

Meeting abstract

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## 229 four dimensional velocity field reconstruction from PC MRI using adaptive divergence free radial basis functions

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### Introduction

Phase Contrast MRI has been used extensively for the reconstruction and visualization of blood flow velocity fields in pediatric applications. However, due to imaging time constraints most of the scans are limited to single plane, 3D PC MRI acquisitions. In the case of patients born with single ventricle congenital heart defects, the ability to visualize in vivo velocity fields in the total cavopulmonary connection (TCPC) in 4D (space + time) is critical for identifying how well the connection is performing clinically.

### Purpose

In this paper a new method for velocity field reconstruction is presented that utilizes blood flow incompressibility as a property for estimating a continuous flow field representation in the TCPC from a stack of contiguous PC MRI.

### Methods

Since blood behaves like an incompressible fluid (divergence of velocity field is zero) in large vessels, this property can be used for reconstructing 4D velocity fields. In order to accomplish this, the following are required: a.) a 3D representation of the vessel anatomy; b.) measurements of all 3 components of velocities inside the vessel over one cardiac cycle; c.) a model for zero divergence interpolation of the measured 3D velocities onto the 3D anatomy. For a), an axial stack of static free breathing steady state free precession with a matrix size is typically

256 × 168 pixels, a pixel size of 1.0 × 1.0 mm<sup>2</sup>, and slice thickness of 3 mm was employed for reconstructing the anatomy. The vessel anatomy was segmented and the nodes inside the vessels were identified. Each node was then transformed to the MRI coordinate system for registration purposes. For b), a stack of 3D retrospectively triggered PC MRI slices in the coronal direction with a matrix size of 320 × 230 pixels, a resolution of 1.25 mm<sup>2</sup>, slice thickness of 6 mm, and 20 cardiac phases were acquired. All scans were performed in the Siemens 1.5 T Avanto scanner at the Children's Hospital of Philadelphia. Using the segmentation from a) the velocity measurements inside the vessel of interest were retained, and the rest were discarded. For c) a divergence free matrix valued radial basis function of the form shown in Figure 1 was

$$V(\vec{x}) = \sum_{j=1}^p \Phi(|\vec{x} - \vec{x}_j|) \vec{c}_j$$
$$\Phi_{\alpha}(x) = \{-\Delta I + \nabla \nabla^T\} \varphi_{\alpha}(x)$$
$$\varphi_{\alpha}(x) = e^{-\alpha \|x\|^2}$$

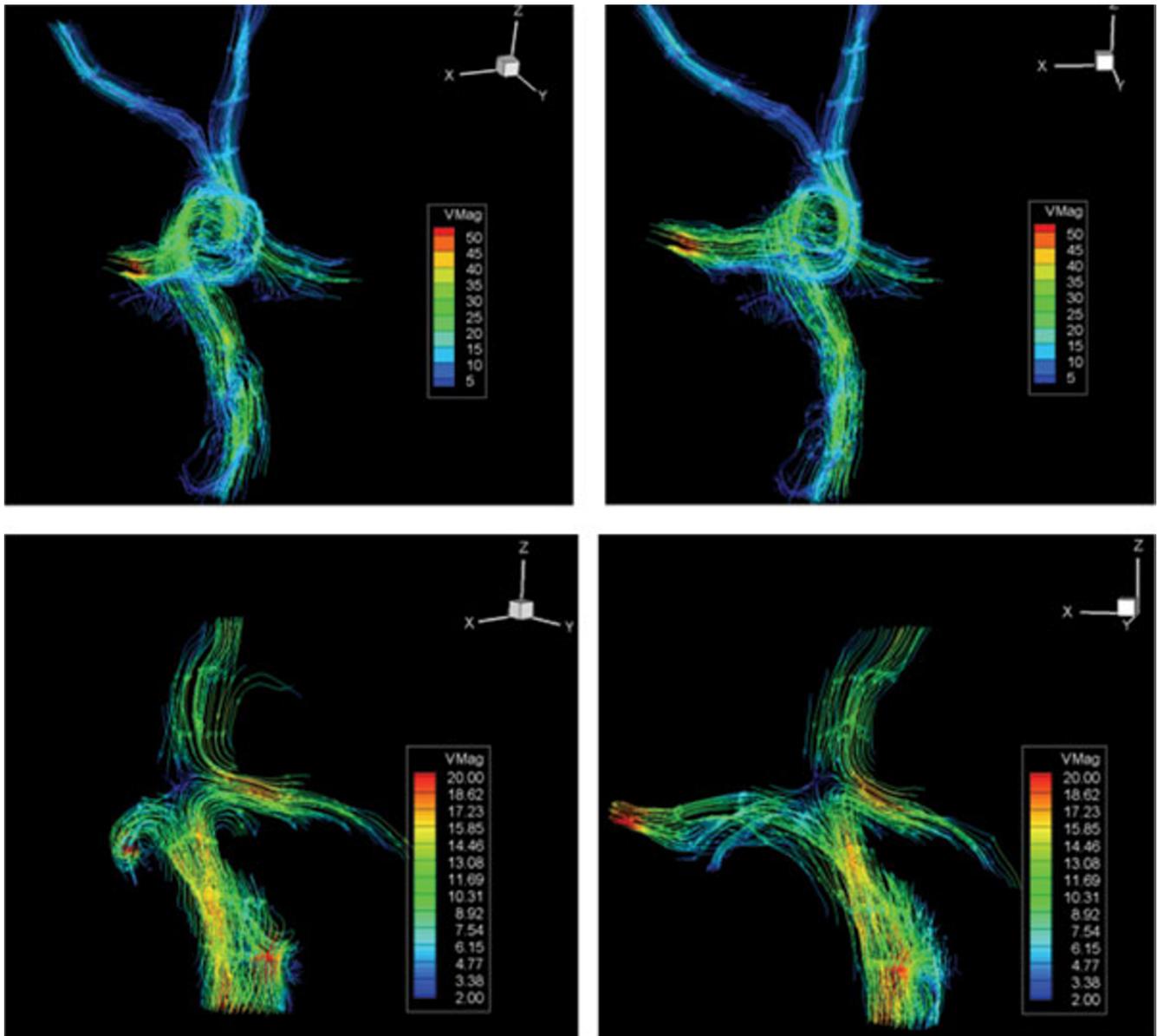
Figure 1

initialized, where  $V(x)$  is the velocity field expressed as a function of the location inside the flow domain.  $\Phi(x)$  is a matrix valued radial basis function which is expressed as a distance function of  $x$  from a set of chosen control points,  $c_j$  is the vector valued interpolation coefficient that is determined using the least squares method, and  $\alpha$  is a scaling parameter that is dependent on the spacing between the control points. It can be shown that the divergence of  $V(x)$  is mathematically 0. To enforce the no-slip condition, the nodes on the vessel surface are used as measurement nodes and are set to 0. Once the value of  $c_j$

for each control point is determined, the velocity at any point inside the vessel lumen can be calculated.

**Results**

The methodology was tested on two in vivo datasets. Shown in Figure 2 are streamtraces color coded by velocity magnitudes inside intra-atrial and extra-cardiac TCPCs. In the former, complex flow structures are evident in the form of vortices, while in the second case the flow is clearly more streamlined.



**Figure 2**

## Conclusion

A new method for velocity field reconstruction is presented that is truly 3D and takes into account the properties of blood in addition to PC MRI velocity measurements. The new technique now allows for improved visualization of blood flow fields from sparsely acquired PC MRI data, while at the same time providing an analytical expression for the velocity field to perform higher order analysis.

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