Modeling Complex Biological Flows in Multi-Scale Systems using the APDEC Framework

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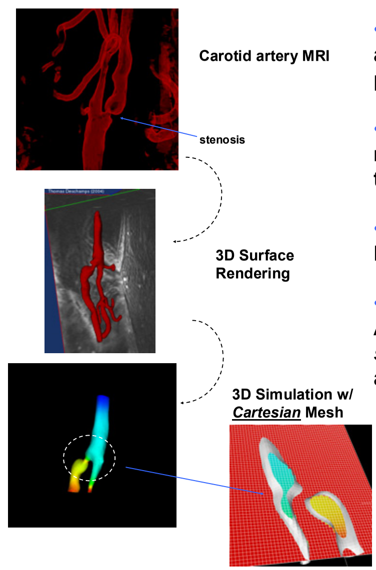
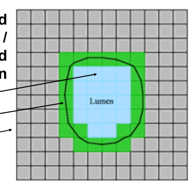
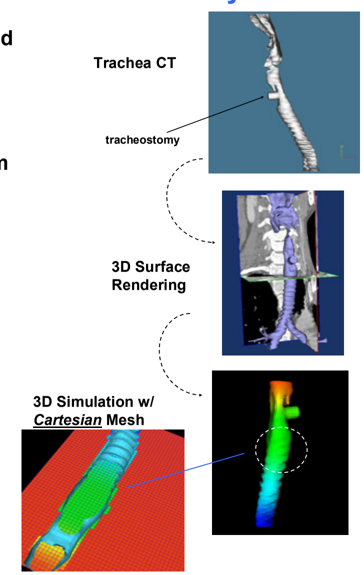
Fast and efficient gridding and simulation from medical image data using embedded boundary methods

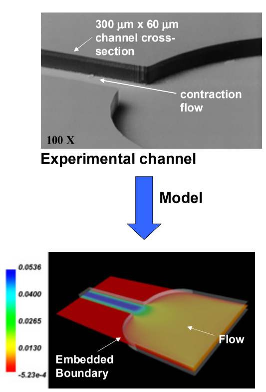


- A simulation capability for complex flows in anatomical vessels and airways can provide clinicians with information on development of pathologies and treatment of disease.
- Accurate methods are needed to (i) extract surface models from medical image data such as CT or MRI and to (ii) simulate flows from these models.
- Surface extraction techniques for body-fitted gridding suffer from loss of geometric detail due to smoothing.
- Using Cartesian embedded boundary grids we have leveraged the APDEC framework to develop an end-to-end technique -- *from surface extraction to meshing to CFD* -- that is fast and retains full anatomical detail.



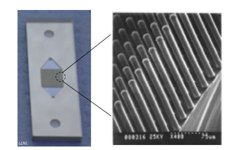


Advanced constitutive modeling of DNA-laden fluids in bioMEMS devices



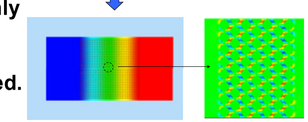
Computed 3D velocity [cm/s]

- Microfluidic technology is the new design strategy for biochemical processors and sensors used in pathogen detection and drug delivery / continuous monitoring systems. This miniaturization strategy requires understanding of the fundamental physics and electro-chemistry of microscale biological flows.
- Biological fluids are inherently particle-laden and, thus, not easy to represent constitutively, especially at the microscale where molecular lengths are comparable to device length scales. For example, a highly concentrated solution of suspended polymer molecules such as DNA may be represented at large, system-level scales with a continuum viscoelastic constitutive model. However, when the geometric length scale is comparable to the inter-polymer spacing, a discrete molecular approximation is needed.
- Using advanced solvers and algorithms with support for particles in the APDEC framework we have developed both continuum and hybrid methods to model a range of concentrations for DNA-laden flows in complex microdevice components. Our viscoelastic continuum algorithm is stable and accurate for a full range of elastic flows including the longstanding High Weissenberg Number Problem; our hybrid particle-fluid approach employs full coupling with short range interactions and promises to compare for the first time discrete representations of DNA concentrated in solution to single phase continuum models.

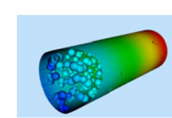


DNA extraction pillar chip

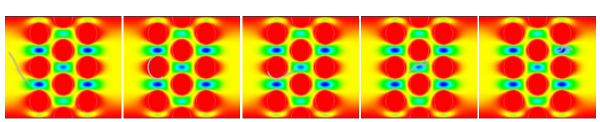
Model



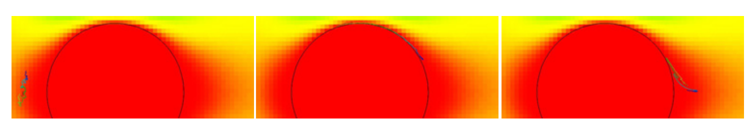
Computed pressure and gradient



Packed bed DNA extraction model



Transport of genomic DNA thru post microarray (left) with short range post and particle interactions (right)



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