X-f Choice: A reconstruction method for under-sampled dynamic data using an adaptive fitting approach

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Introduction: Image acquisition speed is often a constraint for dynamic MRI studies such as Dynamic Contrast-Enhanced MRA (DC-MRA) of the abdomen, which ideally requires the acquisition of volume data sets with high time resolution. Regular under-sampling of dynamic data in the k-space and time (k-t) domain increases the temporal resolution by causing aliasing in the conjugate image and temporal frequency (x-f) domain. The aliases can be effectively removed to give uncorrupted images if dynamic regions with large spectral content overlap with less dynamic information. Sliding window, the simplest alias removal method, amounts to low-pass filtering in f, typically with a constant bandwidth. UNFOLD[1] uses an optimally selected constant width filter to allow more dynamic detail to be retained, but is limited to a factor two speed up. K-t BLAST[2] uses prior knowledge of the signal distribution in x-f space obtained from a low spatial resolution fully sampled training scan to construct an adaptive filter that resolves aliasing by a linear redistribution of the signal. Existing methods often trade alias suppression for spatio-temporal blurring. Here we explore an alternative approach in the context of DC-MRA.

Method: The x-f domain contains an uneven distribution of signals with much more power generally localised around f=0 than towards higher frequencies. As a result aliasing usually mixes signals that are uneven in intensity. We have observed that even with multiple aliases, the signal in x-f space is usually dominated by a single contributor and so it would be faithful to the data to apportion all of the signal to this point, i.e. making an 'x-f choice'. A second issue is that the aliases are coherent signal superpositions, so that magnitude based redistribution inevitably leaves residual phase errors and can under estimate signal magnitude. The linear least squares approach employed by k-t BLAST reapportions the signal based on a 'local' estimate in x-f. This can lead to low pass filtering because noise in training data can obscure the true necessary weightings, especially at high f where the signal is often dominated by noise. Instead we fit the f spectra with an envelope function based on prior knowledge, using a fitting process weighted towards the low f data where SNR is high. This allows signal amplitude to be estimated even in regions where noise dominates. Fitting an envelope function allows narrow spectra overlying wide ones to be removed, conserving high frequency information from the wide spectrum. Where data is rejected, the asymmetric skew of the aliasing pattern means it is possible in many cases to partially fill in missing values using conjugate symmetry. Parallel imaging can be combined with k-t under-sampling, since it is possible to use coil sensitivity data to resolve overlying aliases. For an n fold under sampled problem a given pixel contains n alias contributions, simple x-f choice usually would select one as dominant. If there are χ coil views but n > χ then as a parallel imaging problem it is under determined. The x-f choice approach allows aliases not contributing significantly to be rejected until there are at most χ left, then the problem can be solved using parallel imaging. Often it is possible to reject more than χ aliases so that the coil sensitivities can be used to form a least squares solution. A key issue is the use of prior knowledge to define the fitting function. In the case of DC-MRA, we have used the fact that the arrival of the contrast agent causes a signal increase to construct an envelope function that varies as 1/f away from f= 0 with the f=0 data used as a scaling parameter.

Testing has been carried out using *in-vivo* images from a 3T Philips Intera MRI scanner, and with data based models. Adequately temporally sampled image series were obtained from the single-slice timing scan that is routinely carried out before a DC-MRA study. A full 3D image set consisting of an arterial phase and a late venous phase volume scan from a patient was segmented, allowing vessels and organs to be assigned artificial but realistic rise times to simulate fully time resolved high resolution volume data. Both the model and the *in vivo* data were then sub-sampled as required.

Results

Fig. 1
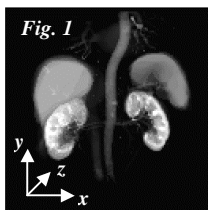
Testing on single slice dynamic *in vivo* data has been successful with acceleration factors of four achieved with no detectable temporal blurring but an increase in noise in dynamic regions (see below). The following results illustrate tests of two facets of the approach: the requirement for x-f to be sparse and the issue of noise obscuring the true contribution in high f regions where SNR is low. Fig.1 shows a reconstruction (projected through z for a single time frame) of the 3D model for 2-fold sub-sampling in the k_x-t plane. Both kidneys lie in this plane causing direct aliasing of regions with dynamic content – i.e. the dynamic regions are not very sparse here. The resulting error is a maximum of 2% in these regions but negligible (<0.1%) in the major vessels where there is genuine sparseness, indicating robustness of the method particularly for the vessels, for which much higher acceleration is possible. No temporal blurring was detected.

Figure 2 shows the effect of noise. Fig 2a is a noise free model representing the dynamic behaviour of arteries and veins, revealing the full extent of the f-spectra. Fig 2b shows how these are mixed by aliasing with a factor 4 and fig 2c shows the same picture with noise added (SNR=20). The extent of the aliasing is obscured leading to temporal blurring if not correctly resolved. Line-fitting to high SNR regions allows estimation of the information content in the areas apparent in fig 2b but lost under noise in fig 2c. The result in this case has no temporal blurring but the noise level in dynamic regions is doubled. This is to be expected since the temporal bandwidth has been increased by a factor four compared with the sparse data. Conversely noise in static regions is reduced by the inherent averaging effect. Combination with parallel imaging allows even more dense aliases to be separated, but can cause noise enhancement (g-factor effect[3]).

Fig. 2

All images are log intensity to reveal small values
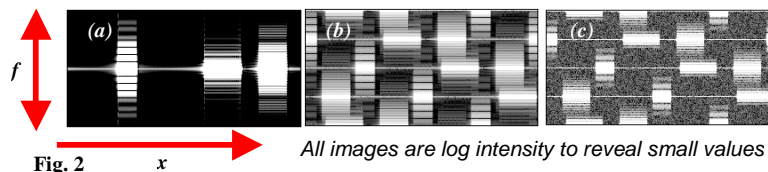
Conclusions: The properties of x-f space mean that in most places aliasing is dominated by a sub-set of the contributions, although this can be obscured by noise. A line-fit approach using an envelope function based on prior knowledge has been proposed to identify the dominant contributors, allowing restoration of required signals while preserving high temporal frequency information. Combining this approach with parallel imaging allows greater degrees of under-sampling to be resolved. The acceleration factor achievable by the reconstruction is limited by sparseness of dynamic content, an inherent speed limit on all such methods. DC-MRA has been selected here as an application but the method can apply to other dynamic imaging situations, the only difference being the model used to fit the f-spectra.

References

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