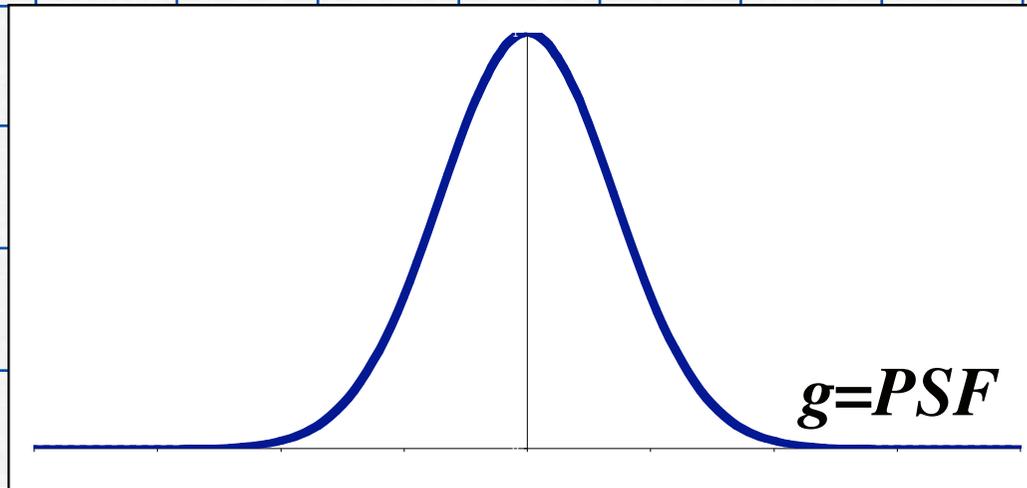


PVEOut

**8th Plenary meeting and
HBM2004 Satellite meeting
Budapest June, 12, 2004**

**A new voxel-based PVE-
correction method developed
inside PVEOut project**

$$PET = C \otimes g$$



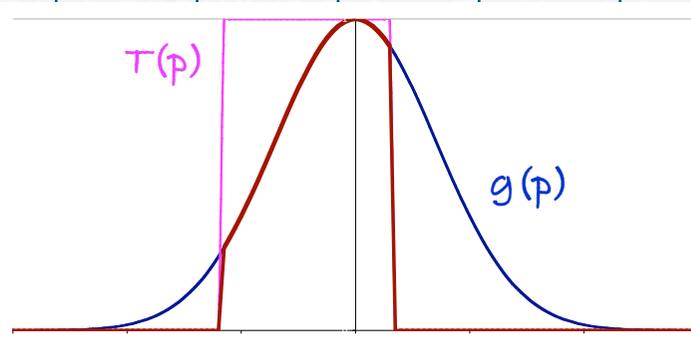
Each point of the radioactivity distribution function C becomes a spot with the shape of the Point Spread Function in the PET.

If C is the radioactivity distribution in the brain, the PET count distribution is:

$$PET(p) = \int_{\text{Volume}} C(\rho) \cdot g(p - \rho) \cdot d\rho + \text{noise}$$

where g (= PSF of scanner) represents the probability function that a point C contributes to PET counts in its neighborhood.

If we know where the tissue is (from segmentation), we have an information which improves the probability function. In fact, locally multiplying $g(p)$ by the function $T(p)$ (equal to 1 where there is tissue and zero otherwise), we obtain a more accurate probability function describing the possible sources of PET counts in p .



PVEOut

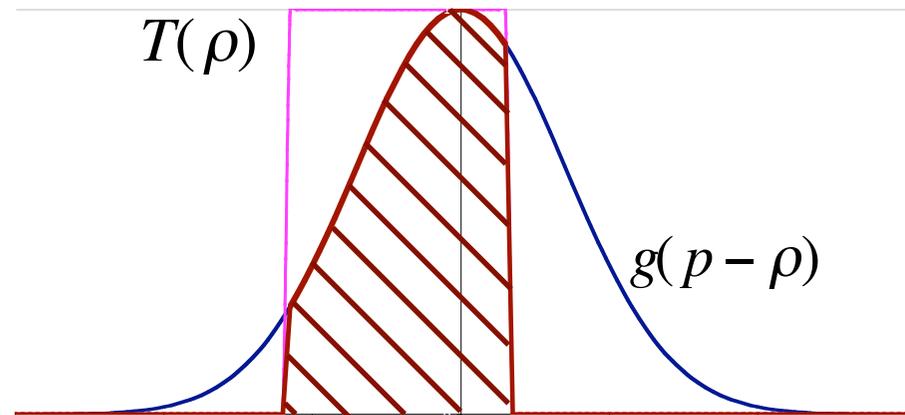
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It can be defined as:

$$g'(p, \rho) = \frac{T(\rho) \cdot g(p - \rho)}{\int_{\text{Volume}} T(\psi) \cdot g(p - \psi) \cdot d\psi}$$

If the denominator is $\neq 0$; $g'(p, \rho) = 0$ otherwise.

It represent the probability
that a PET count in a point p
come from the point ρ .

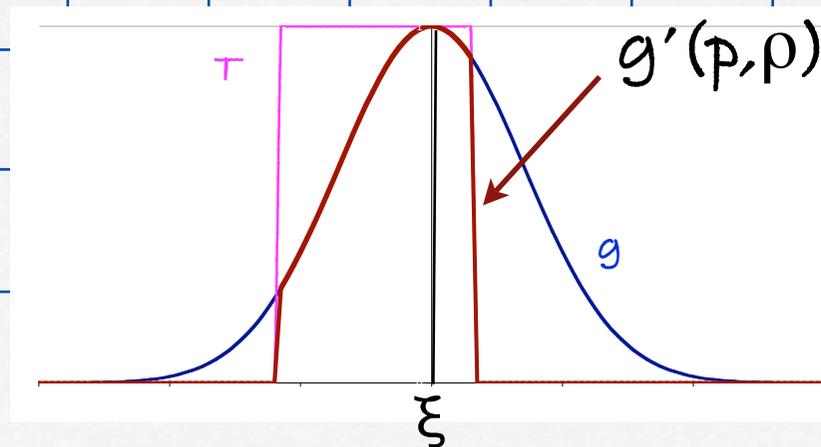


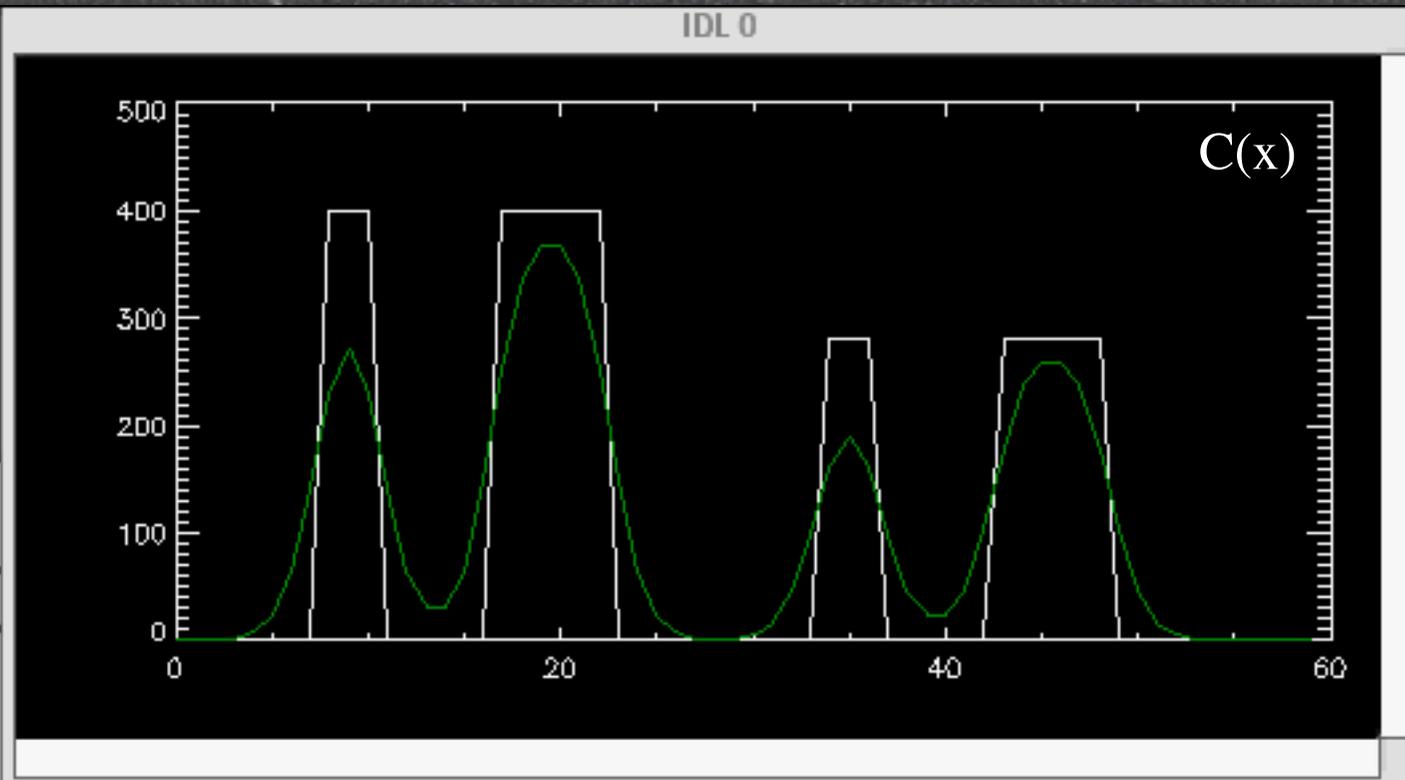
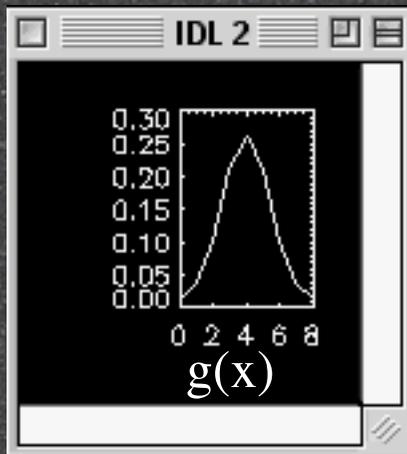
The PVE corrected (recovered) Grey Matter can be calculated as:

$$R_{GMPET}(p) = \int_{Volume} GMPET(\xi) \cdot g'(p, \xi) \cdot d\xi$$

where $GMPET$ represents the distribution of PET counts due to GM alone.

In other words, to reconstruct the activity concentration function C , the proposed algorithm spreads each point ξ of the function PET according to the probability function $g'(p, \rho)$, calculated in the neighbourhood of ξ .





```
Ti=Ti*400.
```

```
TiC = convol(Ti,Gi)
window,2,xsize=128,ysize=
plot,Gi
window,0,xsize=512,ysize=
plot,Ti,yrange=[0,500]
oplot,TiC,color=32768
read,Get
```

```
PET=TiC+randomn(seed,60)
```

```
oplot,PET,color=255
```

```
window,1,xsize=512,ysize=256
```

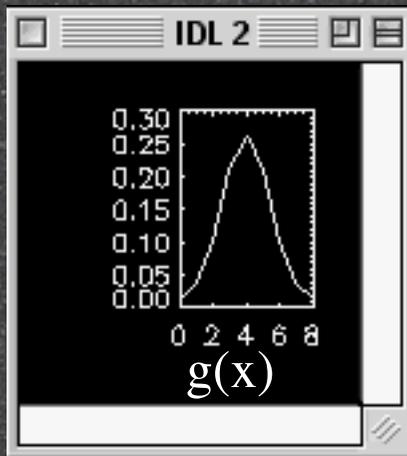
```
; Recuperato Grigia
```

```
spot = fltarr(9)
Cspot = fltarr(9)
recov = fltarr(60)
for i = 4, 55 do begin
    spot=Gi*Ti(i-4:i+4)
    val=total(spot)
    if val GT 0 then begin
        Cspot=spot*PET(i)/val
        recov(i-4:i+4)=recov(i-4:i+4)+Cspot
        plot,recov,yrange=[0,500]
        Cplot=fltarr(60)

        Cplot(i-4:i+4)=Cspot
        oplot,Cplot,color=250
        read,Get
    endif
endif
```

```
endfor
```

```
END
```



```
Ti=Ti*400.
```

```
TiC = convol(Ti,Gi)
window,2,xsize=128,ysize=
plot,Gi
window,0,xsize=512,ysize=
plot,Ti,yrange=[0,500]
oplot,TiC,color=32768
read,Get
```

```
PET=TiC+randomn(seed,60)
```

```
oplot,PET,color=255
```

```
window,1,xsize=512,ysize=256
```

```
;
```

```
spot = fltarr(9)
```

```
Cspot = fltarr(9)
```

```
recov = fltarr(60)
```

```
for i = 4, 55 do begin
```

```
    spot=Gi*Ti(i-4:i+4)
```

```
    val=total(spot)
```

```
    if val GT 0 then begin
```

```
        Cspot=spot*PET(i)/val
```

```
        recov(i-4:i+4)=recov(i-4:i+4)+Cspot
```

```
        plot,recov,yrange=[0,500]
```

```
        Cplot=fltarr(60)
```

```
        Cplot(i-4:i+4)=Cspot
```

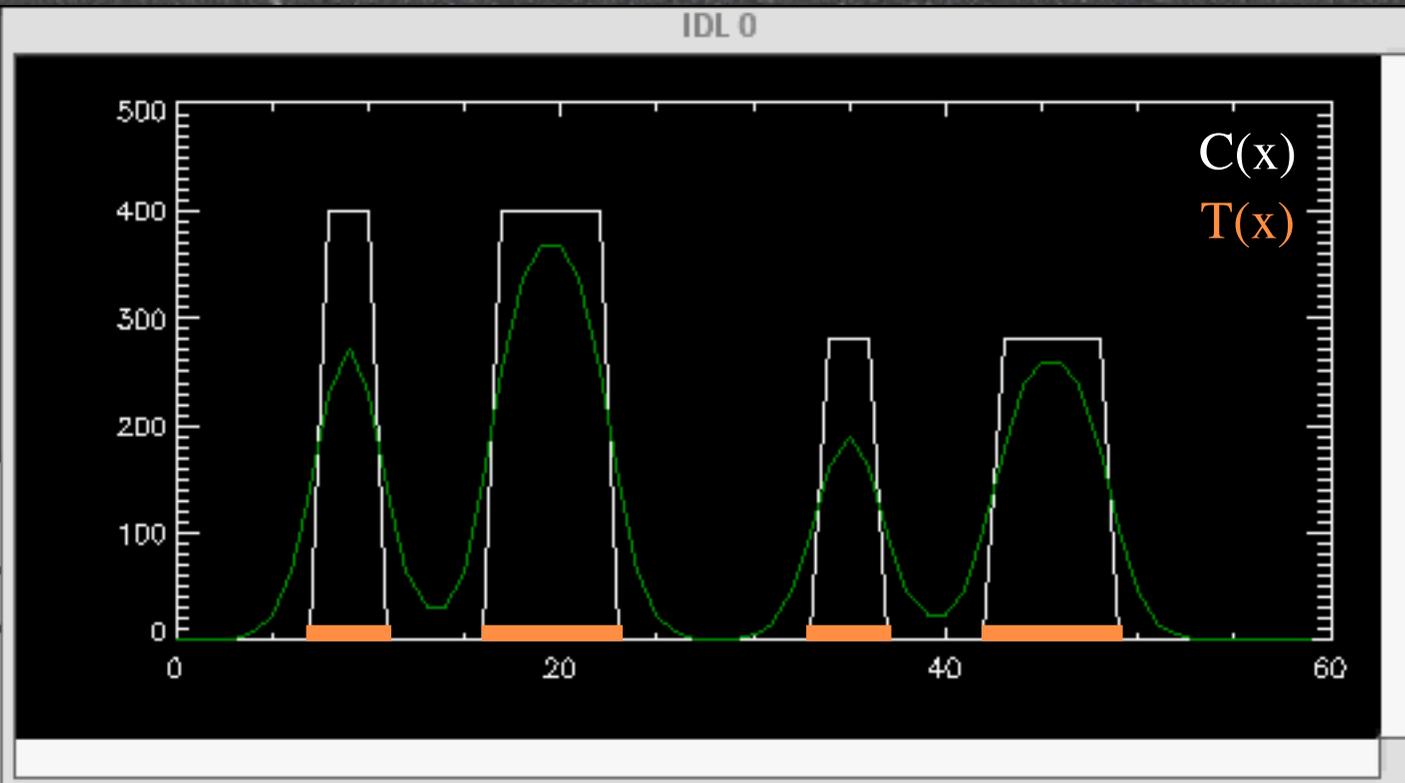
```
        oplot,Cplot,color=250
```

```
        read,Get
```

```
    endif
```

```
endfor
```

```
END
```



Recupero Grigia

IDL 2



```
Ti=Ti*400.
```

```
TiC = convol(Ti,Gi)
window, 2, xsize=128, ysize=128
plot, Gi
window, 0, xsize=512, ysize=512
plot, Ti, yrange=[0, 500]
oplot, TiC, color=32768
read, Gel
```

```
PET=TiC+randomn(seed, 60)
```

```
oplot, PET, color=255
```

```
window, 1, xsize=512, ysize=512
;
spot = fltarr(9)
Cspot = fltarr(9)
recov = fltarr(60)
for i = 4, 55 do begin
    spot=Gi*Ti(i-4:
    val=total(spot)
    if val GT 0 then
        Cspot=s
        recov(i-
        plot, re
        Cplot=f

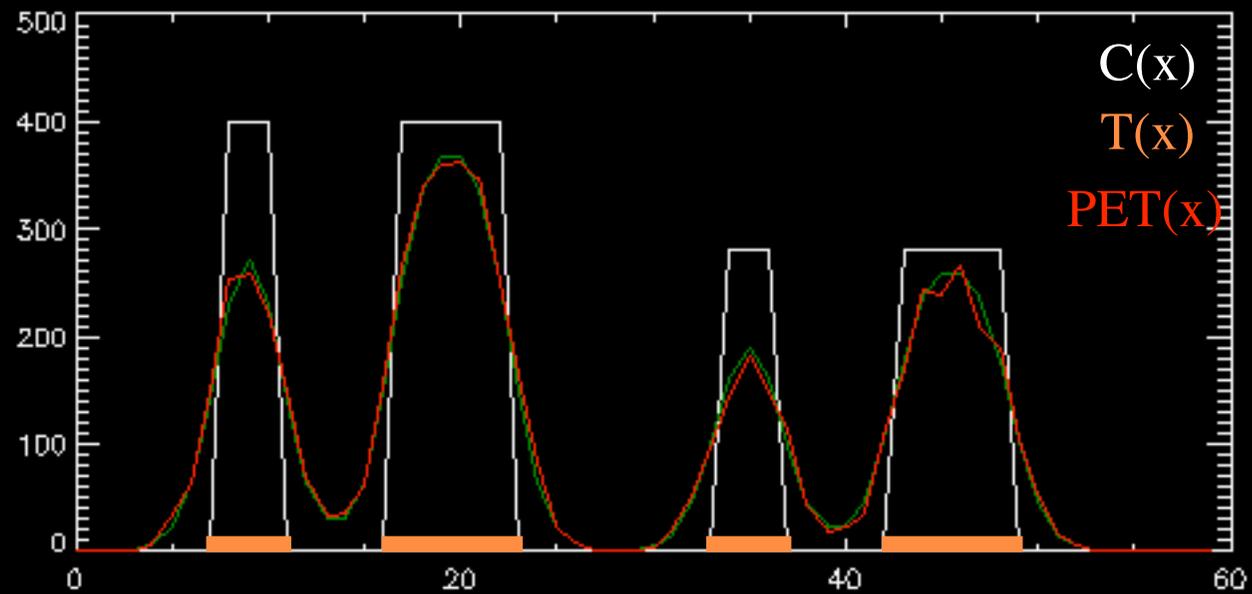
        Cplot(i-
        oplot, C
        read, Gel

    endif
endif
```

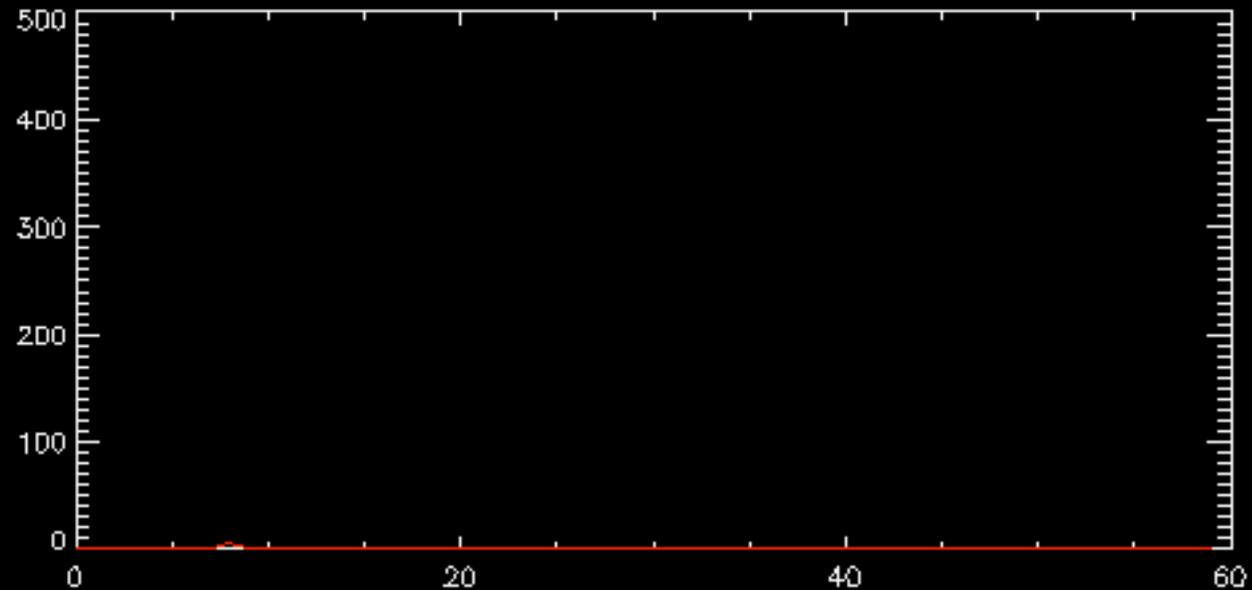
```
endfor
```

```
END
```

IDL 0


 $C(x)$
 $T(x)$
 $PET(x)$

IDL 1



IDL 2



```
Ti=Ti*400.
```

```
TiC = convol(Ti,Gi)
window, 2, xsize=128, ysize=128
plot, Gi
window, 0, xsize=512, ysize=512
plot, Ti, yrange=[0, 500]
oplot, TiC, color=32768
read, Gel
```

```
PET=TiC+randomn(seed, 60)
```

```
oplot, PET, color=255
```

```
window, 1, xsize=512, ysize=512
;
spot = fltarr(9)
Cspot = fltarr(9)
recov = fltarr(60)
for i = 4, 55 do begin
    spot=Gi*Ti(i-4:
    val=total(spot)
    if val GT 0 then
        Cspot=s
        recov(i-
        plot, re
        Cplot=f

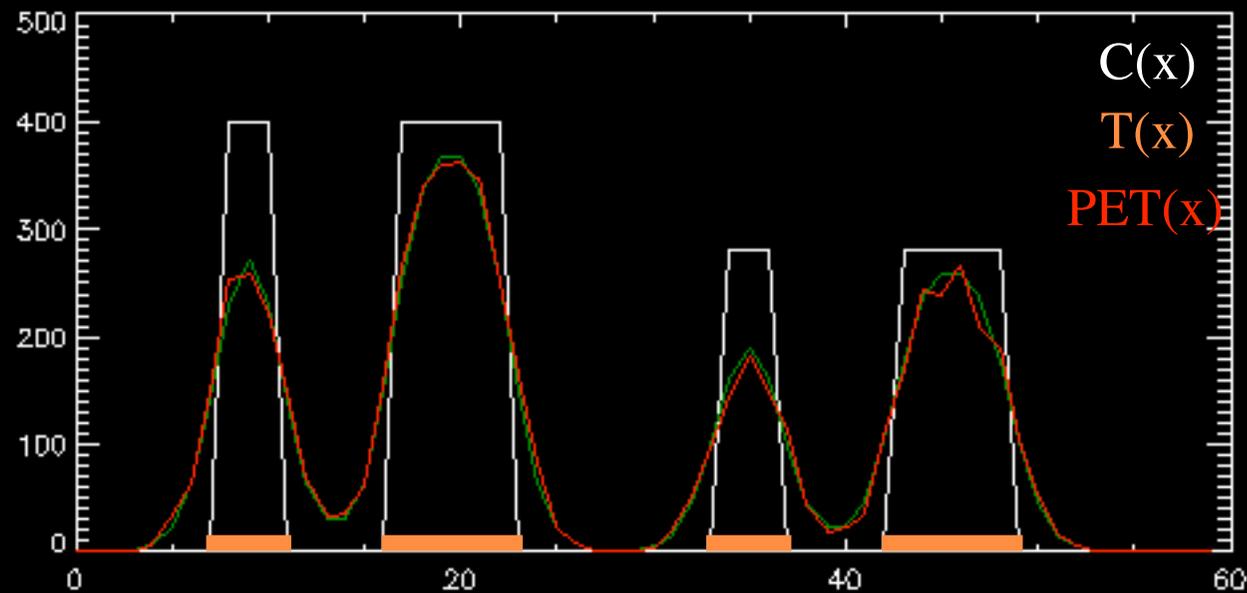
        Cplot(i-
        oplot, C
        read, Gel

    endif
```

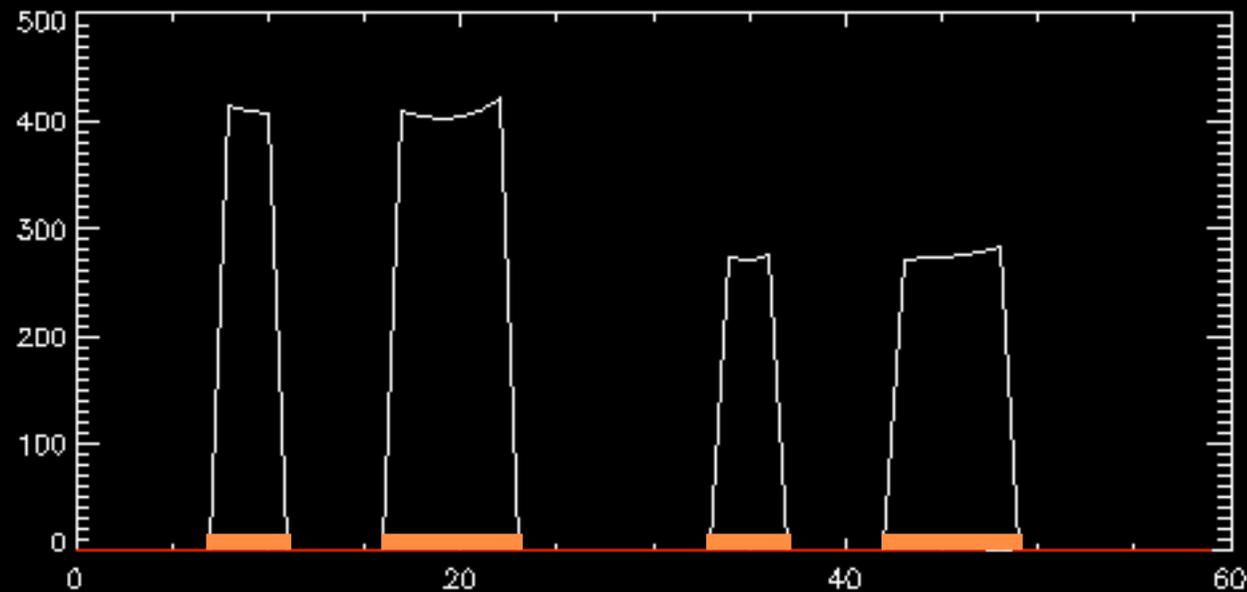
```
endfor
```

```
END
```

IDL 0



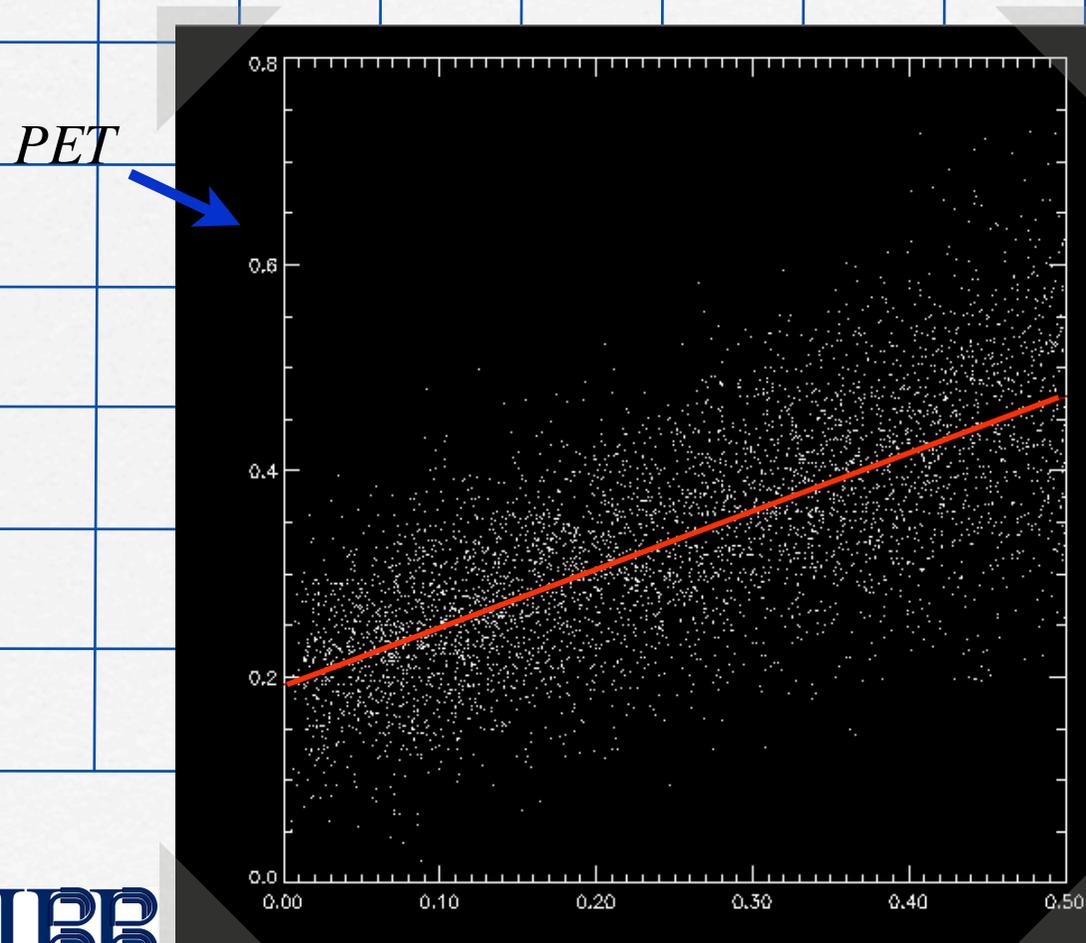
IDL 1



Since the algorithm can operate each time only on one tissue, to apply the method we need:

- Segmented Grey Matter
- Segmented White Matter
- Registered PET
- The Point Spread Function (PSF) of the PET
- A Method for separating GM-PET from WM-PET

WM activity concentration can be estimated:



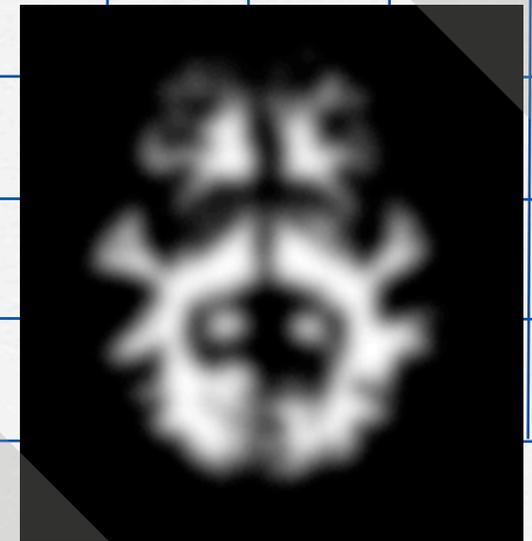
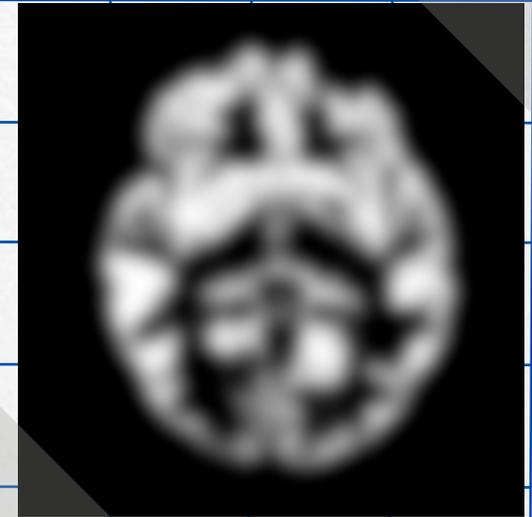
- 1) in Centri semiovali, as proposed by Müller-Gartner;
- 2) using the value calculated with Rousset method;
- 3) from a fitting

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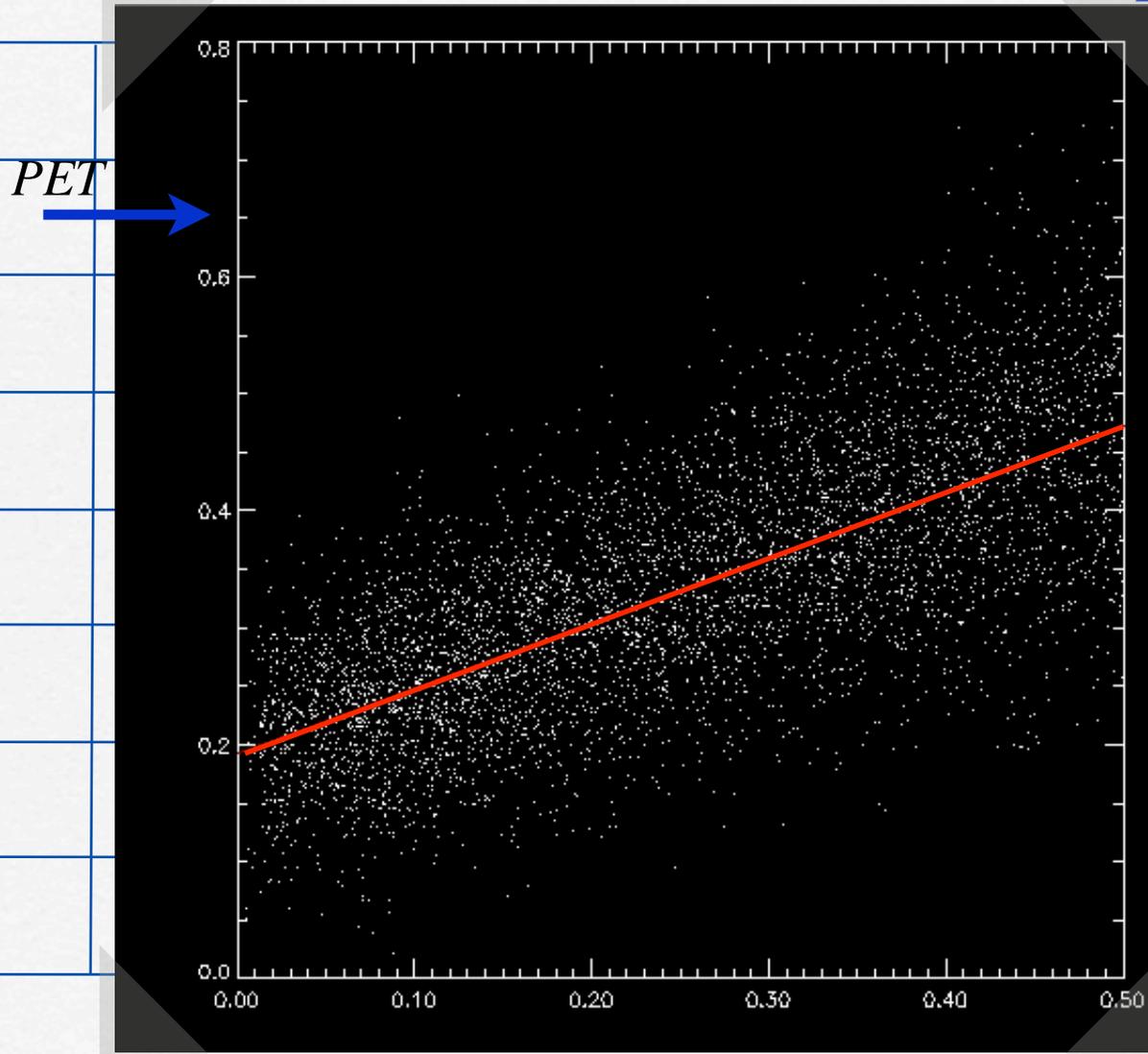
Convoluting the segmented GM
and the segmented WM with
the PSF of the PET, we can
evaluate voxel by voxel the ratio

$$\frac{GM}{GM + WM}$$



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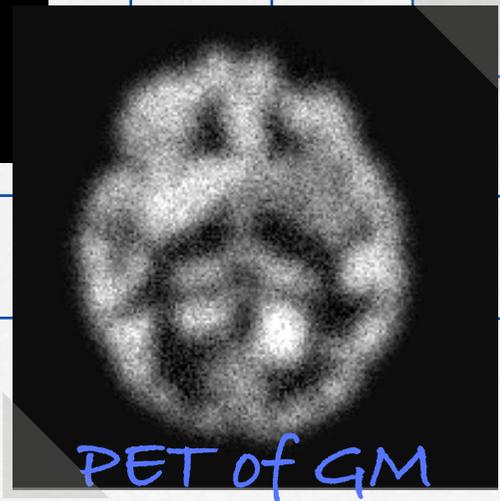
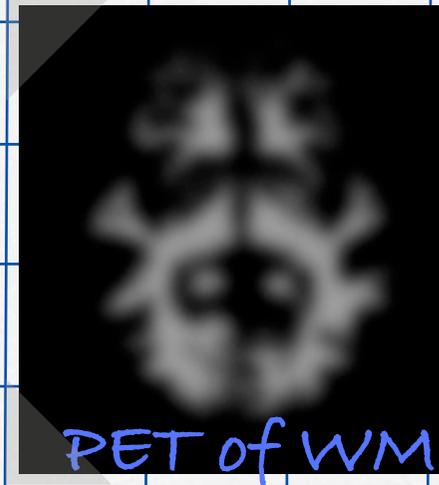
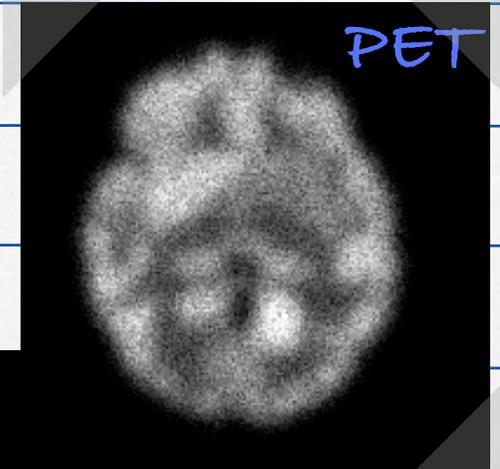
Plotting PET
activity vs. GM
fraction, the
intercept of a fitting
give the estimate of
WM activity
concentration.

$$\frac{GM}{GM + WM}$$

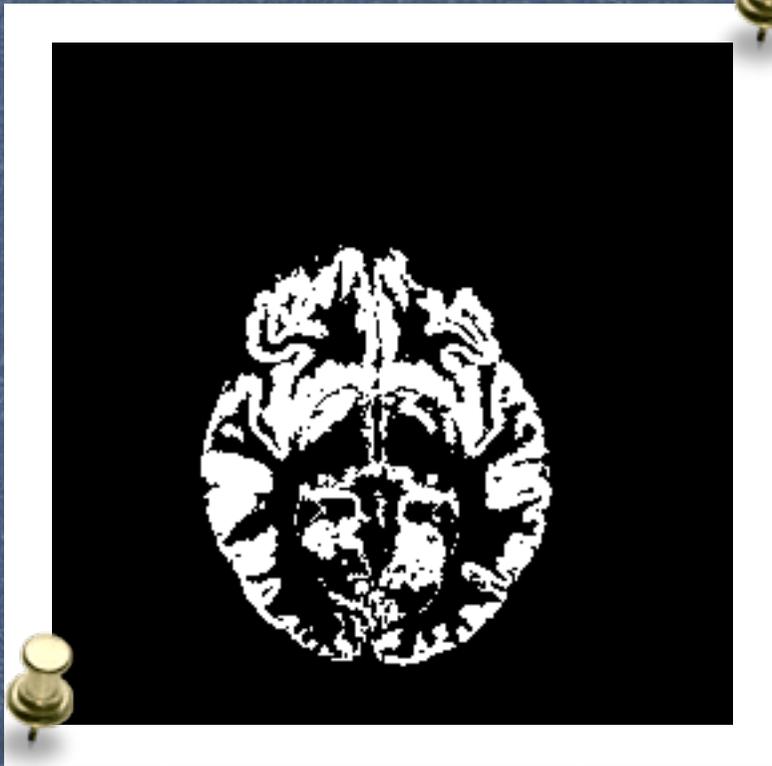
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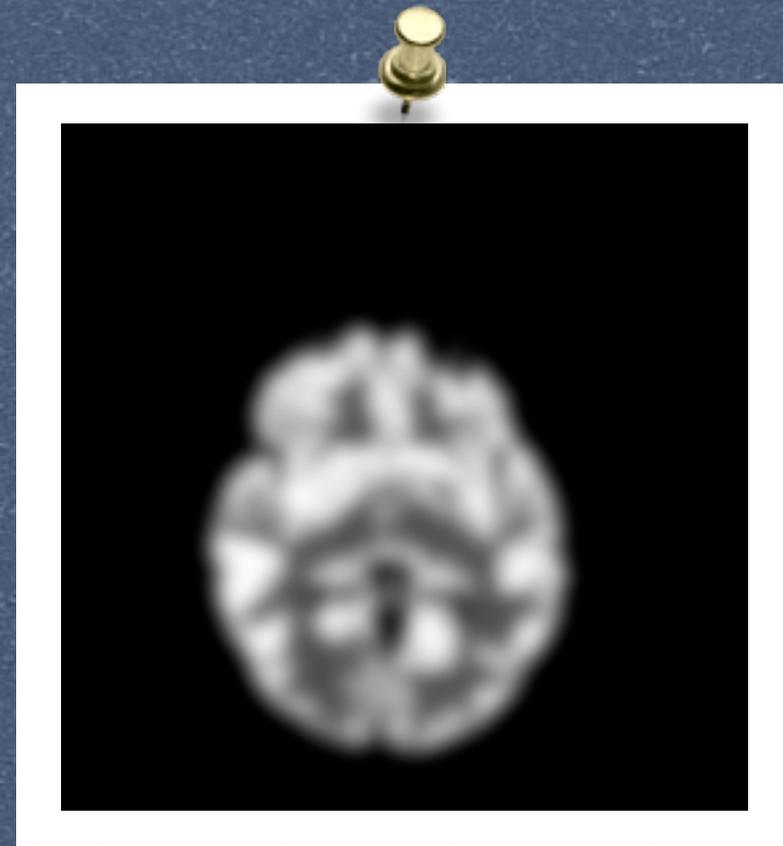
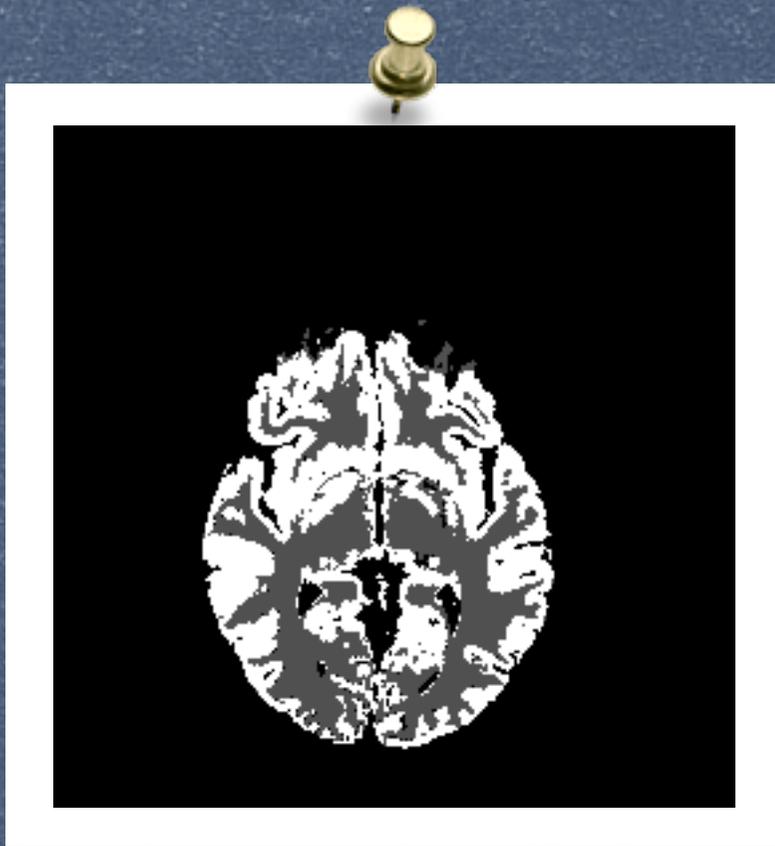
At last, subtracting the scaled convoluted WM from the PET, we separate the contribution of the two tissues to the PET and can apply the PVE correction method separately to GM and WM.



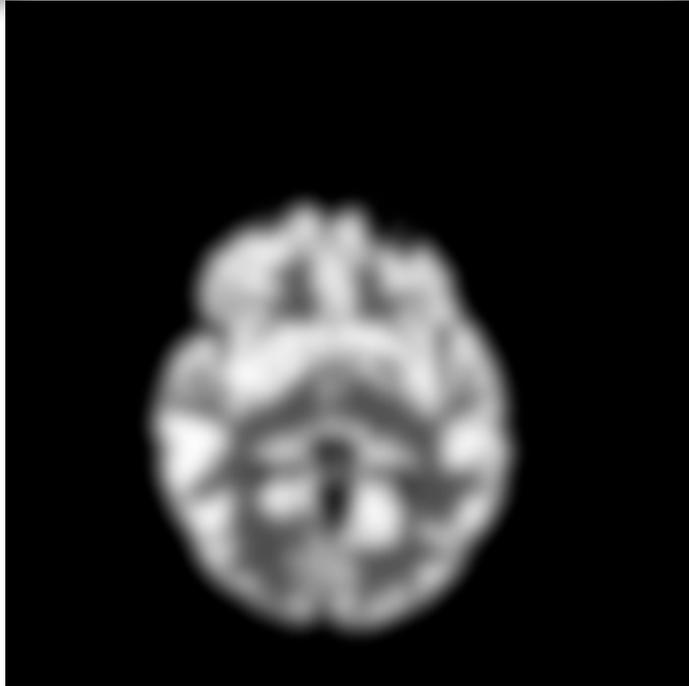
Computer-built phantom



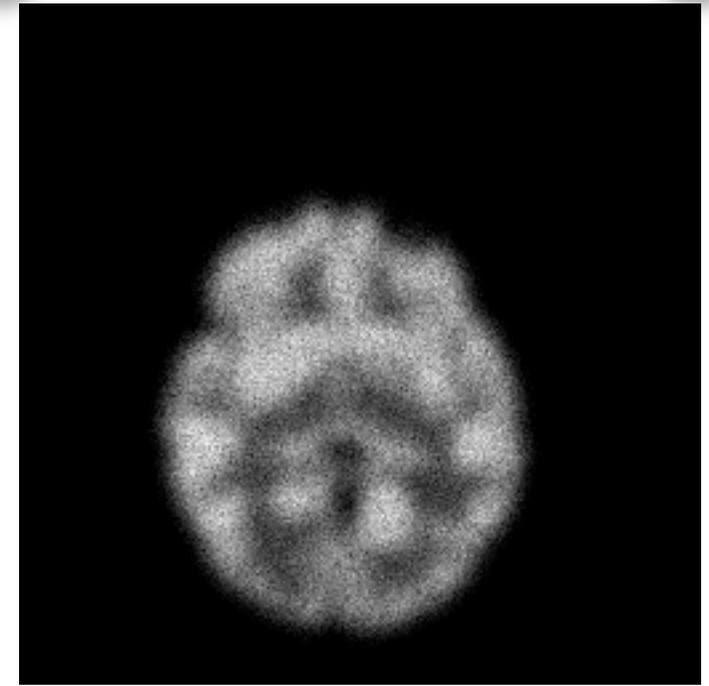
Computer-built phantom



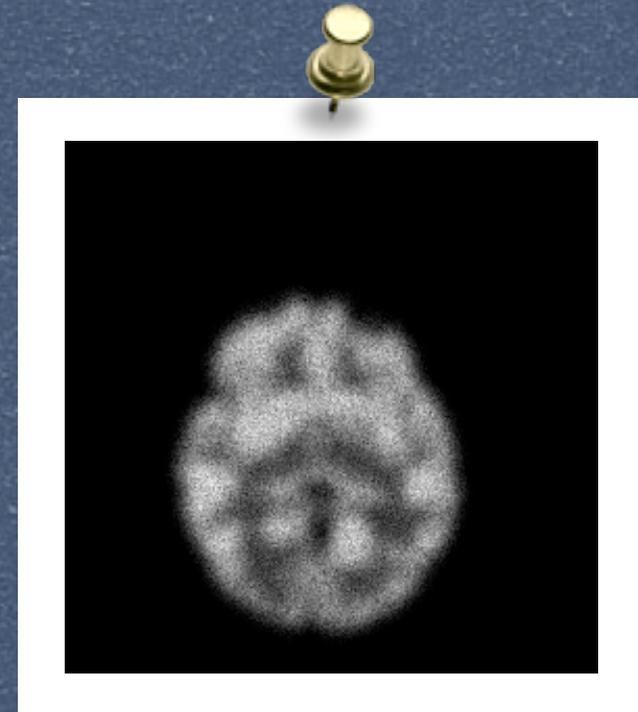
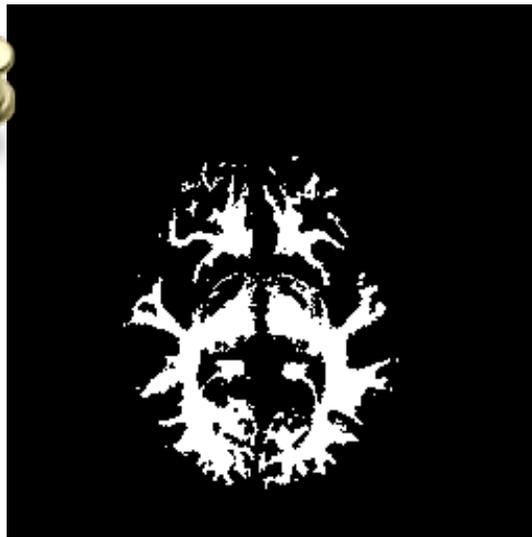
Computer-built phantom



+ noise =

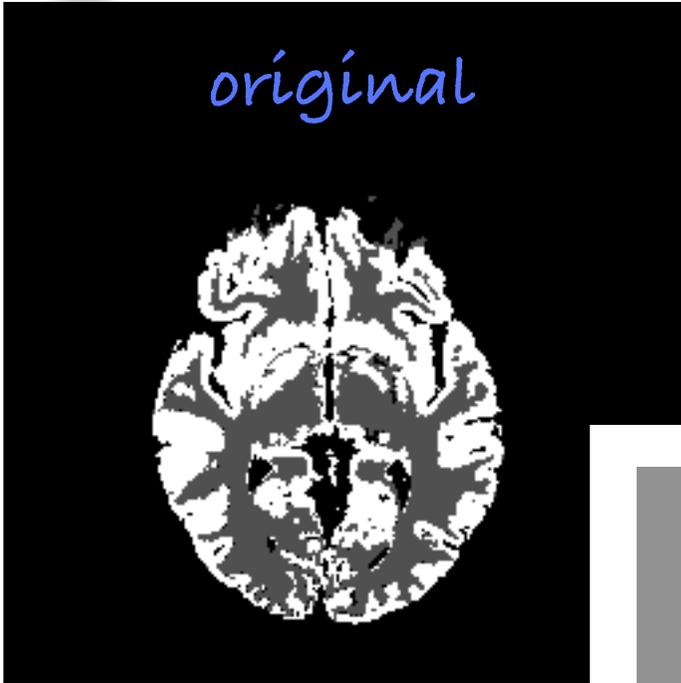


Materials



Results

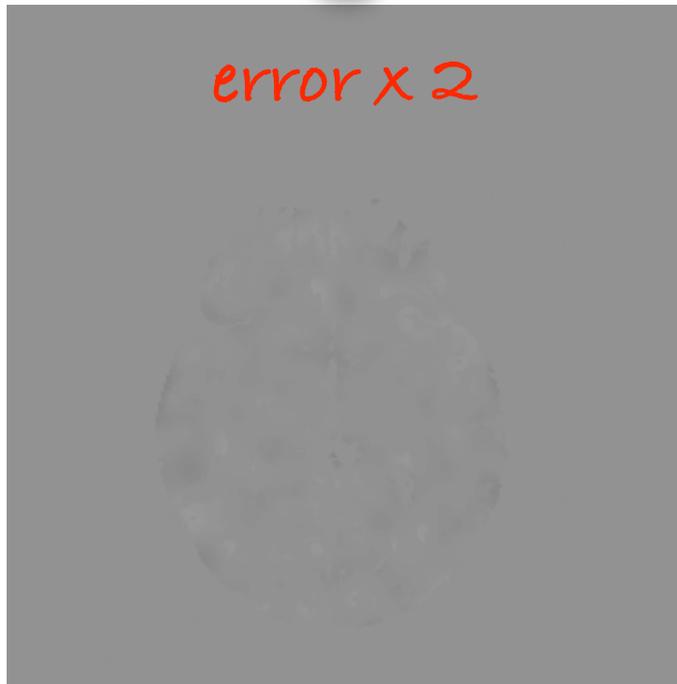
original



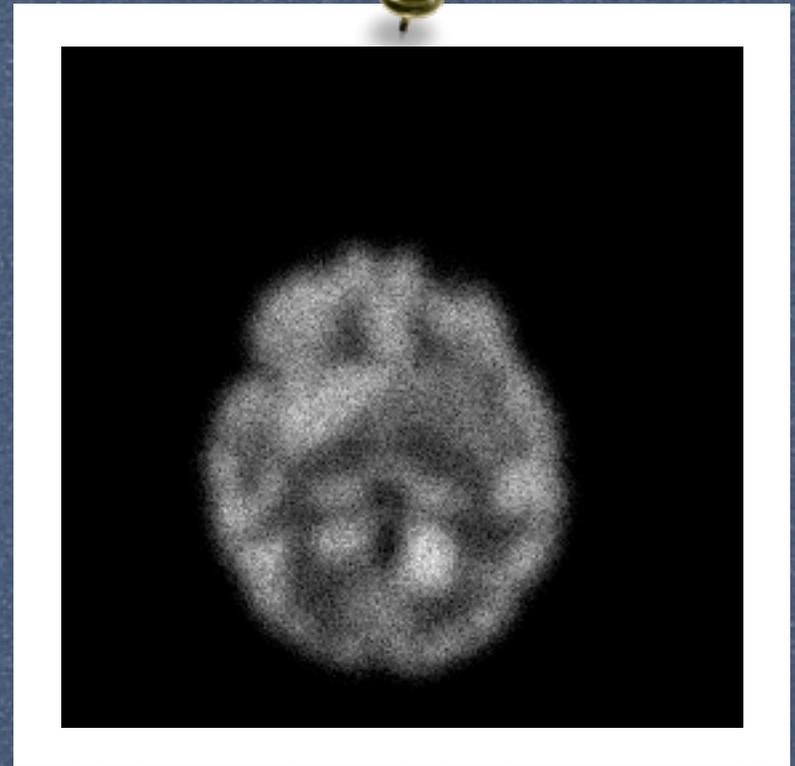
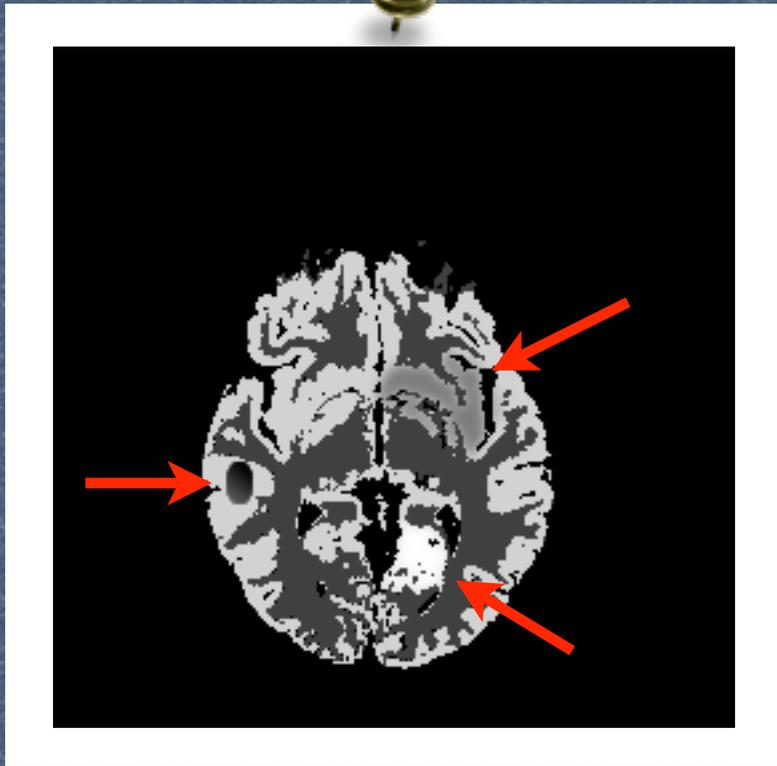
recovered



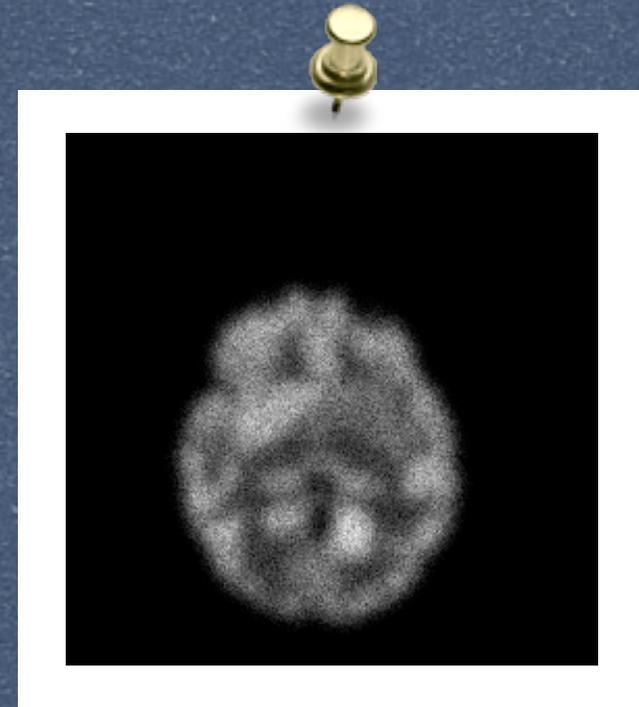
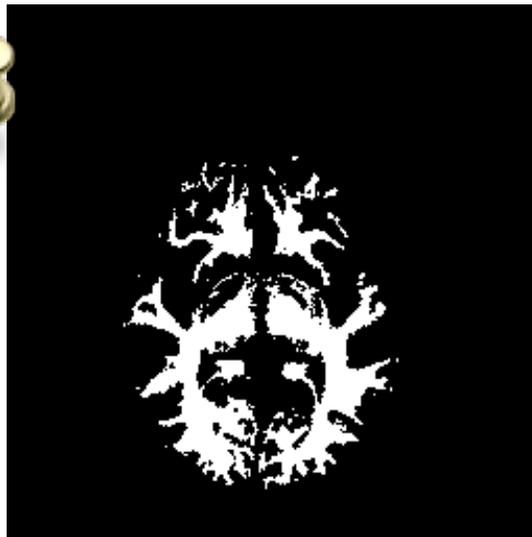
error x 2



Computer-built phantom with “lesions”

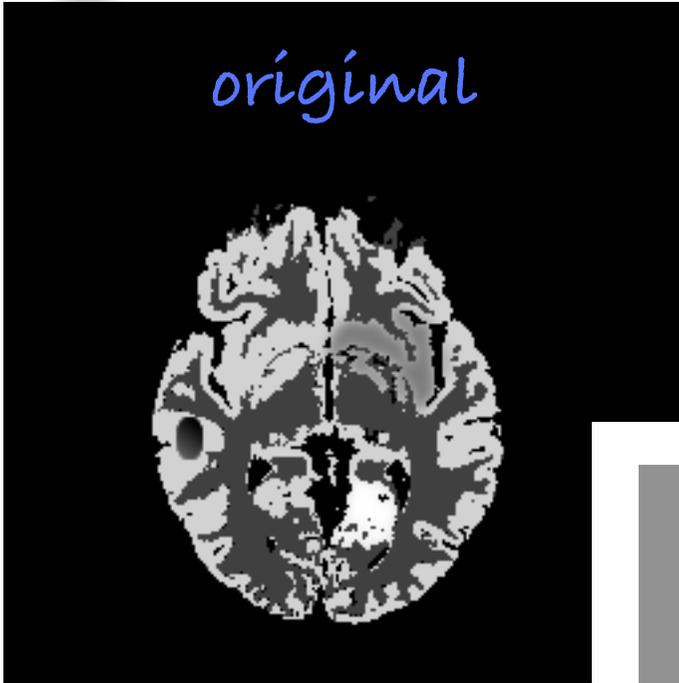


Materials

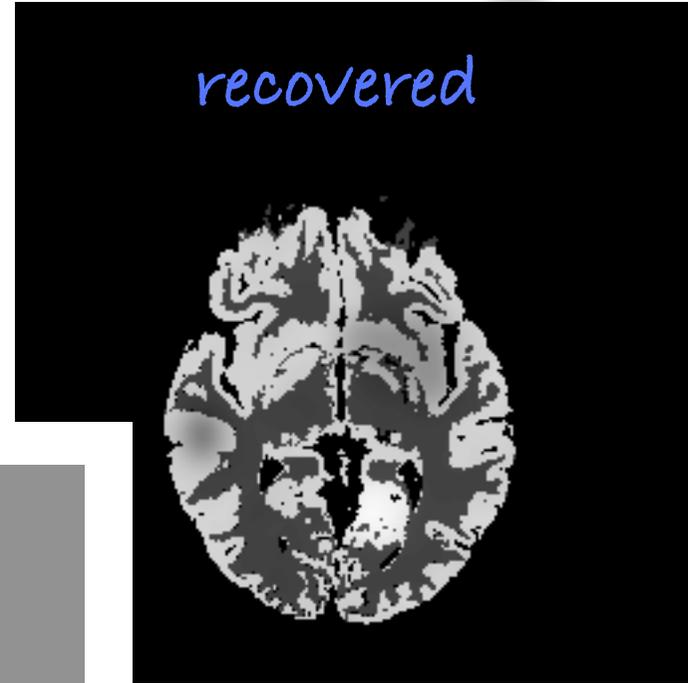


Results

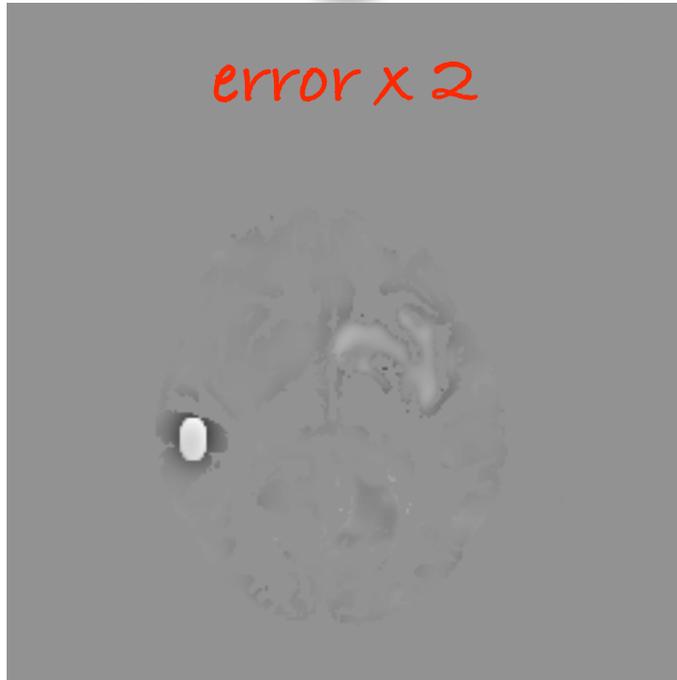
original



recovered

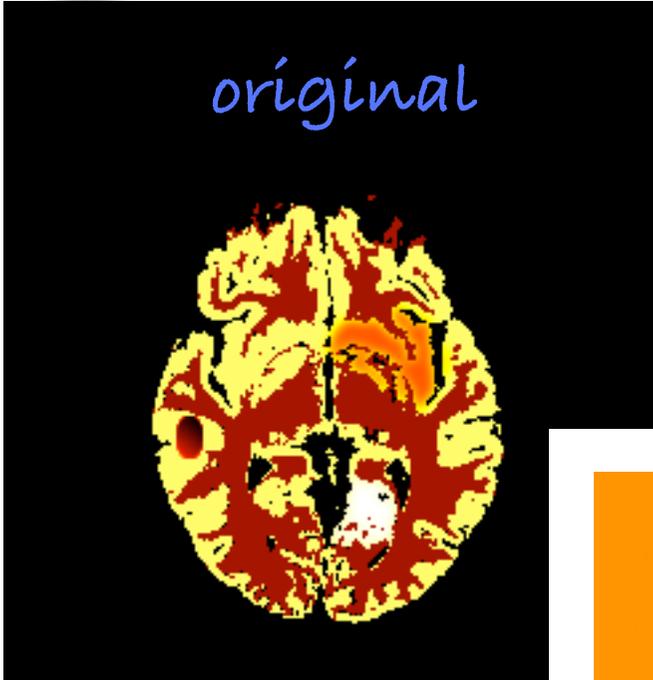


error x 2



Results

original



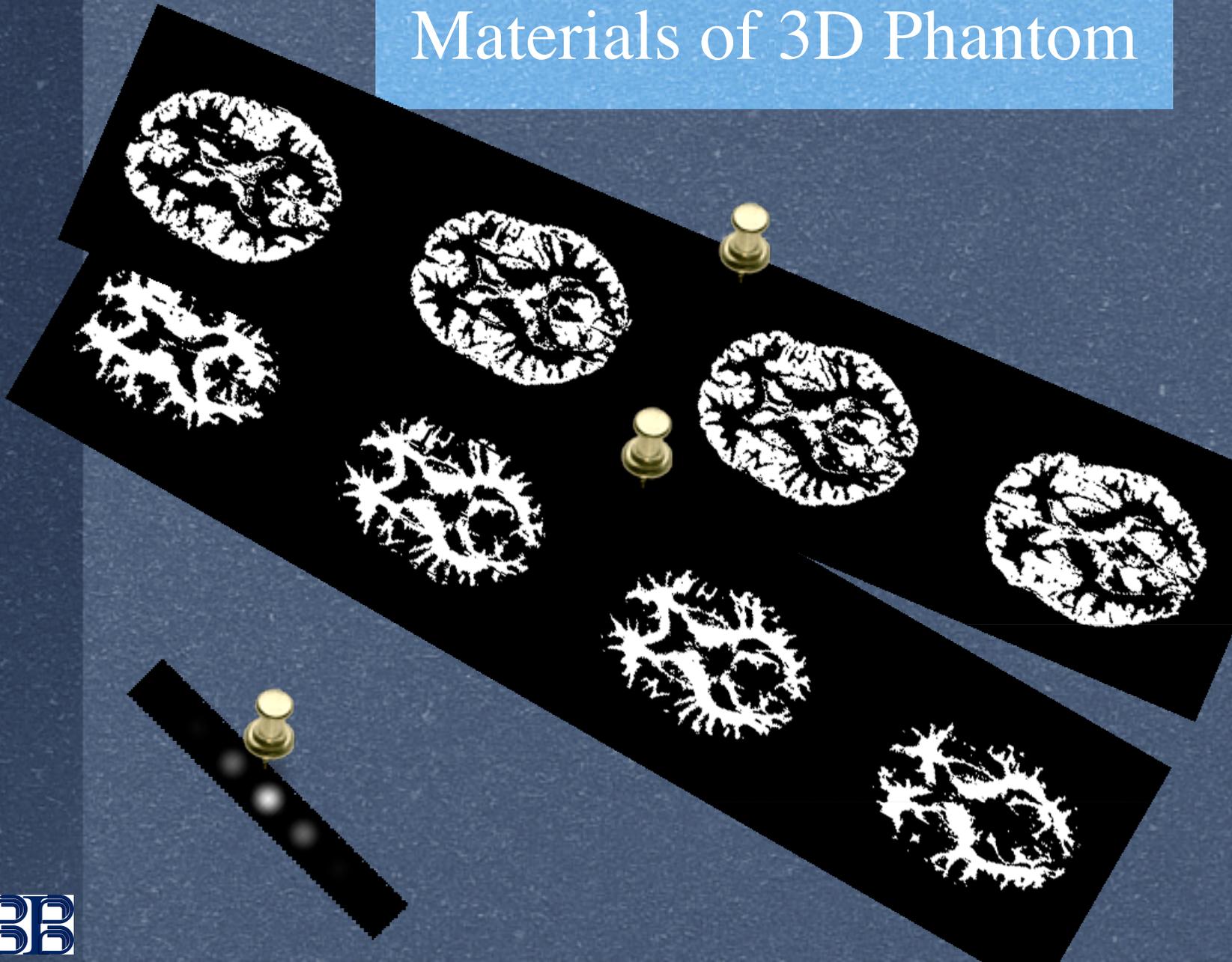
recovered



error x 2



Materials of 3D Phantom



Results

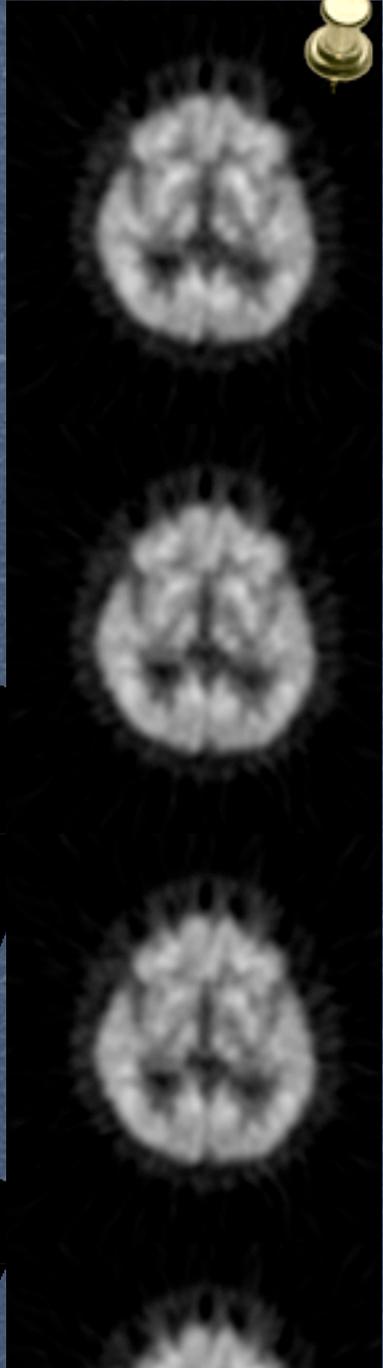
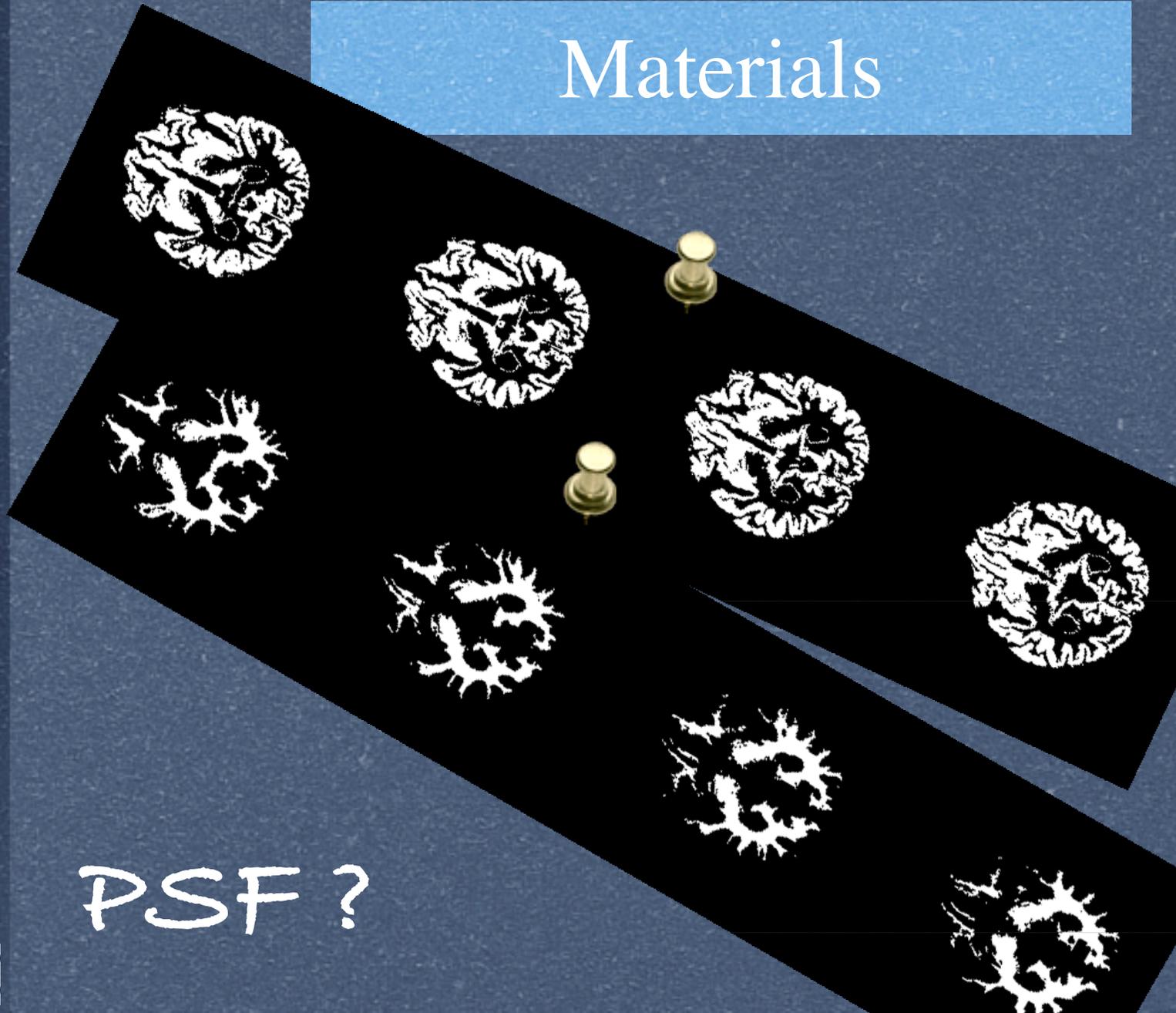


Original values:
GM=255 WM=64

Mean recovered values:
GM=254.69 WM=65.67

Real subject

Materials



PSF ?

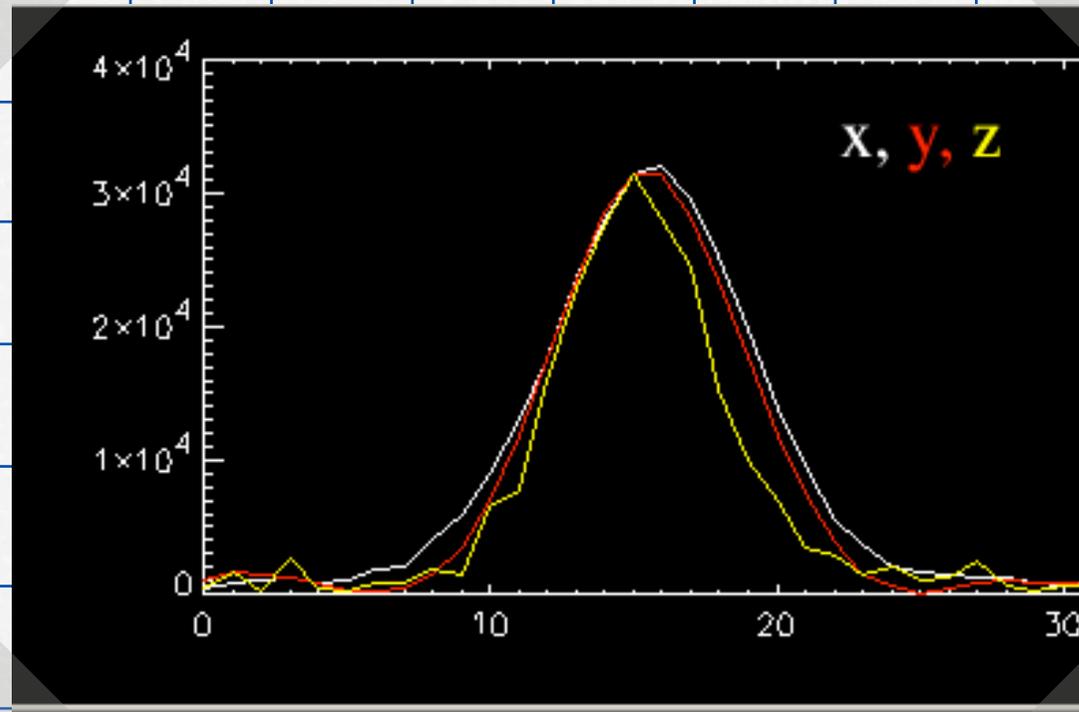
$$PET \cong C \otimes PSF + noise$$

Using a brain segmentation, assuming a concentration ratio of 1/4 between WM and GM, we can define a 3D function Seg similar (in terms of frequency components) to the activity concentration C . Then we may roughly estimate PSF as:

$$PSF \approx F^{-1} \left(\frac{|P\hat{E}T|}{|S\hat{e}g|} \right)$$

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3D PSF

