Deep Learning Applied to Attractor Images Derived from ECG Signals for Detection of Genetic Mutation

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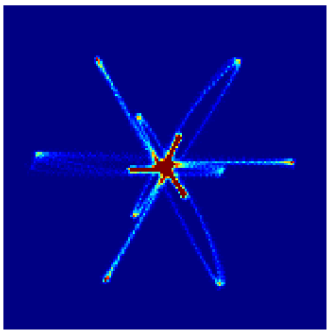
The aim of this work is to distinguish between wild-type mice and $Scn5a^{+/-}$ mice with a heterozygotic sodium channel knockout using short ECG signals. This mutation results in loss of cardiac sodium channel function and is associated with increased ventricular arrhythmogenic risk which can result in sudden cardiac death. Lead I and Lead II ECG signals from wild-type and $Scn5a^{+/-}$ mice are used and the mice are also grouped as female/male and young/old.

We use our novel attractor reconstruction method to generate an attractor from the ECG signal (see Figure) using all of the available waveform data. We have previously extracted a variety of quantitative measures from the attractor and used machine learning to classify each animal as either wild-type or mutant. In this work, we take the attractor images and use these as input to a deep learning algorithm in order to perform the same classification. As there is only data from around 40 mice available, we use a transfer learning approach in which a network that has been pre-trained on millions of images is used as a starting point and the last few layers are changed in order to fine tune the network for the attractor images.



An attractor generated from 10 seconds of mouse ECG data.

Results of the classification are presented for all the data as well as for various groups (e.g. Lead I, Lead II, etc.), all of which show high predictive accuracy. Applying this approach to human ECG data has the potential for detection of genetic mutations associated with conditions such as Brugada syndrome, or indeed other electrophysiological abnormalities, from a single lead ECG signal.