



Deutsche
Gesellschaft
für Nuklearmedizin
e.V.

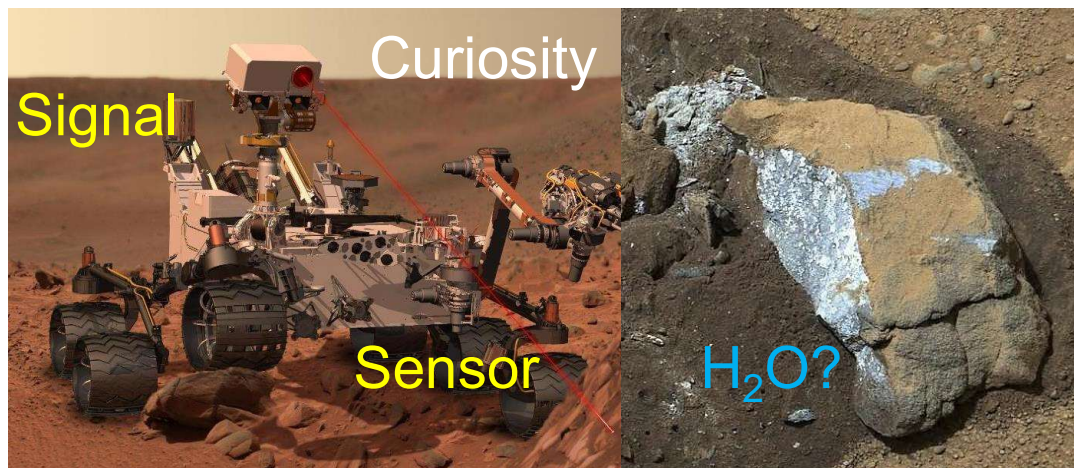
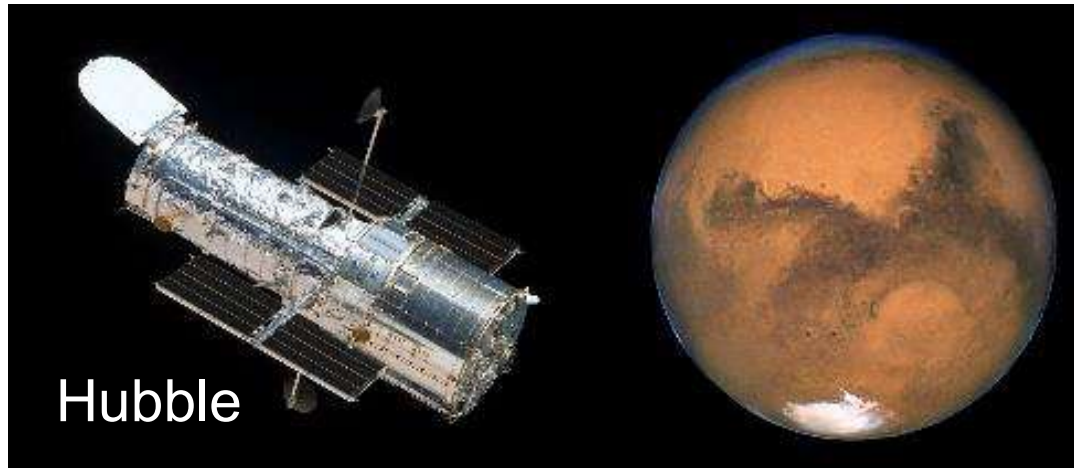
Translational Research in Molecular Imaging and Radionuclid Therapy

August 31 – September 2, 2017

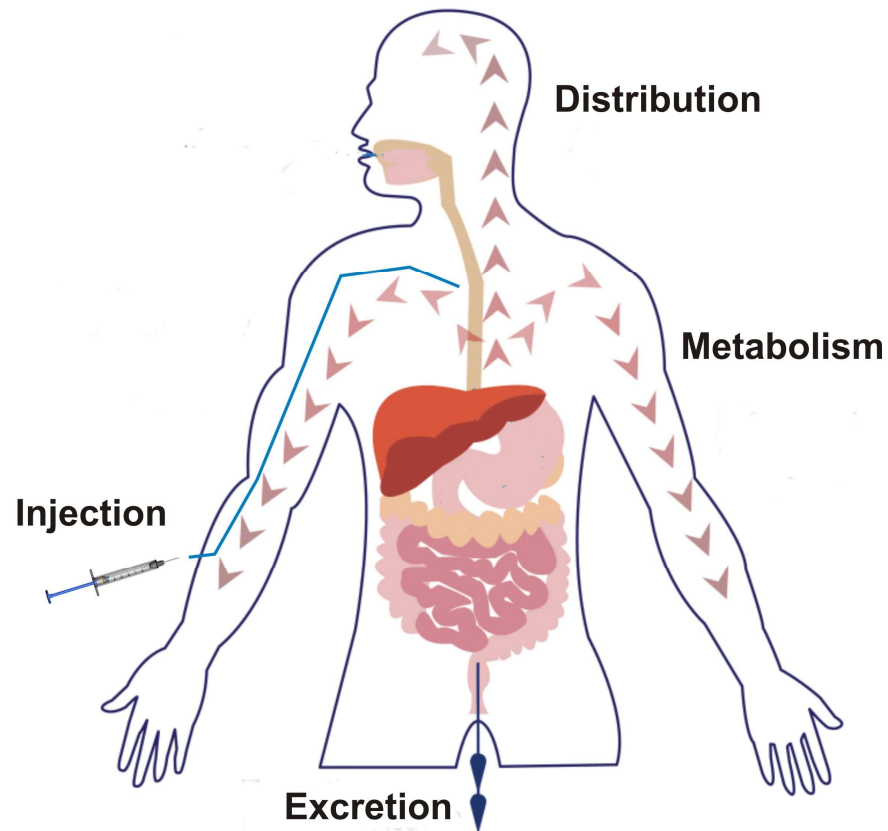
Kinetic Modelling and Quantitative Imaging

Dr. Kuangyu Shi
Dept. Nuclear Medicine
Technische Universität München

Molecular Imaging

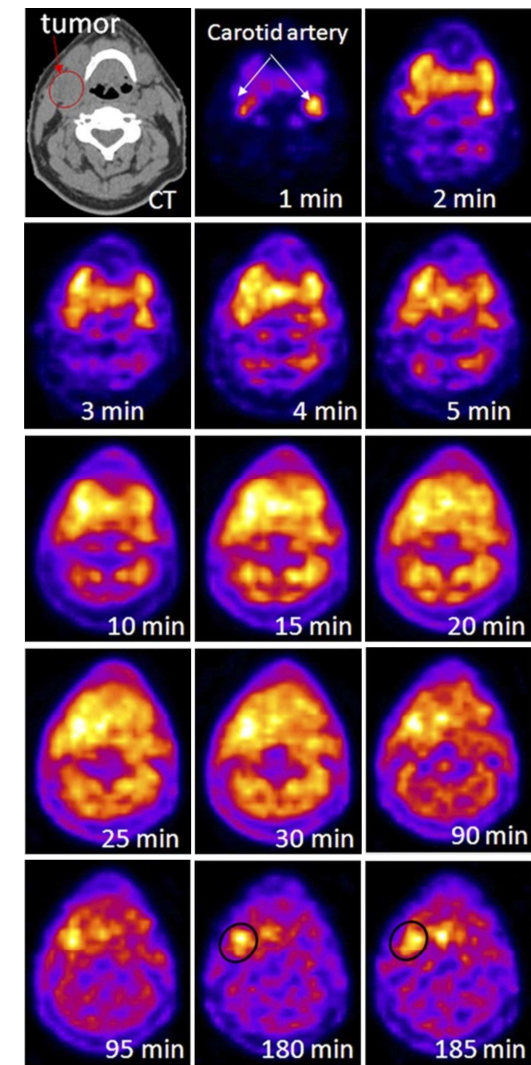


Challenges of Molecular Imaging Quantification



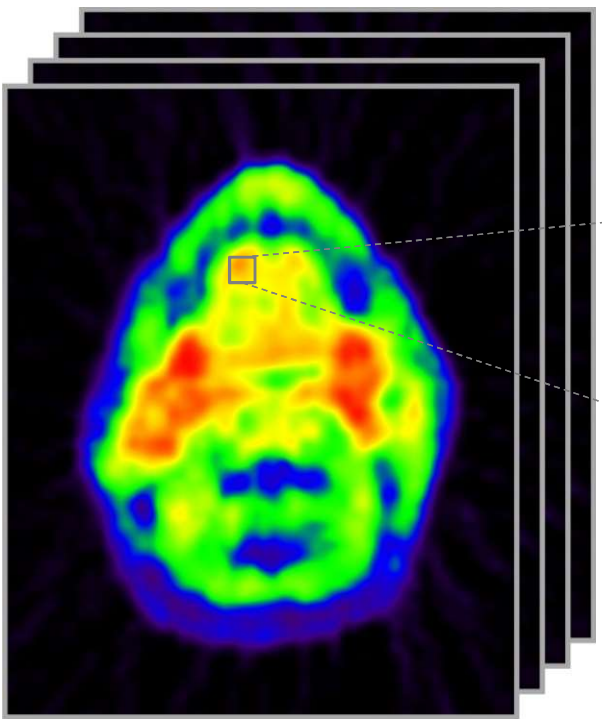
Dynamic imaging signal

Confounding factors



[Carlin & Humm, J Nucl Med 2012]

Quantification of Molecular Imaging



0 6,000 12,000
Activity (Bq/mL)

PET images: ^{18}F -Fmiso

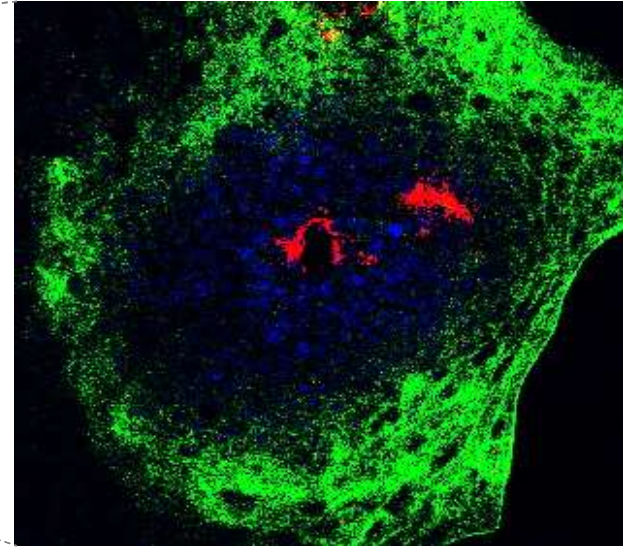
Static Analysis



Dynamic Analysis



■ Microvessel
■ Hypoxia
■ Perfusion

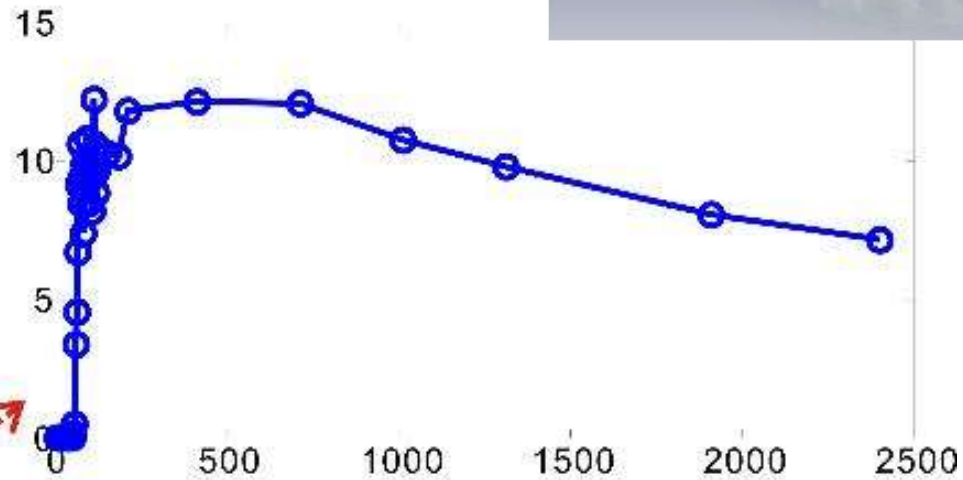
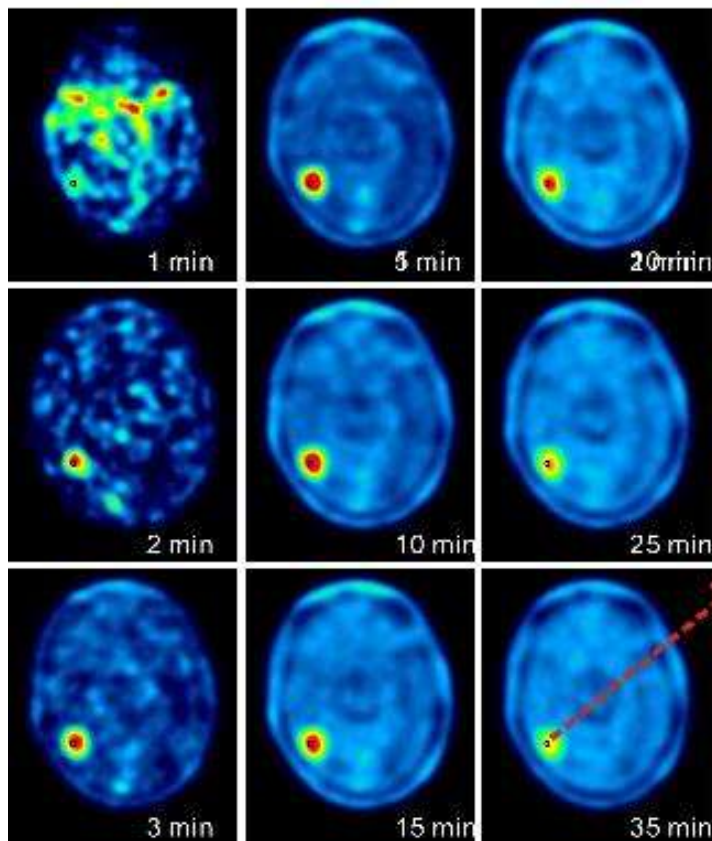


Tumor microenvironment
(immunohistochemistry)

- Qualitative
- Semi-quantitative
- Quantitative

Quantitative Analysis: Dynamic PET & Time-Activity Curve (TAC)

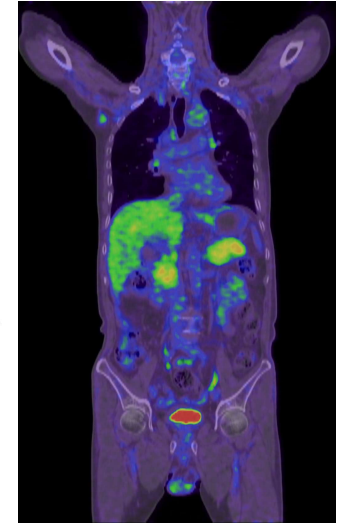
[¹⁸F]FET PET



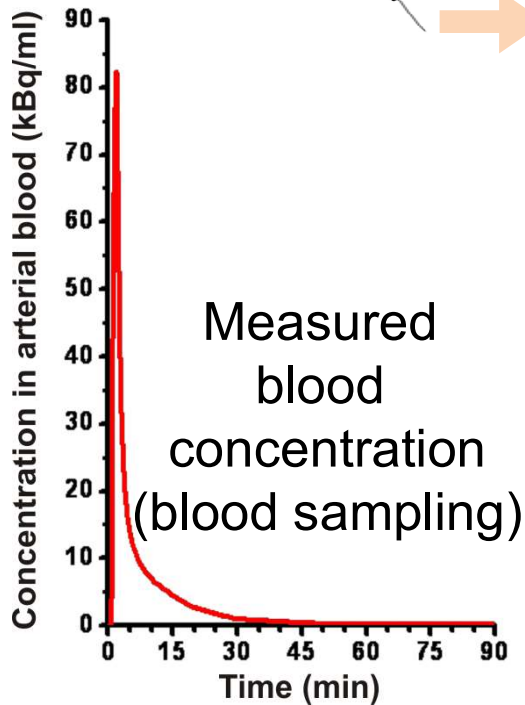
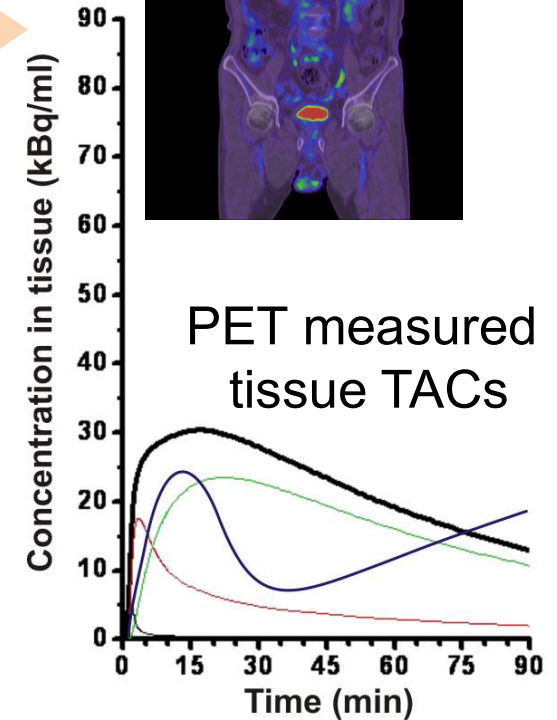
Tracer injection



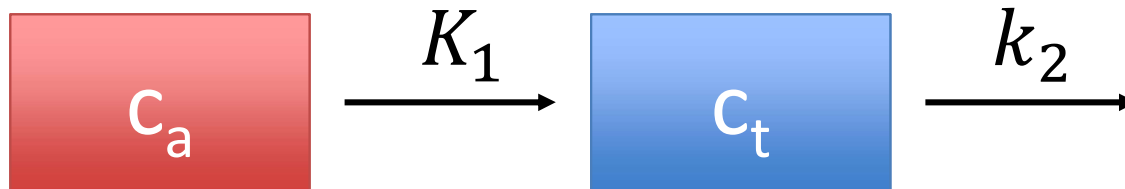
Tissue response



PET measured tissue TACs

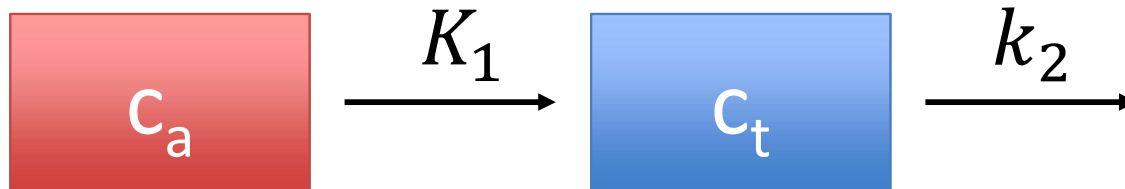


Compartmental Model

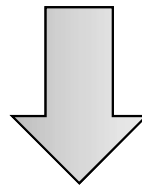


- Compartment: a theoretical volume for tracer
- Instant homogeneous distribution within entire compartment
- Steady-state: constant physiological processes & molecular interactions
- Transport between compartments: pure diffusion
- Linear interconnections among compartments

Compartmental Model



$$\frac{dc_t}{dt} = K_1 c_a - k_2 c_t$$

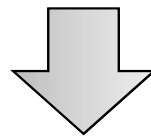
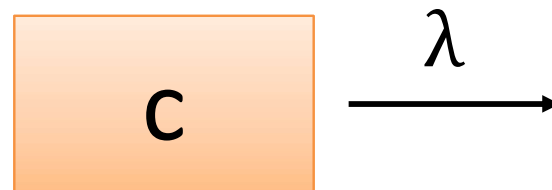


$$c_t = K_1 e^{-k_2 t} \otimes c_a$$

☐ Radioactive decay

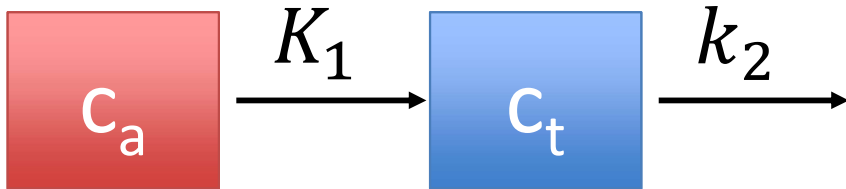
$$\frac{dc}{dt} = -\lambda c$$

☐ Compartmental representation

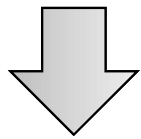


$$c = c_0 e^{-\lambda t}$$

Compartmental Model

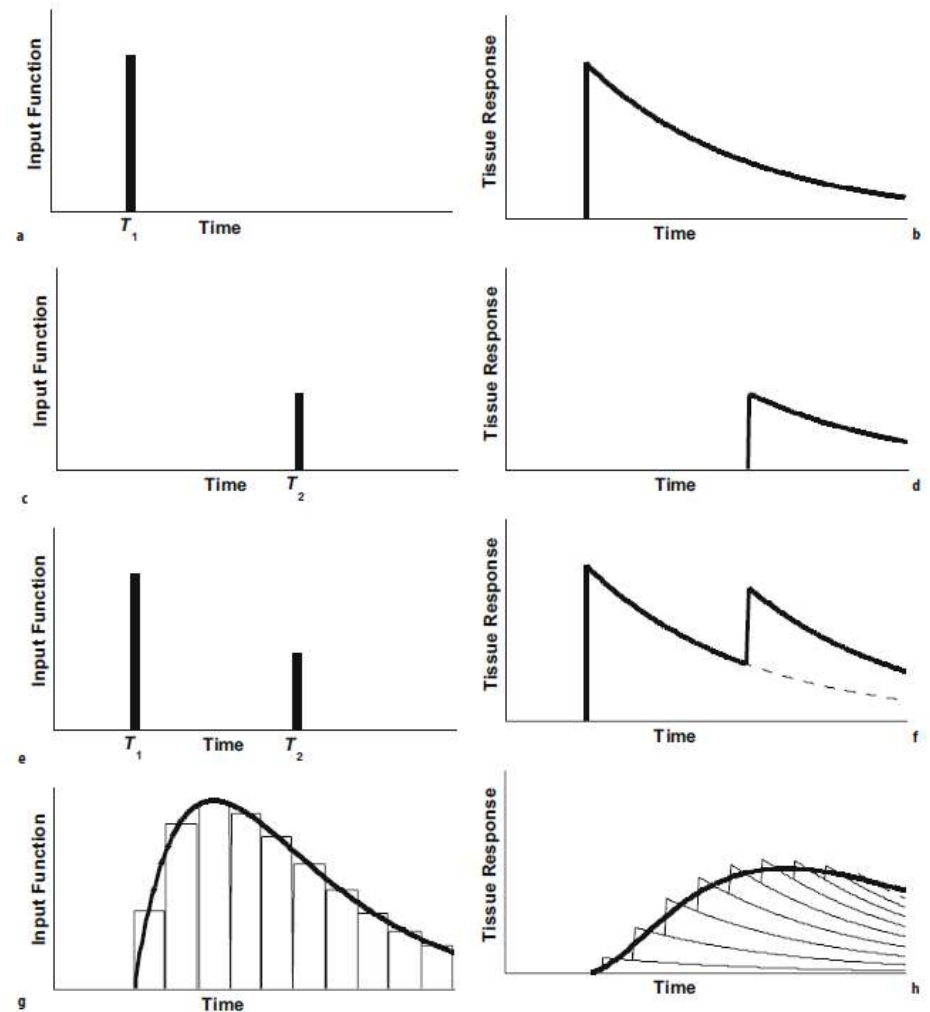


$$c_t = K_1 e^{-k_2 t} \otimes c_a$$



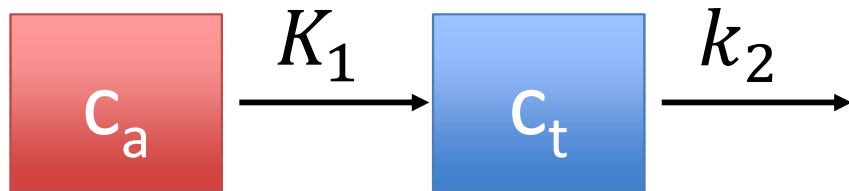
$$c_t(t) = K_1 \int_0^t e^{-k_2(t-\tau)} c_a(\tau) d\tau$$

**Convolution:
sum of system
responses**

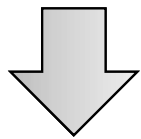


[Carson 2003]

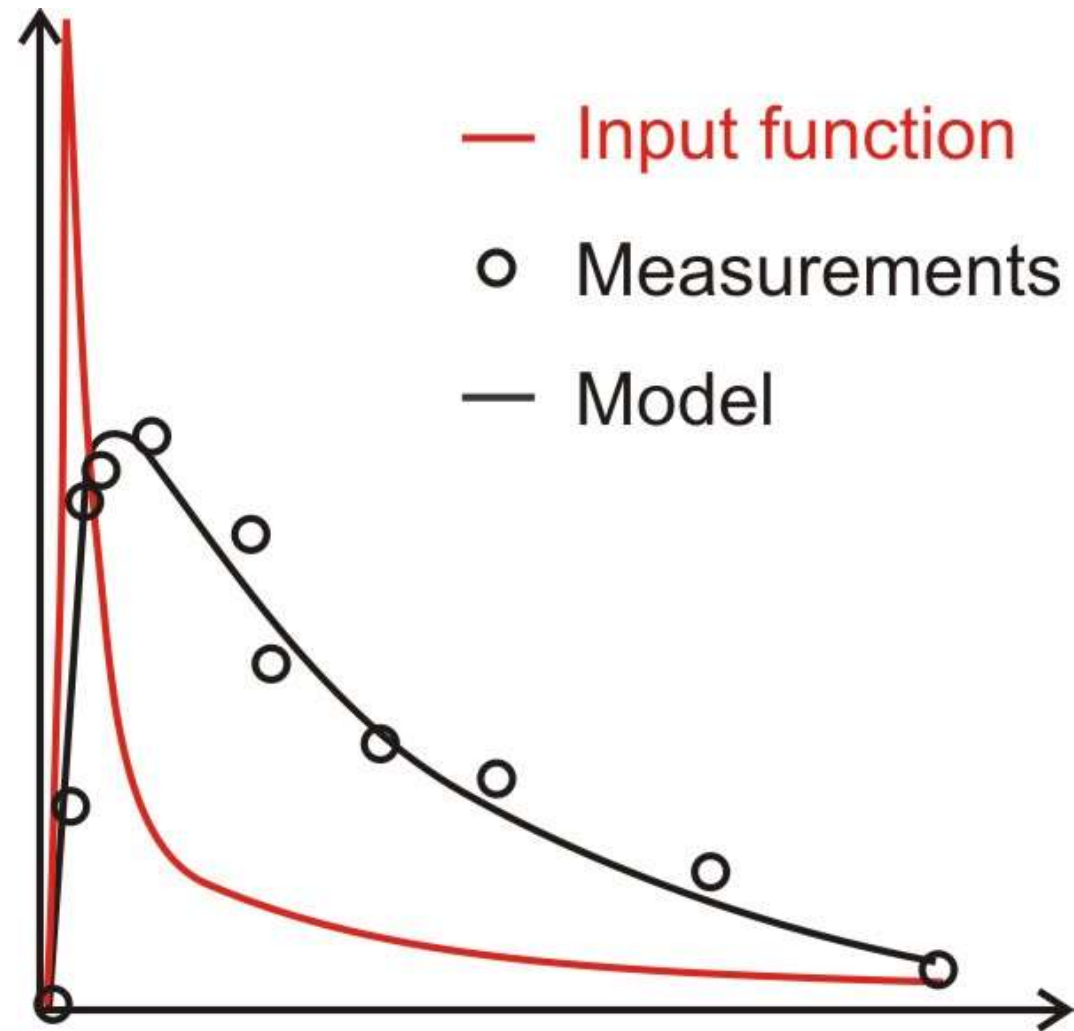
Curve Fitting



$$c_t = K_1 e^{-k_2 t} \otimes c_a$$



$$c_t(t) = K_1 \int_0^t e^{-k_2(t-\tau)} c_a(\tau) d\tau$$



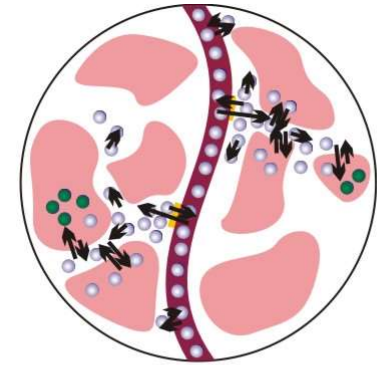
Two Tissue Compartment Model

□ Physiological process

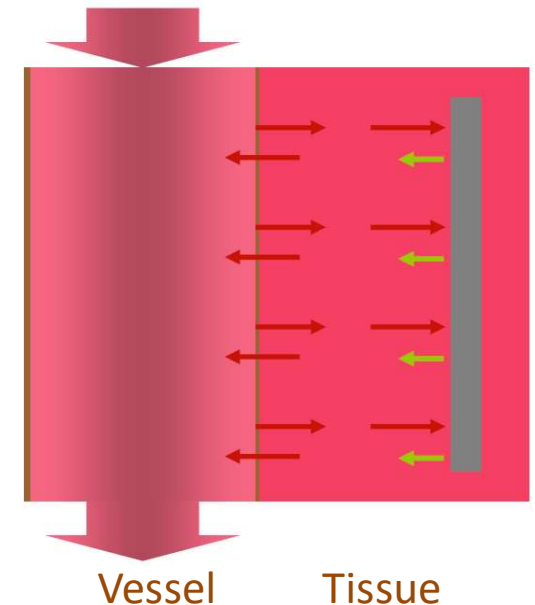
- Free ligand in plasma
- Permeation through endothelium
- Free ligand in tissue
- A fraction binds to receptor
- A fraction dissociates again
- Diffusion back to plasma

□ Model

- Physical / Chemical states
 - => Compartments
 - well mixed homogenous material
 - **Not** physical volume

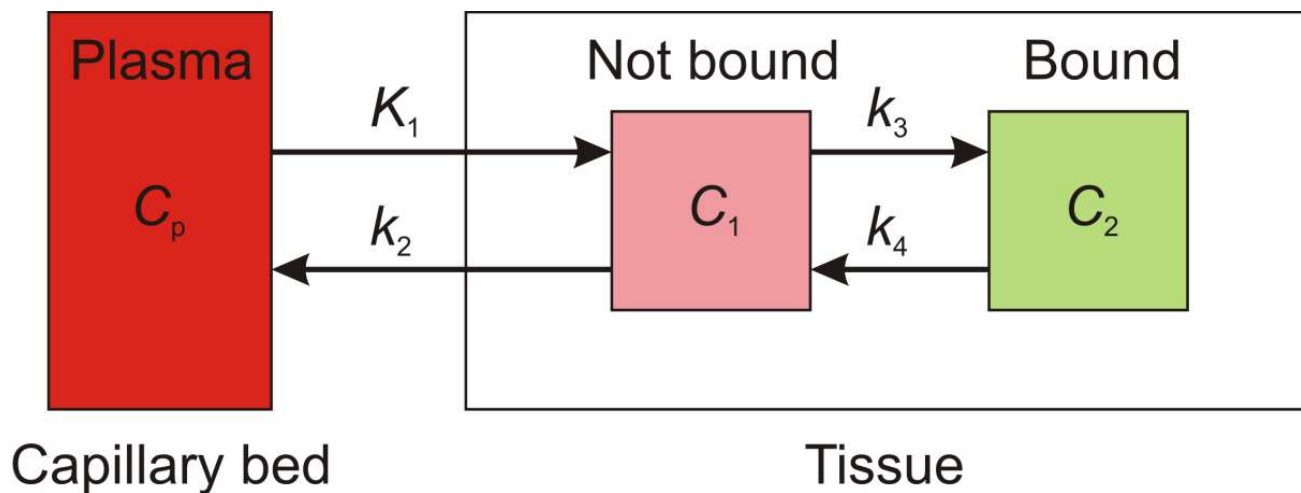


Interstitial+intracellular transport
+metabolism



Two Tissue Compartment Model

- ❑ Fixed number of compartments
- ❑ Transport between compartments: pure diffusion
- ❑ Linear interconnections among compartments
- ❑ First-order process: transfer proportional concentration
- ❑ Constant-coefficient, ODE
- ❑ Curve fitting of TAC



[Watabe H. *et. al. Annals of Nuclear Medicine* 2006]

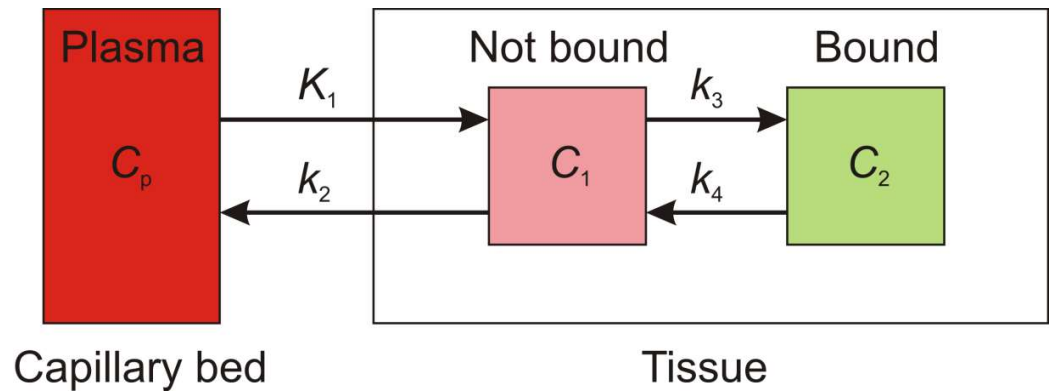
[Gunn R. N. *et. al. J Cereb Blood Flow Metab* 2001]

Two Tissue Compartment Model

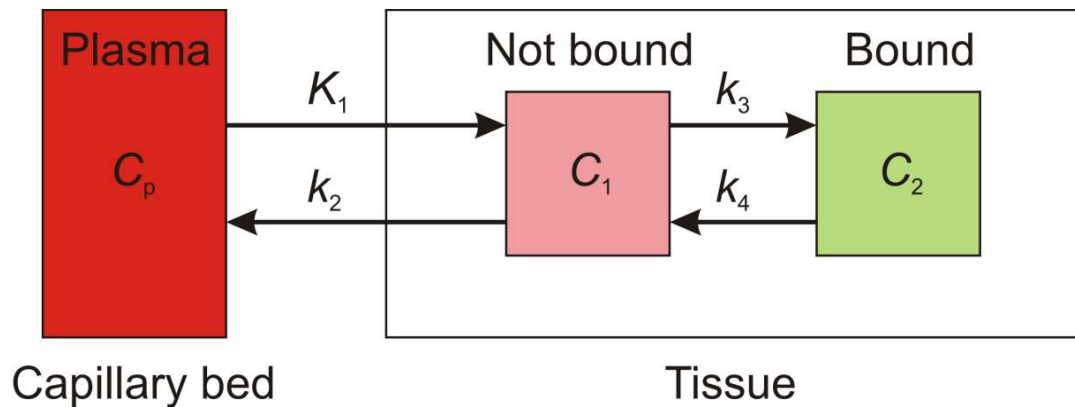
- ❑ Arterial concentration $C_p(t)$: measured
- ❑ Concentration in tissue compartments:
 - $C_1(t)$: free tracer
 - $C_2(t)$: specifically bound tracer
- ❑ Concentration change:

$$\frac{dC_1(t)}{dt} = K_1 C_p(t) - k_2 C_1(t) - k_3 C_1(t) + k_4 C_2(t)$$

$$\frac{dC_2(t)}{dt} = k_3 C_1(t) - k_4 C_2(t)$$



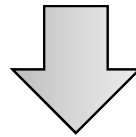
Two Tissue Compartment Model



$$C_{tissue}(t) = C_1(t) + C_2(t)$$

$$\frac{dC_1(t)}{dt} = K_1 C_p(t) - k_2 C_1(t) - k_3 C_1(t) + k_4 C_2(t)$$

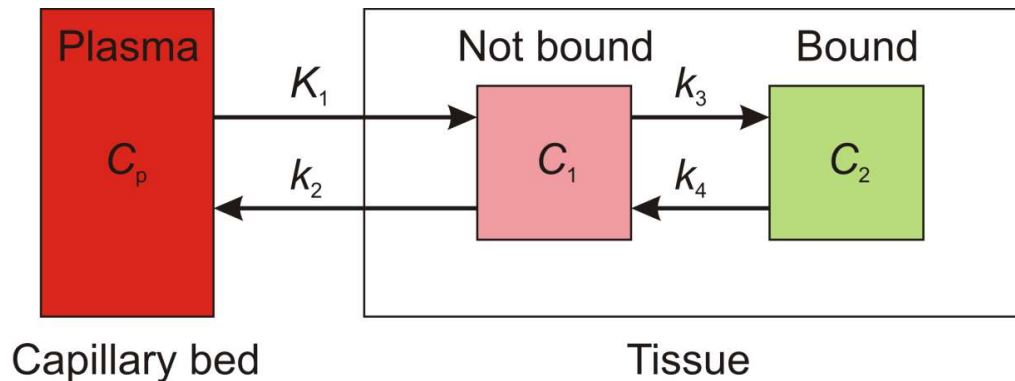
$$\frac{dC_2(t)}{dt} = k_3 C_1(t) - k_4 C_2(t)$$



$$C_1(t) = IRF_1(K_1, k_2, k_3, k_4, t) \otimes C_p(t)$$

$$C_2(t) = IRF_2(K_1, k_2, k_3, k_4, t) \otimes C_p(t)$$

Two Tissue Compartment Model



$$C_{tissue}(t) = C_1(t) + C_2(t)$$

$$C_1(t) = IRF_1(K_1, k_2, k_3, k_4, t) \otimes C_p(t)$$

$$C_2(t) = IRF_2(K_1, k_2, k_3, k_4, t) \otimes C_p(t)$$

$$IRF_1(K_1, k_2, k_3, k_4, t) = \frac{K_1}{(\alpha_2 - \alpha_1)} [(k_4 - \alpha_1)e^{-\alpha_1 t} + (\alpha_2 - k_4)e^{-\alpha_2 t}]$$

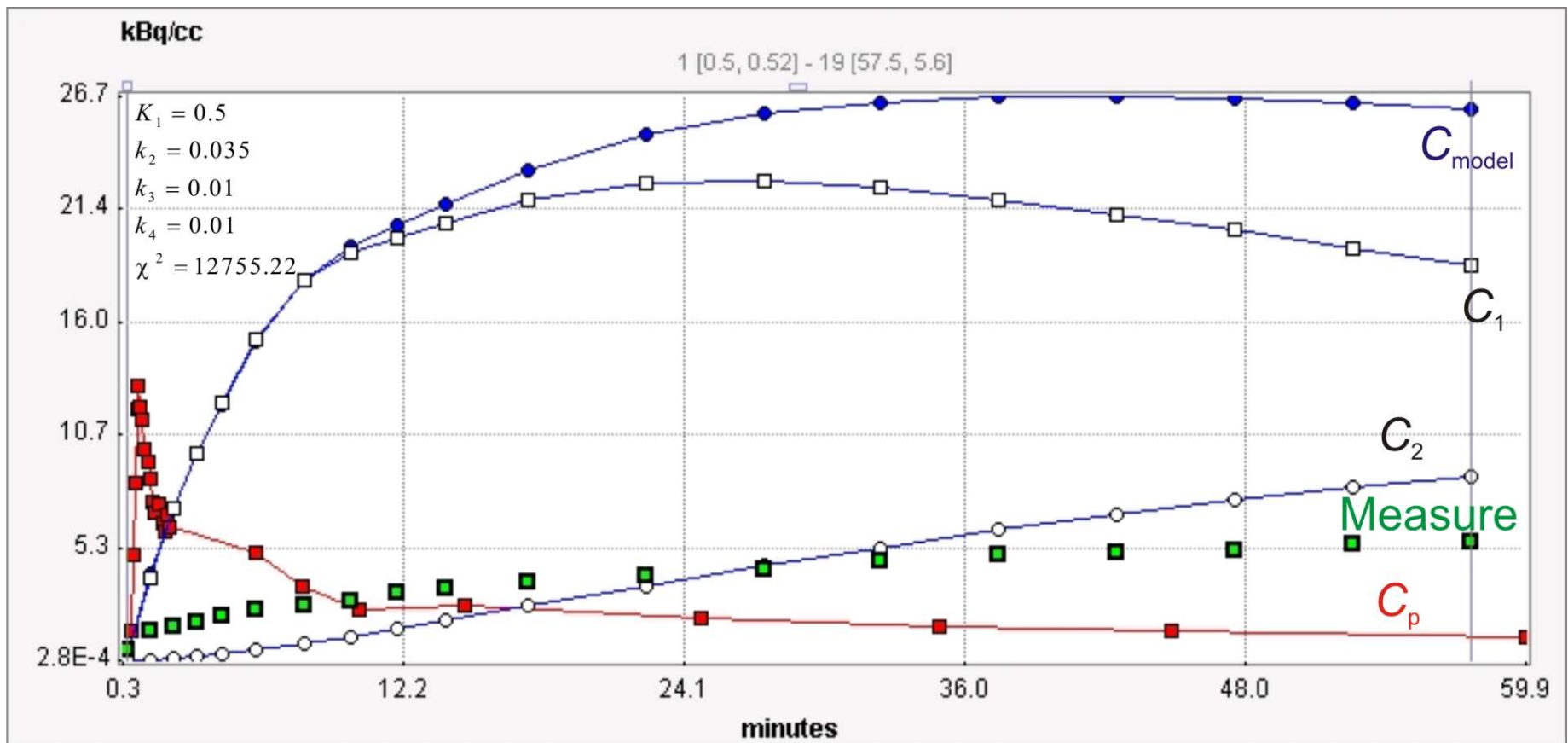
$$IRF_2(K_1, k_2, k_3, k_4, t) = \frac{K_1 k_3}{(\alpha_2 - \alpha_1)} [e^{-\alpha_1 t} + e^{-\alpha_2 t}]$$

$$\alpha_1 = \frac{(k_2 + k_3 + k_4) - \sqrt{(k_2 + k_3 + k_4)^2 - 4k_2 k_4}}{2} \quad \alpha_2 = \frac{(k_2 + k_3 + k_4) + \sqrt{(k_2 + k_3 + k_4)^2 - 4k_2 k_4}}{2}$$

Two Tissue Compartment Model

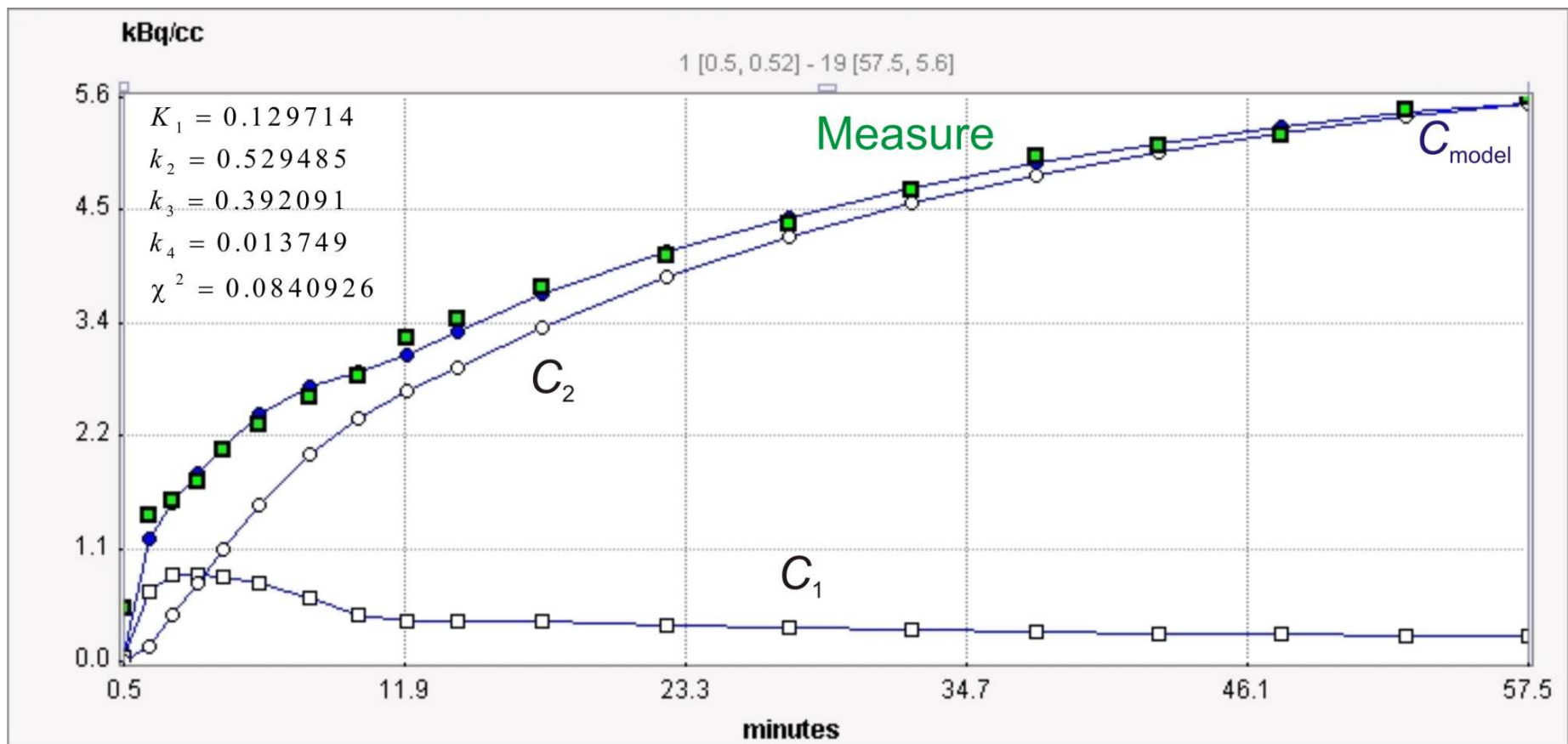
- Given K_1, k_2, k_3, k_4 and $C_p(t)$
- Calculate $C_{\text{model}}(t)$

PMOD



Two Tissue Compartment Model

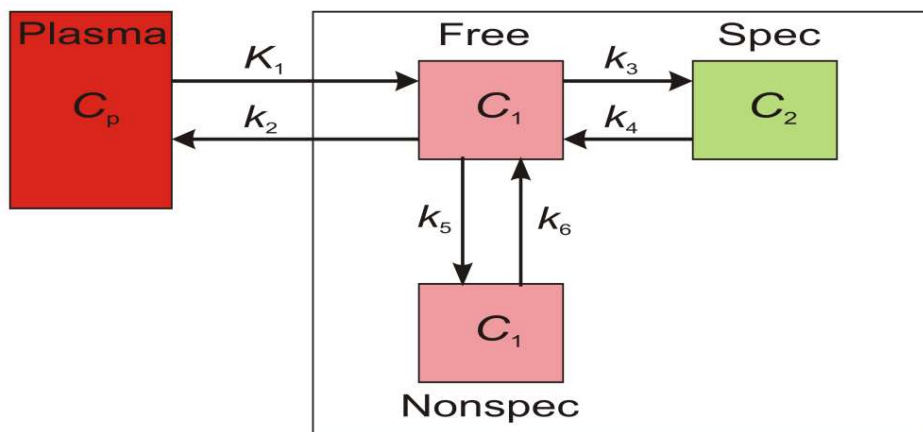
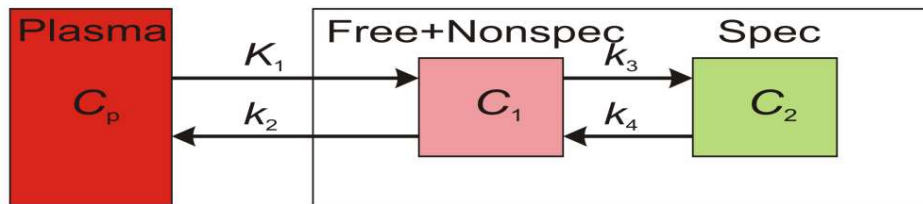
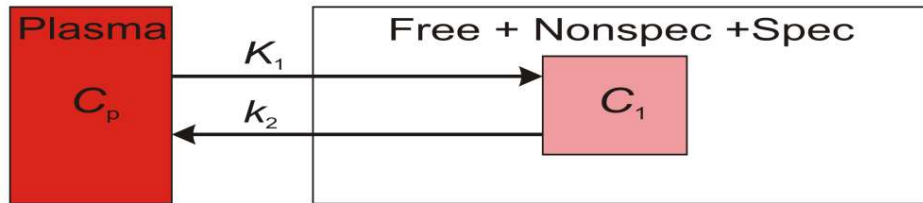
- Criteria of difference between $C_{\text{measure}}(t)$ and $C_{\text{model}}(t)$: χ^2
- Optimization algorithm: modify K_1, k_2, k_3, k_4 to minimize χ^2



Compartmental Model

Capillary bed

Tissue



❑ One compartment

➤ $[^{15}\text{O}]\text{H}_2\text{O}$

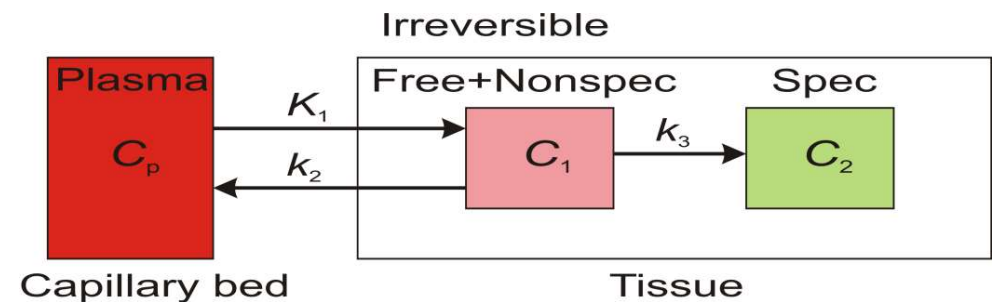
❑ Two compartment

➤ $[^{18}\text{F}]\text{FDG}$

➤ $[^{18}\text{F}]\text{FMISO}$

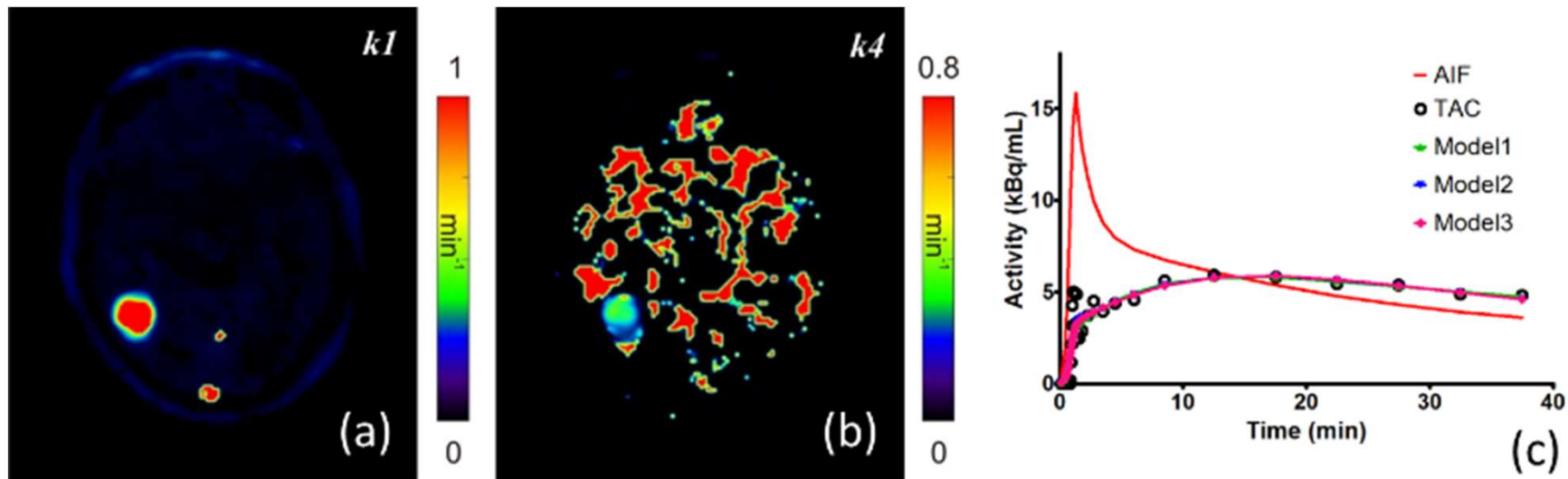
❑ Three compartment

❑ Irreversible model

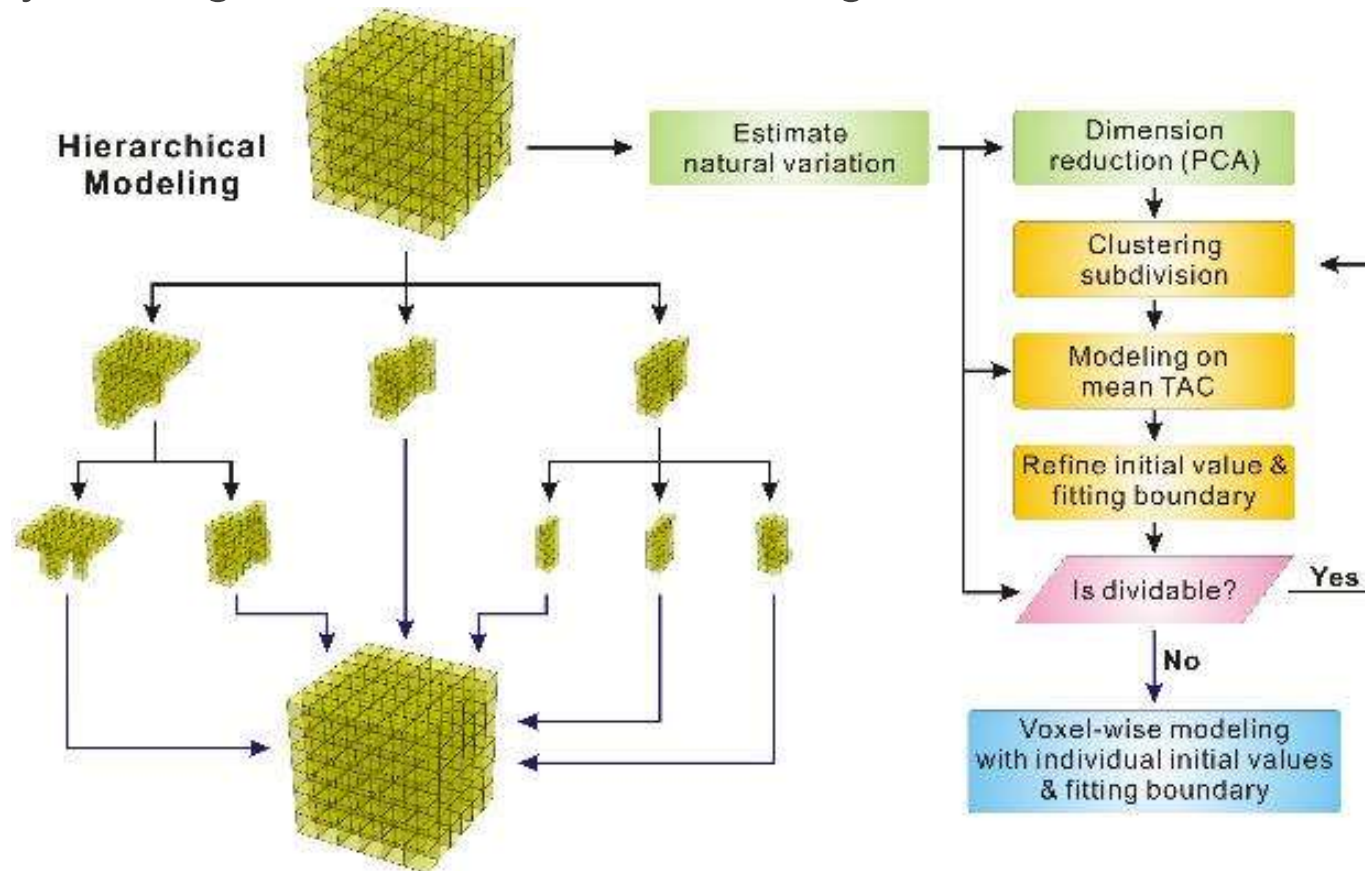


Local Minima of Nonlinear Fitting

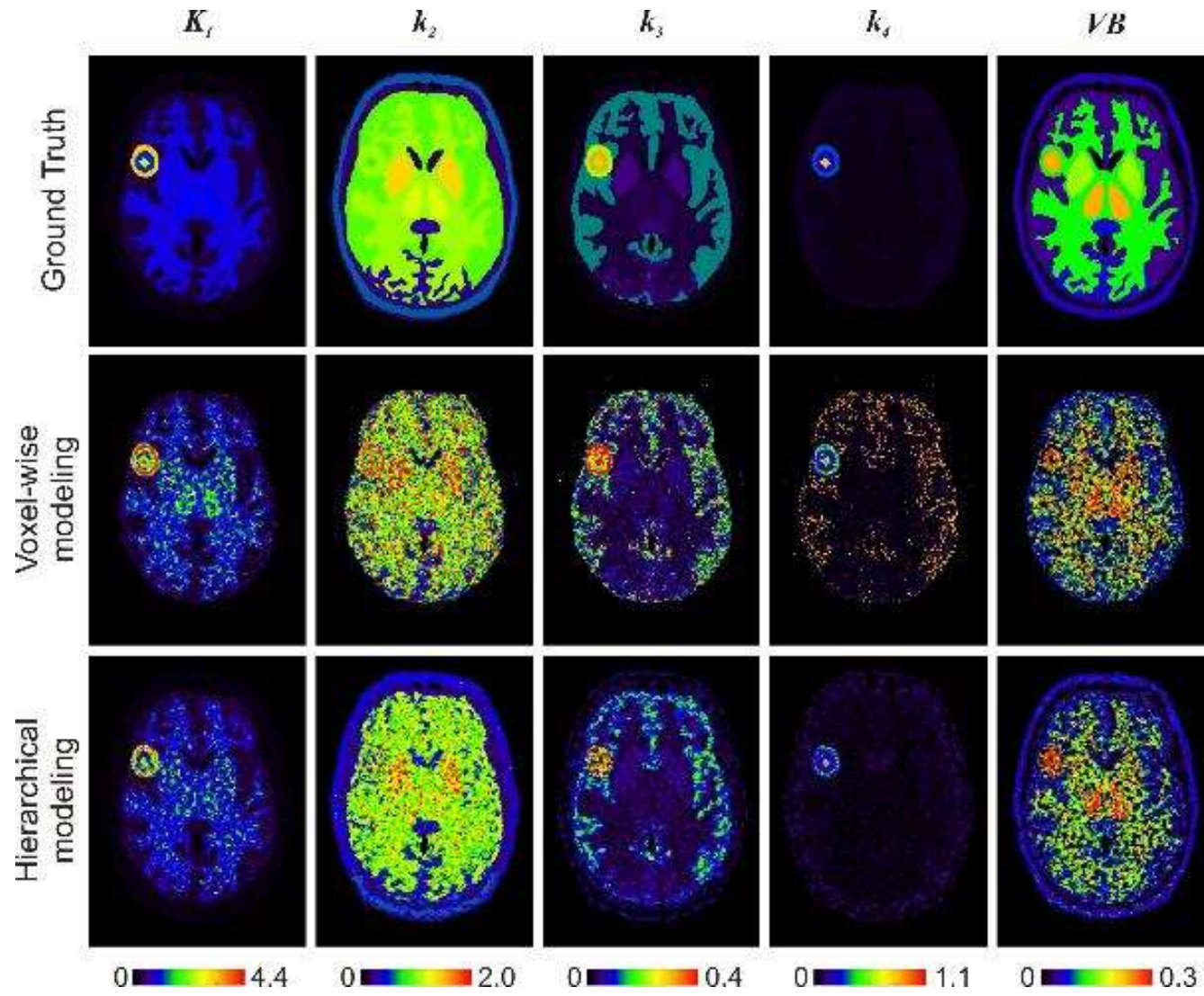
- ❑ a) & b): parametric images (k_1 & k_4) using direct voxel-wise modeling (PMOD) for a slice of Patient #1;
- ❑ c): an example TAC and the three resulting modeling curves fitted using three different sets of initial values:
 - Model1: $\chi^2 = 0.723$; $k_1=0.10$, $k_2=0.12$, $k_3=0.01$, $k_4=0$, $VB=0.14$
 - Model2: $\chi^2 = 0.749$; $k_1=0.81$, $k_2=5.42$, $k_3=0.64$, $k_4=0.11$, $VB=0.05$
 - Model3: $\chi^2 = 0.754$; $k_1=0.15$, $k_2=0.66$, $k_3=0.63$, $k_4=0.20$, $VB=0.13$

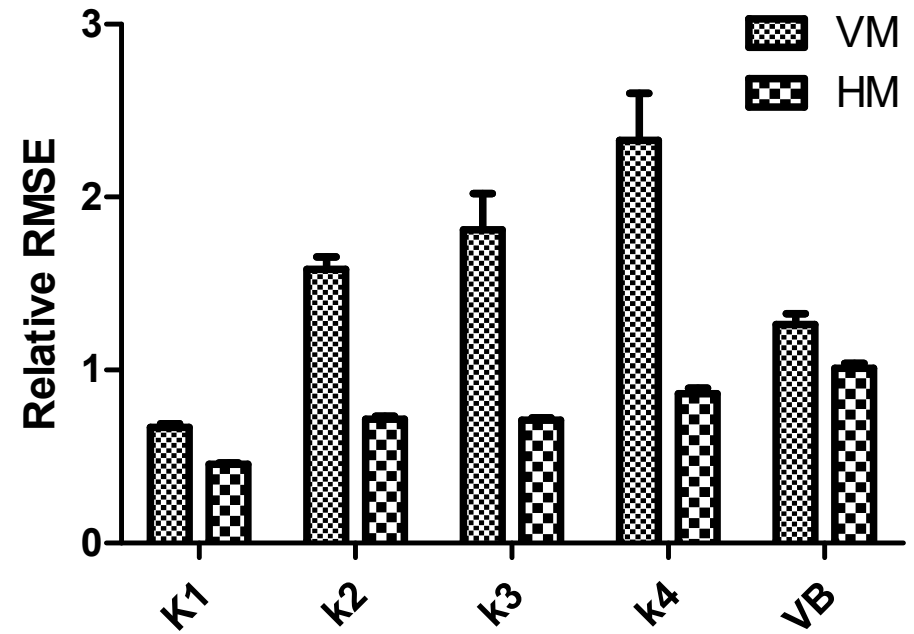
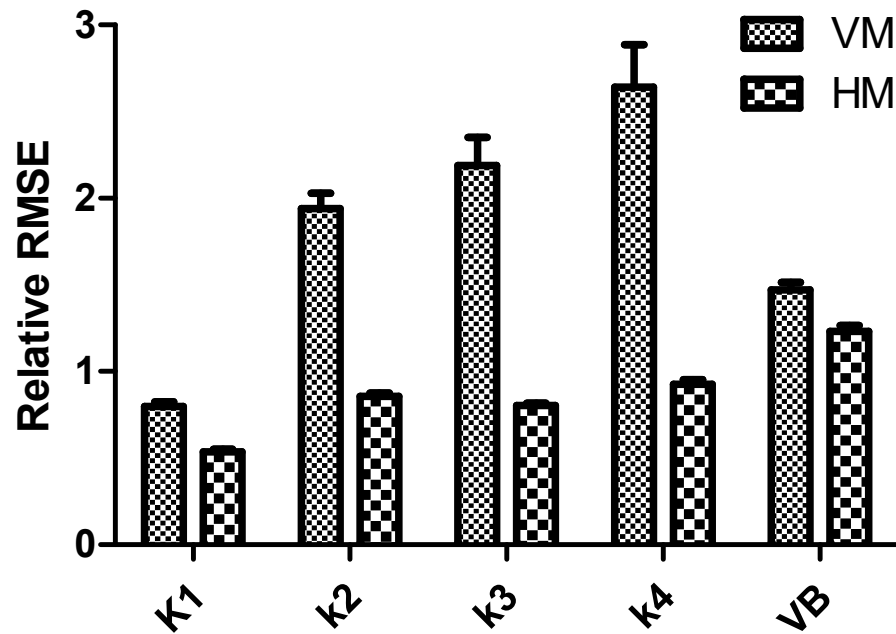


- ❑ Assumption: Similar TACs has similar kinetic parameters
- ❑ Clustering the TACs according to their similarities
- ❑ Gradually refining the initial values and fitting boundaries



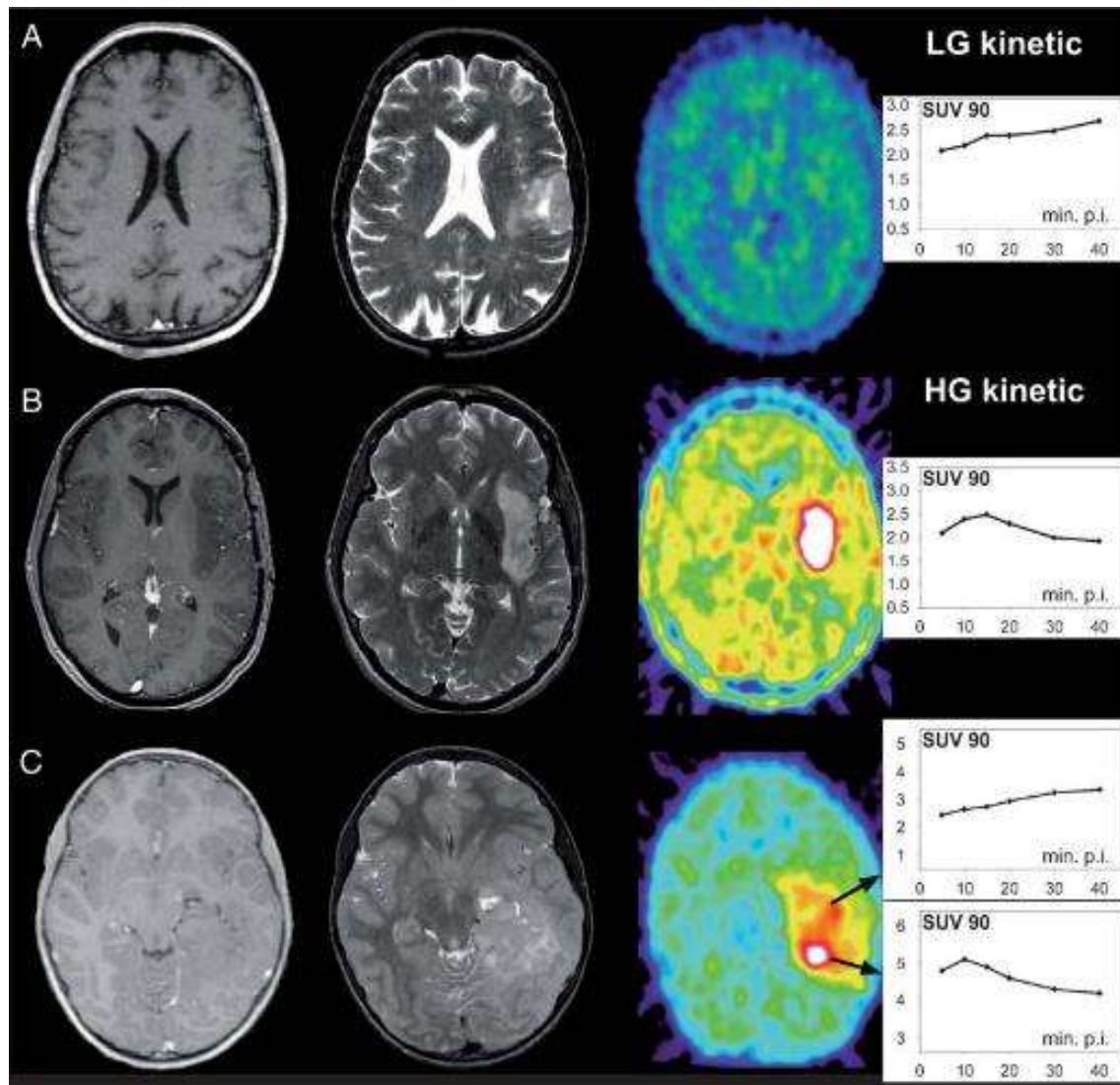
Test on Simulation Phantom





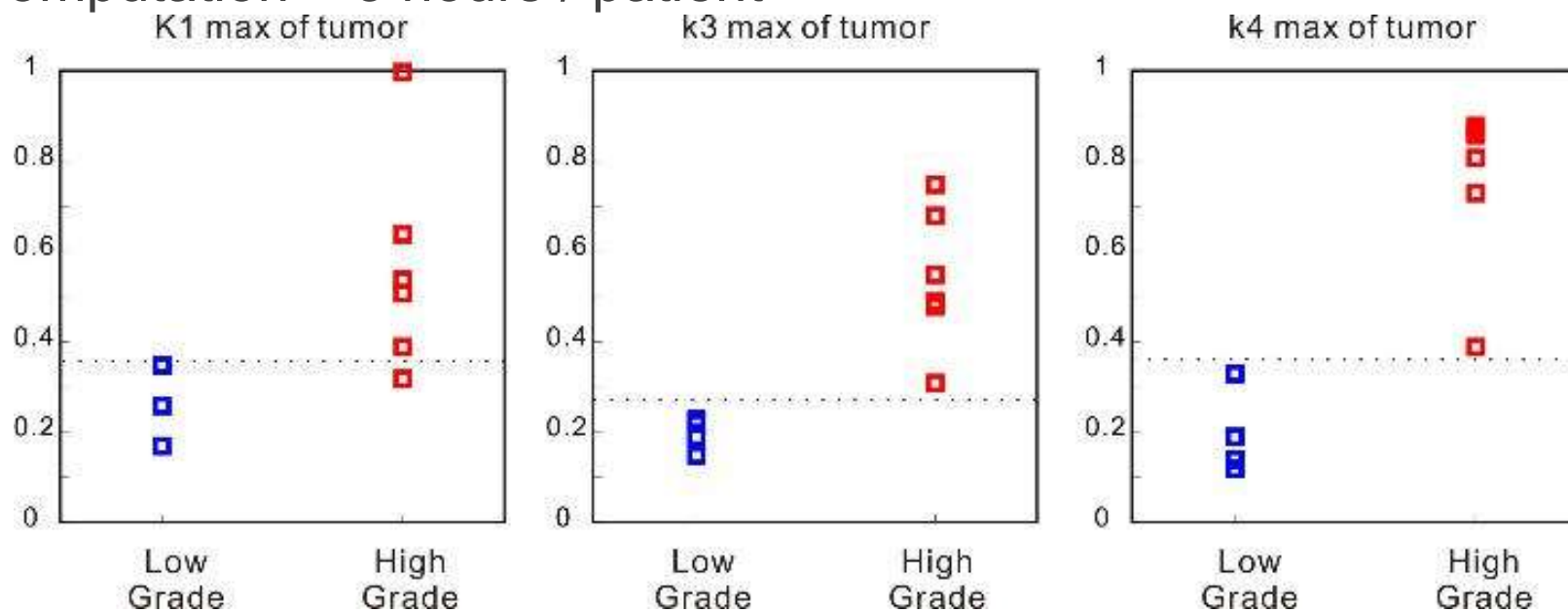
Example Application of Pharmacokinetic Modeling

[¹⁸F]FET

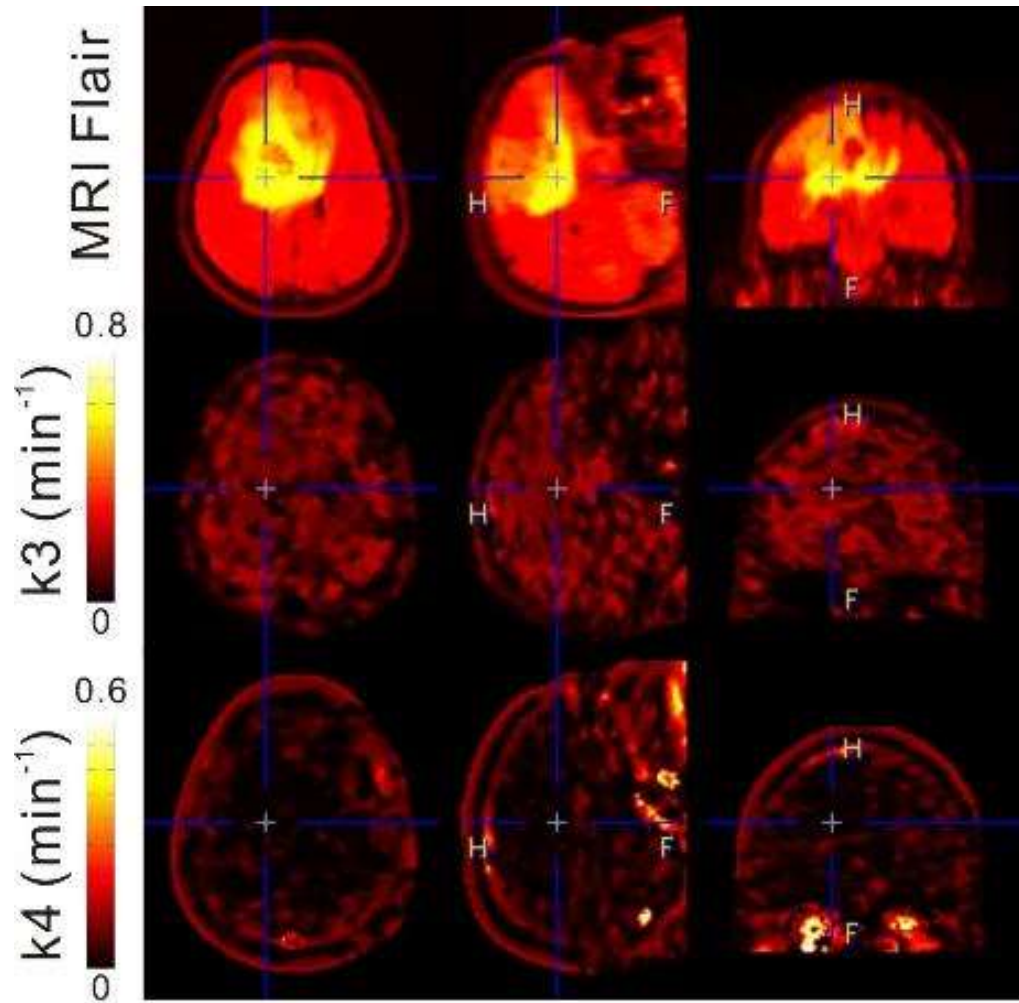


[Kunz et al Neuro
Oncol 2011]

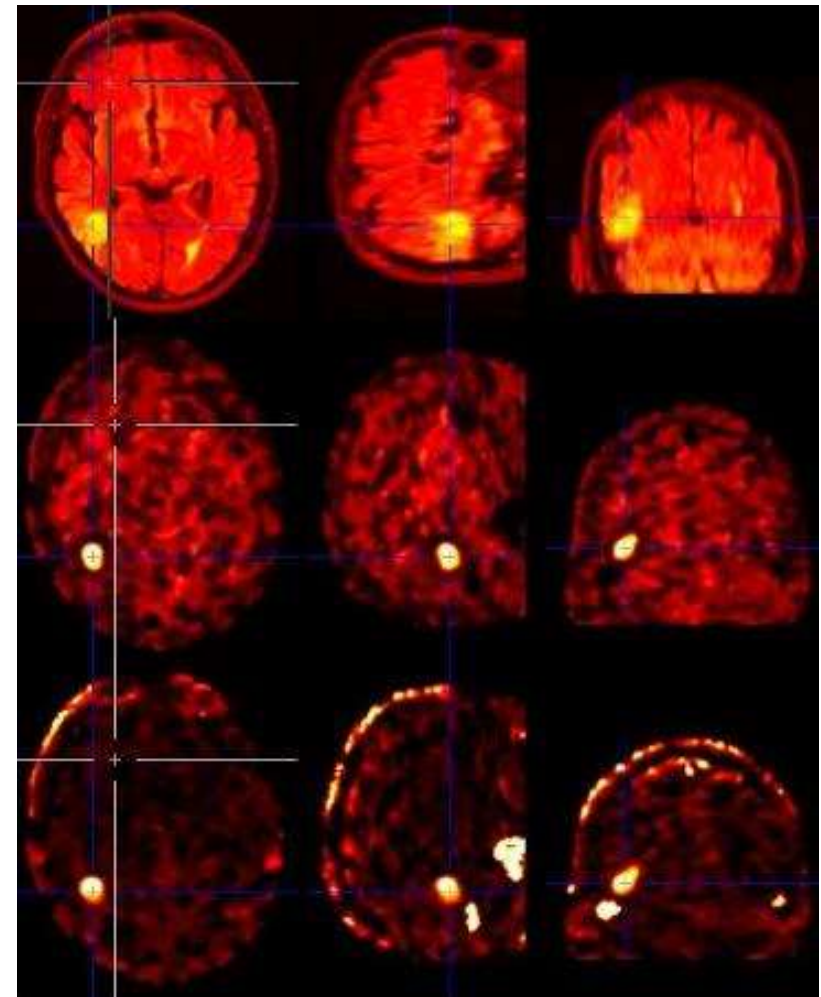
- ❑ 10 Patients: 4 Low Grade (WHO II) , 6 High Grade (WHO III & IV)
- ❑ Dynamic [^{18}F]FET for 40 min (Siemens mMR)
- ❑ OSEM 3D (3 iterations, 21 subsets)
- ❑ Tumor delineation on PET + Flair fusion
- ❑ Image-derived AIF from internal carotid artery (PET + MPRage)
- ❑ Computation < 3 hours / patient



Example Application of Pharmacokinetic Modeling

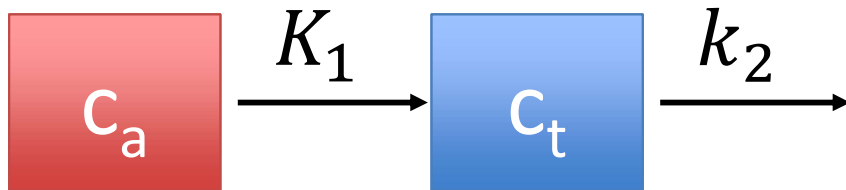


Patient Grade II



Patient Grade IV

Linear Model (Graphical Analysis)




□ Compartment model:

- Non-linear curve fitting
- Time consuming
- Not enough robust

$$\frac{dC_t(t)}{dt} = K_1 C_a(t) - k_2 C_t(t)$$



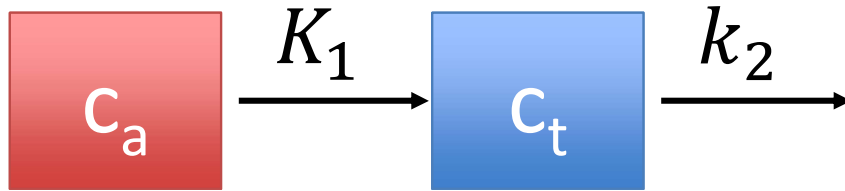
$$C_t(t) = K_1 \int_0^t C_a(t) - k_2 \int_0^t C_t(t)$$



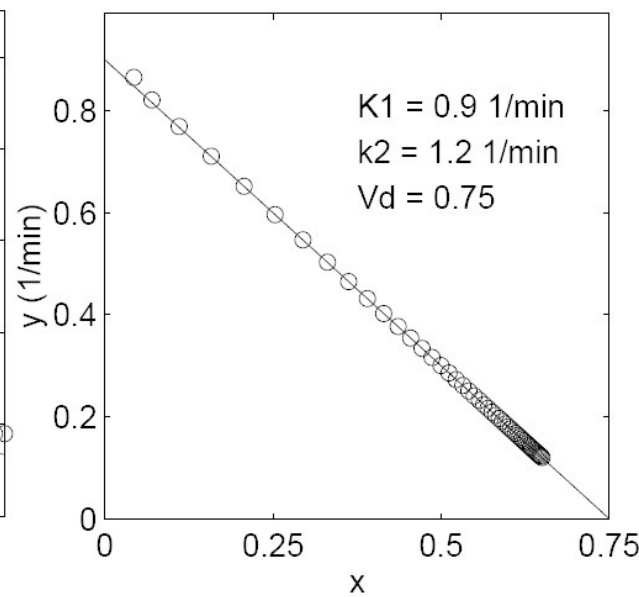
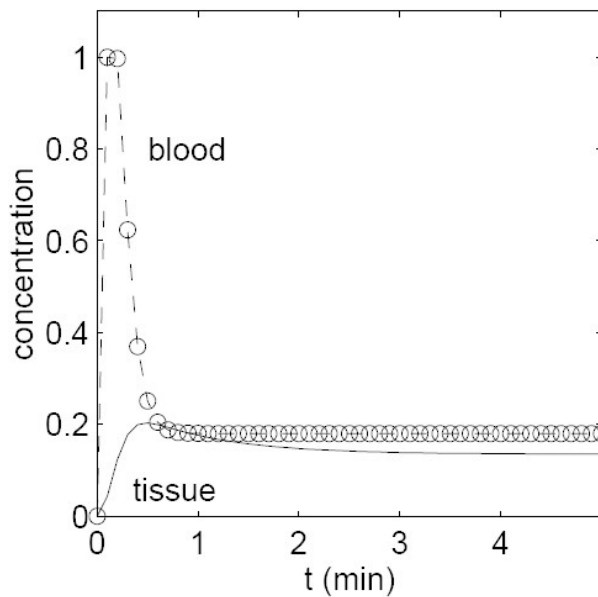
$$c_t = K_1 e^{-k_2 t} \otimes c_a$$

Differential form => integration form
Nonlinear fitting => linear fitting

Linear Model



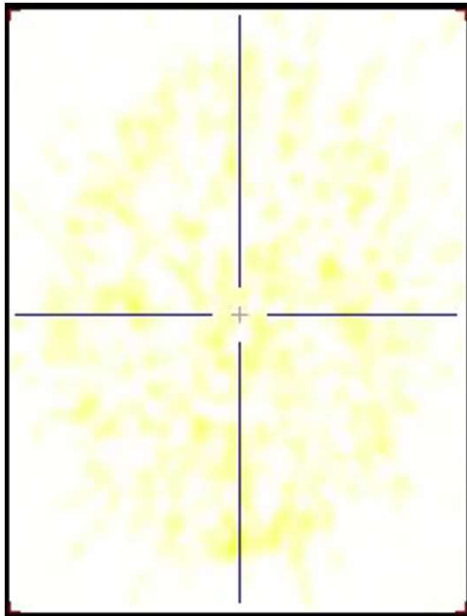
$$\frac{C_t(t)}{\int_0^t C_a(t)} = K_1 - k_2 \frac{\int_0^t C_t(t)}{\int_0^t C_a(t)}$$



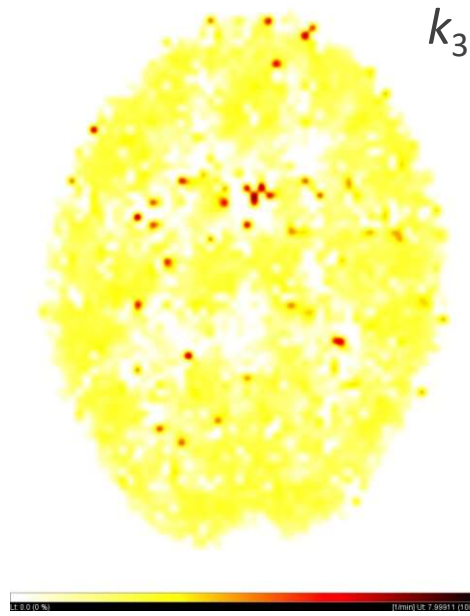
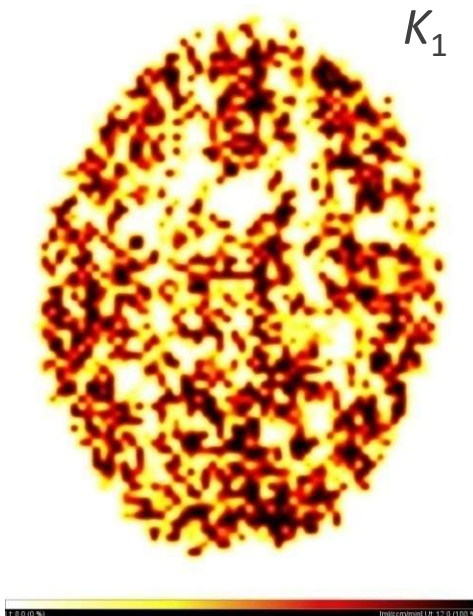
[Maguire R. P. *et. al. PET Pharmacokinetic Course Manual, 2005*]
 [van den Hoff J. *et. al. J. Nuclear Medicine, 1993*]

- Compartment model => Graphical model
- Irreversible two compartment model => Patlak Plot
- Reversible two compartment model => Logan Plot

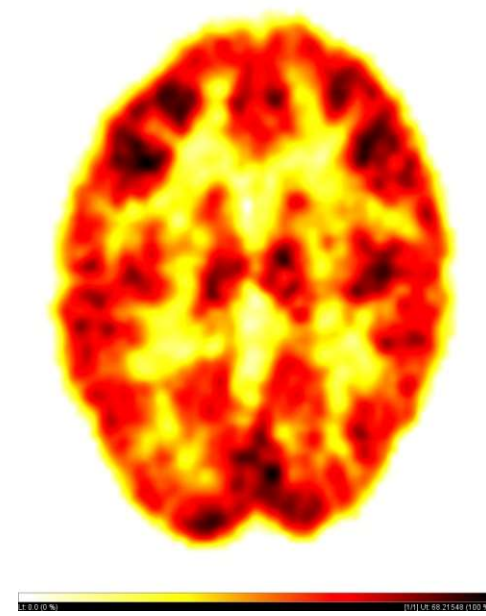
Dynamic PET (1 Slice)



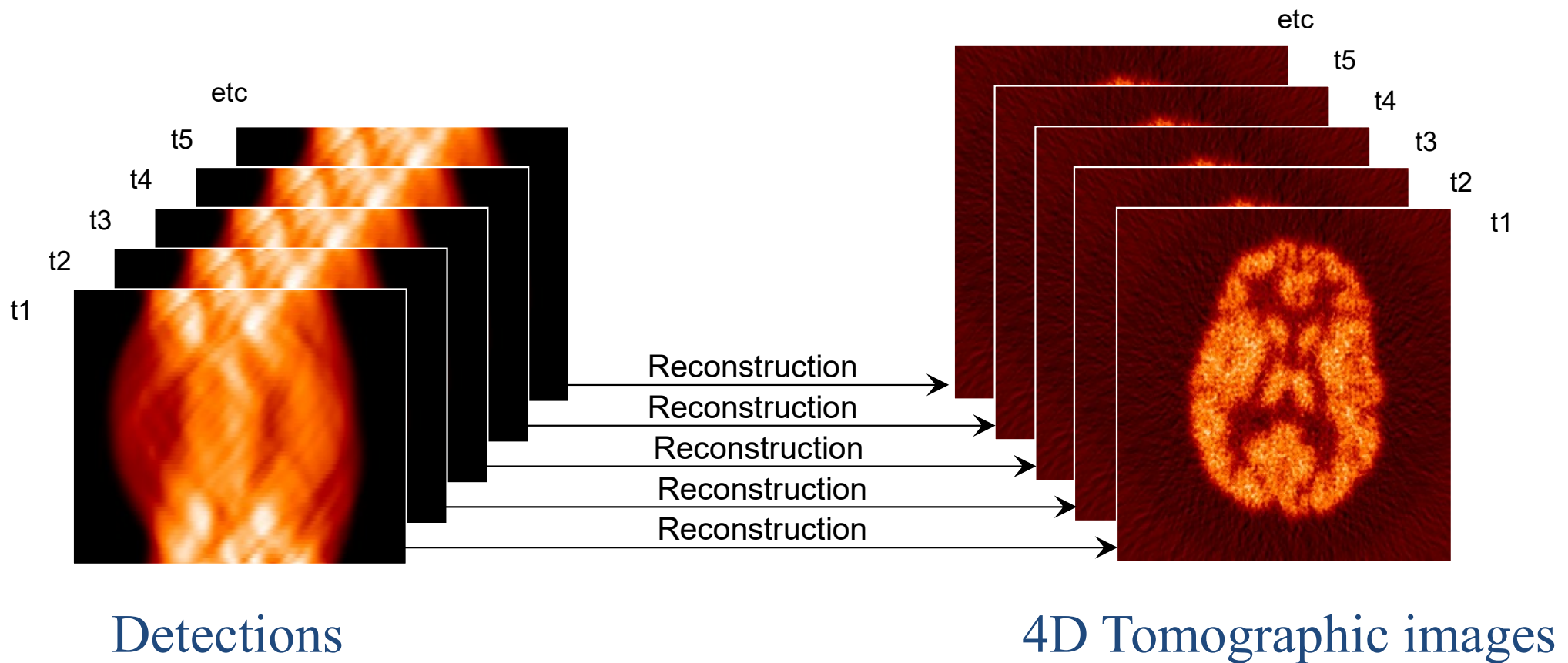
Two Compartment Model (40 min)



Patlak Plot (20 s)

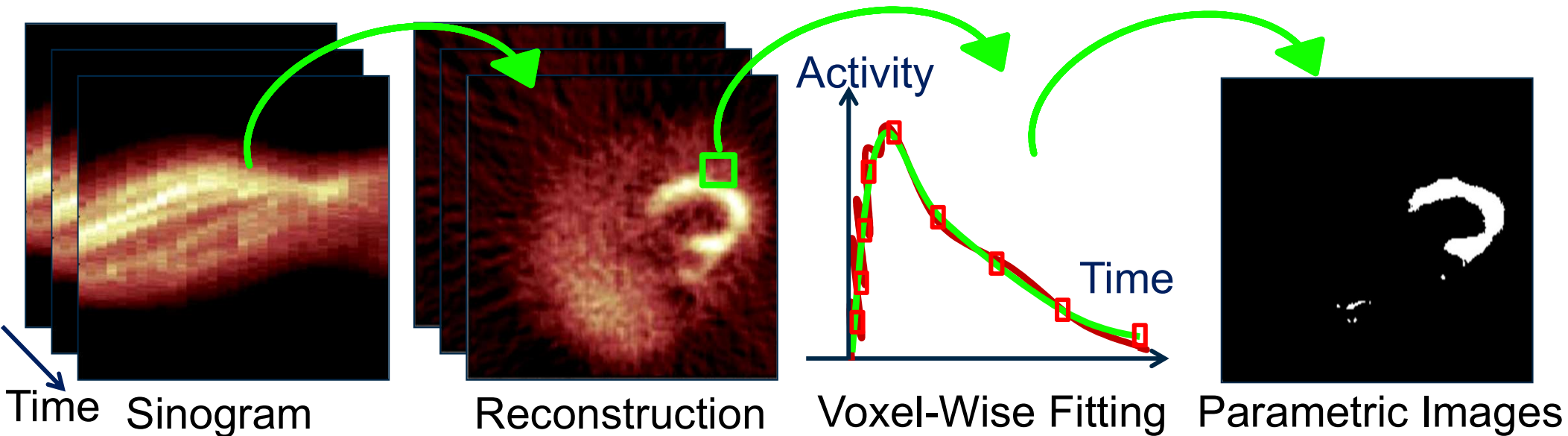


□ PET Reconstruction



[Cheng et al. SNM 2012]

- **Low SNR:**
→ Indirect parametric image generation:



Spatial Information Temporal Information

Advanced Pharmacokinetic Modeling Computing: Direct Parametric Image Reconstruction

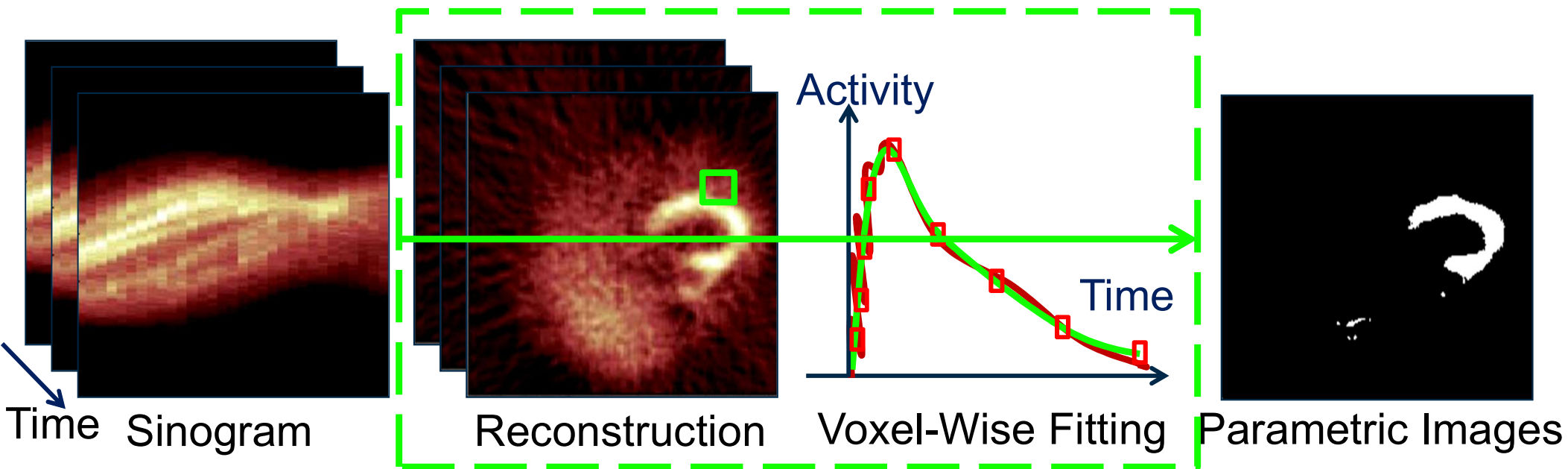
- **Improve SNR:**

→ Direct parametric image reconstruction:

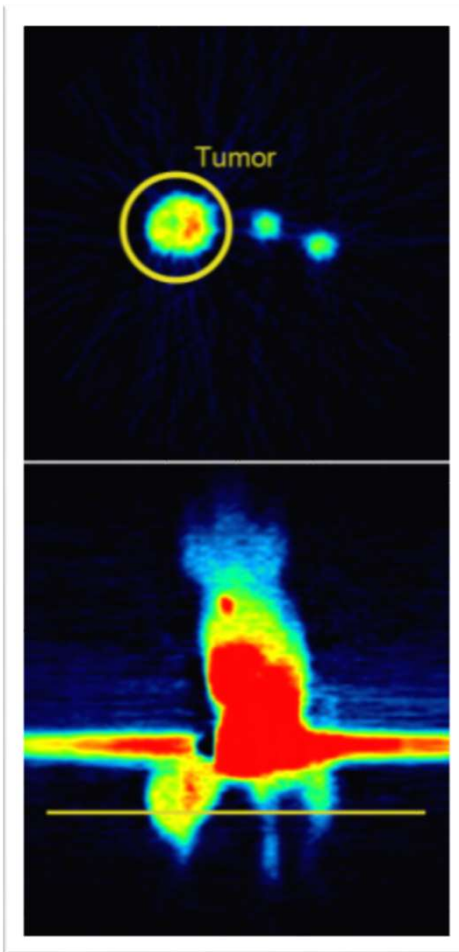
[Mattews et al. Phys. Med. Biol. 1997]

[Tsoumpas et al. Med. Phys. 2008]

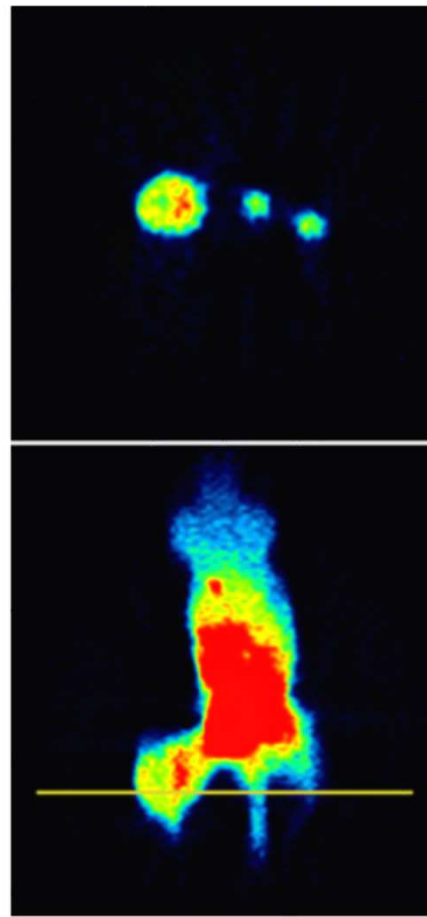
[Wang et al. Phys. Med. Biol. 2008]



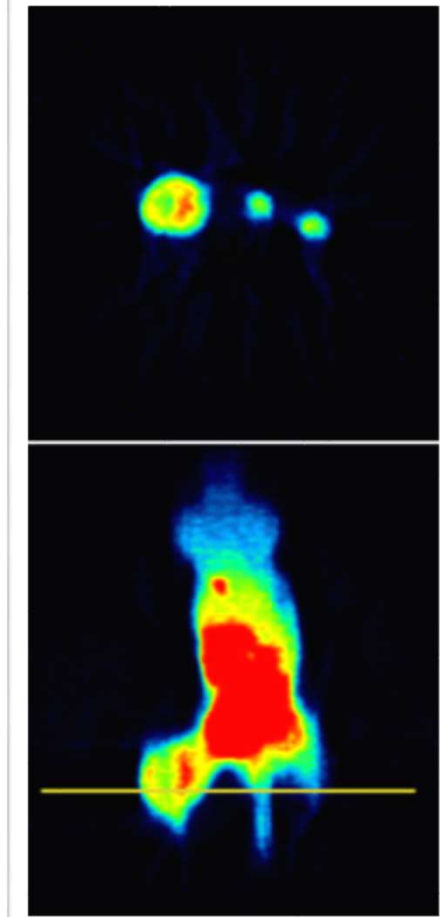
Spatial Information + Temporal Information



FBP + Patlak Model



OSEM + Patlak Model



POSEM + Patlak Model

Indirect Methods

Direct Methods

- ❑ Different tracer: different tumor phenotype
 - [^{18}F]FDG: Glucose metabolism
 - [^{18}F]FMISO: Tumor hypoxia
 - [^{18}F]FLT: Proliferation
 - [^{11}C]Acetate: Oxidative metabolism
- ❑ Pulmonary lesion (16 malignant tumor, 16 tuberculosis, 23 benign lesions)
 - [^{18}F]FDG: sensitivity 87.5% specificity 59.0%
 - [^{18}F]FLT: sensitivity 68.8% specificity 76.9% *[Tian et al. J Nucl Med 2008]*
 - [^{18}F]FDG+[^{18}F]FLT: sensitivity **100%** specificity **89.7%**
- ❑ Hepatocellular carcinoma (99 HCC, 13 cholangiocellular carcinoma)
 - [^{18}F]FDG: sensitivity 60.9% *[Park et al J Nucl Med 2008]*
 - [^{11}C]Acetate: sensitivity 75.4%
 - [^{18}F]FDG+[^{11}C]Acetate: sensitivity **82.7%**

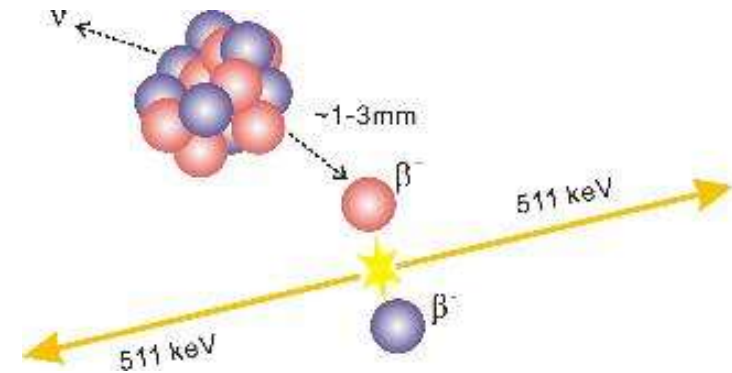
❑ Multi-Tracers and Multi-Scans

- Additional dose from multiple CT scans
- Registration problem
- Staff-consuming, time-consuming

❑ Multiple Tracer in one Scan, technical challenging:

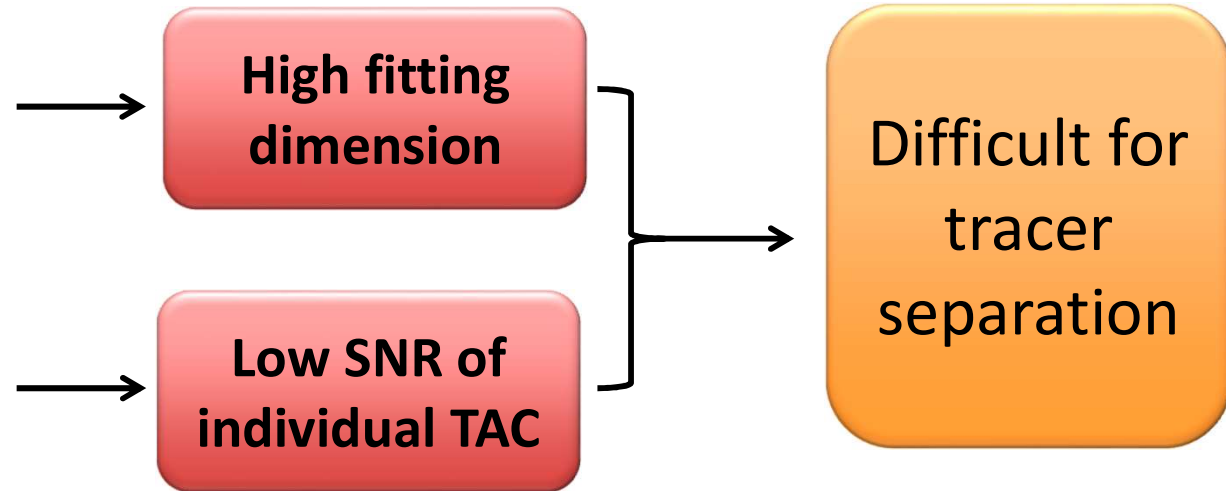
- Different isotopes emitting positrons of different energy
- The gamma photons generated by positron annihilation: same energy level (511KeV)
- Can not be physically differentiated

❑ Identify the individual tracer based on intrinsic pharmacokinetic differences



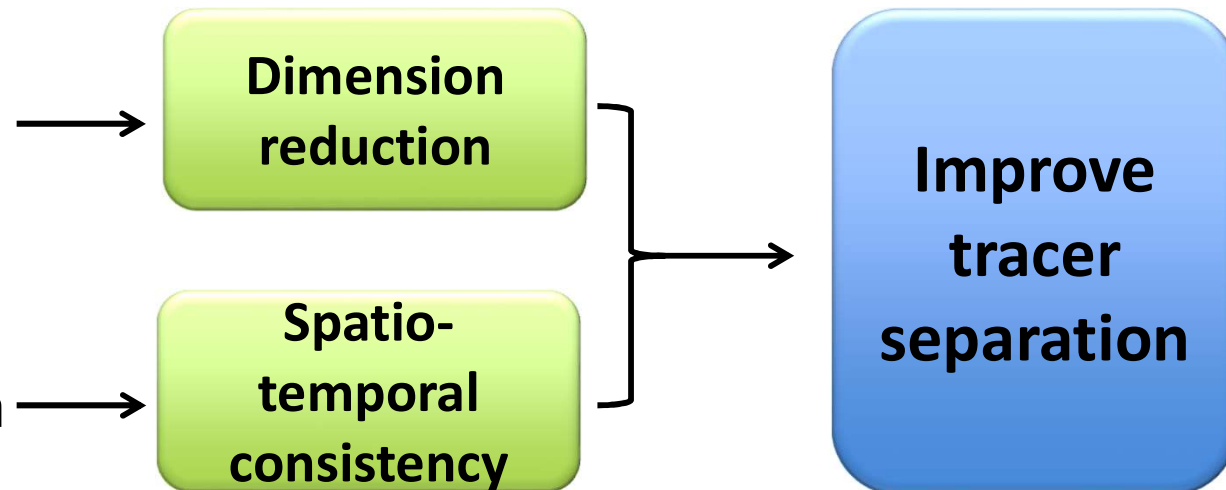
Challenges:

- Multi-tracer Model
- Voxel-wise fitting



Objective:

- Reduced parameter space formulation **(RPS formulation)**
[Kadrmas 2012,2013]
- Direct parametric image reconstruction **(DPIR)**



Parameter Space Reduction

1. Formulate the original multi-tracer model (parameters \mathbf{k}) with parameters θ and \mathbf{v}
2. Regularize the model with the measured TAC C_t as prior knowledge

$$\frac{\partial WSSE}{\partial \theta} = \frac{\partial}{\partial \theta} \left\{ \sum_{t=1}^{N_T} \omega_t (C_t - \hat{C}_t)^2 \right\} = 0$$

3. Results in the representation of \hat{C}_t with \mathbf{v} instead of original parameter \mathbf{k} ;

Direct image reconstruction

1. EM reconstruction of dynamic PET images

[Cheng, ..., Shi. MICCAI 2013]

[Cheng, ..., Shi. PMB 2014]

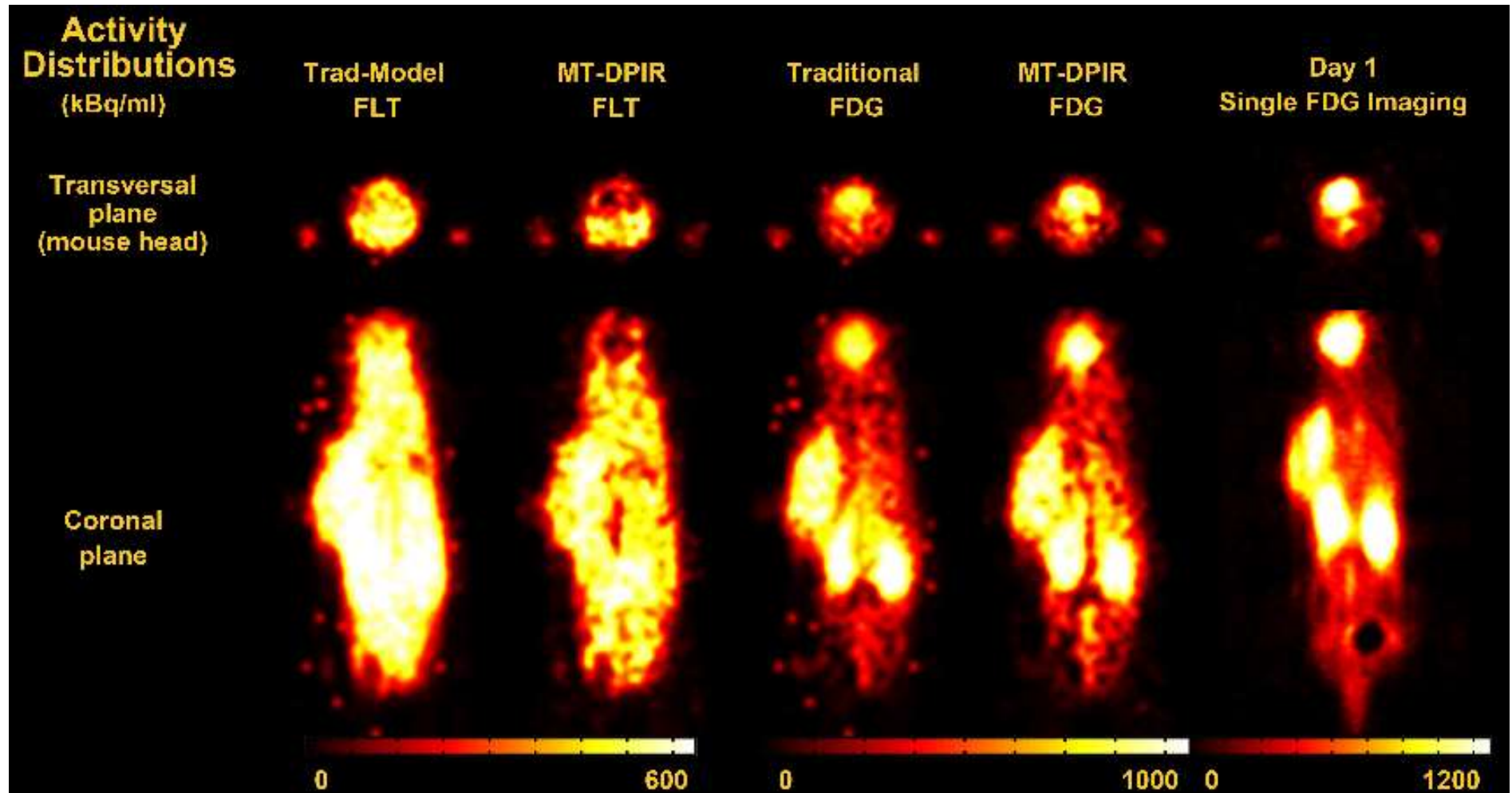
$$\hat{x}_{jt}^{(n+1)} = \frac{x_t(\mathbf{v}_j^{(n)})}{\sum_i a_{ij}} \sum_i a_{ij} \frac{y_{it}}{\sum_{j'} a_{ij'} x_t(\mathbf{v}_{j'}^{(n)}) + r_t + s_t}$$

2. Voxel-wise weighted nonlinear least square fitting (WNLS)

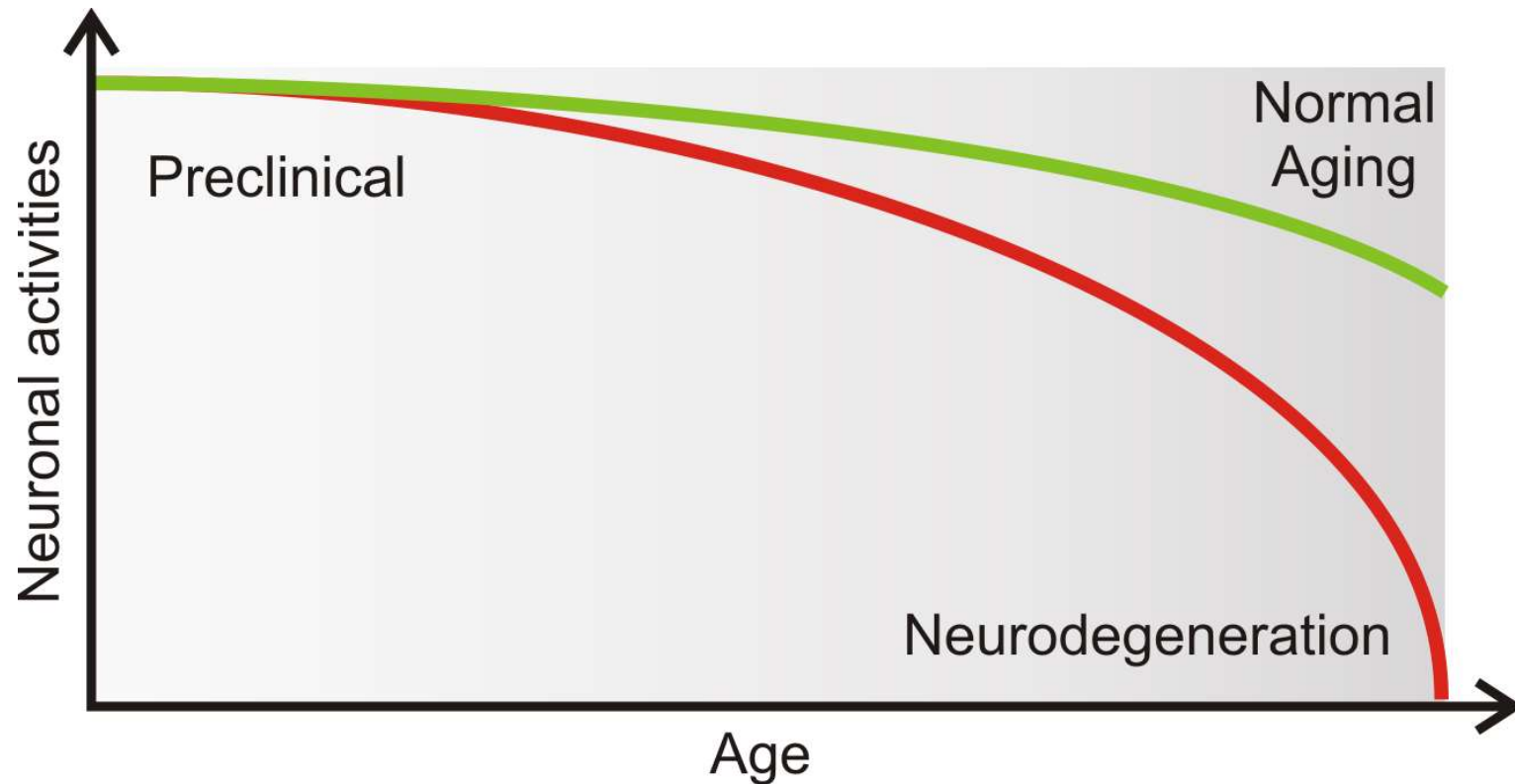
$$\mathbf{v}_j^{(n+1)} = \min_{\mathbf{v}} \sum_{jt} \omega_{jt} \underbrace{(\hat{x}_{jt}^{(n+1)} - x_t(\mathbf{v}_j^{(n)}))^2}_{\text{Nonlinear RPS-Model}}$$

Nonlinear RPS-Model

Selected Results



Semi-Quantitative Analysis: Intensity Normalization for Age Adjustment



- ❑ Confounding factor on metabolic signal: **age-associated metabolic change**
- ❑ Early diagnosis may be more susceptible to this confounding factor

Parkinsonism

- ❑ Atypical parkinsonian syndromes [Goldman & Tanner 1998]
 - Multiple System Atrophy (MSA)
 - Progressive Supranuclear Palsy (PSP)
 - Look like Parkinson's Disease (PD) but much more severe
- ❑ About 20% of PD patients were misdiagnosed
- ❑ Diagnostic error → wrong treatment

How to differentiate the parkinsonism during the early stages of disease?

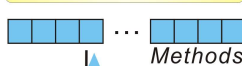
Semi-Quantitative Analysis: Intensity Normalization for Age Adjustment

- ❑ Identify best normalization to describe age-related changes
- ❑ Define a quantity for age adjustment

Spatially Normalized PET Data



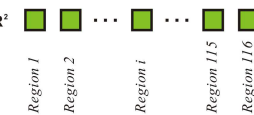
Intensity normalization



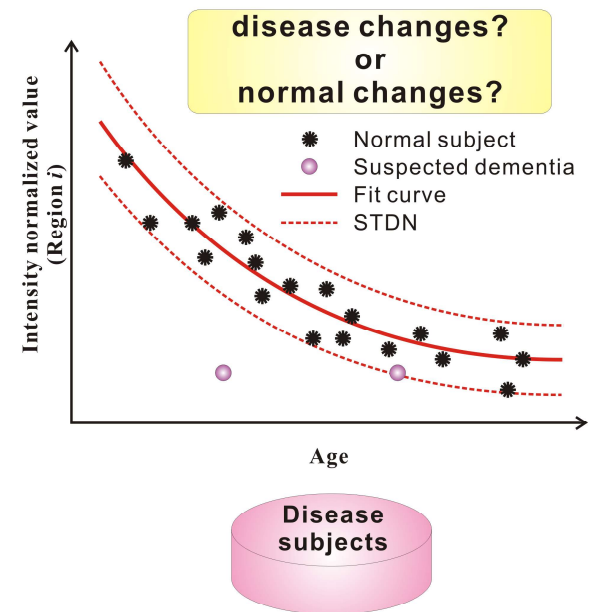
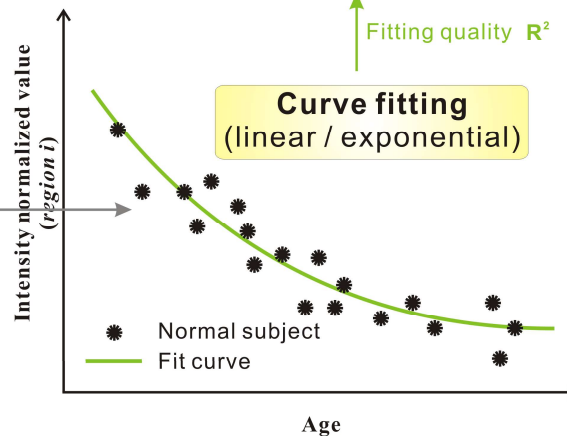
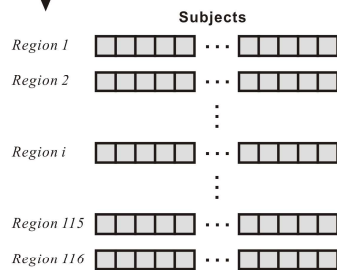
Find best normalization method: $\max(\text{Total Coherence Coefficient})$

Parcellation

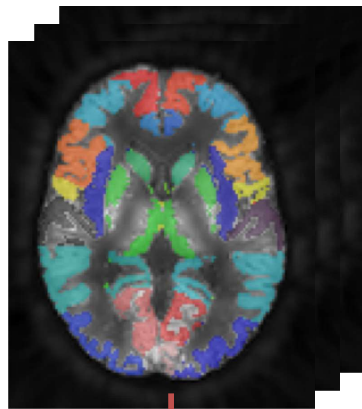
Total Coherence Coefficient: $\text{sum}(R^2)$



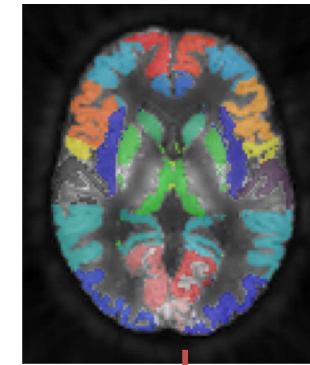
Normal subjects



[Zhang et al. NeuroImage 2017]



Database of ^{18}F -FDG PET of Normal Subjects



New Subject

Regional average

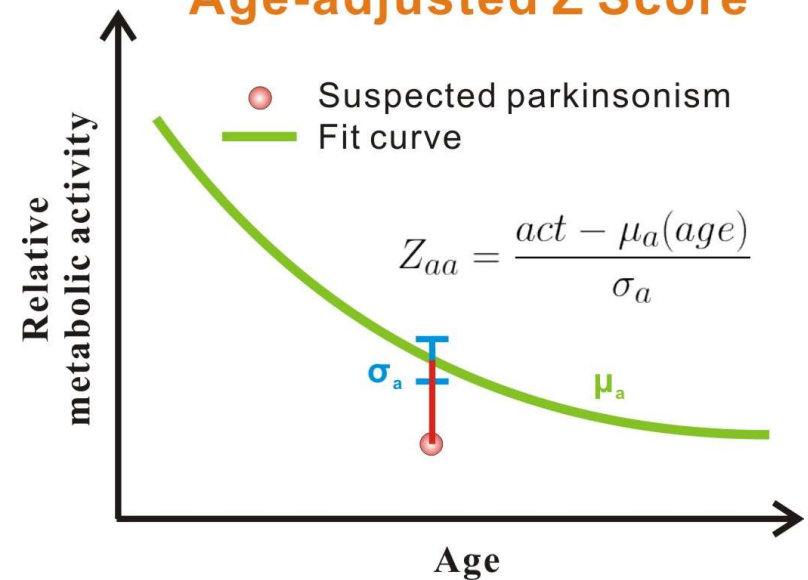
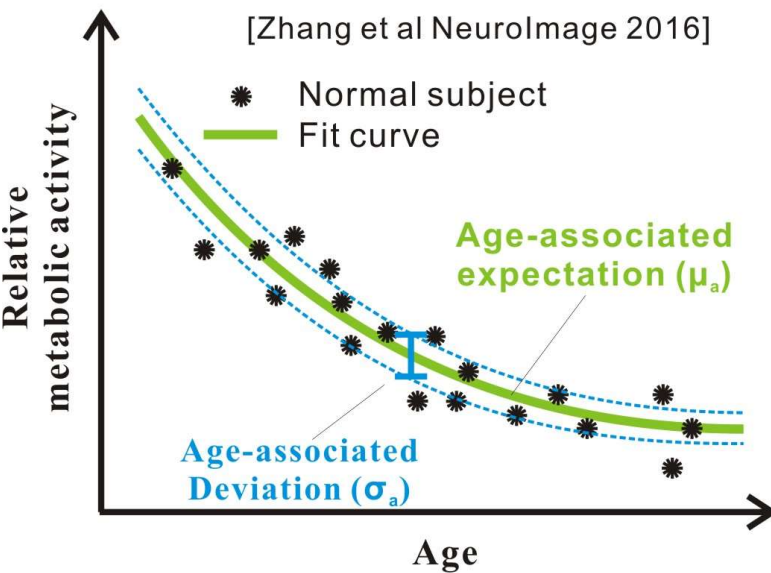
Regional average

Model of Age-related Changes

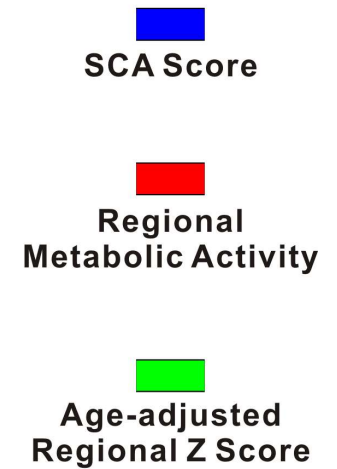
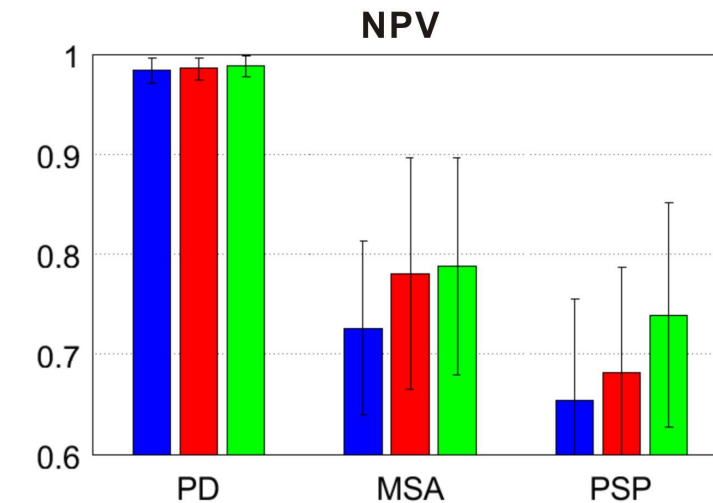
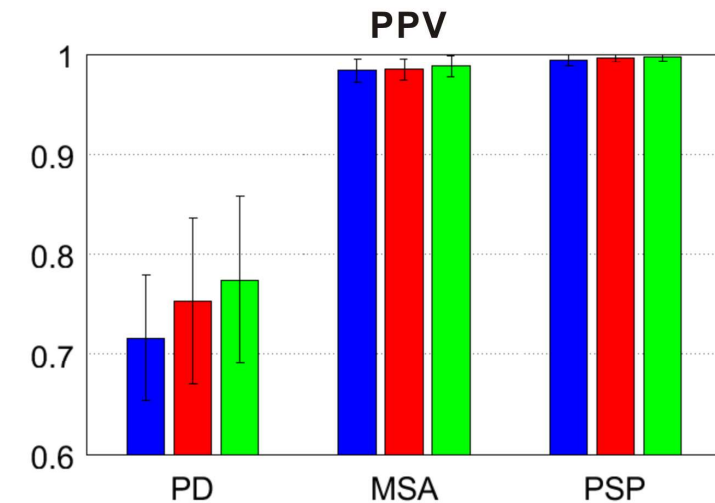
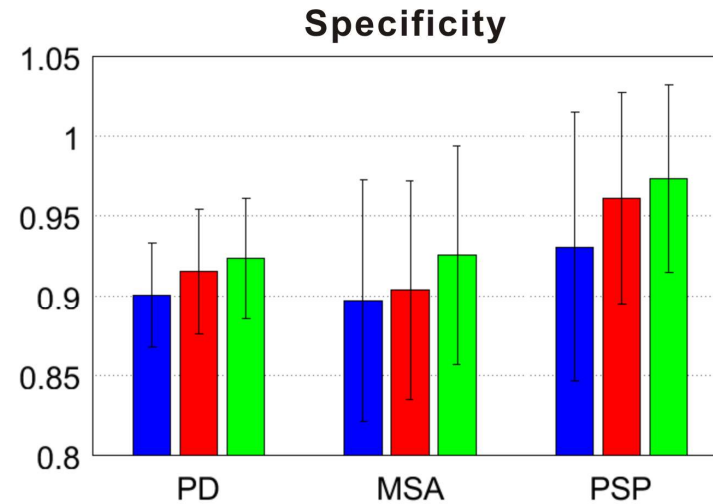
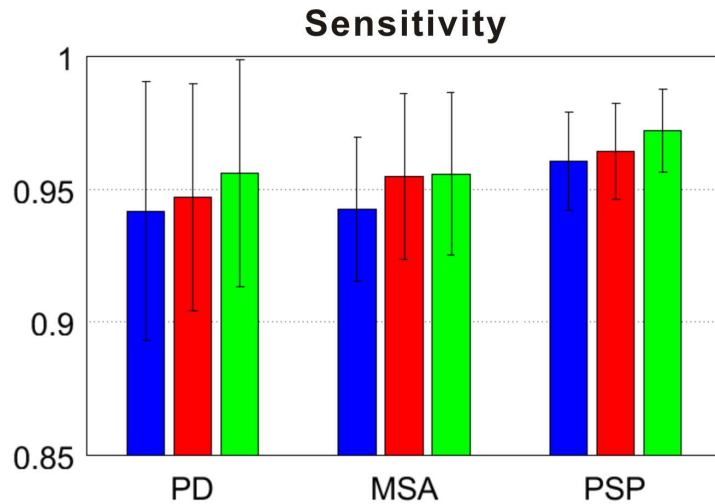
Age-adjusted Z Score

[Zhang et al NeuroImage 2016]

● Suspected parkinsonism
— Fit curve



Semi-Quantitative Analysis: Intensity Normalization for Age Adjustment



❑ Pharmacokinetic modeling

- Quantitative analysis
- Less susceptible to confounding factor but more sensitive to noise
- Improve the robustness:
 - Linearization
 - Utilization of spatial-temporal consistency: direct parametric image reconstruction, hierarchical modeling

❑ Intensity normalization

- Semi-quantitative analysis
- Easily applicable

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Thank you!

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