A Noise Robust Statistical Texture Model

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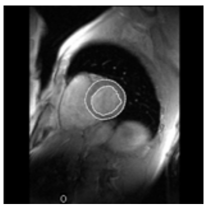
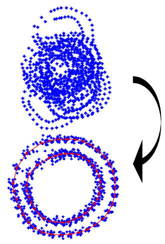
Abstract

The study presents a noise robust low dimensional representation of texture variation present in a training set. The conventional analysis of training textures in the Active Appearance Models (AAMs) segmentation frame-work is extended by the new representation. This is accomplished by augmenting the model with an estimate of the covariance of the noise present in the training data. A compact model is obtained maximizing the signal-to-noise ratio (SNR), thus favouring subspaces rich on signal, and low on noise. The extended method is evaluated on a set of left cardiac ventricles obtained using magnetic resonance imaging (MRI).

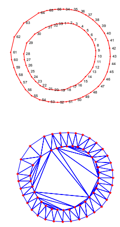
F1: Example annotation of the left ventricle using 66 landmarks

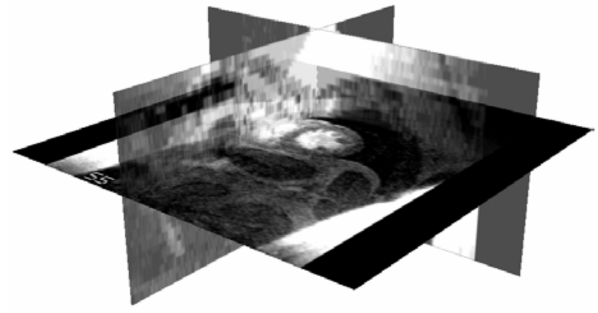


F2: Procrustes alignment



F3: Cardiac prototype and warp mesh





F4: Cardiac MRI volume visualised using three orthogonal cutting planes (secondary planes are semi-transparent)

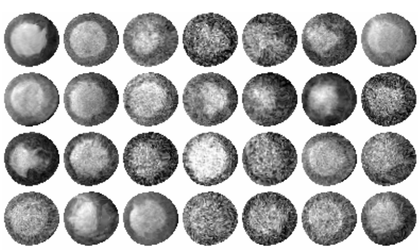
Methods

Active Appearance Models establish a compact parameterisation of object variability, as learned from a training set by estimating a set of latent variables. From these quantities new images similar to the training set can be generated. Objects are defined by marking up each example with points of correspondence over the set either by hand, or by semi- to completely automated methods, see F1-4. Exploiting prior knowledge of the optimisation space, these models can rapidly fit to unseen images, given a reasonable initialisation.

To reduce dimensionality, AAMs traditionally apply a Principal Component (PC) analysis of the training set to synthesise new images. By maximizing the variance only, the PC is modelling any noise present in the training set along with the uncontaminated hidden image data. We propose to extend the AAM framework by augmenting the image representation with noise characteristics. This is accomplished by applying the Minimum Noise Fraction (MNF) transformation.

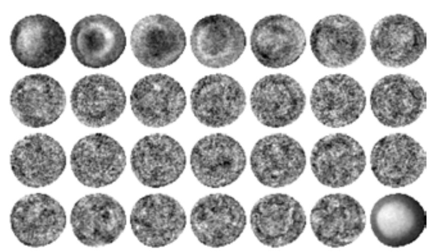
The MNF analysis extracts important otherwise occluded information on the correlation structures of the data, and aims at obtaining a low dimensional model representation. As opposed to the PC transform, the MNF transform takes the spatial nature of the image into account. Whereas the PC transform only requires knowledge of the dispersion (covariance) matrix, the MNF transform requires an estimate of the dispersion matrix of the noise structure as additional information.

F5: Noise contaminated cardiac MRIs



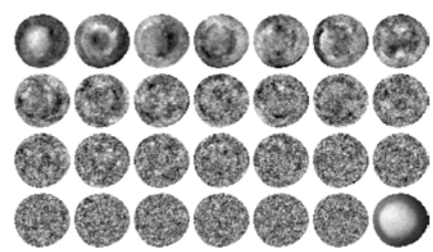
$$\boldsymbol{r}(\boldsymbol{x}) = \boldsymbol{s}(\boldsymbol{x}) + \boldsymbol{n}(\boldsymbol{x})$$

F6: PC decomposition maximising variance



$$\mathrm{V}\{\boldsymbol{a}_i^T \boldsymbol{r}(\boldsymbol{x})\} = \boldsymbol{a}_i^T \boldsymbol{\Sigma} \boldsymbol{a}_i$$

F7: MNF decomposition maximising the signal-to-noise ratio



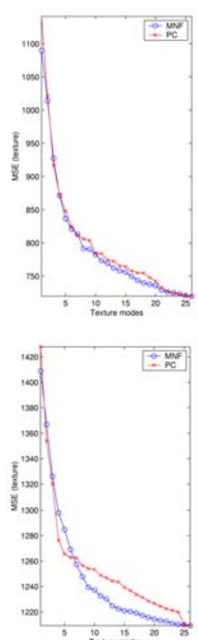
$$\mathrm{SNR}_i = \frac{\mathrm{V}\{\boldsymbol{a}_i^T \boldsymbol{s}(\boldsymbol{x})\}}{\mathrm{V}\{\boldsymbol{a}_i^T \boldsymbol{n}(\boldsymbol{x})\}} = \frac{\boldsymbol{a}_i^T \boldsymbol{\Sigma} \boldsymbol{a}_i}{\boldsymbol{a}_i^T \boldsymbol{\Sigma}_n \boldsymbol{a}_i} - 1$$

Results

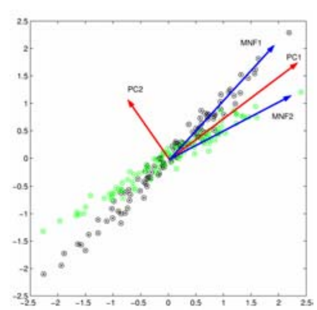
Noise is added to the training data simulating different SNRs, i.e. different quality of the MRIs due to inter-patient, inter-operator variation etc. This is done in order to examine the robustness of the texture representation in the MNF basis compared to the PC basis. Gaussian noise is applied with a standard deviation randomly chosen to produce training images with an SNR down to 6dB. This knowledge of the noise structure is not used in the subsequent analyses. To examine the robustness of the MNF transform, 101 leave-one-out studies were carried out. One on the uncorrupted and 100 on the noise degraded shape-free sets of 28 MRIs. In F5 a random sample of a noise contaminated cardiac MRI data set is shown. F6 and F7 shows the PC and the MNF decompositioning of the data, with the last component representing the mean texture sample. F8 shows the cross-validation results on both uncontaminated data and on the data presented in F5 using the PC and MNF basis representations. F9 shows the metric characteristics and differences between the PC and MNF representation.

To assess the PC and the MNF transforms capabilities in a de facto segmentation setting, a cross-validation study was carried out on the cardiac data set using AAM. The performance is evaluated for both texture and landmark measures. A modest improvement in both these measures and corresponding uncertainties is observed for the MNF AAMs. See F10 for an example segmentation.

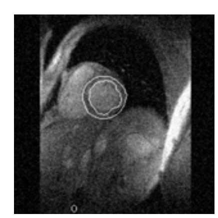
F8: Leave-one-out studies on cardiac MRIs. Without and with noise (top / bottom)



F9: Metric characteristics of the PC and the MNF analysis



F10: Segmentation results on contaminated cardiac MRI using the noise robust texture model



$$\boldsymbol{s} = \overline{\boldsymbol{s}} + \boldsymbol{\Phi}_s \boldsymbol{W}_s^{-1} \boldsymbol{\Phi}_{c,s} \boldsymbol{c}$$

$$\boldsymbol{t} = \overline{\boldsymbol{t}} + \boldsymbol{\Phi}_t \boldsymbol{\Phi}_{c,t} \boldsymbol{c}$$

Conclusion

We have shown that a more compact representation of texture can be obtained by extending the PC to the MNF transformation in the AAM framework. The novel approach shows better performance in leave-one-out representation studies both on original and on noise degraded cardiac MRIs. Thus, by separating important signal from noise the MNF transform generalises better than the PC transform.
In contrast to the PC analysis, the new approach by maximizing SNR is invariant to linear transforma-tions such as scaling of the individual components in the training set. As a consequence, the MNF decomposition is expected to be useful in future AAM studies involving data fusion of multiple features of different nature measured at different scales. This includes derived physiological measures, textual quantities, and multiple imaging modalities.

Moreover, the MNF analysis in itself can be applied as a data driven method probing for uncorrelated modes of biological variation in non-Euclidean space, and thus constitute a useful tool in exploratory analysis of medical data.

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