An extension to UNFOLD to handle breathing motion, and flexibility in k-t sampling schemes

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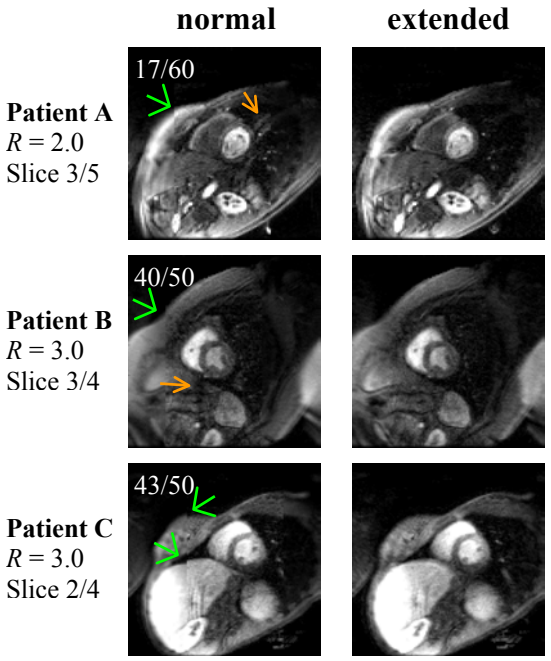
Introduction: "Unaliasing by Fourier-encoding the overlaps in the temporal dimension" (UNFOLD) is a fast-imaging method, used in dynamic imaging [1]. In myocardial-perfusion imaging, it has been reported that breathing motion may confuse the UNFOLD temporal strategy, leading to artifacts [2,3]. This work is an extension to the UNFOLD method, able to handle such disturbances. In the presence of breathing motion, significant artifact suppression was obtained. The method is flexible enough to handle other types of disturbances as well. As a second application, it enabled departures from a usual UNFOLD sampling scheme, in *k-t* space. Accordingly, it introduced new flexibility in the *k-t* sampling, useful (for example) for designing self-calibrated parallel imaging methods.

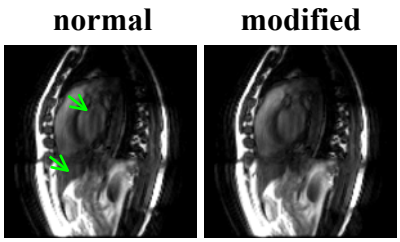
Theory: Suppose that parts of an object, because of motion, receive a modulation $m_d(\vec{k},\nu)$ in the spatial frequency - temporal frequency (i.e., *k-ν*) space. Correcting for the modulation is equivalent to changing reference system, from one attached to the scanner to one attached to the moving features. The acquired data can be represented equally well in a first space Ω_1 (fixed frame), or a second space Ω_2 (moving frame). The goal is to distribute the acquired signal appropriately over these two spaces, apply the UNFOLD-related filters independently in each space, and recombine the resulting data in a common space, e.g., Ω_1. The separation of signals between the two spaces is done by interpreting as much as possible the signal found at intermediate temporal frequencies as truly originating from the Nyquist and/or DC regions, and having "leaked away" due to the effect of $m_d(\vec{k},\nu)$ (i.e., assumption that spectra normally tend to be strongly peaked in the temporal-frequency domain). More specifically, a dot product in function space projects the acquired signal *S* onto unit vectors $h_{\nu 2}$, which represent how signal at a frequency ν_2 in Ω_2 would propagate to intermediate ν frequencies in Ω_1, due to motion: $D = < S, h_{\nu 2} >$. The signal left once all projections have been made is referred to as $P_{\Omega 1}$. With $g_{\nu 2}$ the unit vectors sustaining Ω_2, f_{Ny} and f_{DC} filters to remove the Nyquist and DC regions (HWHM=10% of bandwidth), respectively, the corrected data in *k-ν* space is given by:

$$K(\vec{k},\nu) = \sum_{\nu 2} \frac{{f_{Ny}}^2(\nu_2)\, f_{DC}(\nu_2)\, D(\vec{k},\nu_2)\, g_{\upsilon 2}(\vec{k},\nu)}{\sqrt{\sum_{\nu} \left(f_{Ny}(\nu)\, f_{DC}(\nu)\, g_{\upsilon 2}(\vec{k},\nu) \right)^2}} + (1 - f_{DC}(\nu))\, P_{\Omega 1}.$$

1st application, breathing motion: The figure on the right shows myocardial perfusion results in 3 patients, with both a normal and our extended versions of UNFOLD, for acceleration factors of 2.0, and 3.0 (2.0 from UNFOLD, and 1.5 from variable-density sampling [4]). Green arrows show discontinuity (blurring) artifacts at the transitions between dynamic and less dynamic regions, and orange arrows show ghosting artifacts. A registration algorithm measures the A/P motion of the thorax in the normal results, and our algorithm takes into account that a modulation $m_d(\vec{k},\nu)$, due to this motion, may affect some of the acquired signals. Our approach handles the presence of such modulation, and the artifacts are much suppressed in the images obtained with our extended method. Time frames with a maximum of breathing-related artifacts were selected for display, to showcase the artifact-suppression ability of our approach.



2nd application, changes in sampling scheme: Suppose we sample one line every four in k-space. Four regular, interleaved sampling functions, referred to as *A*, *B*, *C* and *D*, could be used equally well (*A*+*B*+*C*+*D* represents a full sampling). To push aliasing artifacts to the Nyquist frequency, one could alternate in time between *A* and *C*, a sampling strategy referred to here as (*A,C,A,C,A,C,...*) [5], but locations in *B* and *D* would never get sampled. Alternately, one could use a strategy (*A,B,C,D,A,B,C,D,...*) [6,7], but then artifacts are not displaced all the way to Nyquist, and remain overlapped with desired signals. Instead, a non-regular scheme (*A,C,A,C,...A,C,B,D,B,D,...B,D,A,C...*) is used here, so that all locations get sampled (e.g., for self-calibration), but most of the artifact energy is displaced to Nyquist. While normal filtering would lead to artifacts, our approach can better handle variations caused by this discontinuous sampling scheme (figure on the left, sagital images of the thorax).



References: **[1]** Madore *et al*. MRM 1999;42:813. **[2]** Di Bella *et al*. MRM 2003;49:895. **[3]** Ablitt *et al*. JMRI 2004;20:817. **[4]** Pipe. MRM 2000;43:867. **[5]** Madore. MRM 2004;52:310. **[6]** Kellman *et al*. MRM 2001;45:846. **[7]** Tsao *et al*. MRM 2003;50:1031.