# Time Shifted Principle Component Analysis

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## Introduction

Tissue motion in time resolved MR imaging can be classified as voluntary (swallowing, moving in the magnet, etc…) and involuntary/physiological (related to the cardiac cycle, etc…). Since the latter type is periodic it is often modeled with a small number of principle components. As a result, principle component analysis is a popular method of reconstructing undersampled MRI data (1-3). The basic premise is that a time resolved data set can be constrained by keeping only a small number of principal components from the singular value decomposition (SVD). However, modeling the data in this manner can be problematic when two voxels exhibit highly correlated motion that differs by only a small delay in time. In such cases, keeping only a small number of principle components can result in an erroneous temporal shift of voxel signals (Fig. 1). The proposed method preserves these small temporal shits when time resolved data is constrained using principle component analysis.

## Theory

If the signals from two voxels differ only by a multiplicative constant, then a SVD will find that both voxels contain the same principle component. If however, the two signals differ only by a small shift in time, then the SVD will find that each voxel has different principle components. When the signals from two different voxels are identical except for a time delay, then the Fourier Transform of the signals differ only by a linear phase:

$$f(t) \rightarrow f(t+\Delta t) \quad then \quad F(k_t) \rightarrow exp\left(\frac{2\pi i \Delta t}{N_t} \cdot k_t\right) \cdot F(k_t) \qquad [1]$$

Because the two spectrums vary by a linear phase rather than a multiplicative constant, the SVD method is unable to correlate the signal from the two voxels. However, if the linear phase is removed prior to calculating the SVD, then both voxels will have the same principle component. The linear phase can then be added back when the voxel signals are reconstructed from the principle component. In many instances the signal from a given voxel will be a linear combination of multiple principle components, each with their own temporal shift. The general procedure in this case is:

1) Remove the linear phase of the signal. We consider only the central points in the spectrum when calculating the linear phase. The amount of linear phase removed should be noted for later image reconstruction.
2) Find the dominant principle component using SVD.
3) Subtract the scaled and time shifted (use linear phase from step 1) principle component from the data set.
4) Repeat steps 1-3 for the desired number of principle components.

## Results and Discussion

Figure 1 shows data from a 2D CineTSE image reconstruction (4 element receive coil, a resolution of 0.5mm x 0.5mm x 2mm, 12 echoes per train and a TR/TE of 650ms/8ms). Initially a fully sampled data set (12 cardiac phases) is reconstructed with a selected image shown in Fig. 1a and the temporal signal in the two indicated vessels shown in Fig. 1b (signal intensities have been normalized for display purposes). The blood signal intensities in two adjacent vessels are correlated but shifted in time (Fig. 1b). The CineTSE data is then retrospectively undersampled (R=6) and reconstructed using a highly constrained PCA algorithm (constraining the data to contain only a few principle components). The undersampled reconstruction will be some linear combination of the principle components retained. If too many principle components are retained then too little of the undersampling artifact will be removed by the reconstruction process. However, when only a limited number of components are retained, the signal in some voxels might be temporally shifted to obtain the best match to the available principle components (Fig. 1c). This creates a competition between reducing undersampling artifact and retaining the temporal characteristics of our data. If instead, we allow the voxel signals to be a linear combination of the time shifted components, then we can better preserve the temporal behavior of each voxel (Fig. 1d). In the latter case, we are using the same principle components to reconstruct the signal but allow for the possibility that a time shifted version of each component might better match our data. Comparing Fig. 1c/1d to Fig. 1b we see the improved signal matching of the time shifted PCA.

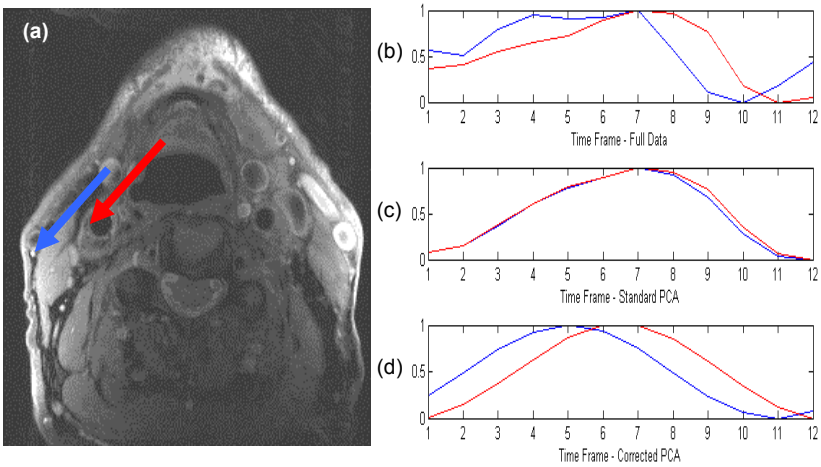


Figure 1: Axial 2D CineTSE data. A select image from the fully sampled data is shown in (a) with vessels of interest indicated by the colored arrows. The blood signal intensity at each of the colored arrows is plotted in the graphs to the right (b-d). The fully sampled data shows how the vessel signals are correlated but shifted in time (b). If the data is highly constrained using a standard PCA algorithm, the signal in the two vessels become aligned in time (c). A time shifted PCA algorithm with the same level of constraint recovers the temporal difference between the two signals (d).

## Conclusion

Principle component analysis is a powerful tool to reconstruct undersampled data. However, when the number of principle components is restricted the temporal characteristics of our data can be altered inadvertently. The proposed method helps to address this concern by reducing the number of principle components needed to reconstruct an undersampled data set using principle component analysis.

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## References

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