Manifold learning characterization of abnormal myocardial motion patterns: application to CRT-induced changes.

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Mechanistic approaches for CRT

Understanding classes of mechanical dyssynchrony

- **C1** = Intra DYS
- **C2** = Inter DYS
- **C3** = Long AV
- **C4** = Short AV
- **C5** = Other

Septal flash: fast inward/outward motion (mechanical dyssynchrony) in the presence of LBBB (electrical dyssynchrony).


http://www.texasheartinstitute.org
(Ab)normal motion / deformation patterns

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<tbody>
<tr>
<td>Displacement</td>
<td>0 → t</td>
<td>Vector</td>
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<tr>
<td>Velocity</td>
<td>t → t+1</td>
<td>Vector</td>
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<td>Strain</td>
<td>0 → t</td>
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<tr>
<td>Strain Rate</td>
<td>t → t+1</td>
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- Motion / deformation extraction: image-based tracking
- Spatiotemporal alignment + statistics: atlas-based techniques

Duchateau et al.  
Med Image Anal (2011)  
(Ab)normal motion / deformation patterns

- Where computational methods can be useful?
  - Quantification + population analysis
  - Learning process (same as clinicians’ practice)

- Currently = voxel-based analysis…

**HOW TO COMPARE PATTERNS QUANTITATIVELY?**
How to compare dyssynchrony patterns?

- Which statistics?
  1. Population modelling
  2. Comparison of individuals to a population

Examples of the learned pattern (septal flash)
Objective: each pathology is modelled as a deviation from normality along a manifold structure.

1. INPUT = 2D motion abnormality maps

2. Manifold-learning problem
   • Training = one specific population (CRT candidates with septal flash)
   • Tested patients = new CRT candidates, volunteers

3. How to compute distances to both normality + learnt population?
a) Manifold-learning from training set

**ISOMAP** = Tenenbaum et al., *Science* (2000)

**Synthetic dataset**

Swiss roll ($P=3$)

**CRT dataset**

N+1 images, $P$ pixels

2D embedding (e.g.)

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Duchateau et al.
*Med Image Anal* (2012)
b) Individual comparison to the whole population

Two consecutive interpolation problems. Analogy with:

Combination of f and g to complete mapping to the manifold:
- Etyngier et al., NIPS (2007)
- Gerber et al., Med Image Anal (2010)

Distances computation

1. Distance to the manifold
2. Distance to normality along the manifold

\[ d_P(I) = \| \hat{I} - I \| \quad \text{and} \quad d_M(I) = \| f(I) - f(I_0) \|. \]
Some important questions

- Linear / non-linear?  ➔ Do I really need to go for non-linear?

- If so:
  - What is the (unknown?) dimensionality of my data?
  - How much noise can be tolerated?
  - Which technique? Which metric on my data?
  - Parameters tuning intrinsic to the technique, e.g. Isomap:
    - Number of neighbours, kernel size, etc.
Distance analysis: baseline data

Duchateau et al.
Distance analysis: evolution with CRT

- Tending to a relevant clustering at baseline
- With pacing ON and follow-up (all CRT candidates, not only SF)
  - Getting further from SF-like pattern
  - Getting closer to normality

Duchateau et al. FIMH (2013)
Distance analysis: understanding CRT outcome

- With pacing ON and follow-up (only SF vs CRT response)
  - Disparition of SF-like pattern
  - Getting closer to normality

- At follow-up:
  - Recovery of a “normal” motion = responders
  - Others: may be responders / non-responders (probably additional factors)

Duchateau et al. FIMH (2013)
**Conclusions**

- Modeling a pathological pattern as deviation from normality
- Need for non-linear analysis
- Comparison of motion patterns *in their whole* (and not just peak or time-to-event measurements)

**Conclusions for CRT:**
- Restoration of normal contraction ➔ Clinical response ➔ Volume response
- Possibility to identify responders with non-typical behaviour (responders with still abnormal motion)
- Further extension to deformation (strain) and other diseases
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  cvREMOD (CEN-20091044), euHeart (FP7-ICT-224495)
Thanks !!! Any questions...?
Inexact interpolation

\[
\left\{ \begin{array}{l}
\arg\min_{f \in \mathcal{F}} \left( \frac{1}{2} \| f \|_{\mathcal{F}}^2 + \frac{\gamma_f}{2} \sum_{i=J+1}^{N} \| f(I_i) - x_i \|^2 \right), \\
\text{under the constraint } \forall j \in [0, J], f(I_j) = x_j.
\end{array} \right.
\]

\[
f(I) = \sum_{i=0}^{N} k_{\mathcal{F}}(I, I_i) \cdot c_i \quad \text{with} \quad C = \left( K_L + \frac{1}{\gamma_f} M \right)^{-1} \cdot X,
\]

Also known as:
- Ridge regression
- Nyström extension
Mapping points to the manifold

Combination of $f$ and $g$ to complete mapping to the manifold:
- Etyngier et al., NIPS (2007)
- Gerber et al., Med Image Anal (2010)
Choice of optimal kernel scale

\[ \sigma_G(x) = \frac{1}{K^2} \sum_{k=1}^{K} \sum_{l=1, l \neq k}^{K} S_C(\text{nn}_k(x), \text{nn}_l(x)). \]

Duchateau et al., GSI-SEE conference (2013)  
= multiscale extension

Duchateau et al., Med Image Anal (2012)  
= locally adapted kernel bandwidth

Geometric harmonics  