Simulation of Heat Transfer in Multilayered Biological Systems Using COMSOL Multiphysics

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ABSTRACT

Analysis of heat flow on the surface of biological or food samples can be achieved through experimental setups. However, these setups lack the capability to analyze and measure heat transfer within the sample. By studying internal heat flow, we gain insights into heat flow patterns within biological or food samples, which aids in optimal preservation. In this study, COMSOL Multiphysics software was employed to develop and execute simulations to observe temperature distribution on the surface and within a biological sample. The simulations focused on heat transfer within a biological context, specifically heat flow from a copper base to a human myocardium sample via a sapphire intermediate stage. Combining infrared camera experiments and COMSOL simulations validated the computational model, providing insights into the intricate temperature distributions and heat transfer patterns within the myocardium sample over time that could not be obtained experimentally, demonstrating the potential of COMSOL modeling to comprehensively study heat flow phenomena in biological contexts and advance understanding of freezing processes in food and biological heat transfer mechanisms.

INTRODUCTION

- In lab experiments, thermal imaging was used to study ice growth inside biological samples.
- Growing ice crystals released heat Fig. 1 (A), and temperature measurements Fig. 1 (B, C) helped calculate growth rates (Celik et al., 2013).
- Heat transfer in a multilayered system (copper base, sapphire layer, myocardium sample) was modeled using COMSOL Multiphysics. This non-invasive method analyzed temperature distribution over time (COMSOL, n.d.).
- Integrating experimental and simulation data provides insights into heat transfer during freezing, aiding applications like food preservation and cryopreservation.

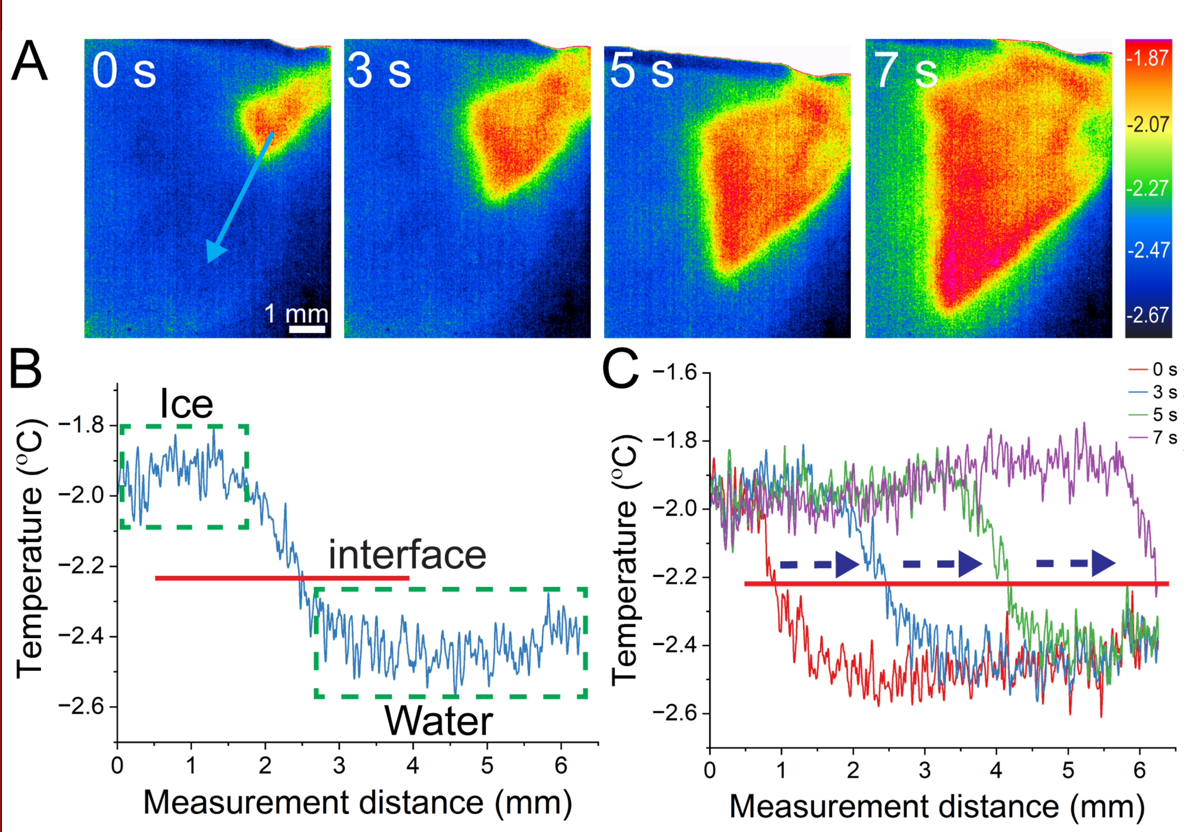


Figure 1

METHODOLOGY

- A time-dependent analysis showed transient heat transfer behavior over simulated time.
- Key steps included meshing the model (Fig. 2, 3), assigning materials properties, and setting up the study parameters.

Key parameters studied (Fig. 4, 5):

- Temperature distribution along the surface from copper base to myocardium surface.
- Temperature distribution within the myocardium sample itself.

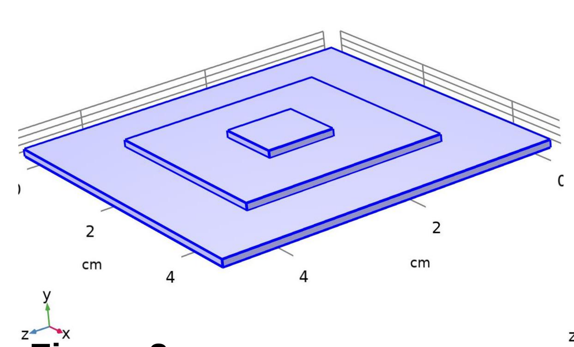


Figure 2

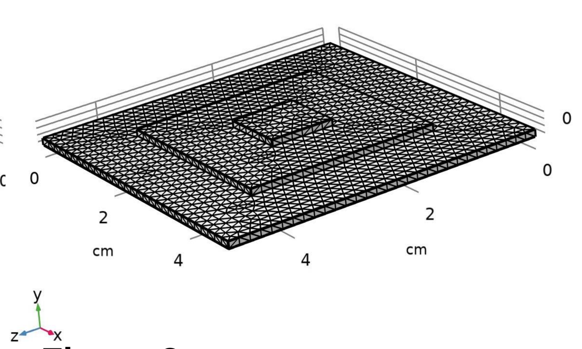


Figure 3

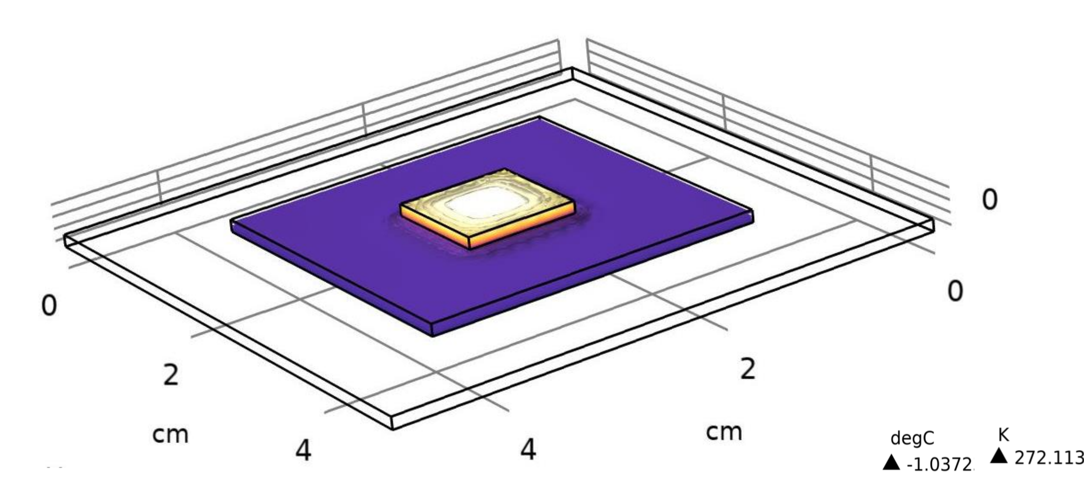


Figure 4

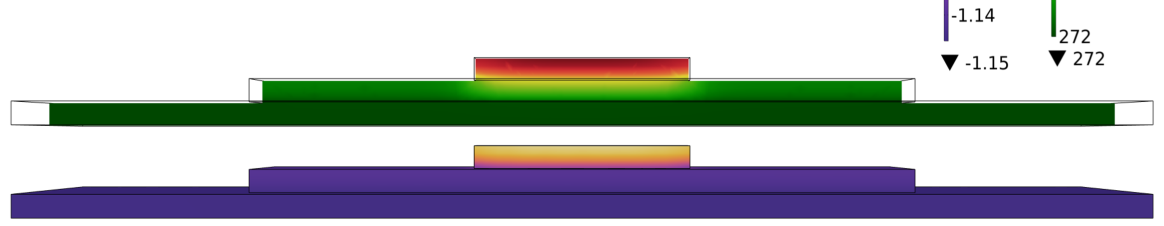
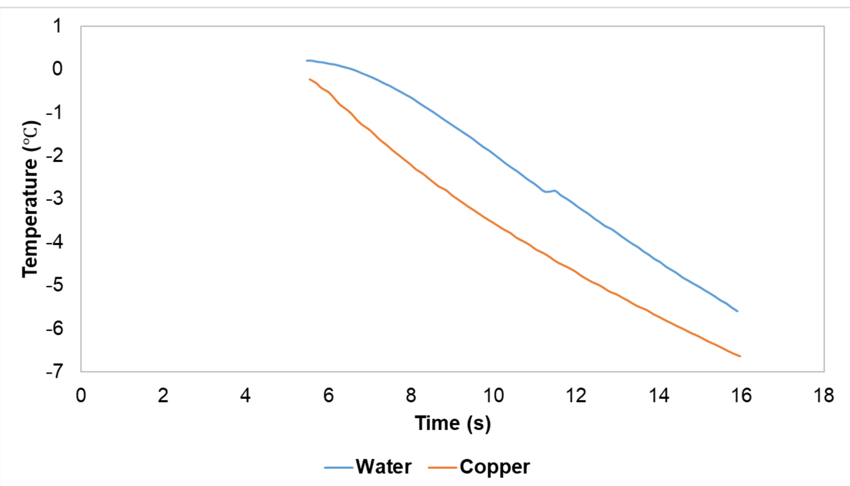


Figure 5

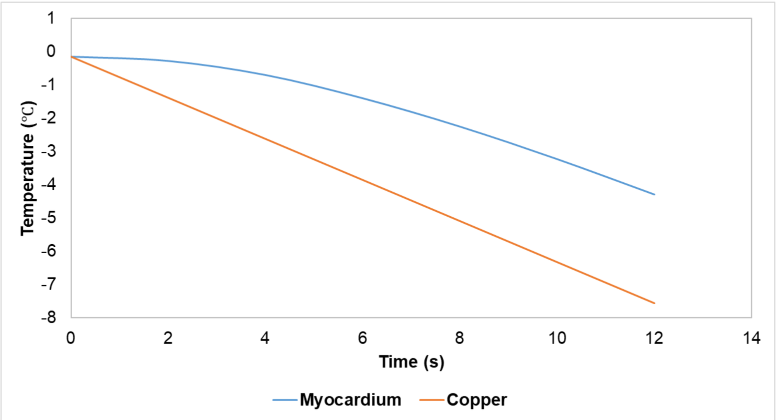
RESULTS

- Fig. 6: The infrared camera used to capture temperature distribution (Graph 1) along the surface of the multilayered system.
- Fig. 4, 5: Temperature distribution simulation inside/within the system (above) and on the surface (below) of the system, respectively.
- Results generated by running the simulation plotted in Graphs 2, 3, 4.
- Graph 2,3: Comparing the temperature distribution received by the IR camera and COMSOL simulation.
- Graph 4: Temperature distribution inside the sample and the copper base.

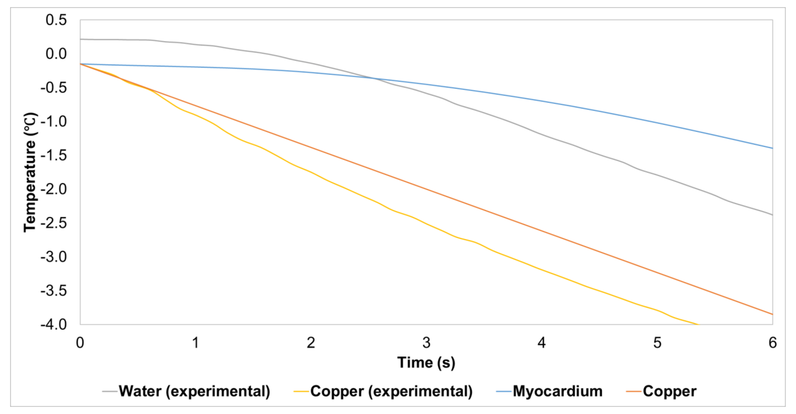
Figure 6



Graph 1

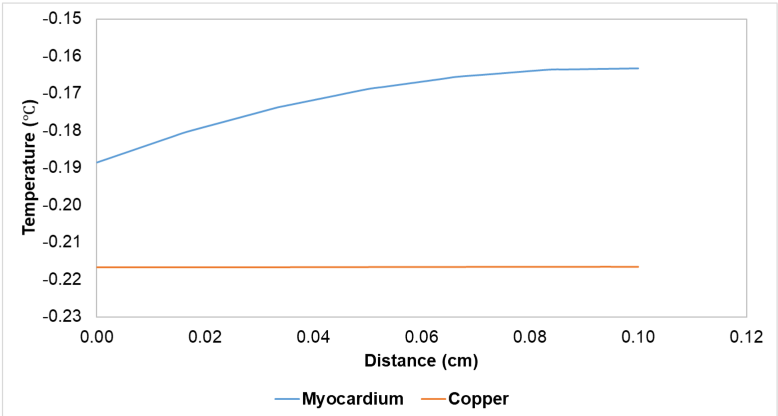


Graph 2



Graph 3

RESULTS, Cont.



Graph 4

DISCUSSION & CONCLUSIONS

- The temperature distributions observed on surfaces by infrared camera experiments agreed with COMSOL simulations, validating the computational model. Notably, COMSOL provided insights into internal heat transfer patterns within the myocardium sample that experiments could not observe. Simulations revealed intricate temperature distributions at varying depths over time, important for understanding biological heat exchange and measuring ice growth in frozen foods.
- This work demonstrates COMSOL modeling's ability to thoroughly examine heat flow in biological contexts, determining surface and internal temperature distributions. It advances understanding of freezing in foods while establishing a foundation for further exploring biological heat transfer mechanisms.

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REFERENCES

Celik, Y., Drori, R., Pertaya-Braun, N., Altan, A., Barton, T., Bar-Dolev, M., Groisman, A., Davies, P. L., & Braslavsky, I. (2013). Microfluidic experiments reveal that antifreeze proteins bound to ice crystals suffice to prevent their growth. Proceedings of the National Academy of Sciences, 110(4), 1309–1314.

COMSOL MULTIPHYSICS® software - understand, predict, and optimize. COMSOL. (n.d.). https://www.comsol.com/comsol-multiphysics