# Personalisation of a 3D Ventricular Electrophysiological Model, using Endocardial & Epicardial Contact Mapping and MRI

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Abstract. Personalisation, i.e. parameter estimation of a cardiac ElectroPhysiology (EP) model is needed to build patient-specific models, which could then be used to understand and predict the complex dynamics involved in patient's pathology. In this paper, we present an EP model personalisation approach applied to an infarcted porcine heart, using contact mapping data and Diffusion Tensor MRI. The contact mapping data was gathered during normal sinus rhythm, on the ventricles *in-vivo*, endocardially as well as epicardially, using a CARTO mapping system. The Diffusion Tensor MRI was then obtained *ex-vivo*, in order to have the true cardiac fibre orientations, for the infarcted heart. Both datasets were then used to build and personalise the 3D ventricular electrophysiological model, with the proposed personalisation approach. Secondly, the effect of using only endocardial mapping or epicardial mapping measurements, on the personalised EP model was also tested.

## 1 Introduction

Modelling of the cardiac electrophysiology has been an important research interest for the last decades, but in order to translate this work into clinical applications, there is an important need for personalisation of such models, i.e. estimation of the model parameters which best fit the simulation to the clinical data. Cardiac model personalisation is required to develop predictive models that can be used to improve therapy planning and guidance.

There is a large variety of cardiac electrophysiology models for myocyte action potential developed at cellular and sub-cellular scales [1–3]. Cardiac tissue and whole-heart electrophysiological computations of these models are based on the principles of reaction-diffusion systems [1]. According to the reaction term computation, these models can be broadly categorised as Biophysical Models (BM), Phenomenological Models (PM) and Generic Models (GM). BM [2,3] model ionic currents and are the most complete and complex but are less suitable for parameter estimation from clinical data due to a high computational cost and to the lack of observability of their parameters. PM [4] are based on PDEs and are of intermediate complexity level and less computationally expensive. GM [5,6] represent simplified action potentials and are the least complex. Simple Eikonal Models (EM) [7] model the action potential propagation in the cardiac tissue without modelling the action potential itself. They can be very fast to compute [8], but less reliable in arrhythmia predictions due to the complexity of both the refractoriness and the curvature of the wavefront.

In this paper, we present a coupled personalisation framework (EK-MS), which is fast and combines the benefits of an Eikonal (EK) model with those of a simplified biophysical model, the Mitchell-Schaeffer (MS) model. The fast 3D EK model is used to estimate the tissue conductivity parameter over the ventricles from the contact mapping of endocardial & epicardial surface potentials, using an adaptive iterative algorithm. This is then used to set the conductivity parameter of the 3D MS model, which could be then used for reliable arrhythmia predictions.

In the past years, authors have focused on the personalisation of the PM and MS model on 3D volumes [9, 10] using optical and MR data. Recently, we have proposed the coupled personalisation approach (EK-MS), with an application to a patient with infarction, using non-contact mapping and 3D MRI [11]. The contributions of this paper are: 1) Application of the EK-MS personalisation approach to an infarcted porcine heart, using contact mapping data and DT-MRI, and 2) Study of the effect of using either endocardial only or epicardial only measurements, on the EP model personalisation.

## 2 3D electrophysiology model with chronic infarction

The models used in the EK-MS personalisation approach are simple Eikonal (EK) model and a simplified biophysical model, the Mitchell-Schaeffer (MS) model.

The EK model simulates the propagation of the depolarization wave in quiescent tissue, ignoring repolarisation phase. The EK model is governed by eikonaldiffusion (ED) equation and is based on anisotropic Fast Marching Method (FMM). More detailed analysis can be found in [8]. The non-linear EK model equation is solved using a fixed point iterative method combined with a very fast eikonal solver, on the bi-ventricular geometry, as explained in [7].

The MS model [12] is a 2-variable simplified biophysical model derived from the 3-variable Fenton Karma (FK) ionic model [13]. It models the transmembrane potential as the sum of a passive diffusive current and several active reactive currents including a sodium ion (influx) current and a potassium ion (outflux) current. Unlike FK model, it does not model the Calcium ion current. More detailed analysis can be found in [12]. The MS model is modelled as reaction diffusion equations and is spatially integrated using a linear tetrahedral mesh of the bi-ventricular myocardium, taking into account the fiber orientation as well, and is temporally integrated using a semi-implicit time integration scheme (MCNAB) [14].

In this paper, we focus only on conductivity estimation, thus chronic scars are modelled with low conductivity in the ischemic zones. While the gray zones (the regions around scars) had conductivity estimated from the data, as shown later. However, we had shown the approach of modelling chronic scars along with APD heterogeneity in [11].

## 3 Contact mapping and MR Dataset Processing

In this paper, we performed the adjustments on an infarcted porcine heart. The acquired data consists of contact mapping data gathered on the ventricles *invivo* during normal sinus rhythm, endocardially as well as epicardially, using a CARTO mapping system, and a Diffusion Tensor MRI (DT-MRI) representing geometry and fiber orientation *ex-vivo*.

The 3D mapping system (CARTO) localizes the extracellular potentials at points in 3D space and on a 3D ventricular geometry acquired by connecting all those points, during the interventional procedure, using invasive catheters. The measurement of extracellular potentials could be unipolar or bipolar (Fig 2(b)). The mapping system then extracts the local activation times (LAT) for the contact points in 3D space and produces a local activation map on the 3D ventricular geometry, representing the action potential wave propagation pattern, as shown in Fig 2(a).

The DT-MRI is used to reconstruct the cardiac fibers using the principal eigenvector of the diffusion tensor. It is also used to create the 3D ventricular model, as shown in Fig 1.

The 3D ventricular geometry acquired using CARTO is then registered to the 3D ventricular model. The measurement contact points of the CARTO, are then projected on to the 3D ventricular geometry using closest points projections (Fig 2(c & d)). Finally, the LATs measured at those points is then interpolated on the endocardial and epicardial surface, to have a rough guess on the action potential wave propagation, as shown in Fig 3.

The interpolated epicardial and endocardial LAT maps on the 3D ventricular model, are then used as input for EP model personalisation. In order to penalise the point projection and interpolation errors, we use the projection distance of the points and the interpolated projection distance maps (Fig 4) as a spatial penalising factor in the conductivity estimation procedure, as explained later.

## 4 Building personalised electrophysiological model

### 4.1 Coupled personalisation approach (EK-MS)

Cardiac tissue conductivity is a crucial feature for the detection of conduction pathologies. The Apparent Conductivity (AC) of the tissue can be measured by a parameter d in the EK model [8]. For computational affordability reasons, we use the simplest EK model for fast tissue conductivity estimation, with an adaptive iterative algorithm based on gradient free optimisation, as explained in details in [8,11]. For reliable pathological predictions with chronic scars, we couple the personalised parameters of the EK model to a relatively more complicated biophysical MS model. The coupling procedure is explained in details in [11].



**Fig. 1.** (a) Volume rendering of DT-MRI to visualize scars (bright in intensity), (b) 3D ventricular model constructed from DT-MRI, with labelled scar zones (black), (c) cardiac fiber construction from DT-MRI, showing the fiber disorientation in and around scars (black contour).



**Fig. 2.** (a) LAT map constructed on a 3D ventricular geometry using CARTO mapping system, (b) Unipolar & bipolar extracellular potentials measured using invasive catheters, (c & d) measurement contact points (red - endocardial & blue - epicardial) gathered in 3D space using CARTO, registered and then projected on the endocardial (c) & epicardial (d) surface respectively, of the 3D ventricular model.



Fig. 3. LAT maps construction from linear interpolation of the measurement contact points (black) for (a) endocardial and (b) epicardial surfaces of the 3D ventricular model.

The input to the algorithm are the linearly interpolated LAT maps on the surface of the ventricular model (Fig 3). The cost function for each zone to minimise, is adapted here, and is given as

$$J(d_{zone}) = \sum_{\forall i \in S \cap zone} \left( PenaltyFactor_i * \left( LAT_i - DT_i^{sim} \left( d_{zone} \right) \right) \right)^2 \quad (1)$$



**Fig. 4.** Projection distance calculated and interpolated from the contact points (black), on to the endocardial surface.

with vertex *i* in zone, belonging to the surface *S* having measures,  $DT^{sim}$  are the simulated depolarisation times from the EK model, and *PenaltyFactor* is computed from the normalisation of interpolated projection distance maps (Fig 4(b & c)), with 1.0 representing lowest distance and  $8.14e^{-9}$  representing the farthest distance.

## 4.2 Application

In order to assess the influence of mapping (endocardial and epicardial) details on the model personalisation, we tested model personalisation with various configurations as follows.

With endocardial and epicardial mapping In the state of the art in clinics, simultaneous endocardial and epicardial mappings are the finest amount of acquisition details possible for capturing the action potential wave propagation dynamics during normal sinus rhythm. Thus we use the apparent conductivity estimated using this mapping data, as the closest approximation of the true tissue conductivity distribution, with the proposed personalisation approach. The mean error on activation times, after model personalisation was 15.93 ms. Fig 5(a & b) shows the activation isochrones after personalisation, and Fig 6(a & b) shows the AC distribution, along with the residual activation time error after optimisation.

With endocardial mapping Now we use only the endocardial mapping, to estimate the AC distribution. The mean error on activation times, after personalisation was 15.26 ms. Fig 5(e) shows matching of the LV endocardial isochrones with Fig 5(a) and data (Fig 3(a)), but has a large misfit of the epicardial isochrones (Fig 5(f) compared against Fig 5(b) and Fig 3(b)). Thus the reproducibility of the isochrones on the epicardial side is highly prone to errors. This is confirmed by the large prediction errors on the epicardial surface, as shown in Fig 7(c).

With epicardial mapping Here we use the epicardial mapping, to estimate the AC distribution. The mean error on activation times, after personalisation was 9.59 ms. Fig 5(c & d) shows good matching of the LV endocardial isochrones, as well as epicardial isochrones with Fig 5(a & b) and data (Fig 3(a & b)). Thus epicardial mapping could be sufficient enough to reproduce the true wave propagation dynamics, as compared to endocardial mapping data. This is confirmed by the low prediction errors on the endocardial surface, as shown in Fig 7(b).



Fig. 5. Volumetric activation times after personalisation using endocardial & epicardial mapping (top row), only epicardial mapping (middle row) and only endocardial mapping (bottom row).

## 5 Conclusion

In this work, we have shown the application of a proposed coupled personalisation framework to the contact mapping data of an infarcted porcine heart. The cardiac fibre orientations estimated from DT-MRI were incorporated inside the model personalisation for a more accurate tissue conductivity estimation. We also tested the influence of mapping details on the model personalisation algorithm. We found that personalisation using epicardial mapping gave a conductivity estimation closest to the one obtained with personalisation using both endocardial and epicardial mapping, and also showed a low prediction error. On



Fig. 6. The first two columns show estimated AC distributions and last two columns show residual error after personalisation, for various configurations explained.



**Fig. 7.** Graph: mean and standard deviation of the difference of AC values estimated for the 3 configurations. Zero mean with low standard deviation shows good agreement between the AC values for a given data point. Other figures show the prediction error on the endocardial side, for personalisation with epicardial mapping (b) and on the epicardial side, for personalisation with endocardial mapping.

the other hand, the personalisation with endocardial mapping had an important deviation from the estimated distribution obtained with both endocardial & epicardial mapping. It also had an important prediction error on the epicardial surface. Thus, within this experimental setting, epicardial mapping proved to be a sufficient acquisition to reproduce a tissue conductivity distribution, closer to the one estimated using both endocardial and epicardial mapping. This was also the case when the personalisation was done on similar data from a clinical case [15]. Such finding has to be tested on other configurations, for different healthy and pathological cases.

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## References

- 1. Fenton, F.H., Cherry, E.M.: Models of cardiac cell. Scholarpedia 3(8) (2008) 1868
- Noble, D., Varghese, A., Kohl, P., Noble, P.: Improved guinea-pig ventricular cell model incorporating a diadic space, IKr and IKs, and length-and tension-dependent processes. The Canadian journal of cardiology 14(1) (1998) 123
- Ten Tusscher, K., Noble, D., Noble, P., Panfilov, A.: A model for human ventricular tissue. American Journal of Physiology- Heart and Circulatory Physiology 286(4) (2004) H1573
- Bueno-Orovio, A., Cherry, E., Fenton, F.: Minimal model for human ventricular action potentials in tissue. Journal of theoretical biology 253(3) (2008) 544–560
- Fitzhugh, R.: Impulses and physiological states in theoretical models of nerve membrane. Biophysical Journal 1(6) (1961) 445–466
- R. Aliev, R., V. Panfilov, A.: A simple two-variable model of cardiac excitation. Chaos, Solitons & Fractals 7(3) (1996) 293–301
- Sermesant, M., Konukoglu, E., Delingette, H., Coudiere, Y., Chinchapatnam, P., Rhode, K., Razavi, R., Ayache, N.: An anisotropic multi-front fast marching method for real-time simulation of cardiac electrophysiology. Volume 4466 of LNCS., Springer (2007) 160–169
- Chinchapatnam, P., Rhode, K., Ginks, M., Rinaldi, C., Lambiase, P., Razavi, R., Arridge, S., Sermesant, M.: Model-based imaging of cardiac apparent conductivity and local conduction velocity for diagnosis and planning of therapy. Medical Imaging, IEEE Transactions on 27(11) (2008) 1631–1642
- Lepiller, D., Sermesant, M., Pop, M., Delingette, H., Wright, G., Ayache, N.: Cardiac electrophysiology model adjustment using the fusion of MR and optical imaging. Volume 5241 of LNCS., Springer (2008) 678–685
- Relan, J., Pop, M., Delingette, H., Wright, G., Ayache, N., Sermesant, M.: Personalisation of a cardiac electrophysiology model using optical mapping and mri for prediction of changes with pacing. Biomedical Engineering, IEEE Transactions on (2011)

- Relan, J., Chinchapatnam, P., Sermesant, M., Rhode, K., Ginks, M., Delingette, H., Rinaldi, C., Razavi, R., Ayache, N.: Coupled personalization of cardiac electrophysiology models for prediction of ischaemic ventricular tachycardia. Interface Focus 1(3) (2011) 396
- Mitchell, C., Schaeffer, D.: A two-current model for the dynamics of cardiac membrane. Bulletin of mathematical biology 65(5) (2003) 767–793
- Fenton, F., Karma, A.: Vortex dynamics in three-dimensional continuous myocardium with fiber rotation: filament instability and fibrillation. Chaos 8(1) (1998) 20–47
- Relan, J., Sermesant, M., Delingette, H., Pop, M., Wright, G., Ayache, N.: Quantitative comparison of two cardiac electrophysiology models using personalisation to optical and mr data. In: Biomedical Imaging: From Nano to Macro, 2009. ISBI'09. IEEE International Symposium on, IEEE (2009) 1027–1030
- 15. Konukoglu, E., Relan, J., Cilingir, U., Menze, B., Chinchapatnam, P., Jadidi, A., Cochet, H., Hocini, M., Delingette, H., Jaïs, P., Haïssaguerre, M., Ayache, N., Sermesant, M.: Efficient probabilistic model personalization integrating uncertainty on data and parameters: Application to eikonal-diffusion models in cardiac electrophysiology. Progress in Biophysics and Molecular Biology (2011) Accepted.