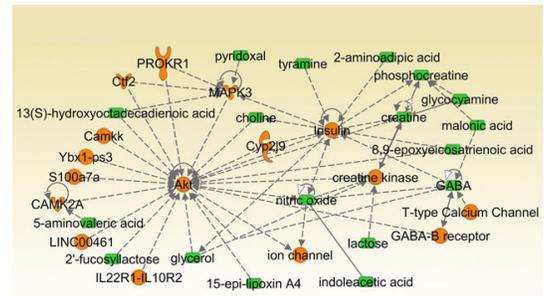


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## Using Machine Learning Models to Better Predict Bladder Cancer Stages

### San Diego Supercomputer Center researchers find novel diagnosis method

The invasive and expensive diagnosis process of bladder cancer, which is one of the most common and aggressive cancers in the United States, may be soon helped by a novel non-invasive diagnostic method thanks to advances in machine learning research at the San Diego Supercomputer Center (SDSC), Moores Cancer Center, and CureMatch Incorporated.



*This chart shows the late stages of bladder cancer, with the proteins shaded in orange and the metabolites shaded in light green. Credit: Elliot Kim and Valentina Kouznetsova, San Diego Supercomputer Center and Moores Cancer Center, UC San Diego*

Research scientists Igor Tsigelny and Valentina Kouznetsova have been working on the development of a machine-learning (ML) model that looks at a patient’s metabolites and their chemical descriptors. The model accurately classifies the stages of bladder cancer in a patient, according to the researchers. Tsigelny is the lead author on a recently published study in the *Metabolomics* journal called ‘Recognition of Early and Late Stages of Bladder Cancer using Metabolites and Machine Learning’.

When a patient experiences early symptoms of bladder cancer (e.g., blood in urine, pain during urination, etc.), the current method of diagnosis is often a painful, invasive series of tests.

“From my point of view, it can be very easy for patients just give a sample of urine and our ML system can produce a “red flag” analysis result telling them to go immediately to an oncologist for testing,” said Tsigelny. “We believe that a lot of early stages and even more advanced stages of bladder cancer go untreated because patients don’t pay attention to mediate pain

signals from the body, and may be thinking that there are less dangerous problems causing the symptoms. Our machine learning model uses metabolites and corresponding genes to determine if a patient has bladder cancer and if so, at what stage.”

More than 81,000 Americans were diagnosed with bladder cancer in 2018 and of those, more than 17,000 died from the condition, [according to statistics](#) from the American Cancer Society.

“The goal of this research is to lower that number and we believe that machine learning models can help us do that,” said Kouznetsova. “Using a variety of computational tools, we studied pathways related to different stages of bladder cancer that can be used for diagnostics and monitoring of cancer progression.”

The researchers trained the software – called multi-layer perceptron or MLP – with the data of urine metabolites of the patients with the different stages of the disease. Each stage has its own profile of metabolites. “MLP analyzes the chemical descriptor of the sets of metabolites related to each stage of cancer and creates AI models of these profiles,” explained Kouznetsova.

Tsigelny, along with his work at UC San Diego, is the chief science officer and co-founder of CureMatch, which provides decision support for doctors in personalized cancer medicine. SDSC Director Michael Norman is a member of the CureMatch Advisory Board.

“With 4.5 million possibilities to combine around 300 FDA-approved cancer drugs, CureMatch targets multiple cancer mutations at the same time and determines the best combination treatment for each patient,” explained Tsigelny. “While this study is not related to the current tasks of CureMatch, it may become so in the future.”

Eden Romm, a bioinformatics specialist at CureMatch, and SDSC Research Experience for High School Students (REHS) participants Elliot Kim and Alan Zhu also participated in this study.

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## MEDIA CONTACT

**Kimberly Mann Bruch**, 858-822-3622, [kbruch@ucsd.edu](mailto:kbruch@ucsd.edu)

**Igor Tsigelny**, 858-822-0953 [itsigel@ucsd.edu](mailto:itsigel@ucsd.edu)

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