



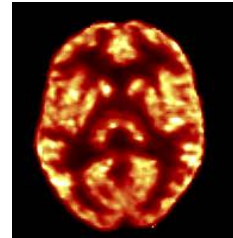
Kinetic Modeling in PET: Madness in the Methods or Method to the Madness

Richard E. Carson, Ph.D.

December 14, 2020

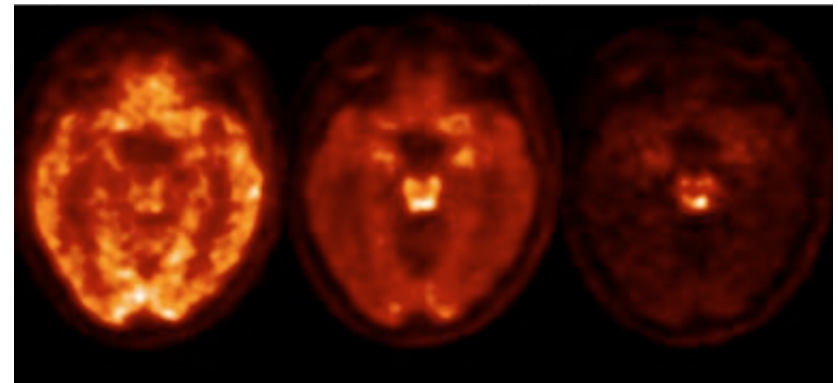
Quantitative Brain PET

- Kinetic Modeling 101
 - Basic modeling methods
- Tracer Development and Validation
 - SV2A Tracer ^{11}C -UCB-J
 - Nonhuman primates
 - Human studies
- Using modeling to separate blood flow and binding changes
- When is modeling important?
 - When might simplified methods be misleading ...
- Simplifications for Brain Imaging
 - Standard Uptake Value Ratio (SUVR) vs. Distribution Volume Ratio (DVR)
 - Time dependent relationships
- Transient Equilibrium
 - Two wrongs can make a right
- Closing thoughts



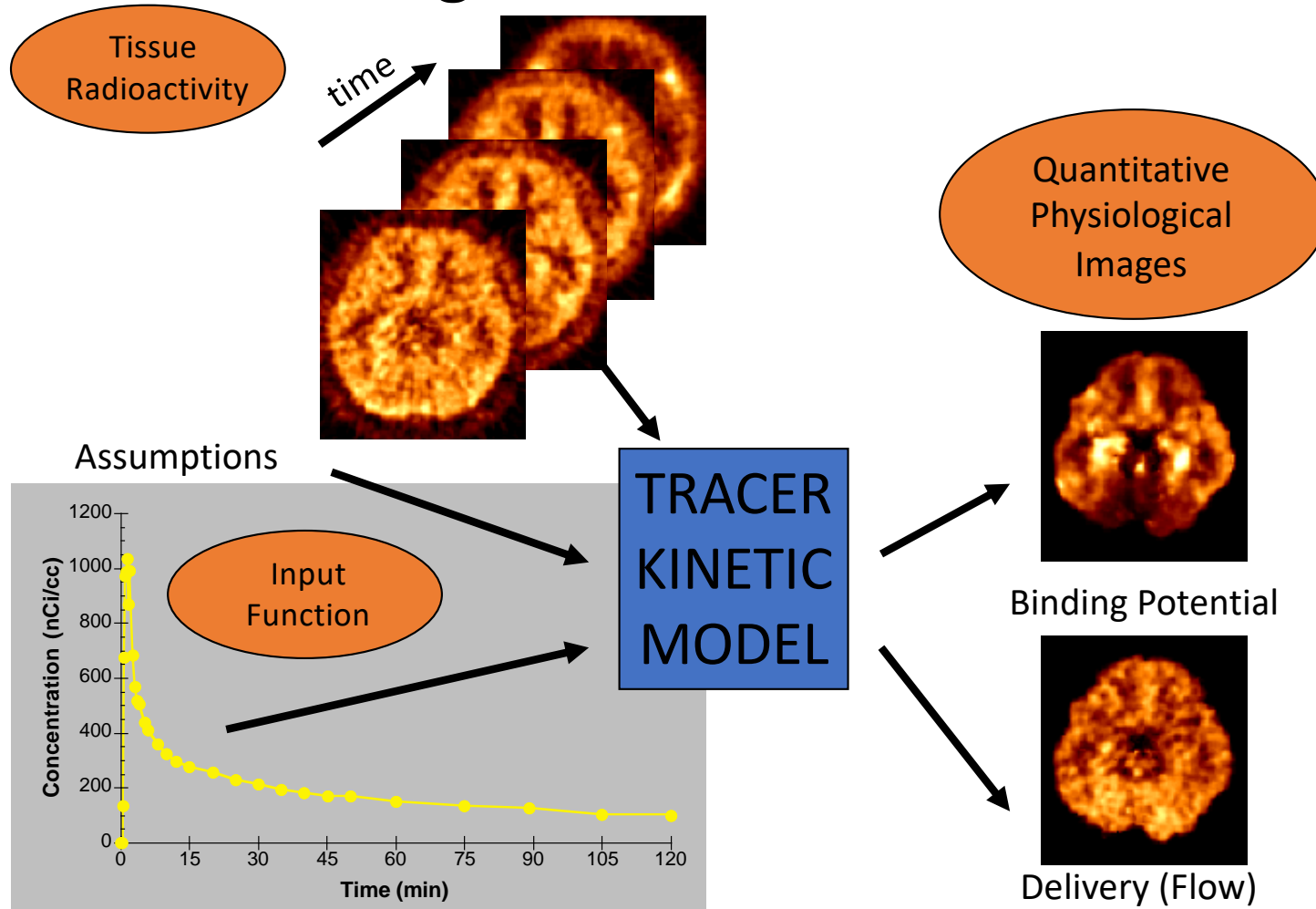
Radioactivity Patterns Change with Time

- Tracer: ^{11}C -AFM
- Target: Serotonin Transporter
- Analog of Selective Serotonin Reuptake Inhibitors (SSRI)
 - Prozac, Zoloft,...
- Time-varying distributions
- Is there a best single time to scan?
- What can we do with dynamic data?
- How to analyze this?



Time (min)	0-10	40-60	90-120
Flow information	+++	++	+
SSRI information	+	++	+++

PET Modeling

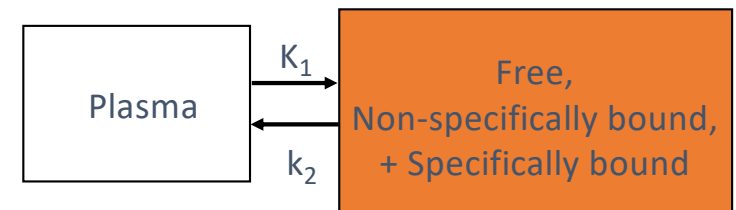


Goals of PET Modeling

- Understand the relationship between the tissue measurements and the underlying physiology (blood flow, metabolism, etc.)
- Account for the effects of tracer availability (input function).
- Determine what parameters can be measured
- Devise study methodology
- Prove that the method measures the parameter(s) of interest.
- Verify that the method is not influenced by other parameters.
- Produce images of physiological parameters (parametric images)
- Produce a **simple and accurate** patient protocol.

Important Kinetic Parameters for Reversible Tracers

- K_1 - tracer delivery
 - Blood flow information
- V_T – volume of distribution (DV)
 - Ratio at **equilibrium** of total tissue concentration to reference fluid
 - metabolite-corrected plasma concentration
 - Units: mL plasma / cm³ tissue
 - Includes free, non-specifically bound, and specifically bound components.
 - Useful for tracers with reversible binding
- DVR – distribution volume ratio
 - V_T in ROI / V_T in reference region
- BP_{ND} – binding potential
 - Specific binding as ratio to nondisplaceable uptake
 - $DVR + 1$



- All these values relate directly to physiological parameters:
 - Receptor concentrations and affinities and blood flow

Methods to estimate V_T and BP

- Fit of dynamic data
 - Need tissue time-activity curve and plasma time-activity curve
 - Fit data to appropriate model
 - Determine V_T from model parameters
 - Model-based method to extrapolate equilibrium conditions from bolus data
 - 2 tissue compartment model:
$$V_T = K_1 / k_2 (1 + k_3 / k_4)$$
 - 1 tissue compartment model (pixel-by-pixel)
$$V_T = K_1 / k_2$$
- Simplified Reference Tissue Model
 - Fit for BP_{ND} directly using TAC from region with no specific binding
 - Plasma input function inferred mathematically from reference TAC

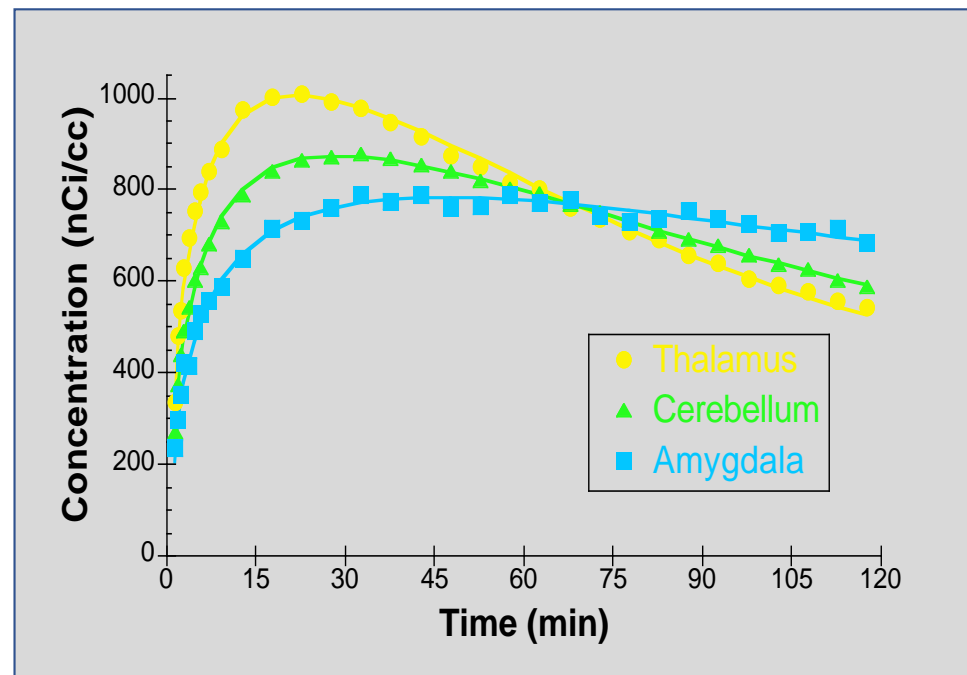
Methods to estimate V_T and BP

- Graphical analysis - Logan plot
 - Transform data to produce a straight line
 - Use part of the data (varies between regions)
 - $V_T = \text{Slope of } \{\text{integral}(C_T) / C_T\} \text{ versus } \{\text{integral}(C_p) / C_T\}$
- Constant infusion
 - At equilibrium, $V_T =$ the ratio of tissue to metabolite-corrected plasma
 - V_T and BP taken directly from the data

Neuroreceptor Imaging

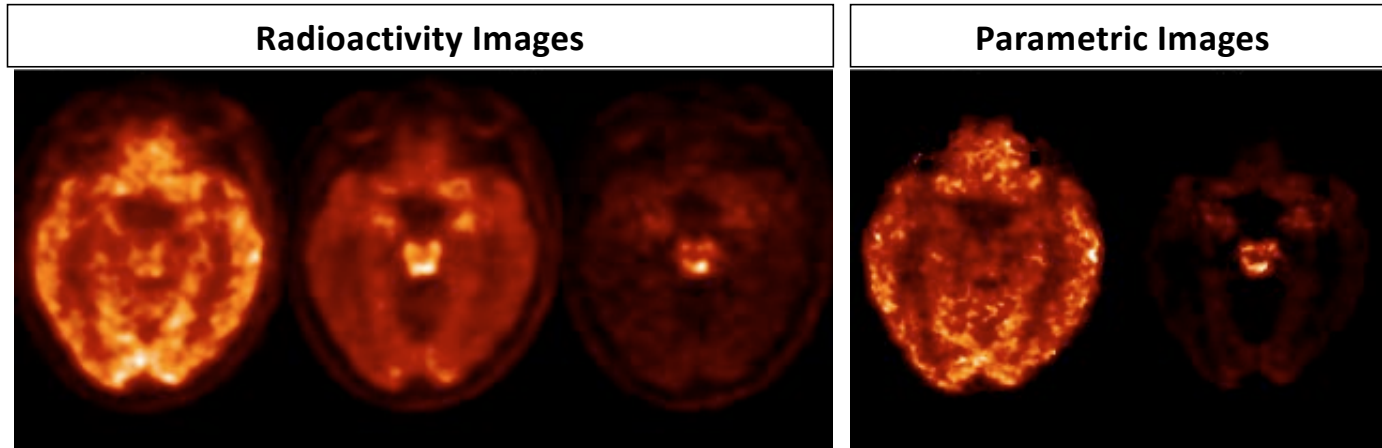
The hard way

- Collect arterial input curve
- Collect scan data (counts)
- Reconstruct multiple images over time
- Define regions-of-interest
- Create time-activity curves
- Do least squares fit to the model
- Extract volumes of distribution and binding potentials



Radioactivity Images vs. Parametric Images

- K_1 - Blood flow
- V_T – Volume of distribution
 - Total binding to serotonin transporters plus nonspecific uptake



Tracer:
 ^{11}C -AFM

Time (min)	0-10 min	40-60 min	90-120 min	K_1	V_T
Flow information	+++	++	+	+++++	
SSRI information	+	++	+++		++++

Reference Tissue Models

- Infer the input function based on the time course of a reference region
- Neuroreceptor studies: reference region has no receptors
- Estimates relative delivery and Binding Potential ($BP = B_{max}/K_d$)
- $C(t)$ ROI TAC
- $C'(t)$ Reference region TAC
- For one tissue-compartment:

$$dC/dt = K_1 C_p - k_2 C$$

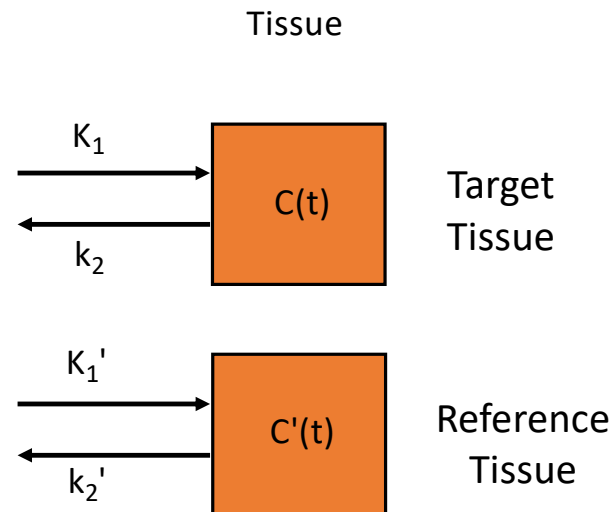
$$dC'/dt = K_1' C_p - k_2' C'$$

- Eliminate C_p (derive)

$$C(t) = R_1 C'(t) + R_1 (k_2' - k_2) C' \cdot \exp(-k_2 t)$$

- R_1 Relative delivery (K_1 / K_1')

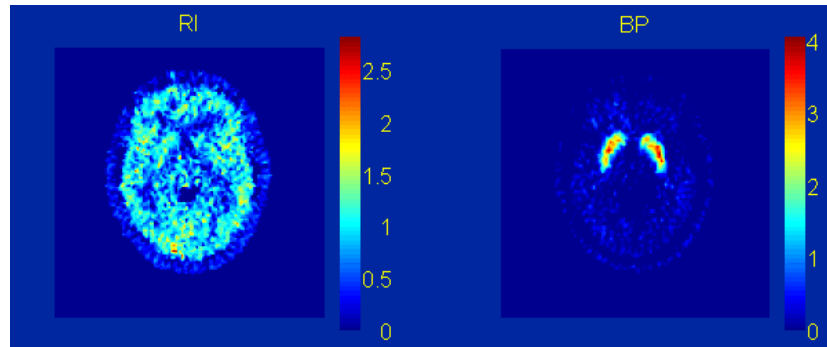
- $BP_{ND} = R_1 k_2' / k_2 - 1$



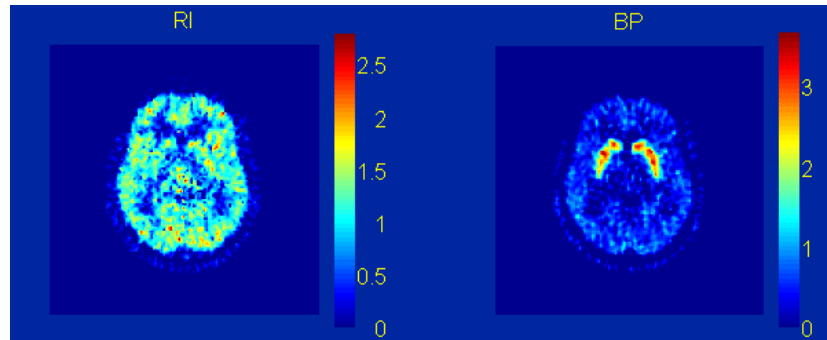
SRTM Images

Relative Delivery and Binding Potential

[¹¹C]Raclopride: D₂
Receptor



[¹¹C]SCH2339: D₁
Receptor



R. Gunn

Medical Research Council
MRC Cyclotron Unit

Logan Graphical Analysis

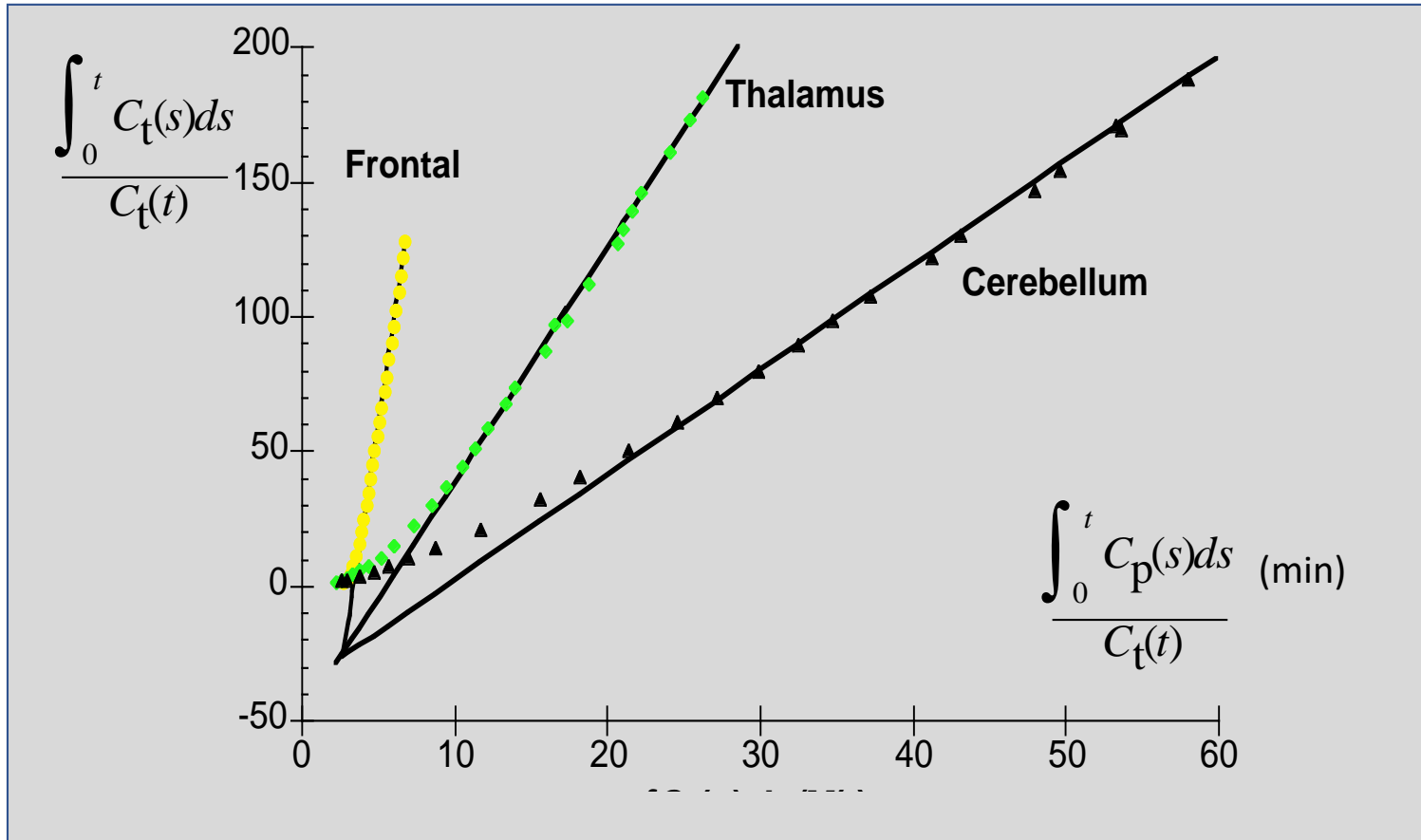
- Appropriate for tracer with reversible binding
- Derived from model with one tissue compartment
- Transforms the data so the final slope is V_T

$$\int C_T dt / C_T = V_T \int C_p dt / C_T + b \quad t > t^*$$

- Model independent

Logan Graphical Analysis

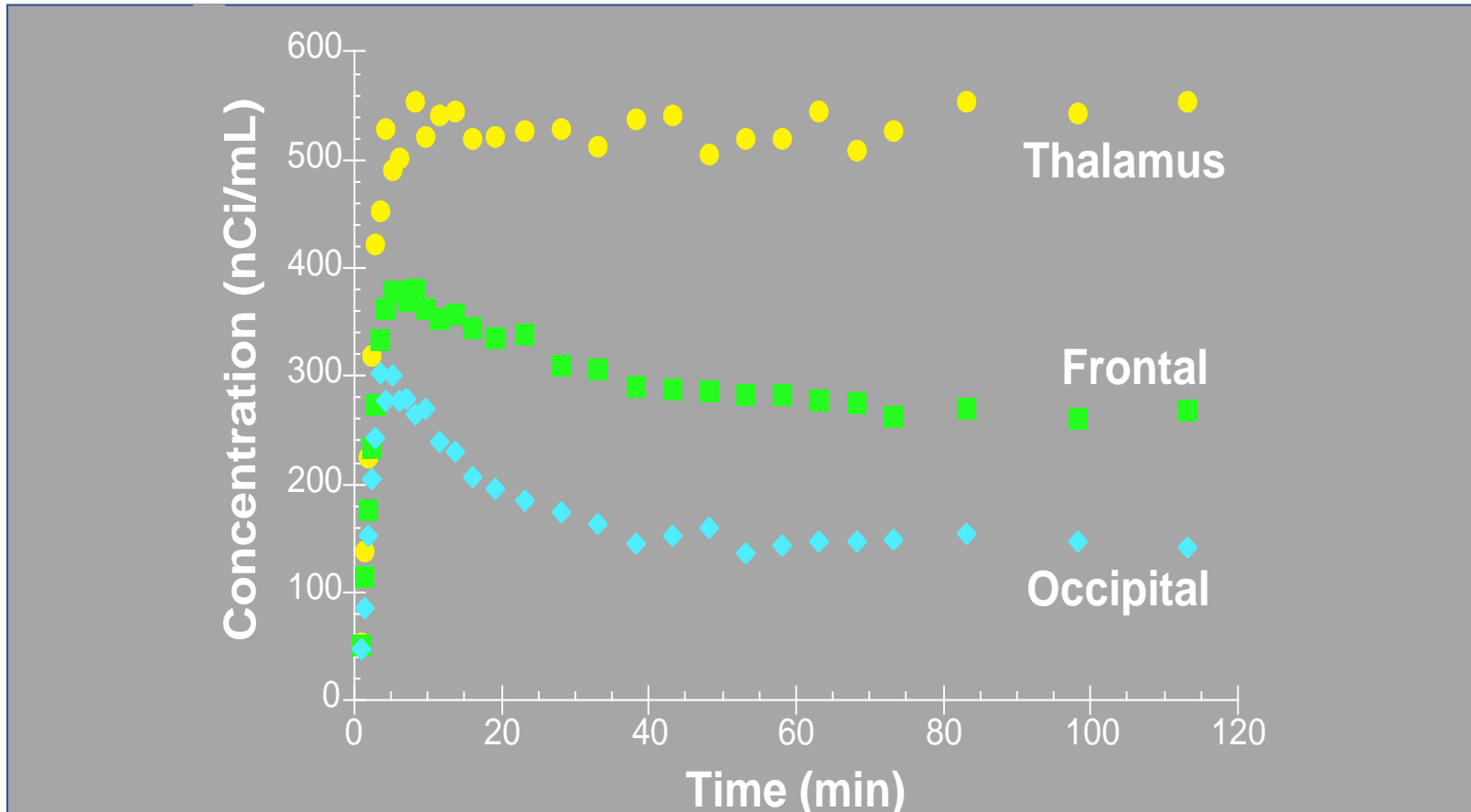
[¹⁸F]FCWAY



Tracer Infusion for Equilibrium Measurements

- Administer tracer as bolus plus continuous infusion
- Achieve true equilibrium in blood and all brain regions
- Model-independent
- Determine V_T directly from concentration ratio of tissue region-of-interest (ROI) to plasma
 - $BP_p = V_T(\text{ROI}) - V_T(\text{BKG})$ proportional to B_{avail} / K_d
- Determine BP_{ND} from tissue concentration ratios
 - $BP_{\text{ND}} = (\text{ROI} / \text{BKG} - 1)$ proportional to B_{avail} / K_d
 - No blood
- For certain tracers, rapid equilibrium achieved if proper bolus fraction is chosen

[¹⁸F]Cyclofoxy Tissue Activity Bolus + Infusion





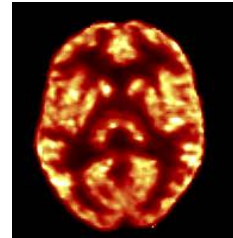
The Challenge



- If we thoroughly understand how a tracer works...
- Can we produce a simple, clinically practical protocol that is patient-friendly, suitable for multi-center trials...
- Without losing too much accuracy...
- So that the practical advantages, which allow us to study many more patients, clearly outweigh any quantitative disadvantages.

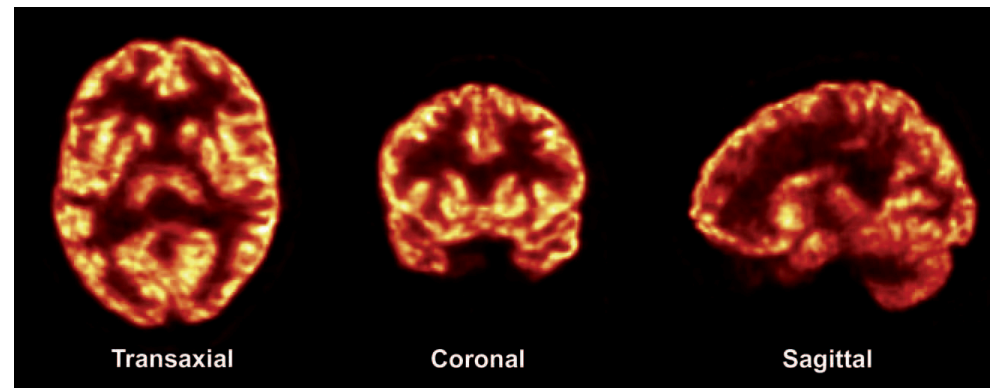
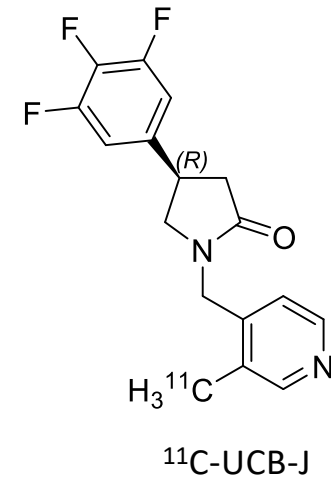
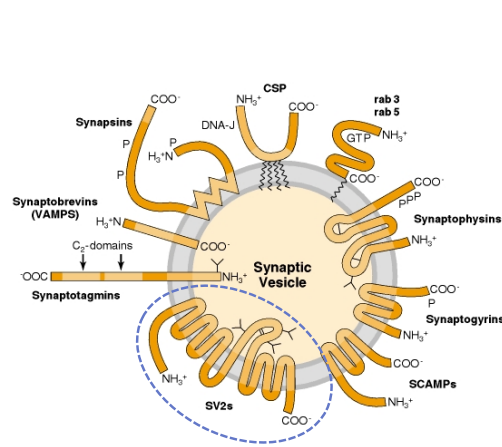
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Developing and Validating a Novel Brain Tracer

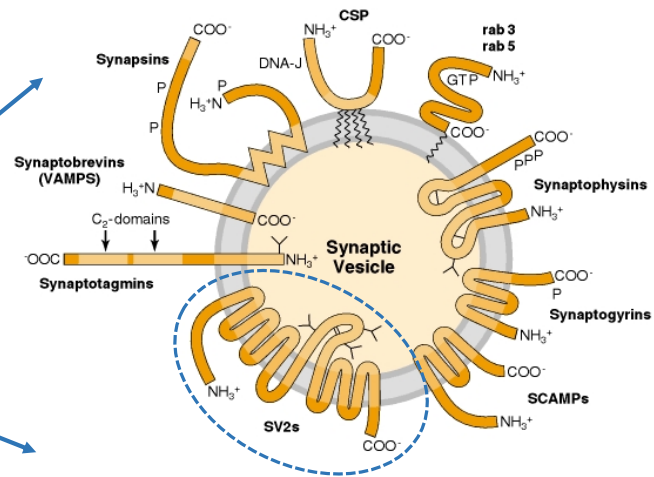
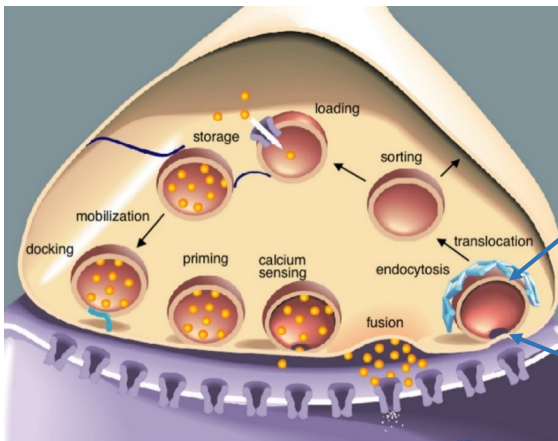
- Identify target
- In vitro evaluations
- Radiochemistry
- Dynamic scans
- Arterial blood samples
- Regional or voxel analysis
- Compartment modeling
- Test/retest
- Blocking studies
- *In vivo / ex vivo* validations



SV2A – Synaptic Density

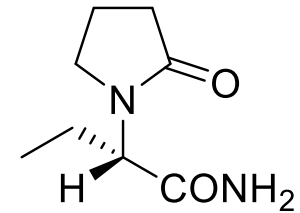
Synaptic Vesicle Glycoprotein 2

- Component of synaptic vesicles, located in presynaptic terminals
- Modulates synaptic exocytosis and endocytosis`
- Radioligand binding to SV2 may be useful for measurement of synaptic density

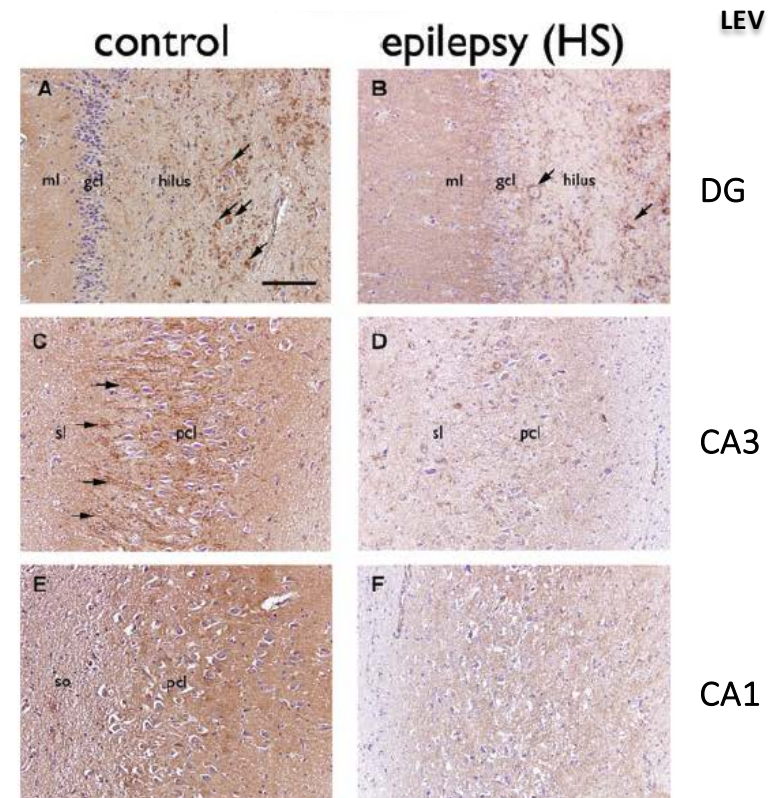


‡Mutch et al., 2011; †Takamori et al., 2006

SV2A in Epilepsy

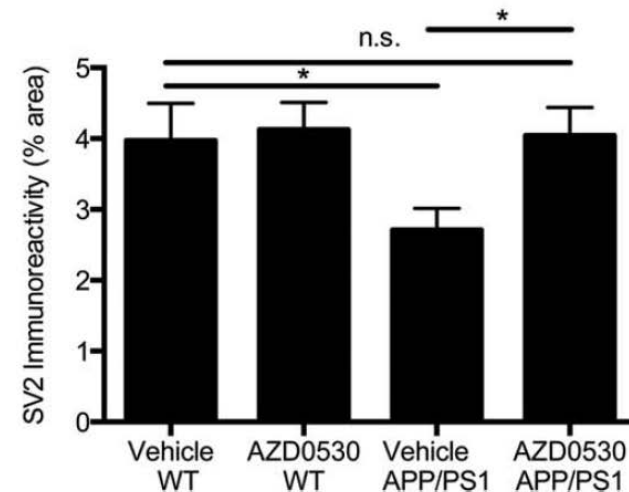


- Validated target of antiepileptic drug *levetiracetam* (LEV; Keppra®)
- Immunocytochemistry and Western blot analysis: reduced SV2A in hippocampus and temporal lobe in TLE with HS (similar results in FCD)
- SV2A in tumor and peritumoral tissue correlated to clinical response to LEV in patients with glioma (response prediction with 91% accuracy)
- Homozygous mutation in SV2A gene results in intractable epilepsy



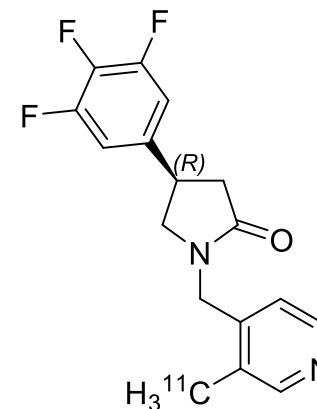
SV2 as Biomarker for Synaptic Density

- Fyn inhibitor AZD0530 reversed memory deficits in AD mouse model
- Rescue of learning and memory impairment was coupled to restoration of synaptic density (no change in A β)
- Recovery of synaptic density was demonstrated using SV2 immunohistochemistry



UCB-J *In Vitro* Binding

Assay/target (37°C)	K_i (nM)
recombinant human SV2A	7
recombinant human SV2B	1995
recombinant human SV2C	100



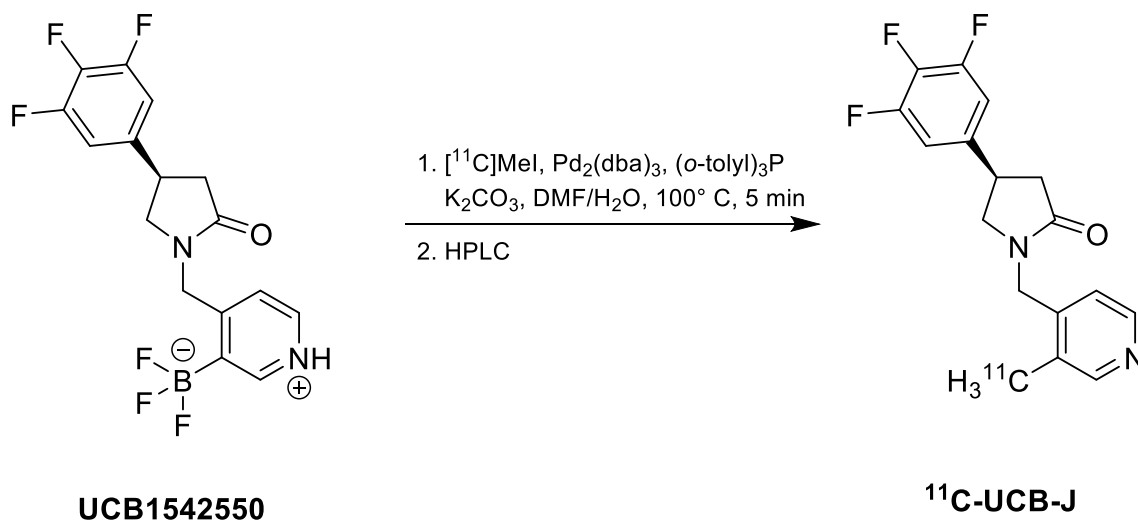
H_1	α_{2A}	α_{1A}	M_2	σ_1	KOR	D_2	5-HT _{1A}	5-HT _{2A}
3	7	-4	2	4	3	2	-2	3

% inhibition of radioligand binding to the targets when tested at 10 μ M in duplicate

†Performed at UCB Pharma (Braine-l'Alleud, Belgium) and at CEREP (Celle-l'Evescault, France)

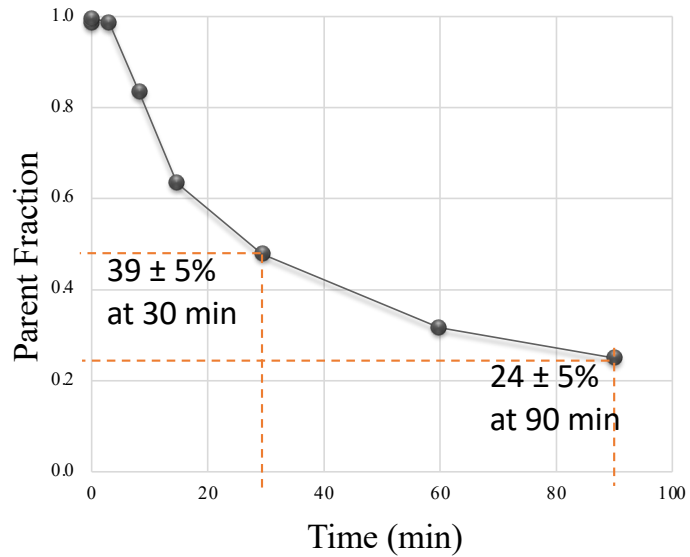
Radiolabeling

- C-[¹¹C]methylation via Suzuki cross-coupling



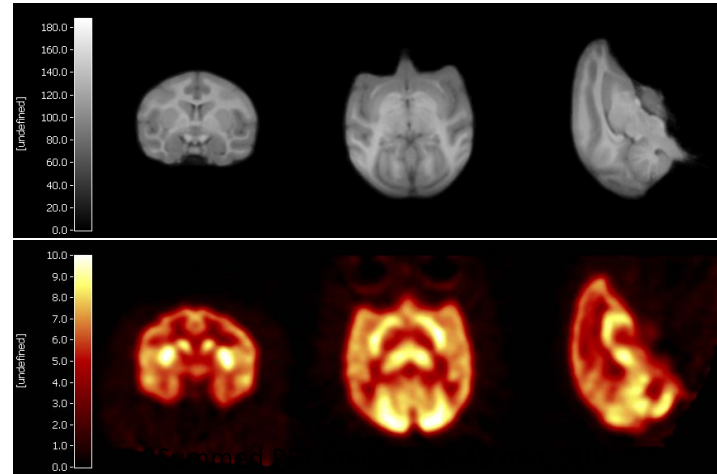
*9% yield @ EOS based on ¹¹CH₃I; >98% CP & RCP;
 S.A. 15.3 ± 7 mCi/nmol (566 ± 258 MBq/nmol) @ EOS (n = 16).*

^{11}C -UCB-J Plasma Analysis & PET Images

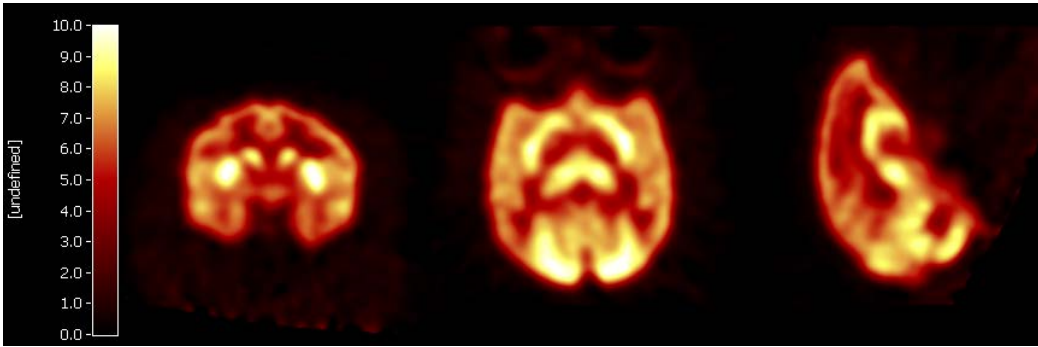


$$f_p = 46 \pm 2\% (n = 10)$$

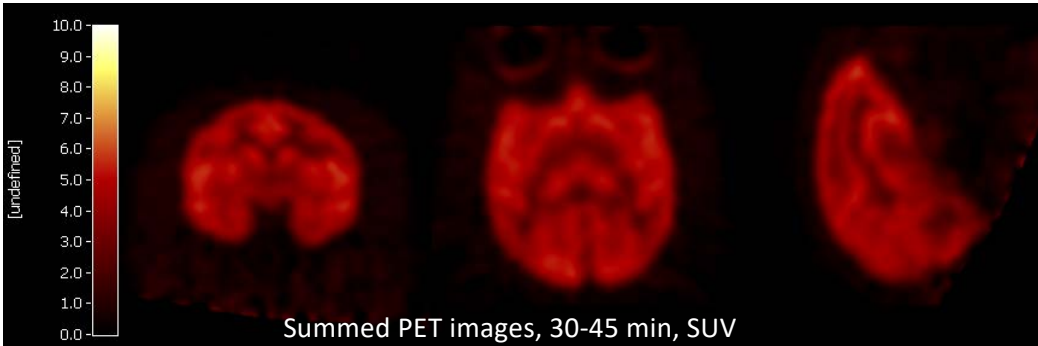
$$\text{Log P} = 2.52 \pm 0.03 (n=9)$$



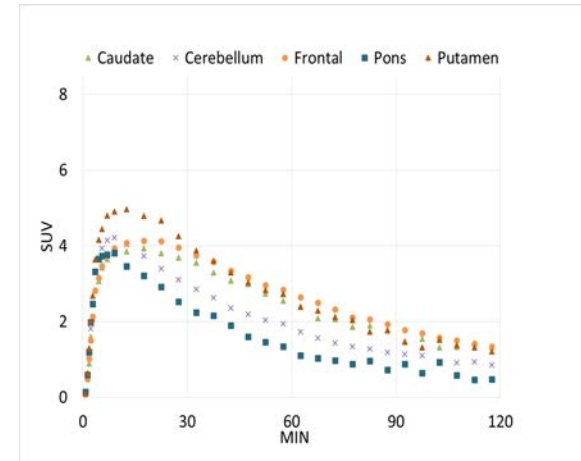
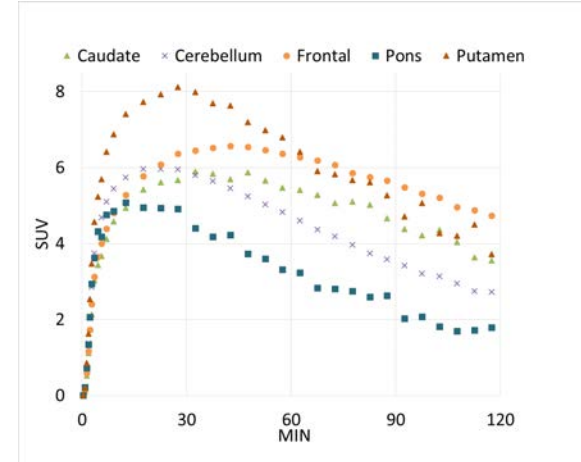
^{11}C -UCB-J Blocking with LEV (10 mg/kg)



Baseline

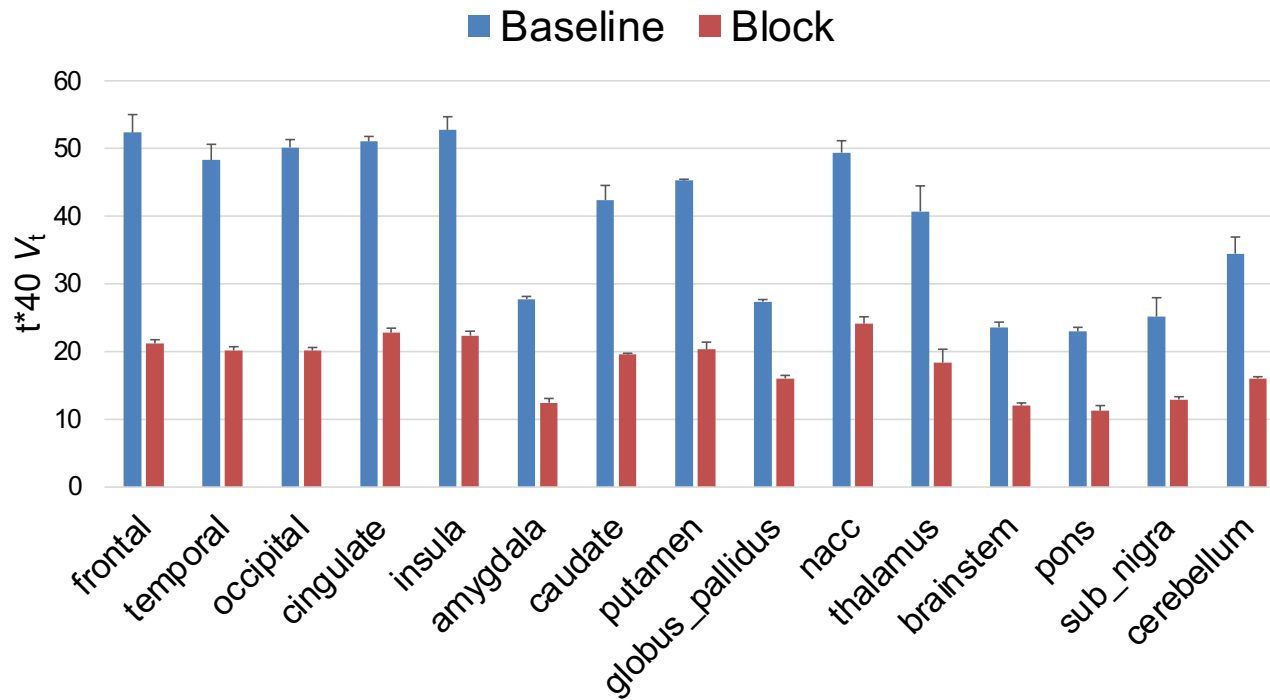


**Blocked
~65% RO**

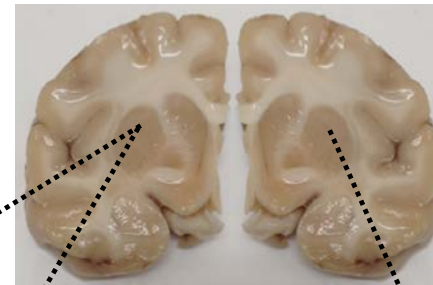
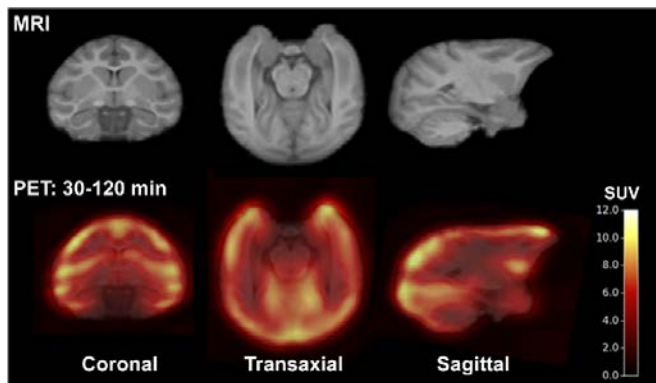


^{11}C -UCB-J Blocking with Levetiracetam

Pre-blocking with 10 mg/kg LEV; $\sim 65\pm 3\%$ occupancy ($n=2$)



Validation study: SV2A vs. Synaptophysin (SYN)

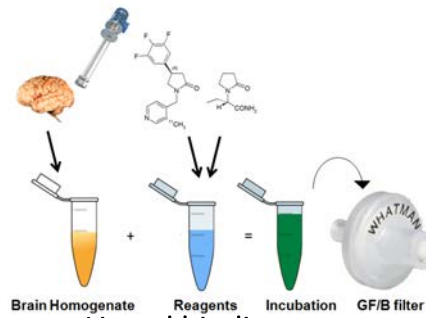


Frozen

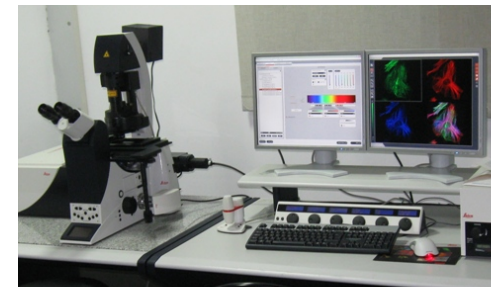
Fixed



Western blot
Regional SV2A - SYN

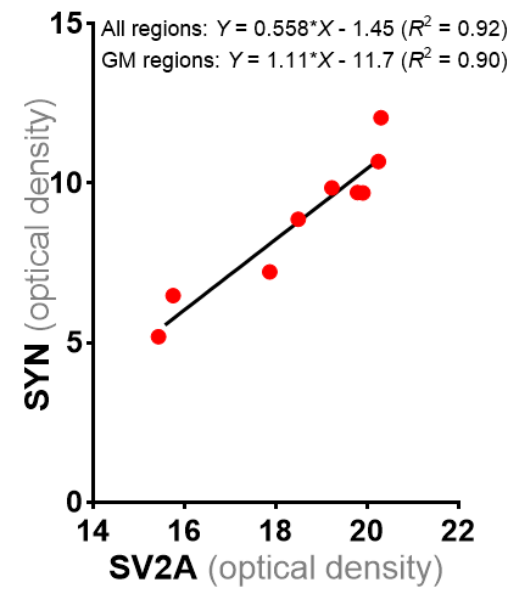
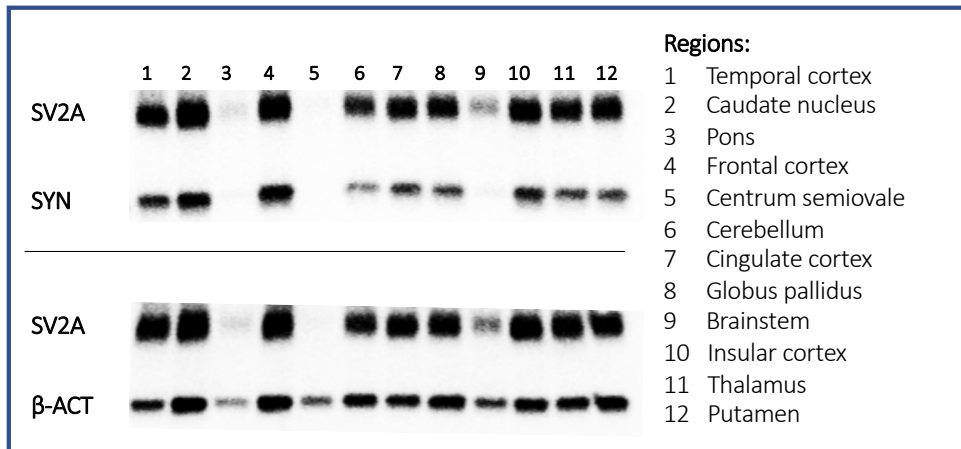


Ligand binding assay
SV2A *in vivo* - *in vitro*



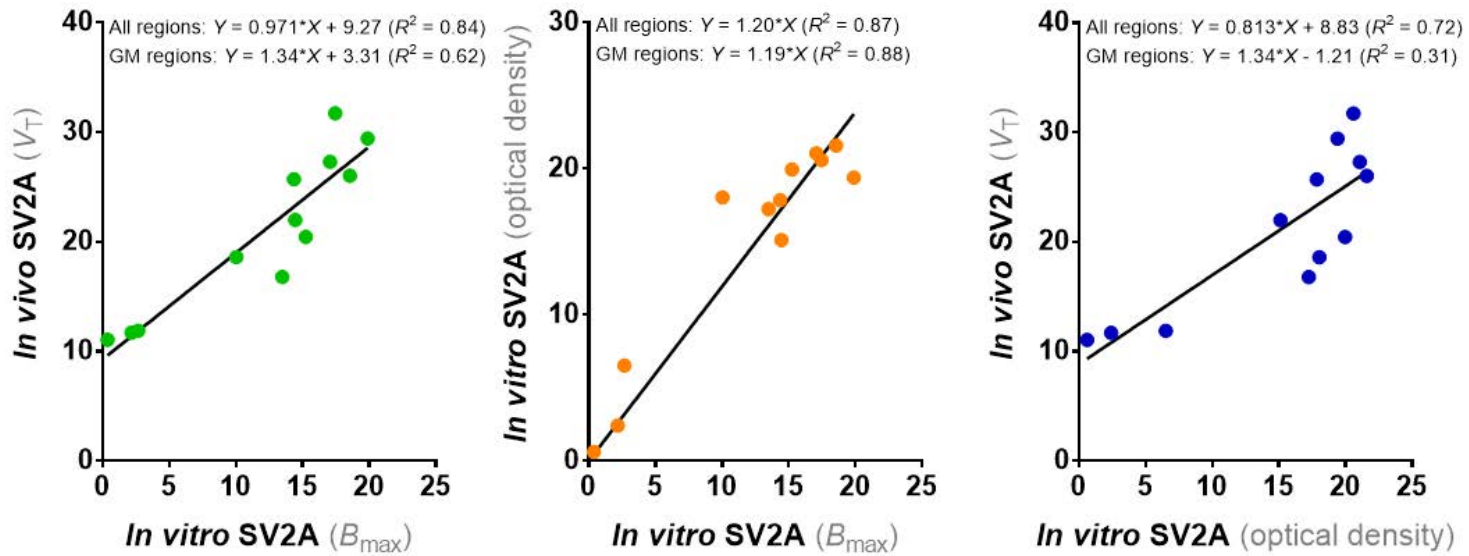
Confocal microscopy
Cellular SV2A - SYN

Western blot analysis



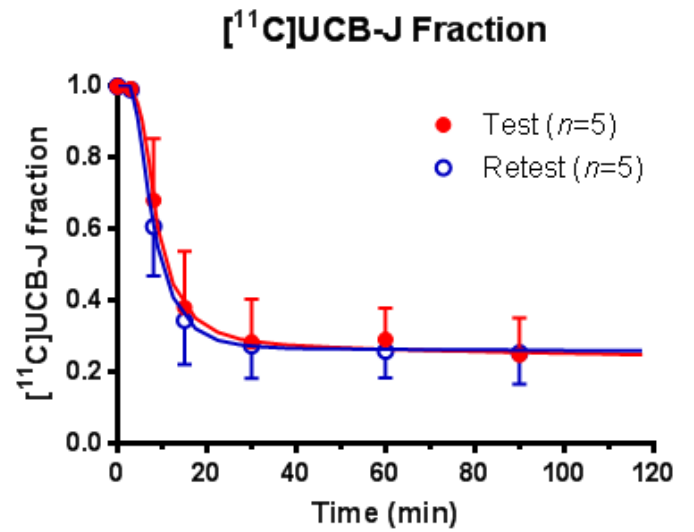
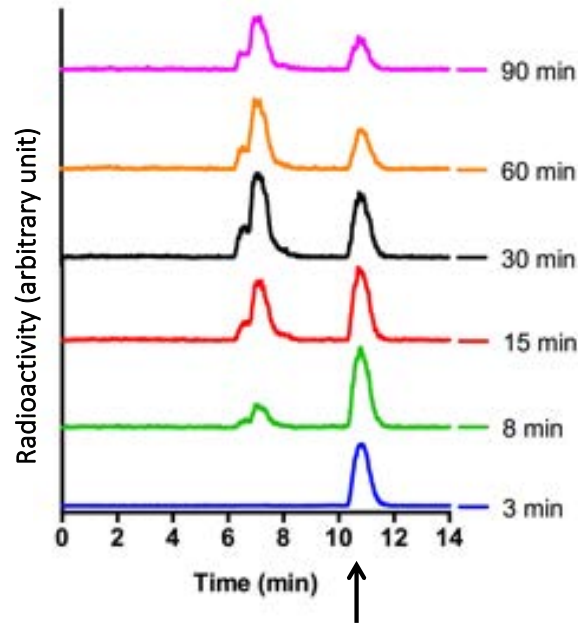
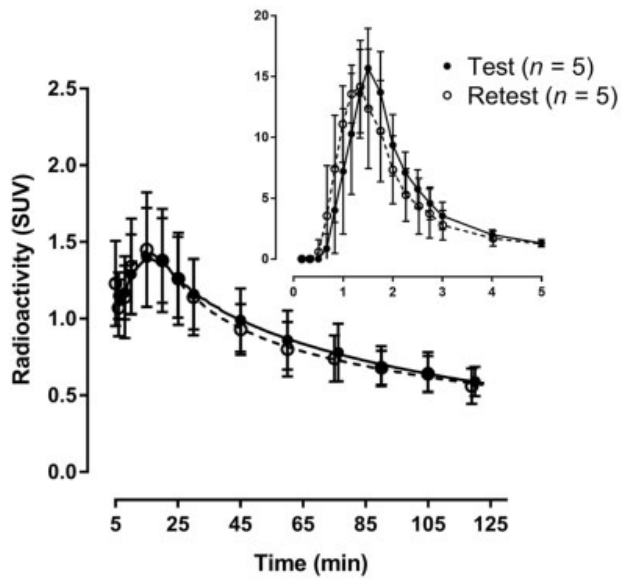
SV2A is valid alternative to SYN

Correlation *in vitro* / *in vivo* SV2A

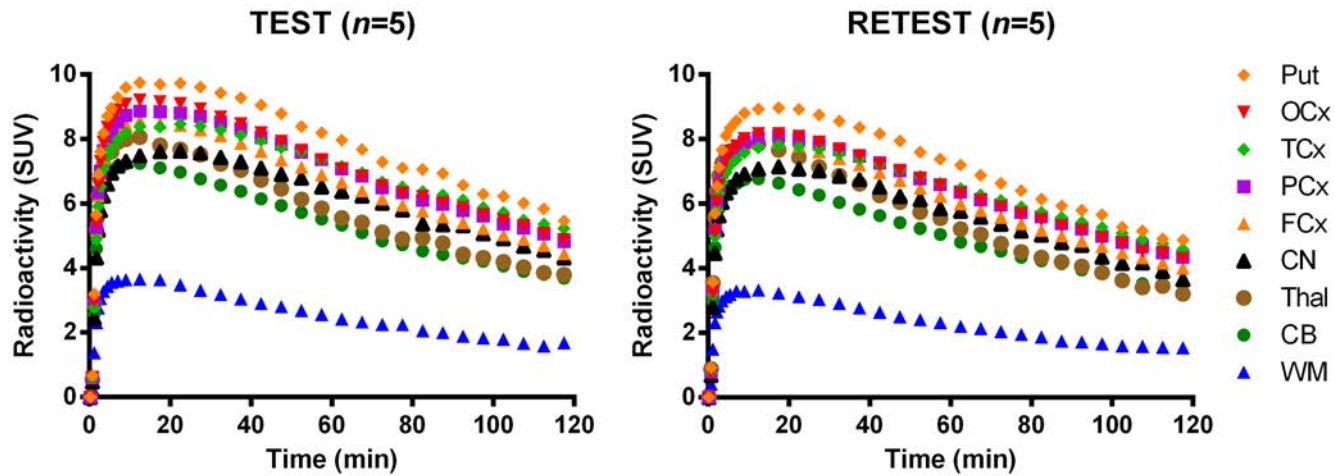
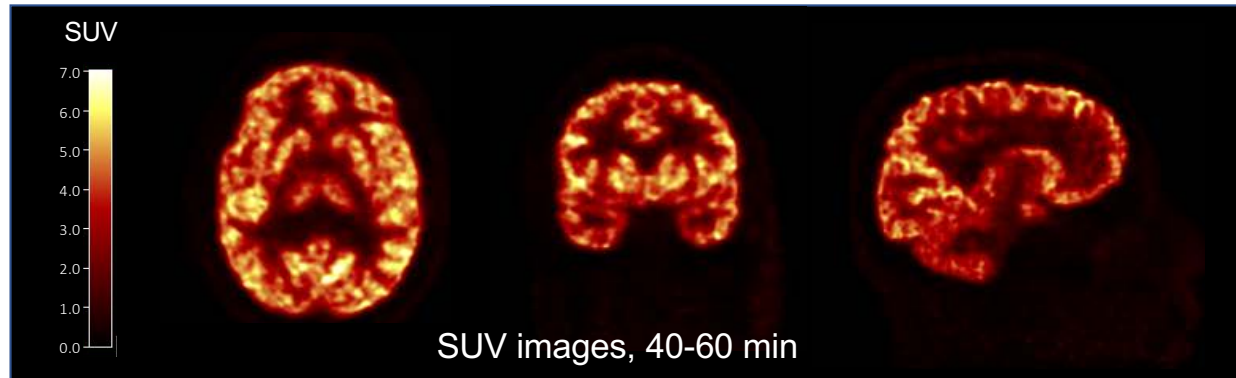


Good regional correlation *in vitro* and *in vivo* SV2A binding
 Regional differences *in vivo* ^{11}C -UCB-J binding relate to SV2A density

Human Arterial Input Function and Radiolabeled Metabolites

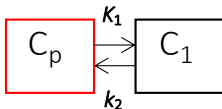


Regional Distribution of ^{11}C -UCB-J

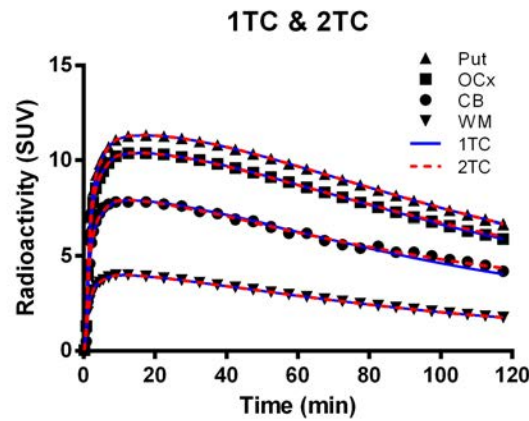
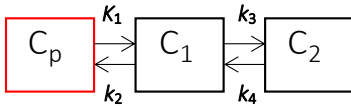


Quantification of Distribution Volume (V_T)

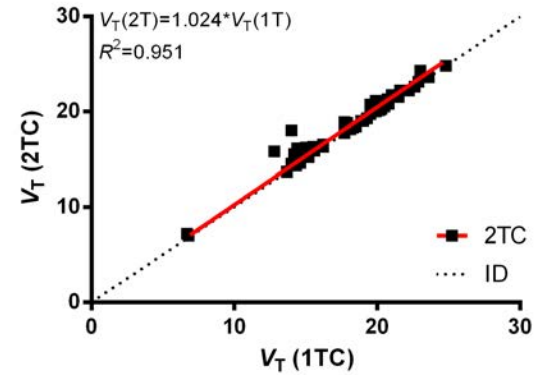
1TC



2TC



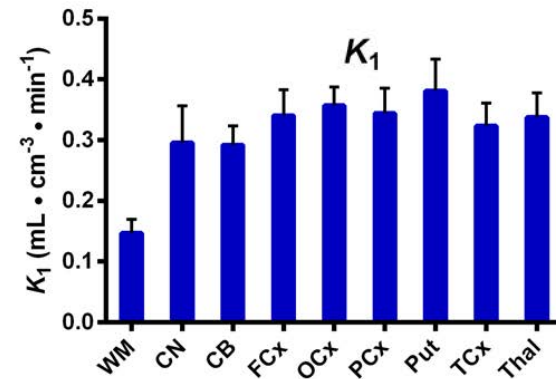
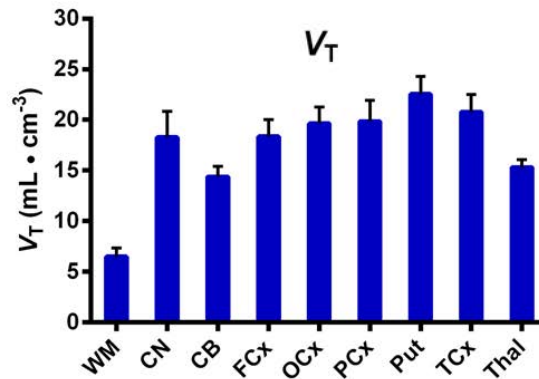
2TC vs. 1TC



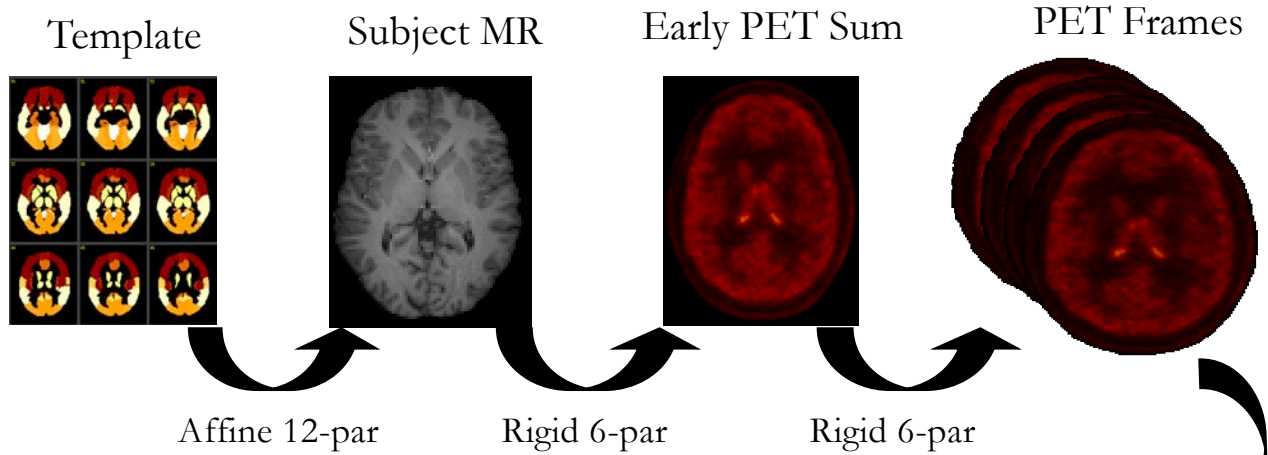
K_1 - Blood flow

V_T - Volume of distribution

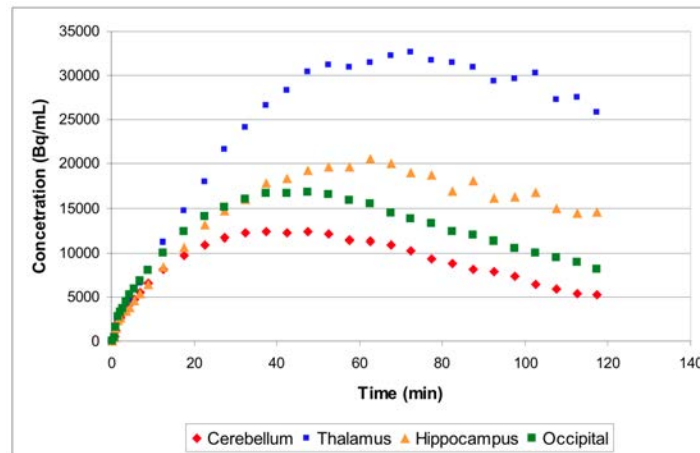
- Total binding to SV2A plus nonspecific uptake



Region Definition and TAC Computation

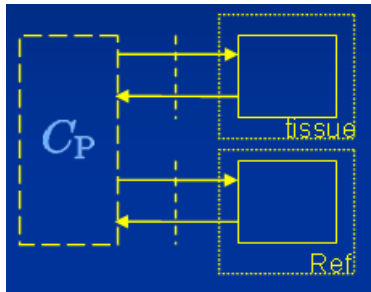


Time Activity Curves (TACs)

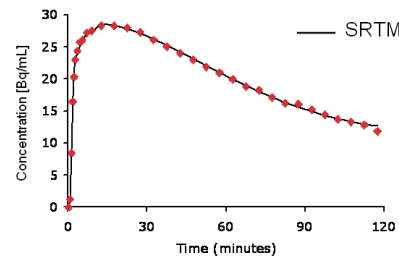


Outcome Measure Computation

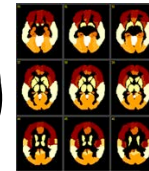
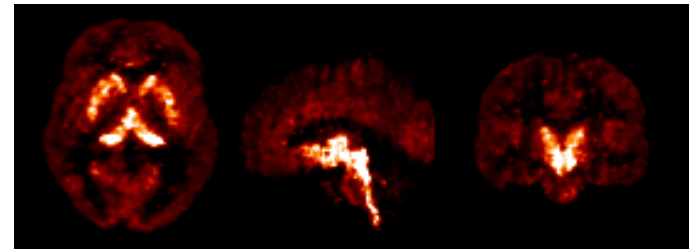
Compartment modeling



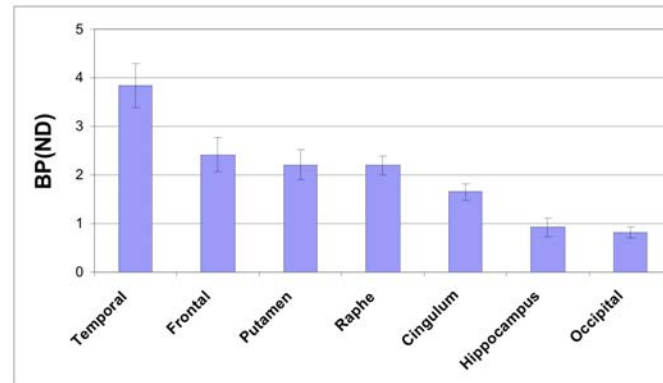
Reference region
TAC fit



BP_{ND} parametric image



Mean regional BP_{ND} values



ROI	BP _{ND}	
	Mean	SD
Temporal	3.850	0.454
Frontal	2.420	0.363
Putamen	2.213	0.304
Raphe	2.194	0.187
Cingulum	1.650	0.164
Hippocampus	0.926	0.188
Occipital	0.817	0.113

Test-Retest Reliability of V_T [%]

Measure	Subject	WM	CN	CB	FCx	OCx	PCx	Put	TCx	Thal
Difference (%)	Subj. 1	-4	0	-1	-2	-6	-4	-2	-4	0
	Subj. 2	3	5	2	3	3	5	4	4	6
	Subj. 3	-7	-9	5	-1	1	1	-7	-4	-1
	Subj. 4	-3	-2	1	-2	-5	-5	2	-3	-1
	Subj. 5	2	0	-1	5	1	1	5	2	4
	Mean	-2	-1	1	1	-1	0	0	-1	2
Absolute Variability (%)	Mean	4	3	2	3	3	3	4	3	3

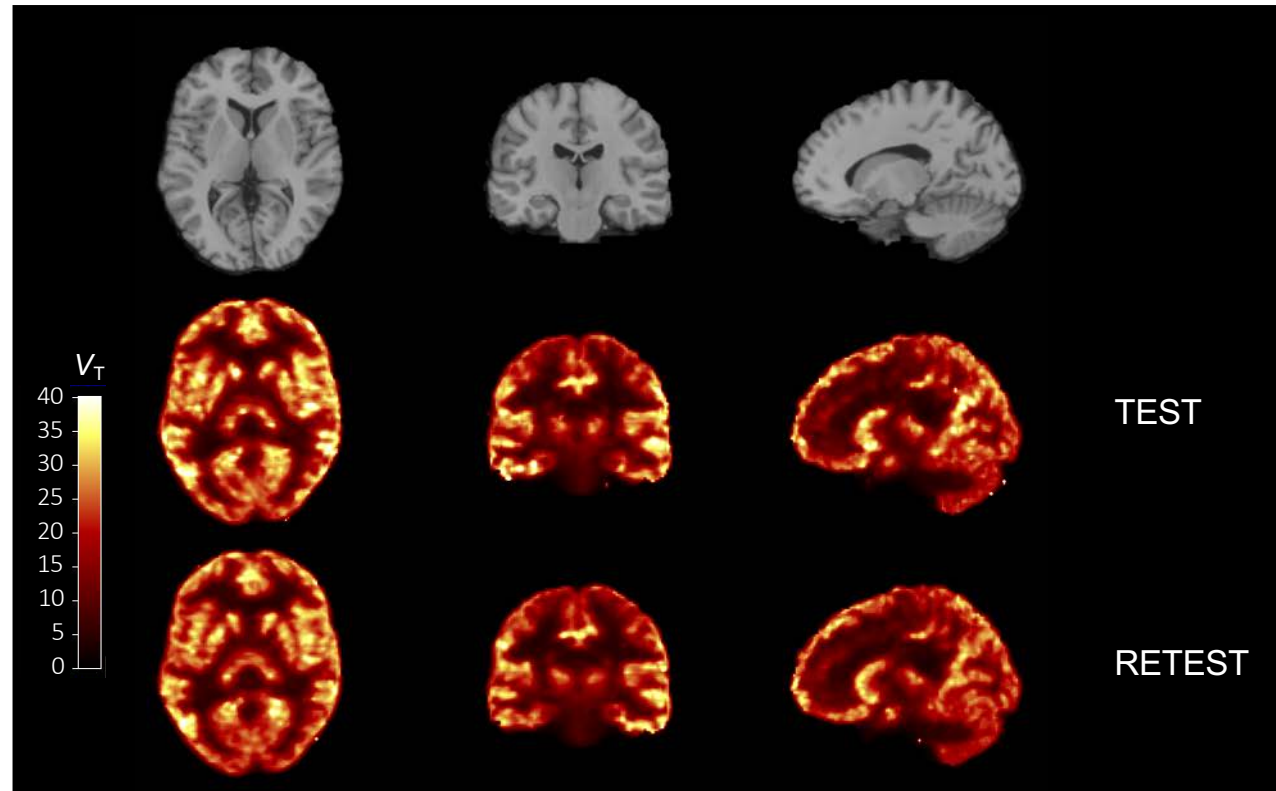
Difference: $(\text{RETEST}-\text{TEST})/((\text{RETEST}+\text{TEST})*0.5)*100\%$

Variability: $|\text{RETEST}-\text{TEST}|/((\text{RETEST}+\text{TEST})*0.5)*100\%$

Parametric Maps of V_T Calculated on Voxel Level

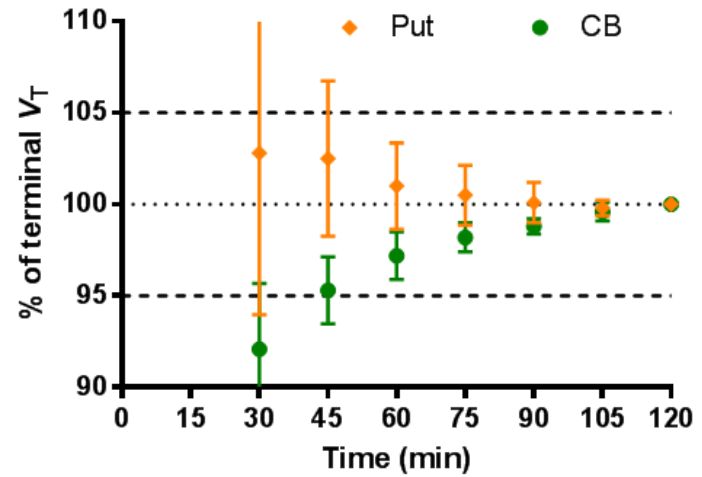
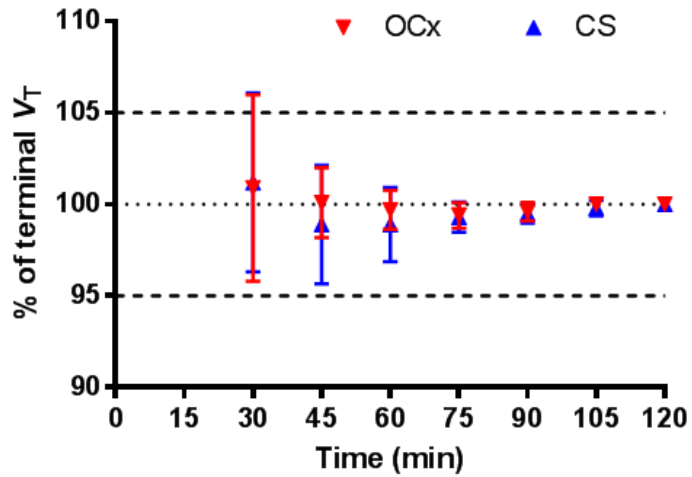
V_T – Volume of distribution

- Total binding to SV2A plus nonspecific uptake



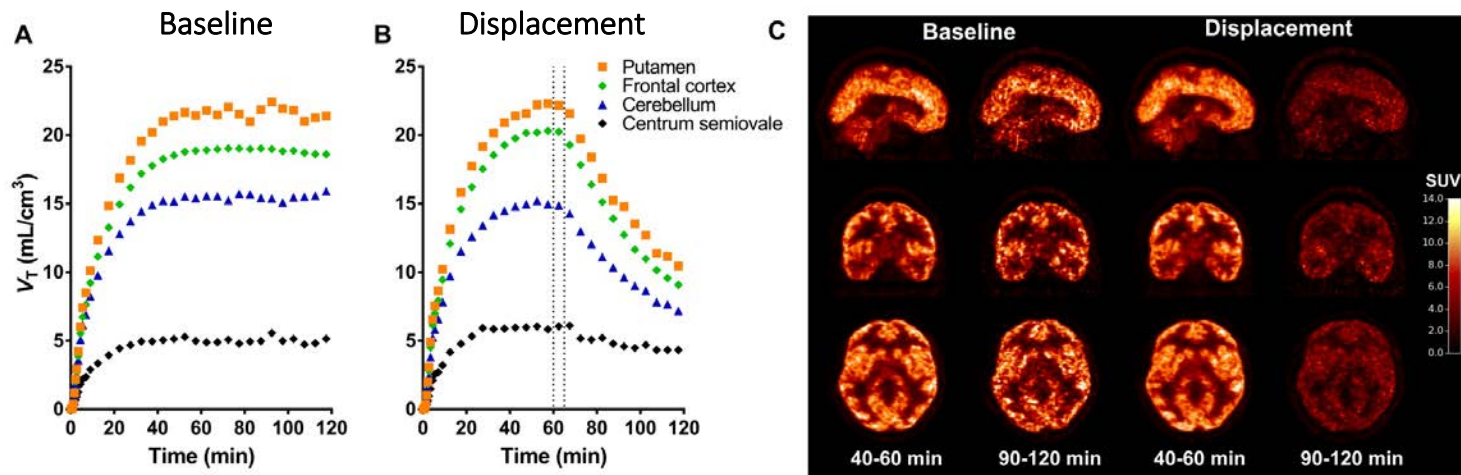
Quantitative V_T images

Stability of V_T over Time



Displacement Studies with Levetiracetam

- Baseline and displacement study
- Very helpful to have approved specific blocking drug
- Levetiracetam (Keppra, 1500 mg i.v. infusion 60-65 min)



Finnema et al, *Sci Transl Med*, 2016

SV2A/Synaptic Density Validation Still a Long Way to Go

- Technical issues:

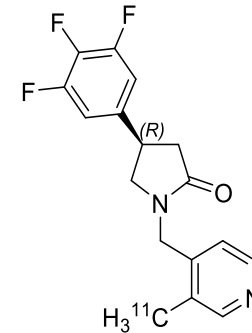
- Choice of outcome measures
- Choice of a reference region
- C-11 vs. F-18

- SV2A as a general marker of synaptic density

- # of SV2A per vesicle and # of vesicles per synapse
- Validation of SV2A as a synaptic density marker in health and diseases
- Effect of vesicle exocytosis and recycling on SV2A binding

- Clinical interpretation:

- Utility in specific diseases to monitor progression
 - Alzheimer's disease, epilepsy, Depression, PTSD, Schizophrenia, Cannabis Use, Cocaine Use, Parkinson's, Alcohol dependence, Multiple Sclerosis, Huntington's Disease, Autism Spectrum Disorder
- Imaging biomarker of synaptic regrowth
 - NCT03493282: Effect of CT1812 Treatment on Brain Synaptic Density
- Utility in animal models: Epilepsy, AD, depression, stroke



SV2A/Synaptic Density Technical Issues

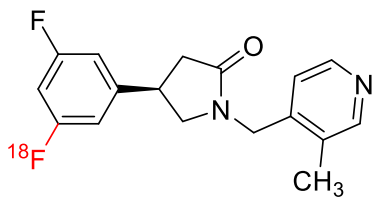
- **Choice of outcome measures**

- V_T
 - Needs arterial data, includes nonspecific binding
- V_T / f_p – correct for protein binding
 - Relevant if there are group differences or substantial intersubject variability in free fraction
- BP (binding potential)
 - Is there an ideal reference region with no specific binding?
- DVR (Distribution volume ratio)
 - Normalize to a suitable region

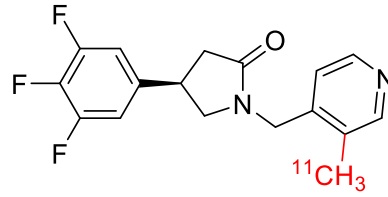
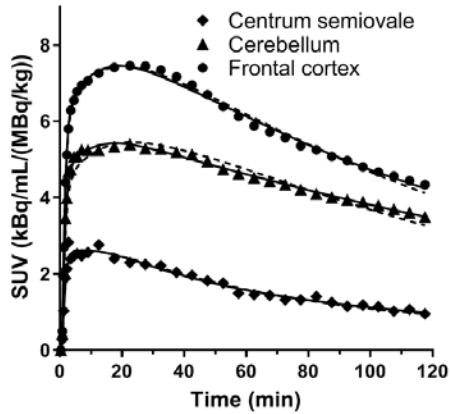
- **Choice of a reference region**

- Centrum semiovale
 - Some specific binding
 - No difference seen in AD, epilepsy, and PD
 - Differences seen in MDD
 - CS is small, so adds noise
 - Sensitive to partial volume effect
- Disease-specific normalizing region
 - Cerebellum in AD

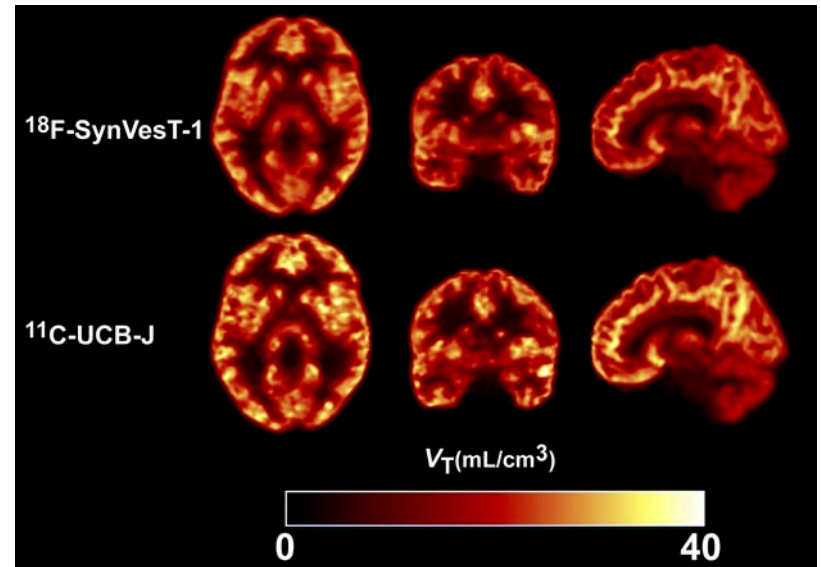
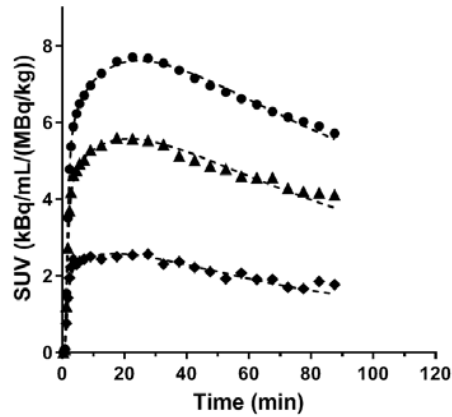
F-18 SV2A Ligand: SynVesT-1



¹⁸F-SynVesT-1



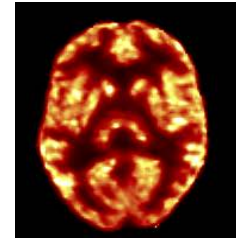
¹¹C-UCB-J



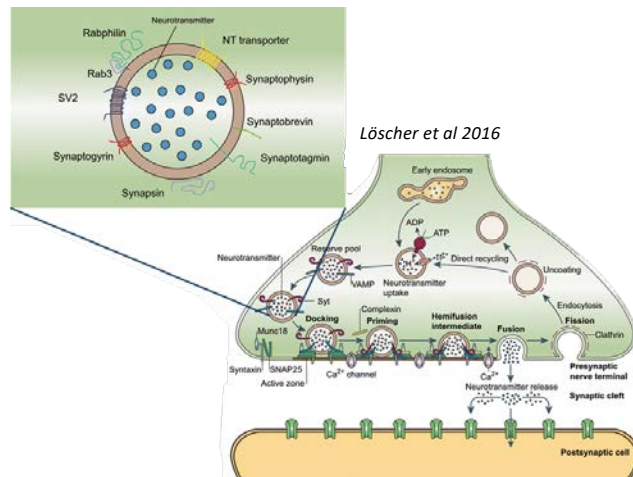
- ¹⁸F-SynVesT-1 vs. ¹¹C-UCB-J: Similarly high brain uptake, fast tissue kinetics and regional distribution

Quantitative Brain PET

- Kinetic Modeling 101
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 - Human studies
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Is the SV2A signal sensitive to neuronal activation?

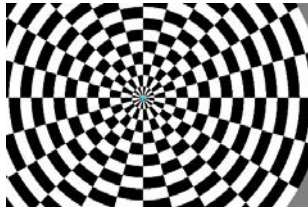


- SV2A is involved in regulating vesicle release, a complex and highly mediated process involving interactions with other proteins or with Ca^{2+}
- **Tracer binding sites may become more or less accessible during active vesicle release. If so, changes in ^{11}C -UCB-J binding would reflect influence of local activity as well as synaptic vesicle number.**
- **Need modeling to separate blood flow effects from changes in binding**

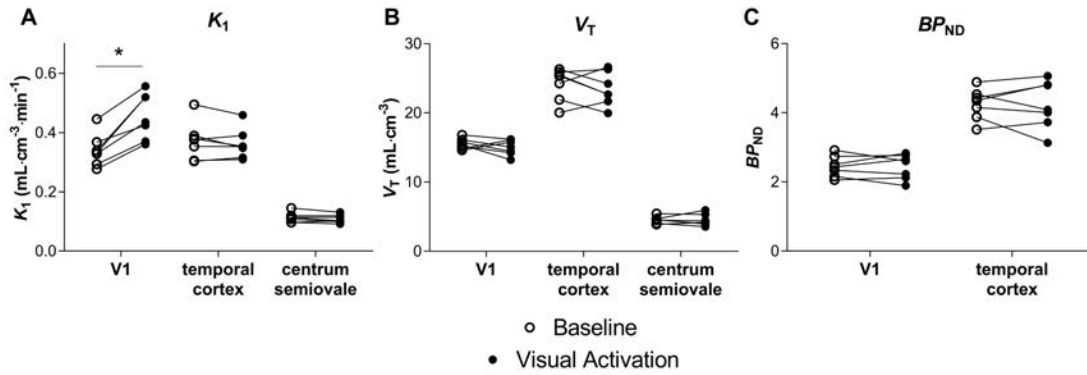
Study Design



- 7 healthy subjects
- 2 [^{11}C]UCB-J scans
 - 60 min. baseline
 - 60 min. with continuous intermittent visual activation
 - 8Hz flickering radial checkerboard
- 1 fMRI scan with checkerboard stimulation
 - 6 x 30s on/off (fMRI-optimized)
 - 3 x 3' on / 2' off (PET-optimized)



Results



- 35% increase in K_1 in primary visual cortex.
- **No change in V_T or BP_{ND} .**

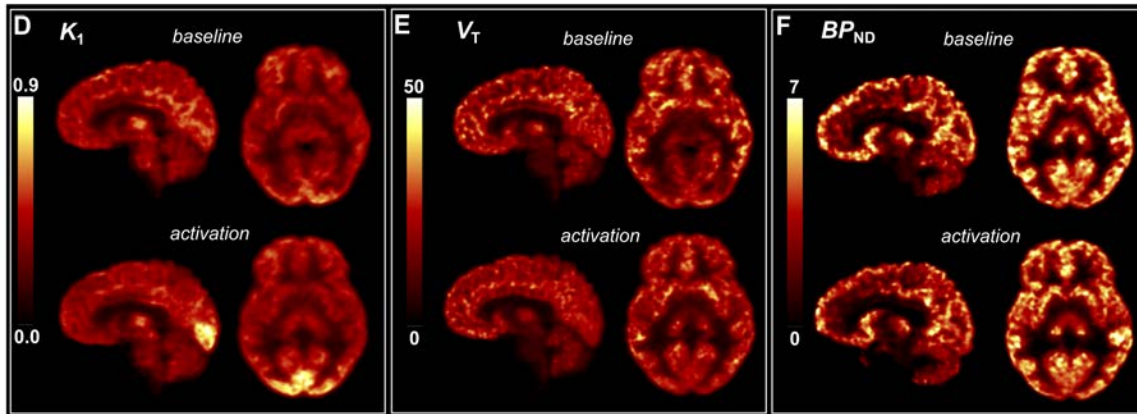


Fig. 4

→ ¹¹C-UCB-J binding is a stable *in vivo* measure of SV2A density despite increased vesicle release.

Results

- fMRI BOLD increase in V1 and LGN.
- PET K1 increase in V1.
- **Change in K1 is correlated with change in fMRI BOLD signal in visual cortex.**

→ K1 tracks brain activity.

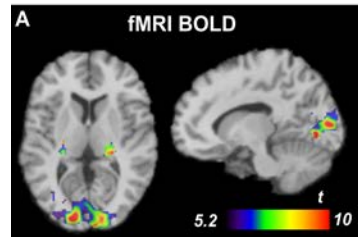


Fig. 3

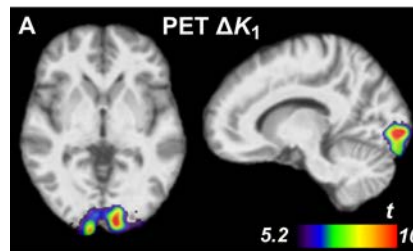
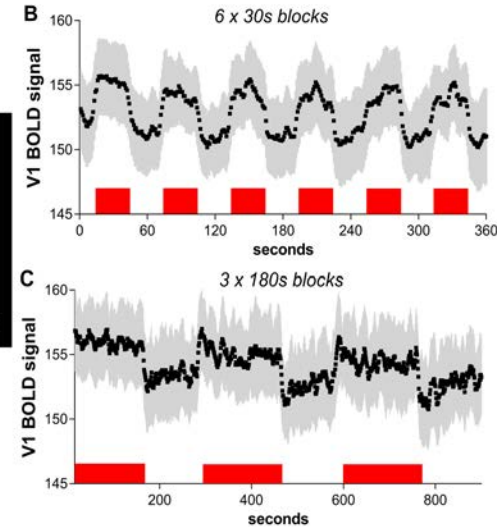
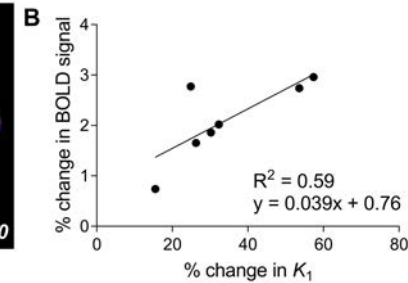
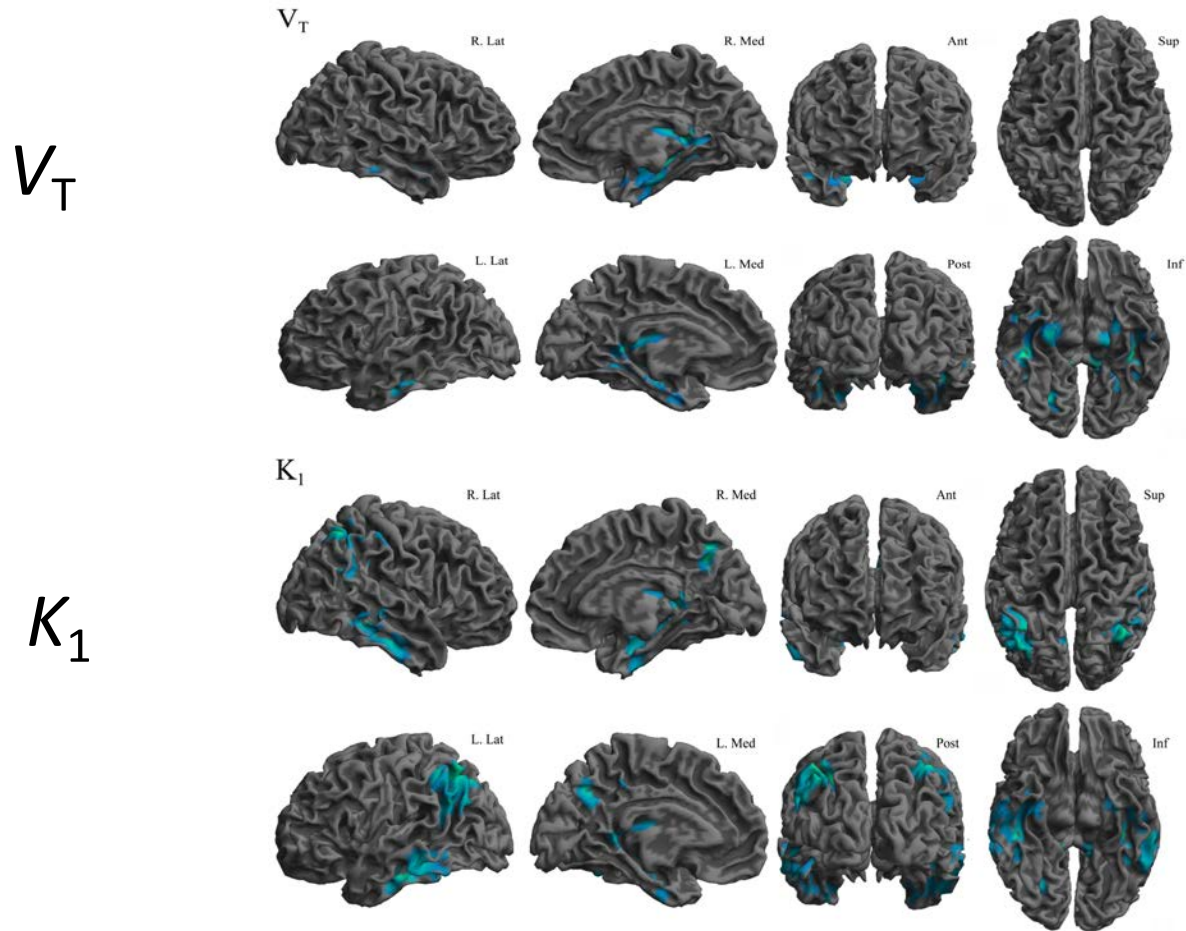


Fig. 5

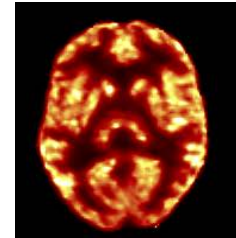


Synaptic Density in Alzheimer's Disease



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Amyloid Example Where Modeling Helps

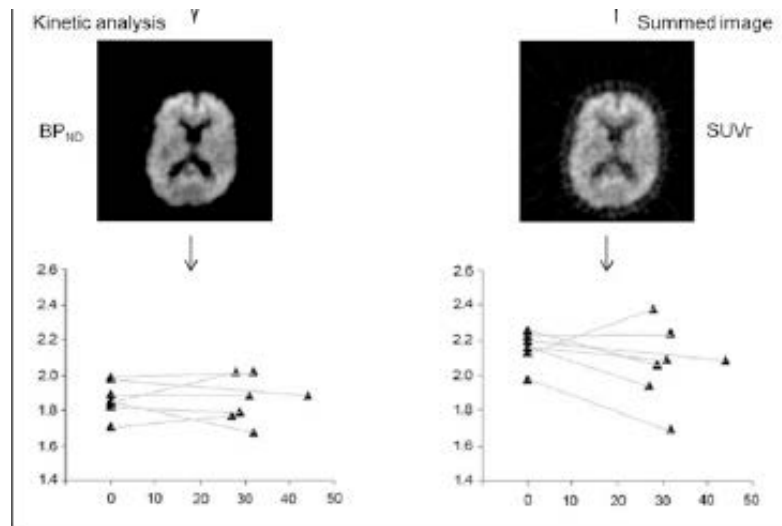


FIGURE 6. BP_{ND} and $SUVr$ (60–90 min after injection) for ^{11}C -Pittsburgh compound B scans of Alzheimer disease patients at 2 time points 2–4 y apart (horizontal axes represent months after baseline scan). Patients did not receive antiamyloid therapy during interval between scans. $SUVr$ shows a small but significant counterintuitive decrease in amyloid load, whereas BP_{ND} remains unchanged.

- Test-retest study
- Less variability in modeling results

Forward to the Past: The Case for Quantitative PET Imaging

Adriaan A. Lammertsma

Department of Radiology and Nuclear Medicine, VU University Medical Center, Amsterdam, The Netherlands

J Nucl Med 2017; 58:1019–1024
DOI: 10.2967/jnumed.116.158029

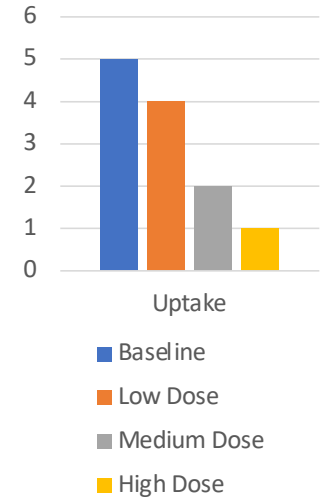
Goals of PET Modeling

- Understand the relationship between the tissue measurements and the underlying physiology (blood flow, metabolism, etc.)
- **Account for the effects of tracer availability (input function).**
- Determine what parameters can be measured
- Devise study methodology
- Prove that the method measures the parameter(s) of interest.
- Verify that the method is not influenced by other parameters.
- Produce images of physiological parameters (parametric images)
- Produce a simple and accurate patient protocol.



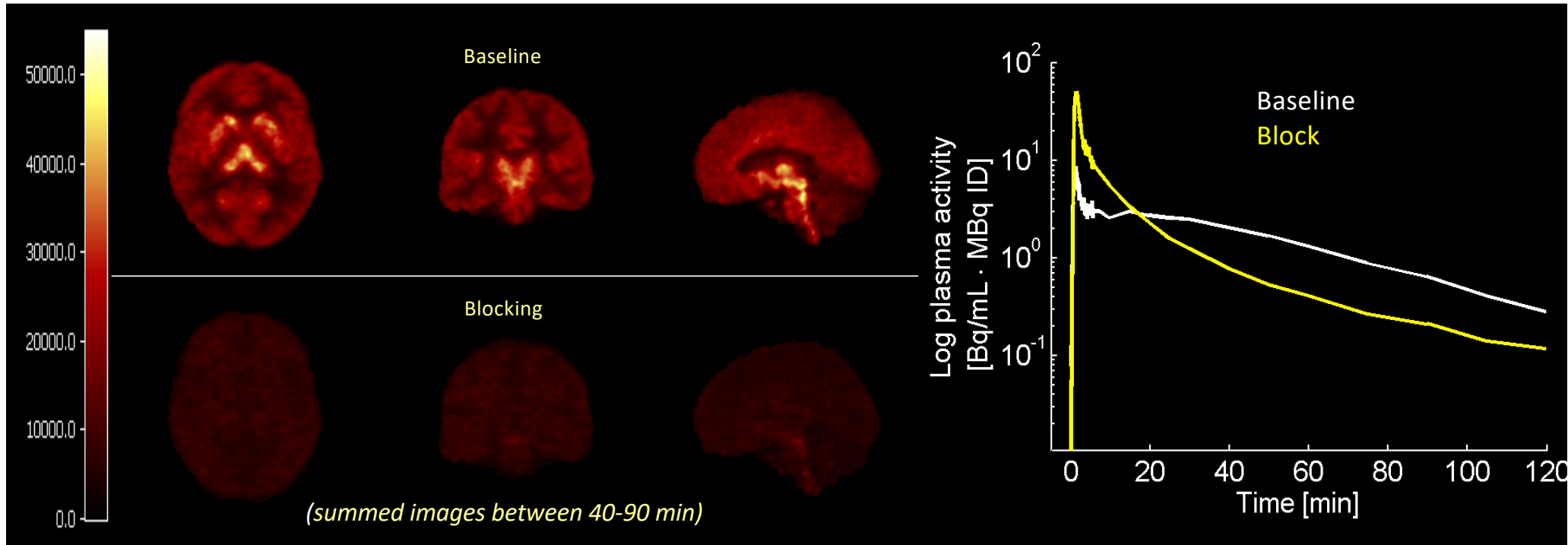
Studying Drug Effects: Input Functions

- Drug and tracer target the same site
- We expect dose-dependent reductions in specific tracer binding following administration of a competing drug
- Typically, blocking drugs reduce tracer in tissue, and increase tracer in the blood
 - Increased bioavailability (the input function)
 - Increased nonspecific uptake
- Net effect depends on relative magnitude of specific and non-specific uptake, and tracer's kinetics

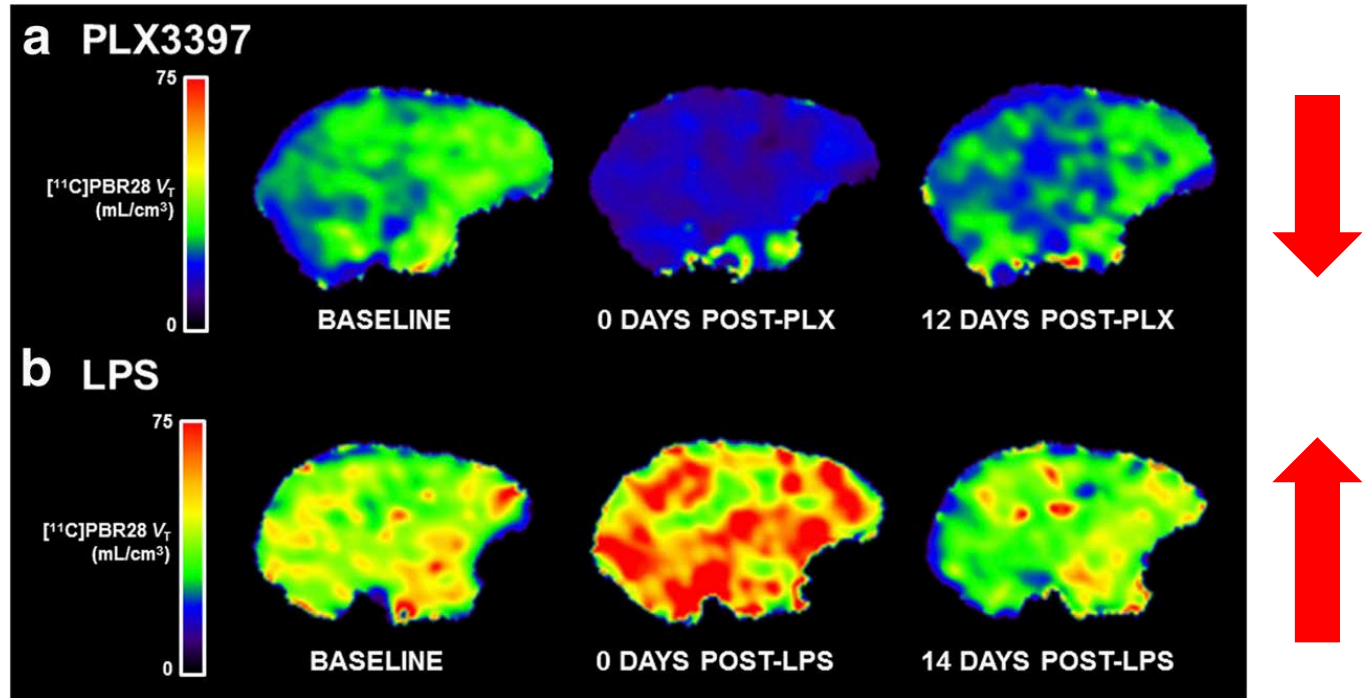




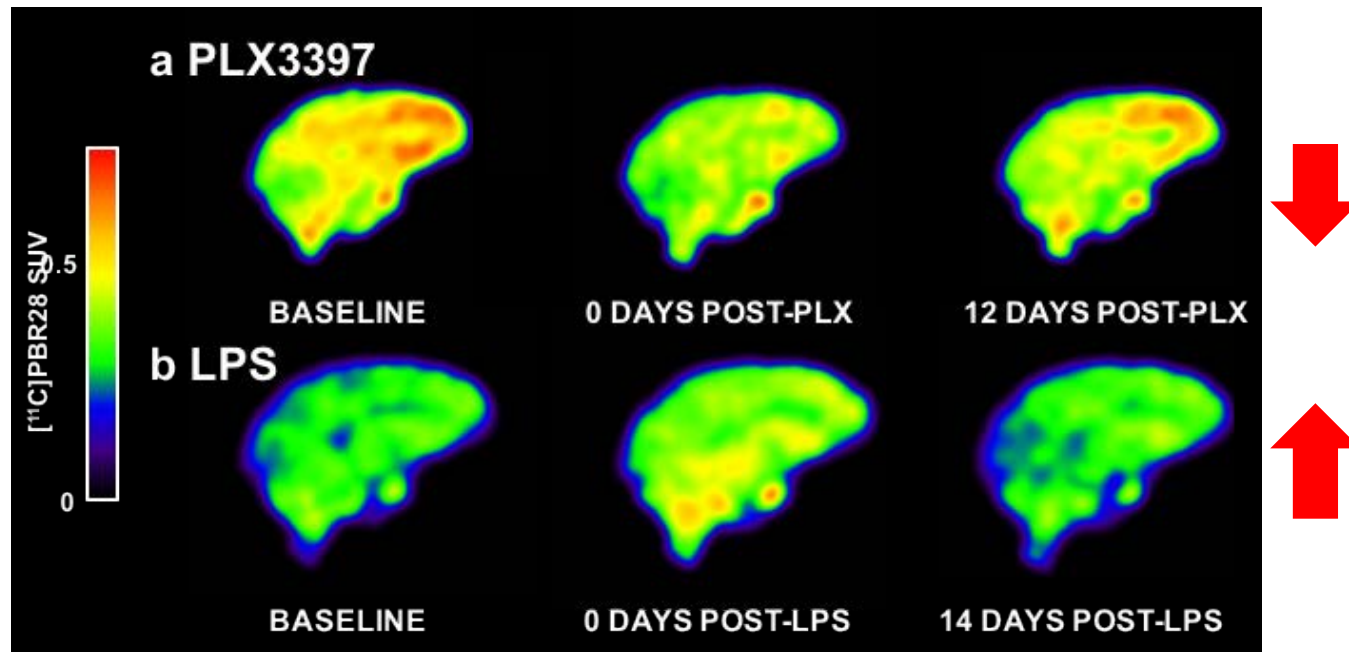
^{11}C -AFM: SERT Tracer Blocking Studies (Citalopram)



Microglial Activation and Depletion Results with Modeling



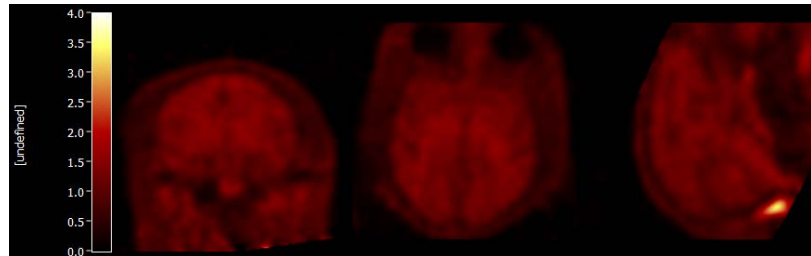
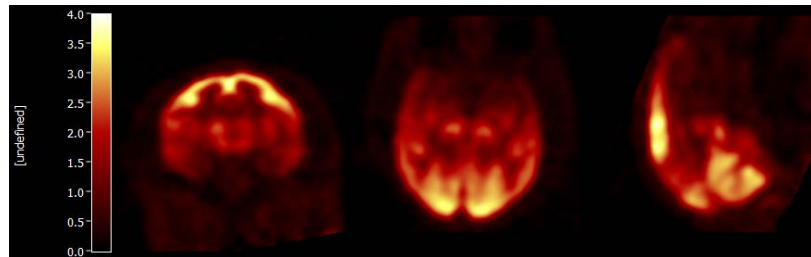
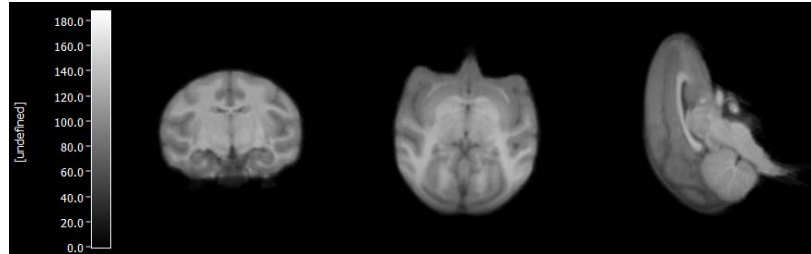
Microglial Activation and Depletion Results without Modeling



Magnitude of change reduced without modeling



Brain Enzyme Inhibitor Study SUV Images



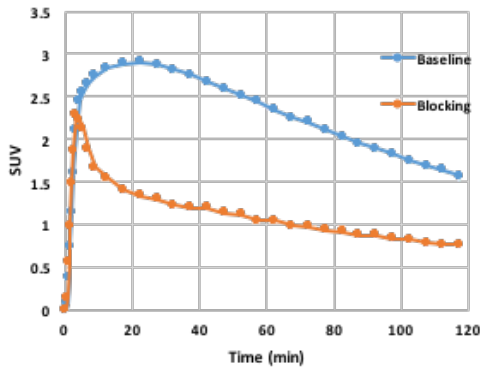
Variation in specific binding among brain regions

Brain Enzyme Inhibitor Study

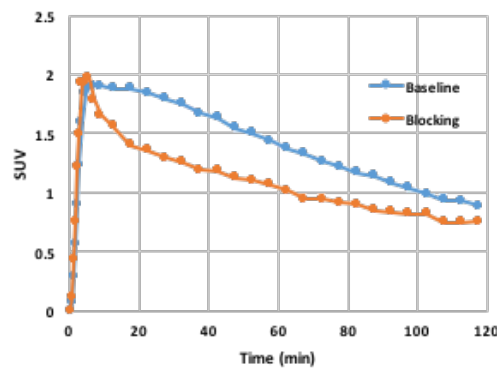
Differences Among Brain Regions Without Modeling

SUV

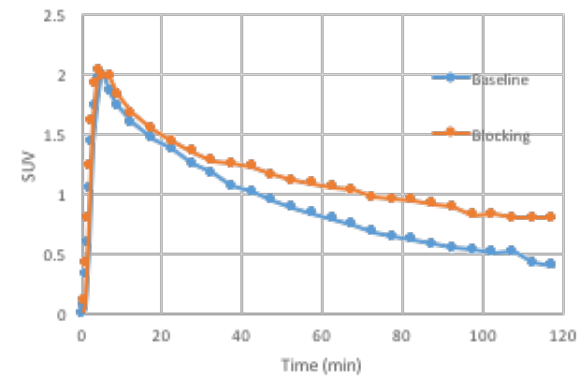
Occipital cortex



Temporal cortex

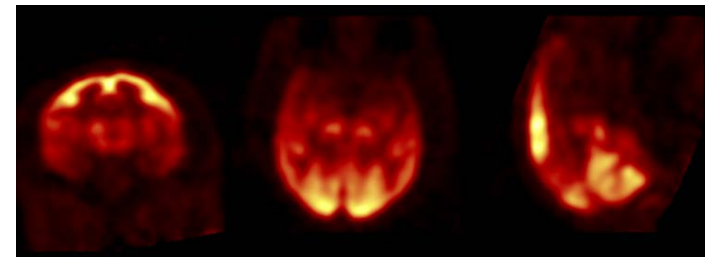


Frontal cortex



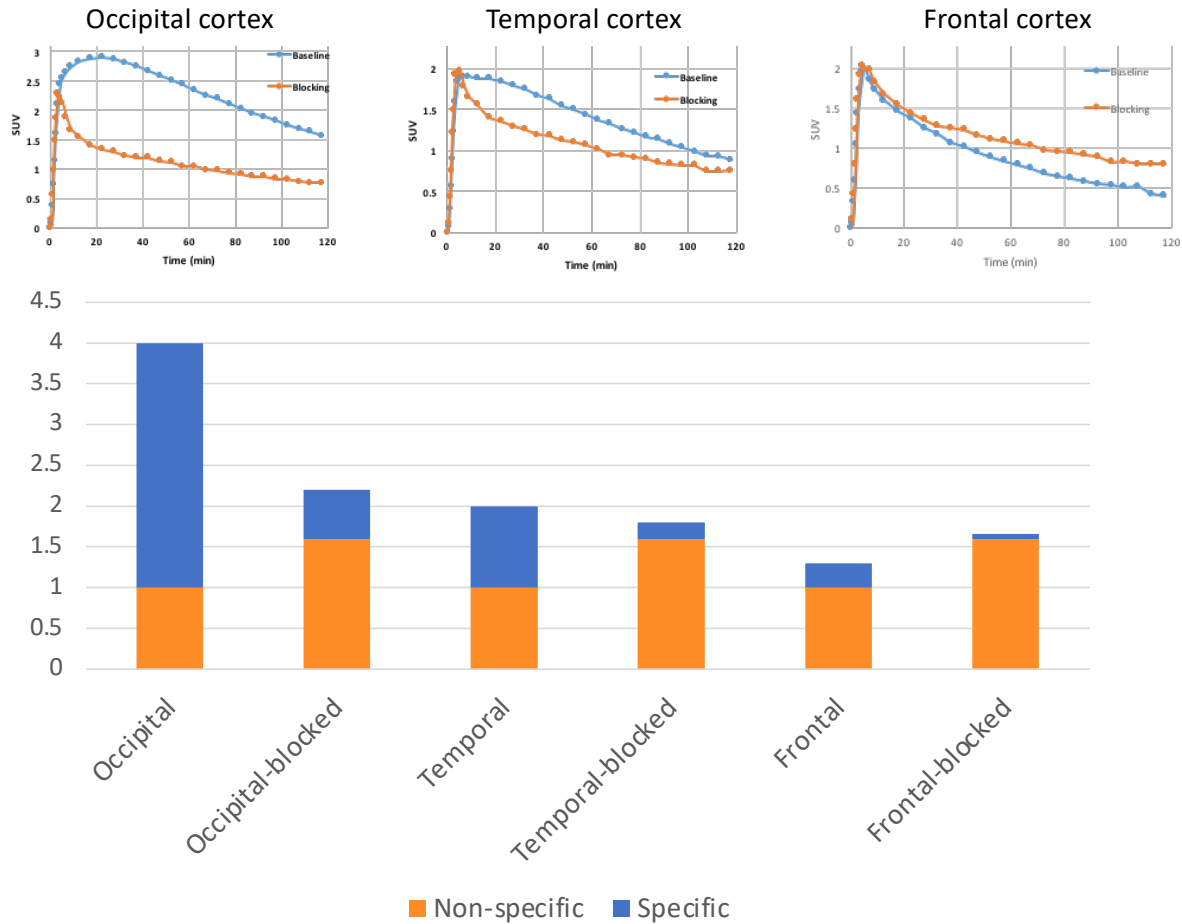
Baseline
Blocking

- Occipital: large decrease
- Temporal: small decrease
- Frontal: small increase!
- ??



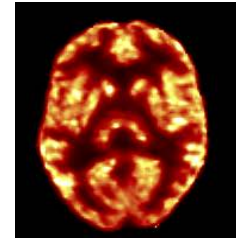
Brain Enzyme Inhibitor Study

Differences Among Brain Regions Without Modeling



Quantitative Brain PET

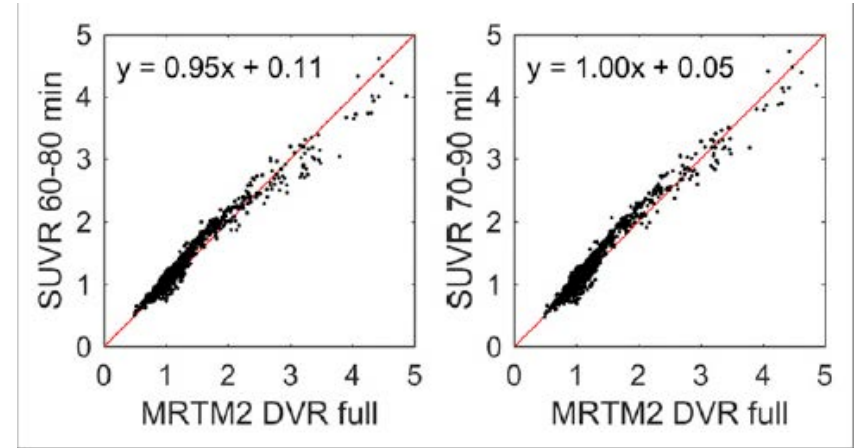
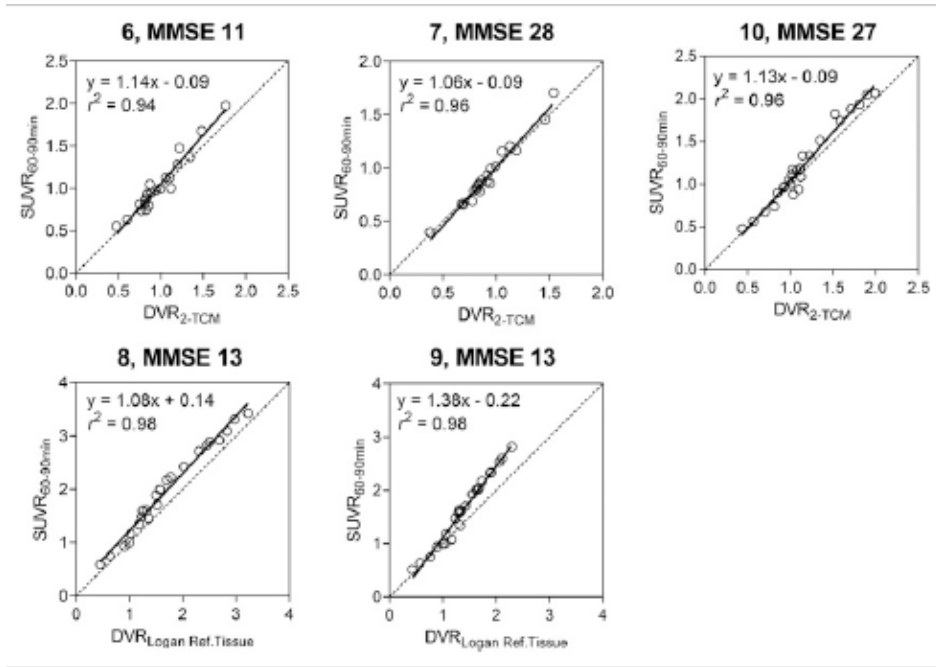
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Simplifications for Brain Imaging

- Use our understanding of the model to produce a protocol and analysis that balances patient simplicity with physiological accuracy
- Find a reference region for normalization – skip the arterial samples
- Look for a static time period that best correlates with the “gold standard” distribution volume ratio **DVR**
- The holy grail: Tissue-to-reference ratio: **SUVR**
- Apply in patient populations and clinical trials

DVR vs. SUVR ¹⁸F-MK6240



Regression	Coefficient	β - (SE)	95% confidence interval	R^2
SUVR (40-60) vs. LGA (full)	Slope	0.814 (0.004)	0.806 to 0.822	0.96
	Intercept	0.245 (0.005)	0.235 to 0.255	
SUVR (50-70) vs. LGA (full)	Slope	0.934 (0.004)	0.926 to 0.941	0.971
	Intercept	0.131 (0.005)	0.122 to 0.141	
SUVR (60-80) vs. LGA (full)	Slope	1.014 (0.004)	1.006 to 1.022	0.972
	Intercept	0.048 (0.005)	0.038 to 0.058	
SUVR (70-90) vs. LGA (full)	Slope	1.073 (0.005)	1.064 to 1.082	0.970
	Intercept	-0.015 (0.006)	-0.026 to -0.004	
SUVR (40-60) vs. MRTM2 (full)	Slope	0.757 (0.004)	0.748 to 0.766	0.947
	Intercept	0.299 (0.006)	0.288 to 0.310	
SUVR (50-70) vs. MRTM2 (full)	Slope	0.869 (0.004)	0.861 to 0.878	0.960
	Intercept	0.192 (0.006)	0.181 to 0.203	
SUVR (60-80) vs. MRTM2 (full)	Slope	0.945 (0.004)	0.937 to 0.954	0.964
	Intercept	0.112 (0.006)	0.101 to 0.123	
SUVR (70-90) vs. MRTM2 (full)	Slope	1.002 (0.005)	0.993 to 1.011	0.964
	Intercept	0.052 (0.006)	0.040 to 0.063	

Lohith et al, JNM, 2019

Bethausen et al, JNM, 2019

Simplifying ^{11}C -UCB-J SV2A Imaging

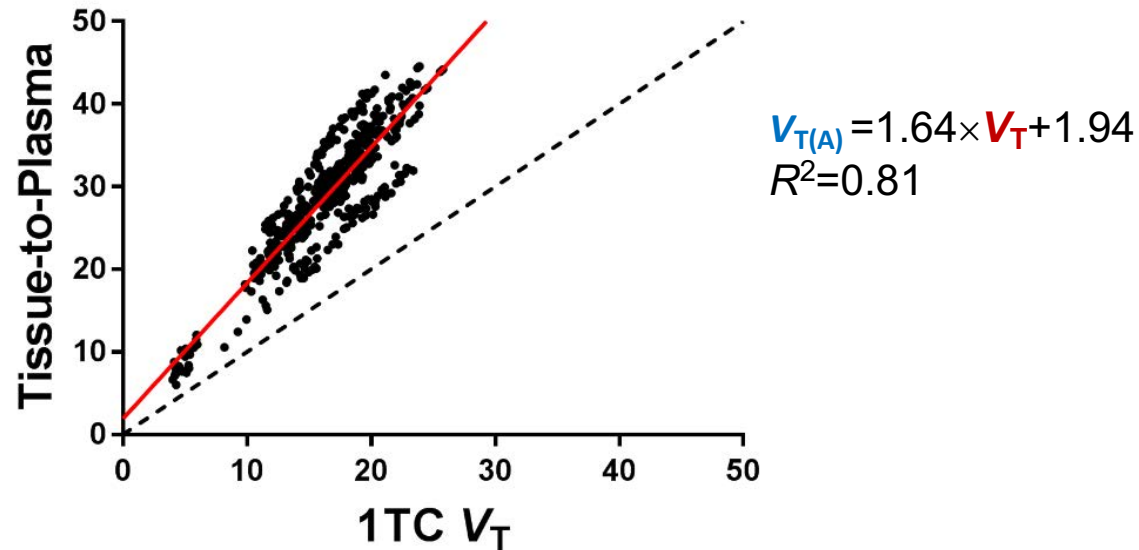
- 90 min scan on the HRRT scanner
 - Bolus injection over 1 min.
 - Arterial blood sampling and metabolite analysis for gold standard values (V_T and BP_{ND}) Reference region = Centrum semiovale
- 2 datasets
 - Healthy controls (HC)
 - Alzheimer's disease (AD)
- Tissue-to-plasma ratio (a.k.a. the apparent volume of distribution, $V_{T(A)}$) compared to V_T
 - Tissue-to-plasma ratio at equilibrium = V_T
- Tissue-to-reference ratio (a.k.a. **SUVR**) compared to **DVR**
 - **SUVR** = $V_{T(A)}(\text{ROI}) / V_{T(A)}(\text{Reference})$
 - **SUVR-1** compared to BP_{ND}



^{11}C -UCB-J: Healthy Control Data Tissue-to-Plasma Ratio



- $V_{T(A)}$ (60-90 min) substantially overestimates V_T



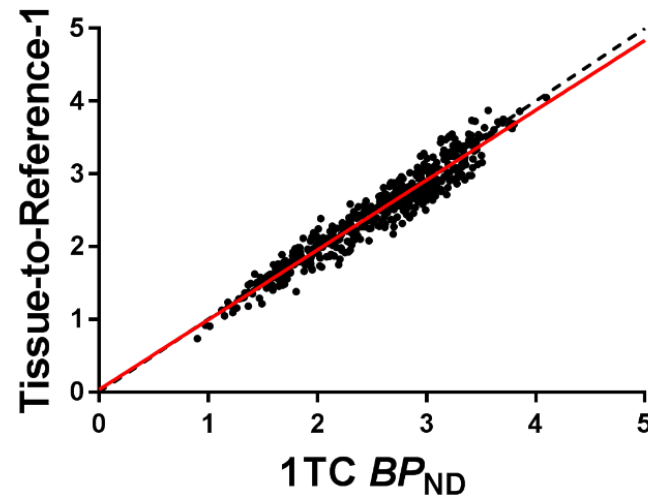
- Why?
 - Plasma and tissue are not at equilibrium



^{11}C -UCB-J: Healthy Control Data Tissue-to-Reference (SUV) Ratio



- **SUVR-1** (60-90 min) very similar to **BP_{ND}**
 - % difference between **SUVR-1** and **BP_{ND}** $-2 \pm 7\%$



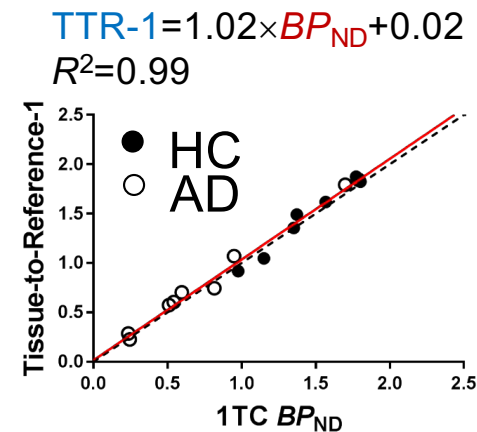
$$\text{SUVR-1} = 0.96 \times BP_{ND} + 0.03$$
$$R^2 = 0.93$$

^{11}C -UCB-J: SUVR in HC/AD comparison

- Hippocampus **SUVR-1** was similar to **BP_{ND}**
 - $4 \pm 10\%$
- The HC-AD group difference was significant using both **BP_{ND}** and **SUVR-1**

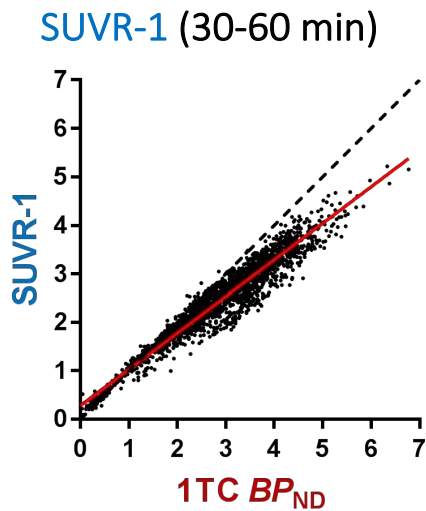
	HC ($n=7$)	AD/MCI ($n=9$)	P -value
BP_{ND}	1.43 ± 0.31	0.82 ± 0.57	0.024
TTR-1	1.45 ± 0.37	0.87 ± 0.59	0.041

- Slightly lower significance

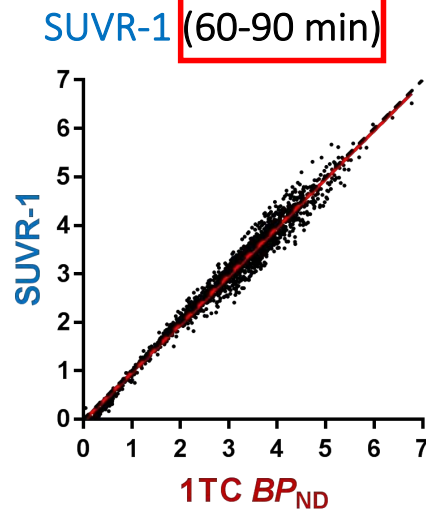




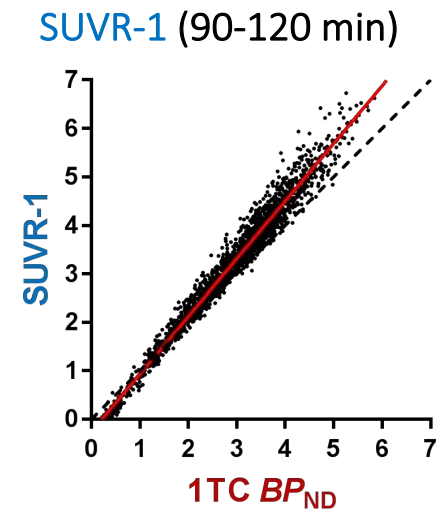
^{11}C -UCB-J agreement between **SUVR-1** and BP_{ND} is time-dependent



$$\text{SUVR-1} = 0.75 \times BP_{\text{ND}} + 0.28$$
$$R^2 = 0.93$$



$$\text{SUVR-1} = 1.00 \times BP_{\text{ND}} - 0.02$$
$$R^2 = 0.98$$



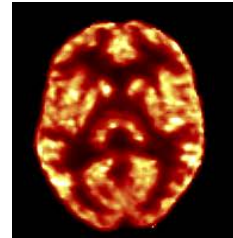
$$\text{SUVR-1} = 1.19 \times BP_{\text{ND}} - 0.25$$
$$R^2 = 0.98$$

- Same as virtually every successful reversible PET tracer
- What's going on?

Naganawa et al, JNM, 2020

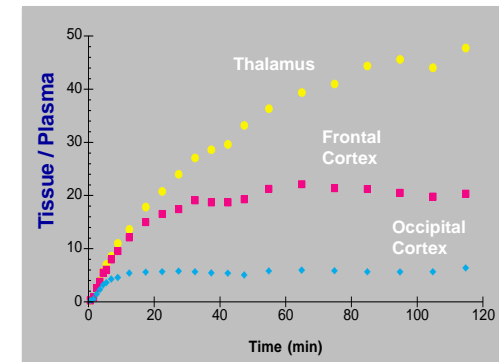
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For a reversible tracer, following a bolus injection...

- As time proceeds, the tissue:plasma ratio typically rises until a constant ratio is reached
 - **Transient equilibrium**
- Typically, higher binding regions take longer to reach transient equilibrium
- The tissue:plasma ratio at transient equilibrium (the apparent volume of distribution, $V_{T(A)}$) is **greater** than the ratio at equilibrium (the true volume of distribution, V_T)
- The faster the plasma clearance, the greater the difference between $V_{T(A)}$ and V_T
- Typically, regions with higher V_T have a greater bias

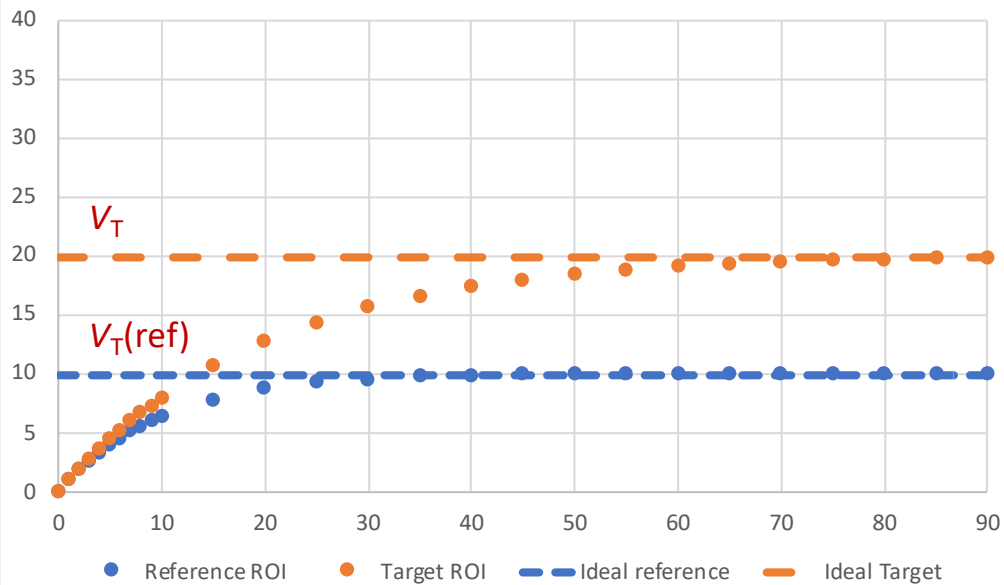


A simple simulation: No plasma clearance

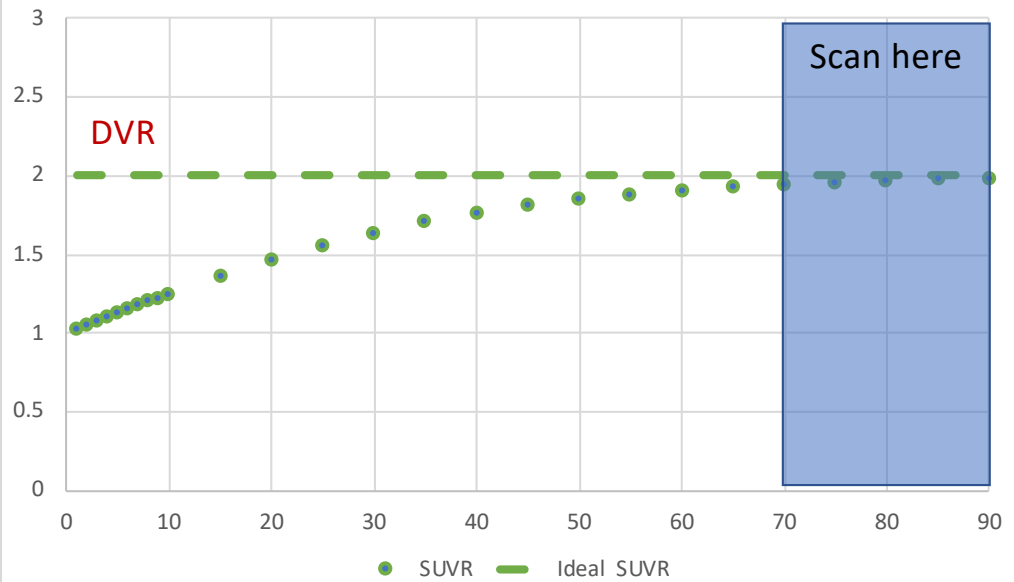
$V_{T(A)}$: Apparent volume of distribution

SUVR

ROI and reference: No plasma clearance



SUVR: No plasma clearance

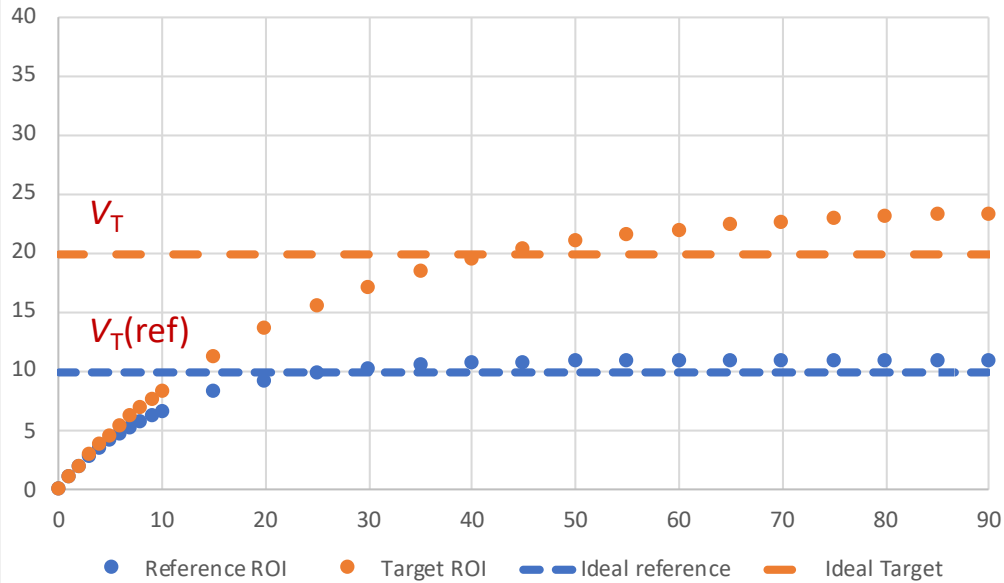


A simple simulation: Slow plasma clearance

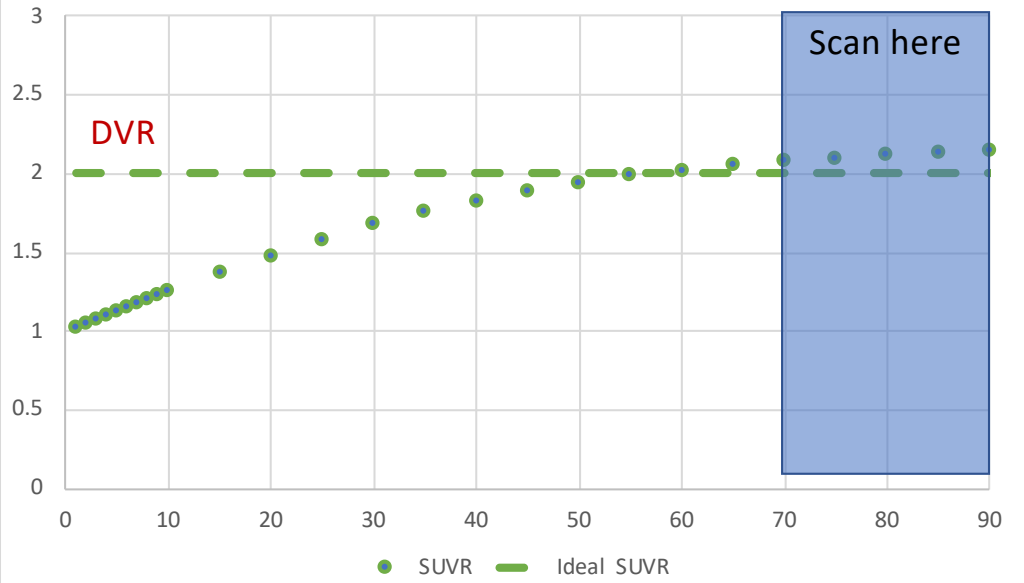
$V_{T(A)}$: Apparent volume of distribution

SUVR

ROI and reference: Slow plasma clearance



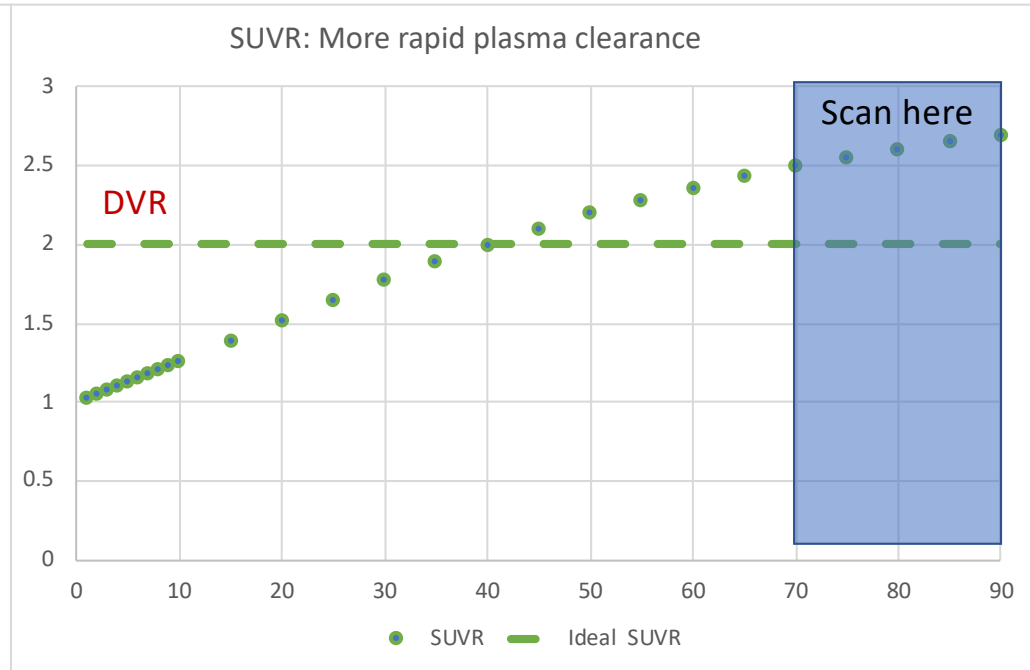
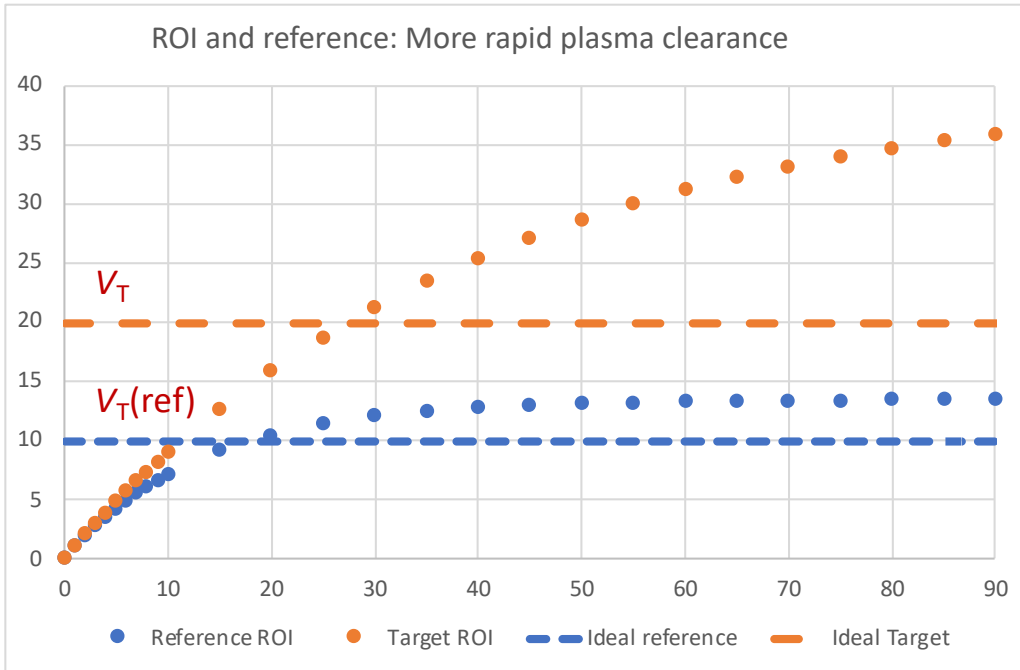
SUVR: Slow plasma clearance



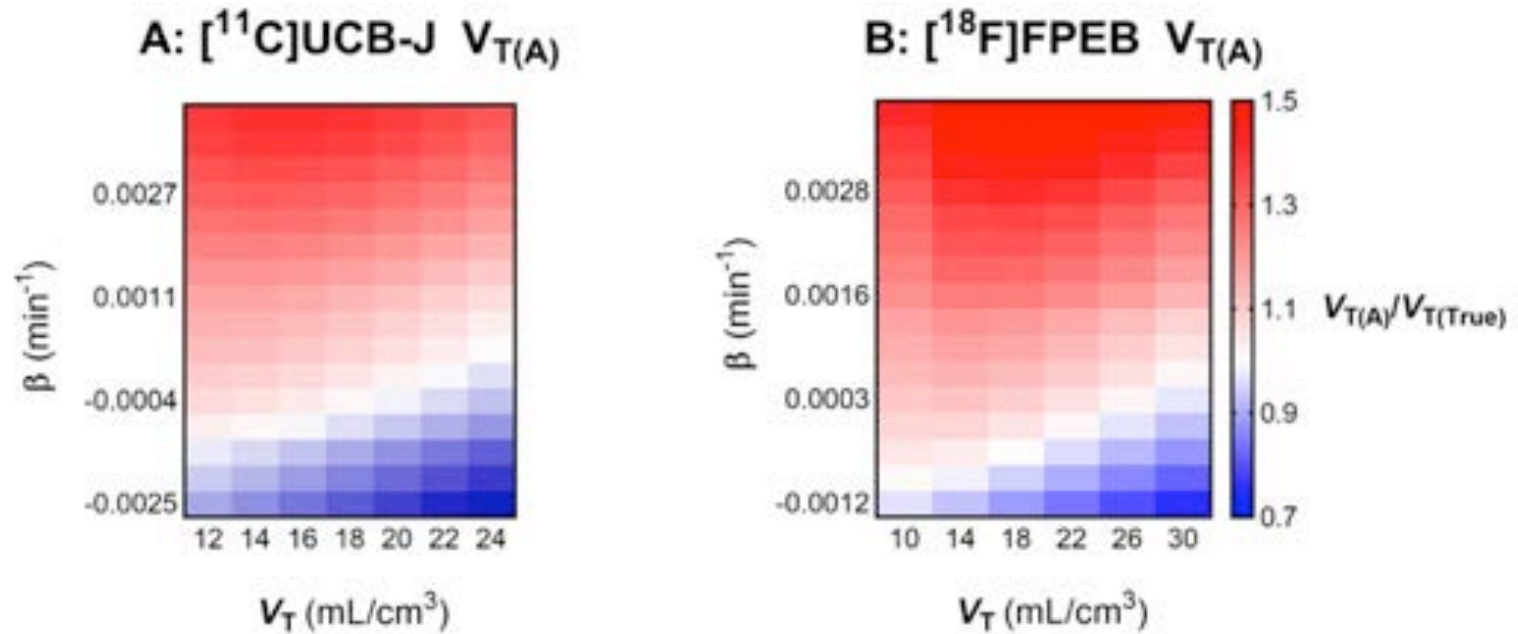
A simple simulation: Faster plasma clearance

$V_{T(A)}$: Apparent volume of distribution

SUVR

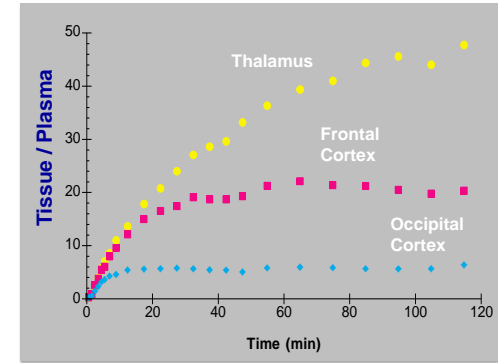


Equilibrium Overshoot Varies with Binding Level as well as Measurement Time



Following a bolus injection...

- The tissue:plasma ratio at transient equilibrium ($V_{T(A)}$) is **greater** than the ratio at equilibrium (V_T)
- The faster the plasma clearance, the greater the difference between $V_{T(A)}$ and V_T
- Regions with higher V_T (typically, the ROI) have a greater bias
- **SUVR** is the ratio of $V_{T(A)}$ of the ROI to $V_{T(A)}$ of the reference region
- So **SUVR** at transient equilibrium, is positively biased with respect to **DVR**.
 - Maybe a little, maybe a lot...
- But, higher binding regions take longer to reach transient equilibrium
- We can “help” by scanning earlier, before transient equilibrium is achieved




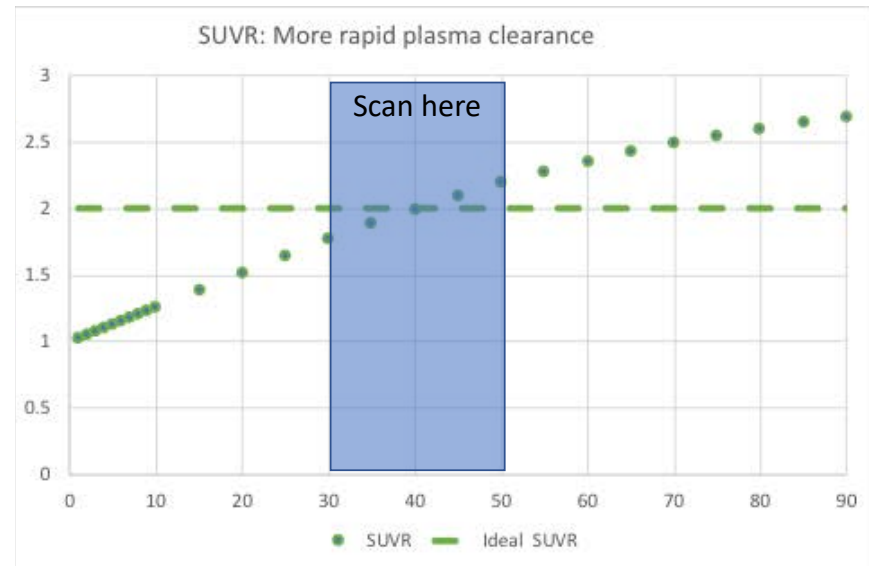
Can two “wrongs” make a right?

- If we wait until transient equilibrium is achieved, **SUVR** will overestimate **DVR**
- If we scan “too early”, we can get the right answer...

- Any imaging scenario with **SUVR = DVR** has 2 factors that cancel each other out

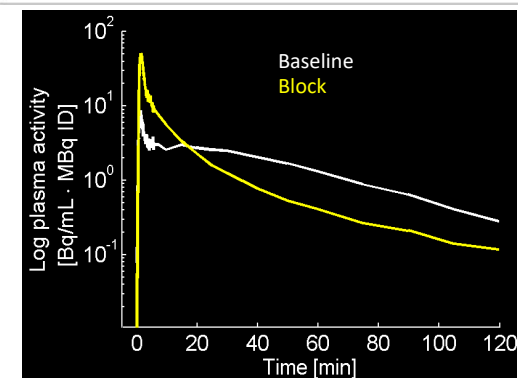
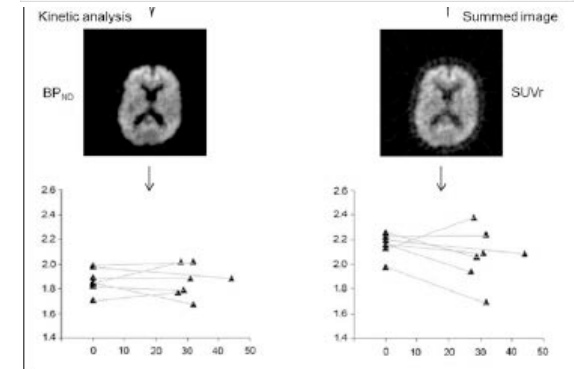
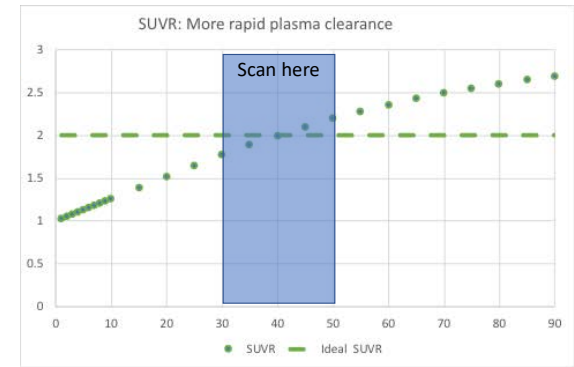
- Transient equilibrium 

- Scanning early 



What could possibly go wrong?

- Will we always get the timing right so that the two effects cancel out?
- “Optimal” time depends on the magnitude of tracer binding
 - Best time varies with extent of disease
- Interindividual variation in tracer plasma clearance
 - Age
 - Sex
- Does drug treatment affect plasma clearance of tracer?

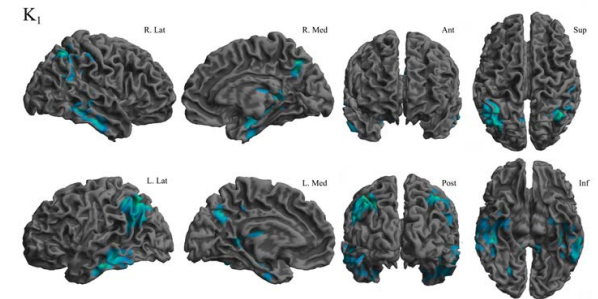


Closing Thoughts

- Modeling methods permit us to measure many aspects of physiology and pathology *in vivo* with great accuracy.
- Great accuracy may not always be clinically important
- Modeling studies tend to be more complex, so we typically trade accuracy for increased patient numbers (and cost)
- Modeling also helps us develop simpler, more patient-friendly assays.
- The simpler methods come with lots of assumptions that are routinely ignored.

Take-home Messages for Simplified Brain Imaging

- Need well-validated tracers with reliable kinetic models
 - Understand all sources of binding *in vivo*
 - Do these validation studies get the priority they need?
- Use the understanding from a well validated model to optimize each simplified scan protocol
 - So far, we just use models to choose the best time for SUVR measurement
- But, also...
 - Understand the factors that corrupt SUVR
 - Understand the impact of these effects on specific study paradigms
 - Correct them (if needed)
- Don't give up on dynamic scans
 - Automatically correct kinetic effects
 - Provide tracer delivery (flow) information (K_1 , R_1)



Acknowledgments

