# Utilising a Genetic Algorithm to Minimise the Number of Leads in Body Surface Mapping for the Electrocardiographic Diagnosis of Myocardial Infarction

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## Abstract

The 80-lead Body Surface Map (BSM) is a diagnostic tool utilised by clinicians for the diagnosis of myocardial infarction (MI) at our centre. The optimum number and placement of leads on the BSM is uncertain. We used Genetic Algorithm (GA) analysis to determine a reduced lead system for the optimal diagnosis of MI. 1106 cases presenting to our centre with ischaemic type chest pain (576 ST Segment Elevation MI, 244 Atypical ECG and 286 Non-MI) were recorded using the 80-lead BSM. A GA was developed to determine a subset of reduced number of leads, with their associated anatomical position within the 80-lead BSM system, while maintaining sensitivity and specificity for MI diagnosis. The GA was run on two separate occasions (Run A and Run B) and the output compared with the 80-Lead BSM. Run A produced a 24 lead system. The sensitivity and specificity for MI diagnosis was 86.40% and 97.55% respectively. Received Operator Characteristic (ROC) curve c-statistic was 0.805. Run B produced a 21 lead system with sensitivity and specificity of 84.84% and 98.25% respectively. ROC curve c-statistic was 0.811. This compares favourably with the 80 lead BSM (sensitivity 90%, specificity 92%, ROC c-statistic 0.850).

## 1. Introduction

The 12-lead ECG plays a pivotal role in the assessmer of patients with suspected Acute Coronary Syndrome (ACS). The 12-lead ECG may show ST-segment change within seconds of an ischaemic insult [1]. Detaile analysis of the ST-segment changes allows the physicia to identify the infarct related artery in patients with ST elevation [2] and risk stratify patients with ST-depressior

Currently in its traditional form, the precordial leads V to V6 provide a panoramic view of the electrical activit of the heart in the horizontal plane but does not full assess the anterior wall of the right ventricle or th posterior wall of the left ventricle. The limb leads grouped in the conventional hexaxial system provide a suboptimal view of the cardiac frontal plane leaving a 60° gap between lead I and II and a 90° gap between lead III and aVR. This results in under detection of injury currents originating in the left ventricular inferior and lateral walls [3].

Interest therefore remains in improving the ability of the ECG to detect MI particularly in those with non-diagnostic ECGs. A method to improve the sensitivity of the ECG is by the application of extra electrodes or "non-standard lead sets" over a larger area of the thorax particularly the right ventricular, high right anterior, posterior and right ventricular territories. This technique is known as body surface potential mapping.

At our centre, in its current format the Body Surface Map (BSM) consists of a flexible plastic anterior and posterior electrode harness together with a recording unit which is portable. The anterior harness contains 64 electrodes, including 3 proximal bipolar limb leads (Mason-Likar position), and a posterior harness with 16 electrodes (Figure 1). This lead configuration enables recording of 77 unipolar ECG signals with respect to the Wilson central terminal.

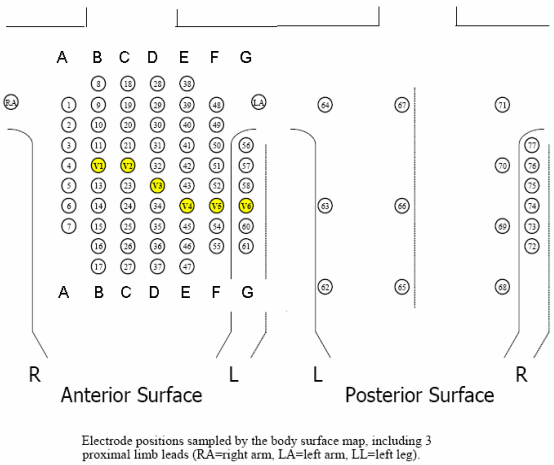


Figure 1. Diagrammatic display of the current layout of the 80 Lead Body Surface Map.

Despite initial promising results, the 80-lead BSM has failed to supersede the 12-lead ECG for initial triage of patients with chest pain. Physicians see the additional leads as increased analytical complexity. This complexity relates to the requirement to sample many channels of ECG information simultaneously and the application of the additional number of chest electrodes viewed as impractical, particularly in acute care.

We propose using a novel approach to reducing the number of leads on the BSM. By utilising a genetic algorithm we aim to provide a reduced lead harness than the 80-lead system, while maintaining sensitivity and specificity for MI diagnosis.

## 1.1. Genetic algorithms

Genetic algorithms (GA) are implemented as a computer simulation of evolution in which populations of solutions are evolved towards a better solution to a problem. The evolution usually starts from a population of randomly generated individuals which represent solutions. The populations evolve in generations. In each generation, the fitness of every individual in the population is evaluated, multiple individuals are optimally selected from the current population (based on their fitness), and recombined (crossover) and possibly randomly mutated to form a new population. The new population is then used in the next iteration of the algorithm. Commonly, the algorithm terminates when either a maximum number of generations has been produced, or a satisfactory fitness level has been reached within the population. If the algorithm has terminated due to a maximum number of generations, a satisfactory solution may or may not have been reached.

# 2. Methods

1106 patients presenting to our centre with ischaemic type chest pain (576 ST Segment Elevation MI, 244 Atypical ECG and 286 Non-MI) were recorded using the 80-lead BSM. All recordings were made within 12 hours of symptom onset. MI was confirmed by elevation of Troponin T > 0.09 umol/l and BSM diagnosis and recording quality confirmed by retrospective analysis by two physicians. A BSM diagnostic algorithm was developed to produce an output (MI or Not MI) depending on the information produced from each lead of the BSM recording [4]. A Genetic Algorithm was developed to determine a subset of reduced number of leads while maintaining sensitivity and specificity for MI diagnosis, based on the output of the BSM algorithm

## 2.1. The genetic algorithm

We adapted a GA previously used in predicting coronary heart disease risk in patients with type 2 diabetes mellitus [5]. For that research, a combination of a GA and Weighted k Nearest Neighbour (WkNN) was used in order to find the feature relevance from a set of markers. The GA dealt with weights for each of the features being analysed where a set of particular weights were modeled as an individual. The fitness was evaluated as each vector of weights was used to classify cases in the database using a WkNN approach. The adaptation from that approach to the present research was to change to feature selection instead and WkNN was substituted by a BSM algorithm.

A rule based algorithm to detect acute MI using up to the 80 lead set (77 unipolar + 3 limb leads) was developed, which produced an output based on the information received from each electrode to determine if the diagnosis was MI or Not-MI. Certain outputs of each lead (e.g. the ST0 elevation/depression, QRS width, T wave inversions etc.) are considered. The algorithm diagnoses Anterior, Posterior, Inferior, Lateral and Right Ventricle MI even in the presence of confounders such as Left Ventricle Hypertrophy, Left Bundle Branch Block, Early Repolarisation and Acute Pericarditis.

An individual for the GA is modeled using a binary vector of 77 elements (the 3 limb leads will be always present). Each element indicates the presence or absence of the corresponding electrode. Thus for example, the full set of leads is represented by a vector of all 77 elements set to 1. A particular subset of electrodes is modeled setting to one the corresponding elements in the vector (the other elements are set to zero). The fitness, as a measure of effectiveness of a particular individual (subset of electrodes), is calculated as the normalised semi-sum of the sensitivity and specificity when it is applied to the database using the algorithm. In general the fitness as defined above favours the full set of electrodes. Therefore we incorporated and additional term to the fitness in order to encourage fewer electrodes in the solutions.

The fitness (f) is calculated as the product of the effectiveness (s) by a factor to encourage solutions with fewer electrodes (n is the number of electrodes used in the solution):

$$f = s(77 - n)/76$$

## 3. Results

Once satisfied that the GA algorithm was producing acceptable, reproducible results, in comparison to 80-lead performance, the algorithm was then run on two final occasions. The outputs from these two final runs (Runs A and B) were used as the two lead sets of the GA as shown in figures 2 and 4. For Run A a 24 lead system was produced with a sensitivity of 86.40 and a specificity of 97.55 for MI diagnosis. The ROC curve and Area Under the Curve (c-statistic) for Run A is shown in Figure 3.

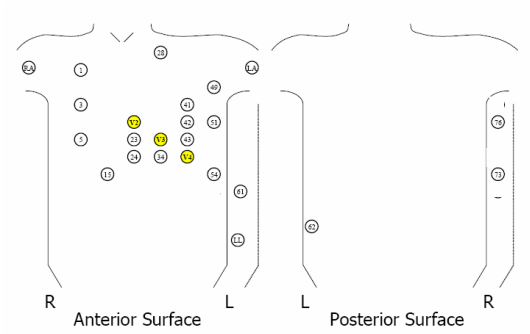


Figure 2: Display of the lead set as produced by Run A of the Genetic Algorithm.

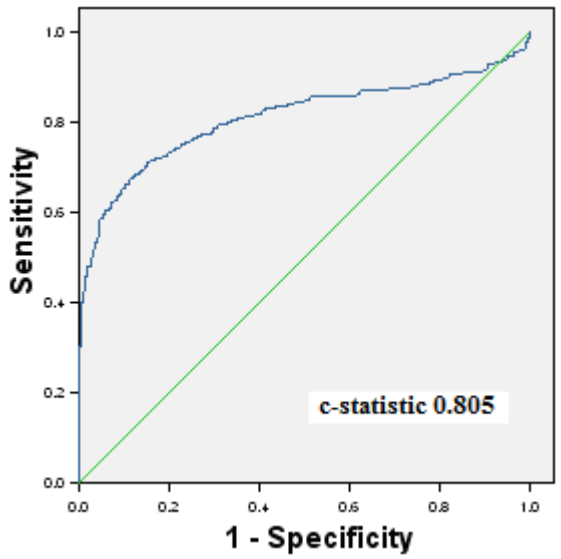


Figure 3: Receiver Operator Characteristic (ROC) curve for the lead set produced by Run A of the Genetic Algorithm.

For Run B a 21 lead system was produced with a sensitivity of 84.84 and specificity of 98.25 for Mi diagnosis. The ROC curve and Area Under the Curve (c-statistic) for Run B is shown in Figure 5. These results can be compared with outputs when all 80 leads of the BSM are used (Table 1).

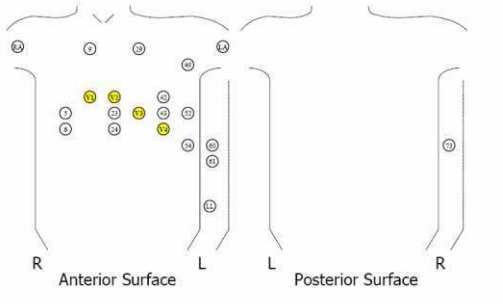


Figure 4: Display of the lead set as produced by Run B of the Genetic Algorithm.

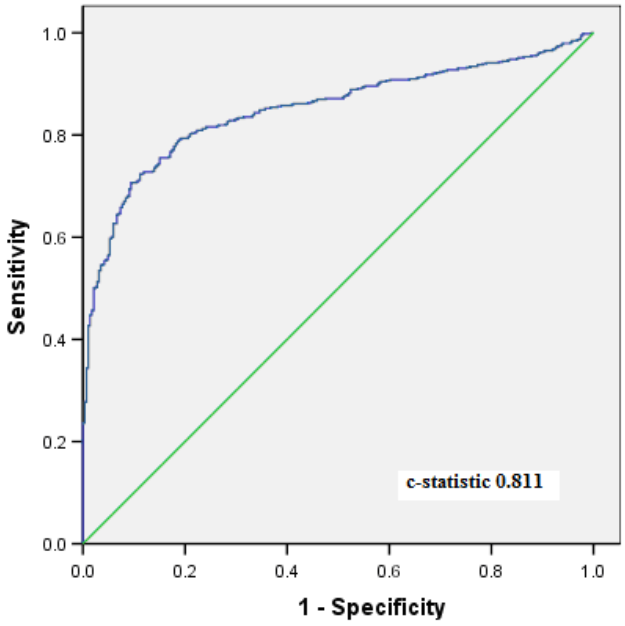


Figure 5: Receiver Operator Characteristic (ROC) curve for the lead set produced by Run B of the Genetic Algorithm.

| | Sensitivity % | Specificity % | c-Statistic (area under the curve) | 95% Confidence Interval |
|---|---|---|---|---|
| Run A | 86.40 | 97.55 | 0.805 | 0.776-0.833 |
| Run B | 84.84 | 98.25 | 0.811 | 0.783-0.839 |
| 80-Lead BSM | 90.12 | 92.00 | 0.850 | 0.824-0.875 |

Table 1: Sensitivity and Specificity and ROC area under the curve (c-statistic- including confidence intervals) for Run A, Run B and the 80-Lead BSM

## 4. Conclusion

The use of a genetic algorithm made it possible to produce two leadsets with these selected variables in producing a reduced lead set for diagnosing MI, while maintaining sensitivity and specificity. The two leadsets produced had subtly different lead positions. This is to be expected given the random nature of lead selection using the genetic algorithm approach. What it does confirm is that there appears to be significant lead redundancy in the 80-lead system, with a multitude of possible leadsets.

This seems to be the first time a genetic algorithm has been used in BSM for lead number/location optimisation. The main draw back with this approach is it reliance on the strength of the diagnostic capabilities of the BSM algorithm. Each generation was produced on the ability to diagnose MI based on the output from the BSM algorithm. Thus, any flaws with the BSM algorithm would reflect in the leads chosen by the GA. Also, most of the posterior leads were ignored, probably because the dataset contained fewer posterior MI, again perhaps a flaw of this system.

Regardless the end result produces new options for producing reduced lead systems for the diagnosis of MI and a novel use of genetic algorithms as a whole.

## Acknowledgements

This work was funded by a Royal Victoria Hospital Research Grant.

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