Spatial Information based DCE-MRI Data Reconstruction and analysis using PCA

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Spatial Information based DCE-MRI Data Reconstruction and analysis using PCA

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Motivation

› Voxel-by-voxel analysis of dynamic contrast enhanced data (DCE) results in pixelated maps in presence of motion and systemic noise

› Using spatial distribution and prior knowledge information for processing of dynamic data can improve the confidence in quantification\textsuperscript{[1-3]}

Objective

› We seek to introduce a block-wise PCA based approach to:
  - reconstruct the DCE-MRI data using the neighborhood information,
  - separate noise from true contrast enhancement
  - preserve the tissue heterogeneity in reconstructed maps.
Background

› Dynamic-4D MRI: Understand the functional and metabolic aspects of disease
› Parametric maps on voxel-by-voxel basis
› Model fits poor due to noise from: patient motion, systemic noise and fluctuations
› Smoothening with simple one-dimensional filter changes the shape of enhancement
› Principal component analysis (PCA) based method previously described for SNR improvement [4]
› Block-wise PCA based approach presented to reconstruct the DCE-MRI and pK map generation

DCE Data

- **Phantom**: DCE phantom as described in [2]
- **MRI system**: 1.5T GE Signa Genesis (GEHC, Waukesha, WI).
- **Patient data**: Two patients with prostate tumor
  - 0.1 mmol/kg Gd-DTPA injected i.v at 0.3 cc/sec for 100 s

<table>
<thead>
<tr>
<th>Anatomy</th>
<th>TE (ms)</th>
<th>TR (ms)</th>
<th>Flip Angle (degree)</th>
<th>Matrix</th>
<th>FOV (mm²)</th>
<th>Slice thickness (mm)</th>
<th>Miscellaneous</th>
</tr>
</thead>
<tbody>
<tr>
<td>Prostate</td>
<td>1.3</td>
<td>3.8</td>
<td>15</td>
<td>256 x 256</td>
<td>260 x 260</td>
<td>6</td>
<td>EIS TORSO coil, 50-65 bolus volumes, ~4.5 s / volume</td>
</tr>
</tbody>
</table>

§ We thank Dr. Adilson Prando (Ressonancia Magnetica Campinas, Brazil) for the data
DCE Data Analysis

› In-house tool developed within the ITK framework.
› DCE signal data converted into concentration with baseline images and fixed tissue T1 = 1317 ms
› Automated AIF detection
› Concentration curves analyzed on voxel-by-voxel basis to obtain:
  - **Semi-quantitative parameters**: Bolus arrival time (BAT), Max-slope, Contrast enhancement
  - **Quantitative pK model**: Two-parameter Toft model, Levenberg-Marquardt fitting to obtain $K_{\text{trans}}$ and $V_e$ estimates

**Single Voxel analysis**: The data analyzed as above is termed as single voxel analysis (SVA).
DCE Data : PCA Analysis

- Block based approach
- For a voxel \( V(x, y, z) \), sweep 3D neighborhood blocks connected to \( V \)
- For each sweep, stack curves in a matrix.
- Perform PCA on stacked matrix and retain first two components with largest variance
- Post all sweeps per voxel, the resulting curve for that voxel is computed as the median of the stacked PCA reconstructed curves.
- Semi-quantitative and pk Model parameters are obtained for PCA recon curve as described earlier
PCA based reconstruction did not introduce any errors [residual error due to reconstruction = 0] in the phantom.
PCA Analysis: Results

Prostate patient data: PCA filtering

The red arrow shows the original curve at a given voxel. The individual sweep PCA curves are shown in blue in same figure.

The PCA smoothened concentration curve is compared to original curve. Note that there is no shift in curve shape or bolus arrival time.
PCA Analysis: pK Model

Prostate patient data: pK model
PCA Analysis : Parametric Maps

› Prostate patient data : Parametric maps and fitting metric
PCA Analysis : Summary

› Prostate patient data : Parameter statistics

<table>
<thead>
<tr>
<th>Parameter</th>
<th>BAT</th>
<th>Max-slope</th>
<th>K\textsubscript{trans}</th>
<th>V\textsubscript{e}</th>
<th>R\textsuperscript{2}</th>
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</thead>
<tbody>
<tr>
<td>Mean_SVA</td>
<td>49.22</td>
<td>0.0117</td>
<td>0.073</td>
<td>0.15</td>
<td>0.77</td>
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<td>Mean_PCA</td>
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<td>0.0063</td>
<td>0.068</td>
<td>0.15</td>
<td>0.91</td>
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<td>Mean_SVA</td>
<td>41.21</td>
<td>0.0115</td>
<td>0.126</td>
<td>0.32</td>
<td>0.89</td>
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<tr>
<td>Mean_PCA</td>
<td>38.81</td>
<td>0.0095</td>
<td>0.123</td>
<td>0.32</td>
<td>0.93</td>
</tr>
</tbody>
</table>

* : Statistically significant difference between SVA and PCA analysis
Discussion & Conclusion

› PCA based filtering using spatial-temporal information improves fidelity of DCE data.
› Concomitant improvement in data fitting to pK-model
› Improvement with PCA filtering is more pronounced for semi-quantitative maps, as they are more susceptible to noise fluctuations
› Other data separation methods such as independent component analysis or total variation filtering can also be investigated in future.