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4D DSA reconstruction using tomosynthesis projections

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Abstract

We investigate the use of tomosynthesis in 4D DSA to improve the accuracy of reconstructed vessel time-attenuation curves (TACs). It is hypothesized that a narrow-angle tomosynthesis dataset for each time point can be exploited to reduce artifacts caused by vessel overlap in individual projections. 4D DSA reconstructs time-resolved 3D angiographic volumes from a typical 3D DSA scan consisting of mask and iodine-enhanced C-arm rotations. Tomosynthesis projections are obtained either from a conventional C-arm rotation, or from an inverse geometry scanning-beam digital x-ray (SBDX) system. In the proposed method, rays of the tomosynthesis dataset which pass through multiple vessels can be ignored, allowing the non-overlapped rays to impart temporal information to the 4D DSA. The technique was tested in simulated scans of 2 mm diameter vessels separated by 2 to 5 cm, with TACs following either early or late enhancement. In standard 4D DSA, overlap artifacts were clearly present. Use of tomosynthesis projections in 4D DSA reduced TAC artifacts caused by vessel overlap, when a sufficient fraction of non-overlapped rays was available in each time frame. In cases where full overlap between vessels occurred, information could be recovered via a proposed image space interpolation technique. SBDX provides a tomosynthesis scan for each frame period in a rotational acquisition, whereas a standard C-arm geometry requires the grouping of multiple frames.

Keywords

4D DSA; digital subtraction angiography; scanning-beam digital x-ray; tomosynthesis; time-attenuation

1. INTRODUCTION

Four-dimensional digital subtraction angiography (4D DSA) is a commercially available technique for interventional neuroradiology that generates a time-resolved set of 3D angiographic volumes from a conventional 3D DSA scan protocol consisting of two rotational C-arm acquisitions: a ‘mask’, without contrast, and a ‘fill’, which is contrast enhanced.^{1–3} A strength of this technique is that it simplifies the intraprocedural 3D visualization of cerebrovascular structures. For example, an early-filling arteriovenous malformation (AVM) can be displayed without later-filling peripheral vessels that would normally occlude the view of the AVM. More recently, it has been recognized that 4D DSA

may be able to provide intraprocedural estimates of blood flow through arterial segments via analysis of the time-attenuation curves (TACs) measured in the vessels.⁴ Such a capability could be used for the pre- and post-treatment visualization of blood flow in the angiographic suite. Towards this goal, this paper investigates the quantitative accuracy of TACs and a potential method for improving accuracy based on the concept of limited-angle tomosynthesis. This method can be applied to either a conventional cone-beam C-arm geometry or an inverse geometry C-arm embodied in the scanning-beam digital x-ray (SBDX) system.^{5,6}

The standard 4D DSA reconstruction algorithm begins with formation of 2D log-subtraction images at each C-arm angle and then 3D DSA reconstruction (e.g. filtered backprojection). An intensity threshold is applied to the 3D DSA to form an image $C(x,y,z)$ termed the *constraining* volume:

$$C(x,y,z)=\begin{cases} DSA_{3D}(x,y,z), & \text{if } DSA_{3D}(x,y,z) > thresh \\ 0, & \text{otherwise} \end{cases} \quad (1)$$

The constraining volume serves to define the positions of contrast-enhanced vessels. Time-resolved 3D volumes are then generated by modifying the intensities in the constraining volume using contrast information contained in the original 2D subtractions. For each angle in the rotational acquisition, the measured 2D subtraction image is divided by a forward projection of the constraining volume. The resulting 2D ratio image is back projected to produce a 3D *weighting* volume. The collection of weighting volumes for all times t in the scan is given by:

$$W(x,y,z,t)=BP_{\theta}\left\{\frac{p(u,v,t)}{FP_{\theta}\{C(x,y,z)\}}\right\} \quad (2)$$

where $p(u,v,t)$ is the 2D DSA image measured at time t and angle θ , $BP\{\cdot\}$ represents unfiltered back projection at view angle θ without distance weighting, and $FP\{\cdot\}$ represents forward projection at view angle θ . The projection p and the forward projection of C may be optionally filtered by a user-specified convolution kernel prior to formation of the ratio, in order to reduce noise in the weighting volumes. Finally, each weighting volume is multiplied by the 3D constraining volume to produce a time series of 3D volumes (4D DSA),

$$T(x,y,z,t)=C(x,y,z)W(x,y,z,t) \quad (3)$$

where each time point t corresponds to a specific C-arm view angle θ . Through this process, a time frame volume is generated for each view angle in the rotational acquisition.

The method of modifying constraining volume intensities with back projected 2D temporal information is well suited to sparse image scenes where non-overlapped views of individual vessels can be obtained for most of the rotational scan. However if, at some time point in the

scan, a ray of measurement passes through two or more vessels, then reliable information on the individual contrast-enhancement levels of these vessels may not be obtained for this particular time.

It is hypothesized that narrow-angle tomosynthesis datasets for each time point can be exploited to reduce artifacts caused by vessel overlap in individual projections. In this work, we define tomosynthesis generally as the acquisition of x-ray images over some limited range of focal spot positions within a short time period, in comparison to the full rotational scan. Each point in the patient volume is imaged by *multiple* rays from a range of angles. We seek to use the non-overlapped rays in a tomosynthesis dataset to mitigate overlap artifacts in 4D DSA. Since the approach potentially involves a tradeoff between artifact reduction and temporal resolution, we explore its application in conventional “slow” tomosynthesis as well as “fast” tomosynthesis provided by an inverse geometry SBDX system.

2. METHODS

2.1 Overlap Artifacts in 4D DSA

The magnitude of a vessel overlap artifact in a 4D DSA reconstruction can be estimated as follows. Consider a ray passing through a single uniform vessel of thickness l and linear attenuation coefficient μ_t (see Fig. 1A).

The value of the 2D DSA image for this ray is the line integral of attenuation coefficient,

$$p_t = \mu_t l \quad (4)$$

In the reconstructed constraining volume, assume this vessel takes on some attenuation coefficient value μ_C :

$$C = \mu_C \quad (5)$$

The weighting value applied to the vessel in the constraining volume is obtained by the procedure outlined in Eq. (2). Forward projection of the constraining volume along the ray yields

$$p_C = \int \mu_C(x) dx = \mu_C l \quad (6)$$

The ratio of the measured projection to the forward projected constraining volume for this ray is

$$p_w = \frac{p_t}{p_C} = \frac{\mu_t l}{\mu_C l} = \frac{\mu_t}{\mu_C} \quad (7)$$

When the 3D weighting volume is generated, this ratio is back projected along the ray of measurement. Therefore, at the position of the vessel, the weighting value is

$$W = BP(p_w) = \frac{\mu_t}{\mu_c} \quad (8)$$

Finally, the time-dependent intensity inside the vessel (μ_t) is equal to the product of the constraining value and the weighting value inside the vessel:

$$T = CW = \mu_c \left(\frac{\mu_t}{\mu_c} \right) = \mu_t \quad (9)$$

This is the expected result for a single vessel. The vessel intensity in the constraining image has been modified to reflect the value that existed at time t . However, in the case where two vessels overlap in a given projection, a different result is obtained. Consider a vessel of interest (“1”) and an overlap vessel (“2”), as shown in Fig. 1B. The intensity for vessel “1” in the constraining volume is

$$C = \mu_{1c} \quad (10)$$

The measured projection through both vessels at time t along the ray is

$$p_t = \mu_{1t}l_1 + \mu_{2t}l_2 \quad (11)$$

The forward projection of the constraining volume now yields:

$$p_c = \int \mu_c(x) dx = \mu_{1c}l_1 + \mu_{2c}l_2 \quad (12)$$

The final result for the time-dependent intensity in the vessel of interest is now:

$$T = CW = \mu_{1c} \left(\frac{\mu_{1t}l_1 + \mu_{2t}l_2}{\mu_{1c}l_1 + \mu_{2c}l_2} \right) \neq \mu_{1t} \quad (13)$$

While the first vessel might be properly reconstructed at other points in time when there is no overlap, at this particular time, the desired result μ_{1t} is not obtained. Instead, the result is a weighted average of the two vessel intensities at time t . This can be seen by rewriting Eq. (13) as

$$T = \mu_{1t} \left(\frac{\mu_{1C} l_1}{\mu_{1C} l_1 + \mu_{2C} l_2} \right) + \mu_{2t} \left(\frac{\mu_{1C} l_2}{\mu_{1C} l_1 + \mu_{2C} l_2} \right) \quad (14)$$

If $\mu_{1C} = \mu_{2C}$, then the result is a simple pathlength-weighted average. In general, errors in the time frame image will occur when the two overlapping vessels have significantly different contrast enhancement at the same time e.g. when an early-filling artery overlaps with a late-filling vein. If the enhancement is identical, then an error will not be evident.

2.2 Tomosynthesis projections on conventional and inverse-geometry C-arms

In this work, we define tomosynthesis generally as the acquisition of x-ray images over some limited range of focal spot positions within a short time period, in comparison to the full rotational scan. It is hypothesized that overlap artifacts in 4D DSA can be mitigated by using a tomosynthesis dataset for each time frame, rather than a single projection view. When tomosynthesis data is used, each point in the patient volume is imaged by *multiple* rays from a range of angles, as shown in Fig 1C. We seek to use the available non-overlapped rays in the 4D DSA reconstruction.

2.2.1 Conventional geometry—Although a conventional C-arm rotation is not usually regarded as a tomosynthesis acquisition, tomosynthesis acquisitions for each time frame in the rotation can be synthesized by grouping the x-ray projections with a sliding view angle window. The full input data to a 4D DSA reconstruction is a set of 2D DSA projections acquired at time points t_i and angles θ_i ($i = 1..F$) where F is the number of frames acquired in a gantry rotation. The *tomosynthesis* dataset for specific angle θ_i is defined as a subset of x-ray projections acquired at angles ranging from $\theta_{i-(N-1)}$ to θ_i , where N is the number of projections within a user-specified tomographic angle. The tomographic angle is defined as the angular span of the rays passing through gantry isocenter. Notice this approach achieves additional angular views of each vessel at the cost of temporal resolution, defined as the width of the temporal acquisition window corresponding to the tomosynthesis dataset. However standard 4D DSA has high temporal resolution. For example, a rotational scan performed with 30 frames/sec detector frame rate can be reconstructed into a 30 frames/sec 4D DSA. In applications where the contrast dynamics are relatively slow, it may be acceptable to trade temporal resolution for tomographic angle.

This study considered a cone-beam x-ray angiographic system with 1201 mm source-to-detector distance, 750 mm source-to-isocenter distance, and a detector consisting of 1240×960 detector elements with 0.308 mm spacing. A short-scan acquisition consisting of 210 view angles evenly distributed over 210 degrees was simulated. Tomosynthesis datasets were generated with 5° , 6° , and 12° tomographic angles. Assuming 30 frame/s detector frame rate, the corresponding temporal resolutions are 167 ms, 200 ms, and 400 ms.

2.2.2 Inverse geometry (SBDX system)—The scanning-beam digital x-ray (SBDX) system is a novel C-arm fluoroscopic/angiographic system for interventional procedures that uses an electronically-scanned spatially-distributed array of focal spots to generate a complete tomosynthesis dataset in each 1/15 sec frame period.^{5,6} As such, this acquisition

geometry can provide the view angles needed for overlap artifact mitigation without a corresponding loss of temporal resolution. Shown in Figure 2 (right side), this system uses an x-ray source with an electron beam that is electronically scanned across a transmission target. The target has 100×100 focal spot positions on a 2.3 mm pitch. A multihole collimator just beyond the target defines a series of x-ray beams. As the electron beam in the x-ray tube performs a raster scan over the focal spot array, the patient is scanned by a series of overlapping x-ray beams. (Figure 2(right) shows only the rays from these x-ray beams that pass through a specific vessel.) The x-ray beams are directed at a 5.3 cm x 10.6 cm high speed photon-counting detector array located at a distance of 150 cm from the target. This geometry and scanning technique provides a complete tomosynthesis scan every 1/15 s, with a tomographic angle of 6° in the axial plane and 3° in the sagittal plane. We refer to this as *fast* tomosynthesis. Details of the current SBDX prototype can be found in Ref. 6.

The SBDX source and detector are mounted to a rotating C-arm, similar to a conventional system, however as the gantry rotates the x-ray beam is also rapidly scanning relative to the x-ray tube. In 4D DSA simulations, we considered a SBDX shortscan rotational acquisition with 210 gantry angles separated by 1 degree. A 71×71 focal spot, 1/15 s scan frame was simulated for each gantry angle, and a 4D DSA time frame was reconstructed using the tomosynthesis data for each gantry angle. Therefore the temporal resolution in the 4D DSA time frames was 66 ms.

2.3 4D DSA reconstruction using tomosynthesis projections

The 4D DSA method was modified to accommodate tomosynthesis data from either imaging geometry. The constraining volume is reconstructed as described in Eq. (1), using all data from the full gantry rotation. Then, for ray orientations acquired during a selected time frame (i.e. the tomosynthesis dataset) we forward project the constraining volume (C). Vessel overlap detection is performed during the forward projection to keep track of rays which can provide reliable measures of vessel intensity during the time frame. In this study, forward projection was implemented by summing samples of the image volume taken at regular intervals along the ray. Intersection of a vessel with the ray was detected by searching the sequence of sample values for an upward transition followed by downward transition. If more than one vessel was detected, the ray was flagged as overlapped.

For non-overlapped rays, we then calculate the ratio of measured projection value to forward projection value. Backprojecting the results yields a weighting volume (W). Next, we calculate the number of weights $N(x,y,z)$ backprojected to each voxel. The N volume was generated by back projecting a binary dataset consisting of ones at all non-overlapped ray positions and zeros at the overlapped ray positions. Finally, we normalize the weighting volume by the number of backprojected weights and multiply the result with the constraining volume. In this new algorithm, the 4D DSA reconstruction is given by

$$T(x, y, z, t) = C(x, y, z)W(x, y, z, t)/N(x, y, z, t) \quad (15)$$

2.4 Simulation studies

The approach was tested with computer-simulated x-ray projections (analytical ray tracings) of a 4D vessel phantom. The phantom consisted of a 2-mm-diameter cylinder at isocenter with early enhancement (*artery*), and four 2-mm-diameter cylinders with late enhancement (*veins*) at separations of 2, 3, 4, and 5 cm with respect to the center of the artery. Vessel diameters and separations were based upon analysis of the typical size and spacing of vessels in the XCAT brain phantom.⁷ The geometry and ground truth time-attenuation curves assigned to the vessels are shown in Figure 3. The vessels were oriented such that, over the course of the scan, the artery overlapped with veins with separation distances of 4 cm, 2 cm, 5 cm, and 3 cm. Each reconstructed image slice consisted of 512×512 square voxels with 0.234 mm pitch resulting in a 120 mm in-plane field-of-view. A total of 385 slices were reconstructed with a 0.5 mm axial pitch.

2.5 Reconstruction parameters

Figure 4 shows an example of the ground truth image (a), constraining image (b), weighting image (c), and time frame image (d) for the conventional C-arm geometry and a 6 degree tomographic angle in the weighting image. In the constraining image the vessels have approximately the same intensity. Multiplication by the weighting image, produces a time frame image (Fig. 4d) with vessel intensities reflecting the ground truth (Fig 4a). An important tunable parameter in 4D DSA is the threshold value used to form the constraining image. Figure 5 compares venous TACs measured from 4D DSA reconstructions with the threshold set to 10% and 30% of the maximum attenuation coefficient in the constraining volume.

Deviations between reconstructed and ground truth TACs are apparent in case of the lower 10% threshold. Examination of the constraining image (Figure 6a) reveals the source of this error: The reconstructed image of the vessel has non-zero values outside of the true vessel area, which can be oriented in the direction of forward projection, leading to erroneous weighting values and bias in the reconstructed TAC.

Specifically, the erroneous increase in pathlength through the vessel increases the denominator of $p_w = \frac{p_L}{p_C} = \frac{\mu_L l}{\mu_C l}$ and reduces the weight value. The vessel artifact demonstrated in Fig. 6(a) is a standard filtered backprojection artifact caused by data inconsistency in the original projection data, i.e. changes in vessel opacification over the course of the rotational acquisition. Thus in 4D DSA reconstruction it is important to set the threshold sufficiently high. However it should also be noted that if the threshold is too high, then the vessel in the constraining image may be eroded and the forward projection may be underestimated. For results reported here, a 30% threshold was used for conventional geometry (35% for inverse geometry). Based on the maximum deviations between measured and ground truth TACs observed in Figure 6, this reduced bias artifacts from 12.5% to 2.5% (relative to the peak ground truth value).

We also investigated the effect of voxel sampling during reconstruction and forward projection by examining different vessel sizes. Small variations in calculated pathlengths can occur due to the discrete nature of the constraining image. As vessel size increases, the

reconstructed vessel has relatively smoother edges (see Figure 7, top row) and these variations are reduced. To study this effect, we simulated vessels with constant attenuation coefficient (0.04 mm^{-1}) vs. time and compared measured with ground truth TACs for different vessel sizes (2mm, 4mm, and 6 mm). Figure 7 bottom row shows the difference between reconstructed and ground truth attenuation coefficients, expressed as a fraction of the corresponding ground truth value. For 2mm (6mm) vessel diameters, reconstructed TACs were found to deviate by up to 2% (<1%) with respect to the ground truth.

3. RESULTS

Time-attenuation curves were measured in the artery and the four veins for each imaging geometry and reconstruction configuration. The curve value at a specific time point was the average within a 3×3 pixel region-of-interest centered on the vessel. The accuracy of each TAC was characterized with two metrics. To quantify overlap artifact level, the maximum absolute deviation between the reconstructed and ground truth TACs was expressed as a percentage of the maximum ground truth value.

$$MaxDev = \frac{\max(|TAC_{4D}(t) - TAC_{truth}(t)|)}{\max(TAC_{truth}(t))} 100 \quad (16)$$

To characterize overall accuracy of the TAC, the relative RMSD was calculated and expressed as a percentage.

$$rRMSD = \frac{\|TAC_{4D}(t) - TAC_{truth}(t)\|_2}{\|TAC_{truth}(t)\|_2} 100 \quad (17)$$

The rRMSD reflects overlap artifacts and also biases that may be present in the entire curve. Results for all imaging geometries, reconstruction configurations, and vessels are summarized in Table 1. Further discussion and selected TACs are presented below for both conventional C-arm geometry and inverse geometry C-arm systems.

3.1 Conventional geometry

Figure 8 compares TACs for arteries and veins at a distance of 30 mm for standard non-tomosynthesis 4D DSA reconstruction (see Fig. 8a), 4D DSA with 12 degree tomographic angle (Fig. 8b), and 4D DSA with 6 degree tomographic angle (Fig. 8c). Overlap artifacts are clearly visible in the case of standard 4D DSA. In the arterial curve there are spikes which deviate towards the venous curve at time points corresponding to overlap, as predicted by Eq. (14). The maximum deviation was 19.8% with respect to ground truth in the case of the artery. Switching to 4D DSA with tomosynthesis projections (6–12 degrees) reduces this overlap artifact to a level of ~4%. For reference, artifacts caused by voxel discretization of a 2 mm vessel (see Fig 7) place the lower bound on maximum deviation at ~2%.

Since smaller vessel separation reduces the fraction of non-overlapped rays available for reconstruction, the benefit from switching to tomosynthesis projections was not apparent in

TACs for veins at a distance of 20 mm to the artery. For larger vein-to-artery separations there was a reduction in the maximum deviation. In the case of the vein at a distance of 40 mm (50 mm) the maximum deviation was 7.0% (5.6 – 6.8%), down from 22.8% (12.8%).

For very narrow tomographic angles or small vessel separation it is possible that some vessel voxels will experience full overlap, meaning all rays passing through the voxel eventually intersect another vessel. To investigate the case where full overlap occurs we lowered the tomographic angle from 6 to 5 degrees. Figure 9(a) compares measured and ground truth TACs using a 5 degree tomographic angle. At the time corresponding to view index 147 (147 degrees), a new artifact appears (compare Fig. 9a to Fig. 8c). The artery and vein TACs indicate maximum deviations at the level of 12.6% and 43.9%, respectively.

The artifact observed with 5 degree tomographic angle was due to voxels inside the vessel which were fully overlapped, and therefore weighted to zero during reconstruction. Figures 10(a) and (d) show zoomed views of artery and vein at the time corresponding to 147° view angle, illustrating the “dropout” of certain voxels due to full overlap. To address this problem, we applied an interpolation technique that smoothly interpolates inward from the voxel values presented on the boundary of the dropout region in each vessel by solving Laplace’s equation (*roifill* function with MATLAB version R2016a). The result of this interpolation is shown in Figures 10(b) and (e) for the artery and vein, respectively. For comparison, Figures 10(c) and (f) show the same vessels reconstructed with a larger tomographic angle (6 degrees) where full overlap does not occur.

Finally, after applying this interpolation method, we revisited the 5-degree tomographic angle case (Figure 9b). Artifacts caused by dropout were greatly reduced. In case of the artery (vein at 30 mm), the maximum deviation with respect to ground truth is 12.6% (43.9%) before interpolation, and 3.9% (3.7%) after interpolation. Results indicate that this image space interpolation method is a feasible approach to reducing TAC artifacts caused by overlaps that are not mitigated by tomosynthesis.

3.2 Inverse geometry (SBDX system)

Results for the SBDX geometry were similar to those obtained with conventional geometry and 6–12 degree tomographic angle. Figure 11a shows SBDX TACs for the artery and the vein at distance of 30 mm from the artery. Figures 11b and 11c show zoomed views of both vessels at a 147 degree gantry angle, where the two vessels would produce overlap artifacts in conventional geometry with standard 4D DSA reconstruction. The SBDX tomographic angle of 6 degrees (in the axial plane) was wide enough to avoid full overlap. Therefore interpolation was not applied. In the case of the artery (vein at 30 mm), the maximum deviation with respect to ground truth was 4.0% (5.6%). SBDX TAC quality was comparable to conventional geometry with 6–12 degree tomographic angle, however with SBDX the tomosynthesis acquisition is obtained in every 1/15 s scan period. The temporal resolution of each 4D DSA time frame is 66 ms for SBDX, in contrast to 200 – 400 ms for conventional geometry (6–12 degree, 30fps).

4. DISCUSSION

4D DSA offers time-resolved vessel visualization and flow analysis in the interventional setting. However, vessel overlap artifacts remain problematic. In this work we present a new tomosynthesis-based 4D DSA reconstruction method that could improve the accuracy of these techniques.

Our method relies on a good understanding of all reconstruction parameters. We studied the effects of varying constraining image thresholds and voxel sampling. Generally, the constraining image threshold must be set at a level to avoid artifacts caused by over- or under-estimation of the projected pathlength through a vessel. Voxel sampling effects are generally reduced as vessel size increases, since larger vessels present smoother edges in a reconstruction. However for small vessels (~2 mm) these effects may place a limit on the TAC accuracy that can be achieved.

In standard 4D DSA reconstruction, overlap artifacts are clearly present in TACs. In this simulation study, incorporation of tomosynthesis reduced the overlap artifact magnitude for 2 mm diameter vessels with vessel separations >3 cm. In cases where full overlap between vessels occurred, information could be recovered via a proposed image space interpolation technique. In a conventional C-arm rotational acquisition, tomosynthesis datasets can be obtained by grouping x-ray projections with a sliding temporal window. In an inverse geometry C-arm with rotational acquisition (SBDX), tomosynthesis datasets are naturally generated for each frame period. The latter geometry is well suited to 4D DSA tasks requiring high temporal resolution. Future work should examine tomosynthesis-based 4D DSA performance in more complex vessel geometries and in the presence of image noise.

5. CONCLUSIONS

Use of tomosynthesis projections in the 4D DSA reconstruction algorithm can reduce TAC artifacts caused by vessel overlap, provided there is a sufficient fraction of non-overlapped rays available in each time frame. In fully overlapped scenarios, image space interpolation techniques are feasible. SBDX can provide a fast tomosynthesis scan for each frame period in a rotational acquisition, whereas a standard C-arm geometry requires the grouping of multiple frames.

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Fig. 1.

In conventional 4D DSA, temporal information is derived from a single angle (A) leading to problems in overlapped views (B). In tomosynthesis-based 4D DSA, multiple rays are available (C) and overlapped rays are ignored.

Fig. 2.

In the slow tomosynthesis approach (left) temporal information comes from a sliding window of a regular C-arm rotational acquisition. The fast tomosynthesis approach (right) uses the SBDX system, which provides a complete tomosynthesis scan in 1/15 s using an electronically scanned focal spot. In either case the 3D constrain volume is generated from a full C-arm rotation.

Fig. 3. Simulated vessel geometry (left), with peripheral veins separated from a central artery. Gantry angle orientation is indicated. The ground truth TACs for artery and vein are shown at right. A view index corresponds to a 1 degree increment in gantry angle. As the rotation proceeds, artery-vein overlap (indicated as black lines labeled ‘A-V Overlap’) occurs for separation distances of 4 cm, 2 cm, 5 cm, and 3 cm.

Fig. 4.

Ground truth (a), constraining (b), weighting (c), and time frame (d) images for conventional C-arm at 30 degree view angle and 6 degree tomographic angle for the time frame reconstruction.

Fig. 5. Reconstructed and ground truth TACs for the vein at 40 mm distance from the artery, with 10% (a) and 30% (b) constraining image thresholds applied.

Fig. 6.

Zoomed views of vein (40 mm distance from artery) at a view angle of 60 degrees, with 10% (a) and 30% (b) constraining image thresholds applied.

Fig. 7.

Top Row: Constraining image with 2 mm, 4 mm, and 6 mm vessel diameter. Bottom Row: Difference between ground truth and reconstructed TACs for different vessel sizes, expressed as a fraction of the ground truth values.

Fig. 8.

Conventional geometry TACs for the artery and the vein at a distance of 30 mm from the artery. (a) Standard 4D DSA algorithm. (b) 4D DSA with 12 degree tomographic angle. (c) 4D DSA with 6 degree tomographic angle.

Fig. 9.

Conventional geometry TACs for 5 degree tomographic angle before (a) and after (b) image space interpolation.

Fig. 10.

Zoomed views of arteries (top row) and veins (30 mm from artery) at a 147 degree view angle, for conventional geometry. (a) and (d), 5 degree tomographic angle. (b) and (e), 5 degree tomographic angle after image space interpolation. (c) and (f), 6 degree tomographic angle.

Fig. 11.

Inverse geometry (*SBDX*) *TACs* for the *artery* and the *vein* at a distance of 30 mm from the artery, (a). Zoomed view of the artery (b) and the vein (c) at a 147 degree gantry angle, for inverse geometry (*SBDX*).

Summary of results for all configurations and vessels. Maximum Deviations (MaxDev) are calculated as the largest absolute difference between measured and ground truth TACs and expressed as a percentage of the peak ground truth value. Relative Root-Mean-Square Deviations (rRMSD) are also expressed percentages.

Table 1

Geometry	Configuration	Artery: MaxDev (rRMSD)	Vein (20 mm): MaxDev (rRMSD)	Vein (30 mm): MaxDev (rRMSD)	Vein (40 mm): MaxDev (rRMSD)	Vein (50 mm): MaxDev (rRMSD)
Conventional	Standard 4D DSA	19.8 (4.5)	4.0 (3.5)	6.6 (3.1)	22.8 (4.4)	12.8 (4.1)
Conventional	12 degree tomo angle	3.9 (2.5)	6.8 (3.7)	6.7 (3.2)	7.0 (3.1)	6.8 (4.0)
Conventional	6 degree tomo angle	4.1 (2.6)	5.7 (3.7)	3.9 (3.1)	7.0 (3.1)	5.6 (3.9)
Conventional	5 degree tomo angle	12.6 (2.8)	19.2 (4.2)	43.9 (5.3)	5.9 (2.9)	5.4 (3.8)
Conventional	5 degree tomo angle with interpolation	3.9 (2.6)	5.0 (3.5)	3.7 (2.9)	5.9 (2.9)	5.4 (3.8)
Inverse	SBDX	4.0 (1.9)	7.8 (5.5)	5.6 (4.5)	9.2 (4.6)	5.3 (3.0)