



Explorative Visual Analysis of Spatio-temporal Regions to Detect Hemodynamic Biomarker Candidates

Adrian Derstroff¹, Simon Leistikow¹, Ali Nahardani^{2,3}, Mahyasadat Ebrahimi^{5,6}, Verena Hoerr^{4,3}, Lars Linsen¹

1 University of Münster, Germany

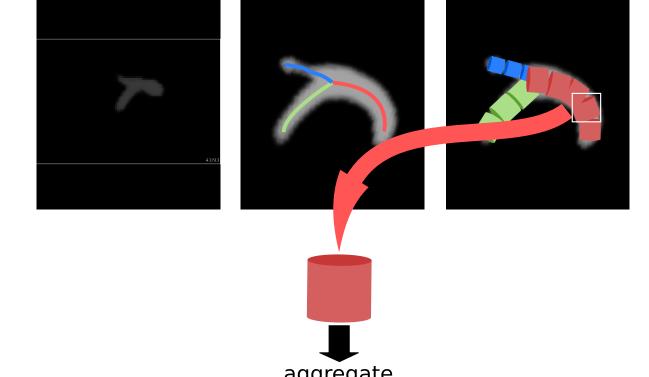
2 Medical Physics Group, Institute of Diagnostic and Interventional Radiology, Jena University Hospital, Friedrich Schiller University Jena, Jena, Germany
3 Heart Center Bonn, Department of Internal Medicine II, University Hospital Bonn, Bonn, Germany
4 Translational Research Imaging Center (TRIC), Clinic for Radiology, University Hospital Münster, Münster, Germany
5 Leipniz-Institute of Photonic Technology, Jena, Germany Friedrich Schiller University Jena, Germany
6 Institute of Physical Chemistry and Abbe Center of Photonics, Jena, Germany

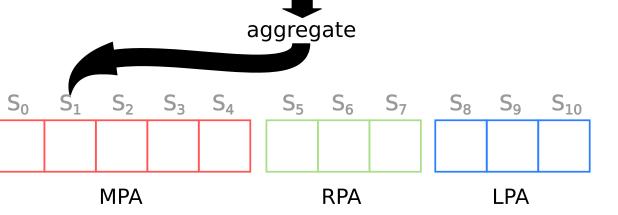
Abstract

Biomarkers are measurable biological properties that allow for distinguishing subjects of different cohorts such as healthy vs. diseased. In the context of diagnosing diseases of the cardiovascular system, researchers aim - among others - at detecting biomarkers in the form of spatio-temporal regions of blood flow obtained by medical imaging or of derived hemodynamical parameters. As the search space for such biomarkers in time-varying volumetric multi-field data is extremely large, we present an interactive visual exploration system to support the analysis of the potential of spatio-temporal regions to discriminate cohorts.

In this poster, we demonstrate our approach based on a sepsis study, conducted by our collaboration partners. The goal hereby is to analyze the effect of sepsis in mice with respect to selected hemodynamic parameters. In this case, a segmentation of the pulmonary artery was performed on 4 baseline animals and 3 with acute sepsis. We were provided with velocity vector fields acquired using 4D-PC-MRI from which we calculate vorticity magnitude and wall shear stress (WSS) for the analysis.

Data Preprocessing Segmentation Centerline Cylinder Samp

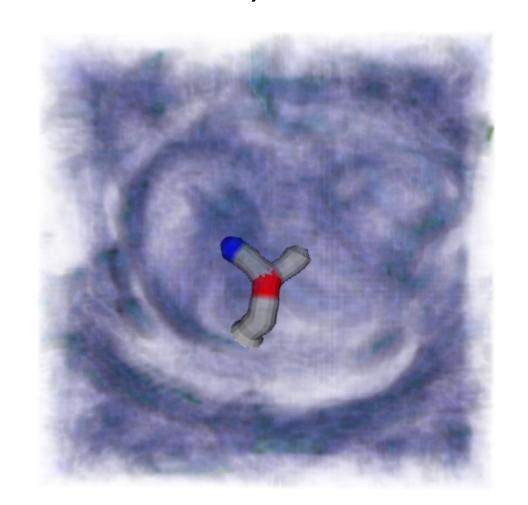




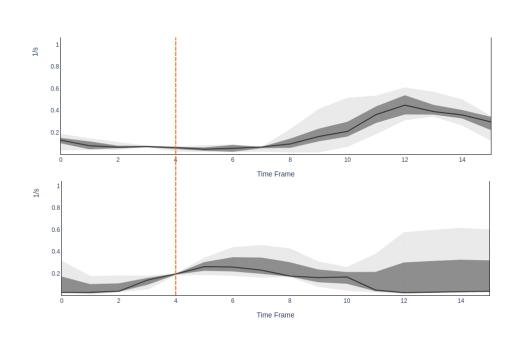
From the segmentation mask of each animal, we extract the centerline and divide each branch into segments of equal length. We accumulate data of each hemodynamic parameter within these segments (i.e. using the mean) to obtain a linear data layout.

Processed Data

An anatomical view allows to assess the spatial domain (selected segment in blue, biomarker in red).

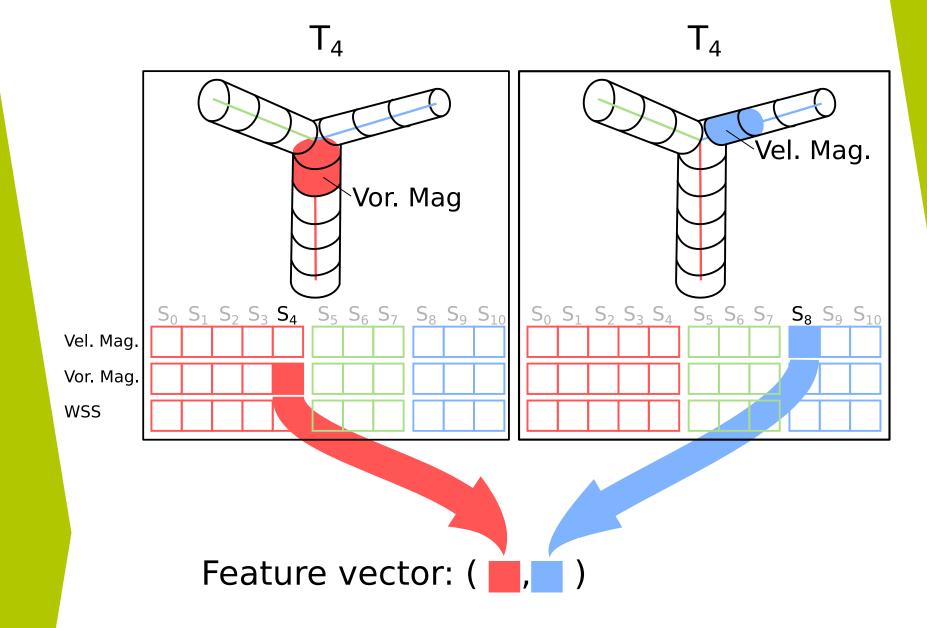


Functional boxplots show the evolution of a selected hemodynamic parameter and segment over time for each cohort.



Detail Visualization

Feature Vector Generation



Layout

We create feature vectors from a set of segment, time frame, and parameters to which we refer as **biomarker**.

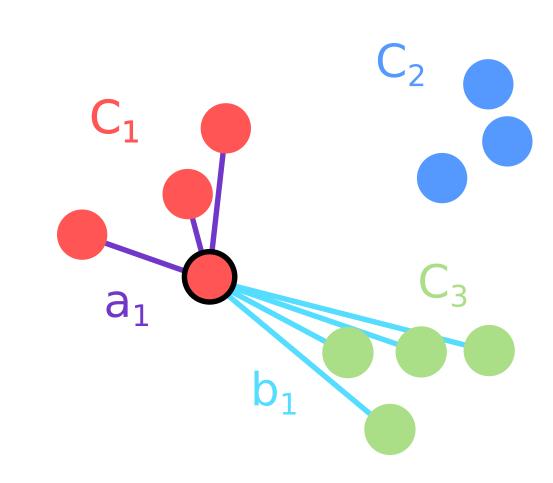
MPA: Main Pulmonary Artery LPA: Left Pulmonary Artery RPA: Right Pulmonary Artery

Biomarker

T₄, S₄, Velocity Magnitude

T₄, S₈, Vorticity Magnitude

Biomarker Potential



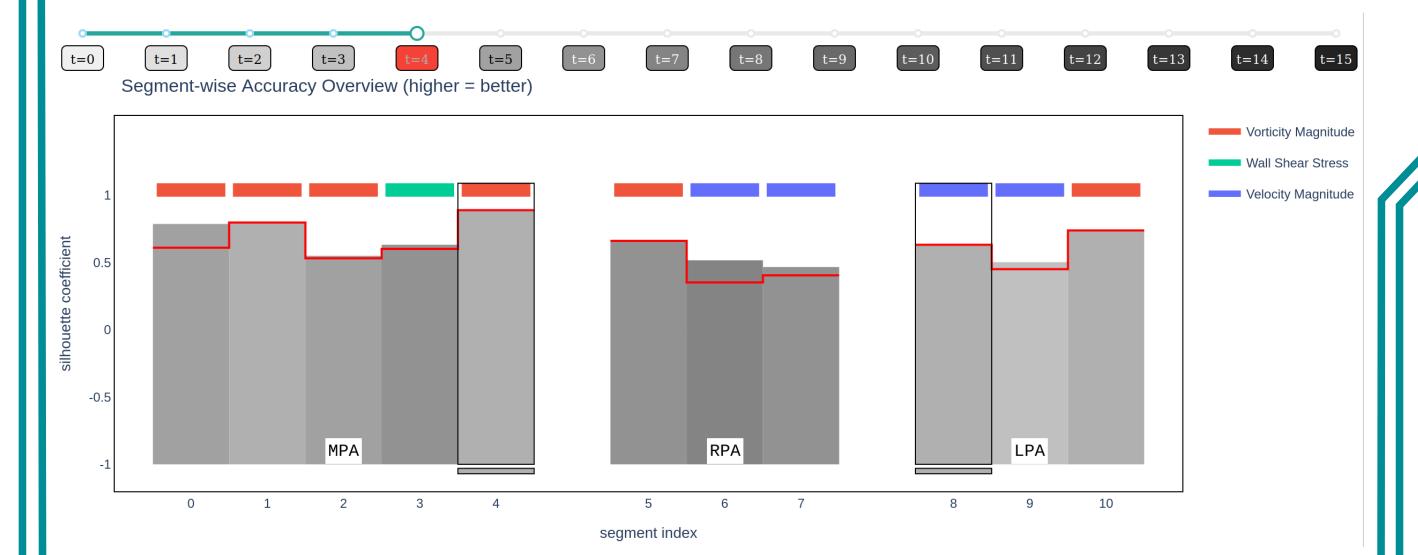
We apply the **field similarity** on all pairs of feature vectors to create a similarity matrix.

To evaluate the potential of such a biomarker, we calculate the **silhouette score**. High silhouette scores are achieved in case of low intra-cohort distances (a) and high inter-cohort distances (b).

Silhouette Score

Similarity Matrix

Clicking on a bar adds the respective segment, time frame and parameter to the biomarker.

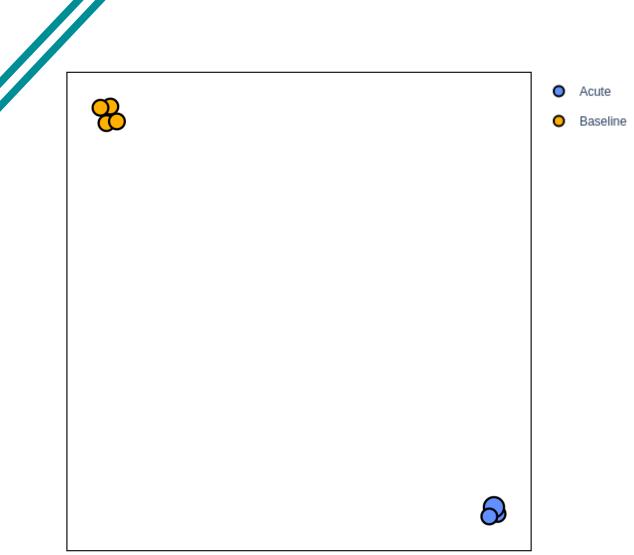


Core to the analysis is our novel overview plot. For each segment (x-axis) a bar encodes the time frame (gray color) and parameter (colored boxes) that achieved the highest silhouette score (y-axis).

A black rectangle depicts the current biomarker selection. The gray boxes below encode the selected time frame.

The red line encodes the silhouette scores of each segment for the selected time frame (using the slider above)

Analysis Overview Visualization



From the similarity matrix we create a low-dimensional embedding using uniform manifold approximation and projection (UMAP), where each animal is represented by a dot, colored by its respective cohort. The embedding is calculated for the current biomarker, hence a good result is when animals of equal cohort are projected next to each other.

Cohort Embedding

