



Biomedical Imaging

Nuclear Imaging (II)

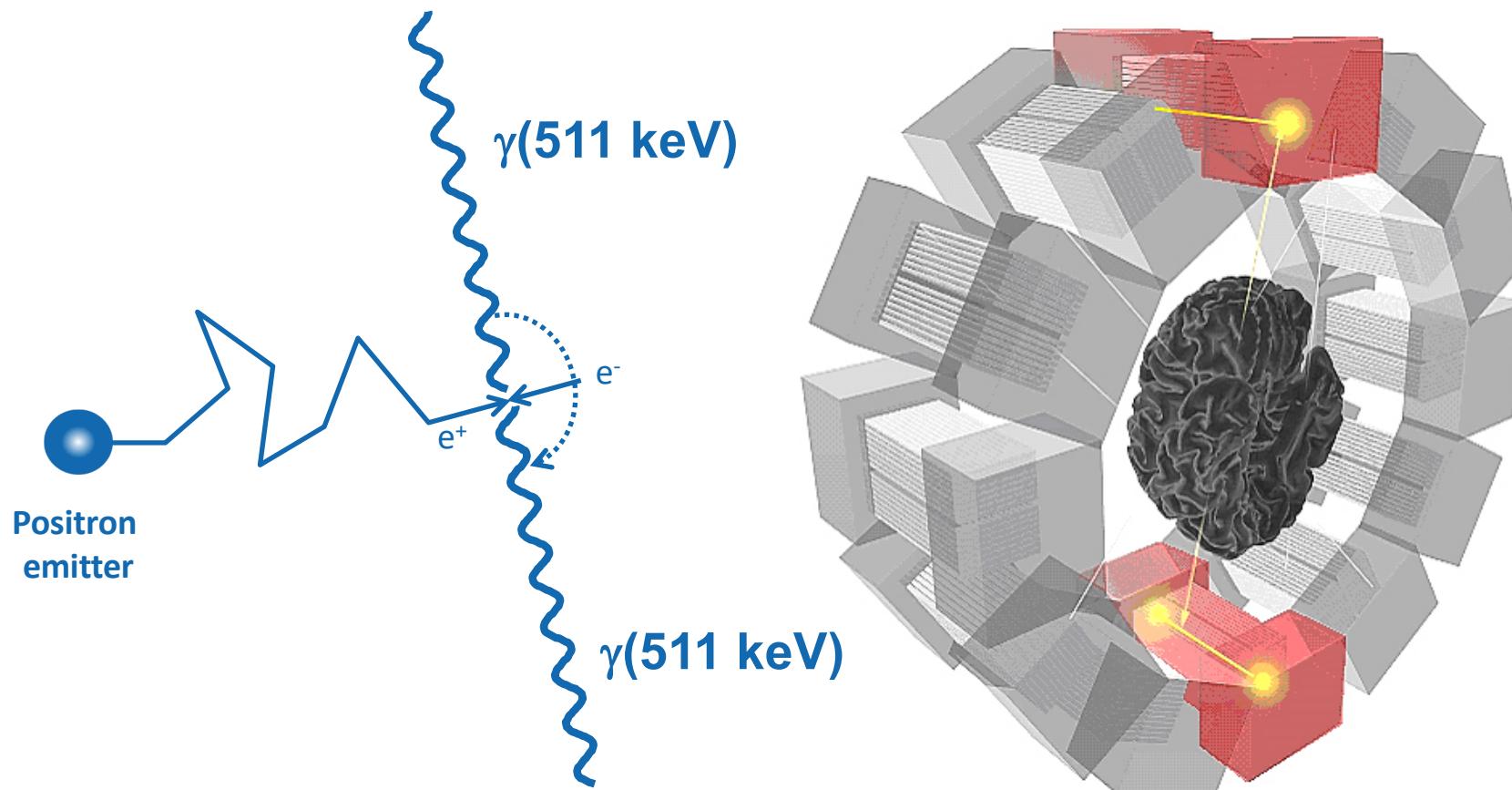
Sebastian Kozerke / Markus Rudin

Institute for Biomedical Engineering, University and ETH Zurich, Switzerland

Today's Learning Objectives

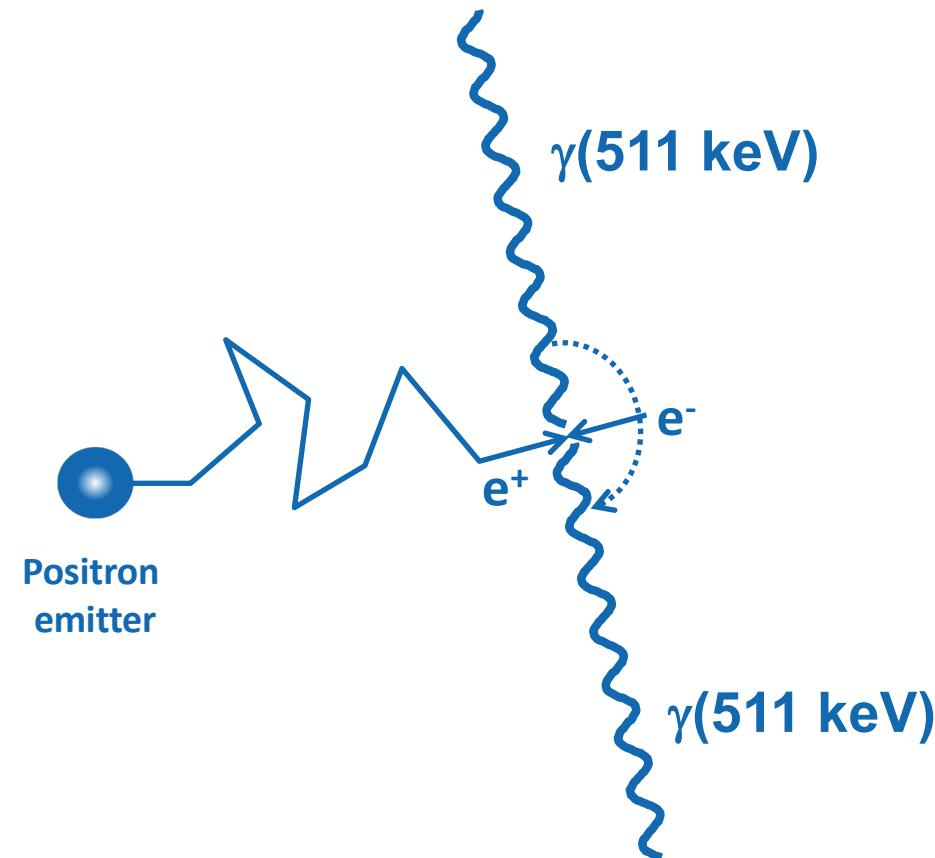
- Explain various PET coincidence events and corrections thereof
- Describe SPECT radioisotope production (Technetium generator)
- Describe PET radioisotope production (cyclotron)
- Derive basic kinetic models for PET tracer quantification
- Implement kinetic modeling for PET (Exercise)

Positron Emission Tomography



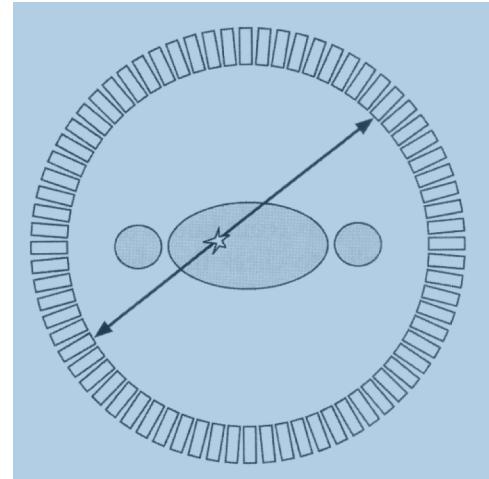
Activity (5 min)

Using the mass of positron/electron, show that the energy of γ -photons is indeed 511 keV ($m_{p,e} = 9.11 \cdot 10^{-31}$ kg; $1 \text{ eV} = 1.6 \cdot 10^{-19} \text{ J}$)!

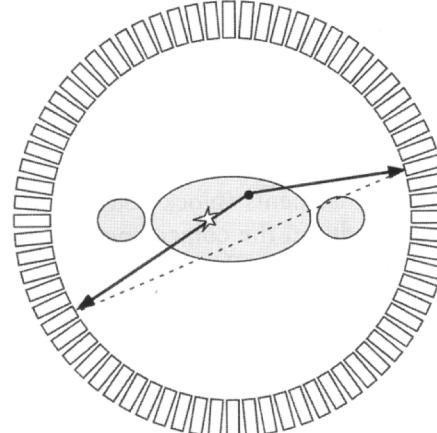


Coincidence types

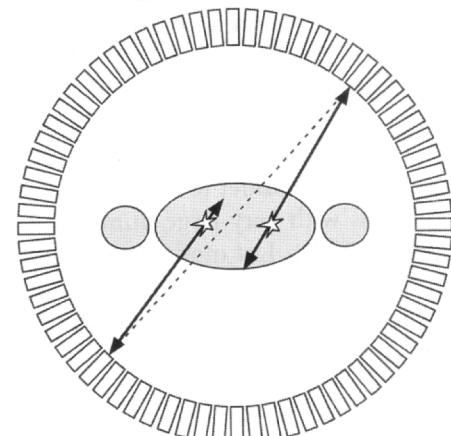
true
coincidence



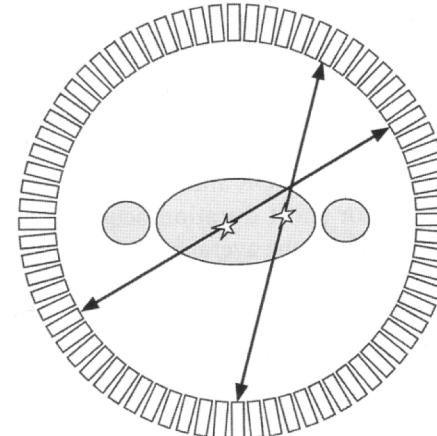
scattered
coincidence



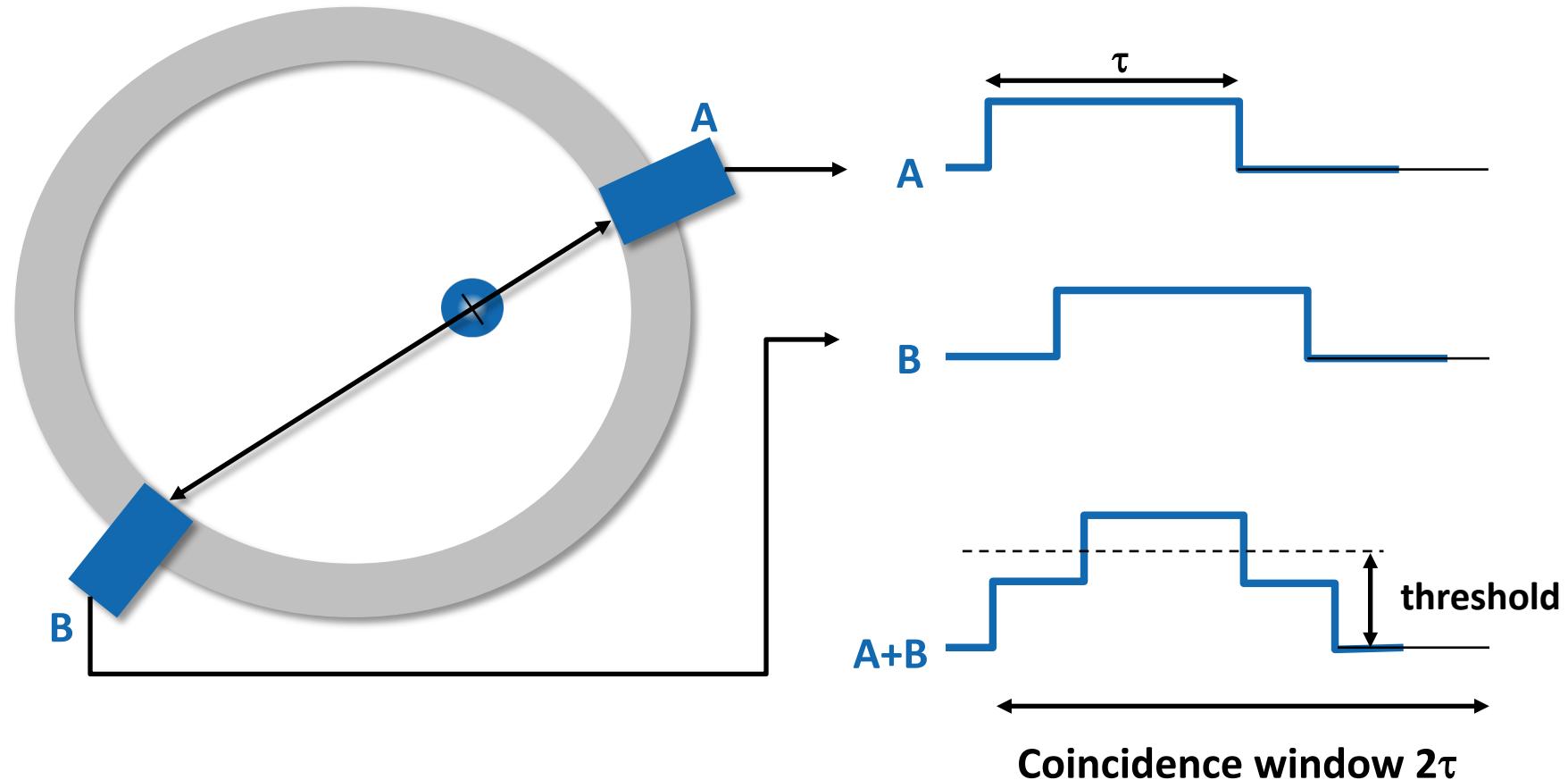
random
coincidence



multiple
coincidence

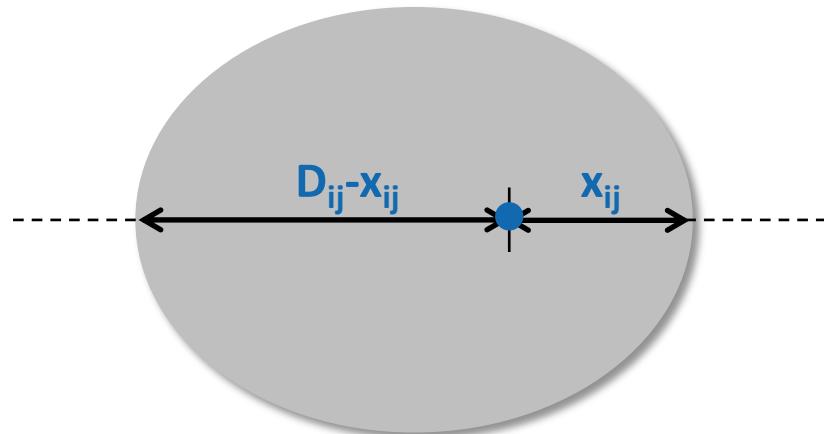


Coincidence detection



Attenuation correction

- Loss of γ -photons due to Compton scattering



$$p_{1ij} = e^{-\mu \cdot x_{ij}}$$

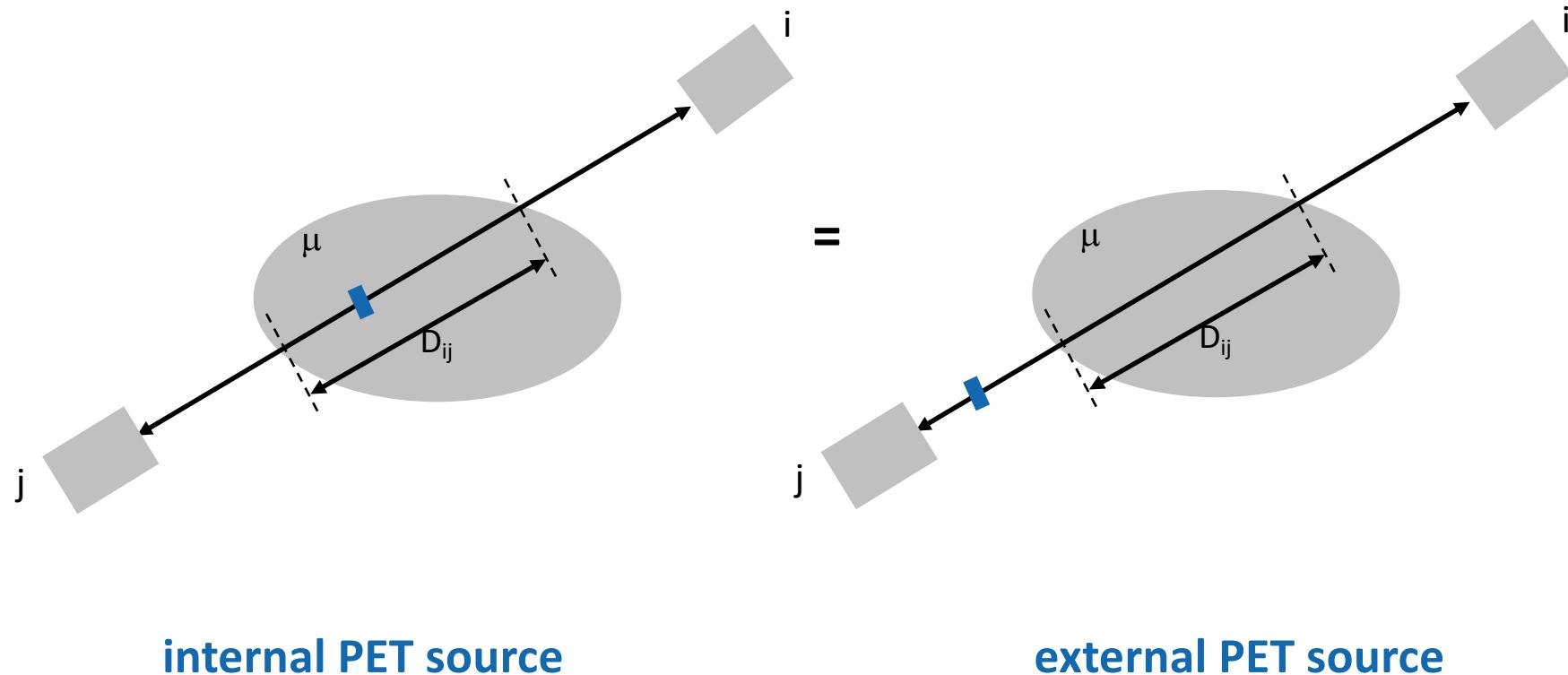
$$p_{2ij} = e^{-\mu \cdot (D_{ij} - x_{ij})}$$

- Total scattering probability

$$p_{ij} = p_{1ij} \cdot p_{2ij} = e^{-\mu \cdot D_{ij}}$$

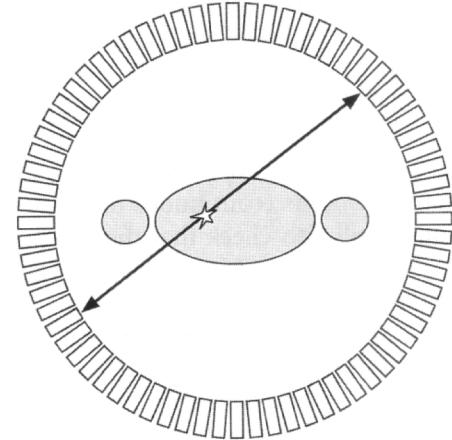
Attenuation correction

$$a_{ij} = \frac{1}{p_{ij}} = e^{\mu \cdot D_{ij}}$$

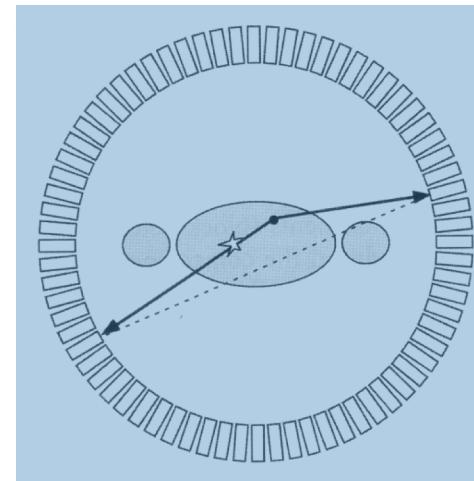


Coincidence types

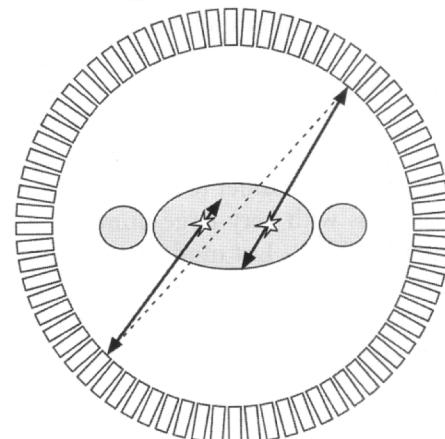
true
coincidence



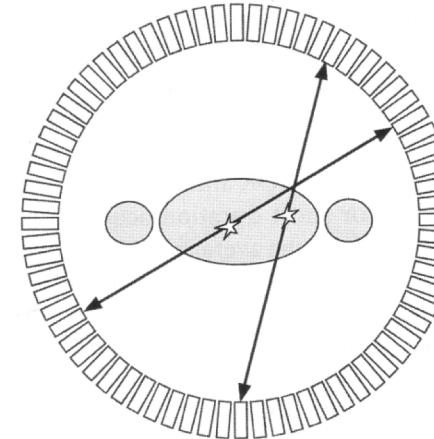
scattered
coincidence



random
coincidence



multiple
coincidence



Scatter correction

Analytical method

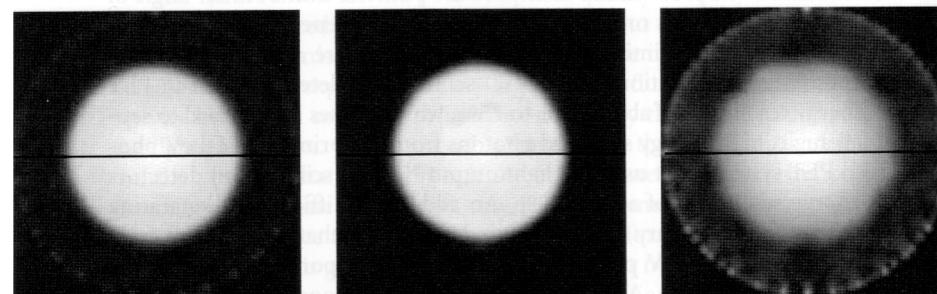
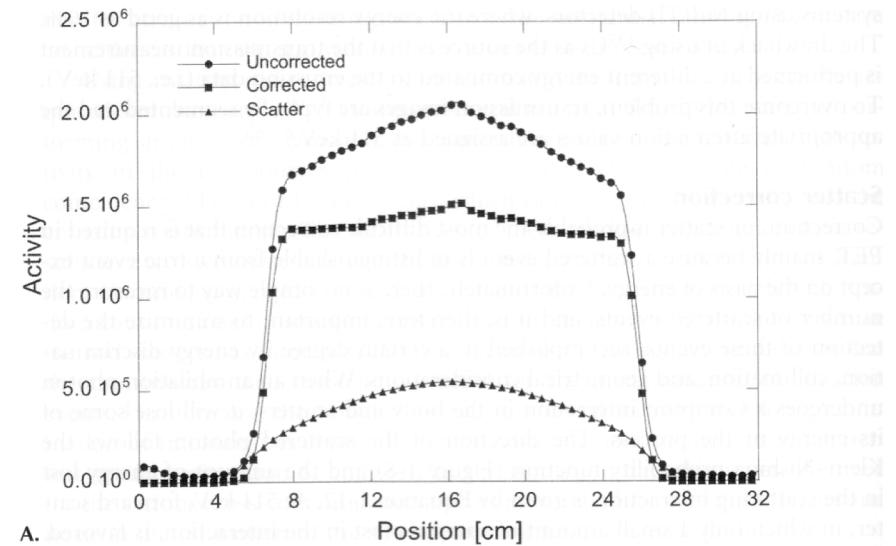
- assumption: scatter distribution varies slowly across scattering medium
- use phantom data to correct for scattered events

Dual energy method

- Energy range 400-600 keV: scattered and true events
- Energy range 200-400 keV: only scattered events

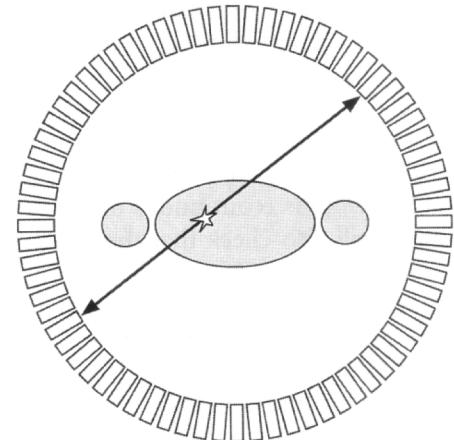
Simulation method

- Reconstruction without scattering correction
- Estimation of scattering correction

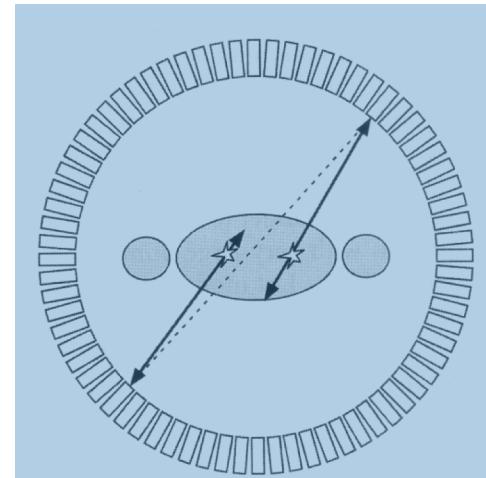
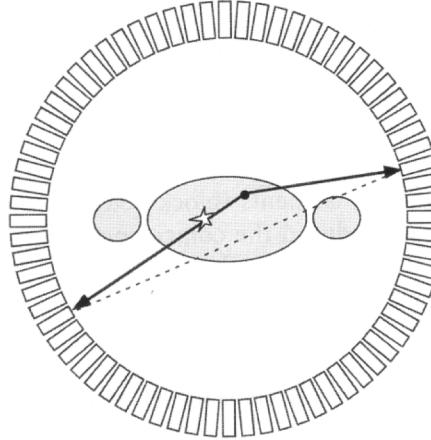


Coincidence types

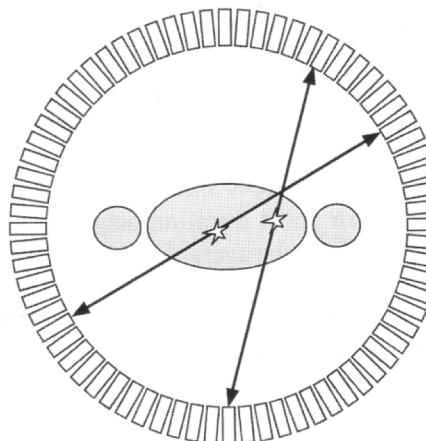
true
coincidence



scattered
coincidence



random
coincidence



multiple
coincidence

Random coincidences

Frequency of random events

Individual photon detection rates of a pair of detectors:

$$N_A, N_B$$

Coincidence window:

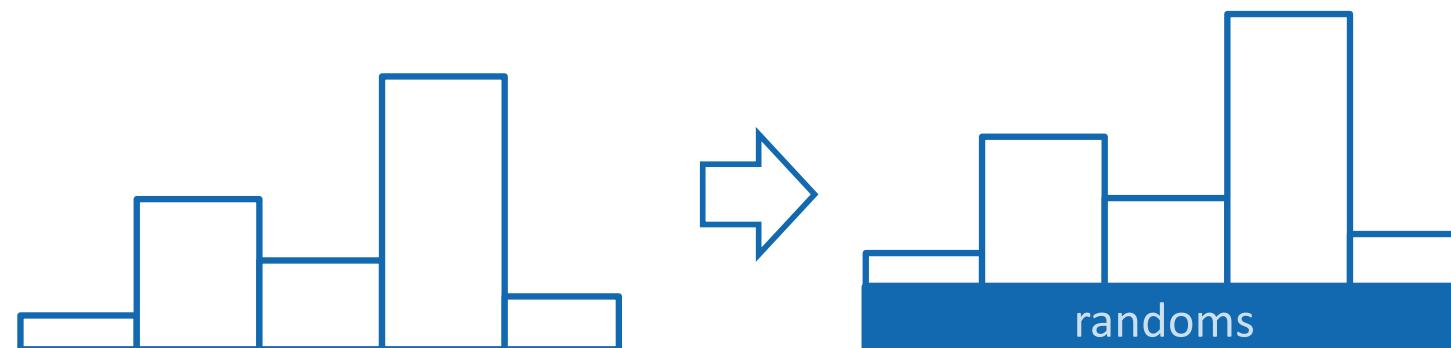
$$2\tau$$

Frequency of random events:

$$N_R = N_A \cdot N_B \cdot 2\tau$$

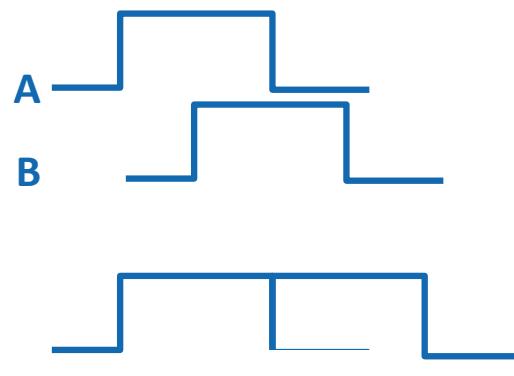
‘Randoms’

- no geometrical information
 - almost uniform distribution across field-of-view
- reduced contrast-to-noise ratio



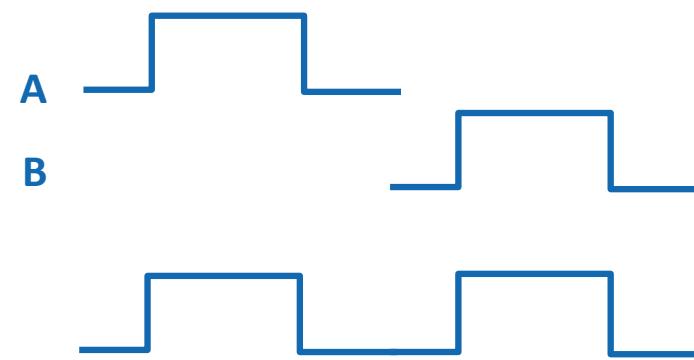
Correction of random coincidences

- Estimate number of ‚randoms‘ for each detector pair: N_1 , N_2 , 2τ must be known
- Measure/estimate number of ‚randoms‘ by adding parallel coincidence circuit



Coincidence window 1

↓
‘trues’ and ‘randoms’ N_{actual}



Coincidence window 2

↓
‘randoms’ $N_{randoms}$

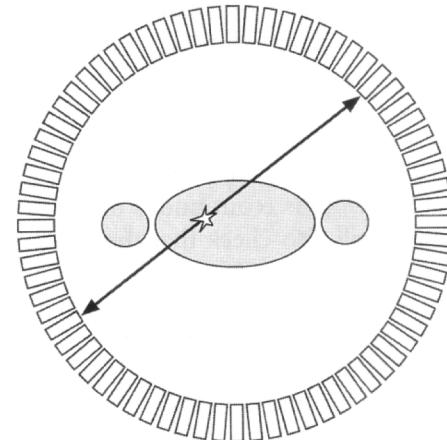
Estimation of number of true events:

$$N_{true} = N_{actual} - N_{randoms}$$

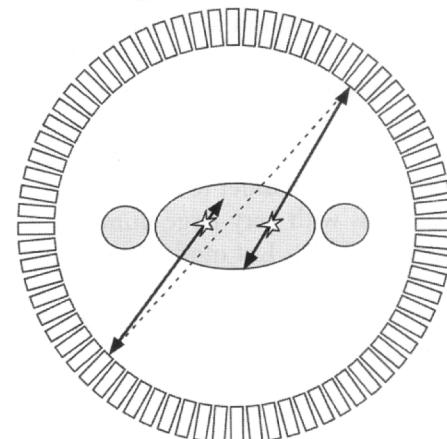
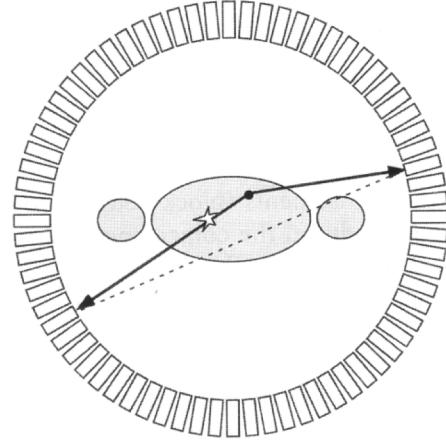


Coincidence types

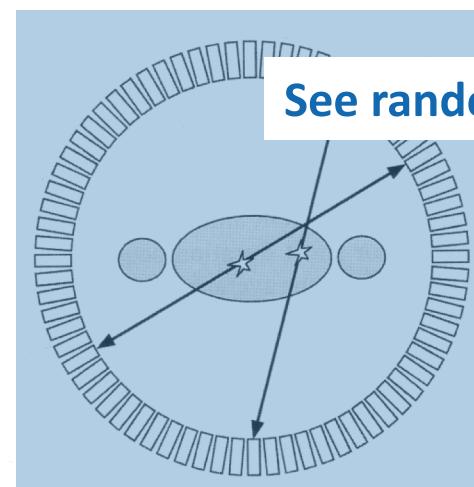
true
coincidence



scattered
coincidence



random
coincidence



multiple
coincidence

See random coincidence

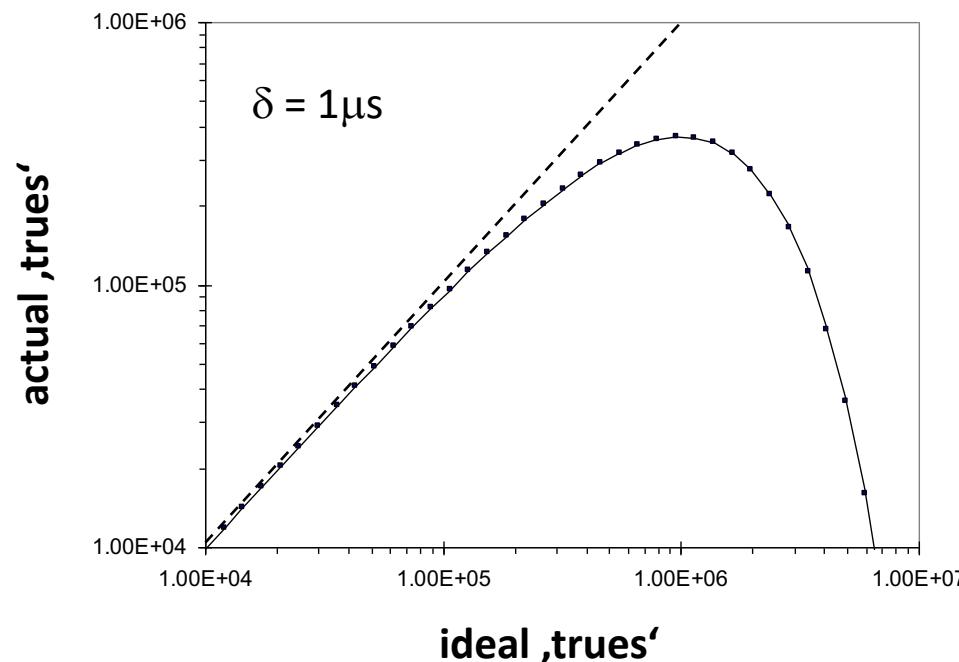
Dead time correction

Detector dead time: **number of events measured < number of true events**

Effect more severe for high activities → high count rate, high fraction of missed events:

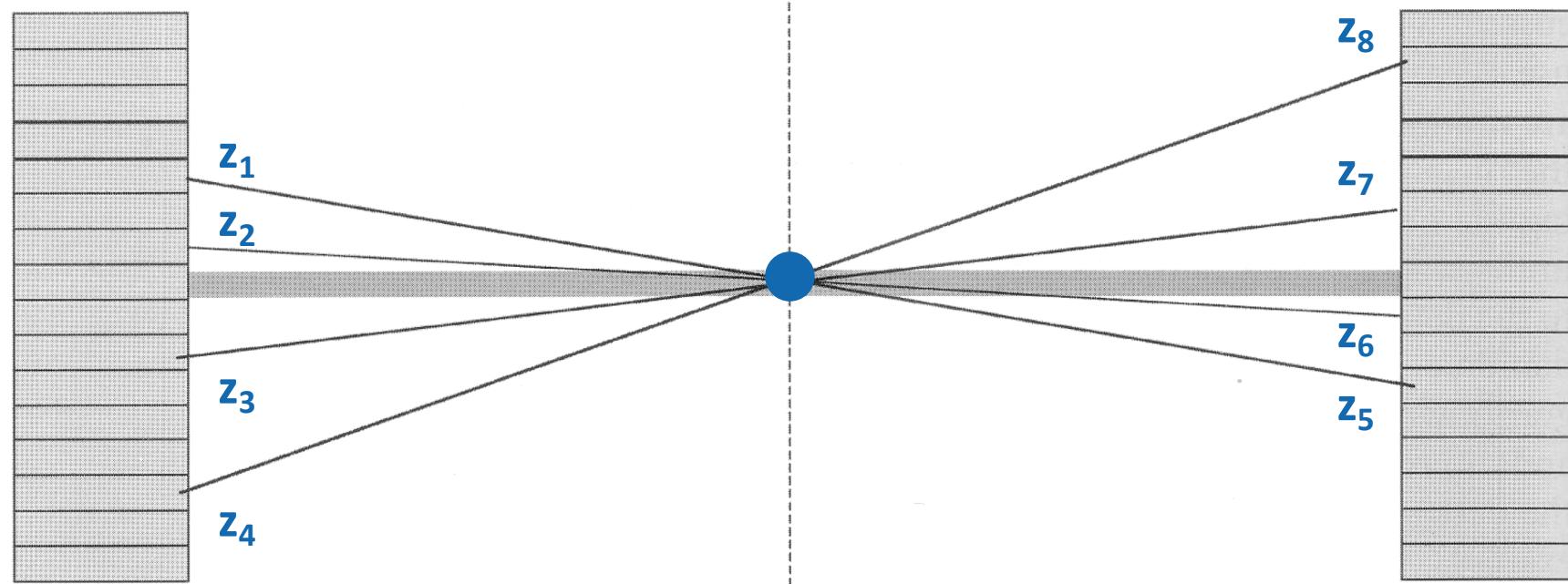
$$N_{\text{actual}} = N_{\text{true}} \cdot e^{-N_{\text{true}} \cdot \delta}$$

δ ...dead time



3D image reconstruction

Data are reduced to a set of **parallel 2D sinograms** by rebinning all sinograms with same z value into the same sinogram



$$z_1 + z_5 = z_2 + z_6 = z_3 + z_7 = z_4 + z_8$$

► Reconstruction of N 2D sinograms



3D image reconstruction

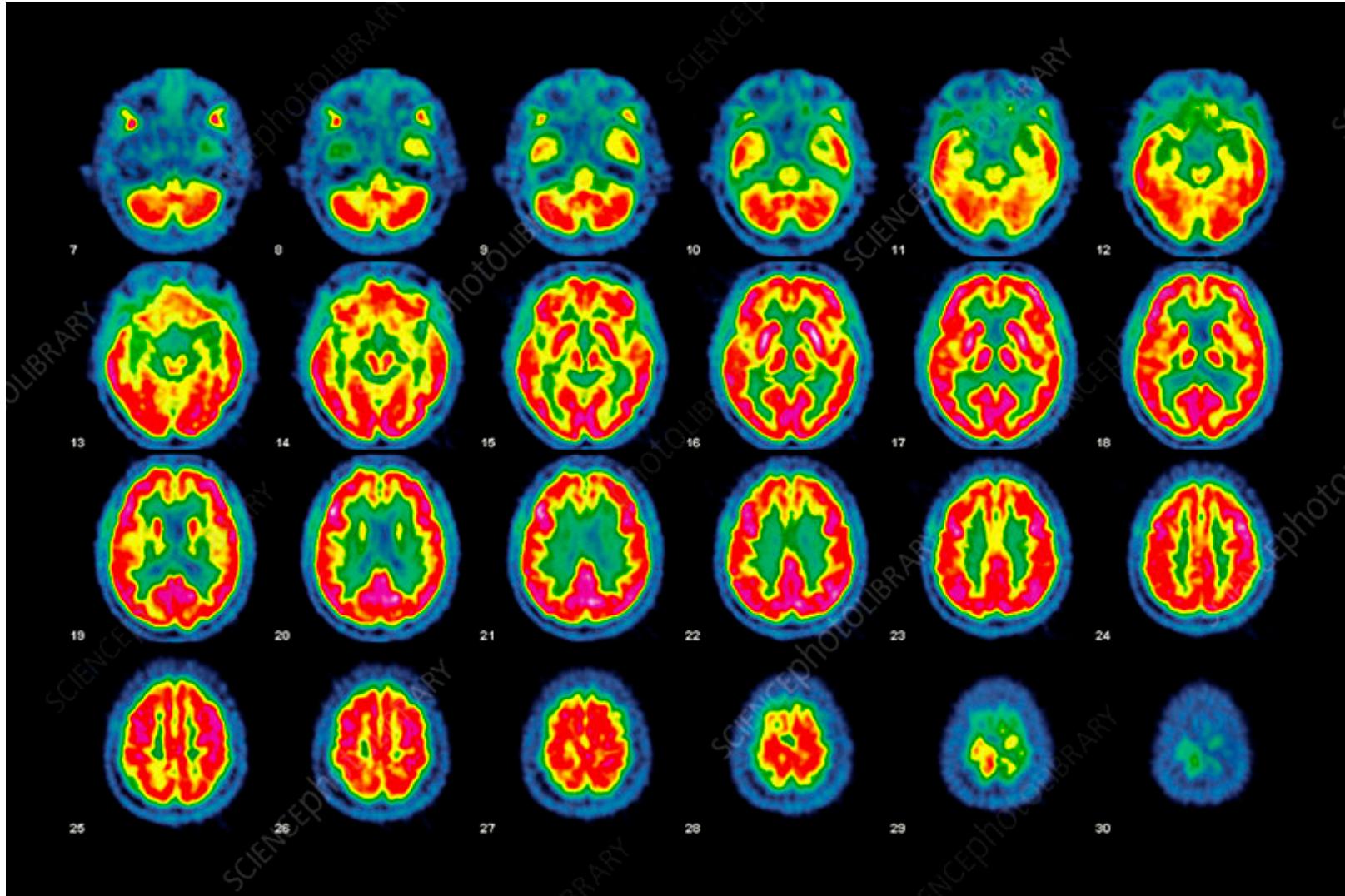


Image noise reduction

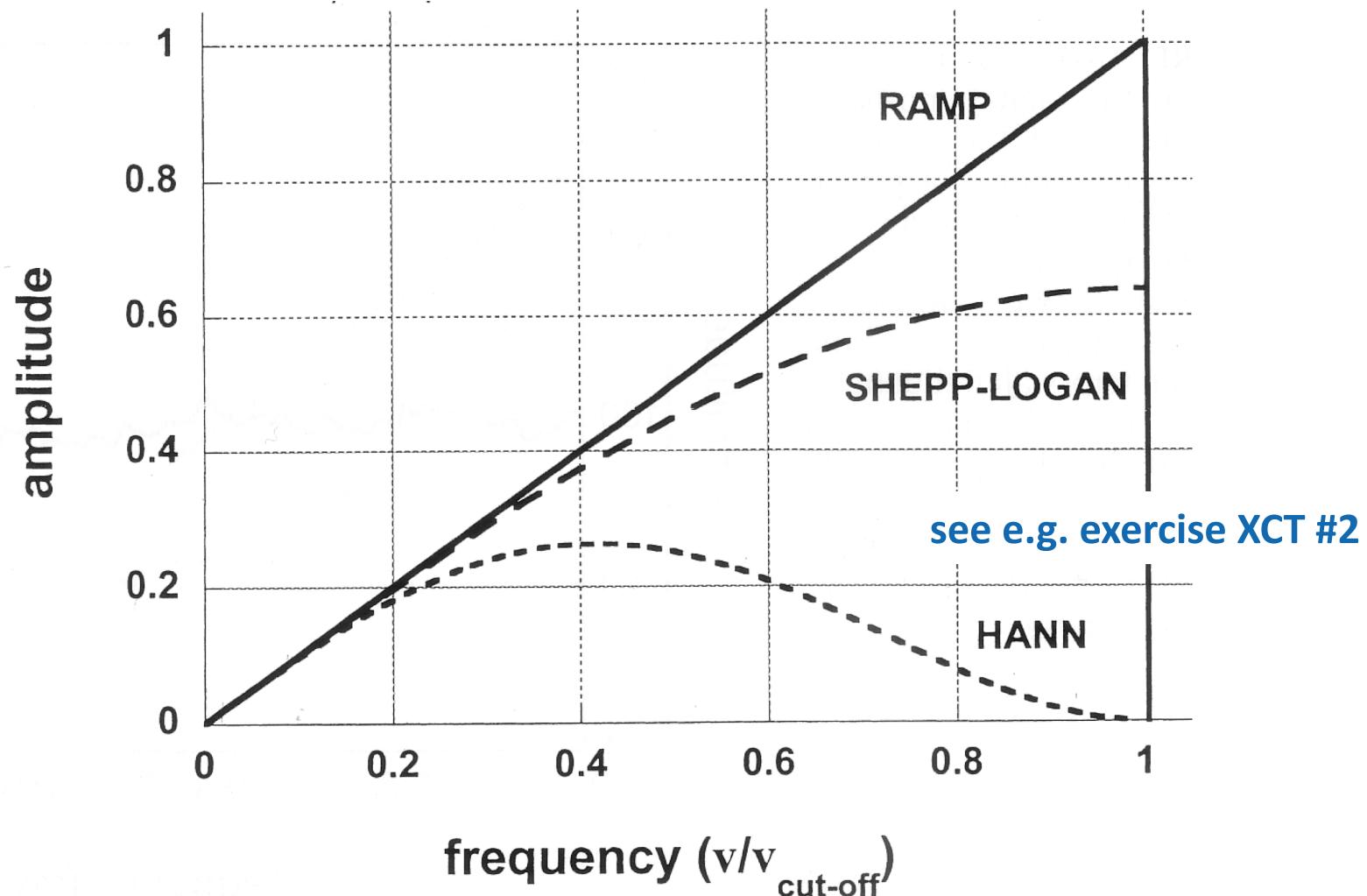
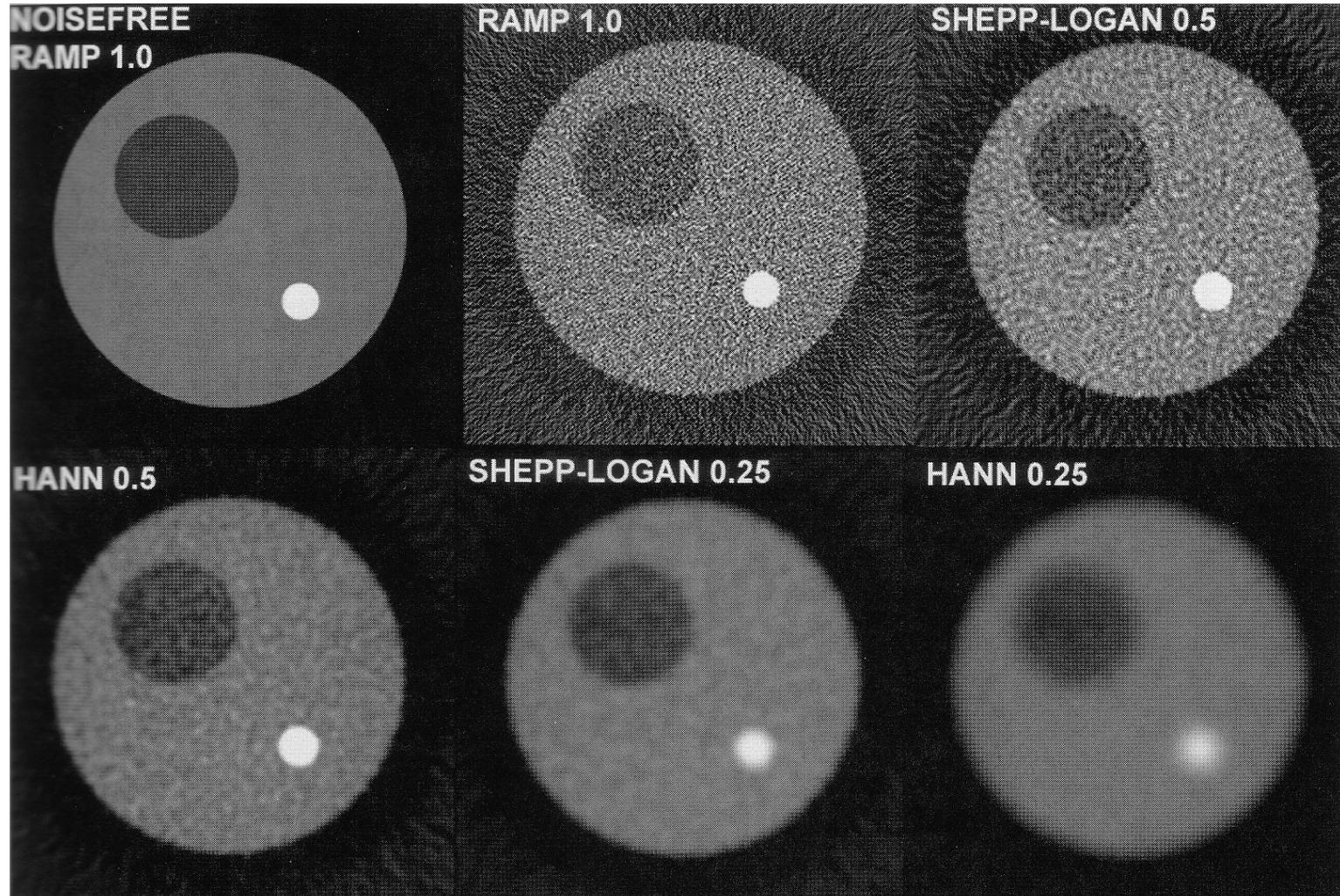


Image noise reduction



Clinical PET scanner



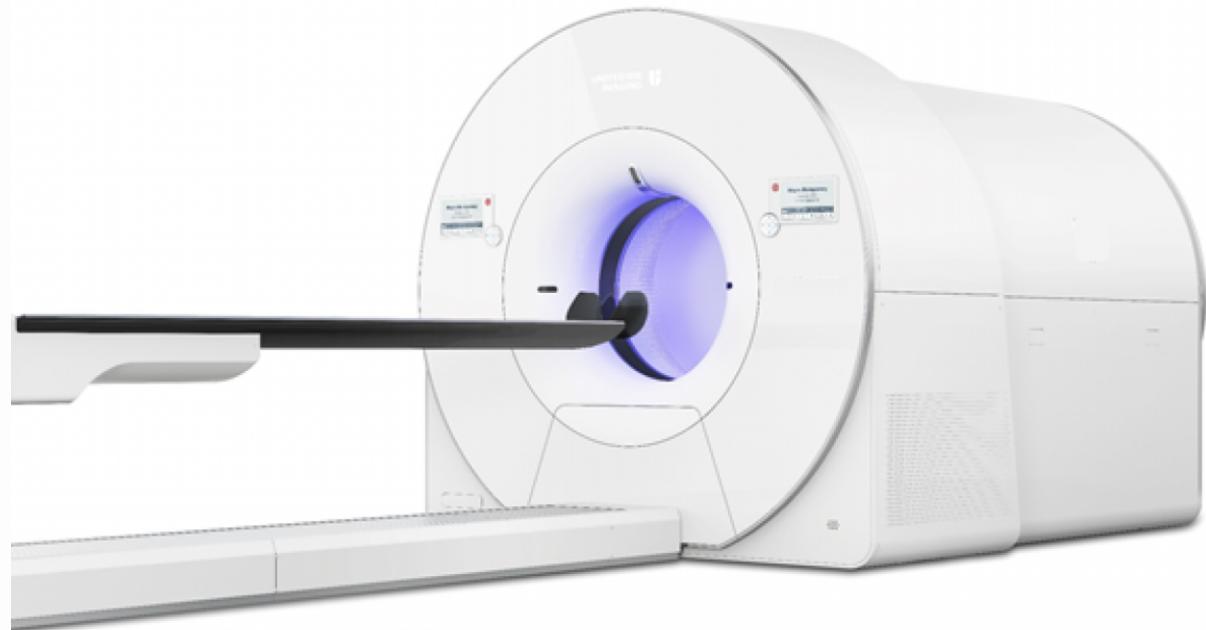
Animal PET scanner



PET/CT scanner



Total body PET scanner



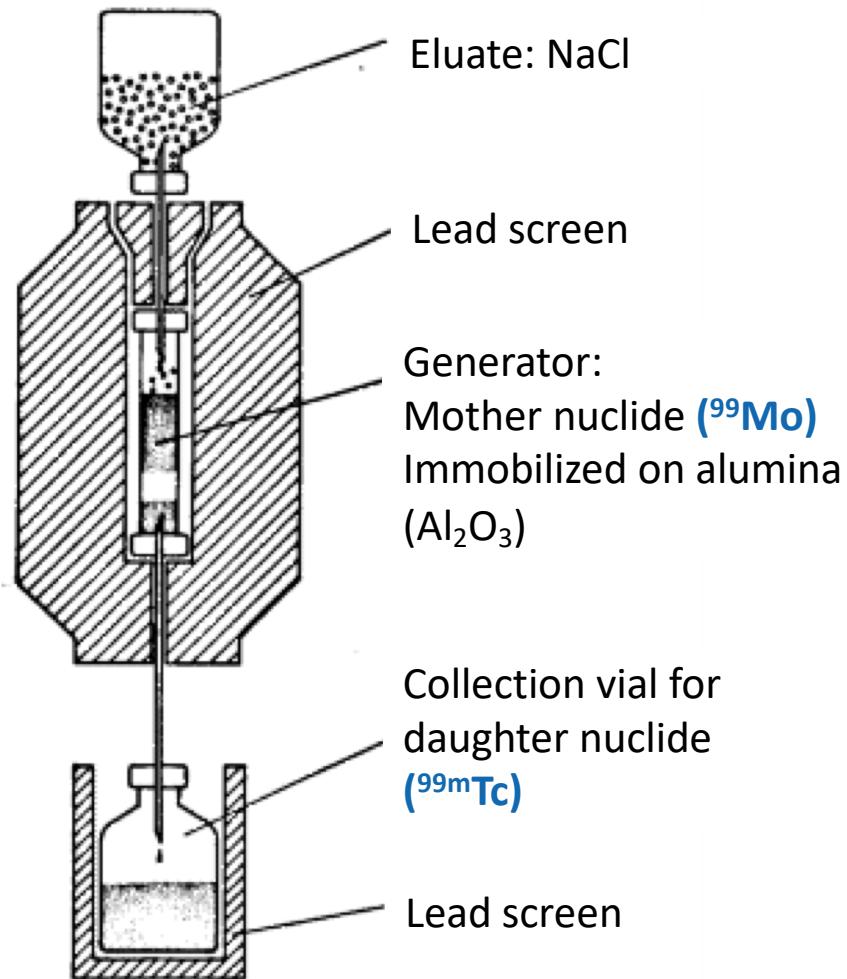


Radiotracer Production

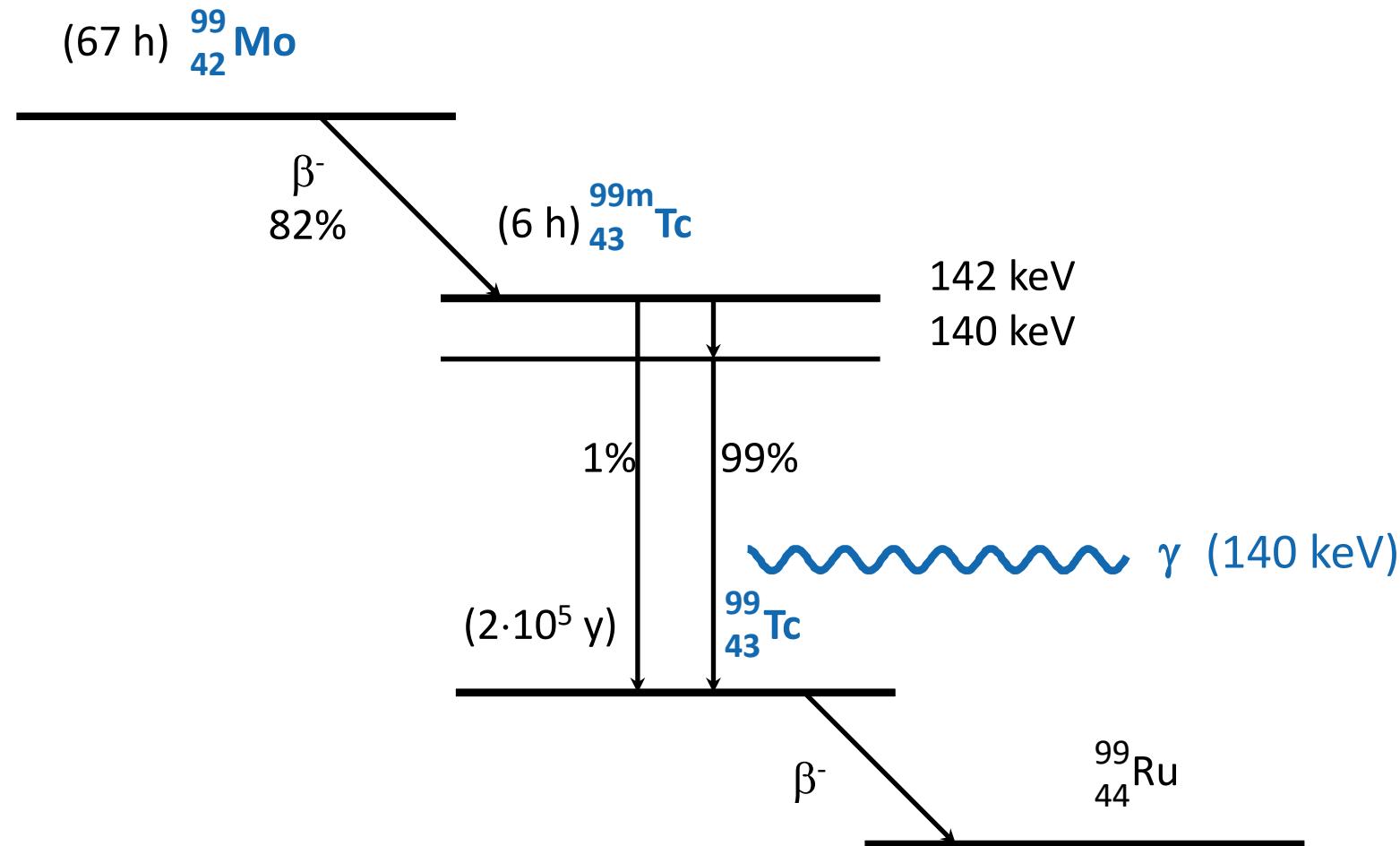
SPECT radioisotopes

Radioisotope	Energy (keV)	Half-life	Production
^{67}Ga	93, 185, 300	3.3d	cyclotron
$^{99\text{m}}\text{Tc}$	140	6h	generator
^{111}In	173, 247	67h	cyclotron
^{123}I	160	13h	cyclotron
^{133}Xe	81	5.2d	reactor
^{201}Tl	60, 83	73h	cyclotron

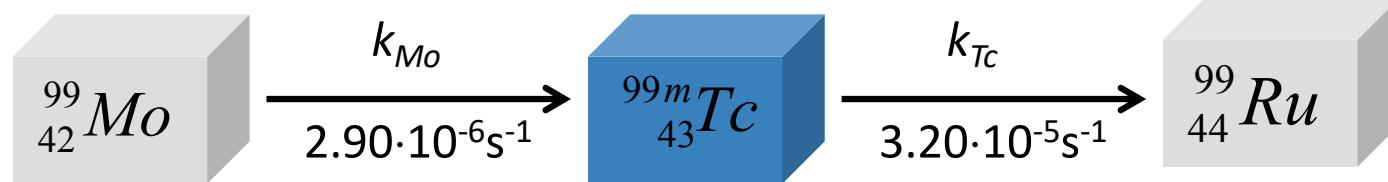
Technetium generator



Technetium generator



Technetium generator



Kinetic equations:

$$\frac{d}{dt} N_{^{99}Mo} = -k_{Mo} \cdot N_{^{99}Mo}$$

$$\frac{d}{dt} N_{^{99m}Tc} = +k_{Mo} \cdot N_{^{99}Mo} - k_{Tc} \cdot N_{^{99m}Tc}$$

Solution:

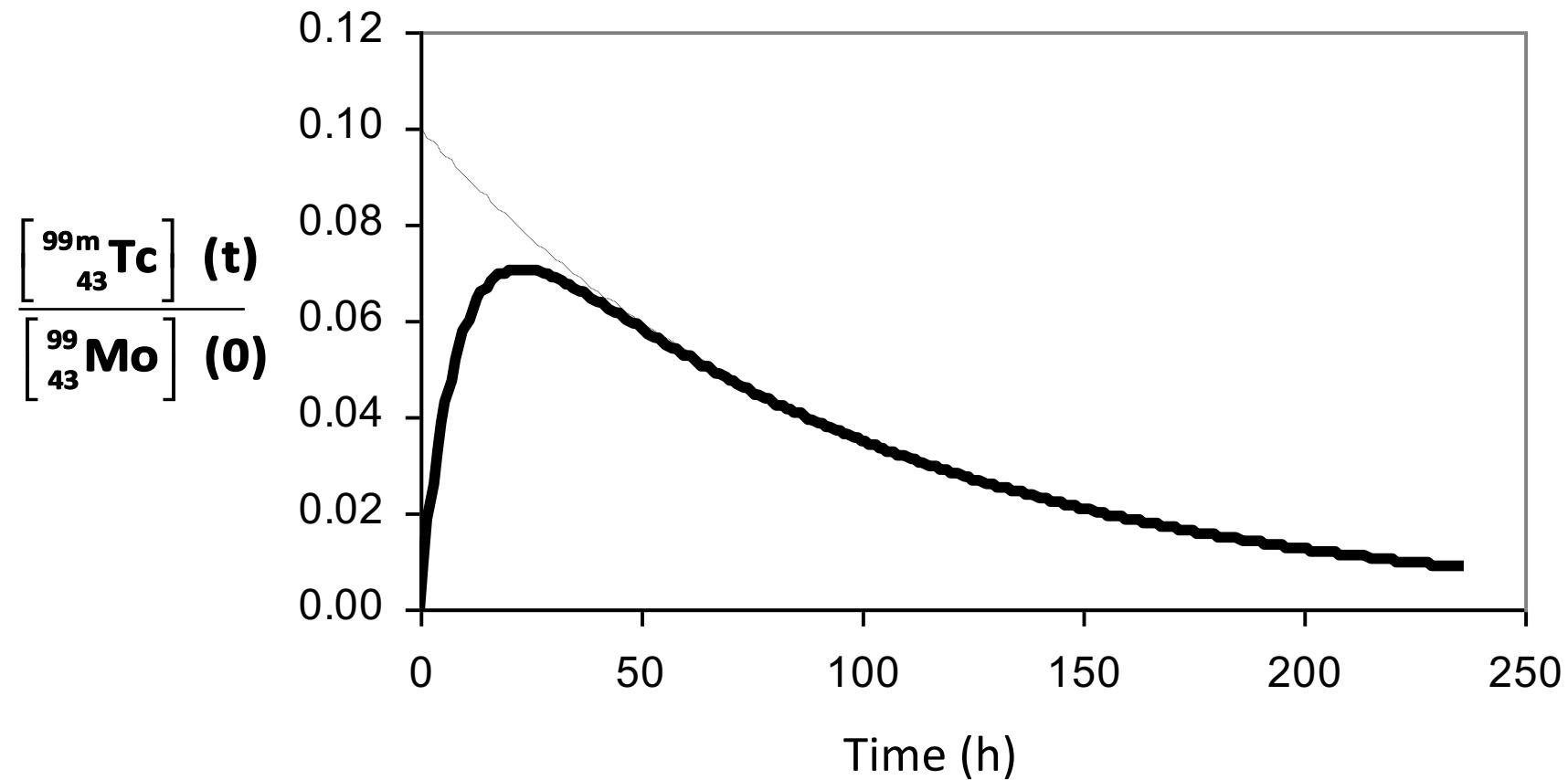
$$N_{^{99m}Tc}(t) = N_{^{99}Mo}(0) \cdot \frac{k_{Mo}}{k_{Tc} - k_{Mo}} \cdot \left\{ \exp(-k_{mo} \cdot t) - \exp(-k_{Tc} \cdot t) \right\}$$

Radioactivity of ^{99m}Tc :

$$Q_{^{99m}Tc}(t) = k_{Tc} \cdot N_{^{99m}Tc}(t) = N_{^{99}Mo}(0) \cdot \frac{k_{Mo} \cdot k_{Tc}}{k_{Tc} - k_{Mo}} \cdot \left\{ \exp(-k_{mo} \cdot t) - \exp(-k_{Tc} \cdot t) \right\}$$



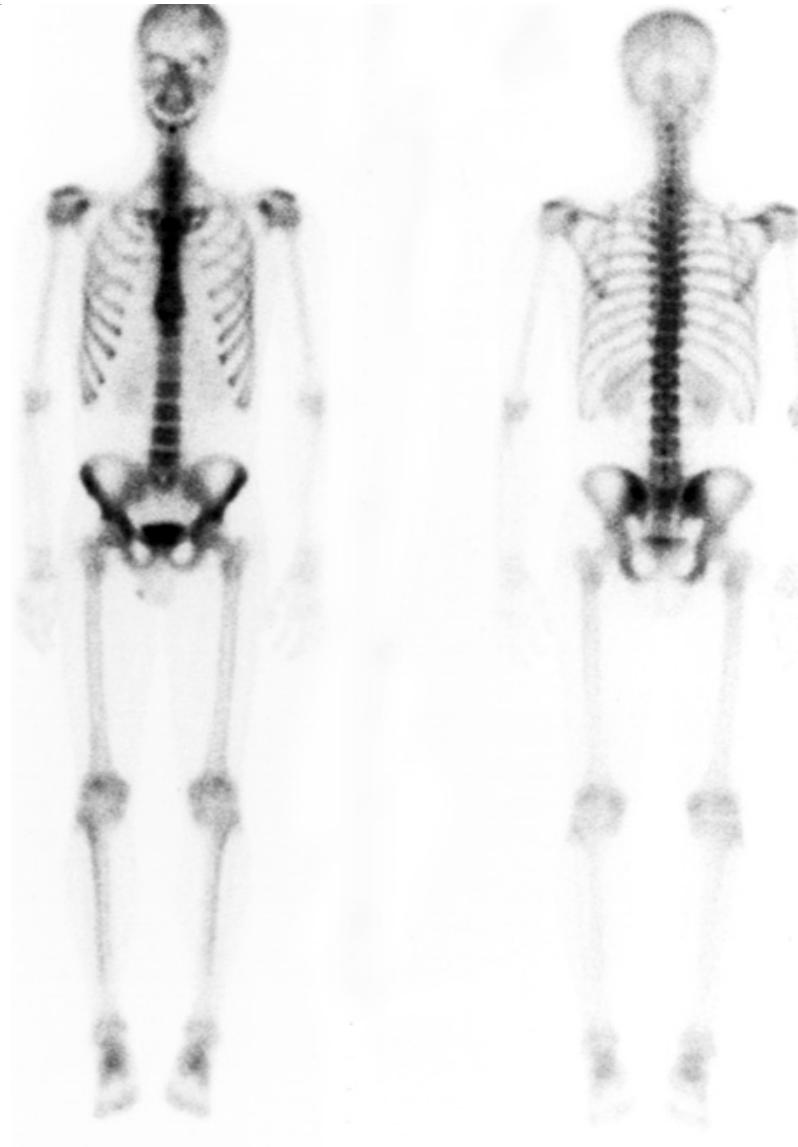
Technetium generator



Technetium tracers

Radiolabel	Ligand	Application
$^{99m}\text{TcO}_4\text{-Na}$	Sodium pertechnetate	Thyroid function
$^{99m}\text{Tc-HSA}$	Human serum albumine	Blood pool, cardiac function
$^{99m}\text{Tc-HSA}$	Human serum albumine (microspheres)	Regional perfusion, vascular patency
$^{99m}\text{Tc-MIBI}$	2-methoxy-isobutylisonitril	Myocardial function
$^{99m}\text{Tc-HMPAO}$	Hexamethyl-propylenaminoxim	Cerebral perfusion
$^{99m}\text{Tc-HEDP}$	Hydroxyl-ethylene-diphosphonate	Bone metabolism / formation
$^{99m}\text{Tc-MDP}$	Methylene-diphosphonate	Bone metabolism / formation
$^{99m}\text{Tc-DTPA}$	Diethylene-triamine-tetraacetate	Kidney function, lung function

SPECT imaging of bone



PET radioisotopes

Radionuclide	Half-life	E _{max} (MeV)	e ⁺ decay (%)
¹¹ C	20.4 min	0.96	100
¹³ N	10 min	1.20	100
¹⁵ O	2 min	1.73	100
¹⁸ F	110 min	0.63	97
²² Na	2.6 y	0.55	90
⁶² Cu	9.7 min	2.93	97
⁶⁴ Cu	12.7 h	0.65	29
⁶⁸ Ga	67.6 min	1.89	89
⁷⁶ Br	16.2 h	Various	56
⁸² Rb	1.3 min	2.60, 3.38	96
¹²⁴ I	4.2 d	1.53, 2.14	23

Production of ^{18}F radionuclide

©de pinxi

<https://www.youtube.com/watch?v=zD1fnNAmAPk>

Properties of ^{18}F radionuclides

- Lifetime 110 min
- Lifetime reasonably long for chemical synthesis
- Lifetime long enough to allow for shipping of labeled compound
- ^{18}F PET does not require on-site cyclotron
- Studies can be repeated in relatively short time intervals

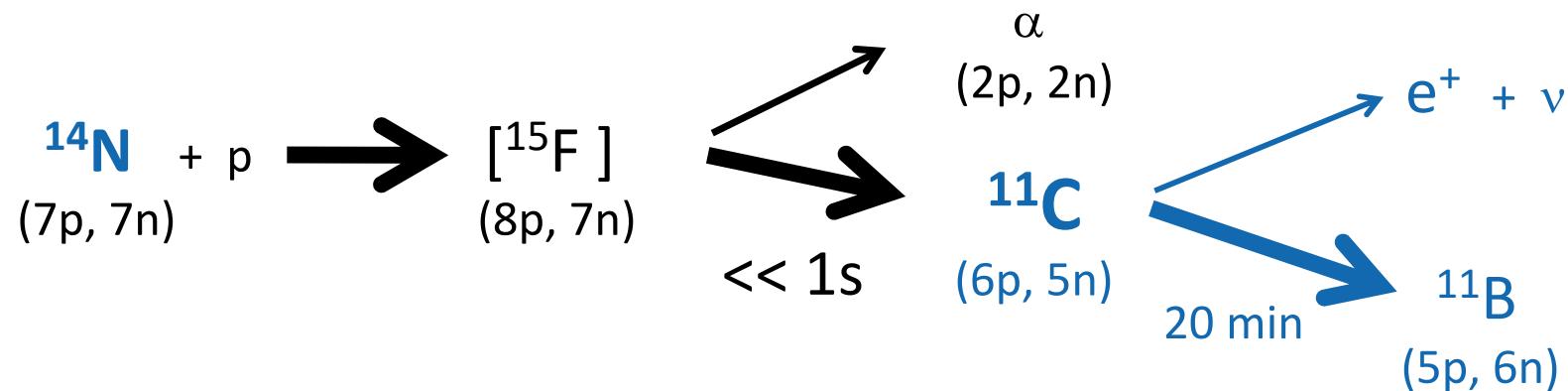
but

- Pharmacokinetics different from native, endogenous compound

PET radioisotopes

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Production of ^{11}C radionuclide



Proton
capture
Proton source:
cyclotron

Metastable nucleus $(t_{1/2} \ll 1s)$

Positron emitter *Stabilization by positron emission*

Stable nucleus

Stabilization by emission of α-particle

Chemical synthesis

Properties of ^{11}C radionuclides

- All organic compounds contain C and can be labeled in principle
- Pharmacokinetic properties identical to that of 'cold' parent compound
- Studies of drug biodistribution / PK
- Receptor affinity identical to that of parent compound

but

- Short half life (20 min)
- Chemical synthesis difficult due to time constraints



Quantitative PET Analysis

Quantitative PET – definitions

Injected dose per gram of tissue:

$$\%ID/g = \frac{c_t \cdot v_t}{D_{inj}} \cdot \frac{1}{m_t} \cdot 100\%$$

c_t tissue concentration

v_t volume of tissue ROI

m_t mass of tissue ROI

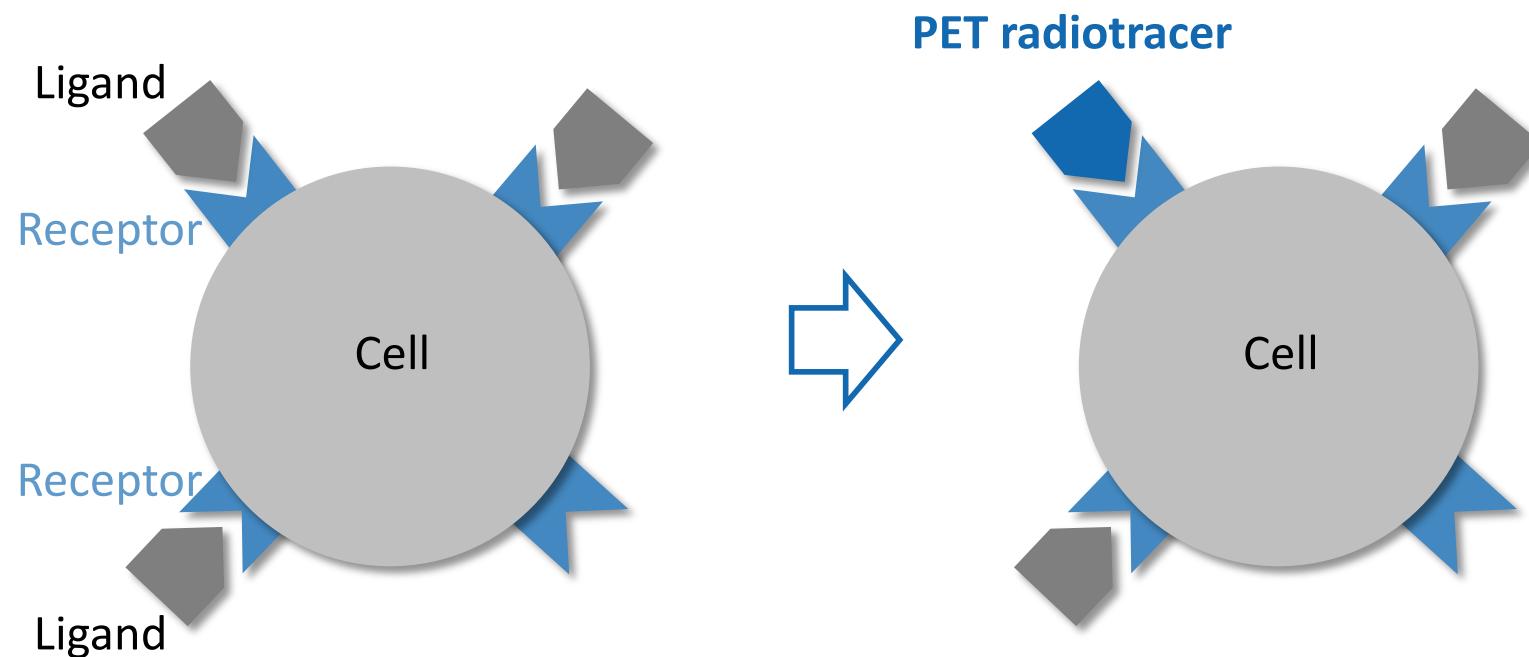
D_{inj} injected dose

Standardized Uptake Value (SUV):

$$SUV = [\%ID/g] \cdot M / 100 = \frac{c_t \cdot v_t}{D_{inj}} \cdot \frac{1}{m_t} \cdot M$$

M : Body mass

Quantitative PET – receptor binding



Quantitative PET – receptor binding

Receptor Binding:



Equilibrium constant:

$$K_d = \frac{k_{off}}{k_{on}} = \frac{[L] \cdot [R]}{[RL]} \quad k_{off} \cdot [RL] = k_{on} \cdot [R] \cdot [L]$$

(principle of microreversibility)

Mass conservation for receptor:

$$[R_T] = [R] + [RL]$$

yields

$$K_d = \frac{[L]}{[RL]} \cdot ([R_T] - [RL])$$

or the receptor binding

$$\frac{[RL]}{[R_t]} = \frac{[L]}{K_d + [L]}$$

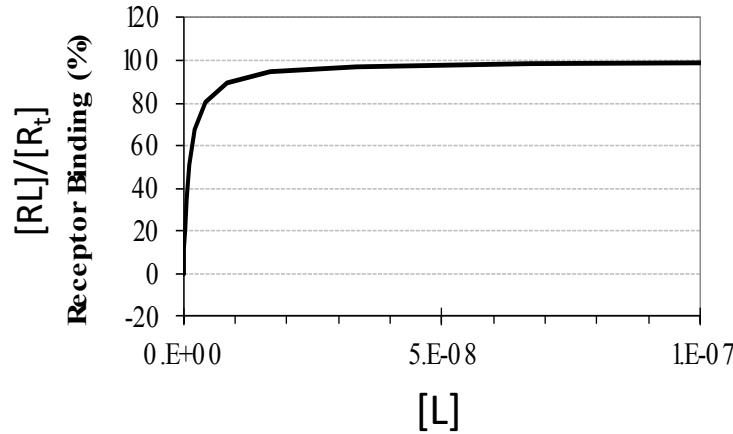
and the Scatchard equation

$$\frac{[RL]}{[L]} = -\frac{1}{K_d} \cdot [RL] + \frac{[R_T]}{K_d}$$

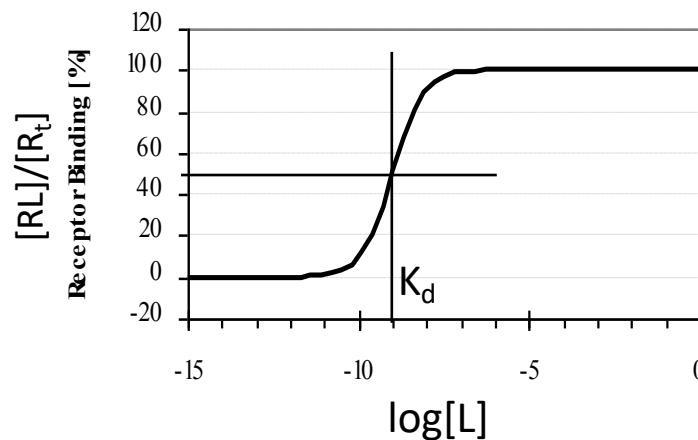
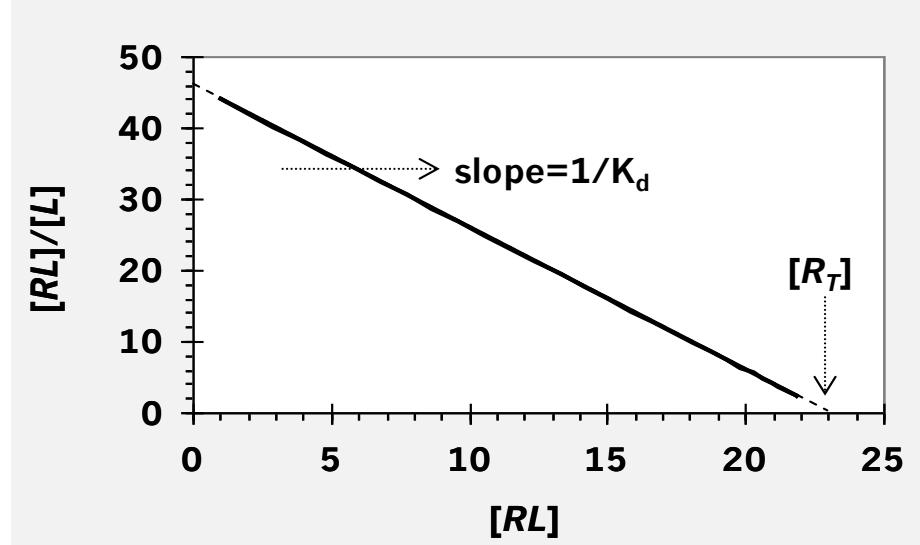


Quantitative PET – receptor binding

Binding plot



Scatchard plot



$$\frac{[RL]}{[L]} = -\frac{1}{K_d} \cdot [RL] + \frac{[R_T]}{K_d}$$

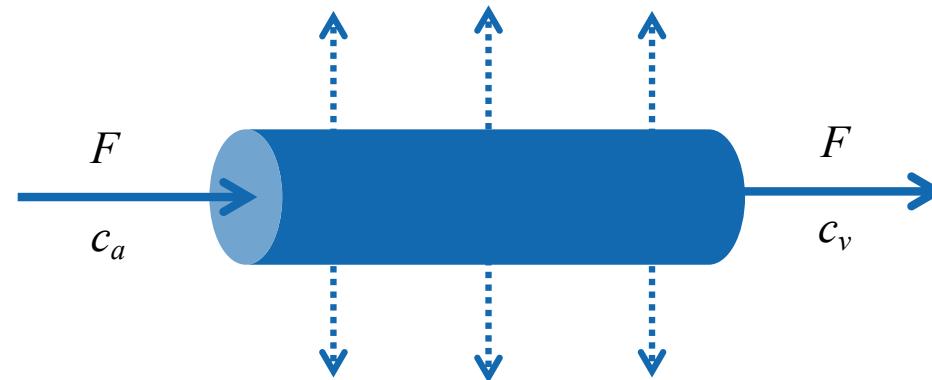
for $[RL] \ll [R_T]$

$$\frac{[RL]}{[L]} = \frac{[R_T]}{K_d} = \frac{B_{max}}{K_d}$$

B_{max} : maximum binding capacity

Quantitative PET – tracer extraction

Tracer extraction from capillaries

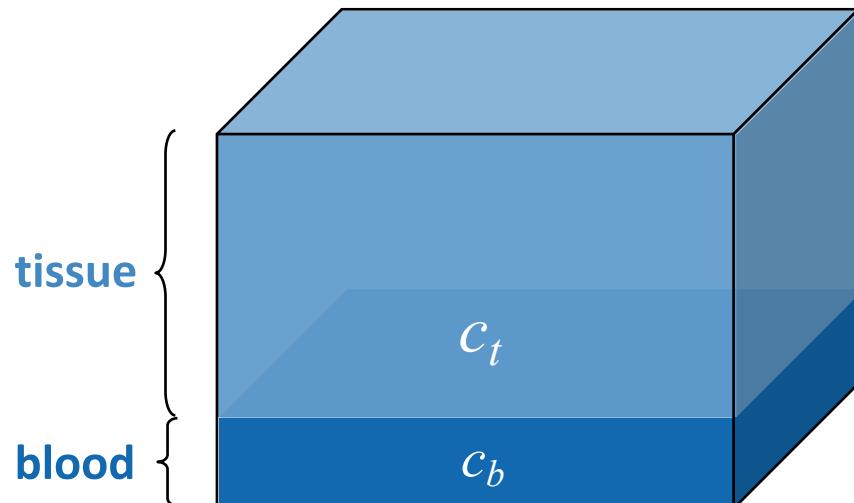
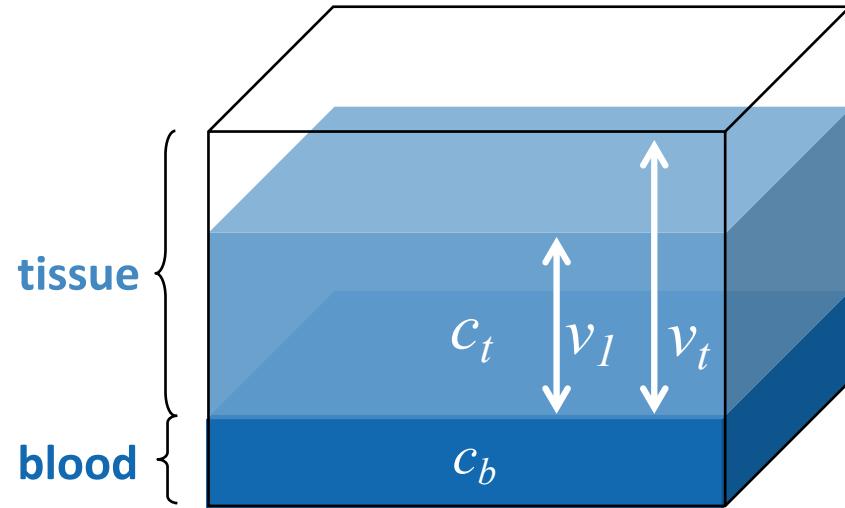


The amount of tracer extracted from capillaries depends on capillary surface S , the vascular permeability P and the blood flow F :

$$E = 1 - \exp(-P \cdot S / F)$$

Renkin-Crone equation

Quantitative PET – volume distribution



Distribution volume

$$V_d = V_1 + V_b = V_t \cdot \frac{c_t}{c_b} + V_b$$

Tracer experiment

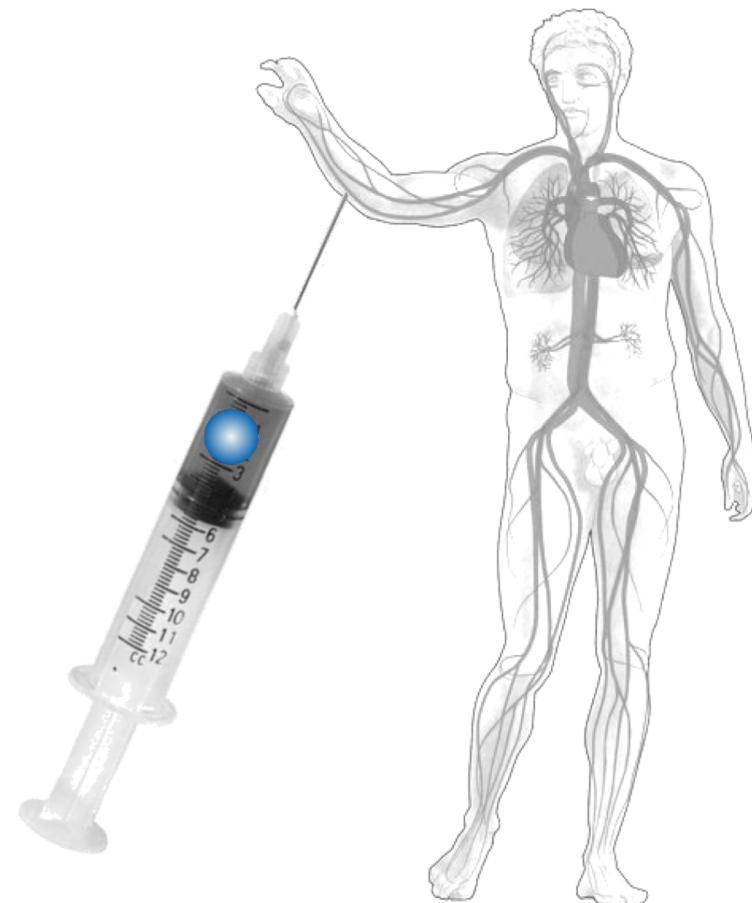
$$V_d = \frac{M}{c_b}$$

M : total amount of tracer

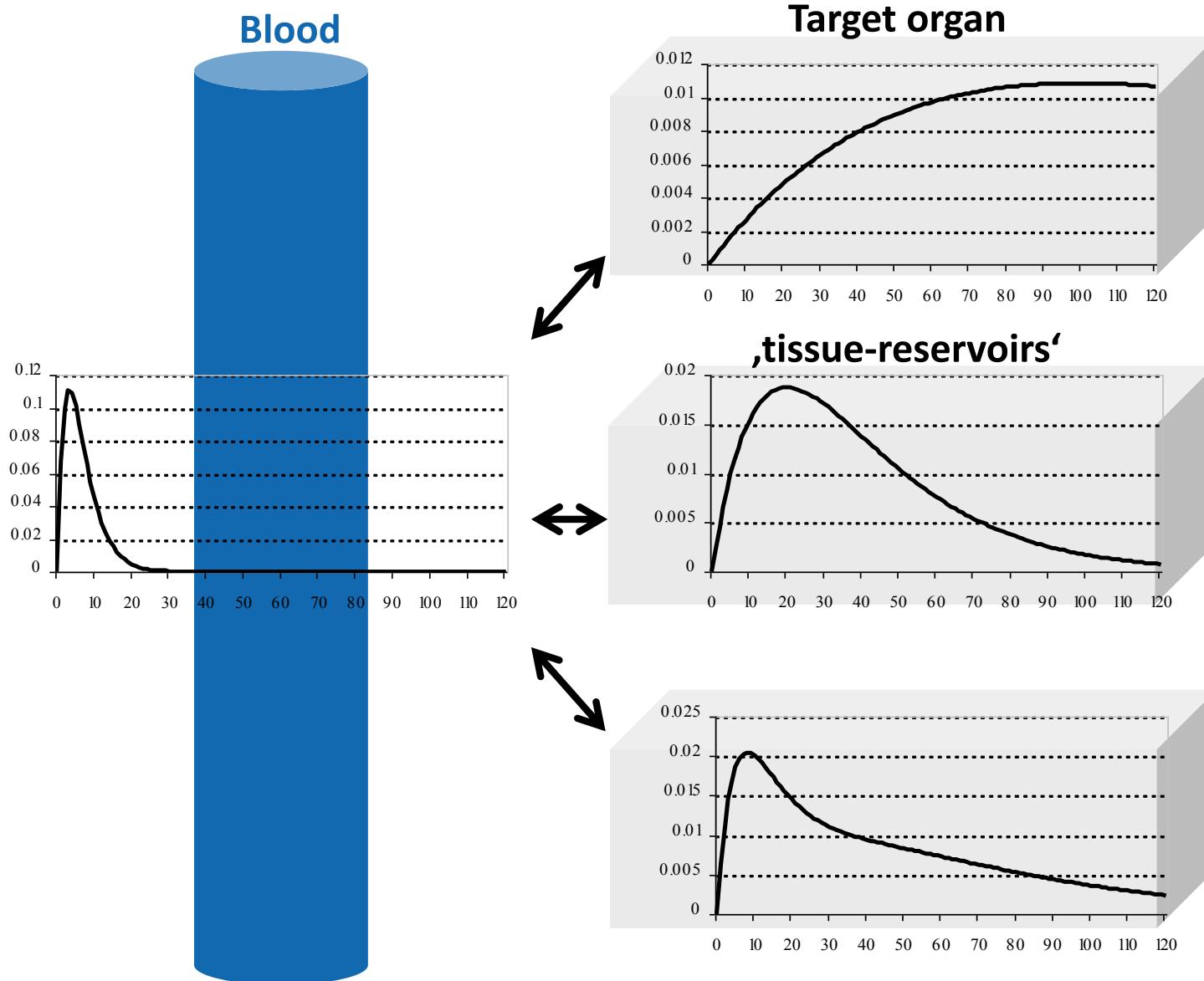
Clicker Activity (5 min)

After administration of 1 $\mu\text{g}/\text{kg}$ of a tracer into a patient of 70 kg body mass, an average blood concentration of 1.4 $\mu\text{g}/\text{l}$ is measured. What is the distribution volume?

- 5 l
- 500 ml
- 50 l
- 10 l



Quantitative PET – compartment modeling



Quantitative PET – modeling of receptor binding

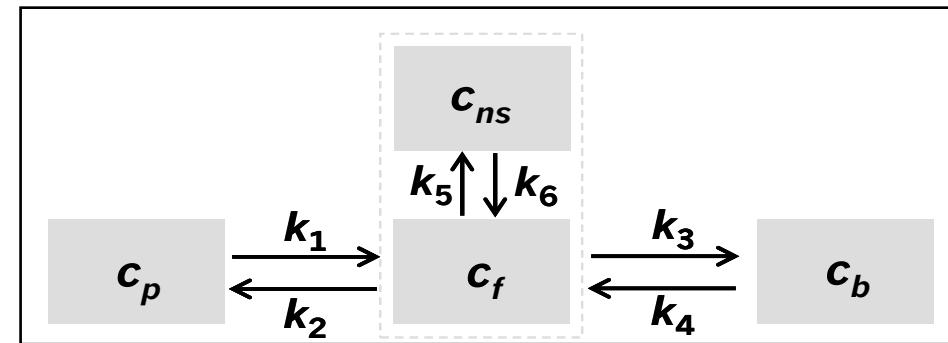
Tracer fraction in tissue compartments

p : plasma

f : free (in tissue)

ns : non-specific bound

b : bound

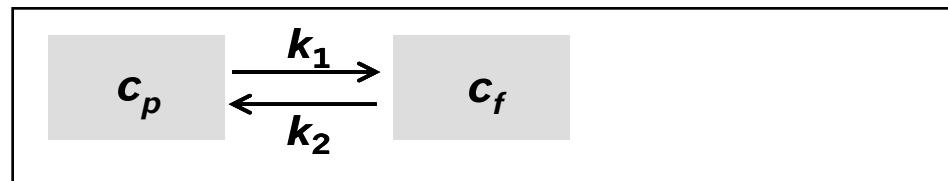
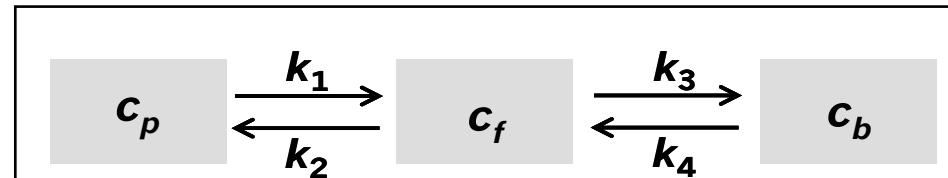


PET activity at time t :

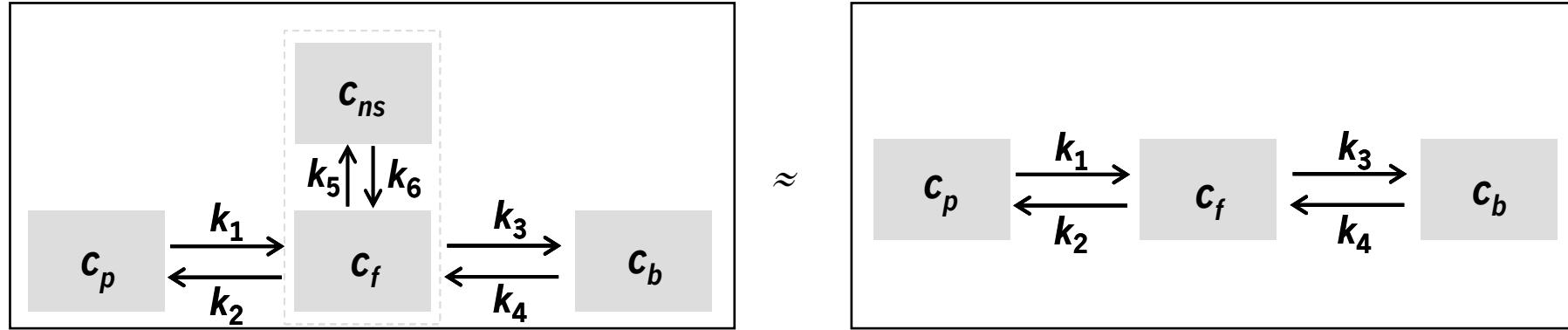
$$c_t^*(t) = \sum_i v_i \cdot c_i^*(t)$$

$i = p, f, ns, b$

v_i fractional volume of compartment



Quantitative PET – modeling of receptor binding



Equilibrium free / non-specifically bound tracer instantaneous: $c_f = f_2 \cdot (c_f + c_{ns})$

Kinetic equations:

$$\frac{dc_f}{dt} = k_1 \cdot c_p - (k_2 + k_3) \cdot c_f + k_4 \cdot c_b$$

$$\frac{dc_b}{dt} = k_3 \cdot c_f - k_4 \cdot c_b$$

with rate constants:

$$k_3 = k_{on} \cdot [R]$$

$$k_4 = k_{off}$$

$$k_1 = F \cdot (1 - \exp(-P \cdot S / F))$$

$$k_2 = k_1 \cdot c_p / c_f$$

Renkin-Crone:

$$E = 1 - \exp(-P \cdot S / F)$$



Quantitative PET – tracer kinetics for receptor binding

Solution for compartment expressing receptor:

$$c_t(t) = c_f(t) + c_b(t) = k_1 \cdot \sum_{i=1}^2 a_i \cdot \exp(-\alpha_i \cdot t) \otimes c_p(t)$$

with coefficients

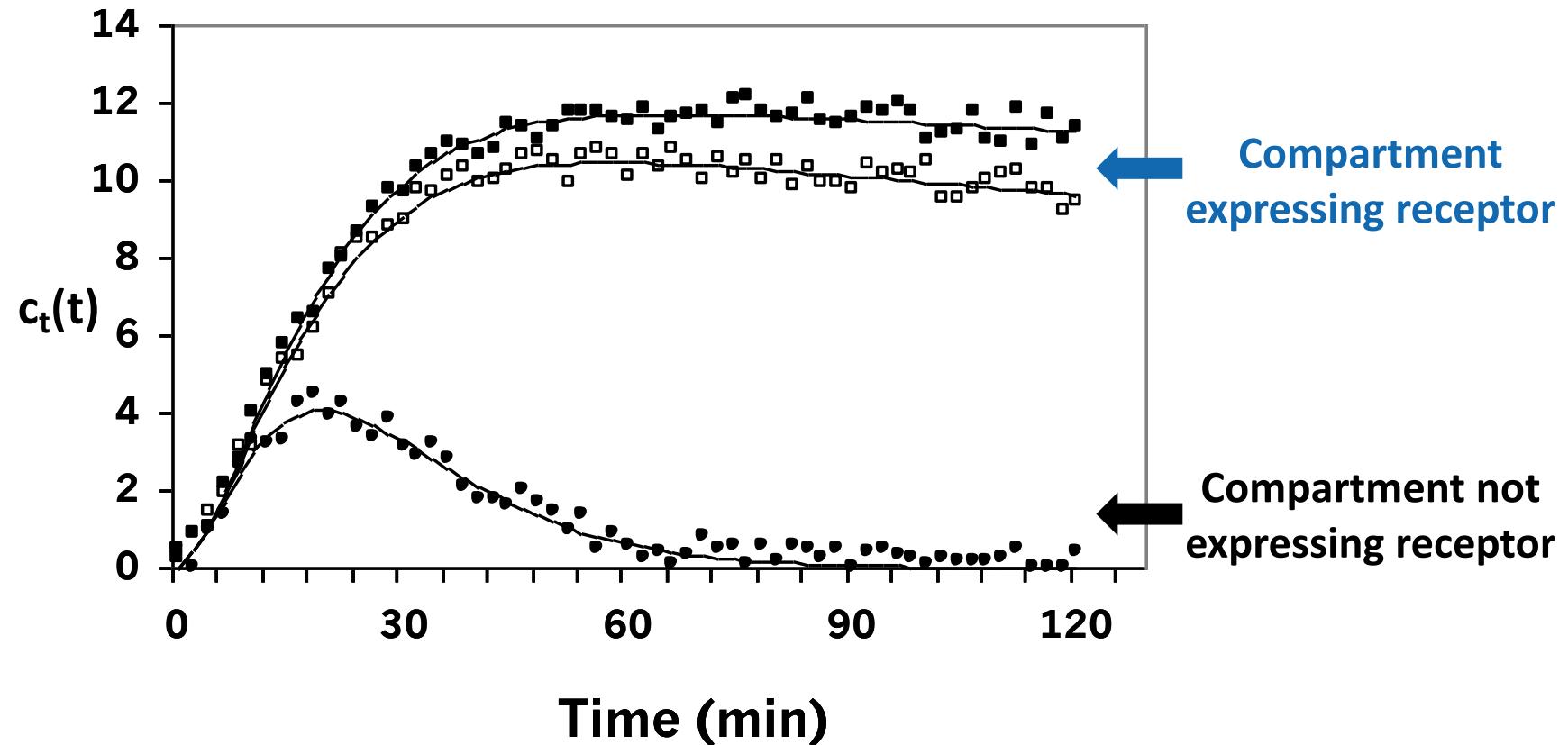
$$a_1 = \frac{k_3 + k_4 - \alpha_2}{\alpha_2 - \alpha_1}$$

$$a_2 = -\frac{k_3 + k_4 - \alpha_1}{\alpha_2 - \alpha_1}$$

Solution for compartment not expressing receptor:

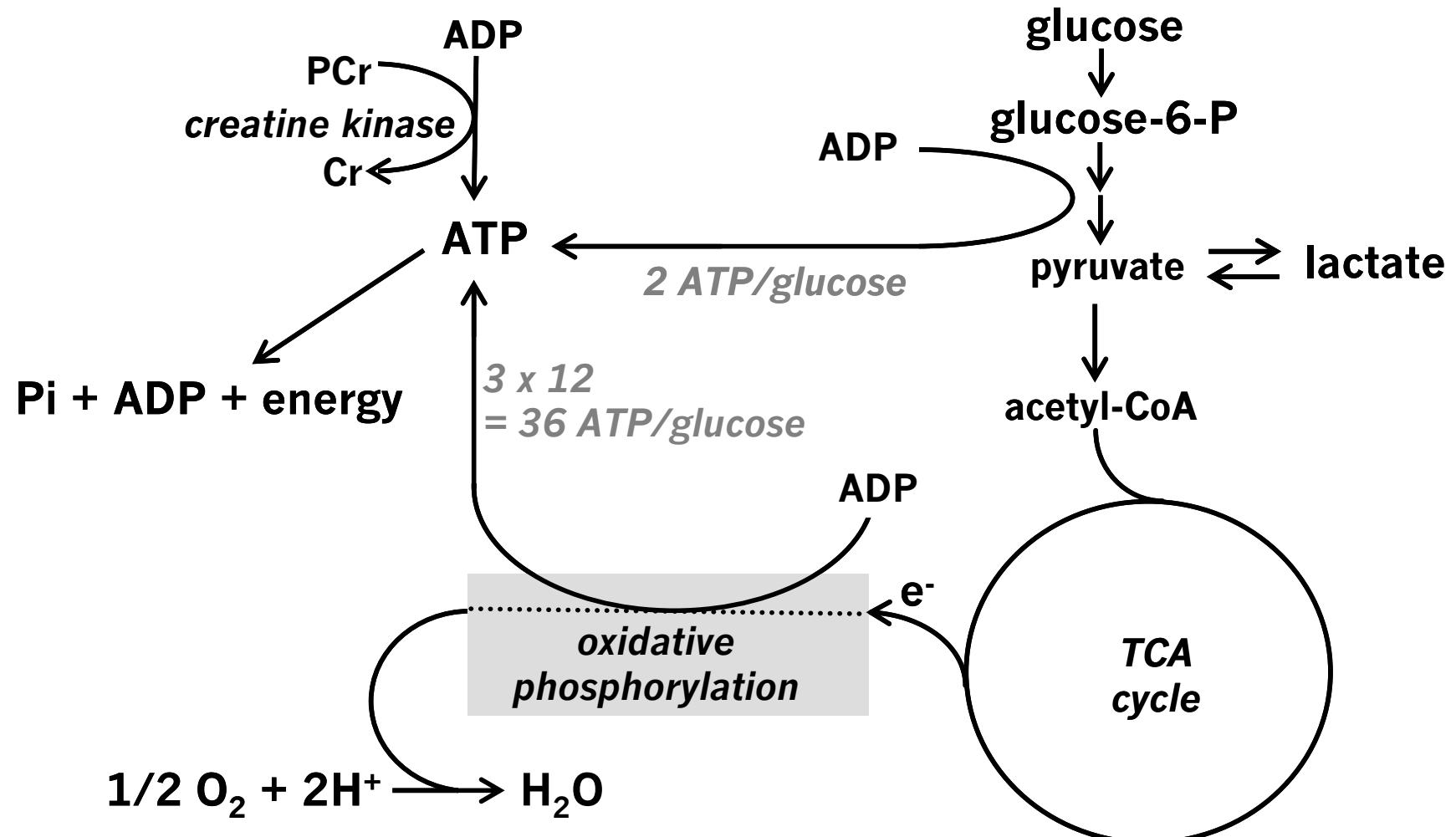
$$c_t(t) = c_f(t) = k_1 \cdot \exp(-k_2 \cdot t) \otimes c_p(t)$$

Quantitative PET – tracer binding example



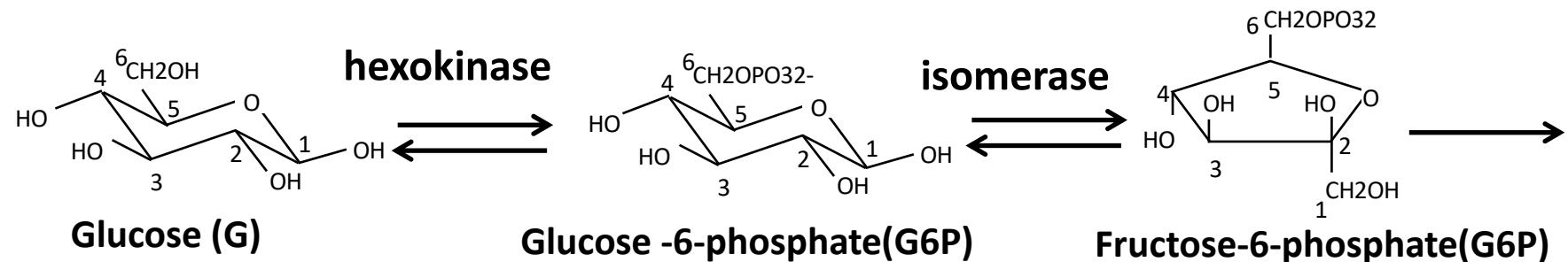
$$k_1 = 1 \text{ min}^{-1}, k_2 = 0.1 \text{ min}^{-1}, k_3 = 1 \text{ min}^{-1} \text{ and } 0.5 \text{ min}^{-1}, k_4 = 0.01 \text{ min}^{-1}$$

Quantitative PET – cell energy metabolism

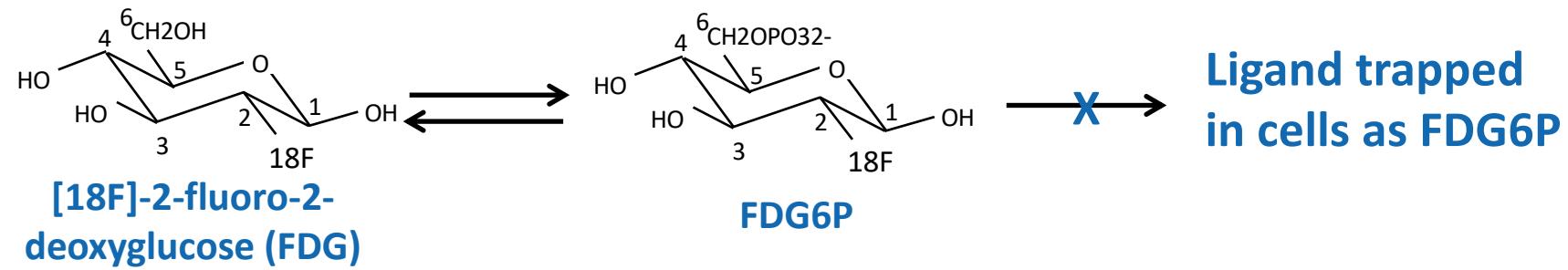


Quantitative PET – cell energy metabolism

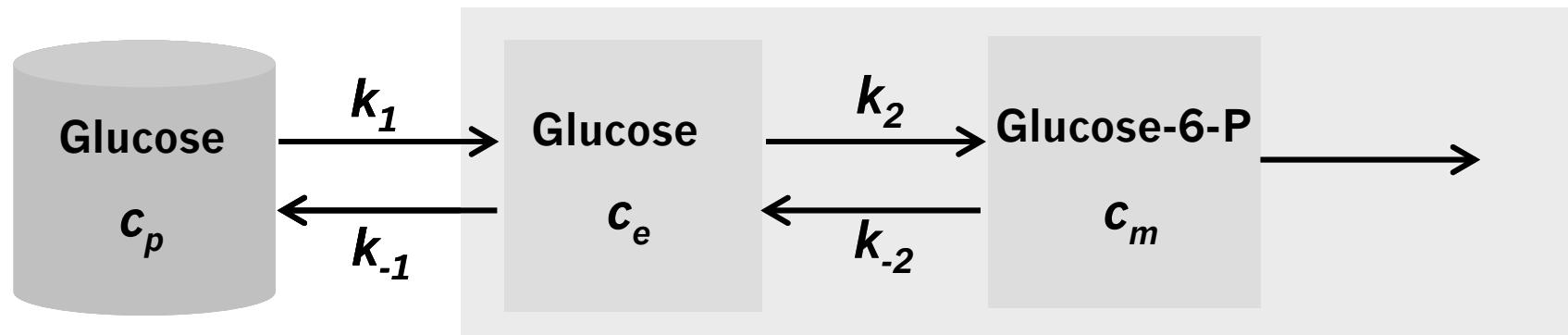
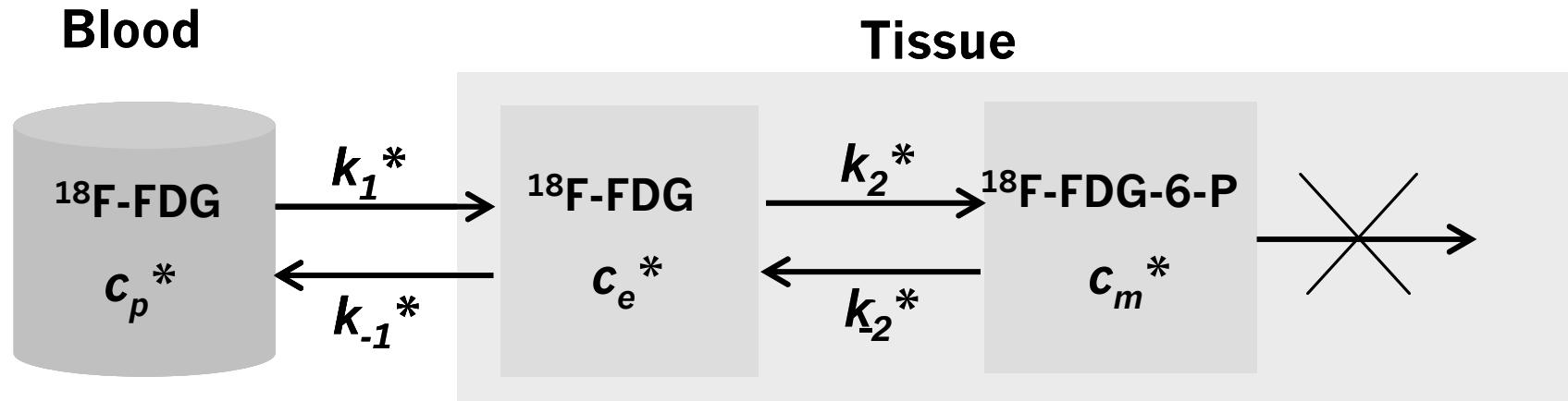
Native glucose utilization



FDG PET deoxyglucose utilization



Quantitative PET – FDG compartment models



Quantitative PET – FDG compartment models

Total tracer concentration in tissue

$$c_t^* = \frac{1}{V} (v_p \cdot c_p^* + v_t \cdot (c_e^* + c_m^*)) \approx \frac{1}{V} (V \cdot c_e^* + V \cdot c_m^*) = c_e^* + c_m^*$$

(assume $v_p \ll v_t \approx V$)

Kinetic equations for tracer:

$$\frac{dc_e^*}{dt} = k_1^* \cdot c_p^* - (k_{-1}^* + k_2^*) \cdot c_e^* + k_{-2}^* \cdot c_m^*$$

$$\frac{dc_m^*}{dt} = k_2^* \cdot c_e^* - k_{-2}^* \cdot c_m^*$$

Solution:

$$c_e^*(t) = k_1^* \cdot \int_0^t c_p^*(t') \cdot \exp\{-(k_{-1}^* + k_2^*) \cdot (t - t')\} \cdot dt' = k_1^* \cdot \exp\{-(k_{-1}^* + k_2^*) \cdot t\} \otimes c_p^*(t)$$

Quantitative PET – FDG compartment models

Metabolic rate of FDG:

$$v_{FDGMR} = k_2^* \cdot c_e^*(t) \approx \frac{k_1^* \cdot k_2^*}{k_{-1}^* + k_2^*} \cdot c_p^*(t)$$

Metabolic rate of glucose (glucose utilization):

$$v_{GluMR} \approx \frac{k_1 \cdot k_2}{k_{-1} + k_2} \cdot c_p(t) \approx \frac{1}{LC} \cdot \frac{k_1^* \cdot k_2^*}{k_{-1}^* + k_2^*} \cdot c_p(t)$$

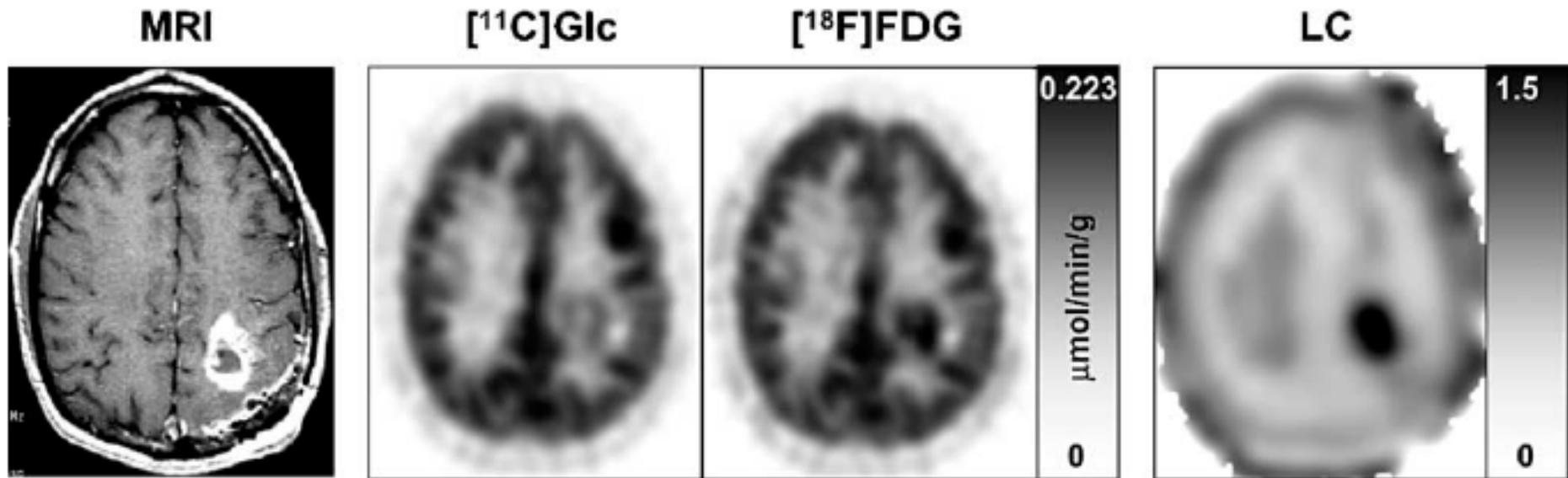


Lumped constant (ca. 0.6 in humans)

Correction factor to translate measured reaction rate for FDG to that for glucose

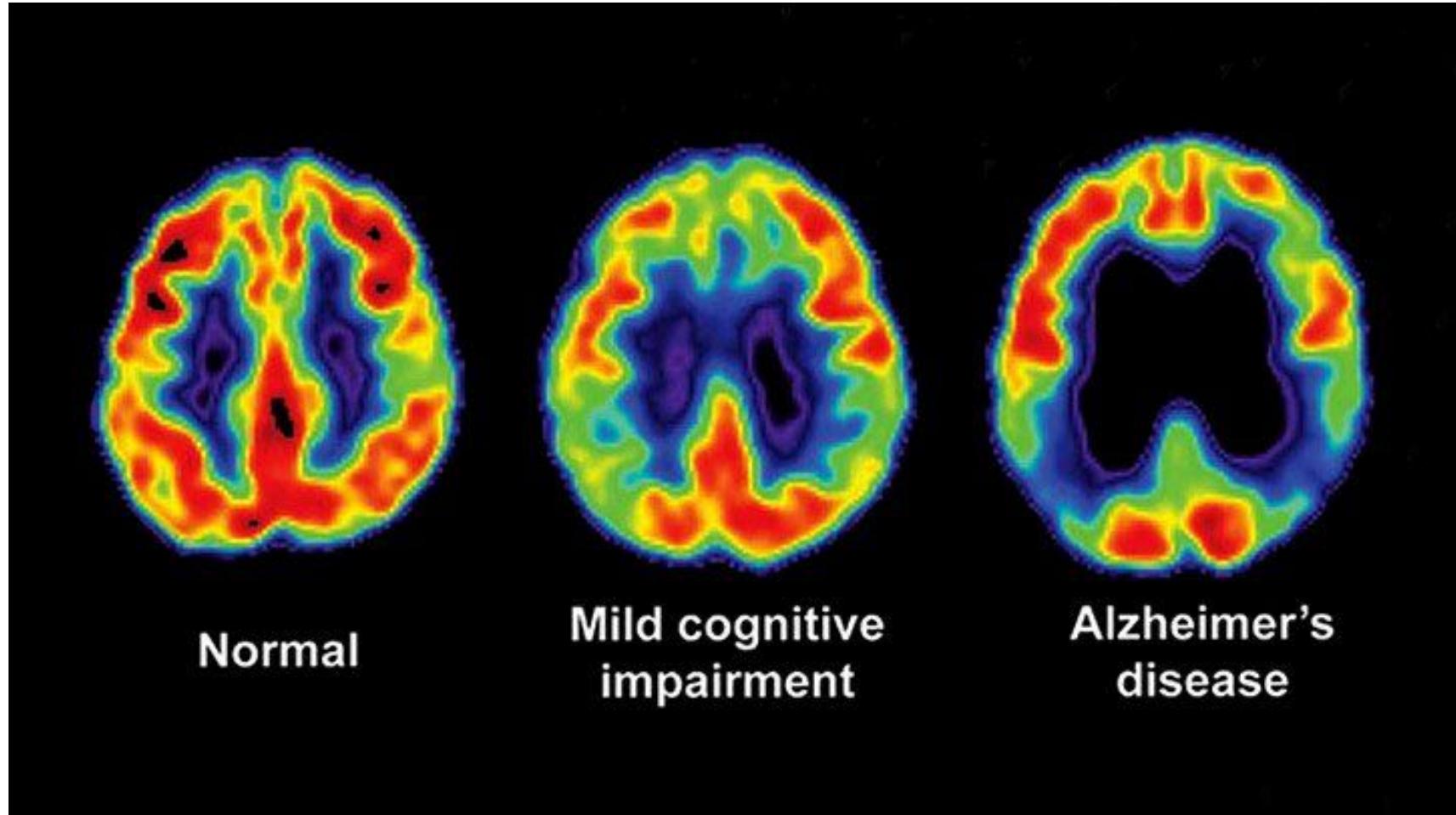


Quantitative PET – FDG lumped constant



Patient with brain glioma. The panels include calculated metabolic rate for the true tracer $[1-^{11}\text{C}]$ glucose and the analog FDG. The two PET images were divided ($\text{PET}_{\text{FDG}}/\text{PET}_{\text{glc}}$) on a pixel-by-pixel basis to provide an image of regional variation of the lumped constant LC.

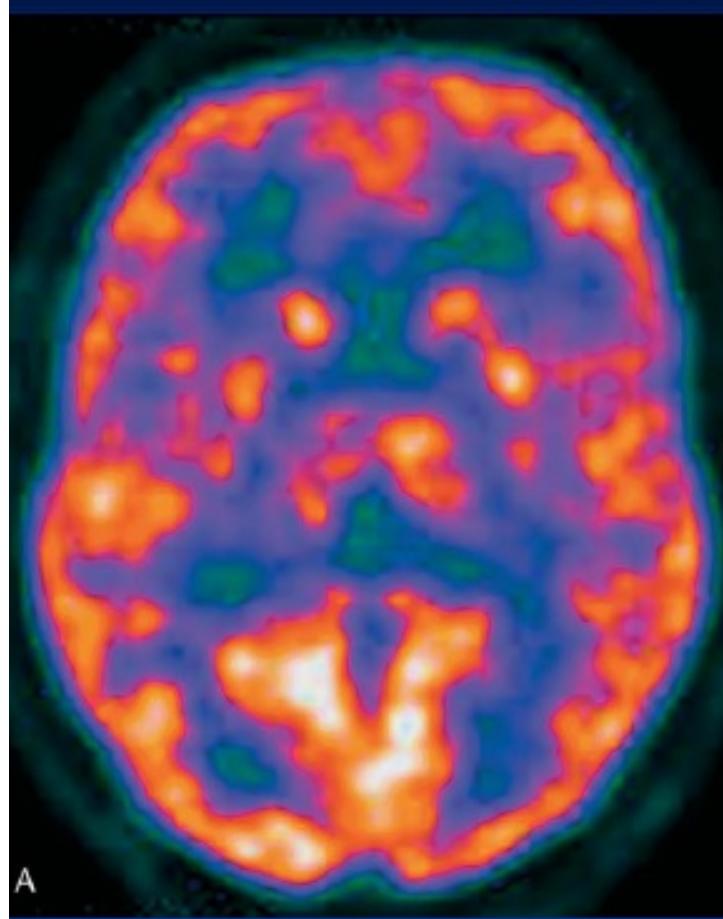
Application – FDG PET of Alzheimer disease



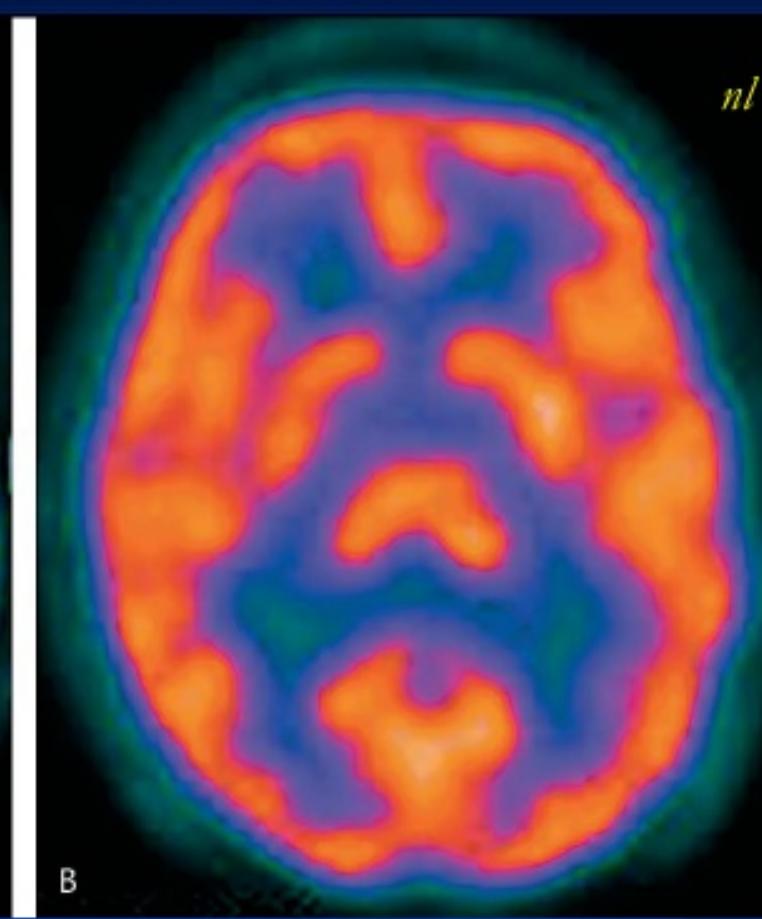
Reduced FDG PET activity in Alzheimer patient compared to age-matched control

Application – FDG PET of cocaine abuse

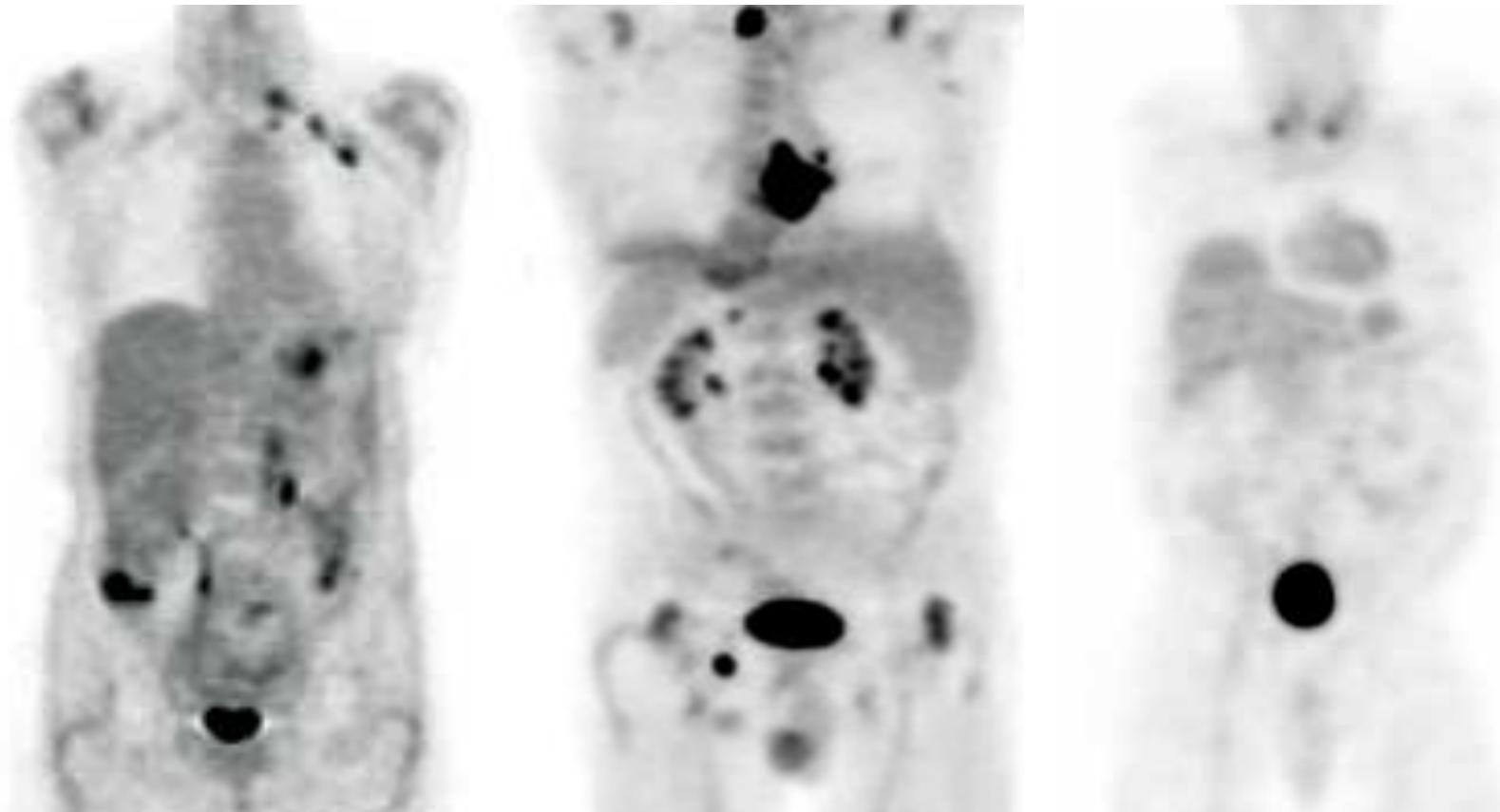
Cocaine abuse



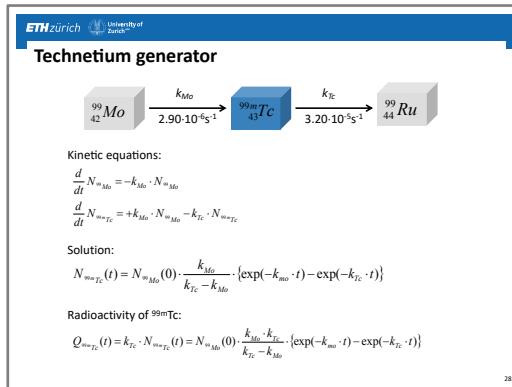
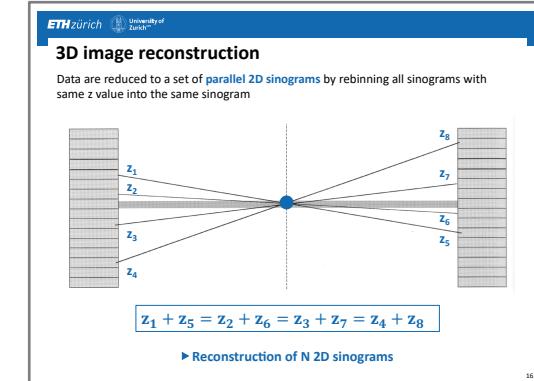
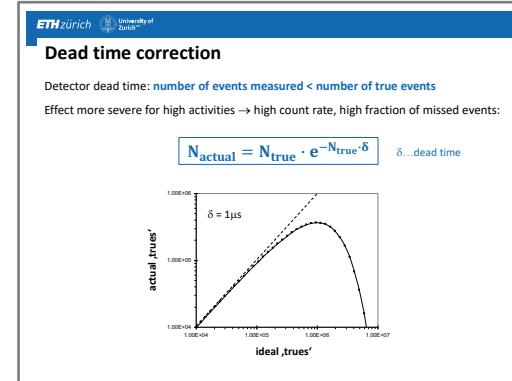
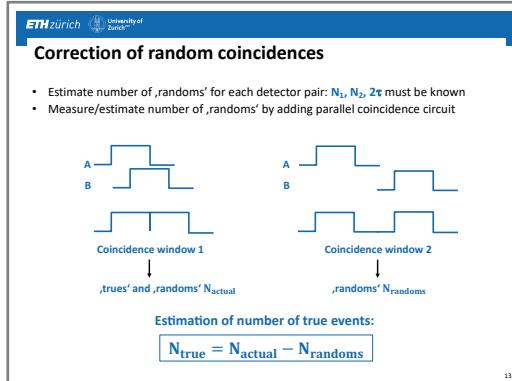
Normal



Application – FDG PET of cancer metastases



“The most important slides”



Quantitative PET – receptor binding

Receptor Binding: $L + R \leftrightarrow RL$ (L : Ligand, R : Receptor)

Equilibrium constant: $K_d = \frac{k_{off}}{k_{on}} = \frac{[L] \cdot [R]}{[RL]}$ $k_{off} \cdot [RL] = k_{on} \cdot [R] \cdot [L]$

(principle of microreversibility)

Mass conservation for receptor: $[R_f] = [R] + [RL]$

yields $K_d = \frac{[L]}{[RL]} \cdot ([R_f] - [RL])$

or the receptor binding $\frac{[RL]}{[L]} = \frac{[L]}{K_d + [L]}$

and the Scatchard equation $\frac{[RL]}{[L]} = -\frac{1}{K_d} \cdot [RL] + \frac{[R_f]}{K_d}$

41

Quantitative PET – modeling of receptor binding

Equilibrium free / non-specifically bound tracer instantaneous: $c_f = f_2 \cdot (c_f + c_m)$

Kinetic equations:

$$\frac{dc_f}{dt} = k_1 \cdot c_p - (k_2 + k_3) \cdot c_f + k_4 \cdot c_b$$

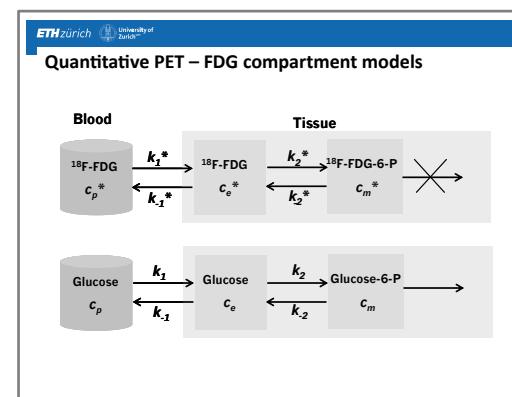
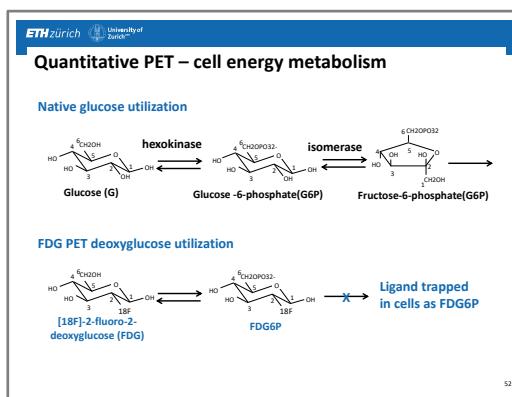
$$\frac{dc_b}{dt} = k_3 \cdot c_f - k_4 \cdot c_b$$

with rate constants: $k_1 = k_{on} \cdot [R]$ $k_1 = F \cdot (1 - \exp(-P \cdot S/F))$

$$k_2 = k_{off}$$
 $k_2 = k_1 \cdot c_p / c_f$

Renkin-Crone: $E = 1 - \exp(-P \cdot S/F)$

48



Quantitative PET – FDG compartment models

Metabolic rate of FDG:

$$V_{FDGMR} = k_1^* \cdot c_e^*(t) \approx \frac{k_1^* \cdot k_2^*}{k_{-1}^* + k_2^*} \cdot c_p(t)$$

Metabolic rate of glucose (glucose utilization):

$$V_{GlucMR} \approx \frac{k_1 \cdot k_2}{k_{-1} + k_2} \cdot c_p(t) \approx \frac{1}{LC} \cdot \frac{k_1^* \cdot k_2^*}{k_{-1}^* + k_2^*} \cdot c_p(t)$$

Lumped constant (ca. 0.6 in humans):

Correction factor to translate measured reaction rate for FDG to that for glucose

55