



## Feasibility of a semi-automated method for cardiac conduction velocity analysis of high-resolution activation maps

Ashish N. Doshi<sup>a,1</sup>, Richard D. Walton<sup>b,1</sup>, Sébastien P. Krul<sup>c</sup>, Joris R. de Groot<sup>d</sup>, Olivier Bernus<sup>b,e</sup>, Igor R. Efimov<sup>a,b,d</sup>, Bastiaan J. Boukens<sup>d,\*,2</sup>, Ruben Coronel<sup>b,c,\*,2</sup>

<sup>a</sup> Department of Biomedical Engineering, Washington University, St Louis, USA

<sup>b</sup> L'Institut de Rythmologie et de Modélisation Cardiaque (LIRYC), Fondation Université Bordeaux, Bordeaux, France

<sup>c</sup> Heart Center, Departments of Experimental Cardiology, Cardiology, and Cardiothoracic Surgery, Academic Medical Center, University of Amsterdam, Amsterdam, Netherlands

<sup>d</sup> Department of Biomedical Engineering, George Washington University, Washington D.C., USA

<sup>e</sup> Centre de Recherche Cardio-Thoracique de Bordeaux Inserm U1045, Université de Bordeaux, Bordeaux, France

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### ABSTRACT

Myocardial conduction velocity is important for the genesis of arrhythmias. In the normal heart, conduction is primarily dependent on fiber direction (anisotropy) and may be discontinuous at sites with tissue heterogeneities (trabeculated or fibrotic tissue). We present a semi-automated method for the accurate measurement of conduction velocity based on high-resolution activation mapping following central stimulation. The method was applied to activation maps created from myocardium from man, sheep and mouse with anisotropic and discontinuous conduction. Advantages of the presented method over existing methods are discussed.

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### 1. Introduction

Cardiac conduction velocity is an important determinant of arrhythmogenesis [1]. Slow and discontinuous conduction facilitate the initiation and maintenance of reentrant arrhythmias [1,2]. In healthy myocardium, conduction along the myocyte fiber direction (longitudinal) is faster than perpendicular to the fiber direction (transverse), resulting in a typical anisotropic activation pattern. Processes such as aging, ischemia, edema, heart failure, infarction and inflammation alter conduction [3–7]. For example, fibrosis may increase longitudinal conduction velocity by lateral insulation of myocyte fibers [2,8] or decrease conduction velocity by generating small myocardial discontinuities [9]. These factors increase the risk of ventricular fibrillation by setting the stage for conduction block and the onset of re-entry. [1,10].

Although the basis for measuring conduction velocity is simple (the distance traveled by a cardiac impulse during a predefined time), the

method for calculating conduction velocity is disputed. The complex, three-dimensional architecture of the myocardium results in non-uniform and regionally-complex activation spread. Consequently, the measurement of conduction velocity is inaccurate when estimated from epicardial or endocardial activation maps recorded at a distance from the stimulation site. Stimulation from within the field of recording sites, however, does allow accurate measurement of conduction velocities, as conduction close to the site of stimulation can be assumed to be two-dimensional [11]. Thus, the technique allows differentiation between conduction along and across the fiber direction.

Currently, high-density optical and electrical mapping are the methods of choice for measuring conduction in experimental cardiac electrophysiology [12]. These techniques permit recording of local activation times and calculation of local activation vectors in a regular grid. Two methods are commonly used to estimate conduction velocity. The single vector method measures conduction velocity between two points that are manually selected along the perceived longitudinal axis and perpendicular to it (Fig. 1A) [13]. The multiple vector method estimates conduction velocity by calculating local velocity vectors at each recording site and placing each vector into a bin based on its direction (Fig. 1B–D) [14]. The bins with the largest number of vectors indicate the transverse direction, whereas the bins with the highest average vector magnitude indicate the longitudinal direction. Bin size is chosen such that there exist an adequate number of vectors in each bin. Despite the large number of data points, the multi vector method

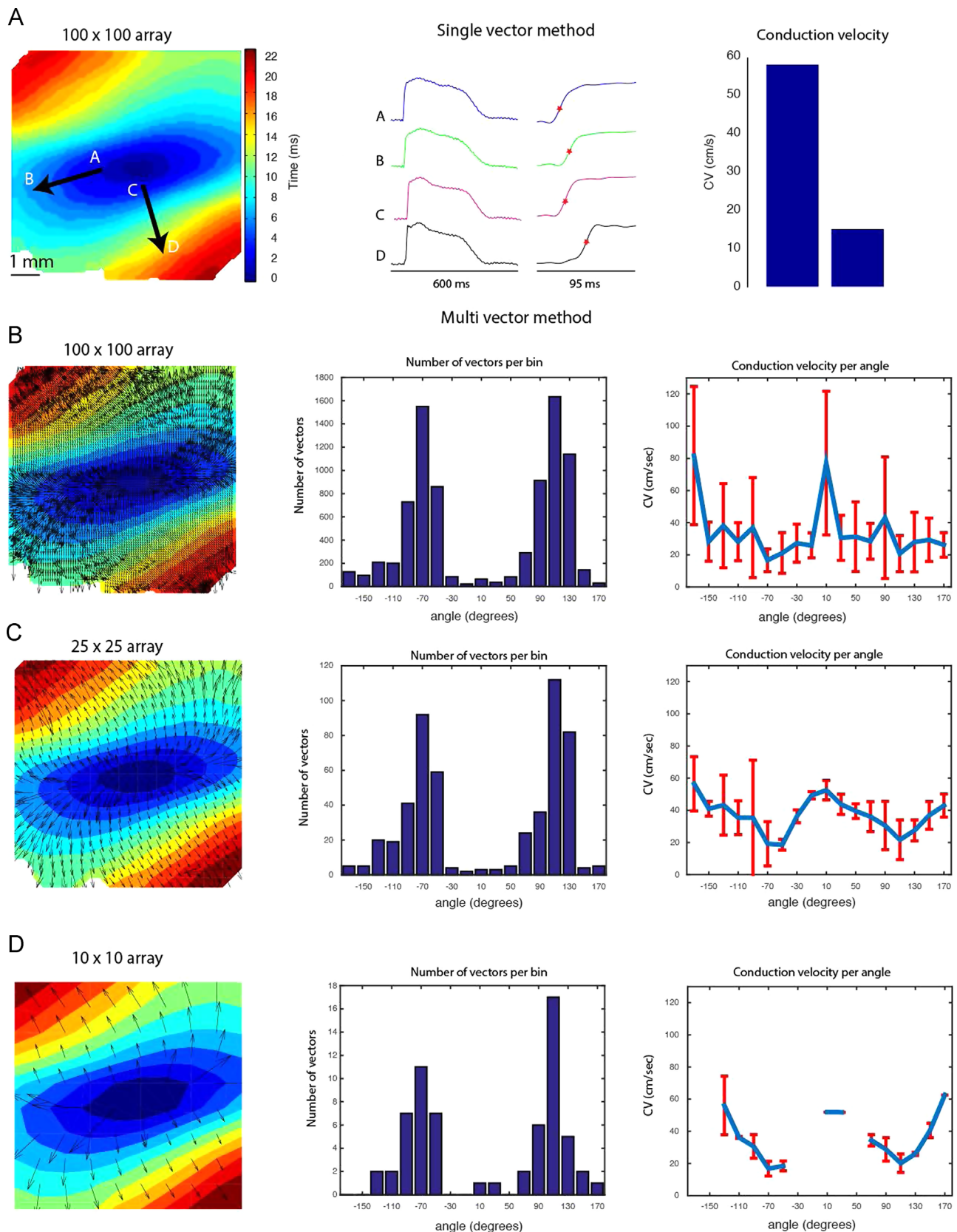
\* Correspondence to: Department Biomedical Engineering George Washington University 800 22nd St NW Room 5600 Washington, DC 20052, USA. Tel.: +1 314 662 1772.

\*\* Corresponding author at: Department Experimental Cardiology Academic Medical Center, Meibergdreef 9 1105 AZ Amsterdam, The Netherlands. Tel.: +31 20 5663267.

E-mail address: [bjboukens@gwu.edu](mailto:bjboukens@gwu.edu) (B.J. Boukens).

<sup>1</sup> Authors contributed equally.

<sup>2</sup> Authors contributed equally.



**Fig. 1.** The single and multi vector method for calculating conduction velocity. A. (Left panel) Activation map of the epicardium of a left ventricular wedge preparation from human heart during central stimulation. Black arrows indicate the directions in which either longitudinal (A-B arrow) or transverse (C-D arrow) conduction velocity was calculated. (Middle panel) Optical action potentials from the regions indicated on the activation map, with activation times (time of greatest action potential upstroke) noted. (Right panel) Longitudinal and transversal conduction velocity as measured via the single-vector method. B. (Left panel) Activation map of A with superimposed vectors as calculated by the multi vector method [19] (Middle panel). Histogram indicating the number of vectors per direction. (Right panel) Average conduction velocity for each direction, calculated using the multi vector method. C and D show the same as in B but for a  $25 \times 25$  array and a  $10 \times 10$  array, respectively. CV, conduction velocity.

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