Bolus Chasing Computed Tomography Angiography Using Local Maximum Tracking Method

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Abstract: Tracking bolus peak position is a crucial issue for computed tomography angiography (CTA). In this paper, a local maximum tracking method is proposed and tested using real patient data. The method uses a second order polynomial to approximate bolus density function locally. By estimating the local maximum density position at next sampling time, bolus peak trajectory is closely followed. Experiments with Magnetic Resonance Angiography (MRA) patient data show a significant performance improvement using the proposed tracking method over the conventional constant speed counterpart.

Keywords: Bolus Chasing; Computed Tomography Angiography; Local Adaptive Control

Reference

Biographical notes:

1 INTRODUCTION

It was reported in American Heart Association news 12/06/2005 that more than 12 million Americans suffer from peripheral arterial disease (PDA). Today, more and more clinics use Computed Tomography (CT) Angiography to evaluate patients with PDA (Fleischmann, 2006; Sheafor, 1998). Before performing a CT scanning, one injects a certain amount of contrast material (bolus) into a vein, and administrates it through a temporal narrow window (CT gantry) during the whole period. Better diagnosis image needs to scan higher enhancement of the bolus while it travels along the artery. In the ideal case, the bolus peak enhancement and the patient table are synchronized.

In clinic, CT operator uses CT fluoroscopy to monitor the bolus arrival and then moves CT table at a pre-set
constant scanning speed. This is far from optimal because bolus rarely moves at a constant speed due to its complex dynamics which is determined by many factors, such as patient characteristics, contrast injection (Bae, 2003; Sheafar, 1998). Non-synchronization means more dose and radiation exposure to the patient. Also, the Mis-alignment will result in worse diagnosis image.

Recently, more and more works have been published on CT contrast enhancements. Some investigated the relationship of contrast enhancement and patient demographics, detailed in Filippo (2002). However, little correlation has been found except patient weight; Some studied optimal bolus geometry (Bae, 1998, 2000; Becker, 2003; Fleischmann, 2000; Kopka, 1996); Some worked on the bolus dynamics and model (Blomley, 1997; Claussen, 1998; Fleischmann, 1999). The later two are concentrated on obtaining a prolonged peak geometry by optimizing the injection pattern. A problem with these approaches is that these methods are not practical due to unknown patient’s characteristics. To obtain a better diagnosis image with a lower dose, bolus chasing technique is a practical way which tracks the peak enhancement of the bolus during CT scanning. In Wang (2000), a full bolus dynamic model was developed and based on this model, bolus concentration can be computed with respect to time as well as location. This model assumes all the information with respect to unknown patient’s parameters and is therefore impractical. Some bolus tracking methods are proposed in the literature, e.g., for X-Ray Periperal Angiography Wu (1998) and for Magnetic Resonance Angiography (MRA) (Ho, 1999; Kruger, 2005). In Kruger (2005), a dual-velocity continuously moving table acquisition for MRA is proposed. It demonstrated that with a higher velocity for upper part of body, and lower velocity for lower part of body produces a better diagnosis image. In other words, a constant speed is not the optimal method for CT scanning. Though these methods are useful, bolus chasing in DSA or MRA is quite different from bolus chasing in CTA. In DSA and MRA, the field of view is much wider, while in CTA, the field of view is very narrow which makes chasing much harder.

In our previous work, the bolus dynamic was studied Cai (2006b) and a peak position prediction method was proposed and applied to an experiment with actual bolus peak trajectory data Bai (2003). Using the assumption that current bolus peak position is available all the time, the controller shows good prediction capability for next peak position even with certain noise. Recently, a dispersion tracking method based on bolus local information Cai (2006a) was proposed that demonstrates good tracking results with actual bolus peak enhancement data. However, it needs the information on the peak value which is not available during the scanning. The above two methods have to be modified for on-line applications due to some assumptions.

The contribution of the paper is a local maximum tracking method that shows promising results on the actual bolus data. The paper is organized as follows. Section 2 studies bolus geometry and dynamics based on the actual MRA data. A model describing the bolus dynamics is developed. In section 3, we present the local maximum tracking method. Section 4 gives the numerical results using the actual patient data. Comparisons with the conventional constant speed table control scheme are made that demonstrate superior performance of the proposed method.

## 2 Bolus Model Development

### 2.1 Bolus Model Review

Bolus model is a crucial step in the bolus chasing CTA. Only after a reasonable model is obtained, the bolus tracking becomes possible. There exist several ways to describe a bolus propagation characteristics:

- Spatial curves that describe bolus densities along the artery at a certain time instant (see Figure 3 bottom plot);
- Temporal curves that describe bolus densities at a certain location (see Figure 3 top plot);
- 3D bolus profiles that combine the former two.

Much work has been reported in the literature to fit a bolus profile with temporal curves. In Blomley (1997), a Gamma variate function was suggested to describe the aortic time-density curve

\[
B(t) = k(t - t_0)^a e^{\frac{(t - t_0)}{\tau}}
\]  

where \( B \) represents the bolus density of the contrast, \( k, a \) and \( b \) are fitting parameters, \( t \) is time and \( t_0 \) is the arrival time of contrast bolus at the aortic region. (1) has advantages to calculate the curve peak height, curve mean transit time and rise time. In Stow (1954), empirical formula

\[
B(t) = C_p e^{-kln^2 \frac{(t - t_a)}{(t_p - t_a)}}
\]

was proposed, where \( C_p \) and \( t \) denotes maximum concentration and time respectively, and \( k, t_a, t_p \) are fitting parameters. Both of above two models work well for a typical bolus temporal curve locally. The problem is that neither is able to fit the bolus curve for a large range, for example, the whole aorta area.

Another well known function is the lagged normal density model Bass (1966),

\[
B(t) = \frac{m_i}{Q} \left( \frac{1}{\sqrt{2\pi}\sigma} \otimes e^{-\frac{(t - t_0)^2}{2\sigma^2}} \right) \left( 1 e^{-\frac{t}{\tau}} \right)
\]

where \( t \) is time, \( m_i \) the contrast material injected, \( Q \) the flow rate and \( \otimes \) denotes the convolution. \( \sigma, t_e \) and \( \tau \) are fitting parameters. The term in the bracket is the convolution of Gaussian function and unit decay function, whose area is one. It has been shown that this model improves the previous two functions.
2.2 3D Bolus Fitting

It is highly desirable to be able to compute the bolus density at any time instant and at any location in the region of interest after the contrast injection based on a model. Clearly, a simple model is preferred that will facilitate the design and validation of the controller. Unfortunately, no such a model exists in the literature. To develop such a model, we have collected a large number of Magnetic Resonance Angiography (MRA\textsuperscript{1}) data from the University of Iowa Hospital and Clinic, which show the bolus dynamic in the aorta area as a function of time and location. The data is in the form of a sequence of images with the frame rate one second per image. Figure 1 (a) shows one frame of the MRA image. To develop a bolus dynamic model, we first extract the bolus information from the MRA data as follows:

1. Define the region of interest (ROI) in the frame, see Figure 1 (b);
2. Filtered each frame with a low pass filter;
3. Subtract the 5th frame from each frame (the 1st frame has too much transients, see Figure 1 (c)) to reduce the background noises;
4. Mask ROI to each frame and set zero to all the pixels out of the ROI (see Figure 1 (d);
5. Calculate the mean pixel value for each row in the ROI. A spatial curve is obtained for that frame (moment);
6. Repeat 2)-5) for each frame till the last frame.

A 3D bolus profile is obtained after combining all spatial curves together (x-location, y-time, z-pixel value)(see Figure 2). Typical bolus temporal and spatial curves are shown in Figure 3.

Once a bolus profile is established, the next step is to fit it into a 3D parametric model. In this work, we adopt the model (3). However, to have a single model for a wide range of the region of interest, we allow \( m_i/Q = K(y), \tau(y), \sigma(y) \) and \( t_c(y) \) be functions of location \( y \). This leads to

\[
B(t, y) = \frac{K(y)}{\tau(y)\sqrt{\pi}} e^{-\frac{t - t_c(y)}{\tau(y)^2}} \int_{-\frac{\alpha(y)}{\sqrt{\tau(y)}}}^{t - \alpha(y)} z^{-2}dz \quad (4)
\]

where \( \alpha(y) = t_c(y) + \frac{\sigma(y)^2}{\tau(y)} \). Immediately, we face a difficulty that though the model (4) is parametric, no a priori information on the function forms of \( K(y), \sigma(y), \tau(y) \) and \( \alpha(y) \) are available. On the other hand, however, note that the actual bolus dynamic \( B(t, y) \) is available supplied by the MRA data. Moreover, at a given location, say at \( y = y_i \), the unknown parameters \( K_i = K(y_i), \sigma_i = \sigma(y_i), \tau_i = \tau(y_i) \) and \( \alpha_i = \alpha(y_i) \) are constants independent of time that provide the information on the bolus density at

\textsuperscript{1}The unit of MRA pixel value is different from CTA. In this paper, we treat pixel value in the MRA image as density level.
Table 1: Fitting error for 8 patients

<table>
<thead>
<tr>
<th>Patient</th>
<th>Fitting error</th>
<th>Fitting error</th>
</tr>
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<tbody>
<tr>
<td>1</td>
<td>0.0053</td>
<td>0.0064</td>
</tr>
<tr>
<td>2</td>
<td>0.0056</td>
<td>0.0043</td>
</tr>
<tr>
<td>3</td>
<td>0.0051</td>
<td>0.0109</td>
</tr>
<tr>
<td>4</td>
<td>0.0085</td>
<td>0.0207</td>
</tr>
</tbody>
</table>

The goal of control is to synchronize the table position with the bolus peak at each time by adaptively control the CT table. By doing so, the signal to noise ratio could be maximized. The on line bolus dynamics information is obtained by the re-constructed CT images which is at $\Delta t = 1/3$ second per rotation. The overall control system consists of four components. The first one is imaging acquiring and processing that provides real time bolus density at scanned location. The second one is a predictor. Based on a bolus dynamics model and observed measurements, it predicts future bolus peak position. Since the bolus dynamics is unknown, the model inevitably involves some unknown parameters. Thus, the estimator is the third part that estimates unknown parameters on-line. The final part is a patient table driven by a motor. The motor takes information from the predictor and moves the table so that the imaging aperture and the bolus are synchronized. For the CT table part, most existing control systems use an AC or DC stepping motor servo system to move the table. Mechanically and electronically speaking, the system is very complicated for patient comfort and safety. Because of the stepping motor serve system, however, the mathematical equation that describes the CT table motion is surprisingly simple. In addition, the currently available stepping motor servo systems in CT are able to move the patient table very quickly and precisely. Therefore, the key in this control system is on line estimation and prediction.

3.1 Global model

Control based on the global model (5) seems to be trivial. If the model (5) and the parameters $K(y)$, $\sigma(y)$, $\tau(y)$ and $\alpha(y)$ were available, the peak density of $B(t,y)$ for any given time $t$ would be calculated and the control is to move the patient table to that location. There exist several inherent difficulties however. Some are fundamental and others are practical. First, the parameters $K(y)$, $\sigma(y)$, $\tau(y)$ and $\alpha(y)$ are unknown. To implement any control scheme, those parameters have to be estimated on line. The problem is that the field of view for a CT is about 10mm wide, i.e., only local information within 10mm can be detected from the constructed CT images. Therefore, on line estimation of those parameters for the entire region is theoretically impossible. Secondly, the model (5) is highly nonlinear in those unknown parameters and the outcomes of adaptive estimation algorithms are often local minima that depend largely on the initial guess. Even if the global information were available, no adaptive algorithms would guarantee that the obtained estimates could be close to the true but unknown values, which is confirmed again and again by a large number of computer simulations. This is a serious problem for control design. Thus, the global model (5) does provide valuable insights on the bolus dynamics. Control based on this global model on the other hand does not seem possible.

3.2 Local model

To overcome the problem with the global model, we propose a control scheme based on a local model. The idea is
At time $t_k = k\Delta t$ and location $y_k$, the control scheme has to determine the bolus peak position at time $t_{k+1} = (k+1)\Delta t$.

$$y_{k+1} = \arg\max_{y \geq y_k} B(t_{k+1}, y)$$

Since $\Delta t$ is small, it is justified to assume that $y_{k+1} - y_k$ is reasonably small.

Though highly nonlinear, the global model (5) is fairly smooth. Thus, given the current bolus density value $B(t_k, y_k)$, its neighborhood information can be accurately estimated by a second order Taylor expansion

$$B(t, y) \approx B(t_k, y_k) + \nabla_t B|_{(t_k, y_k)}(t - t_k) + \nabla_y B|_{(t_k, y_k)}(y - y_k) + \frac{1}{2} (t - t_k)^T \nabla^2 B|_{(t_k, y_k)} (t - t_k)(y - y_k)$$

$$= a_0 + a_1 t + a_2 y + a_3 t^2 + a_4 ty + a_5 y^2$$

for some $a_0, a_1, a_2, a_3, a_4$ and $a_5$, which will be obtained on line through adaptive estimation algorithms. Figure 5 shows one simulation where the dash line is the actual bolus density function at $t_{k+1} = (k+1)\Delta t$ as a function of location $y$ given by the global model and the solid line is obtained by the second order polynomial approximation expanded at the point $(t_k, y_k)$. Clearly, in the neighborhood of $(t_k, y_k)$, they are close.

There are several issues in implementing the local control scheme. First is how to extract local bolus information on line. Note that most of commercially available CT today are multi-sliced, i.e., with one rotation of the gantry, multislices of images are constructed. For simplicity, we assume three slice per rotation in this work. Now, suppose the current time and location are $t_k = k\Delta t$ and $y_k$ respectively. With one rotation, the bolus density values at $y_k, y_k + \Delta y$ and $y_k - \Delta y$ are obtained. Combined with two previous consecutive measurements at times $t_{k-1}$ and $t_{k-2}$, nine point values are observed

$$B(t_{k-3+i}, y_{k-3+i} + (j-2)\Delta y), \ i, j = 1, 2, 3. \quad (7)$$

The second issue is to estimates the coefficients $a_i$ in the Taylor expansion. This is accomplished by the least squares

$$a_i = \arg\min_{a_i} \sum_{i=1}^{3} \sum_{j=1}^{3} \left( B(t_{k-3+i}, y_{k-3+i} + (j-2)\Delta y) - \left[ a_0 + a_1 t_{k-3+i} + a_2 y_{k-3+i} + (j-2)\Delta y) + a_3 t_{k-3+i}^2 + a_4 (y_{k-3+i} + (j-2)\Delta y) t_{k-3+i} + a_5 (y_{k-3+i} + (j-2)\Delta y)^2 \right] \right)^2$$

The last step is to determine the bolus peak at time $(k + 1)\Delta t$ which is accomplished by maximizing

$$y_{k+1} = \arg\max_y \{ a_0 + a_1 t_{k+1} + a_2 y + a_3 t_{k+1}^2 + a_4 y t_{k+1} + a_5 y^2 \}$$

under the constraint $y_{k+1} \in (y_k + y_i, y_k + y_u)$, where $y_i$ and $y_u$ are lower bound and upper bound of the CT travel length during $\Delta t$, respectively. In the experiments, we set $y_u = V_{\max} \Delta t$, which is limited by the maximum table velocity $V_{\max}$, and $y_i = 0$. The idea is illustrated in Figure 6, where the solid curve represents the bolus peak trajectory and stars denote the positions where the bolus density are measured, totally nine points, which are used to estimated the coefficients of the Taylor expansion. The bold bar is the search area for the bolus peak location at time $t_{k+1} = (k+1)\Delta t$.

Figure 7 summarizes the control scheme, where threshold is set to determine when to start the controller. Once the observed bolus density reaches the threshold, controller is activated. Otherwise, we continue to scan the starting position.
4 Results

In this section, we test the proposed local maximum tracking (local adaptive) method on the actual MRA data. Recall again tracking the bolus peak position at each time is the control objective. In order to show the advantage of this control method, we compare the results with constant speed method, which is the gold standard in clinic practice.

4.1 Tracking error and density comparison

The maximum velocity for the local adaptive method is set to 10 cm/sec (Fuchs, 2003), which is acceptable for most conventional CT tables. Sampling time is again set to $\Delta t = 1/3$ seconds. Therefore, the maximum search range is 10 cm/3 = 3.33 cm in the local method. Constant speed was set to 3 cm/sec, which is proved to be a good velocity in clinic applications. Threshold was set to 3 for both local adaptive method and constant speed method. Figures 8-11 show the simulation results. In all figures, the top plots show the peak trajectory over time for actual MRA data (dashed), local adaptive method (solid) and constant speed (dotted); the bottom plots show the actual density values for corresponding trajectory.

A higher bolus density will produce a higher SNR (signal to noise ratio), which results in a better image quality. Therefore, comparing the highest achievable density value and the density valued achieved by the proposed control method would be an effective criterion. Also, it is useful to compare the density values achieved by the proposed method and the conventional constant speed control method respectively. The results are summarized in Figure 12. In Figure 12 (a), "Mean Density" denotes the mean density over the scanning time; while in Figure 12 (b) and (c), "Maximum Density Error" and "Maximum Density Error" are the mean and the maximum of the difference between the observed density and the actual maximum density over the scanning time, respectively. We compare all of the three values for the proposed local adaptive method and the conventional constant speed method. It can be seen that the proposed local adaptive method increases the mean density value by over 25% and decreases the density error by 35%. In addition, the maximum density error is reduced under around 5, which is good to the CT image.

4.2 Robustness on starting time (threshold)

Accurately estimating the bolus arrival time and activating the control is a critical part of CTA (Hittmair, 2001; Paulson, 1998; Schweiger, 1998). In particular, the traditional constant speed control is extremely sensitive with respect to the activating time. Activating the control either too early or too late comprises the performance substantially. In practice, a test bolus with a small dose is often administered to test the arrival. A problem is that the arrival times for a small dose contrast and the full dose contrast are not necessarily consistent. The other way is to monitor on line the arrival of the leading edge of the contrast bolus. A problem is what constitutes the leading edge that has to be compared to a prescribed threshold. If the threshold is...
One advantage of the proposed local adaptive control is its adaptability. Because of that, the method is very robust with the activating time. Figures 8 and 13 are simulation results for different thresholds (3 and 7, respectively) based on Patient #1 data. It is noticed that the performance for local adaptive method does not change much, while the performance of constant speed method improves for threshold 7. In Figure 14, we plot the performance of local adaptive method (red star) and constant speed (black cross) against a set of threshold, where performance is measured by percentage of the mean observed density over the maximum density during the scanning time. It shows that the local adaptive method is robust and performs equally well for a wide range of thresholds. While for the constant speed method, the performance gets better with higher threshold, and it varies greatly depending on the choice of the "correct value of threshold", which is easily taken as the highest density of the bolus. Unfortunately, the highest density is unknown before the scanning, and threshold being higher than observed will not start the CT table automatically. On the other hand, we can choose a relatively low threshold for local adaptive method and the performance would be almost same as "the best threshold" does.
5 Conclusion

In this paper, a local adaptive tracking method is proposed based on actual MRA data and practical CT specifications. The objective is to synchronize the bolus peak position and CT gantry leading to a higher SNR. Simulation results show that bolus peak position is well estimated by using a local 2nd order polynomial function as approximation function. Comparison with the conventional constant speed method demonstrates the increased average density and robustness to a wide range of thresholds. Future work will be focused on validating the method in clinical trials.

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