Table S1. MSC and AIC for 1 TCM and 2 TCM

	MSC			AIC		
	2TCM	1TCM	p paired t-test	2TCM	1TCM	p paired t-test
Cerebellar ctx	4.7±2.2	2.6±1.4	3.90E-10	-196.4±16.4	-128.7±16.0	3.90E-10
Temporal ctx	5.8±2.6	2.9±1.6	4.80E-10	-224.7±23.1	-133.6±19.2	4.80E-10
Prefrontal ctx	5.6±2.6	3.1±1.7	4.90E-08	-216.4±26.7	-137.7±20.7	4.90E-08
Caudate head	4.2±2.1	3.8±1.9	1.50E-03	-160.2±13.4	-147.3±14.5	1.50E-03
Putamen	4.7±2.2	3.6±1.8	4.70E-06	-174.6±16.9	-141.5±19.0	4.70E-06
Thalamus	4.5±2.3	3.6±1.9	2.00E-06	-169.9±12.6	-140.1±14.6	2.00E-06
Ant cingulate ctx	4.4±2.1	3.3±1.7	6.00E-06	-181.8±18.5	-146.4±18.3	6.00E-06
Pons	3.9±1.9	3.1±1.7	2.80E-06	-176.9±13.9	-151.1±19.9	2.80E-06

Table S2. Test-retest of total distribution volume (V_T) for different scan lengths. BSSD: between-subject standard deviation WSSD: within-subject standard deviation. CV=%Standard deviation/mean. TRV: the mean across the subjects of the ratio absolute value of the difference between measurements to average of the measurements, ICC: intraclass correlation coefficient

	90 minutes					60 minutes					45 minutes				
	Mean	BSSD (%CV)	WSSD (%CV)	TRV±SD (%)	ICC	Mean	BSSD (%CV)	WSSD (%CV)	TRV±SD (%)	ICC	Mean	BSSD (%CV)	WSSD (%CV)	TRV±SD (%)	ICC
Cerebellar ctx	22.4	5.3(23)	2.0(9)	11± 7	0.739	22.6	5.0(22)	2.5(11)	14± 9	0.603	22.5	4.3(19)	3.0(13)	16±10	0.345
Temporal ctx	33.3	5.4(16)	3.4(10)	12± 9	0.438	33.3	5.3(16)	3.6(11)	13± 9	0.365	32.8	5.0(15)	3.7(11)	14± 9	0.306
Prefrontal ctx	33	4.7(14)	3.2(10)	11± 9	0.379	33	4.5(13)	3.6(11)	13± 9	0.22	33	4.1(12)	3.7(11)	13±10	0.106
Caudate head	59.2	11.8(20)	7.4(12)	15± 6	0.442	79.9	83.2(104)	79.0(99)	34±47	0.052	62.3	16.8(27)	15.5(25)	22±22	0.079
Putamen	52.2	9.5(18)	5.8(11)	13± 9	0.457	52.8	11.1(21)	7.4(14)	17±11	0.383	51.8	9.0(17)	7.6(15)	19± 8	0.162
Thalamus	55.2	9.1(16)	4.4(8)	10± 7	0.615	56.5	9.1(16)	5.1(9)	12± 6	0.519	57.5	8.5(15)	9.4(16)	20±10	-0.099
Ant cingulate ctx	40.2	7.0(17)	4.3(11)	13±10	0.445	39.8	7.3(18)	4.9(12)	14±12	0.376	40.7	8.9(22)	7.7(19)	23±12	0.14
Pons	33.4	11.1(33)	3.1(9)	11± 9	0.856	34.7	13.1(38)	3.8(11)	12±13	0.842	34.9	12.1(35)	3.8(11)	14± 9	0.824

Table S3. Test-retest of total distribution volume (V_T) for Logan Graphical method using t*=7.75 min and 90 minutes of data. Same nomenclature as in table 2

	Mean	BSSD (%CV)	WSSD (%CV)	TRV±SD (%)	ICC
Cerebellar ctx	21.7	5.2(24)	1.7(8)	10±7	0.805
Temporal ctx	32.8	5.2(16)	3.2(10)	11±9	0.456
Prefrontal ctx	32.6	4.9(15)	2.9(9)	11±7	0.472
Caudate head	55.2	12.3(22)	6.8(12)	15±8	0.531
Putamen	50.7	9.5(19)	5.5(11)	13±8	0.497
Thalamus	53.1	8.9(17)	3.9(7)	10±6	0.678
Ant cingulate ctx	39.1	6.5(17)	3.8(10)	12±8	0.501
Pons	31.2	10.1(32)	3.0(10)	12±9	0.84

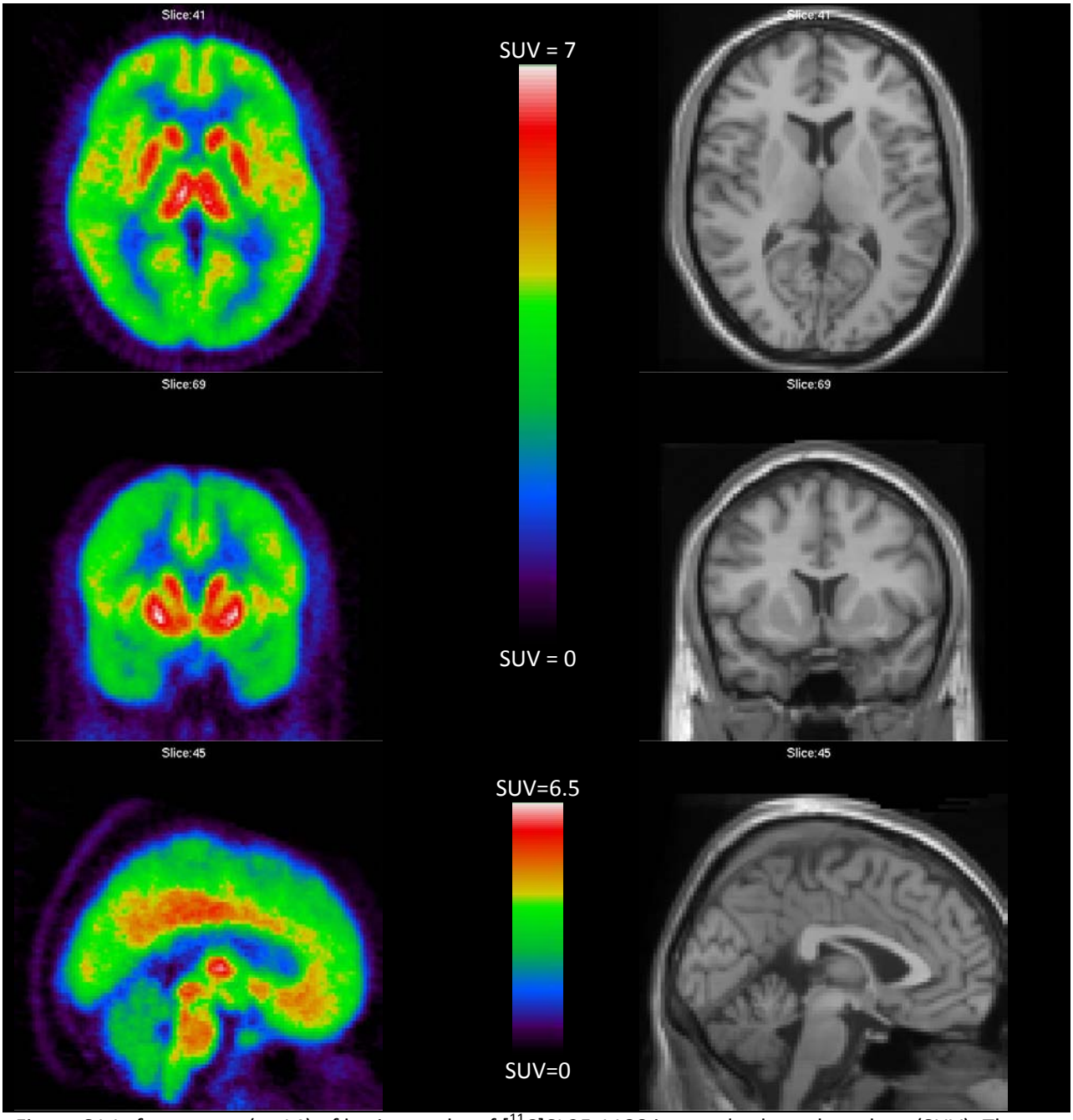

Figure S1.Left: average (n=14) of brain uptake of [^{11}C]SL25.1188 in standard uptake values (SUV). The images were normalized to the MNI/ICBM space. Right: Single subject MRI in the same standard space for anatomical reference. In the top axial view 14 mm superior to anterior commissure (AC), middle: +6 mm anterior to the AC, bottom: interhemisphere plane.

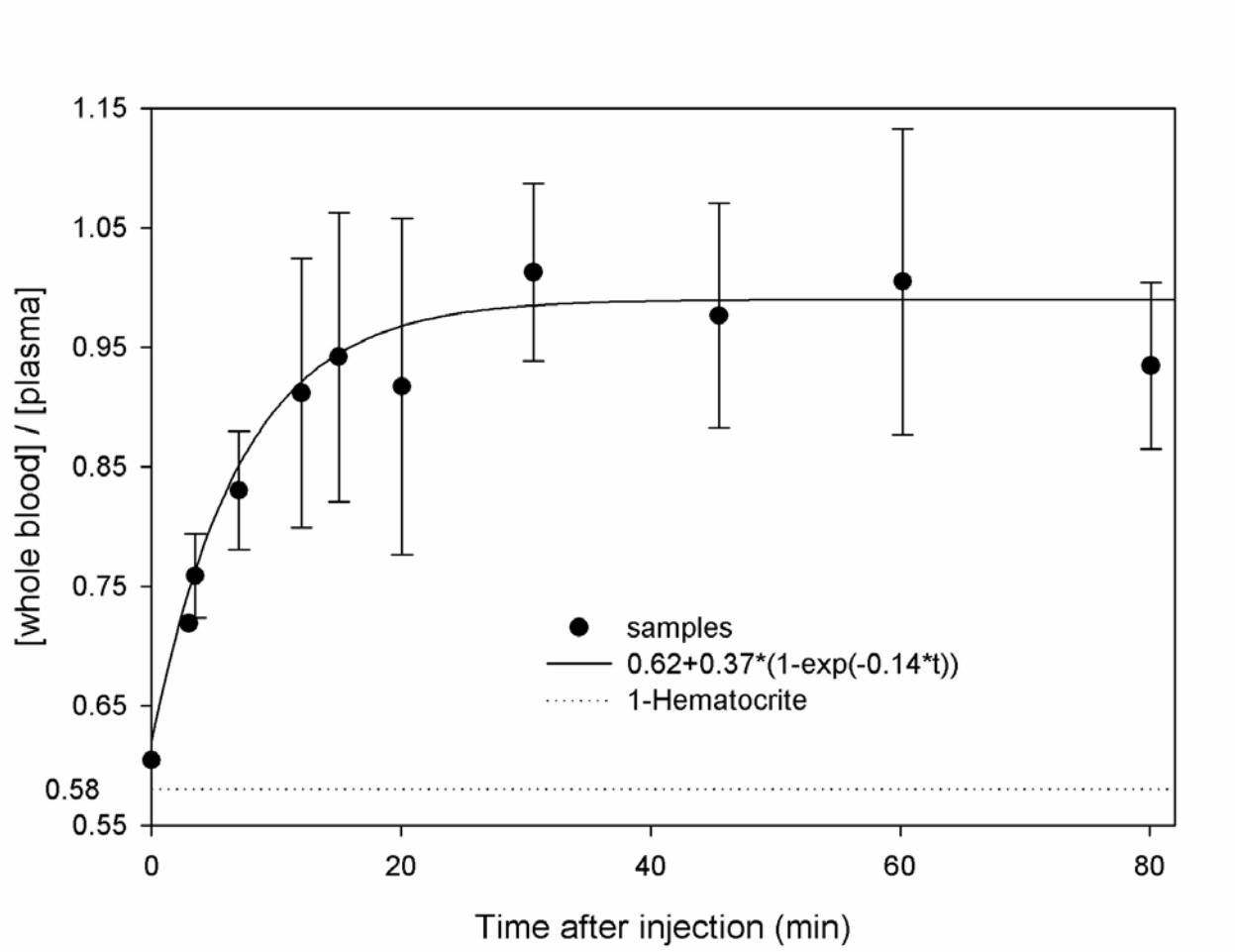

Figure S2. Temporal evolution of the ratio radioactivity in whole blood to plasma. Dark circles after 3 minutes represent discrete samples (mean±SD) for 14 scans (7 subjects scanned twice). Sample at t=3 is based in a single scan. Sample at t=0 is an in vitro measurement in a single subject. The solid line is a monoexponential function using the average (n=14) coefficients from the best fit for each scan data. The intercept is close to the value (1-hematocrit) showed as the dotted horizontal line.

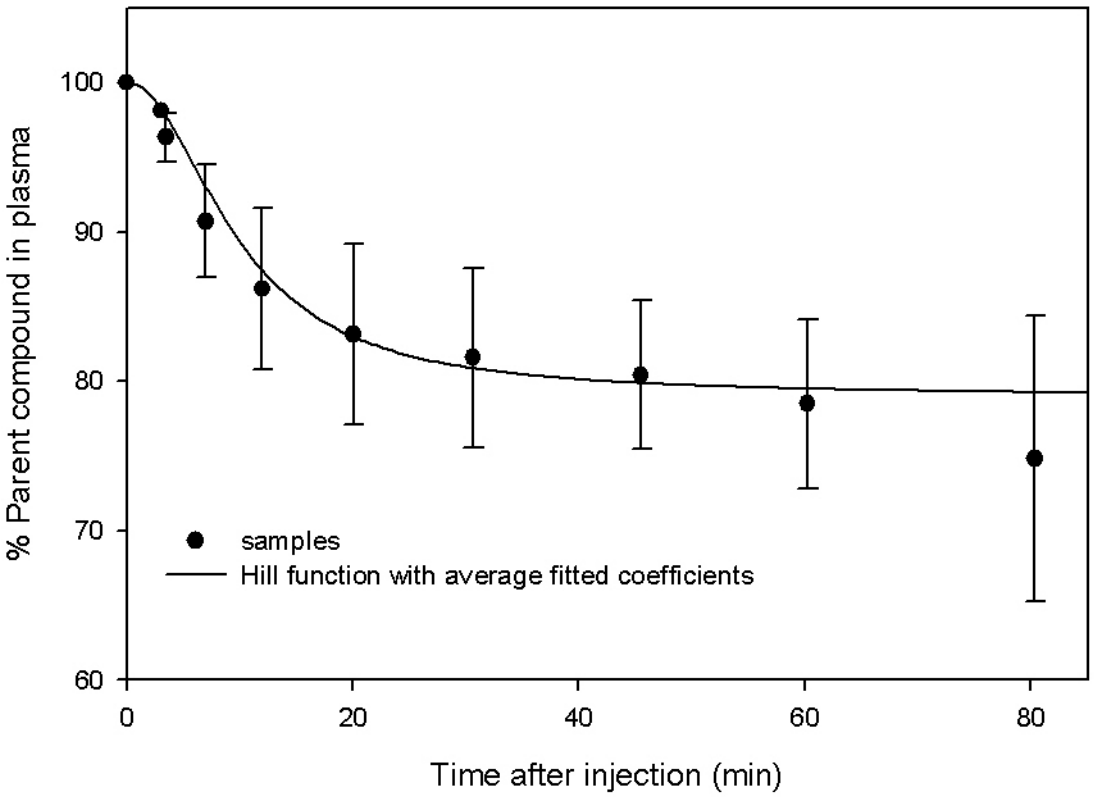

Figure S3. Temporal evolution of the fraction of parent compound in plasma determined by Reverse-phase radiochromatogram. Dark circles after 3 minutes represent discrete samples (mean±SD) for 14 scans (7 subjects scanned twice). Sample at t=3 is based in a single scan. It is assumed that at time of injection (Sample at t=0) all the radioactivity is parent compound. The solid line represents is a hill function using the average (n=14) coefficients from the best fit for each scan data.

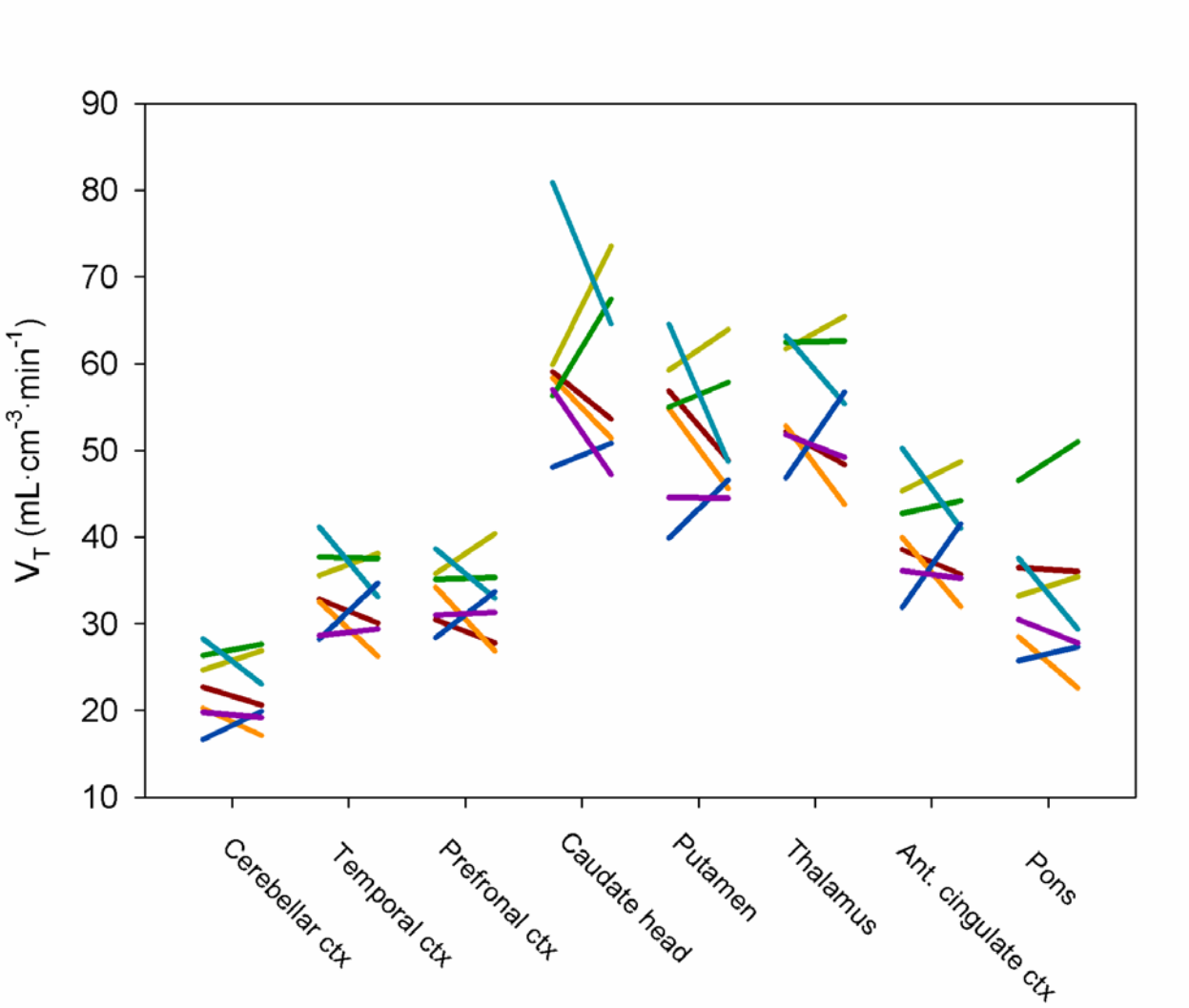

Figure S4. Total distribution volume (V_T) test retest value for each one of the seven subjects (identify by a color) and each region of interest. V_T was calculated using the 90 minutes data.

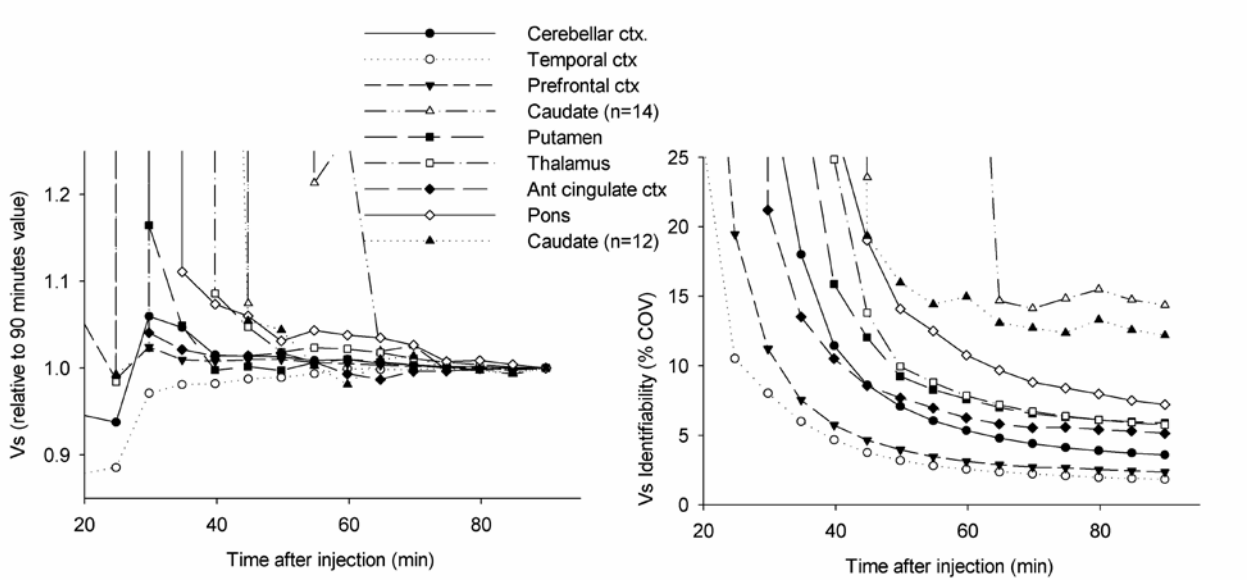

Figure S5. Regional average convergence of V_S to the final value at 90 min. For all the regions the 14 scans are considered. For the caudate an average of 12 scans are shown as 2 TACs gave solutions with low identifiability for a length of scan below 70 min.

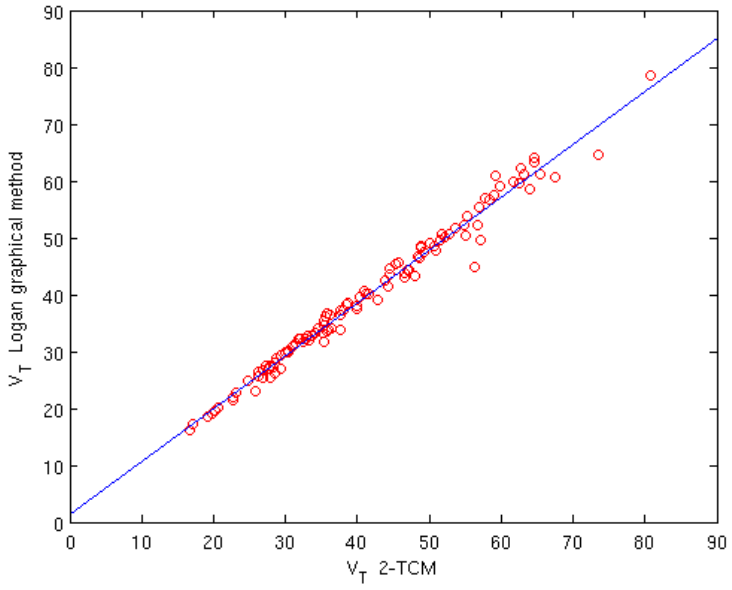

Figure S6. Correlation between total distribution volume (V_T) estimated with the 2 tissue compartment model (2-TCM) and Logan graphical method using t*=7.75 min. (r^2 =0.98)

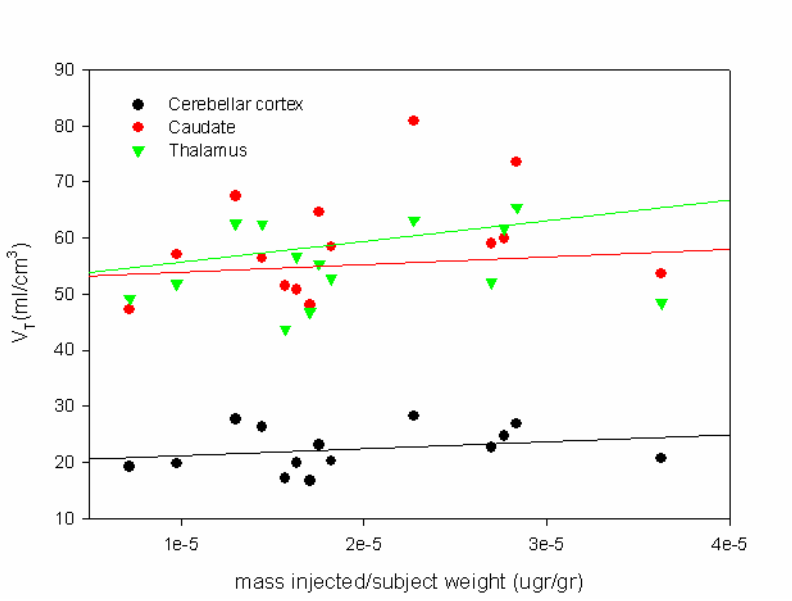

Figure S7. No correlation was observed between total distribution volume (V_T) and mass injected.

Simulation Study to show properties of the deconvolution algorithm used.

A rectangular shape bolus was simulated as one ideally injected with an infusion pump for 1 minute: activity of 100 units between 10 and 70 seconds. Grid of 1 second for 5400 sec. (line in black in figures S8, S9, S10)

The bolus was convolved with a monoexponential $d(t) = \frac{1}{\tau} e^{-t/\tau}$ with a dispersion constant $\tau = 10\,\text{sec}$ to simulate the curve measured by the ABSS (line in red in figures S8, S9, S10).

Scripts were run in Matlab 7.11.

1. **Noise free.**

The iterative algorithm described in the section "method" in the paper was applied with 10, 30 and 300 iterations. (Figure S8)

Conclusion: when more iterations are applied, the shape of the deconvolved data is closer to the original. Low number of iterations attenuates some high frequency components smoothing the borders of the rectangular shape.

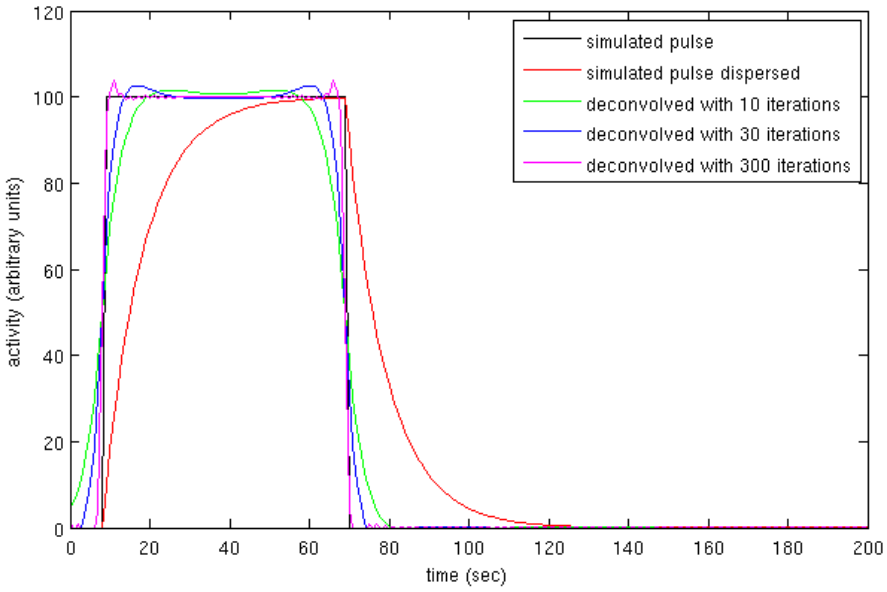

Figure S8. Dispersion correction as a function of number of iteration of the iterative deconvolution algorithm on noise free data

2. Presence of noise.

This example illustrates the noise propagation with the number of iterations

Two kind of noise were tested:

1) A Gaussian noise with standard deviation of 2 activity units was added to the convolved curve (red curve, simulating ABSS measured data). Figure S9.

2) A Gaussian noise with standard deviation of 2 activity units plus a Gaussian noise with standard deviation of 5% of the noise-free activity was added to the convolved curve (red curve, simulating ABSS measured data). Figure S10.

Conclusion: In the presence of noise too many iteration (e.g. 300) amplify the noise during the deconvolution. Too little iterations (e.g. 10) attenuate the high frequencies too much. 30 iterations show a good compromise to recover the original shape.

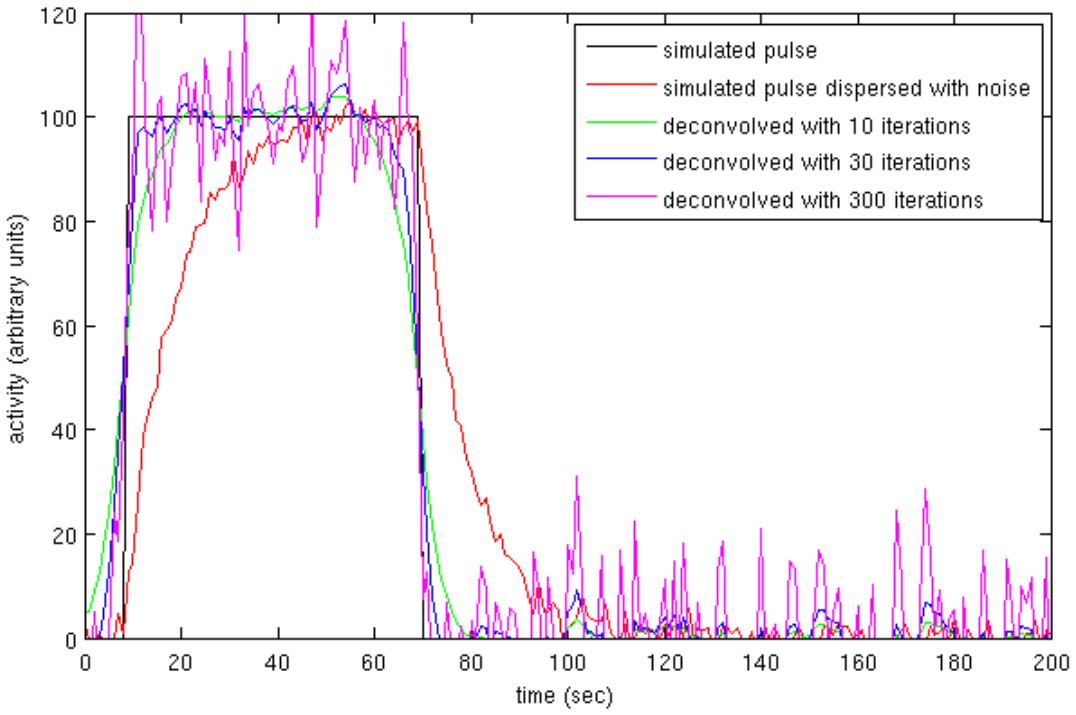

Figure S9. Dispersion correction as a function of number of iteration of the iterative deconvolution algorithm on data with Gaussian noise independent of the activity value.

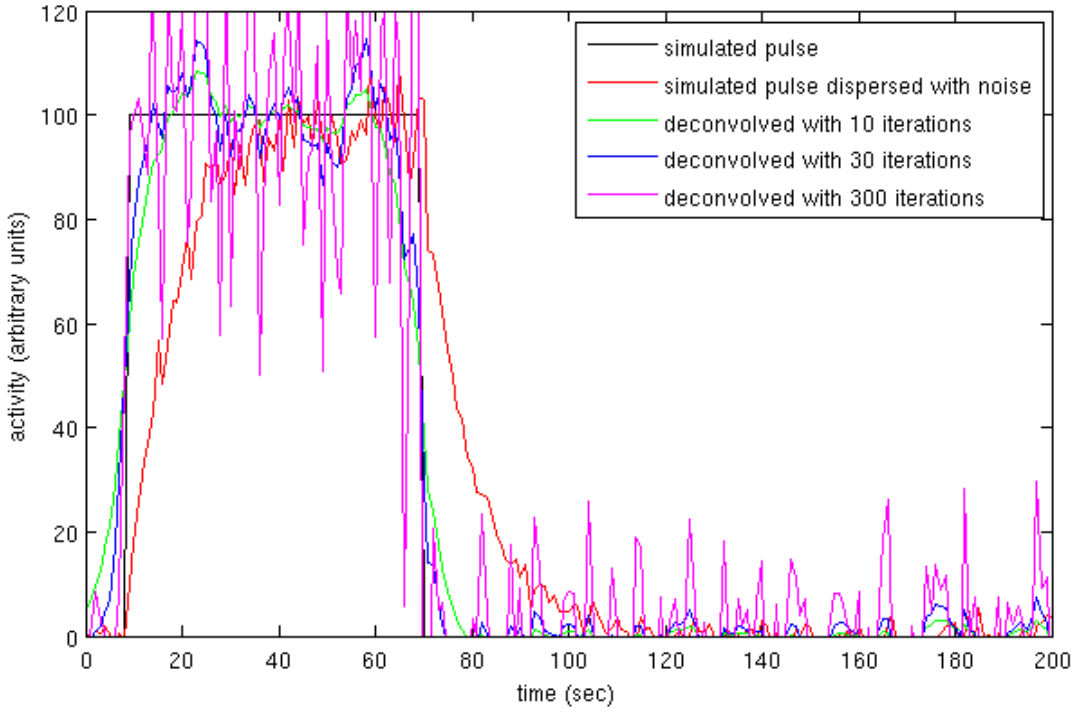

Figure S10. Dispersion correction as a function of number of iteration of the iterative deconvolution algorithm on data with Gaussian noise dependent plus independent of the activity value (see text).

3. Real data

Figure S11 illustrates the algorithm in real data (single subject) using 30 iterations ($\tau = 10\,\mathrm{sec}$) which shows a good tradeoff between filtering noise and keeping high frequencies. (Figure S11). The exponential convolution of the dispersion corrected curve makes complete overlap with the original data.

Figure S12 illustrate the average input function (n=14) with dispersion correction and without dispersion correction.

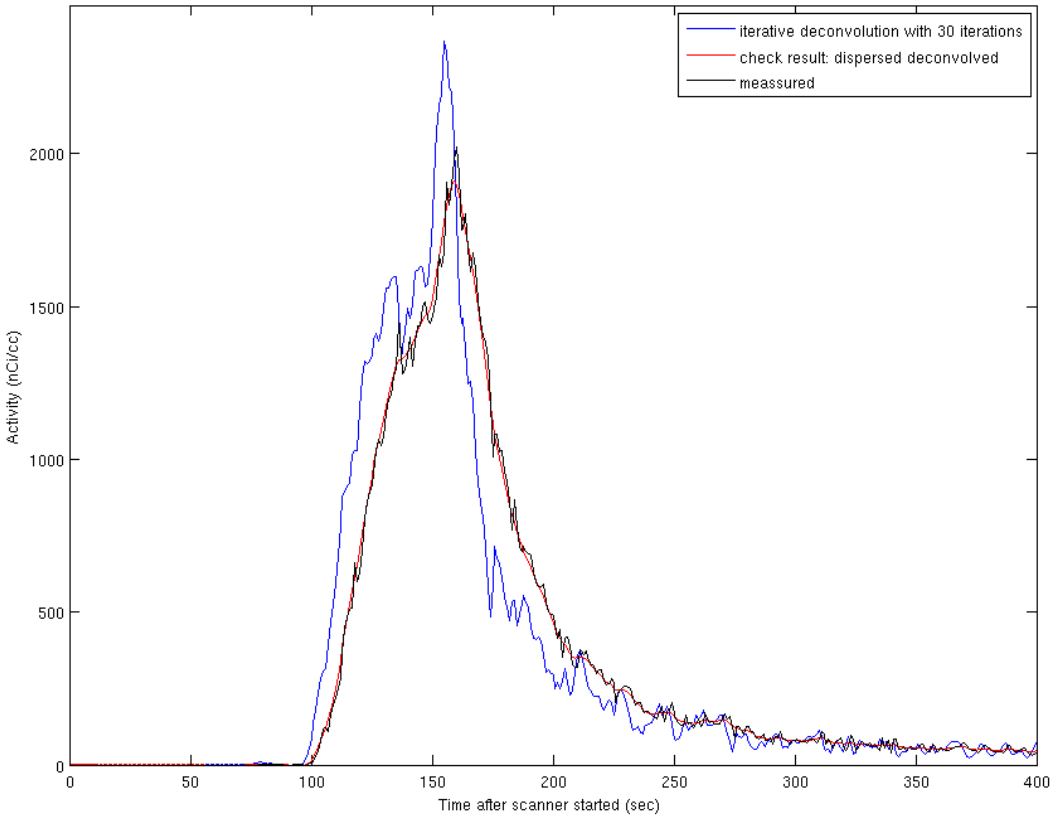

Figure S11. The black curve is the ABSS data measure and preprocessed (interpolated in a grid of 1 sec for 5400 sec). The blue curve is the deconvolved data (dispersion corrected curve with $\tau = 10\,\mathrm{sec}$). The red curve is a verification of the result: the deconvolved data was convolved again to verify the overlap with the original data.

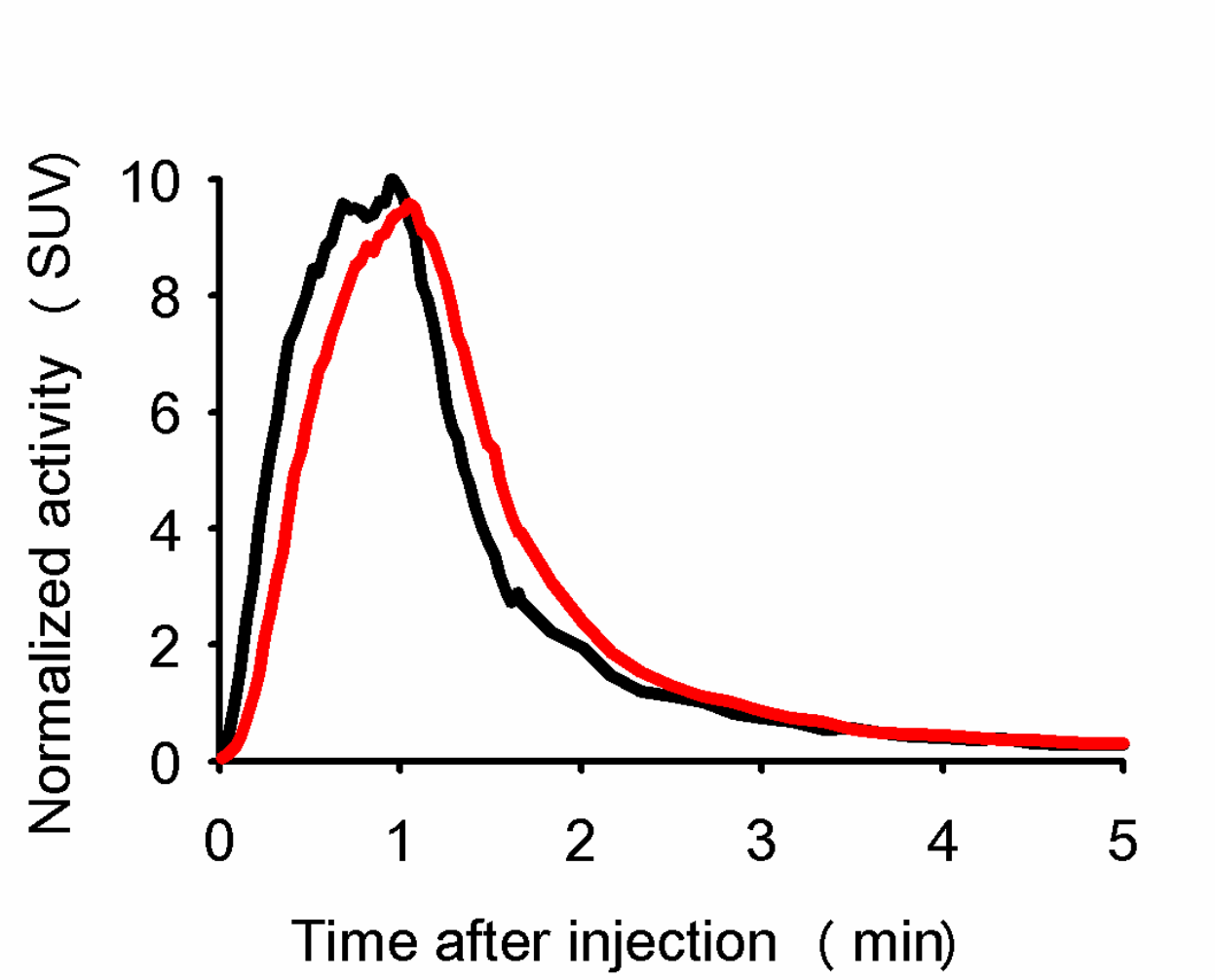

Figure S12. The average input function (n=14) with dispersion correction $\tau = 10\,\mathrm{sec}$ (black) and without dispersion correction (red).