

Team creates framework to provide optimal personalized treatment options for esophageal cancer patients

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A multidisciplinary team of researchers that included 14 graduate students from The University of Texas at Arlington has created a new framework to provide optimal personalized treatment options for individuals with esophageal cancer.

"Esophageal cancer is an unusually diverse disease with many heterogeneities and cancerous origins, which have been shown to be

leading factors for [drug resistance](#) in the patients," said Souvik Roy, assistant professor of mathematics. "That's why timely and effective treatment strategies are key to combating it."

Esophageal cancer starts when [cancerous cells](#) form in the lining of the esophagus, which is the hollow, muscular tube that moves food and liquid from the throat to the stomach. Risk factors include [tobacco use](#), heavy alcohol use, gastric reflux and older age. The symptoms of the disease are easy to miss since they're so common, including indigestion and heartburn.

As there are no ideal screening techniques for esophageal cancer like there are mammograms for [breast cancer](#), only about 22% of people diagnosed with the cancer live more than five years. Typically, by the time the cancer is found, it has progressed to the point where there are fewer effective [treatment options](#) available.

Roy and his College of Nursing and Health Innovation colleague Zui Pan worked with 14 graduate students to create a modeling framework that incorporates various heterogeneous factors that facilitate the progression of esophageal cancer. The graduate students were a part of a MATH 5392 class in Fall 2022 titled "Modeling and Optimal Control of Ordinary Differential Equations."

Their [research](#) appears in the *Journal of Mathematical Biology*.

"Imagine a software application where you can input [real-time](#) esophageal cancer data along with available drug information and possible patient interactions, then receive a recommended optimal course of treatments," Roy said. "It would make the clinician's job much easier, and hopefully, improve survival rates for this dreaded disease."

Roy's students came to the class with a variety of individual research

interests, including applied and computational math, [data science](#), computer science and computational neuroscience. Over the semester, they were not only trained on topics related to ordinary differential equations, modeling techniques in mathematical biology, and optimal control, but also worked on individual assignments. The results from the assignments were collected and assimilated to form the content of the publication.

The mathematical framework they created uses a three-step process:

- building a pharmacokinetic model to determine the ideal pharmaceutical dose for an individual's body using a combination of mathematical models
- sensitivity analysis to determine the most sensitive parameters facilitating the cancer progression
- an optimal control model to select the type and number of combination drugs and optimal dosage profiles

They then tested the framework with different synthetic patient data generated by other models in literature. It demonstrated optimal treatment regimens for patients with potentially high accuracy for controlling esophageal cancer.

"This work presents a new mathematical framework that depicts a new way of modeling cancer heterogeneities by using different interaction laws and assessing combination treatment strategies, all targeting a class of signaling pathways that are over-expressive in [esophageal cancer](#) patients," Roy said. "We're hopeful this will add a new tool to the armamentarium clinicians can use to fight this disease."

More information: Souvik Roy et al, A robust optimal control framework for controlling aberrant RTK signaling pathways in esophageal cancer, *Journal of Mathematical Biology* (2024). [DOI:](#)

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