Computational Modeling and Simulation of the Human Duodenum

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Abstract

Introduction: Worldwide attention in the computational modeling and simulation of the human intestine is increasing in order to help understand its complex behavior and improve health [1,2,3]. Computational fluid dynamics (CFD) is an affordable and essential tool to understand the mechanics and transport phenomena of the intestine, thereby advancing the diagnosis and treatment of gastrointestinal related diseases, such as diabetes or obesity. The aim of this work is to develop a CFD model, which will mimic the human duodenum (Figure 1). The CFD model couples peristaltic motions of the duodenum wall together with the flow of chyme, known as a fluid-structure interaction coupling. The fluid flow of chyme is described by Navier-Stokes equations to capture the phenomena of the system, while the duodenum contractions are approximated by the smoothed Heaviside step function to describe peristaltic movements. Mixing of chyme, caused by peristalsis, is monitored through the particle tracing module physics. A simplified biochemical reaction, hydrolysing starch and producing glucose, is added to the computational duodenum model to validate the convection-diffusion equation and the flux of glucose through the porous duodenum wall. Several parametric studies for different flow viscosities, loads and elasticity of the duodenum-like porous silicone tube are performed to validate the accuracy of the computational duodenum model. Use of COMSOL Multiphysics: The CFD model of the human duodenum is entirely modeled with COMSOL Multiphysics 4.2a. It consists of five different interfaces. The first interface, Free and Porous Media Flow, describes the laminar Newtonian fluid flow of chyme in the main flow channel, whereas Brinkman equations model the fluid flow through the porous duodenum wall. The second interface, Solid Mechanics, applies the smoothed Heaviside step function and external load to mimic peristaltic movements of the silicone tube. The third interface, Moving Mesh, adds mesh displacements and velocities to the existing model and couples the second and the first interfaces into the complex fluid-structure interaction computational model. The fourth interface, Particle Tracing for Fluid Flow, contributes to the duodenum model by tracing solid particles and their mixing with the fluid flow. The last interface, Transport of Diluted Species, models convection and diffusion phenomena inside the silicone tube and in the porous wall together with the simplified hydrolysis reaction of starch producing glucose. Results: Figure 2 shows the velocity field in the axial direction and spatial velocity field of flow. Figure 3 shows the particle trajectories. Figure 4 shows the concentration field and inward diffusive flux of glucose. The duodenum geometry and mesh are modeled as the axis symmetric model where all figures are taken for dynamic viscosity 0.1 Pa*s at the same time step 2.5 s. Conclusion: The complex computational duodenum model gives a thorough understanding of mechanics and transport phenomena inside the

human duodenum, which is beneficial for production of healthier food and drugs with higher absorption rate. The future work will focus on the fabrication of the in-vitro human duodenum prototype and comparing experimental and computational results in order to validate both approaches.

Reference

1. M. Taghipoor et al., Mathematical Modeling of Transport and Degradation of Feedstuffs in the Small Intestine, Journal of Theoretical Biology, 294, 114-121 (2012).
2. A. Tharakan et al., Mass Transfer and Nutrient Absorption in a Simulated Model of Small Intestine, Journal of Food Science, 75, E339-E346 (2010).
3. B. R. Stoll et al., A Theory of Molecular Absorption from the Small Intestine, Chemical Engineering Science, 55, 473-489 (2000).

Figures used in the abstract

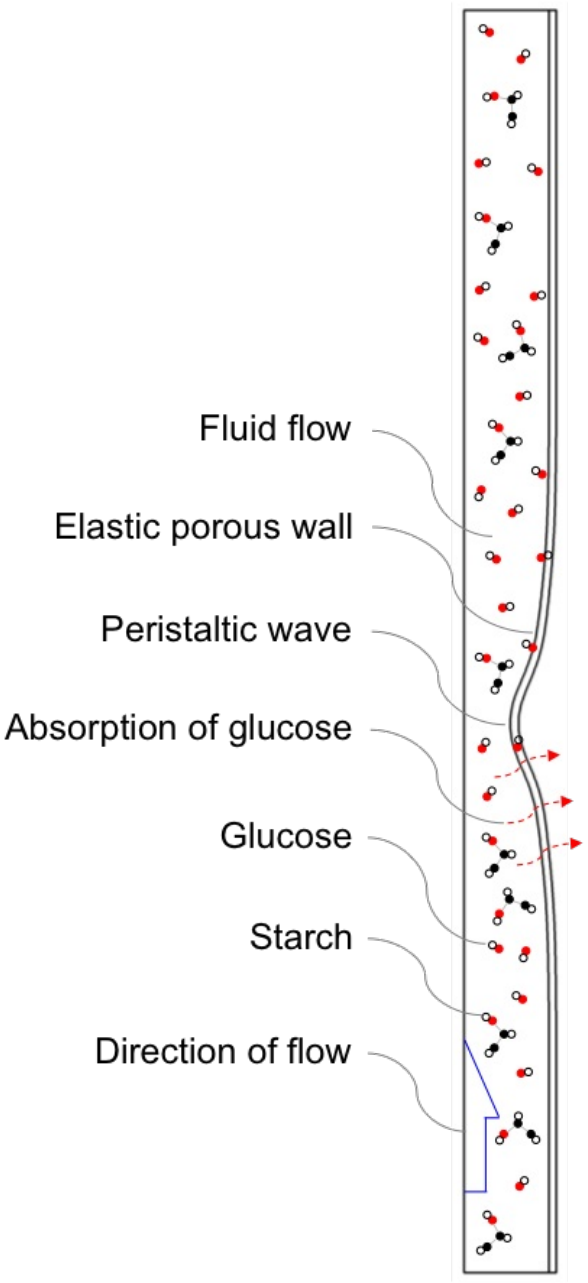

Figure 1: Axis symmetric geometry of the computational duodenum model.

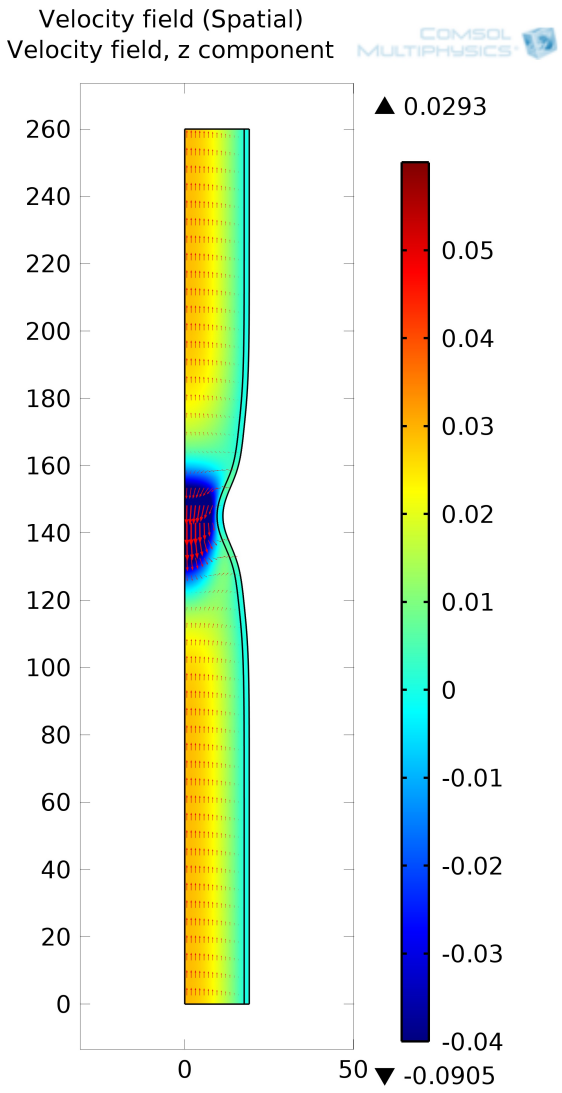

Figure 2: Velocity field of fluid in the axial direction and spatial velocity field of fluid for dynamic viscosity 0.1 Pas and time step 2.5 s.

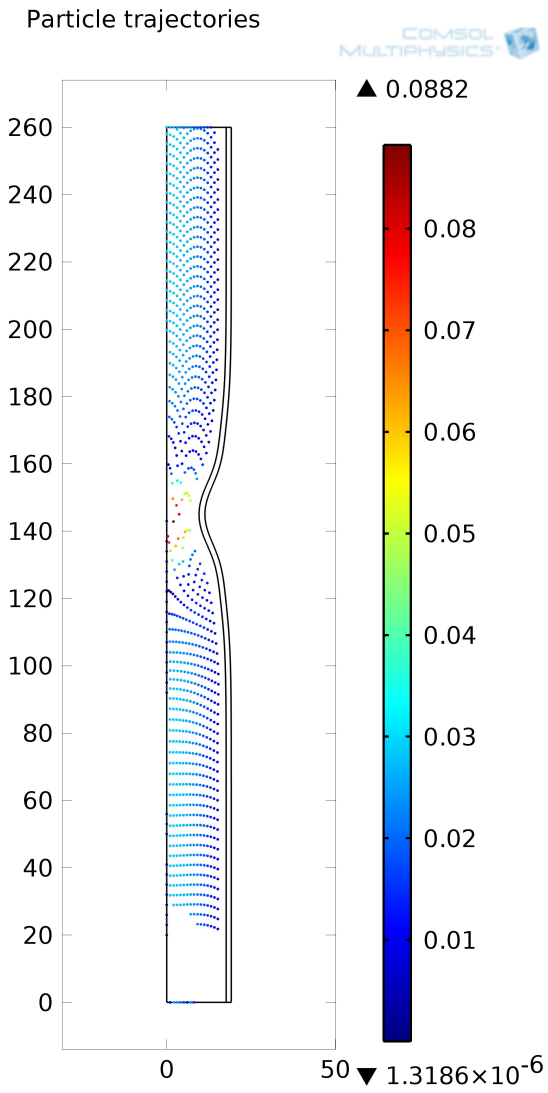

Figure 3: Particle trajectories of fluid for dynamic viscosity 0.1 Pas and time step 2.5 s.

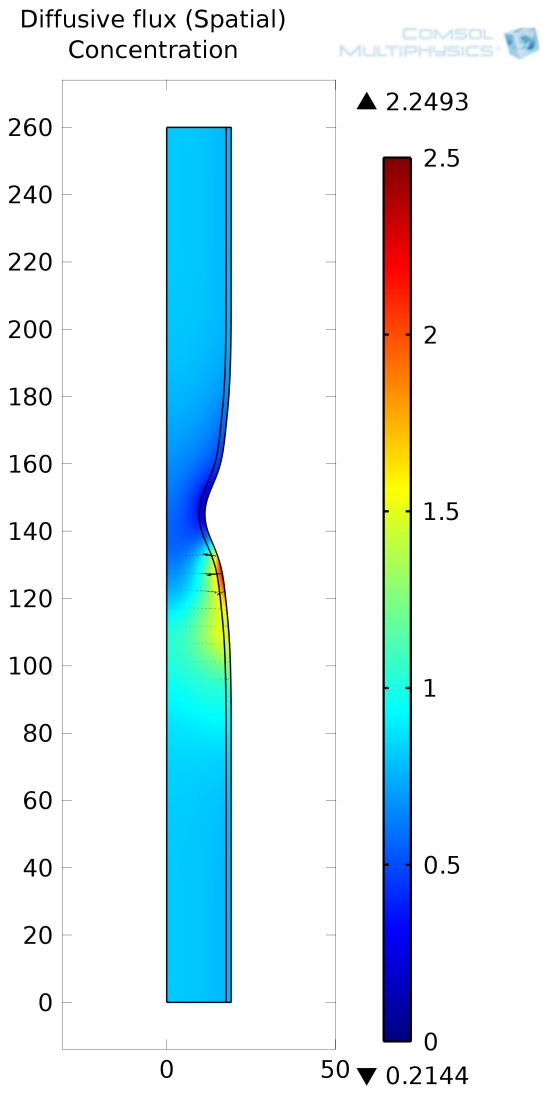

Figure 4: Concentration field of glucose and inward diffusive flux of glucose through the porous wall for dynamic viscosity 0.1 Pas and time step 2.5 s.