Autoencoder in Time-Series Analysis for Unsupervised Tissue Characterisation in a Large Unlabelled Medical Image Dataset

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Introduction

- The challenges in medical data
  - Data-labelling is challenging even for trained radiologists
  - Image acquisition protocols may not be well documented
- DCE-MRI
  - An imaging protocol to acquire a series of images by time after an injection of a contrast agent into the patient
  - The change of the contrast of the successive images represent the observed tissue's blood perfusion dynamics and vascular permeability
- Our approach
  - Use unsupervised feature-learning approach to automatically learn how to classify different tissue types based on the contrast changes:
  - Time-series analysis of DCE-MRI contrast change signals using single-layer sparse autoencoder

Single-Layer Sparse Autoencoder

- An algorithm for unsupervised feature learning with symmetrical bi-layer neural networks of two visible layers (input & output layer), and one hidden layer (encoding layer) [1], [2]
- The activation of each unit in the hidden layer is defined as

$$f(x) = g(Wx + b),$$

where
- $g(z) = 1/(1 + exp(-z))$: logistic sigmoid function for a vector z
- W: weight vector between visible & hidden nodes, b: bias

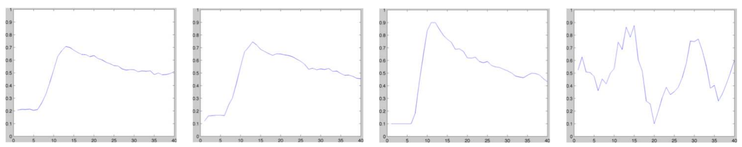
- The cost function is given as:

$$J_{\text{sparse}}(W, b) = J(W, b) + \beta \sum_{j=1}^{s_2} \text{KL}(\rho \parallel \hat{\rho}_j),$$

where
- $J(W, b)$: likelihood cost function between the input & output of the autoencoder
- $\beta \sum_{j=1}^{s_2} \text{KL}(\rho \parallel \hat{\rho}_j)$: Kullback-Leibler (KL) divergence to encourage the average activation of each hidden unit
- $\hat{\rho}_j$: activation of each hidden unit, ρ: desired level of sparsity
- β: the sparsity penalty term, s_2 number of hidden units

Application to Time-series Analysis of DCE-MRI Data

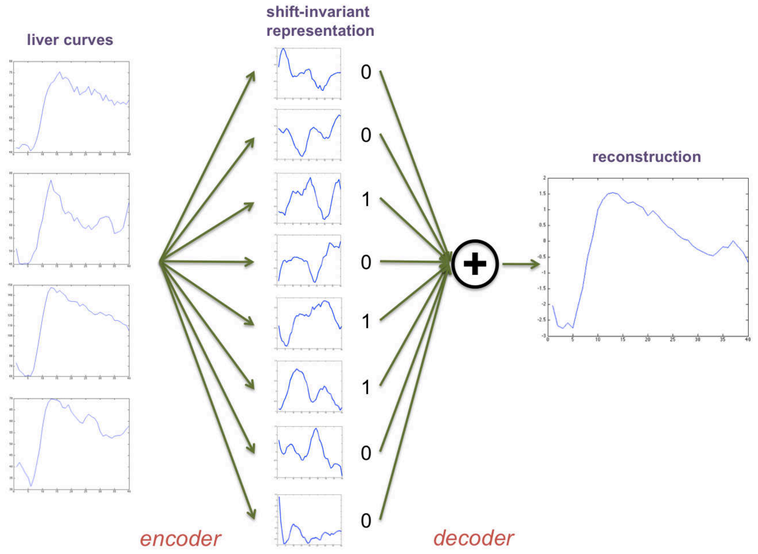
- Data
  - DCE-MRI study of tumors in different organs, where the majority are liver metastases
  - 46 scans having 40 time-points in each DCE-MRI measurement, each time point producing an image volume of 256×256×12 voxels
  - Total of 22,080 (46×40×12) images
- Time-series signals



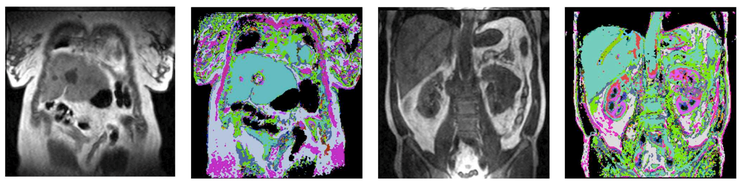
a liver signal | a non-liver signal | a non-liver signal | a signal affected by motion

Results

- Encoder-decoder setting for the time-series analysis

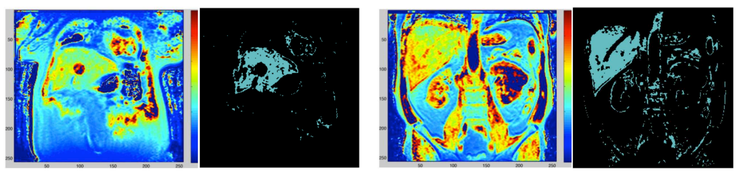


- Unsupervised tissue-type classification



T1 liver scan | automatic tissue-type classification | T1 kidney scan | automatic tissue-type classification

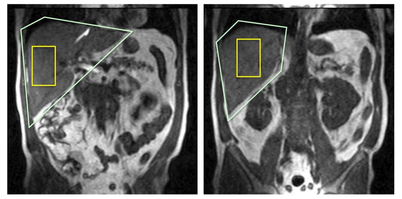
- Comparison to threshold-based methods



T1 range in heat-map (0<T1<1200) for an image of the training dataset | After filtering with the T1 range of the liver for the image of the training dataset (500<T1<700) | T1 range in heat-map (0<T1<1200) for an image in the test dataset | After filtering with the T1 range of the liver for the image in the test dataset (550<T1<900)

- An absolute value range varies according to case by case (patient (condition), measurement pulse sequence, scanning device, etc.), but the contrast change over time (shape of the signal curves) is more constant
- Our method is robuster & more generic, across images of varying circumstances than the threshold-based methods

Performance Evaluation



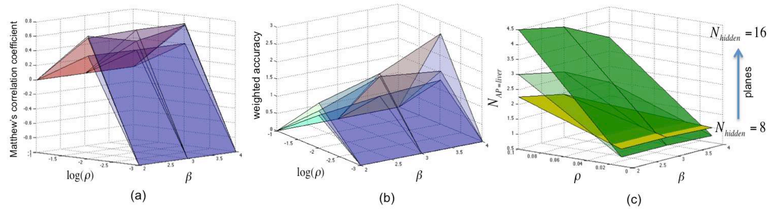
- Evaluate the performance with liver tissue classification
  - Liver is an organ with tissues of homogeneous characteristics
  - It is easier to sample the liver-tissues & non-liver-tissues in a semi-automatic way than the other tissue types
  - Although other tissue types give consistent results as well
- 7118 liver-tissues and 18519 non-liver tissues were sampled from a different dataset (kidney patient scan) than the training dataset (liver patient scan)
- Performance evaluation with Matthew's correlation coefficient (MCC) (a), weighted accuracy (b), Number of encoding patterns for liver tissue (c), for various parameter settings

$$\text{MCC} = \frac{TP \times TN - FP \times FN}{\sqrt{(TP + FP)(TP + FN)(TN + FP)(TN + FN)}}$$

$$\text{weighted accuracy} = \beta Acc^{+} + (1 - \beta) Acc^{-}$$

$$Acc^{+}(\text{True Positive Rate}) = \frac{TP}{TP + FN}$$

$$Acc^{-}(\text{True Negative Rate}) = \frac{TN}{TN + FP},$$



Conclusions

- A robust & generic automatic tissue type classification with single-layer sparse autoencoder
- Performance evaluation for different parameter settings

Acknowledgement

We acknowledge the support received from the CRUK and EPSRC Cancer Imaging Centre in association with the MRC and Department of Health (England) grant C1060/A10334, also NHS funding to the NIHR Biomedical Research Centre.

References

[1] A. Coates, H. Lee, and A. NG, "An analysis of single-layer networks in unsupervised feature learning," *Journal of Machine Learning Research*, vol. 15, p. 48109.

[2] I. Goodfellow, Q. Le, A. Saxe, H. Lee, and A. Ng, "Measuring invariances in deep networks," *Advances in neural information processing systems*, vol. 22, pp. 646-654, 2009.

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