

# PET Quantification using STIR

**STIR User's Meeting**  
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# PET Quantification

Image elements should correspond to concentration of the injected radiotracer

What corrections are necessary for it:

- Attenuation
- Scatter
- Motion
- Randoms
- Normalization
- Dead Time

# Overview of the talk

PET Quantification using STIR:

3D Scatter Correction

Parametric Reconstruction

Theory

How to use

Examples

Limitations & Future Work

# 3D Scatter Correction

## Single Scatter Simulation - SSS

The scatter probabilities are estimated by Klein-Nishina formula for each possible scatter point in the transmission image.

$$P_{AB} = \int_{\text{scatter volume}} \left( \frac{\sigma_{AS} \sigma_{BS}}{r_{AS}^2 r_{BS}^2} \right) (P_{ASB} + P_{BSA}) dS$$
$$P_{ASB} = \epsilon_{AS}(E) e^{-\int_A^S \mu(E,l) dl} \int_A^S \lambda(l) \frac{d\mu(E, S, \theta)}{d\Omega} e^{-\int_S^B \mu(E',l) dl} \epsilon_{BS}(E')$$
$$P_{BSA} = \epsilon_{BS}(E) e^{-\int_B^S \mu(E,l) dl} \int_B^S \lambda(l) \frac{d\mu(E, S, \theta)}{d\Omega} e^{-\int_S^A \mu(E',l) dl} \epsilon_{AS}(E')$$

## Compensation for multiple and out of the FoV scattering

Each plane of the scatter estimation is scaled by an appropriate factor

# Implementation in STIR

## Scatter Buildblock classes and relative files

`ScatterEstimationByBin`

`sample_scatter_points`

`scatter_estimate_for_one_scatter_point`

`integral_scattpoint_det`

`cached_factors`

`scatter_estimate_for_all_scatter_points`

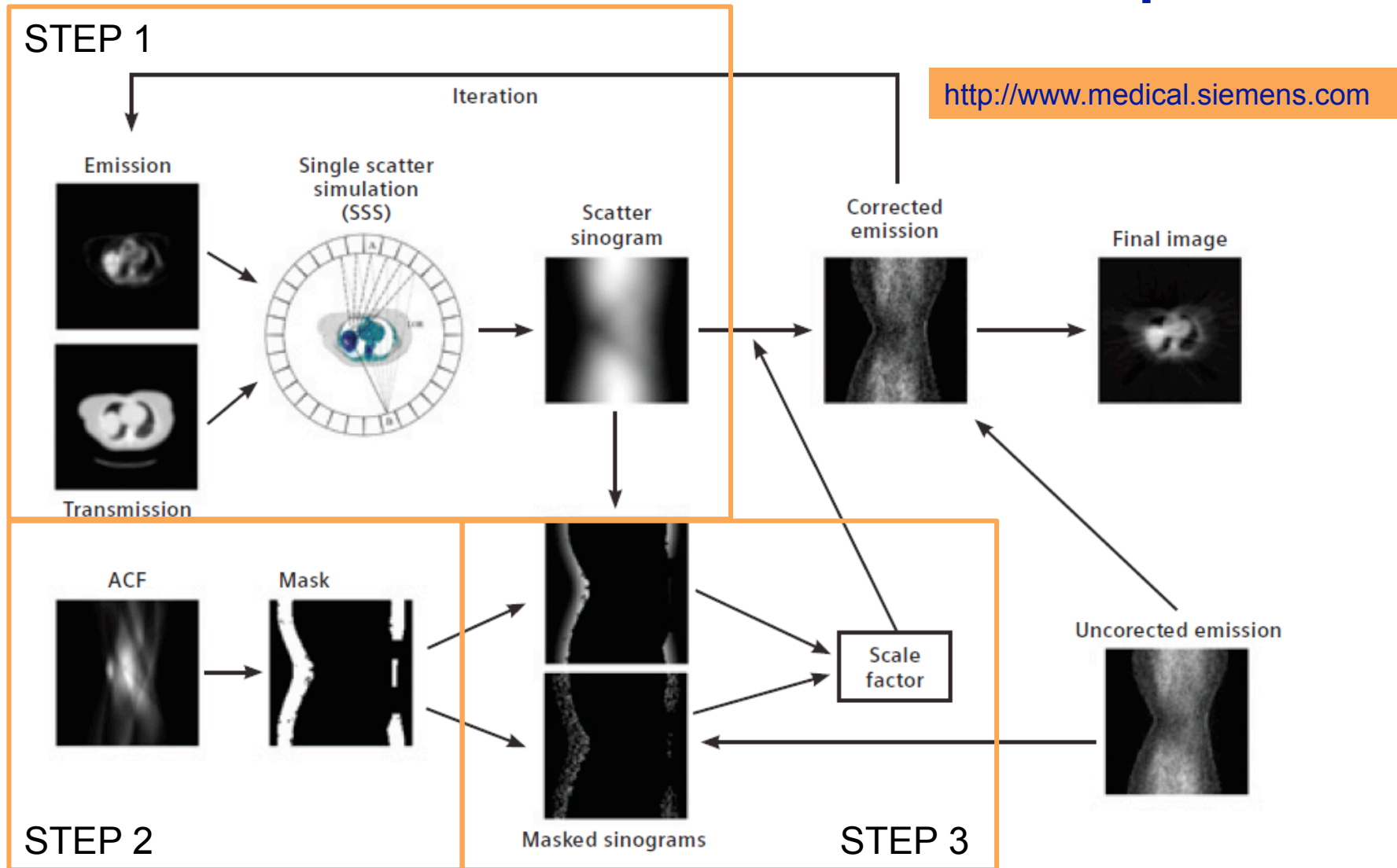
`estimate_scatter`

`upsample_and_fit_scatter_estimate`

`create_tail_mask_from_ACFs`

`scale_single_scatter`

# Scatter Correction in 4 steps



Watson CC "New, Faster, Image-Based Scatter Correction for 3D PET" *IEEE Trans. Nucl. Sci.* 47 (4) 1587-1594, 2000

# STIR How To: Scatter Correct

STEP 1: estimate\_scatter scatter.par

```
attenuation_threshold :=.01
random :=0
use_cache :=1
energy_resolution :=.22
lower_energy_threshold :=350
upper_energy_threshold :=650

activity_image_filename := ${ACTIVITY_IMAGE}
density_image_filename := ${DENSITY_IMAGE}
density_image_for_scatter_points_filename:=${LOW_RES_DENSITY_IMAGE}
template_proj_data_filename := ${TEMPLATE}

output_filename_prefix :=${OUTPUT_PREFIX}

End Scatter Estimation Parameters:=
```

# STIR How To: Scatter Correct

STEP 2: `create_tail_mask_from_ACFs`

```
--ACF-filename <projdata>  
--ACF-threshold <number (1.01)>  
--output-filename <projdata>  
--safety-margin <0>
```

STEP 3: `scale_single_scatter`

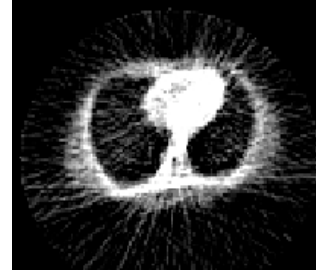
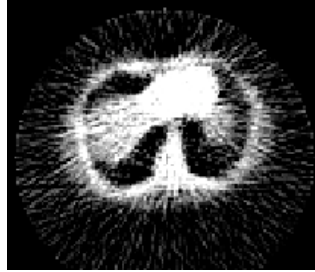
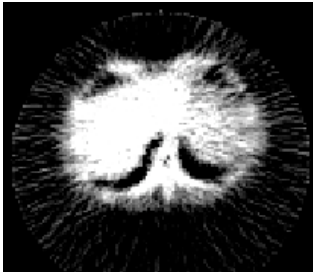
```
--min-scale-factor <number>  
--max-scale-factor <number>  
--remove-interleaving <1|0>  
--half-filter-width <number>  
--output-filename <filename>  
--data-to-fit <filename>  
--data-to-scale <filename>  
--weights <filename>
```

STEP 4: Remove Scatter Estimate and repeat steps (1) and (3).  
Then, average the two scatter estimates.

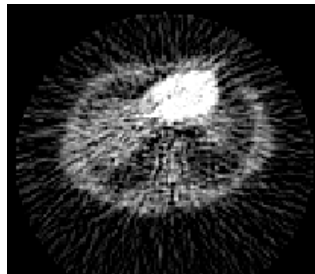
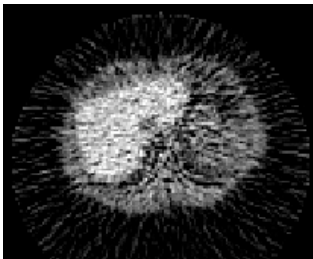


# Phantom Results

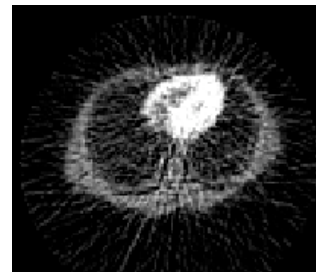
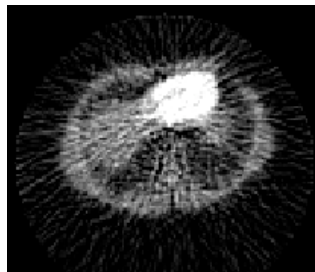
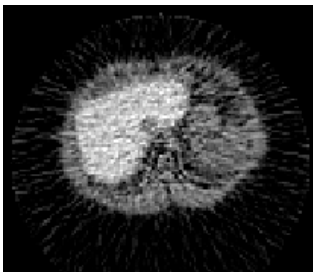
Not corrected



Corrected with SSS



SimSET total scatter corrected



# Implementation in STIR

- Current Limitations - Potential Optimizations:
  - Three separate executables: merge all in one
  - Upsampling for oblique sinograms is handled in a simple way: (pseudo)-inverse SSRB
- Potential Extensions
  - ToF scatter correction
  - Scatter estimation for List Mode data

# Relevant Literature

- Tsoumpas C *et al.* “Evaluation of the Single Scatter Simulation Algorithm Implemented in the STIR Library” 2004 IEEE NSS-MIC, Rome.
- Aguiar P *et al.* “Assessment of scattered photons on the quantification of small animal PET studies” *EANM*, Athens, Greece, 2006.
- Dikaios N “Scatter correction in 3D PET”, MSc Thesis, Patras, Greece, 2006.
- Polycarpou I “Evaluation of Scatter Correction Approaches in PET”, MSc Thesis, King’s College London, 2009.

# Overview

PET Quantification using STIR:

3D Scatter Correction

Parametric Reconstruction

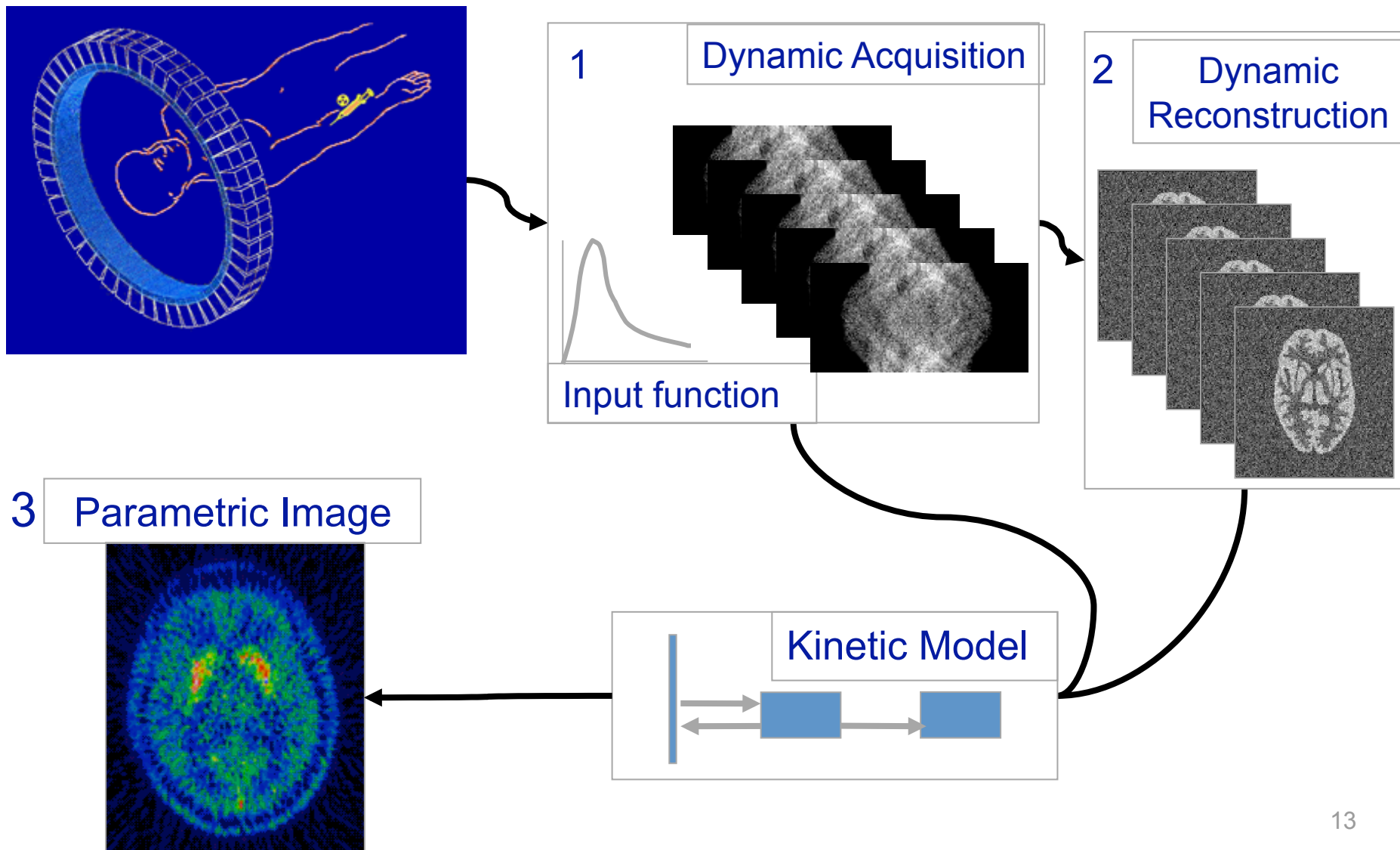
Theory

How to use

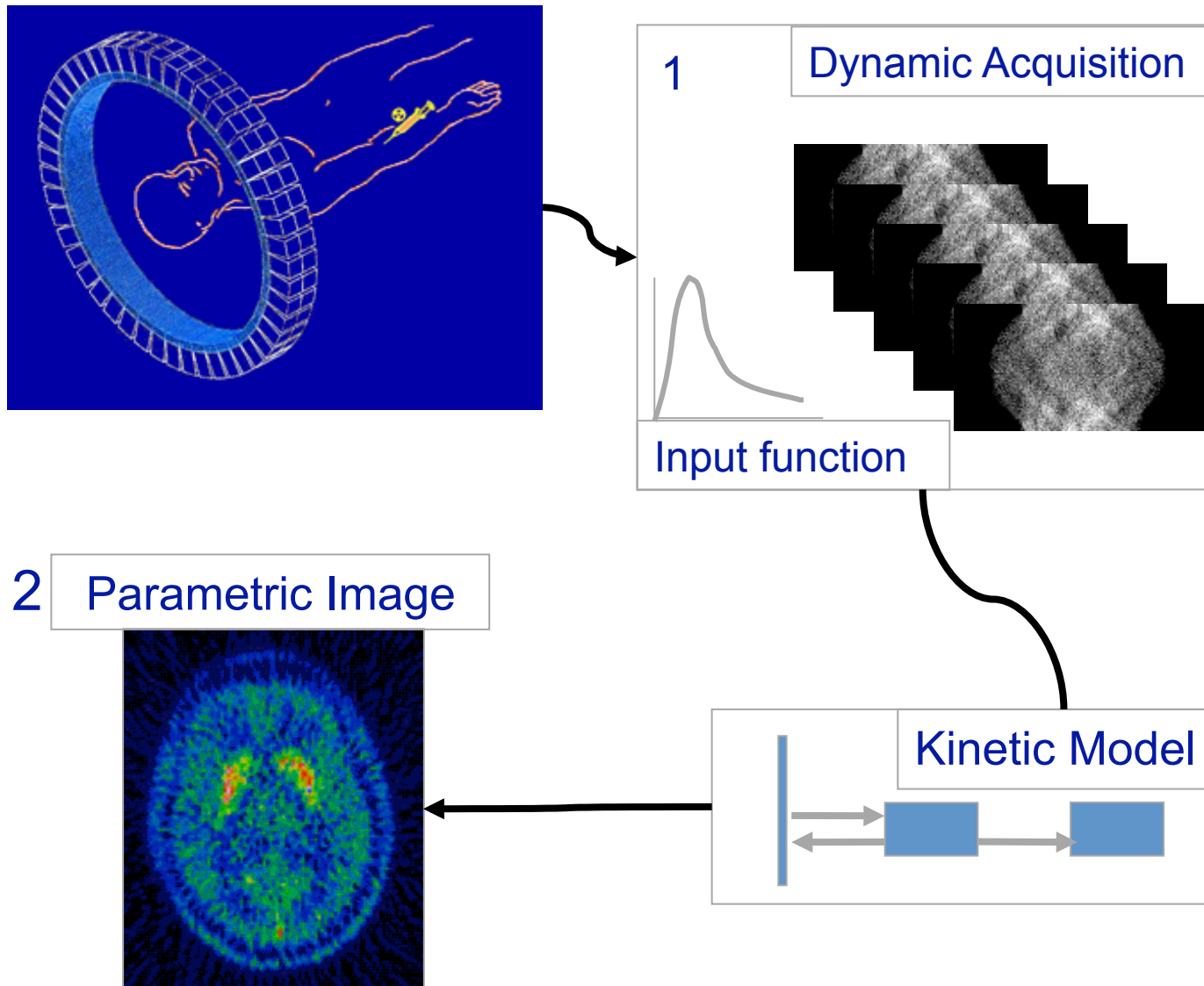
Examples

Limitations & Future Work

# Quantitative dynamic studies



# Parametric Reconstruction



# Why Direct Reconstruction?

- Image Reconstruction: FBP does not offer high resolution and quality parametric images, thus OSEM would be preferable. However, the statistical properties of the reconstructed images are not well approximated with normal distribution for OSEM (*Foundations of Image Science, Barrett & Myers*).
- Kinetic Modelling: Assume Normal Distribution of emission images within repeated measurements.

# Parametric Reconstruction

An iterative algorithm based on OSEM that integrates the kinetic model in reconstruction

$$K_{vk}^{(n+1)} = K_{vk}^{(n)} \frac{1}{\sum_{b,f} P_{bvf} M_{kf}} \sum_{b,f} P_{bvf} \left( \frac{Y_{bf}}{\sum_{\tilde{k}, \tilde{v}} P_{b\tilde{v}f} (K_{\tilde{v}\tilde{k}}^{(n)} M_{\tilde{k}f}) + S_{bf} + R_{bf}} M_{kf} \right)$$

$K$ : Kinetic Parameter

$M$ : Linear Kinetic Model Matrix

$S, R$ : Scatter and Random Sinograms

$P$ : System Matrix (including scanner geometry, attenuation, normalisation etc.)

$Y$ : Projection Data

$b, f, v, k$ : notations for sinogram, bins, time frames, voxels, kinetic parameter

C. Tsoumpas, F.E. Turkheimer, K. Thielemans, "Study of direct and indirect parametric estimation methods of linear models in dynamic positron emission tomography." *Med Phys*, 2008.



# Implementation in STIR

## Modelling Buildblock classes and relative classes

ParametricDiscretisedDensity

KineticModel

KineticParameters

PatlakPlot

ModelMatrix

PlasmaSample/PlasmaData

PoissonLogLikelihoodWithLinearKineticModelAndDynamicProjectionData

DynamicProjData

DynamicDiscretisedDensity

POSMAPOSL/POSSPS

# STIR How To: Modelling

## Indirect Patlak Plot

### Example for Reference Tissue

```
Patlak Plot Parameters:=  
  
time frame definition filename:=time.fdef  
starting frame := 23  
calibration factor := 1  
scale factor := 1  
blood data filename := ref.roi  
; In seconds  
Time Shift := 0  
In total counts := 0  
In correct scale := 1  
  
end Patlak Plot Parameters:=
```

### Example for Plasma Input Function

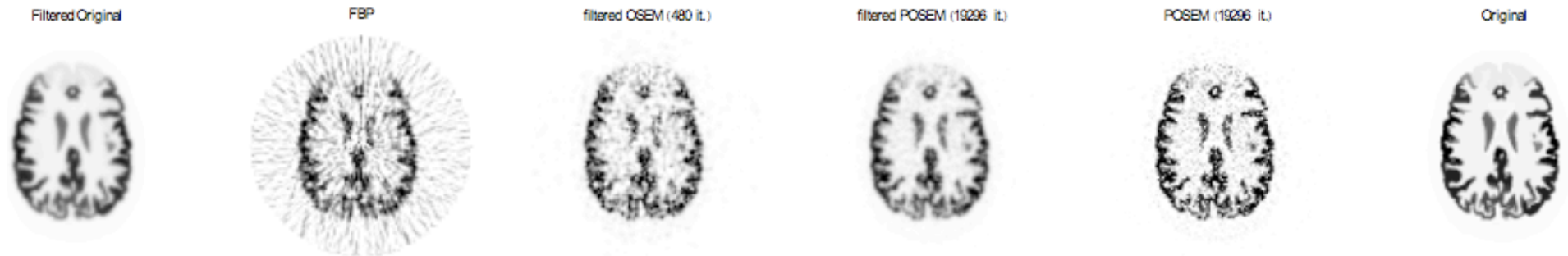
```
Patlak Plot Parameters:=  
  
time frame definition filename:=time.fdef  
starting frame := 23  
calibration factor := 1942  
scale factor := 1  
blood data filename := plasma.tac  
; In seconds  
Time Shift := 15  
In total counts := 0  
In correct scale := 1  
  
end Patlak Plot Parameters:=
```

## Direct Reconstruction (POSMAPOSL or POSSPS)

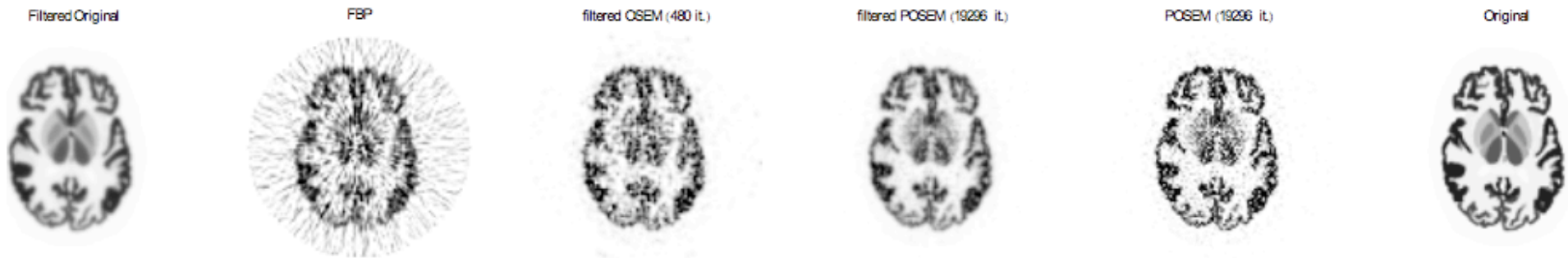
```
objective function  
type:=PoissonLogLikelihoodWithLinearKineticModelAndDynamicProjectionData
```

# Comparison of converged images of a single realization

FDG uptake for the plane 23

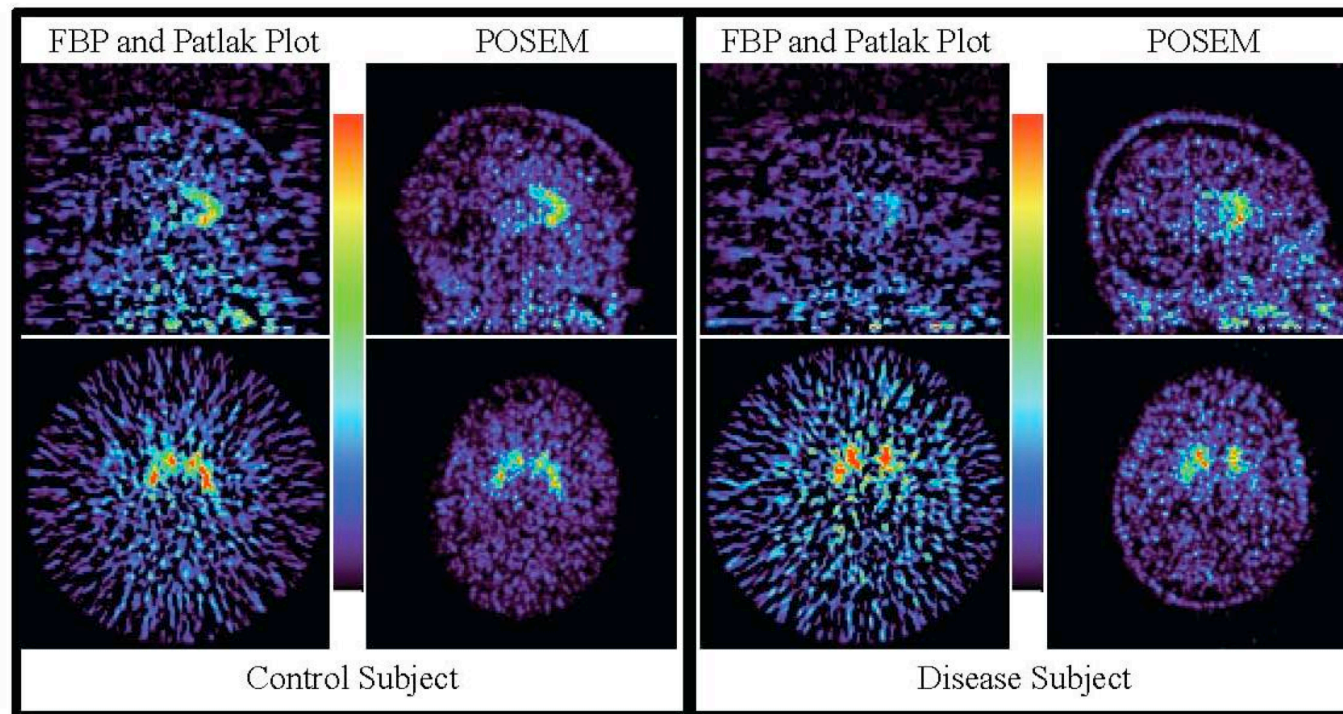


FDG uptake for the plane 30



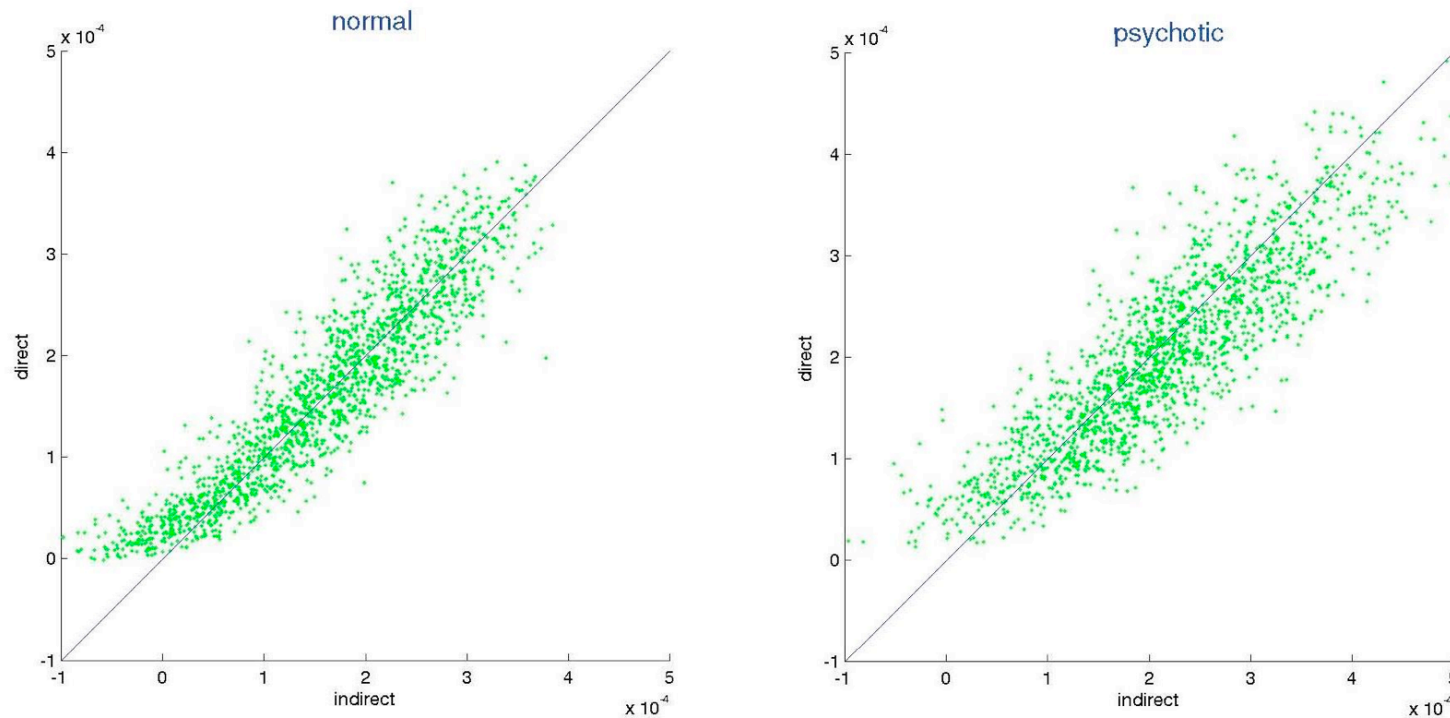
Two transaxial planes of the phantom images for one noise realization for the FDG uptake reconstructed with the different methods. Inverse grey scale was used ranging from 0 to the maximum of the original parametric planes. (Note that the last 96 POSEM iterations were performed with PMLEM)

# Example of an FDOPA study



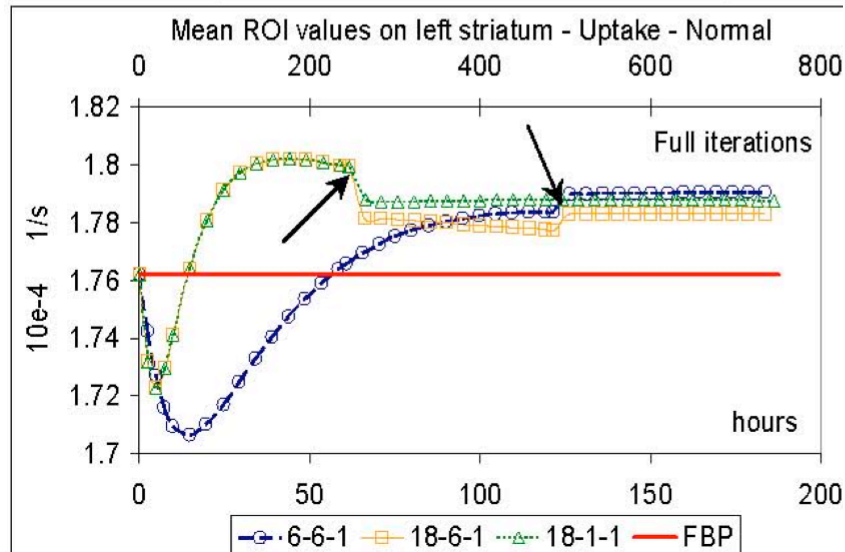
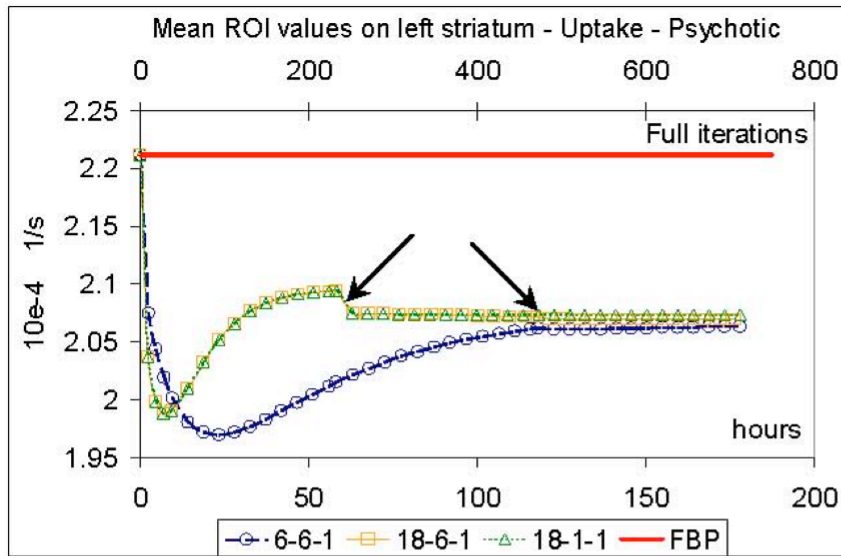
Comparison of parametric maps for a patient and a healthy volunteer on a large axial FoV and high sensitivity PET scanner.

# Quantitative Comparison



Voxel-wise scatter plots comparing the quantitative values in the left and right striatum for a normal (left side) and an abnormal (right side) subject.

# Need for Speed



The mean ROI values (left) and standard deviation (right) for the tracer uptake on the left striatum are presented for a psychotic (up) and a normal (down) study. Three different descending subsets schemes are presented.

G. Angelis, *et al.* WMIC, Nice, France, 2008.

# Implementation in STIR

- Current Limitation:
  - Compilation only by defining the NUM\_PARAMS as preprocessor variable
- Possible Optimization:
  - POSMAPOSL could use less fwd-projection steps
  - Much faster convergence using alternates steps direct reconstruction (Wang and Qi, 2009 TMI)
- Potential Extensions
  - Straight integration of other algorithms
  - Additional temporal basis (e.g. Spectral Analysis, B-Splines)
  - List-Mode based direct reconstruction

# PET Quantification

What next?

- Motion Correction
- *Randoms*
- *Normalization*
- *Dead Time*

However, details from the scanner manufacturers are not easily accessible.



# Acknowledgments

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