

Low Dose CT Perfusion using K-Means Clustering

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Introduction and Goals

Being a high dose technique, dynamic CT perfusion is normally performed with low mAs values. Noise has a dramatic impact on functional maps to be obtained, and hence has to be reduced.

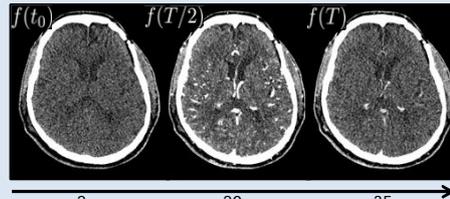


Fig 1. Low dose CT images of the same slice acquired over time.

K-means clustering (k)

Indicating with T the total number of time points acquired, each voxel can be interpreted as an array of T values (the CT value for each time point).

In matrix form, we would have $N_x N_y N_z$ columns (number of entries) and T rows (dimension of entries).

$$\begin{bmatrix} f(0,0) & \dots & f(N_x N_y N_z, 0) \\ \vdots & \vdots & \vdots \\ f(0,T) & \dots & f(N_x N_y N_z, T) \end{bmatrix}$$

A k-means clustering algorithm is run to iteratively classify each entry according to their distance, in the T-dimensional space, from each k center calculated as:

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

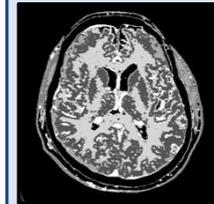


Fig 3. Clustering mask with 4 classes.

A mask is generated, containing the clustering information. Successively, voxels will be filtered together only if they belong to the same class.

Guiding Image (g)

To improve the TIPS filter, an additional weight is introduced² ($w(\hat{s})$), via a guiding image obtained as the pure temporal average for every voxel except for the ones containing edges and small vessels, where a mix between temporal average and temporal maximum intensity projection was used.

$$w(\hat{s})$$

k-gTIPS

$$f^*(\mathbf{r}, t) = \frac{1}{\eta(\mathbf{r})} \sum_{\mathbf{i}} w(\mathbf{i}) w(s) w(\hat{s}) \delta(c(\mathbf{i}), c(\mathbf{i} + \mathbf{i})) f(\mathbf{r} + \mathbf{i}, t)$$

$$\delta(c(\mathbf{r}), c(\mathbf{r} + \mathbf{i})) = \begin{cases} 1 & \text{if } c(\mathbf{r}) = c(\mathbf{r} + \mathbf{i}) \\ 0 & \text{if } c(\mathbf{r}) \neq c(\mathbf{r} + \mathbf{i}) \end{cases}$$

TIPS filter

The TIPS filter¹ weights each voxels according to both the Euclidean distance ($|\mathbf{i}|$) and the similarity (s) of their time-intensity profile (TIP). The similarity is the sum of squared differences of the CT values of the two voxels at each time step.

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

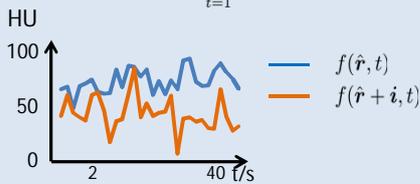


Fig 2. Example of time-intensity profiles. The blue curve is taken in a grey matter voxel, orange curve is a white matter voxel.

Results and Conclusions

The TIPS filter shows the best CNR improvements, but loss in spatial resolution. The gTIPS shows the best trade-off of spatial resolution and CNR for the CT images. The introduction of k-clustering step has significant benefits in the functional maps quality.

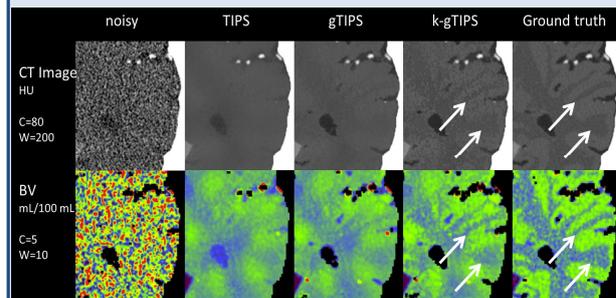


Fig 4. Example of CT images and blood volume maps of a digital phantom for different types of filters.

Phantom (values normalized to noisy dataset)

	$\Delta CT / \Delta x$	CNR_{CT}	CNR_{maps}
noisy	1	1	1
ground truth	1.08	8.75	100
TIPS	0.20	8.7	2
gTIPS	0.81	7.53	3
k-gTIPS	0.94	3.96	66

Clinical cases (values normalized to noisy dataset)

	$\Delta CT / \Delta x$	CNR_{CT}	CNR_{maps}
noisy	1	1	1
TIPS	0.40	6.63	7.85
gTIPS	0.60	5.77	7.93
k-gTIPS	1.83	3.99	14.72

Fig 5. Spatial resolution and image quality improvement of CT images and functional maps for phantom and clinical cases, for different types of filters implementations.

Acknowledgments

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