

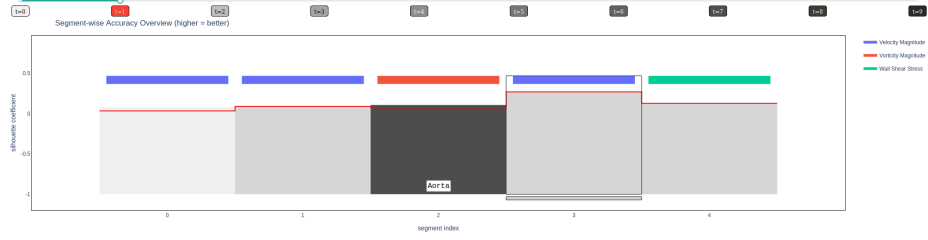
Explorative Visual Analysis of Spatio-temporal
Regions to Detect Hemodynamic Biomarker
Candidates - APPENDIX

May 4, 2022

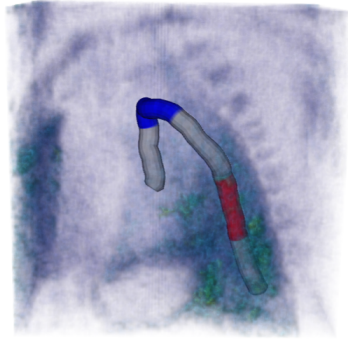
1 Right Heart Overload Condition Dataset

The effect of right heart overload condition is usually analyzed at the pulmonary artery that transports the blood from the right heart to the lungs. The aorta may not be a good candidate to observe hemodynamic effects of the right heart overload condition. However, as the circulatory system is an interconnected system there still might be some observable differences between the different disease progressions. Thus the hypothesis would be that it might be possible to see some differences, while it might not be possible to separate all three classes. When looking at the overview visualization in Figure 1 (a) segment 3 with time frame 1 and velocity magnitude yielded the highest silhouette score. The low-dimensional embedding shows, that the currently selected biomarker is unable to separate any of the cohorts. Then, when comparing the velocity magnitude for segment 3 it seems evident, that the functional boxplots of all three cohorts (d)-(f) are hard to separate.

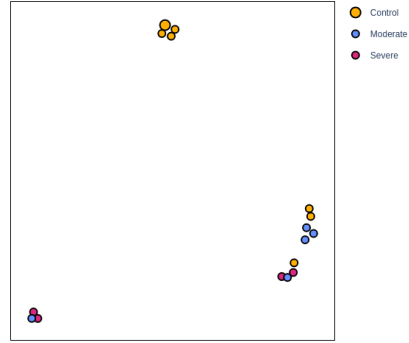
As it is not possible to separate all cohorts a sub-selection is performed in Figure 2 to see if the control and severe cohorts can be separated. The cohort plot (a) shows that it is almost possible to separate the control and severe cohorts. Comparing this outlier with the rest of the severe cohort (d) shows that the velocity magnitude profile of the outlier is very close to that of the severe cohort (e)-(f), while the rest of the control cohorts compared to the severe cohort is different enough for time frame 1 (h)-(i). This indicates that it is not possible to separate the two cohorts and supports our hypothesis.



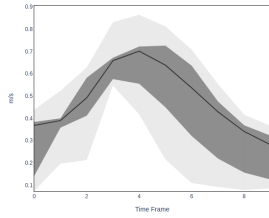
(a) Analysis overview visualization of the right heart overload dataset, using 5 segments. Velocity and vorticity magnitude as well as wall shear stress are depicted.



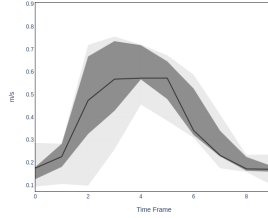
(b) Anatomical image depicting the currently selected biomarker candidate.



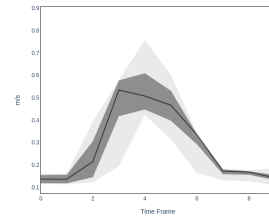
(c) Low-dim. emb. showing all cohorts.



(d) Funct. boxplot control



(e) Funct. boxplot moderate



(f) Funct. boxplot severe

Figure 1: Analysis of the right heart overload condition dataset in the aorta of rats. It is not possible to separate all cohorts.

2 Sepsis Dataset

For the sepsis dataset the pulmonary artery was chosen where we suspected to see a separation between the baseline and the acute cohorts. The last segment of the main pulmonary artery (MPA) yielded the highest silhouette score for time frame 4 and vorticity magnitude Figure 3. By looking at the functional boxplots (d) and (e) a difference in the vorticity magnitude can be observed. The low-dimensional embedding (c) also indicates that it is possible to separate

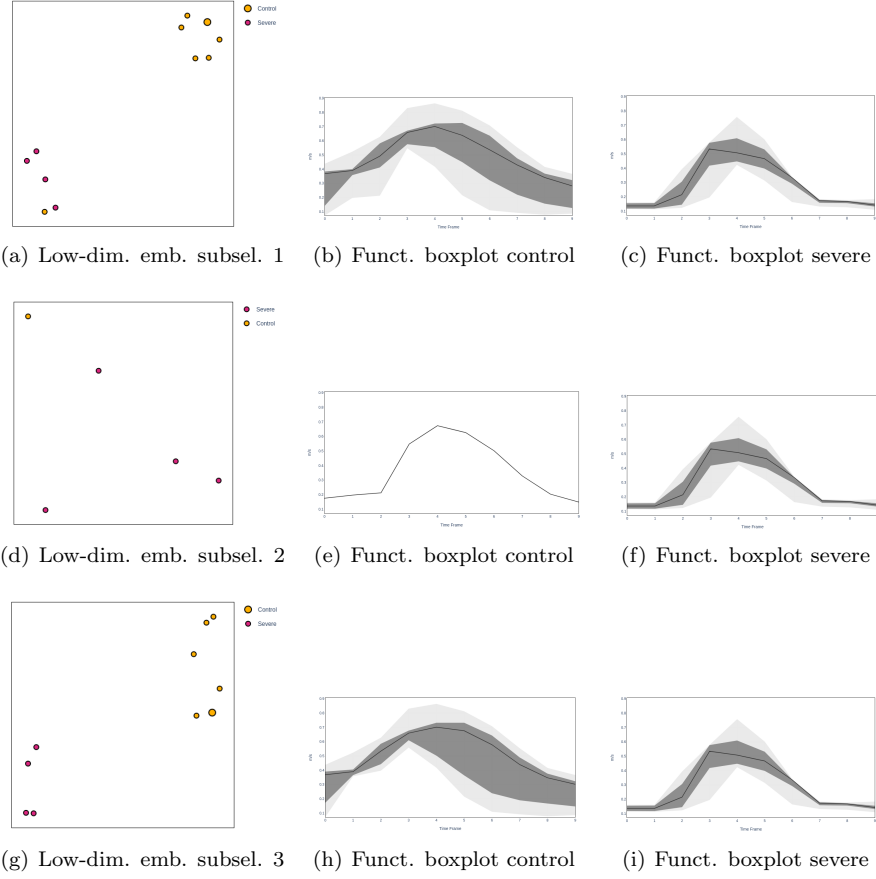
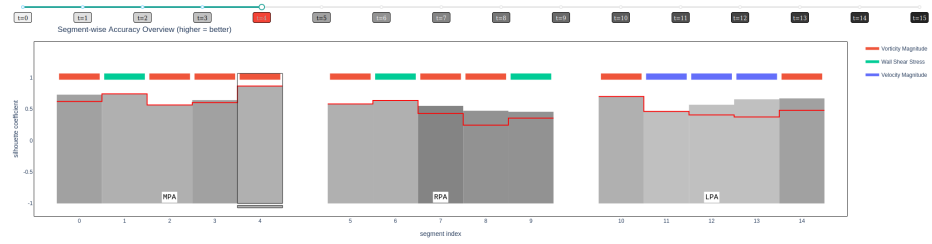
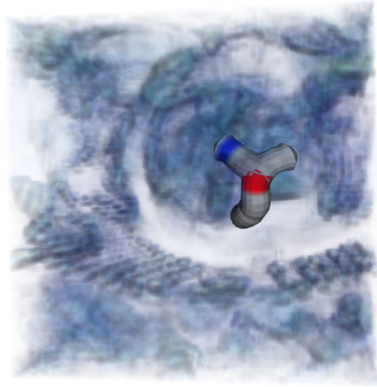


Figure 2: Sub-selection of the right heart overload dataset. Trying to separate the control and severe cohort fails as there is one outlier in the control cohort that is closer to severe cohort (a).

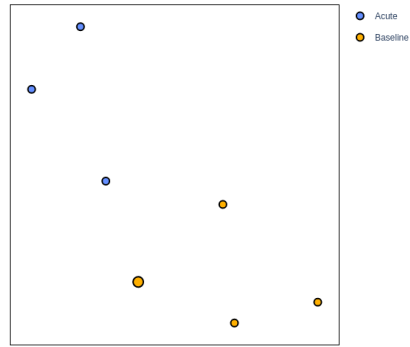
both cohorts with the selected biomarker.



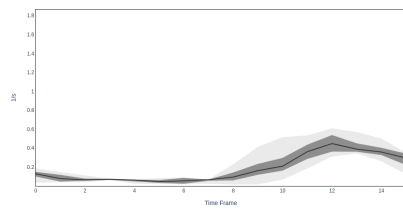
(a) Analysis overview visualization of the sepsis dataset, using 5 segments. Velocity and vorticity magnitude as well as wall shear stress are depicted.



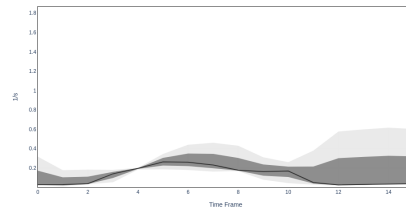
(b) Anatomical image depicting the currently selected biomarker candidate



(c) Low-dimensional embedding



(d) Funct. boxplot baseline



(e) Funct. boxplot acute

Figure 3: Analysis of the sepsis dataset. Using the last segment of the main pulmonary artery (MPA) with time frame 4 and the vorticity magnitude it is possible to separate the baseline from the acute cohort.