Machine Learning in Cardiac Imaging

Andrew King
School of Biomedical Engineering and Imaging Sciences
King’s College London
Outline

LEARNING FROM CLINICIANS
1. Incorporating non-imaging data into image-based machine learning
2. Exploiting multi-modal imaging data

MACHINE LEARNING IN ACQUISITION/RECONSTRUCTION/ANALYSIS
3. Automated quality control in large-scale imaging databases
4. Machine learning for robust MR reconstruction
Learning from cardiologists

How do doctors make clinical decisions?

Imaging data

Patient record

Experience
1. Incorporating non-imaging data into image-based machine learning

Background

- Cardiac resynchronisation therapy (CRT) involves implanting a pacemaker to treat heart failure
- Using standard clinical selection criteria, ~30% of patients do not respond to treatment
- Research in the clinical literature has identified specific activation patterns that are associated with CRT response*, but these require manual inspection of imaging data by expert cardiologists

Aim

- Use machine learning to automatically learn imaging/non-imaging features to predict positive CRT response

* Sohal et al., JACC, 2013; Jackson et al, Heart Rhythm 2014
Data

Database:
34 patients selected for CRT
Pre-treatment tagged/cine/LGE MR
Follow-up data (positive/negative response to treatment)
Non-imaging data:

<table>
<thead>
<tr>
<th>Biomarker</th>
<th>Description</th>
<th>Mean/std dev</th>
<th>Frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>Aetiology</td>
<td>Ischaemic/non-ischaemic</td>
<td>NA</td>
<td>13/21</td>
</tr>
<tr>
<td>EDV&lt;sub&gt;m&lt;/sub&gt;</td>
<td>End-Diastolic Volume from 3D geometry (cm&lt;sup&gt;3&lt;/sup&gt;)</td>
<td>281/127</td>
<td>NA</td>
</tr>
<tr>
<td>EDV</td>
<td>End-Diastolic Volume from 2D echo (cm&lt;sup&gt;3&lt;/sup&gt;)</td>
<td>214/91</td>
<td>NA</td>
</tr>
<tr>
<td>ESV</td>
<td>End-Systolic Volume from 2D echo (cm&lt;sup&gt;3&lt;/sup&gt;)</td>
<td>164/84</td>
<td>NA</td>
</tr>
<tr>
<td>EF</td>
<td>Ejection Fraction from 2D echo (%)</td>
<td>24.7/9.3</td>
<td>NA</td>
</tr>
<tr>
<td>Gender</td>
<td>Male/Female</td>
<td>NA</td>
<td>24/10</td>
</tr>
<tr>
<td>LBBB</td>
<td>Strict Left-Bundle Branch Block: yes/no</td>
<td>NA</td>
<td>23/11</td>
</tr>
<tr>
<td>NYHA</td>
<td>New York Heart Association classes (I-IV)</td>
<td>2.7/0.5</td>
<td>NA</td>
</tr>
<tr>
<td>QOL</td>
<td>Quality of Life questionnaire score</td>
<td>48/27</td>
<td>NA</td>
</tr>
<tr>
<td>QRS&lt;sub&gt;dur&lt;/sub&gt;</td>
<td>QRS duration (ms)</td>
<td>146/22</td>
<td>NA</td>
</tr>
<tr>
<td>QRS&lt;sub&gt;cat&lt;/sub&gt;</td>
<td>QRS category &lt; 150 ms/ &gt; 150 ms</td>
<td>NA</td>
<td>18/16</td>
</tr>
<tr>
<td>Rhythm</td>
<td>Sinus/Atrial fibrillation</td>
<td>NA</td>
<td>28/6</td>
</tr>
<tr>
<td>6MWD</td>
<td>6 min walking distance (m)</td>
<td>269/137</td>
<td>NA</td>
</tr>
</tbody>
</table>

Peressutti et al, Med Image Anal, 2017

A. King – Machine Learning in Cardiac Imaging
Multiple kernel learning

Peressutti et al, Med Image Anal, 2017

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Motion atlas

Segmentation of LV from cine MR:

Motion estimation from tagged MR:

Transport of motion/deformation data:

Peressutti et al, Med Image Anal, 2017
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Random projections with task-based subspace rejection

Motion Descriptors

L Random Projections

D << F

LDA with Subspace Rejection

Peressutti et al, Med Image Anal, 2017

A. King – Machine Learning in Cardiac Imaging
Multiple kernel learning for CRT response prediction - results

Classification results:

<table>
<thead>
<tr>
<th></th>
<th>Non-motion kernels only</th>
<th>Motion kernels only</th>
<th>Both motion and non-motion kernels</th>
</tr>
</thead>
<tbody>
<tr>
<td>Accuracy</td>
<td>85.3</td>
<td>88.2</td>
<td>91.2</td>
</tr>
<tr>
<td>Sensitivity</td>
<td>100</td>
<td>100</td>
<td>100</td>
</tr>
<tr>
<td>Specificity</td>
<td>37.5</td>
<td>50</td>
<td>62.5</td>
</tr>
<tr>
<td>PPV</td>
<td>83.8</td>
<td>86.7</td>
<td>89.7</td>
</tr>
<tr>
<td>NPV</td>
<td>100</td>
<td>100</td>
<td>100</td>
</tr>
</tbody>
</table>

Sensitivity = proportion of responders chosen for treatment
Specificity = proportion of non-responders who would not be chosen for treatment

Peressutti et al, Med Image Anal, 2017
Multiple kernel learning for CRT response prediction – kernel weights

Peressutti et al, Med Image Anal, 2017
CRT response prediction – the role of spatial scale of the motion features

Sensitivity = proportion of responders chosen for treatment
Specificity = proportion of non-responders who would not be chosen for treatment

Sinclair et al, Med Image Anal, 2018
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Learning from cardiologists

How do doctors make clinical decisions?

Imaging data

Patient record

Experience

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2. Exploiting multi-modal imaging data

Background:

- MR is considered to be the ‘gold standard’ for cardiac functional assessment
- US is more commonly used due to its low cost, ease of use and portability
Exploiting multi-modal imaging data

Aim:
• Use a database of paired MR/US data sets to exploit multimodal data in a diagnostic pipeline
• Pipeline should be based on data from a single modality (US)
A multimodal cardiac motion atlas

Puyol-Anton et al., Med Image Anal, 2017

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Multiview dimensionality reduction

Multi-view dimensionality reduction algorithms

- **Canonical correlation analysis (CCA)** on MR/US displacements
  - Determines directions where X and Y have maximum *correlation* between modalities
- **Partial least squares regression (PLS)** on MR/US displacements
  - Determines directions where X and Y have maximum *covariance* between modalities

Single view dimensionality reduction algorithm

- **Principal component analysis (PCA)** on MR displacements only
  - Determines directions of maximum data *variance* in single modality
Multimodal atlas: results

- CCA and PLS have lower errors than PCA.
- PLS has lower errors and better reconstructed volumes compared to CCA.

$E_d(MR-US)$ – embedding error
$E_D(MR-MR)$ – Reconstruction error for MR
$E_D(US-US)$ – Reconstruction error for US
$E_D(MR-US)$ – Prediction error

Puyol-Anton et al., Med Image Anal, 2017
The task

Classification of normal vs. dilated cardiomyopathy:

Clinical database:
- 50 healthy volunteers
- 14 dilated cardiomyopathy patients

Image protocol (LV):
- Multi-slice short-axis MR sequence
- 3D tagged MR sequence (3DTAG).
- 3D apical ultrasound sequence (3DUS).

Stratified k-fold cross-validation
- Imbalanced data
- # low dimensions set to retain 90% of the variance
- 8 folds and 100 repetitions

Puyol-Anton et al., IEEE Trans Biomed Eng, 2018

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Multiview classification

2.a. Single modality US method

<table>
<thead>
<tr>
<th>Method</th>
<th>Sensitivity (%)</th>
<th>Specificity (%)</th>
<th>Accuracy (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>PCA_{US} + LDA</td>
<td>74.79 (15.8)</td>
<td>71.05 (28.6)</td>
<td>78.57 (10.1)</td>
</tr>
<tr>
<td>PCA_{US} + SVM_{rbf}</td>
<td>87.32 (12.9)</td>
<td>84.50 (23.2)</td>
<td>90.14 (6.6)</td>
</tr>
</tbody>
</table>

3. Multiple modality two-step method

<table>
<thead>
<tr>
<th>Method</th>
<th>Sensitivity (%)</th>
<th>Specificity (%)</th>
<th>Accuracy (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>PLS + LDA</td>
<td>80.07 (16.8)*</td>
<td>75.51 (27.1)</td>
<td>81.86 (9.5)</td>
</tr>
<tr>
<td>PLS + SVM_{rbf}</td>
<td>90.39 (12.1)*</td>
<td>87.50 (21.8)</td>
<td>90.57 (10.9)</td>
</tr>
</tbody>
</table>

Puyol-Anton et al., IEEE Trans Biomed Eng, 2018

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Multiview learning

Puyol-Anton et al., IEEE Trans Biomed Eng, 2018

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Multiview learning

1. Multiple modality one-step method

<table>
<thead>
<tr>
<th>MR displacements</th>
</tr>
</thead>
<tbody>
<tr>
<td>$X_1$</td>
</tr>
<tr>
<td>...</td>
</tr>
<tr>
<td>$X_k$</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>US displacements</th>
</tr>
</thead>
<tbody>
<tr>
<td>$Z_1$</td>
</tr>
<tr>
<td>...</td>
</tr>
<tr>
<td>$Z_k$</td>
</tr>
</tbody>
</table>

MLDA/MvLapSVM

2. Single modality methods

2.a - Baseline - US-only

<table>
<thead>
<tr>
<th>US displacements</th>
</tr>
</thead>
<tbody>
<tr>
<td>$Z_1$</td>
</tr>
<tr>
<td>...</td>
</tr>
<tr>
<td>$Z_k$</td>
</tr>
</tbody>
</table>

PCA

LDA/SVM$_{rbf}$

2.b - MR-only

<table>
<thead>
<tr>
<th>MR displacements</th>
</tr>
</thead>
<tbody>
<tr>
<td>$X_1$</td>
</tr>
<tr>
<td>...</td>
</tr>
<tr>
<td>$X_k$</td>
</tr>
</tbody>
</table>

PCA

LDA/SVM$_{rbf}$

Puyol-Anton et al., IEEE Trans Biomed Eng, 2018
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Multiview learning - results

- One-step multiview learning outperforms two-step approach

- One-step multiview learning performs almost as well as the ‘gold standard’ of MR-based classification

Puyol-Anton et al., IEEE Trans Biomed Eng, 2018

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**Proposed method**

<table>
<thead>
<tr>
<th>Method</th>
<th>BACC (%)</th>
<th>SEN (%)</th>
<th>SPE (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>MLDA</td>
<td>82.18 (15.0)*</td>
<td>80.50 (26.5)</td>
<td>83.86 (9.9)</td>
</tr>
<tr>
<td>MvLapSVM</td>
<td>92.71 (10.4)*</td>
<td>89.00 (20.8)</td>
<td>95.14 (6.8)</td>
</tr>
</tbody>
</table>

**Comparative approaches**

<table>
<thead>
<tr>
<th>Method</th>
<th>BACC (%)</th>
<th>SEN (%)</th>
<th>SPE (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. Multiple modality one-step method</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MLDA</td>
<td>82.18 (15.0)*</td>
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<tr>
<td>2.a. Single modality US method</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
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<td>74.79 (15.8)</td>
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<td>78.57 (10.1)</td>
</tr>
<tr>
<td>PCA$<em>{US}$ + SVM$</em>{rbf}$</td>
<td>87.32 (12.9)</td>
<td>84.50 (23.2)</td>
<td>90.14 (6.6)</td>
</tr>
<tr>
<td>2.b. Single modality MR method</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>PCA$_{MR}$ + LDA</td>
<td>84.21 (15.4)*</td>
<td>74.00 (28.8)</td>
<td>90.43 (6.8)</td>
</tr>
<tr>
<td>PCA$<em>{MR}$ + SVM$</em>{rbf}$</td>
<td>90.89 (11.7)*</td>
<td>86.50 (22.3)</td>
<td>95.29 (6.7)</td>
</tr>
<tr>
<td>3. Multiple modality two-step method</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>PLS + LDA</td>
<td>80.07 (16.8)*</td>
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<td>90.39 (12.1)*</td>
<td>87.50 (21.8)</td>
<td>90.57 (10.9)</td>
</tr>
</tbody>
</table>

BACC: balanced accuracy
SEN: sensitivity
SPE: specificity

* Student’s t-test (99% confidence)
Regional multiview learning

Weighted majority voting:

For each AHA segment each subject is classified. The results are combined using weighted majority voting with weights determined at training by a randomised search on hyper parameters.

Puyol-Anton et al., IEEE Trans Biomed Eng, 2018
Regional multiview learning - results

<table>
<thead>
<tr>
<th>Global Methods</th>
<th>BACC (%)</th>
<th>SEN (%)</th>
<th>SPE (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>MLDA</td>
<td>82.18 (15.0)</td>
<td>80.50 (26.5)</td>
<td>83.86 (9.9)</td>
</tr>
<tr>
<td>MvLapSVM</td>
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</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Regional Methods</th>
<th>BACC (%)</th>
<th>SEN (%)</th>
<th>SPE (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>MLDA</td>
<td>87.71 (12.6)*</td>
<td>85.00 (23.1)</td>
<td>90.43 (6.7)</td>
</tr>
<tr>
<td>MvLapSVM</td>
<td>94.32 (11.1)*</td>
<td>93.00 (17.5)</td>
<td>96.57 (6.2)</td>
</tr>
</tbody>
</table>

- Regional approach has higher accuracy
- Highest accuracy was 94% using regional MvLapSVM.

BACC: balanced accuracy
SEN: sensitivity
SPEL: specificity

* Student’s t-test (99% confidence)

Puyol-Anton et al., IEEE Trans Biomed Eng, 2018

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SmartHeart project

5 year grant involving:
- King’s College London
- Imperial College London
- Queen Mary University London
- Oxford University

“To develop a diagnosis-driven ‘smart MR scanner’ that it is no longer a mere imaging device but instead becomes a highly sophisticated diagnostic tool” …
3. Automated quality control in large-scale imaging databases

Cardiac MR

• Need for high quality images
• Wide range of artefacts
• Manual labelling tedious for large datasets
• Need for automatic quality assessment tools

Adopted from Ferreira et al., JCMR, 2013.

• UK Biobank is a large scale database of imaging/non-imaging data
• Will eventually consist of cardiac MR images from 100,000 subjects (currently ~27,000)
Cardiac MR quality issues

1. **Off-axis (4ch)**
   - Left Ventricular Outflow Tract
   - 5 chamber look

2. **Motion related artefacts (SAX)**
   - Breathing
   - Mis-triggering
   - Arrhythmia

* Oksuz et al., ISBI 2018

$ Oksuz et al., MICCAI 2018

Good Planning

Bad Planning

Good Quality

Motion Artefact

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4-chamber cine cardiac MR

- Good 4-chamber CMR image shows all chambers clearly, enables right and left atrium analysis
- Planned using 2-chamber and short axis images
- Mistakes in planning lead to ‘off axis’ images

2-chamber view  Short axis view  4-chamber view

Oksuz et al., ISBI 2018
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Left ventricular outflow tract (LVOT)

- Off-axis acquisitions often show the Left Ventricular Outflow Tract (LVOT)
- Challenges RA and LA analysis
- Automatic LVOT detection can assist automatic quality control/planning

Good Planning  Bad Planning

Oksuz et al., ISBI 2018

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Method

1. Contrast Normalisation
2. Region of Interest Extraction
3. Training a CNN Model

Input: 2D 4chamber cardiac MR

Output: LVOT = 0 or 1

- Similar to Lenet* Model
- Dropout 0.5 after each layer
- ReLU Activation

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Experimental results

**Dataset:**
- 123 Good Quality Image and 123 LVOT images from UK Biobank
- 5 temporal frames of each sequence, 615 images for each class

<table>
<thead>
<tr>
<th>Methods</th>
<th>Accuracy</th>
<th>Precision</th>
<th>Recall</th>
</tr>
</thead>
<tbody>
<tr>
<td>K-Nearest Neighbours</td>
<td>0.613</td>
<td>0.604</td>
<td>0.602</td>
</tr>
<tr>
<td>Linear SVM</td>
<td>0.732</td>
<td>0.741</td>
<td>0.736</td>
</tr>
<tr>
<td>Decision Tree</td>
<td>0.651</td>
<td>0.626</td>
<td>0.619</td>
</tr>
<tr>
<td>Random Forests</td>
<td>0.598</td>
<td>0.613</td>
<td>0.610</td>
</tr>
<tr>
<td>Adaboost</td>
<td>0.718</td>
<td>0.729</td>
<td>0.727</td>
</tr>
<tr>
<td>Naive Bayesian</td>
<td>0.653</td>
<td>0.625</td>
<td>0.637</td>
</tr>
<tr>
<td>Discriminant Analysis</td>
<td>0.669</td>
<td>0.684</td>
<td>0.643</td>
</tr>
<tr>
<td><strong>CNN w.o Augmentation</strong></td>
<td><strong>0.801</strong></td>
<td><strong>0.811</strong></td>
<td><strong>0.781</strong></td>
</tr>
<tr>
<td><strong>CNN</strong></td>
<td><strong>0.826</strong></td>
<td><strong>0.828</strong></td>
<td><strong>0.821</strong></td>
</tr>
</tbody>
</table>

\[
\text{Accuracy} = \frac{TP + TN}{TP + FP + FN + TN}
\]
\[
\text{Precision} = \frac{TP}{TP + FP}
\]
\[
\text{Recall} = \frac{TP}{TP + FN}
\]

* Zhou et al., CVPR, 2016

Oksuz et al., ISBI 2018
Cardiac MR quality issues

1. **Off-axis (4ch)**
   Left Ventricular Outflow Tract
   5 chamber look

2. **Motion related issues (SAX)**
   Breathing
   Mis-triggering
   Arrhythmia

*Oksuz et al., MICCAI 2018*
Cardiac cine MR acquisition

...etc.

complete k-space matrix must be obtained for each point in cardiac cycle

Oksuz et al., MICCAI 2018
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Dataset

• **105 subjects** with motion artefacts (breathing, mistriggering, arrhythmia)
• 53 for mistriggering, 23 for breathing, 24 arrhythmia, 4 mixed
• **105 artefact images, 3360 good quality images**
• **DATA IMBALANCE …**

Arrhythmia  Breathing  Mistriggering  Good Quality

Oksuz et al., MICCAI 2018
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Data imbalance

1. **More data**
   - Difficult task in many medical imaging applications.
   - Not plausible to generate more real low quality medical data.

2. **Resampling dataset**
   - Add copies of instances from the under-represented class.
   - Delete some data from the over-represented class.

3. **Generate synthetic samples**
   - Generate synthetic examples that best represent the original data from the under-represented class.

Oksuz et al., MICCAI 2018
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K-space corruption

Frame i

Frame i+j

Corrupted Frame i

Frame i k-space

Frame i+j k-space

Frame i corrupted k-space

Oksuz et al., MICCAI 2018
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Synthetic images

Different corruption levels of k-space

HIGH QUALITY  LOW QUALITY

Good quality  Motion artefact  K-space corrupted image

Oksuz et al., MICCAI 2018
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3D CNN model

3D INPUT

2D+time sequence

50X80x80

C1
32@
3x3x3

C2
64@
3x3x3

C3
128@
3x3x3

C4
128@
3x3x3

C5
128@
2x2x2

C6
256@
2x2x2

P1
Pooling
1x2x2

P2
Pooling
1x2x2

P3
Pooling
1x2x2

P4
Pooling
1x2x2

OUTPUT

Good Quality
or
Artefact

1024

2

Oksuz et al., MICCAI 2018

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Experimental Results

**Dataset:**
- 105 Artefact Images, 3360 Good quality Images
- Dataset balanced with augmentation

<table>
<thead>
<tr>
<th>Methods</th>
<th>Accuracy</th>
<th>Precision</th>
<th>Recall</th>
<th>F1-score</th>
</tr>
</thead>
<tbody>
<tr>
<td>K-Nearest Neighbours</td>
<td>0.952</td>
<td>0.074</td>
<td>0.268</td>
<td>0.116</td>
</tr>
<tr>
<td>Linear SVM</td>
<td>0.968</td>
<td>0.721</td>
<td>0.385</td>
<td>0.502</td>
</tr>
<tr>
<td>Decision Tree</td>
<td>0.951</td>
<td>0.250</td>
<td>0.385</td>
<td>0.303</td>
</tr>
<tr>
<td>Random Forests</td>
<td>0.958</td>
<td>0.320</td>
<td>0.315</td>
<td>0.317</td>
</tr>
<tr>
<td>Adaboost</td>
<td>0.960</td>
<td>0.230</td>
<td>0.567</td>
<td>0.327</td>
</tr>
<tr>
<td>Naive Bayesian</td>
<td>0.801</td>
<td>0.527</td>
<td>0.183</td>
<td>0.111</td>
</tr>
<tr>
<td>Variance of Laplacian</td>
<td>0.958</td>
<td>0.113</td>
<td>0.161</td>
<td>0.133</td>
</tr>
<tr>
<td>NIQE *</td>
<td>0.958</td>
<td>0.210</td>
<td>0.248</td>
<td>0.227</td>
</tr>
<tr>
<td>CNN with no augmentation</td>
<td>0.968</td>
<td>0.700</td>
<td>0.466</td>
<td>0.560</td>
</tr>
<tr>
<td>CNN with translational augmentation</td>
<td>0.974</td>
<td>0.750</td>
<td>0.600</td>
<td>0.667</td>
</tr>
<tr>
<td>CNN with k-space augmentation</td>
<td>0.977</td>
<td>0.779</td>
<td>0.642</td>
<td>0.704</td>
</tr>
<tr>
<td>CNN with k-space + translational augmentation</td>
<td>0.982</td>
<td>0.809</td>
<td>0.652</td>
<td>0.722</td>
</tr>
</tbody>
</table>

Precision = \( \frac{TP}{TP + FP} \)  
Recall = \( \frac{TP}{TP + FN} \)  
Accuracy = \( \frac{TP + TN}{TP + FP + FN + TN} \)  
F1 score = \( \frac{2 \times (\text{Recall} \times \text{Precision})}{\text{Recall} + \text{Precision}} \)

Oksuz et al., MICCAI 2018  

A. King – Machine Learning in Cardiac Imaging
Use of UK biobank data for analysis of factors influencing cardiac health

**STACOM poster:** Puyol-Anton, et al. “Learning associations between clinical information and motion-based descriptors using a large scale MR-derived cardiac motion atlas”
5 year grant involving:
- King’s College London
- Imperial College London
- Queen Mary University London
- Oxford University

“To develop a diagnosis-driven ‘smart MR scanner’ that it is no longer a mere imaging device but instead becomes a highly sophisticated diagnostic tool” …
4. Machine learning for robust MR reconstruction

Aim:
MR motion artefact correction during reconstruction

Approaches:
• Denoising in image space (c to a)
• Denoising in k-space (d to b)
• End-to-end (d to a)*

Oksuz et al., MICCAI MLMIR, 2018

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Automap

Image reconstruction by domain transform manifold learning

- Developed for high quality image reconstruction from under-sampled k-space
- Insufficient image quality for corrupted k-space

Oksuz et al., MICCAI MLMIR, 2018

* Zhu et al., Nature, 2018
Automap-GAN setup

Adversarial setup for motion artefact correction

- Improved robustness and deblurring of the image outputs

Oksuz et al., MICCAI MLMIR, 2018

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Experimental results

**Dataset:**
- Synthetically generated corruptions
- 75000 2D images for training, 2500 for testing

<table>
<thead>
<tr>
<th>Methods</th>
<th>RMSE</th>
<th>PSNR</th>
<th>SSIM</th>
</tr>
</thead>
<tbody>
<tr>
<td>Inverse Fourier Transform</td>
<td>0.045</td>
<td>27.8</td>
<td><strong>0.883</strong></td>
</tr>
<tr>
<td>Proposed-ImageNET</td>
<td>0.032</td>
<td>31.1</td>
<td>0.766</td>
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<tr>
<td>Automap-Cardiac</td>
<td>0.029</td>
<td>32.7</td>
<td>0.814</td>
</tr>
<tr>
<td>Proposed-Cardiac</td>
<td><strong>0.027</strong></td>
<td><strong>35.1</strong></td>
<td><strong>0.850</strong></td>
</tr>
</tbody>
</table>

\[
\text{RMSE} = \sqrt{\frac{1}{N_x N_y} \sum_{x=0}^{N_x} \sum_{y=0}^{N_y} (r(x, y) - p(x, y))^2}
\]

\[
\text{PSNR} = 20 \log_{10} \left( \frac{\sum_{x=0}^{N_x} \sum_{y=0}^{N_y} r(x, y)^2}{\sum_{x=0}^{N_x} \sum_{y=0}^{N_y} (r(x, y) - p(x, y))^2} \right)
\]

\[
\text{SSIM}(x, y) = \frac{(2\mu_x \mu_y + c_1)(2\sigma_{xy} + c_2)}{\mu_x^2 + \mu_y^2 + c_1(\sigma_x^2 + \sigma_y^2 + c_2)}
\]

In-vivo example

(a) K-space  (b) Motion corrupted image  (c) Proposed

Oksuz et al., MICCAI MLMIR, 2018

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QUESTIONS ??

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UK Biobank:  http://www.ukbiobank.ac.uk/

biobank uk  smartheart  EPSRC
(Application 17806)