Preliminary Study on the MR Temperature Mapping using Center Array-Sequencing Phase Unwrapping Algorithm

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Purpose : To investigate the feasibility and accuracy of Proton Resonance Frequency (PRF) shift based magnetic resonance (MR) temperature mapping utilizing the self-developed center array-sequencing phase unwrapping (PU) method for non-invasive temperature monitoring.

Materials and Methods : The computer simulation was done on the PU algorithm for performance evaluation before further application to MR thermometry. The MR experiments were conducted in two approaches namely PU experiment, and temperature mapping experiment based on the PU technique with all the image post-processing implemented in MATLAB. A 1.5T MR scanner employing a knee coil with T2* GRE (Gradient Recalled Echo) pulse sequence were used throughout the experiments. Various subjects such as water phantom, orange, and agarose gel phantom were used for the assessment of the self-developed PU algorithm. The MR temperature mapping experiment was initially attempted on the agarose gel phantom only with the application of a custom-made thermoregulating water pump as the heating source. Heat was generated to the phantom via hot water circulation whilst temperature variation was observed with T-type thermocouple. The PU program was implemented on the reconstructed wrapped phase images prior to map the temperature distribution of subjects. As the temperature change is directly proportional to the phase difference map, the absolute temperature could be estimated from the summation of the computed temperature difference with the measured ambient temperature of subjects.

Results : The PU technique successfully recovered and removed the phase wrapping artifacts on MR phase images with various subjects by producing a smooth and continuous phase map thus producing a more reliable temperature map.

Conclusion : This work presented a rapid, and robust self-developed center array-sequencing PU algorithm feasible for the application of MR temperature mapping according to the PRF phase shift property.

Index words : MR phase image
Image processing
Phase Unwrapping (PU)
MR temperature mapping

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Introduction

The 2D Fourier Transform (FT) of the complex (real and imaginary) raw data results in complex output that could be converted to magnitude and phase images. Information, such as field inhomogeneity or the velocity of blood flow, can be encoded in the phase of the MRI signal. Nevertheless, due to the ambiguity in interpreting the information conveyed by the phase of the signal, the magnitude of the complex MRI signal is the information that is primarily used for clinical diagnosis. This will inevitably result in the loss of important information which is and can only be encoded in the phase of the signal (1, 2).

This study only dealt with the reconstructed phase image for unwrapping and temperature mapping purposes. The phase of any complex signal represents a rotation, with direction and amplitude, and is characterized as a single quantity by coherent processing and it is an important property of many classes of signals. However, given any complex data, the phase can only be derived as modulo-2π which gives a scalar value (known as the principal value) contained in a given range, usually $[-\pi, \pi)$ and the true phase rotation cannot be known unambiguously from a single scalar value. For instance, rotations $\pi/2$ and $-3\pi/2$ are indistinguishable since $-3\pi/2$ falls outside the unambiguous range $[-\pi, \pi)$ and is hence wrapped around. In this work, the specific artifact - phase wrapping, is first to be eliminated by the self-developed phase unwrapping (PU) technique before the computation of MR temperature distribution (3, 4).

Artifacts often corrupt MRI images. Wrapping operation is a nonlinear process which implies that the acquisition system can only measure phase modulo-2π, the so-called principal phase values, or wrapped phase values because the absolute phase is wrapped into the interval $[-\pi, \pi)$. In phase unwrapping, the problem at hand is to estimate the number of integer multiples of 2 π to be added to the wrapped map in order to render a map of the true phase (5, 6). Mathematically, the PU operation is expressed as follows:

$$\phi(x) = \psi(x) + 2\pi k(x) \quad [1]$$

where $\phi(x)$ is the estimated unwrapped function (the absolute value), $\psi(x)$ is the measured (wrapped) modulo-2π phase value, and $k(x)$ is the integer value at each pixel which specifies the corrective offset required, and x is a spatial variable (7, 8).

Figure 1 plots the true and wrapped phase of Equation 1. It is seen that the wrapped phase $\psi(x)$ is plotted as the sawtooth pattern shown by the dashed line. An estimate denoted by $\phi(x)$ can be obtained by adding an appropriate multiple of 2π radians to $\psi(x)$. Visually it is easily determined that nothing needs to be added to $\psi(x)$ for $0 \leq x \leq 40$ to give a correct estimate of the unwrapped phase within that same interval. Similarly, for $40 \leq x \leq 140$, one multiple of 2π must be added, whereas $2 \times 2\pi$ must be added in the interval $140 \leq x \leq 250$ (2).

PU finds many important applications in MRI, ranging from field mapping to flow imaging. Many PU algorithms have been proposed in the past to improve the noise immunity of the unwrapping algorithms. These existing unwrapping techniques for MR applications are based on approaches such as path following algorithms, minimum norm methods, Bayesian approach, and parametric algorithms. These methods can lead to unacceptably complicating algorithms and the requirements of branch cuts and seed point selection. The proposed PU approaches the path following technique by devising an improved, more rapid, and simpler algorithm for the purpose of MR thermal mapping.

MRI is playing an increasingly important role in local drug delivery and in the control of local hyperthermia

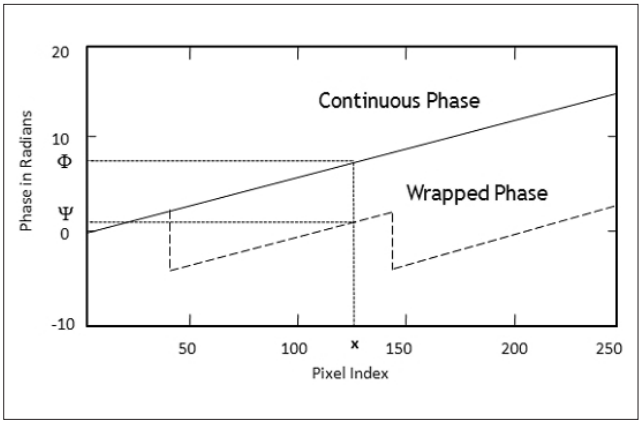

Fig. 1. Plot of the true and wrapped phase of Equation 1. The true phase is a linear function of x (solid line), whereas the wrapped phase $\psi(x)$ is the sawtooth function (dashed line). Phase unwrapping is accomplished by detecting the wrapped phase jumps and adding an appropriate multiple of 2π radians [2]

for drug activation and thermotherapy - temperature measurement and temperature mapping. MRI temperature measurement may be based on various parameters: relaxation time T1, diffusion coefficient (D), Proton Resonance Frequency (PRF), proton spectroscopic imaging, and temperature-sensitive contrast agents as illustrated in Table 1 (10, 11). These vary with respect to sensitivity, the linearity of the effects with temperature, their dependence on coagulation, dependence on field strength, and the question of whether absolute or relative temperature is measured (12, 13). They also differ in their sensitivity to pulse sequences, speed, potential artifacts, and motion sensitivity. PRF shift is currently the most commonly used temperature sensitive MR parameter especially for most mid or high field ($\geq$1T) applications as it achieved excellent linearity and near-independence with respect to tissue type, together with good temperature sensitivity (14, 15). As the phase change will depend on the temperature change, this principle will be used to compute temperature maps for the rest of the work (16, 17).

The novel approach of this work is to integrate the self-developed center array-sequencing PU technique with the PRF phase shift based temperature mapping method in order to effectively improve the precision of thermal map by removing the phase wrapping artifacts that normally corrupted the MRI phase images. The stand-alone program has been investigated using the simulation and MR experimental data with various subjects that demonstrated the possibility of mapping MR temperature variation according to the self-developed PU program.

Materials and Methods

All MR experiments were conducted at the Pusan Paik Hospital on a 1.5T MRI scanner (Signa Echospeed, General Electric, Milwaukee, WI, USA) using a knee coil. As temperature-related frequency shift can be detected using phase images obtained from a gradient echo sequence, the T2* Gradient Recalled Echo (GRE) sequence was applied throughout the experiments. The MRI parameters employed throughout this study are summarized in Table 2. The experiments were approached in two ways, namely the center array-sequencing PU experiment for the evaluation of the PU program and MR thermal mapping experiment using the PU method for the assessment of the possibility in this integrated work. The center array-sequencing PU has been tested with both simulated and experimental data, where the subjects included water phantom, orange, and agarose gel phantom which generated a variety of wrapping patterns. The preliminary attempt for mapping MR temperature distribution using the self-developed PU method has been tested with agarose gel phantom only. The water phantom was filled with copper (II) sulfate pentahydrate and sodium chloride reagents in a cylindrical bottle, which is also known as the lower extremity coil phantom. The agarose gel (Bio-

Table 1. Comparison of Several Techniques for NMR Temperature Imaging [9]

	Absolute or relative temperature	Linearity	Sensitivity	Spatial resolution	Temporal resolution (acq. Time)	Motion artifacts	Sequence type	Field dependence of the effect[a]
Diffusion	Relative	−	−/+	+	+	—	SE (GE)[b]	Negligible
T_1	Relative	−	−	+	+	−/+	SE (GE)[b]	Less at high field
PRF	Relative	+ +	+[c]	+	+ +	−/+	GE	Linear increase with field
Spectroscopy	Absolute	+ +	−/+	—	—	−	SE or GE	Linear increase with field
Temperature-sensitive contrast agent	Absolute	—	+ +	−/+	−/+	−/+	SE (GE)[b]	Small

[a]Not taking into account the approximately linear increase of SNR with increasing B0 field
[b]Spin echo (SE) preferred above gradient echo (GE) to avoid phase dispersion due to PRF effect
[c]For high field
* + + = excellent; + = good; −/+ = average; − = poor; — = very poor.

Rad Laboratories) phantom (3%) was filled in a petri dish with dimension: $\phi \times H = 90 \times 20$ mm^2. In order to increase the SNR level, 0.6mM/l $MnCl_2$ was added to the gel. After the acquisition of the MR raw data, another self-developed MRI image reconstruction program in Visual C++ was implemented to generate the respective phase images for further image processing. The entire image processing in this work was predominantly performed offline and executed in MATLAB - MR temperature mapping using PU technique.

A. Center Array-Sequencing PU Experiment

The simulated wrapped phase image is acquired via a self-developed simulation program. The 256×256 simulated image has three phase jumps with added salt and pepper noise, and is elliptically shaped as shown in Figure 2. The robustness of the algorithm to noise was also examined on the simulated wrapped phase images when the amount of added noise was increased which synthetically deteriorated the SNR levels.

In principle, phase unwrapping is simple but in practice it is rather more difficult to implement. The problem is that it is highly sensitive to errors in regions with low signal-to-noise. These errors can propagate into areas with high signals, and lead to a catastrophic failure of the unwrapping process. The simple unwrapping algorithm which was presented in the previous work (9) used the recursive 1D technique that executed in the horizontal manner without considering the phase wrapping directions for the estimation of $k(x)$ values. This simple PU method initiated from the top leftmost pixel and unwrapped whenever there is phase discontinuity. This could result an erroneous unwrapped map that is not suitable and reliable for estimation of temperature variation. The performance of the currently proposed center array-sequencing PU method was compared with the previously suggested PU algorithm to demonstrate the reliability characteristic.

The revised center array-sequencing algorithm was to estimate the corrective offset $k(x)$ in Equation 1 which is the multiples of 2π values. To do this, each pixel value in the phase image is compared to its right, left, top, and bottom neighbors followed by a subtraction from the subsequent pixel that grows from the image center pixel out to the boundary pixels on each individual MR wrapped phase image. If the calculated phase difference value is identified as a phase jump, an appropriate number of integer multiples of 2π is to be added to the wrapped map in order to render a map of the true phase. When the wrapping is occurred in the negative direction which has the phase change from $+\pi$ to $-\pi$, it is needed to add the multiples of 2π to the current value. Likewise, if the wrapping is occurred in the positive direction which has the phase change from $-\pi$ to $+\pi$, it is needed to subtract the multiples of 2π to the current value. The summation of two subsequent phase difference values is also assessed in order to verify the contiguous phase variation from the genuine phase jump. When the contiguous phase variation is detected, there will be no PU operation and the current phase values will be maintained. In short, the proposed PU algorithm comprises of four principal steps namely pixel values conversion, phase values comparison, determination of phase jumps, and computation of k values.

In order to apply the PU method for MR temperature mapping, phase difference maps were acquired by subtracting a reference phase map from the objective phase map after the PU operation. Consider two sets of real (R) and imaginary (I) components acquired at two

Table 2. MRI Parameters Employed for the MRI Experiments with Various Subjects that are Applicable for Both the Phase Unwrapping and Temperature Mapping Experiments

Parameters \ Subjects	Water Phantom	Orange	Agarose Gel Phantom
TR (msec)	100	150	100
TE (msec)	15	30	20
Matrix	256×256	256×256	256×128
Field of View (mm)	160	240	120
Flip angle (°)	50	60	50
NEX	4	4	4
Slice Thickness (mm)	5	10	3

different time points; the phase difference ($\Delta\phi$) in radians is obtained by calculating the arctangent of the ratio of the imaginary part to the real part:

$$\Delta\phi = \phi_1 - \phi_2 = tan^{-1}\{(R_2I_1 - R_1I_2)/(R_1R_2 + I_1I_2)\} \quad [2]$$

B. MR Temperature Mapping Experiment

This experiment was approached by the application of the agarose gel phantom using the same conditions and MRI parameters as in the PU experiment. The heating source was a custom-made thermoregulating water pump which circulated boiling water to the phantom surface in a boxy heating chamber. Temperature measurement was done by a T-type thermocouple connected to the FLUKE 52$^{K/J\ Thermometer}$ thermocouple reader. Scanning was done while the subject was cooling down and raw data were reconstructed into the respective phase images before further post-processing was done.

In order to apply PU methods for MR thermal mapping, two datasets are acquired which differ only in the degree to which the phase is influenced by the parameter of interest. One dataset is used as a reference, and subtracted from the phase of the other. In this way, uninteresting phase components that are common to both images, such as the transmitter or receiver characteristics, or those of the digital filtering, are removed. Only the effect of the parameter remains. In this work, the reference images at ambient temperature (T_I = 22.3° C) were acquired before heating. The PU algorithm was applied where necessary before further quantification was performed. The temperature-induced phase changes obtained by subtracting the reference phase map from the objective phase map show up as areas where there is still

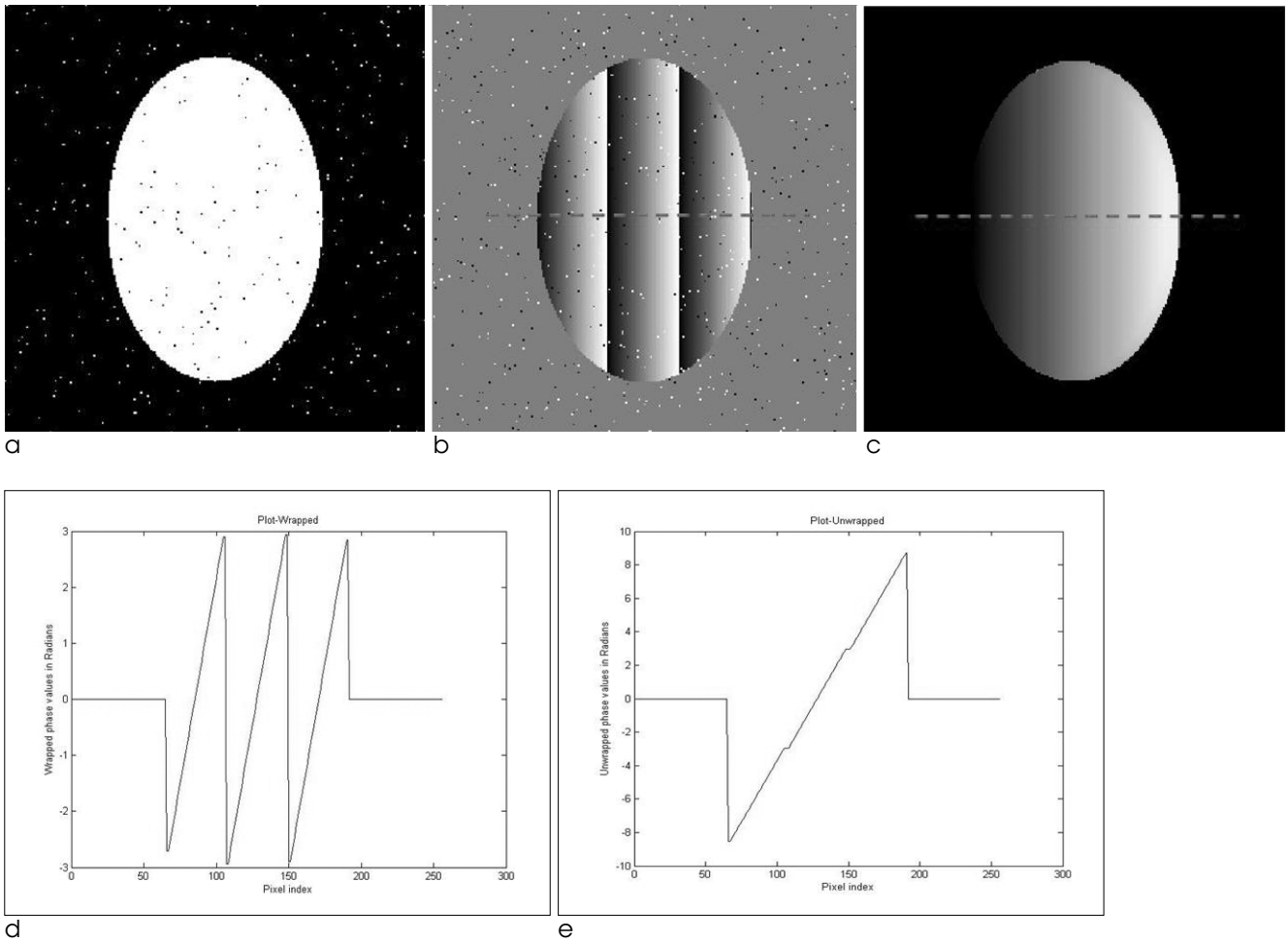

Fig. 2. Performance of center array-sequencing phase unwrapping algorithm on the simulated MR wrapped phase image added with salt and pepper noise. (a) Simulated MR magnitude image, (b) Simulated wrapped phase image, (c) Unwrapped phase image by the proposed method, (d) Horizontal plot of (b), and (e) Horizontal plot of (c).

residual signal after subtraction. Thus, the phase difference map was generated for the estimation of temperature variation.

Temperature-related frequency shift can be detected using phase images obtained from a gradient echo sequence. PRF shift thermometry uses changes in the phase of GRE images to estimate the relative temperature change ΔT, as given by:

$$\Delta T = \frac{\Delta \phi}{\gamma B_0 \alpha T_E} \quad [3]$$

where γ is the gyromagnetic ratio of hydrogen proton, B_0 is the strength of the magnetic field, T_E is the echo time in seconds, and α is the chemical shift per temperature change in units of ppm/° C.

Hence the change in temperature is approximately linearly proportional to the phase difference change. Assuming that the ambient temperature is denoted by T_I, hence the absolute temperature T_{abs}, could be estimated from:

$$T_{abs} = \Delta T + T_I \quad [4]$$

Thermocouple measurements were recorded before and during thermoregulating water pump application to determine absolute and maximal temperature increase. Thus temperature maps were computed to visualize temperature distribution

Results

A. MR Phase Unwrapping

The proposed center array-sequencing PU algorithm has been executed on both the simulated and experimental data. Figure 2 shows the MR simulated

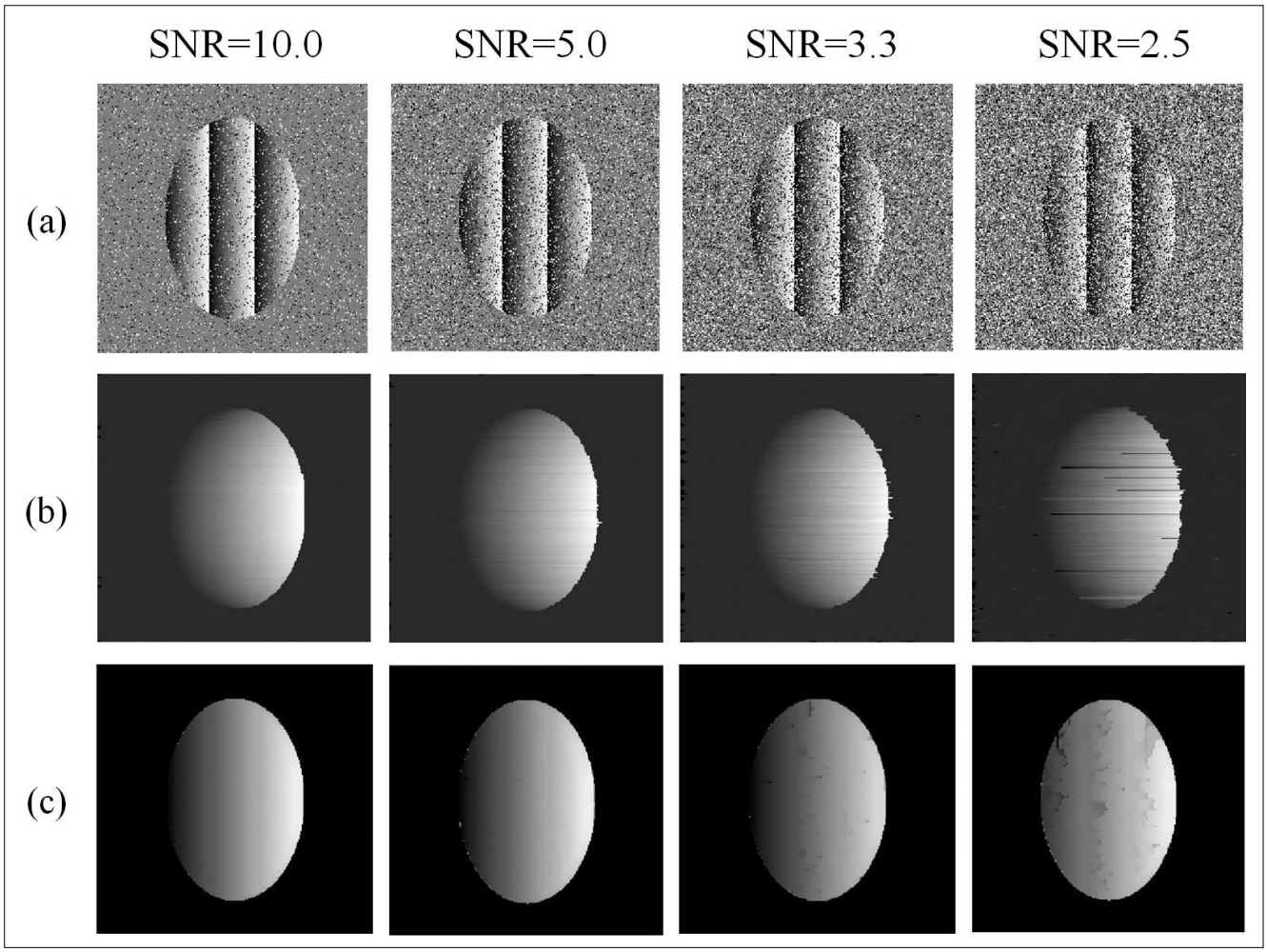

Fig. 3. Simulation of a wrapped phase map is shown in row (a). From left to right, the SNR deteriorates when the added salt and pepper noise level increases as indicated in the top row. Row (b) shows the result from applying the previously proposed [9] phase unwrapping method to the corresponding image in (a). Row (c) displays the improvement of unwrapping by implementing the proposed center array-sequencing phase unwrapping method.

magnitude (a) and phase (b) images with added salt and pepper noise. The wrapped phase image is scaled into the range of $[-\pi, \pi)$ that is represented in black and white for display. Apparently, the self-developed PU technique has successfully recovered those phase wrapping artifacts on the MR simulated phase image by producing a continuous and smooth phase map as illustrated in Figure 2(c). The performance and effectiveness of the proposed algorithm were analyzed by the plots of horizontal profiles along the middle line of the wrapped and unwrapped phase images. Figure 2(d) shows that the three phase jumps are constrained to the range of $[-\pi, \pi)$ whereas Figure 2(e) shows that the self-developed center array-sequencing algorithm has effectively rendered the wrapped phase to a smooth continuous plot of the unwrapped phase values.

In order to assess the robustness of the algorithm, the effect of noise was studied. Figure 3 demonstrates the noise test by adding various amounts of salt and pepper noise to the simulated wrapped phase image that generates a set of synthetic images with different SNR levels (Figure 3(a)). In comparison, the result of the previously suggested phase unwrapping method (Figure 3(b)) shows the propagation of several streak flaws, originating at the physical discontinuity throughout the entire image. The resultant unwrapped phase images in Figure 3(c) verified that the proposed PU method is highly immune to the effect of noise, making the center array-sequencing PU technique very robust.

MR experiments were investigated with three kinds of subjects: water phantom, orange, and agarose gel phantom. Figure 4 compares the performance of the

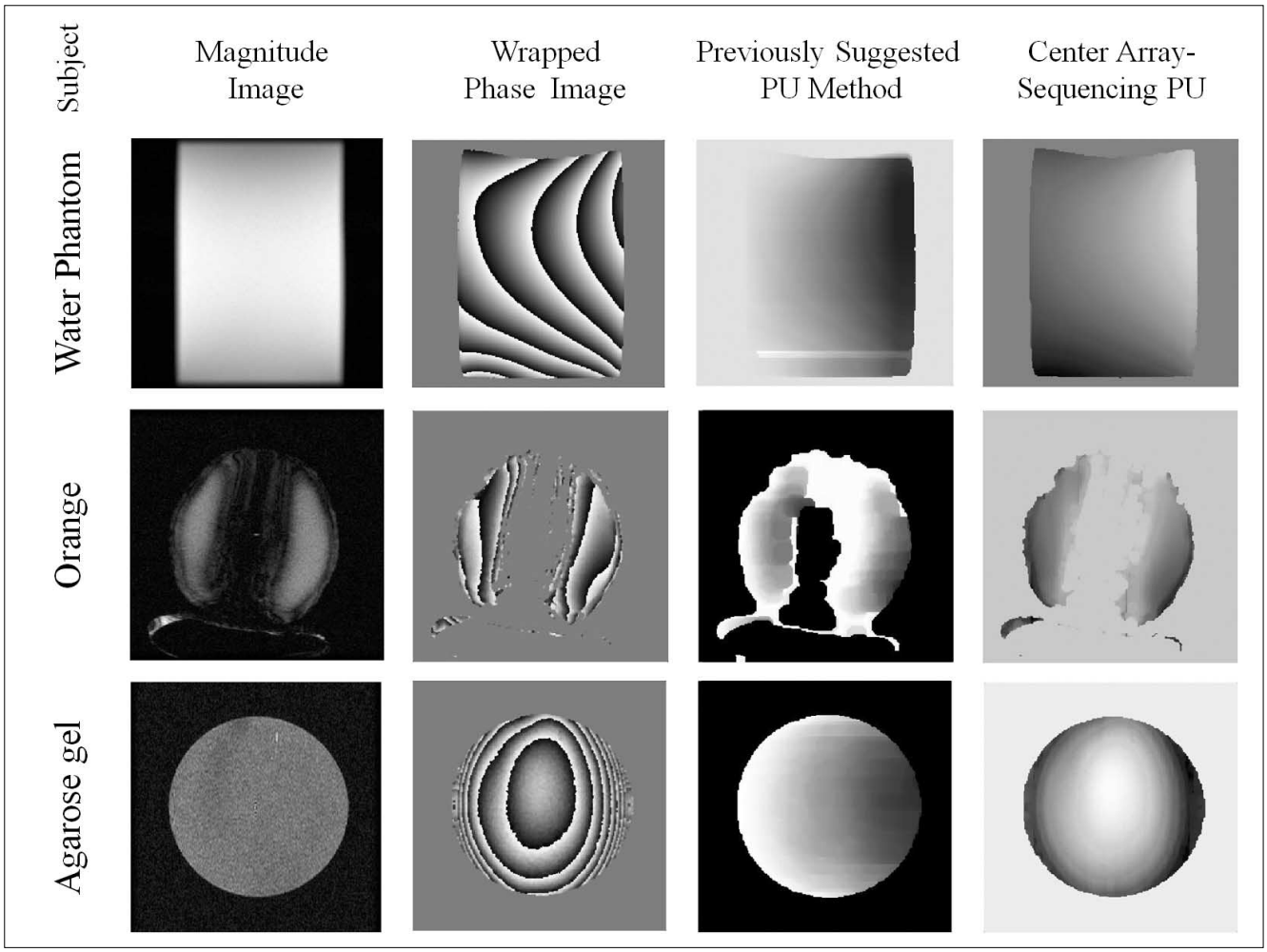

Fig. 4. Comparison between the previously suggested [9] and center array-sequencing phase unwrapping method on the MR wrapped phase images with various subjects

previously work on PU with the currently proposed PU method using various subjects as stated before. In these experiments, the PU algorithms were approached with three different phase wrapping fashion created by the subjects. As shown in the figure, the previously suggested PU method failed to recover the artifacts. Conversely, the center array-sequencing PU method successfully recuperates the phase wrapping artifacts regardless of the diverse wrapping patterns.

Table 3 presents the characteristics of the existing path following algorithms and their comparison with the proposed center array-sequencing PU method. The column labeled 'Identifies Residues?' indicates whether or not the algorithm explicitly identifies residues. The last column indicates whether or not the algorithm requires a quality map. Center array-sequencing and Flynn's minimum discontinuity algorithm can be used with or without a quality map (processing time for images with matrix 256×256 is only 1.198seconds). This table validates that the proposed PU method is

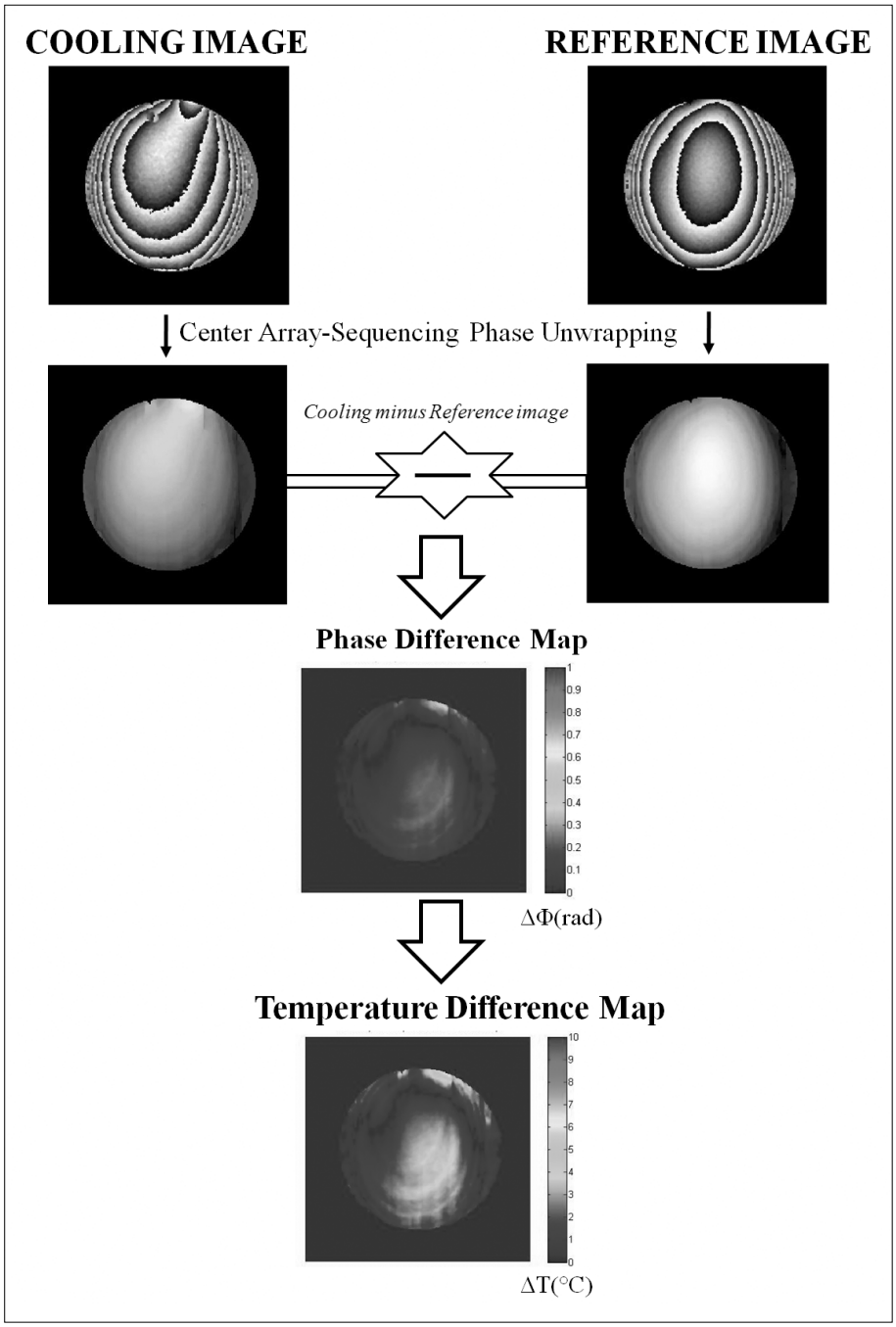

Fig. 5. Generation of phase difference and temperature change maps from the subtraction of unwrapped MR phase images

most rapid in comparison with other path following PU.

B. MR Temperature Mapping

PRF shift thermometry uses changes in the phase from the subtraction of the reference and objective phase maps to estimate the temperature change map. The reference image is referred to the agarose gel phantom imaged at ambient temperature, without the application of heating source; whilst the objective image is regarded to the agarose gel phantom imaged with varying temperature, after the application of

Table 3. Characteristics of the Existing Path-following Algorithms and Their Comparison with the Proposed Center Array-sequencing PU Method

Algorithm	Execution Time	Identifies Residues?	Quality Map Required?
Center array-sequencing	3 sec	n	y/n
Goldstein	30 sec	y	n
Quality	3 min	n	y
Mask cut	4 min	y	y
Flynn	20 min	n	y/n

Note: Besides the proposed algorithm which uses MATLAB, the rest of the algorithms were implemented in Visual C++. The execution times are given in minutes for a 1024×1024-pixels phase array on an IBM RS/6000 workstation. [2]

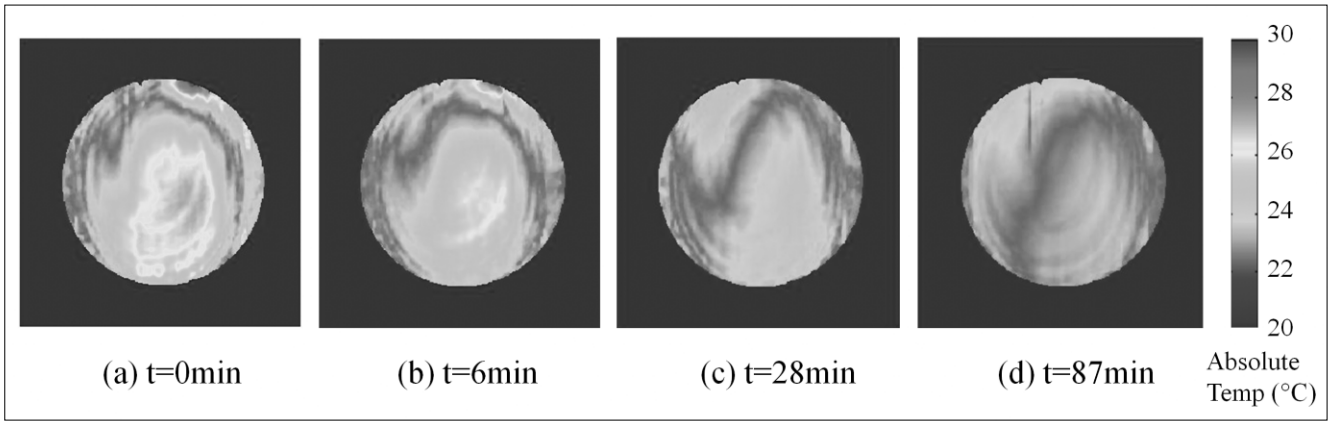

Fig. 6. MR absolute temperature maps when the agarose gel phantom is cooling down (a) Initial time, (b) 6min, (c) 28min, and (d) 87min later

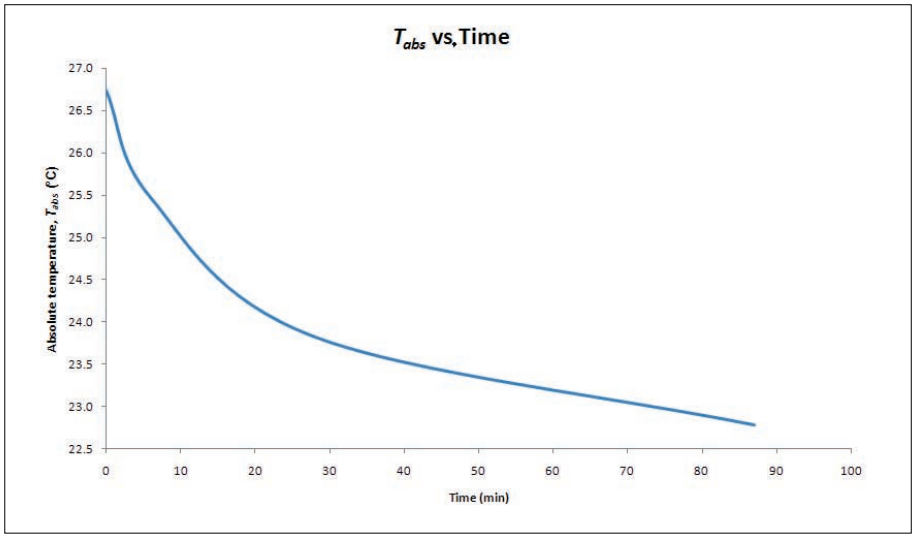

Fig. 7. Plot of the absolute temperature vs time for a period of 87 minutes from the center pixel value of the estimated absolute temperature maps

heating source.

Figure 5 presents the generation of the phase difference and temperature change maps from the subtraction of unwrapped MR phase images. As could be observed from the figure, the phase wrapping fashions between the reference and objective images reconstructed from the experimental raw data are different from each other. The resultant unwrapped phase images for both the reference and objective phase maps verified that the proposed PU technique is consistent and effective. Thus, phase difference map could be generated by subtracting reference phase map from the objective phase map after the PU operation. The generated phase difference map provides the linear relationship with the temperature change. The temperature difference map estimated from the phase difference map is obtained according to the Equation 3 in comparison with the temperature values measured by the thermocouple.

The maximum temperature induced in this experiment was 29.8° C before the cooling down process and the ambient temperature was recorded as 22.3° C. Figure 6 depicts the computed absolute temperature with time according to the Equation 4. Maximum temperature map is shown in Figure 6(a) with the estimated maximum absolute temperature T_{abs} = 29.8° C. As time passes by until t = 87 minutes (Figure 6(d)), the temperature distribution of the phantom reaches closely to the initial temperature T_I. The plot of the estimated absolute temperature with time for a period of 87 minutes is illustrated in Figure 7 according to the center pixel values obtained from the absolute temperature maps. The plot confirms that temperature change decreases with time in the cooling condition which is on the contrary to the heating condition.

Discussion and Conclusions

This study challenges the conventional MR thermometry by integrating the self-developed center array-sequencing phase unwrapping technique with temperature mapping for the sake of achieving a higher precision and reliable temperature monitoring especially during hyperthermic procedures. PRF shift thermal maps generated from magnetic resonance phase difference imaging provide thermal surgery guidance. It could be predicted that as temperature increases, more phase wraps will be generated with various wrapping fashions. The computed phase difference map and the estimated temperature difference map are reasonable to provide a means for the approximation of absolute temperature maps.

Future works include the assessment of reliability and confirmation of these results ex vivo. Numerous experiments should be done to verify the consistency of this work on clinical cases as well as to investigate the practicability of implementing real time monitoring of MR temperature variation with time. Further medical application of this study includes MRI guided hyperthermia surgery. In conclusion, this work has presented a robust PU technique feasible for the application of MR temperature mapping according to the PRF phase shift property.

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Center Array-Sequencing 위상펼침 기법의 MR 온도영상 적용에 관한 기초연구

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이광식[2] · 전재량[3] · 은충기[3] · 문치웅[1]

목적: 물체 내부의 온도를 비침습적으로 측정할 수 있는 양성자 공명 주파수 이동에 의한 MR 온도영상의 재구성에 center array-sequencing 위상펼침(PU) 기법을 적용시켜 그 성능 및 유용성을 평가하고자 하였다.
대상 및 방법: MR 온도 영상에 앞서 잡음 수준이 다른 타원형 팬텀들을 컴퓨터 모의 실험으로 제작하고 제안된 PU방법을 적용시켜 잡음에 대한 성능을 평가하였다. MR 실험은 PU 실험과 이를 이용한 온도분포영상획득 실험으로 구분하여 수행되었다. 1.5T MR 영상장치에서 무릎코일과 T2* 경사자장에코 펄스열을 이용하여 MR 영상을 얻었다. 물통, 오렌지, 아가젤 등의 팬텀을 실험 대상으로 하였고 자체 제작된 온수펌프 장치로 팬텀의 온도를 조절하였다. T 형 열전쌍 온도측정장치로 팬텀 온도를 측정하고 MR 온도영상 결과와 비교하였다. 획득된 MR영상의 위상분포는 제안된 PU방법으로 위상을 편 후 온도분포 영상을 재구성하였다. 가열 전 후의 온도변화와 MR 영상의 위상변화 관계를 이용하여 아가젤 팬텀 내의 MR온도분포 영상을 구하였다.
결과: 제안된 center array-sequencing PU 알고리즘을 이용하여 여러 팬텀에 대한 MR 위상영상의 접힘 현상을 기존 방법보다 간편하고 빠르게 제거할 수 있었고 이를 이용하여 MR 온도영상을 획득할 수 있었다.
결론: 본 연구는 제안된 center array-sequencing 위상펼침 방법이 잡음에 강하고 처리 속도가 빠를 뿐만 아니라 양성자 공명 주파수 이동의 성질을 이용한 MR 온도 영상 획득에 성공적으로 적용될 수 있음을 보였다.

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