Computationally Efficient Velocity Profile Solutions for Cardiac Haemodynamics

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Introduction

A minimal cardiac model has been developed which accurately captures the essential dynamics of the cardiovascular system to assist medical staff in diagnosis and treatment selection. Including time varying resistance around heart valves produces significantly different haemodynamic response. However the increased complexity has significant extra computational cost reducing the ability to easily identify model parameters

Objective

To reformulate the model for rapid solution with minimal error and suitable for easy parameter identification.

Result

Speed increases up to 16.6 times were seen with errors less than 1%. Very fast simulation enables the time varying resistance to be readily included in the optimization required to match the model to patient data. This is important as it enables more physiological accuracy with minimal cost in increased computation, enabling greater clinical application of these models.

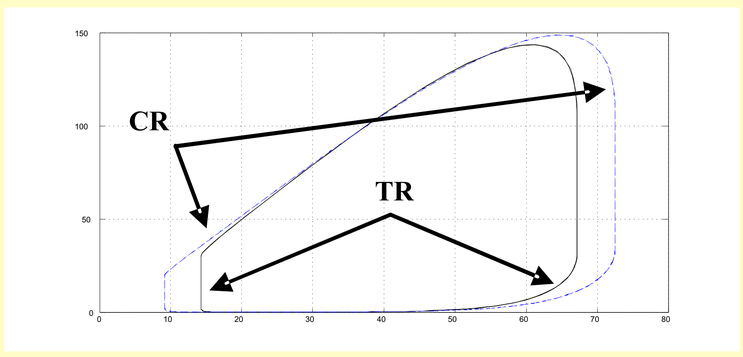

Fig. 2. Pressure volume curve for time varying resistance (TR) and constant resistance (CR) models.

Model and Method

Equations (1)-(3) are solved by a finite element method where the radius r0 is equally spaced into N nodes and the N derivatives ur and urr are approximated by finite differences. These equations are coupled and non-linear. After simulation of the model with a wide range of parameters it was found that the volume could be represented by parabolas and straight lines as shown in Figure 1. Most of the unknown parameters can be measured leaving at most four constant unknowns, one for each parabola. Note that if ultra-sonography is used then the volume could be calculated for each time point giving the whole volume profile. With this new definition of volume the differential equations become linear with an analytical solution and they only have to be simulated through one heartbeat since the volume is already in the steady state form.

Single chamber model

$$\frac{dV}{dt} \quad Q_{in} \quad Q_{out} \tag{1}$$

$$\frac{u_{in}}{t} \quad \frac{1}{l}\frac{P_2 \quad P_1}{r \quad r} \quad r\frac{u_{in}(r,t)}{r} \tag{2}$$

$$\frac{u_{out}}{t} \quad \frac{1}{l}\frac{P_3 \quad P_2}{r \quad r} \quad r\frac{u_{out}(r,t)}{r} \tag{3}$$

$$P_2 \quad e(t)E_{es}(V \quad V_d) \quad (1 \quad e(t))P_0(e^{(V \quad V_0)})$$

$$e(t) \quad e^{80(t \quad 0.375)}$$

New model (three nodes)

$$\frac{d\underline{u}}{dt} \quad A\underline{u} \quad \underline{F}(t),$$

$$\underline{F}(t) \quad \frac{1}{l}\frac{P_2 \quad P_1}{1 \quad 1}, \quad \underline{u}(0) \quad \underline{0},$$

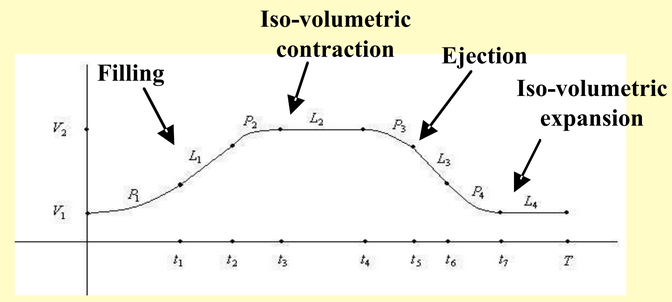

Fig. 1. Representation of the volume in terms of parabolas and straight lines with cardiac cycle phases shown

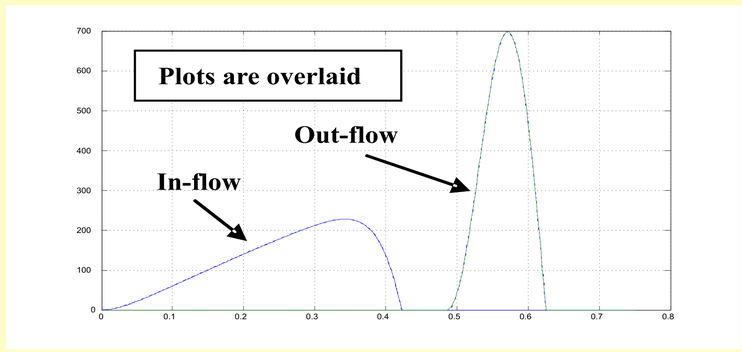

Fig. 3. The flows of the new method (dashed) versus old method (solid)

TABLE 1
COMPARING THE COMPUTATIONAL TIME OF THE OLD METHOD TO THE NEW METHOD

Nodes	CPU time (seconds)			Mean error (%)	
	Old method	New Method	Speed Increase (x)	Q_1	Q_2
20	2.1	0.15	14	0.4	1.8
30	2.4	0.16	15	0.3	0.7
40	2.6	0.18	14.4	0.2	0.4
60	3.4	0.24	14.2	0.3	0.3
80	4.4	0.3	14.7	0.3	0.3
100	5.3	0.32	16.6	0.3	0.3

Conclusions

The new method does not make use of the analytical solution which would give greater computational savings. Speed increases up to 16.6 times were seen with errors less than 1%. Very fast simulation enables the time varying resistance to be readily included in the optimization required to match the model to patient data. This is important as it enables more physiological accuracy with minimal cost in increased computation, enabling greater clinical application of these models.