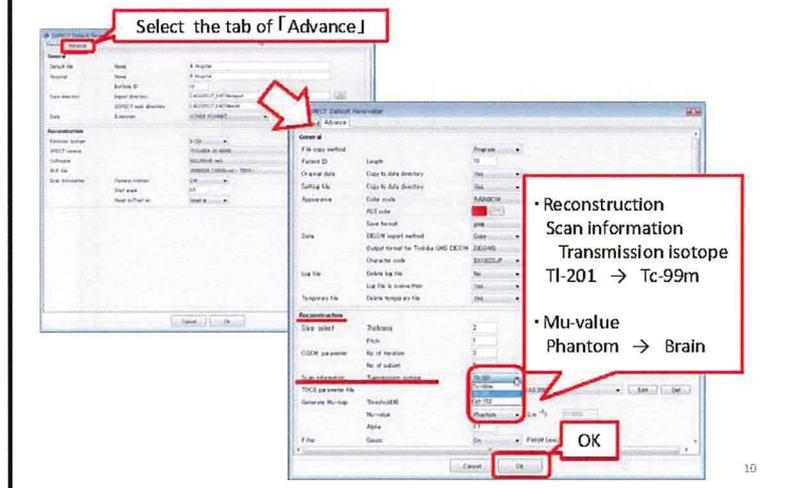
If QSPECT work directory DON'T exist, create the work directory.

2

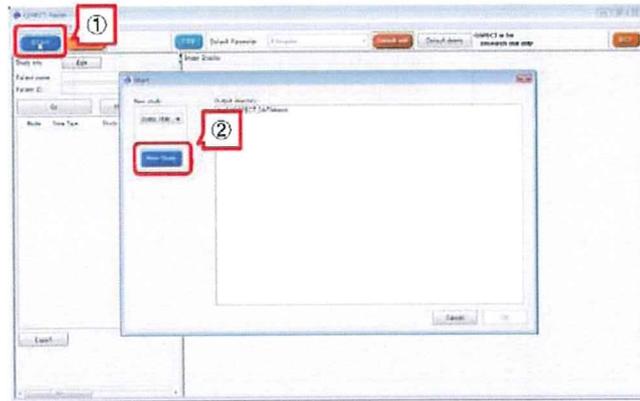
Set up QSPECT default



Set up QSPECT default

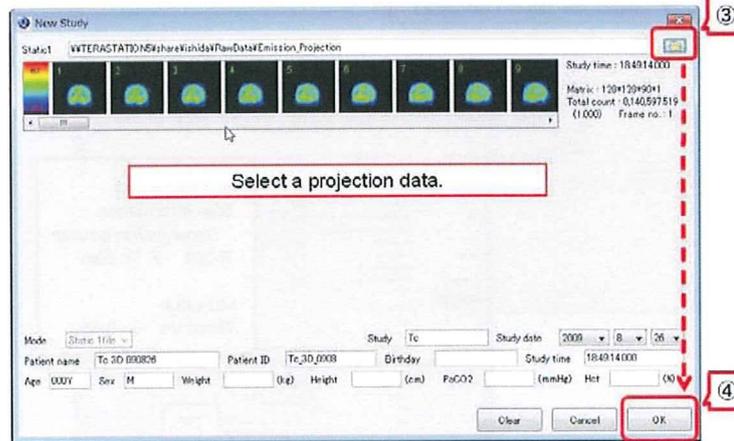


How to reconstruct a projection data



11

How to reconstruct a projection data



12

How to reconstruct a projection data

(1) Click a Generate Mu-map button, and then make a mu-map by threshold.
 (2) Run reconstruction.

15

How to reconstruct a projection data

⑨ You can reslice a reconstruction image what you drag a cross shape bar.

15

QSPECT

(Quantitative SPECT image reconstruction)

For Heart

定量SPECT画像再構成パッケージ(QSPECT)
の心筋領域での利用について

March 2007

Department of Investigative Radiology, Advanced-Medical Engineering Center,
National Cardiovascular Center Research Institute

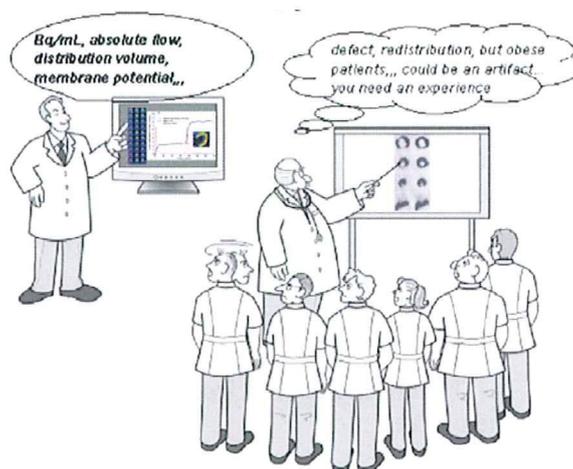
Preface

Nuclear Medicine is a unique modality, and provides images which reflect fundamental biophysiological functions in various organs, such as perfusion, metabolic rates of particular substrates, receptor binding potential. Mathematical model-based analysis of regional kinetics (uptake and clearance) of the radiotracer potentially allows quantification of functional parameters from the images. Physiological parameter estimation using kinetic analysis is well established in positron emission tomography (PET), mainly in the brain, but also in the myocardium, skeletal muscle and other regions. In contrast, dynamic single photon emission computed tomography (SPECT) studies, particularly when performed with a single detector system, have been limited by SPECT's low sensitivity, poor resolution and restricted dynamic frame rate due to the need for mechanical rotation of the detector. The widespread introduction of multi-detector SPECT systems, with their improved sensitivity and increased frame rate and advances in SPECT attenuation and scatter correction have opened the opportunity for SPECT to invade the traditional PET territory of physiological parameter estimation.

We have recently developed a noble technique for quantitative SPECT reconstruction in order to assess accurately the radioactivity distribution in the body. The technique involved a transmission-dependent convolution subtraction (TDCS) method for scatter compensation, and the ordered-subset maximum-likelihood expectation maximization (OSEM) reconstruction including the attenuation correction. The former is originally proposed by Meikle et al (1994) and further optimized by Narita (1997, 1998) and other investigators (Iida et al., 1998a, Iida et al., 1998b, Kim et al., 2001). It has then been demonstrated that this strategy enables absolute quantitation of radioactivity distribution in brain and thorax regions, and further shown that physiologic functional images such as cerebral blood flow and myocardial perfusion may be quantitated by means of the compartmental model analysis.

A program package, QSPECT, has been developed in National Cardiovascular Center (NCVC), so as to provide absolute quantitation of regional radioactivity in the body from existing projection data sets obtained using clinical SPECT scanners. with particular focus

on quantitation of physiological functions in myocardial SPECT studies. The program is written with JAVA interface and can run on Windows-XP platform. The program can handle several data formats including Dicom and Analyze. This note briefly overview this package. How-to-use will also be presented. We hope that this program will be of a help in the area of clinical research.



Contents

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 - TDCS for scatter correction
 - OSEM reconstruction
 - Collimator dependency
 - Validation experiments
- Literatures

Specification of QSPECT program

- Reconstruction is carried out according to OSEM with attenuation correction. Projection data should be geometric-mean (GM) for parallel-beam.
- Transmission-dependent convolution subtraction (TDCS) method has been employed as scatter correction. Attenuation-to-scatter fraction tables are presented for ^{99m}Tc , ^{201}Tl , ^{123}I isotopes. The table for ^{123}I includes collimator penetration process determined empirically for various collimators from various manufacturers.
- μ map from TCT (or edge-detection for brain).
- Mmap generated from X-ray CT ma also be of use
- Pixel counts are presented in units of Bq/mL. (BCF (Bq Calibration Factor) needs to be defined prior to use)

Pixel counts (Bq/mL) are independent of

- Scan duration
- The number of heads
- Kinds of collimator
- Pixel size (64x64 or 128x128 etc)
- Radioisotope
- Manufacturer
- etc
- JAVA interface, with C code as the foundation.
- R/W format: Dicom, Analyze, and Dr.View.
- Runs on Windows (XP) with JAVA 1.4.1 or more. CPU 3GHz. Memory 512 MB. Disk space>30MB. Display > XGA (1024x768).
 - Emission Projection File should be
 - Uniformity corrected.
 - Parallel-beam (need to be converted to parallel-beam equivalent if acquired by fanbeam collimator)
 - File format should be Dicom, Analyze or Dr.View

1. Input Files

a) Projection file

File name should have 18 characters as a general rule. Maximum 23 characters. Our rule is as follows.

File Name : **[patient ID]_[date]_[modality]_[type].(ext)**
 - Patient ID : 7 characters
 - Date : 3 characters (ymd : year-month-day)
 - Modality : 1 character
 - Type: 4 characters (2 characters for acquisition, 2 characters for study)
 - Ext : Extension (dcm for DICOM, hdr/img for ANALYZE)

Example)

1234567_44b_s_p1sr.dcm
 Patient ID : 1234567
 Study date : 11 April 2004
 Acquisition equipment : SPECT
 Data type : reconstructed static image from 1st static scan data

Data format should be either Dicom, Analyze or Dr.View.

b) Attenuation mu-map file

This program can read mu-map for given radioisotopes. This file should be in Analyze format, and should have units of cm^{-1} . Pixel counts may be approximately 0.15 for ^{99m}Tc in water. Two-dimensional mu-maps should be defined at each slice pixel in the projection data.

The mu-map may also be generated in this program by defining edge of attenuation-uncorrected FBP images. This option may be used for some brain studies.

2. Temporary Files

File format is ANALYZE.

[img-file-name]_UNIMAP: uniform attenuation-map generated by using edge-detection (if mu-map is defined by edge-detection program)

[img-file-name]_Scat: Estimated scatter-component projection

[img-file-name]_Prim: Scatter-corrected projection (with geometric mean typed)

[img-file-name]_ACSC: Reconstructed image with attenuation + scatter correction

[img-file-name]_NoAC: Reconstructed image with no attenuation using FBP

[img-file-name]_UNIMAP_MuAP: Transmission projection calculated from Mu map

3. Output File

Output file name can be defined in the user-interface window. Default file name is defined by replacing 18th character with "r". File format is the same as input file format (Dicom, Analyze, Dr.View).

Input file...ex) 1234567_44b_s_ils_.img
 Output file (default) . . . ex)
 1234567_44b_s_ilsr.img

4. Parameter Files

def.txt: Default parameters are saved into this file by [File]->[Default]->[Save]. Thickness, Pitch, Iteration, Subset, Camera Rotation, Start Angle, Head-In/Feet-In, Emission Isotope, Transmission Isotope, BCF, TDCS parameter, Threshold(%), Mu-value, cm^{-1}

env.txt: Parameter set by [Settings]->[Options] are save into this file. Data directory, temporary directory etc.

para.txt: Parameter values set on the menu window are saved into this file. Slice Select, Scan Information, OSEM Parameter, etc

QSPECT_000_S_BCF.txt: Bequerrel calibration factor (BCF)

QSPECT_000_S_BCF_Default.txt: BCF defaults

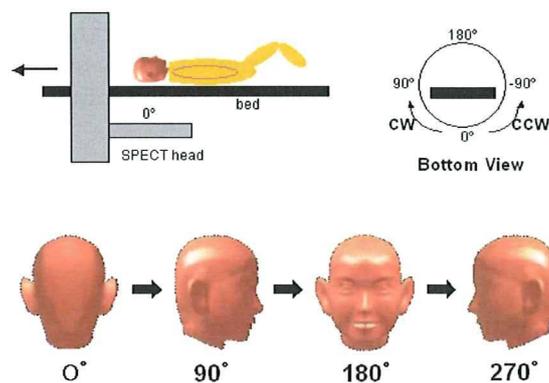
[image-file-name].time:

Number of frames, Acquisition time for each view for each frame, Number of Heads

5. Definition of acquisition setting

QSPECT has an original definition of axis of coordinates. You should set up parameters (camera-rotation, start-angle, subject-position)

so as to show projection as below.



Projection data should be displayed as in this figure in the main menu window. Set three parameters of camera-rotation, start-angle, subject-position, so as to display as this.

	Rotation	Start Angle	Orientation
	CW	0	Head-in
	CW	90	Head-in
	CCW	0	Head-in
	CW	0	Feet-in

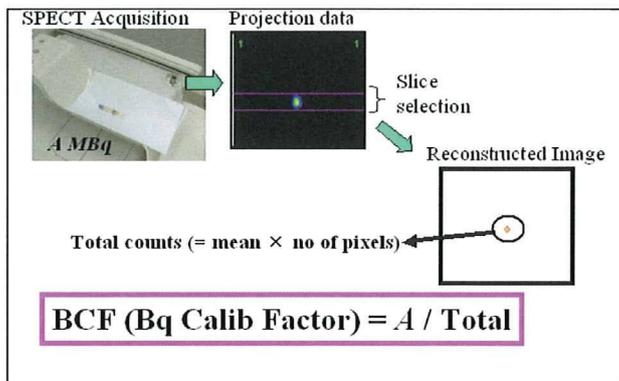
Example of set-up parameters (Rotation, Start Angle, Orientation)

Operation of the program

1. Settings

a) BCF (Becquerel Calibration Factor)

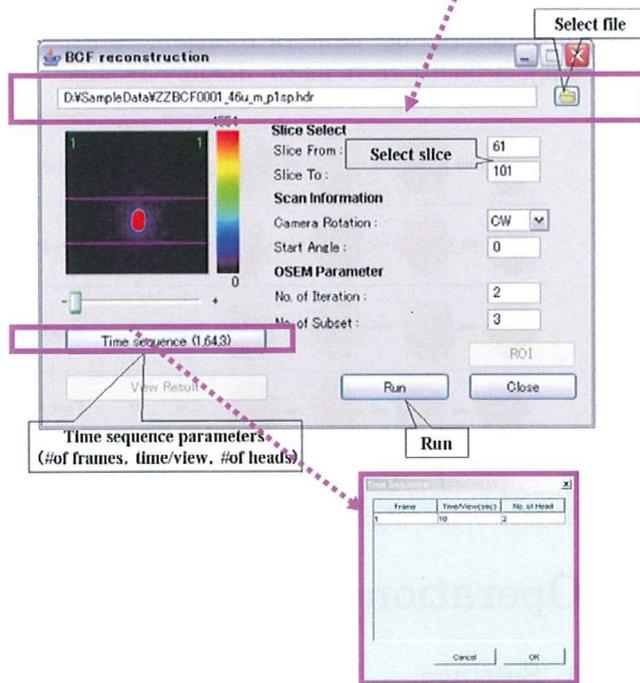
Prior to use QSPECT, BCF needs to be defined. This can be done by scanning a small syringe of known radioactivity, typically supplied from radio-pharmaceutical companies.



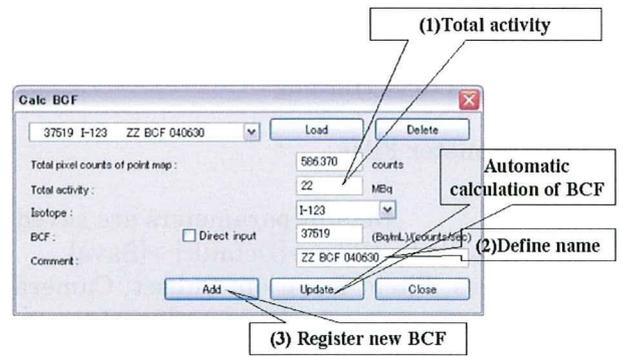
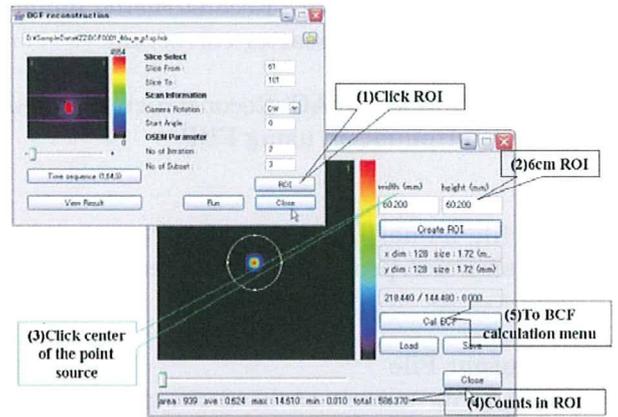
To define BCF in QSPECT, select BCF reconstruction menu in Settings, and do reconstruction for a single-slice projection that covers the whole activity. BCF can then be calculated as the true radioactivity over the pixel counts of the reconstructed image.

Settings→BCF reconstruction

Hot Source Projection Data



Columns in Time sequence need to be filled as:
 The number of frames (1 if single time frame)
 Acquisition time (sec)/View
 Number of heads (SPECT cameras)



BCF((Bq/mL)/(counts/sec)):

$$BCF = \frac{\text{Time activity (MBq)}}{\text{(Total pixel count of point map (counts))}}$$

b) TDCS parameter for ¹²³I

TDCS scatter correction technique requires a previously-determined attenuation-to-scatter fraction table for each isotope. Previous studies demonstrated that collimator dependency of this table was minimal, and virtually the same table can be applied to most isotopes such as ^{99m}Tc and ²⁰¹Tl. ¹²³I has a unique problem associated with the penetration of high-energy photons which cause large background over the whole field-of-view. TDCS algorithm could include empirically this fraction by defining a constant background in the attenuation-to-scatter fraction table. However, this constant significantly depends on the design parameters of the collimator. The QSPECT program includes several tables for most commercially available collimators. Chose appropriate TDCS parameter values in Settings, if one wish to use QSPECT for ¹²³I compounds. This is needed only for ¹²³I, but the same parameter

sets can practically be applied to other isotopes such as ^{201}Tl and $^{99\text{m}}\text{Tc}$.

c) Data Directory

Default directories can be set by selecting Options in Settings.

2. Image Reconstruction

To run:
QSPECT>QSPECT Reconstruction

1. Select Emission Projection File:

QSPECT can load multiple image files to reconstruct images using a common mu-map data.



2. Confirm and set scan information

- CCW/CW CW(clockwise) or CCW (counterclockwise)
- Start angle 0 or 90 or 180 or -90 only
- Head/feet-in
- Matrix size (displayed automatically by use of data information)
- # of frames (displayed automatically by use of data information)
- # of projections (displayed automatically by use of data information)
- Emission isotope (TDCS parameters will automatically defined)

Transmission isotope

BCF value

3. Define reconstruction parameters

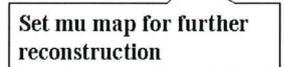
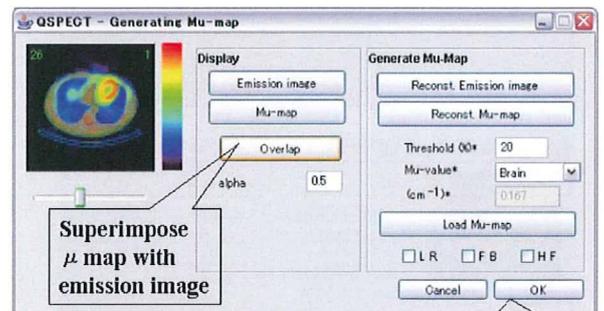
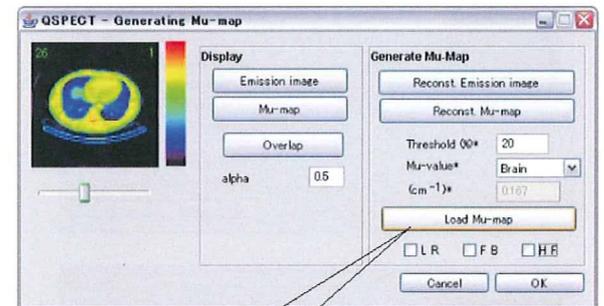
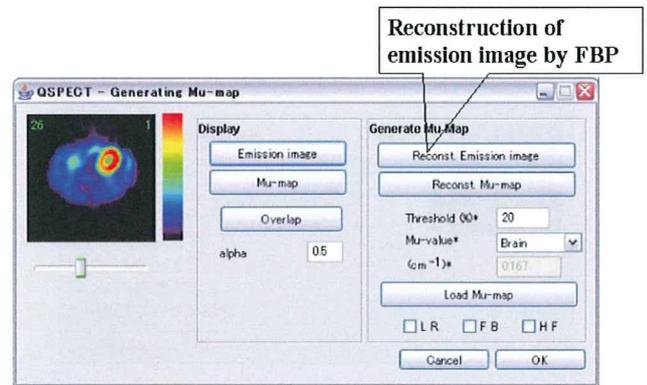
- Slice From:
- Slice To:
- Thickness: unit of pixel
- Pitch: unit of pixel
- No. of planes (determined automatically)
- No. of frame unit of integer

4. OSEM Parameter

- No. of Iteration:
- No. of Subset:
- Attenuation Map File:

5. Generating Mu-map

This menu can be used to define previously-determined attenuation mu map. The mu map can be superimposed to emission images reconstructed without attenuation or scatter correction by FBP, so that the mu map is obtained at the consistent position with emission data.



Mu map images can be flipped by selecting LR, FB, and HF switches

LR: Left or Right

FB: Front or Back

HF: Head or Foot

Multiple columns can be selected, and after finding the suitable direction, click OK. The mu image can be coordinated so as to become consistent with the emission projection data. .

