

High Quality High Spatial Resolution Functional Classification in Low Dose Dynamic CT Perfusion Using Singular Value Decomposition (SVD) and K-Means Clustering

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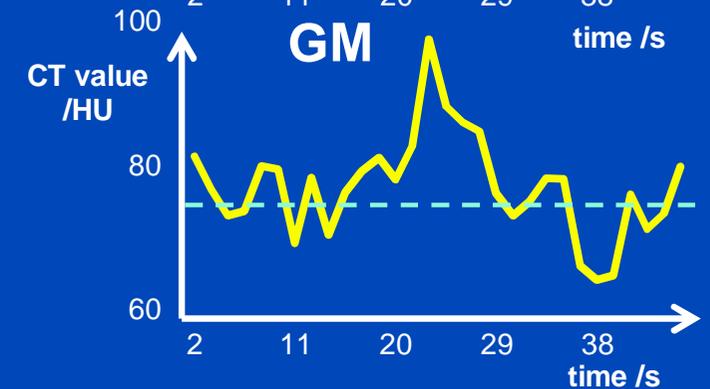
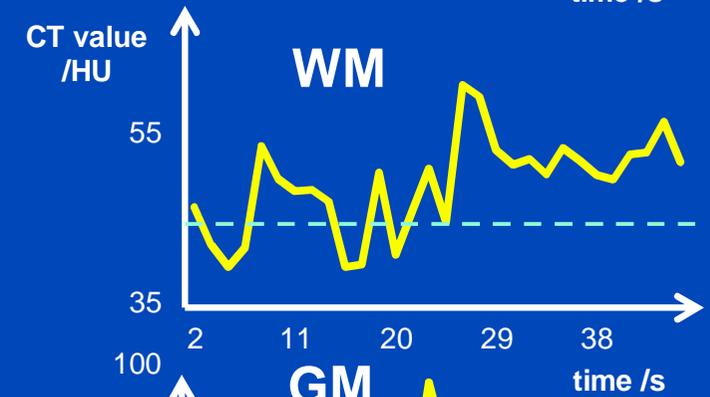
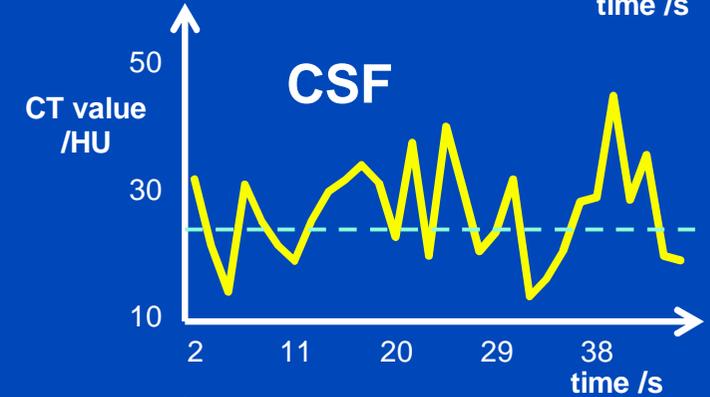
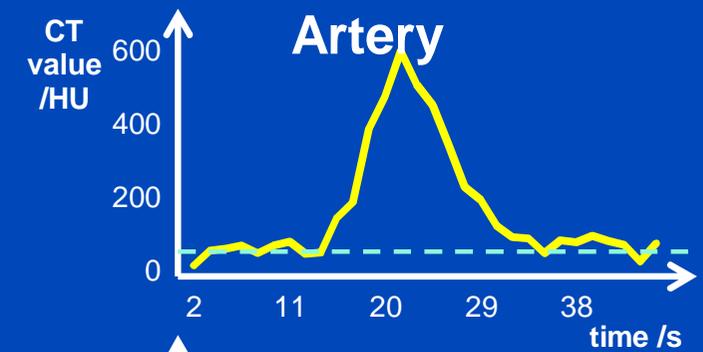
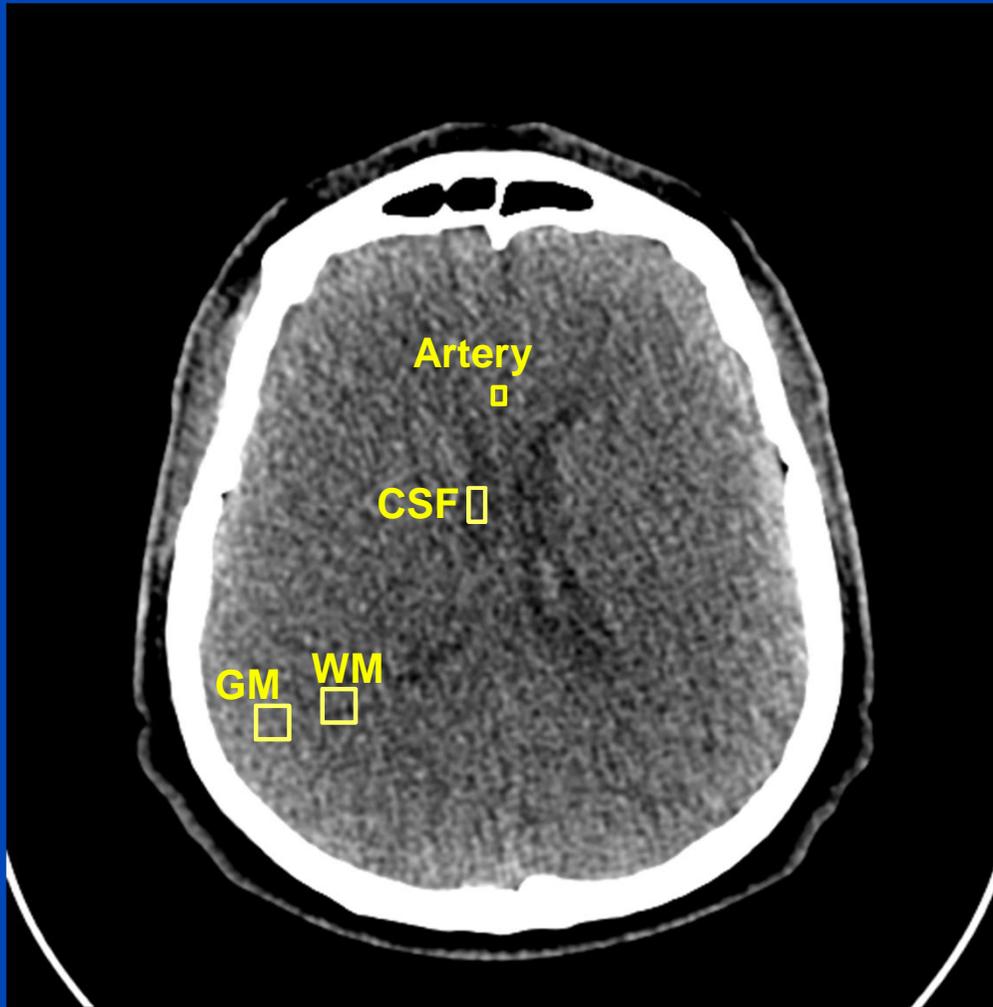
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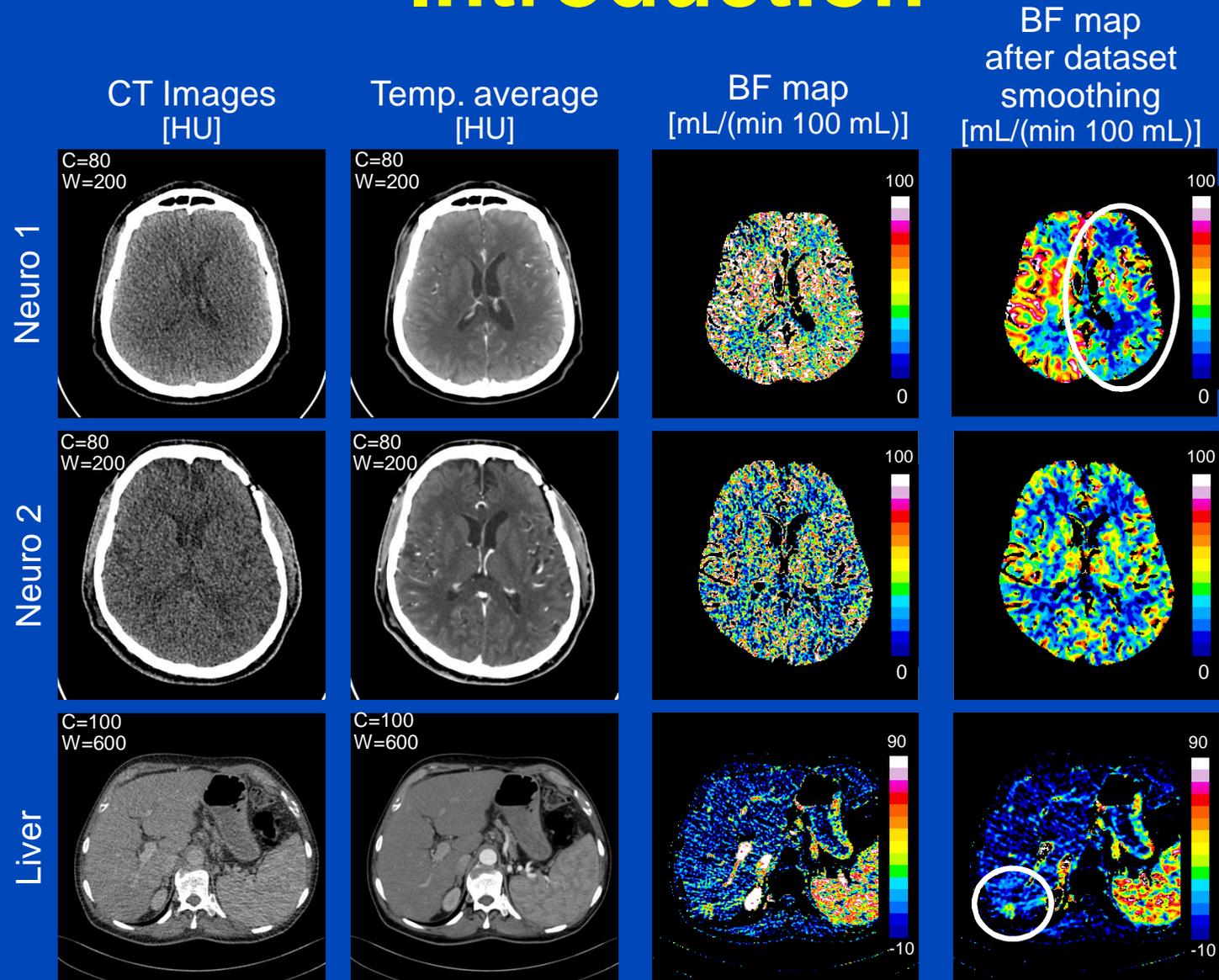
Introduction

In low dose CTP, TACs SNR is very poor.



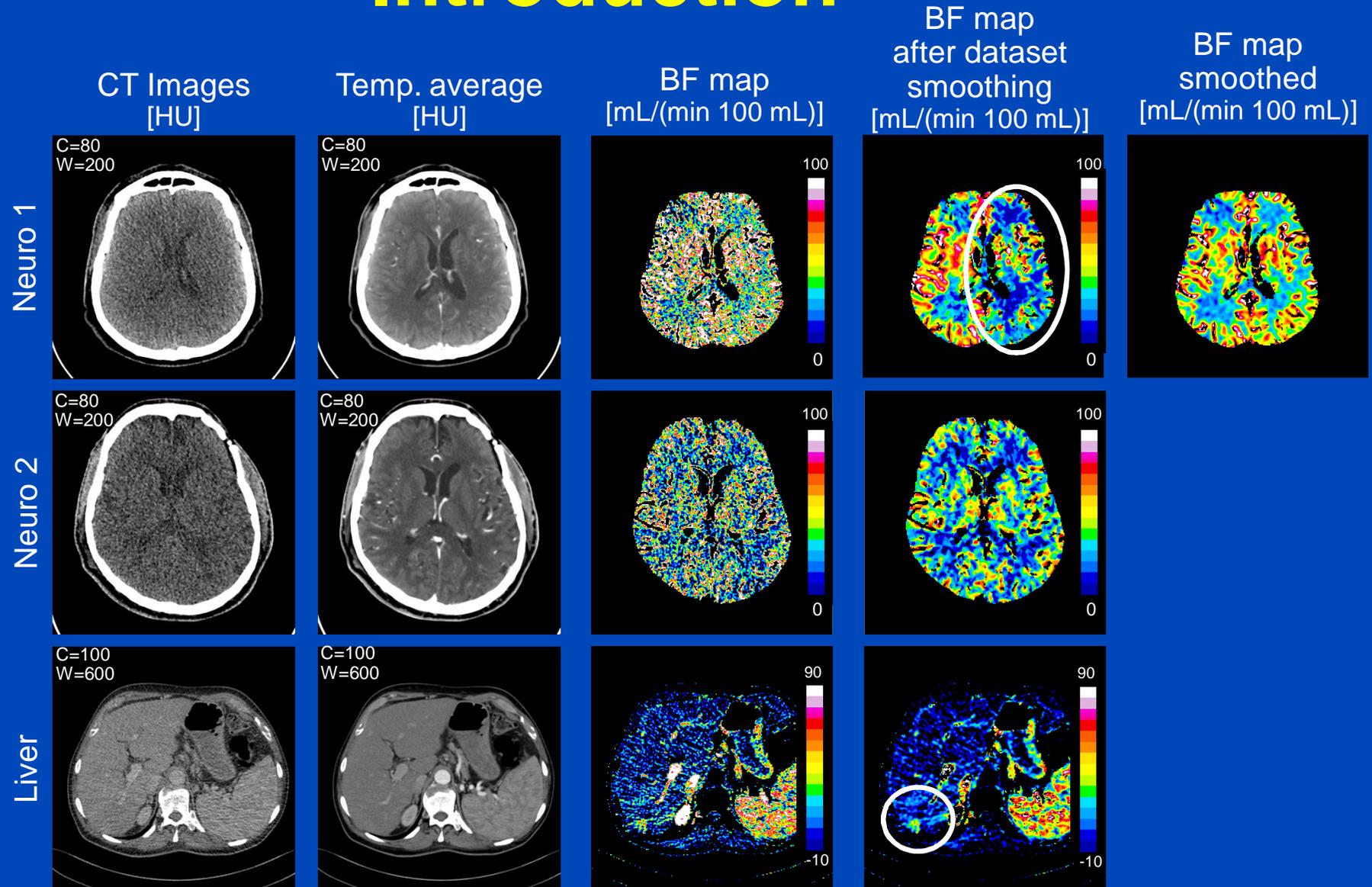
C = 80 HU, W = 200 HU

Introduction



In this study we aim at detecting the functional similarity between the voxels, independently from the maps.

Introduction



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Introduction

other methods - TIPS

Time-intensity profile similarity - TIPS^{1,2}:

$$s(\mathbf{r}_1, \mathbf{r}_2) = \frac{\sum_{t=1}^T (f(\mathbf{r}_1, t) - f(\mathbf{r}_2, t))^2}{2T\sigma_s^2}$$

$$\sigma_s^2 = \frac{1}{N_{\text{ROI}}(N_{\text{ROI}} - 1)T} \sum_{\mathbf{r}_1, \mathbf{r}_2 \in \text{ROI}} \sum_{t=1}^T (f(\mathbf{r}_1, t) - f(\mathbf{r}_2, t))^2$$

f Unfiltered image

$\mathbf{r} = (i, j, k)$ Voxel index

t Temporal index

ROI Homogeneous non-enhancing ROI

¹Mendrik et al. "TIPS bilateral noise reduction in 4D CT perfusion scans produces high-quality cerebral blood flow maps." , *Phys Med Biol* 56, (2011).

²Li et al. "A robust noise reduction technique for time resolved CT." , *Med Phys* 43, (2016).

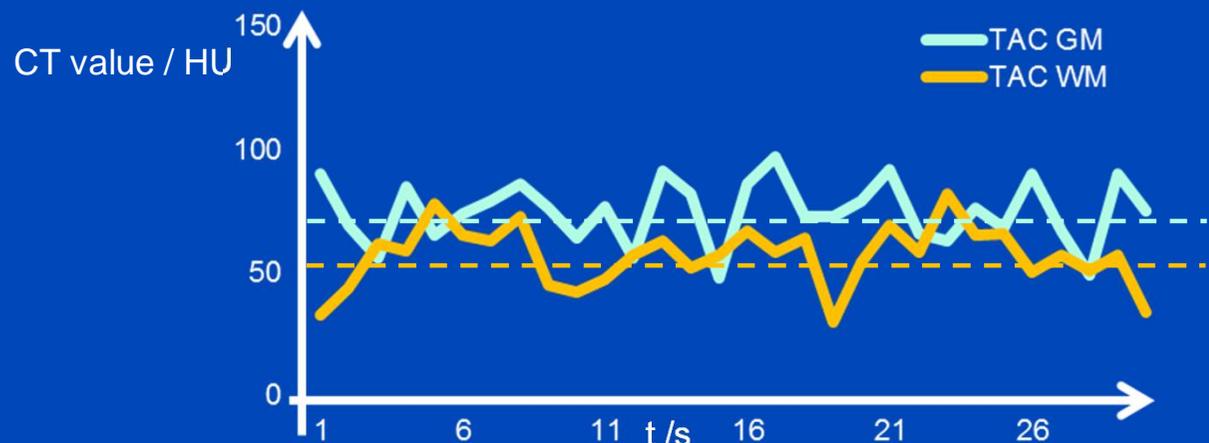
Introduction

other methods - TIPS

TIPS limitations for low dose CT perfusion:

- The sum of squared differences between the TACs mainly depends on their baseline* difference.
- If baseline is removed, the sum of squared differences is dominated by the temporal noise.

$$s(\mathbf{r}_1, \mathbf{r}_2) = \frac{\sum_{t=1}^T (f(\mathbf{r}_1, t) - f(\mathbf{r}_2, t))^2}{2T\sigma_s^2}$$



* the baseline is defined as the temporal average of all time points prior to contrast media arrival in the arteries.

Introduction

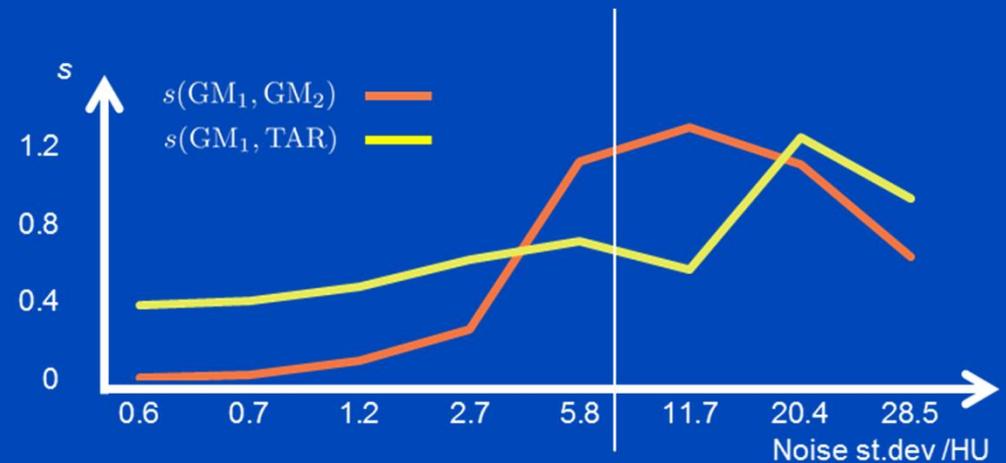
other methods - TIPS

TIPS similarity between:

- Two voxels with the identical TAC $s(\text{GM}_1, \text{GM}_2)$
- Two voxels with different TACs $s(\text{GM}_1, \text{TAR})$

After baseline subtraction and for different noise levels simulations:

$$s(\mathbf{r}_1, \mathbf{r}_2) = \frac{\sum_{t=1}^T (f(\mathbf{r}_1, t) - f(\mathbf{r}_2, t))^2}{2T\sigma_s^2}$$



Introduction

TIPS clustering

To visualize the TIPS similarity results, we perform a k-means clustering using the TIPS similarity formula as a distance measure:

- The k-means centroids are initialized with K=5 random voxels.
- We calculate the sum of squared differences between each voxel and each centroid, and assign each voxel to the cluster with the lowest distance:

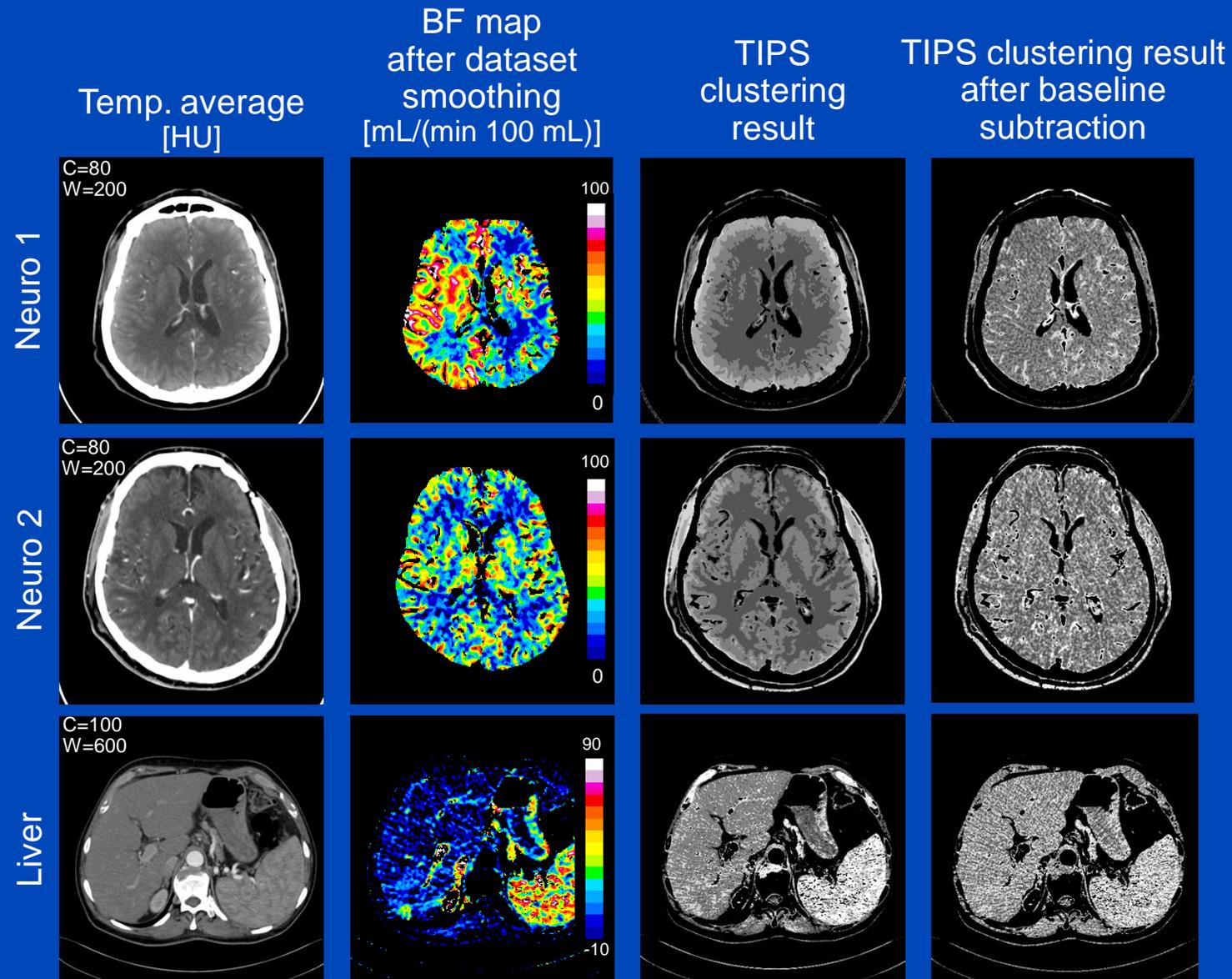
$$d_k(\mathbf{r}) = \frac{1}{T} \sum_{t=1}^T (f(\mathbf{r}, t) - c_k(\mathbf{r}, t))^2$$

$$m(\mathbf{r}) = \arg \min_k d_k(\mathbf{r})$$

- The centroids are updated as the average of all voxels belonging to its cluster.
- Steps 2 and 3 are repeated until 99.99% of the voxels do not change cluster anymore.

Introduction

TIPS clustering



Material and Methods

SVD

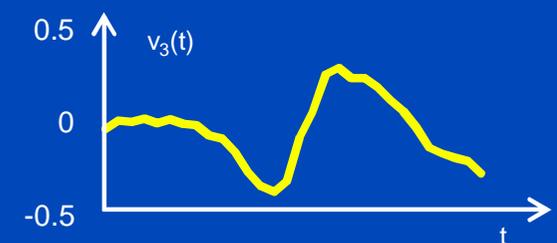
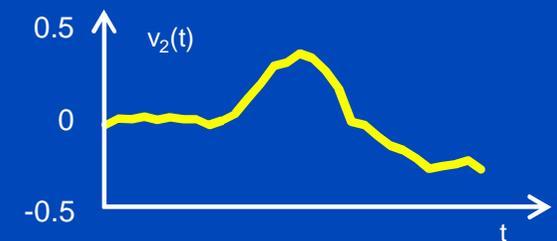
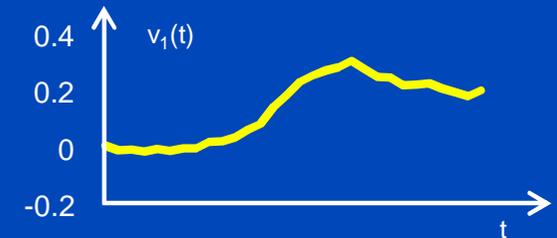
We subtract the baseline from the dataset, and re-arrange all the temporal volumes as columns of a matrix D .

Then we perform the singular value decomposition (SVD) .

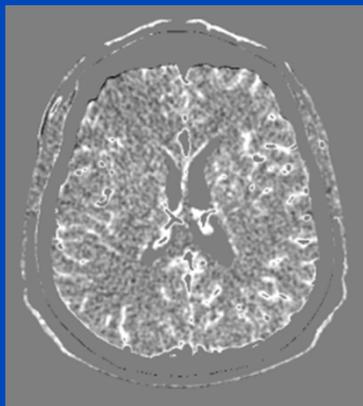
$$D = \begin{pmatrix} f(1,1) & \cdots & f(1,T) \\ \vdots & \cdots & \vdots \\ f(N_v,1) & \cdots & f(N_v,T) \end{pmatrix}$$

$$D = U\Sigma V^T$$

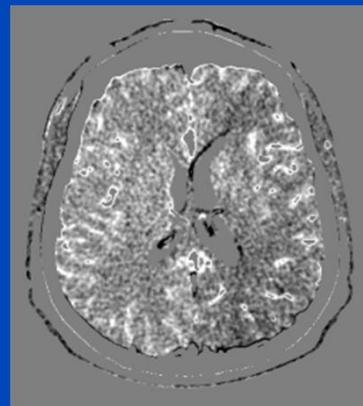
$$u_i(\mathbf{r}) = \frac{1}{\sigma_i} \sum_{t=1}^T f(\mathbf{r}, t) v_i(t)$$



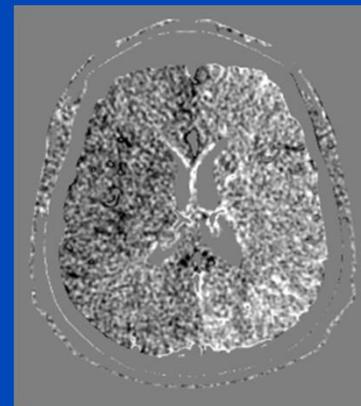
$u_1(\mathbf{r})$



$u_2(\mathbf{r})$



$u_3(\mathbf{r})$



$C = 0, W = 0.01$

⁴Gao H. et al "Robust principal component analysis-based four-dimensional computed tomography.", *Phys Med Biol* **56**, (2011).

⁵Gou S. et al "CT image sequence restoration based on sparse and low-rank decomposition.", *PLoS One* **8**, (2013).

Material and Methods

edge-preserving smoothing

We smooth the singular vectors with a guided bilateral filter, where the guiding image is the temporal average image.

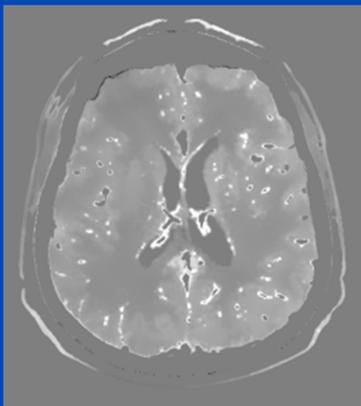
$$u_i^*(\mathbf{r}) = \frac{\sum_{\rho} w_d(\rho) w_g(\mathbf{r}, \rho) u(\mathbf{r} + \rho)}{\sum_{\rho} w_d(\rho) w_g(\mathbf{r}, \rho)}$$

$$w_d(\mathbf{r} + \rho) = \frac{1}{\sqrt{2\pi}\sigma_d} e^{-\frac{|\rho|^2}{2\sigma_d^2}}$$

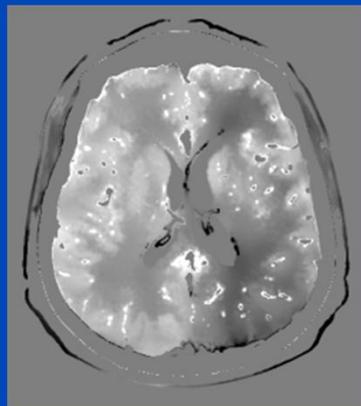
$$w_g(\mathbf{r} + \rho) = \frac{1}{\sqrt{2\pi}\sigma_g} e^{-\frac{(g(\mathbf{r}) - g(\mathbf{r} + \rho))^2}{2\sigma_g^2}}$$

$$g(\mathbf{r}) = (1/T) \sum_{t=1}^T f(\mathbf{r}, t)$$

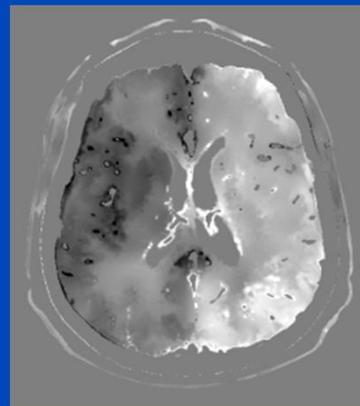
$u_1^*(\mathbf{r})$



$u_2^*(\mathbf{r})$



$u_3^*(\mathbf{r})$



C = 0, W = 0.01

Material and Methods

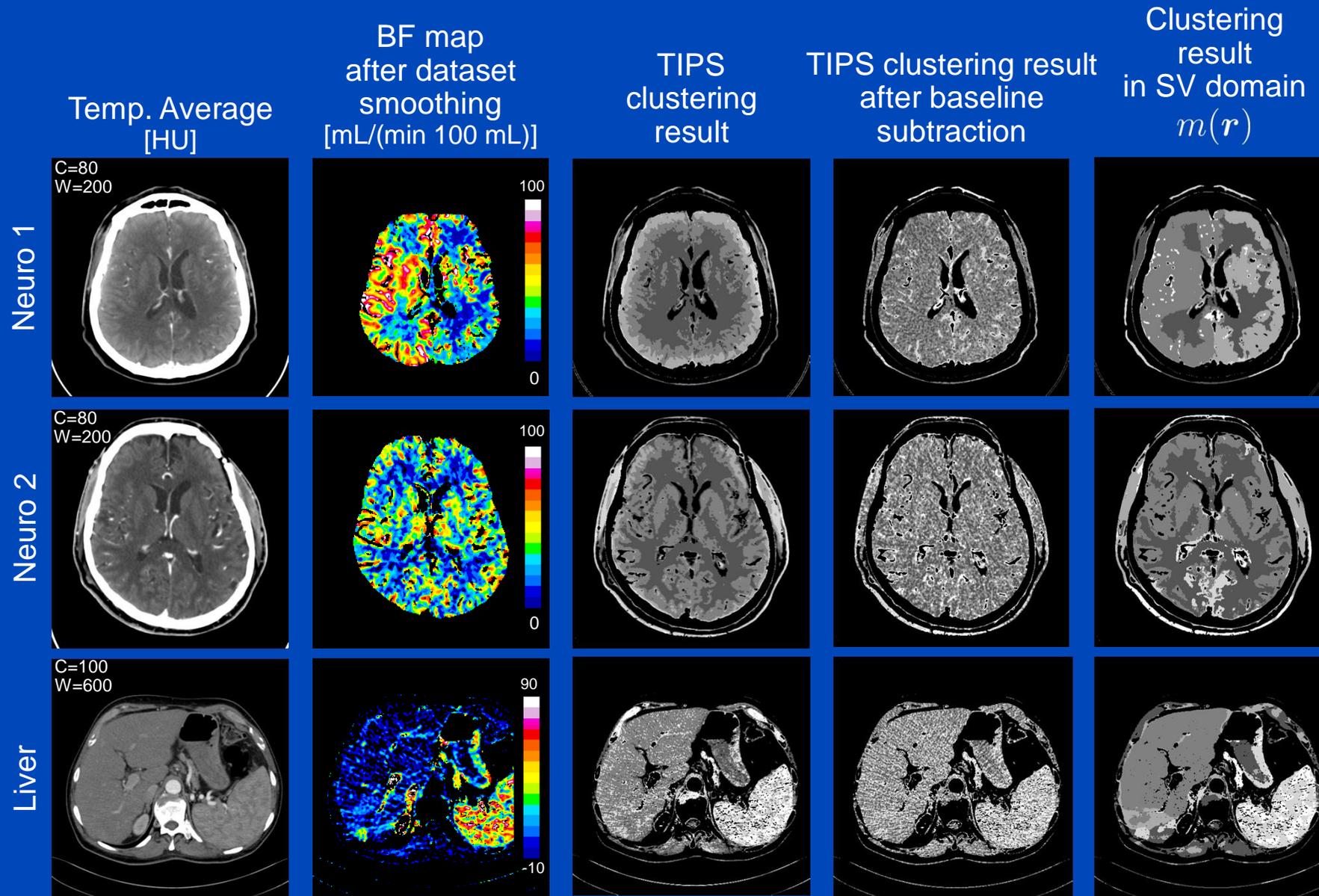
clustering

We used the same k-means clustering algorithm as before, but now it is performed in the singular vectors domain, rather than in temporal domain.

$$d_k(\mathbf{r}) = \frac{1}{3} \sum_{i=1}^3 (u_i^*(\mathbf{r}) - c_{k,i}(\mathbf{r}))^2$$

$$m(\mathbf{r}) = \arg \min_k d_k(\mathbf{r})$$

Results

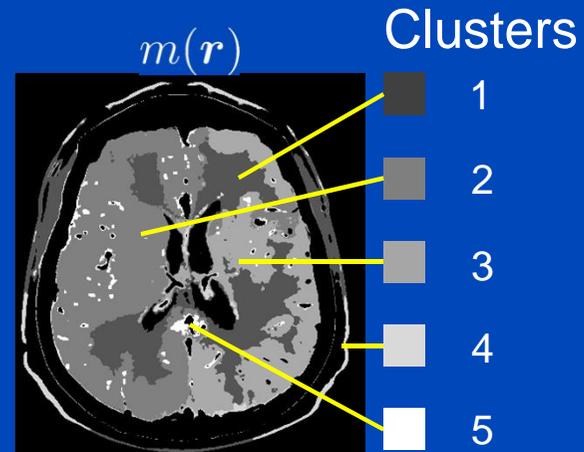


Results

Neuro 1

$$d_k(\mathbf{r}) = \frac{1}{3} \sum_{i=1}^3 (u_i^*(\mathbf{r}) - c_{k,i}(\mathbf{r}))^2$$

$$m(\mathbf{r}) = \arg \min_k d_k(\mathbf{r})$$



BF map
after dataset
smoothing
[mL/(min 100 mL)]

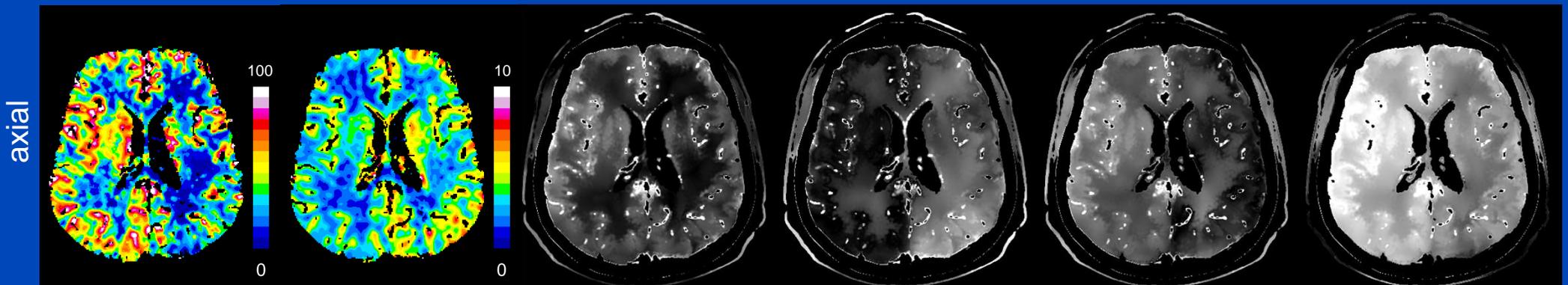
BV map
after dataset
smoothing
[mL/100 mL]

$d_1(r)$

$d_2(r)$

$d_3(r)$

$d_4(r)$



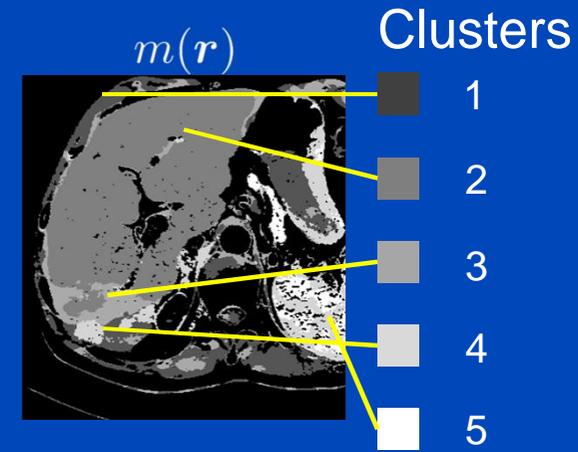
The fifth cluster groups the vessels and $d_5(r)$ is not displayed here.

Results

Liver

$$d_k(\mathbf{r}) = \frac{1}{3} \sum_{i=1}^3 (u_i^*(\mathbf{r}) - c_{k,i}(\mathbf{r}))^2$$

$$m(\mathbf{r}) = \arg \min_k d_k(\mathbf{r})$$



ALP map
after dataset
smoothing
[mL/(min 100 mL)]

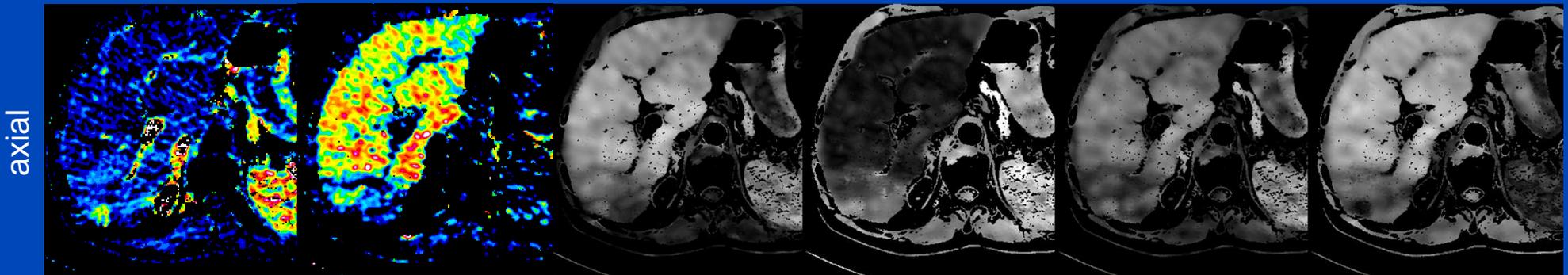
PVP map
after dataset
smoothing
[mL/(min 100 mL)]

$d_1(\mathbf{r})$

$d_2(\mathbf{r})$

$d_3(\mathbf{r})$

$d_4(\mathbf{r})$



Outlook

preliminary results

These distance maps could be used to guide a smoothing of the dataset before the maps calculation.

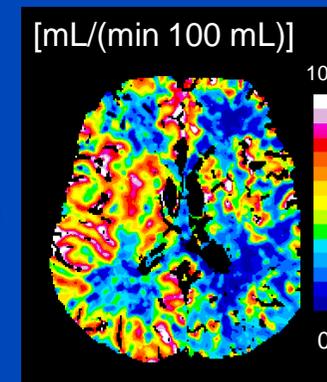
$$f^*(\mathbf{r}, t) = \frac{\sum_{\rho} w_d(\rho) w_s(\mathbf{r}, \rho) f(\mathbf{r} + \rho, t)}{\sum_{\rho} w_d(\rho) w_s(\mathbf{r}, \rho)}$$

$$w_s(\mathbf{r} + \rho) = \frac{1}{\sqrt{2\pi}\sigma_i} e^{-\frac{(d_i(\mathbf{r}) - d_i(\mathbf{r} + \rho))^2}{2\sigma_i^2}}$$

Where i is the cluster the voxel \mathbf{r} belongs to.

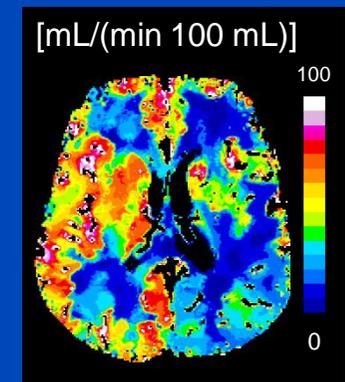
σ_i is the standard deviation of the distances from the i^{th} centroid of all voxels belonging to the cluster i .

After smoothing
the dataset with
Gaussian



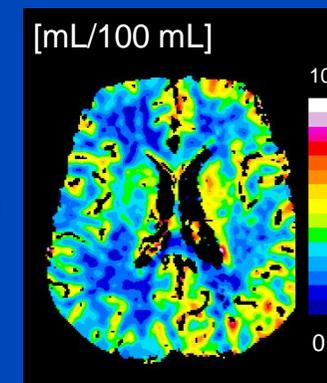
CNR = 3

After smoothing
the dataset with
distance maps

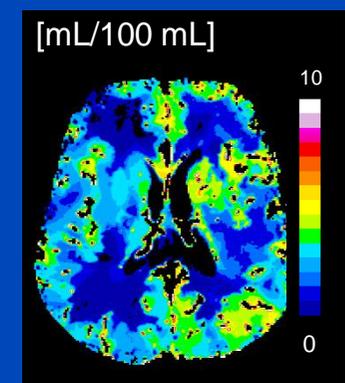


CNR = 8

BV



CNR = 26



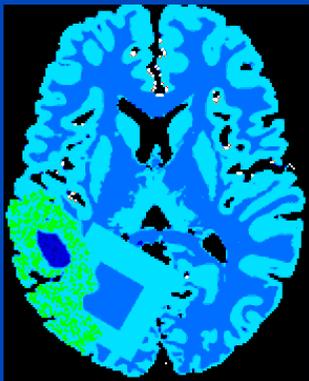
CNR = 58

Phantom Study

preliminary results

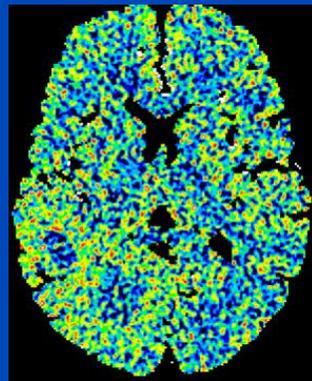
Phantom simulation with ischemic region. Results on blood volume maps: our approach (on the right side) is better able to preserve original shape and signal of the ischemic region.

Ground truth



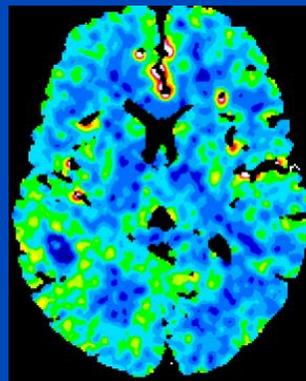
GM: 3.5
WM: 2
TAR: 3.75
NVT: 1.25

BV map obtained from noisy dataset (simulating 80 kV, 100 mAs, 5 mm)



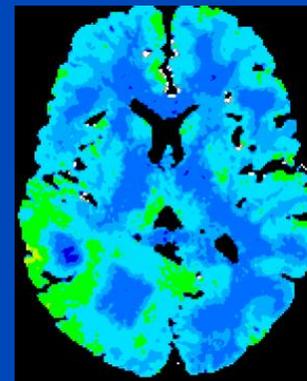
GM: 4
WM: 2.6
TAR: 4.2
NVT: 2.2

BV map obtained after smoothing the dataset with Gaussian



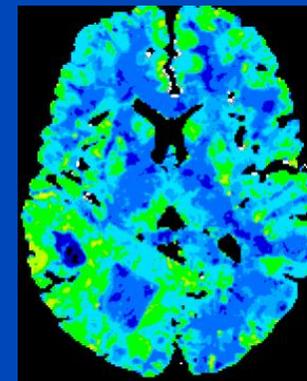
GM: 3.6
WM: 2.2
TAR: 4
NVT: 1.5

BV map obtained after smoothing the dataset with TIPS

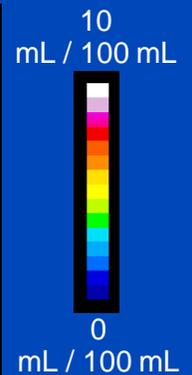


GM: 3.4
WM: 2.2
TAR: 3.8
NVT: 2.1

BV map obtained after smoothing the dataset with our method



GM: 3.6
WM: 2
TAR: 3.9
NVT: 1.2



Conclusions

- The proposed method correctly separated voxels with different functional features.
- It proved to be more robust than the TIPS method for functional similarity measurements (independently from the perfusion model) in dynamic CTP, and robust to spatial and temporal noise.
- Computational times are significantly lower than in the TIPS method, due to the dimensionality reduction.
- Potential use of such algorithm, in low dose dynamic CT perfusion, could be:
 - to efficiently guide a dataset smoothing before maps calculation, or a smoothing of the maps themselves,
 - to provide more information when the maps are too noisy or blurred, which can be used both as a second reader, or to help the radiologists in lesion detection and segmentation.

Thank You!

This presentation will soon be available at www.dkfz.de/ct

Job opportunities through DKFZ's international PhD or Postdoctoral Fellowship programs (www.dkfz.de), or directly through Marc Kachelrieß (marc.kachelriess@dkfz.de).

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