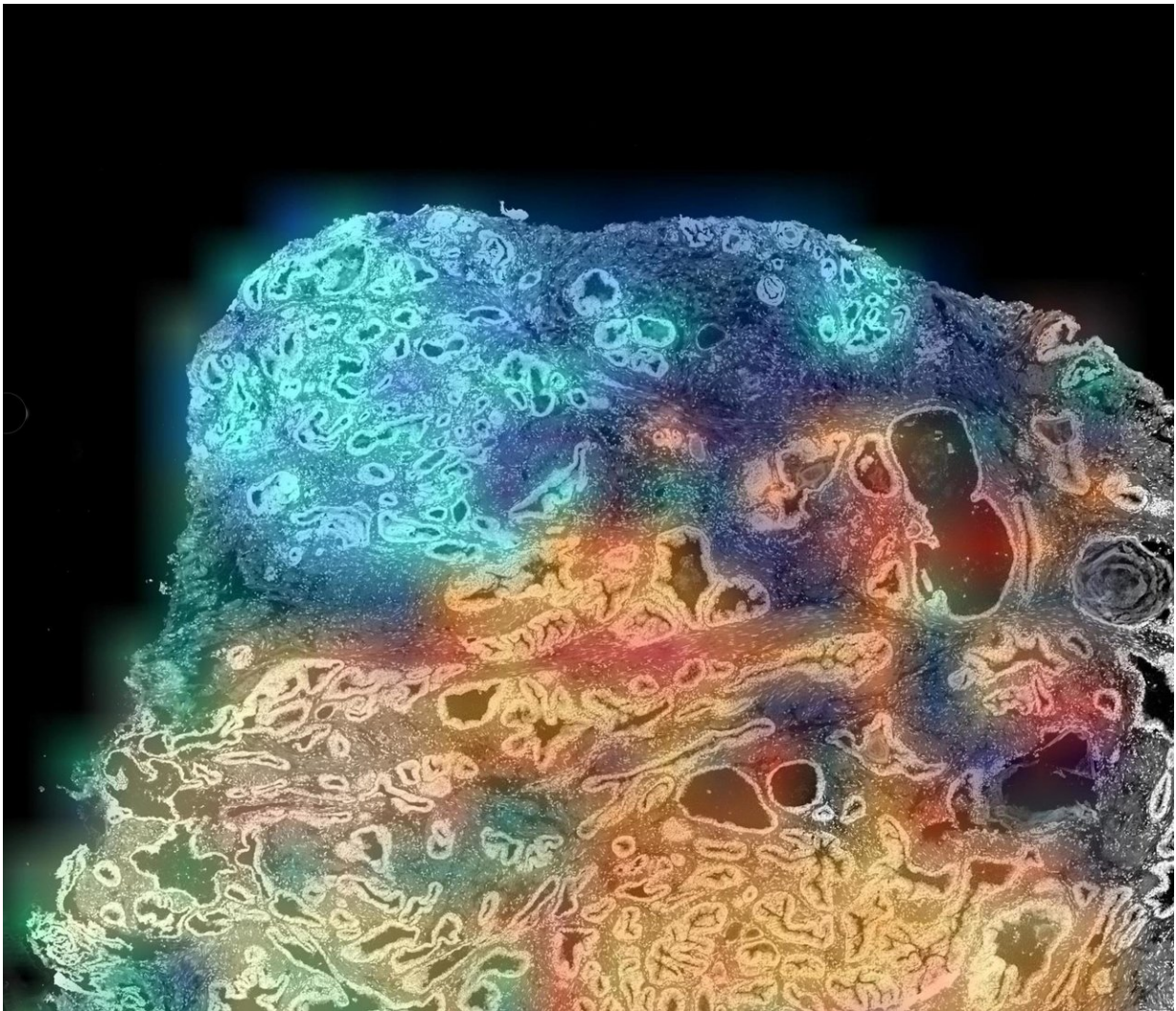


Prostate cancer diagnosis and treatment could improve with AI

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Focused AI analysis of a part of a prostate containing a tumor clone (blue). The AI signature is superimposed on the morphological tissue image. This confirms that the AI signature indirectly overlaps with tumor cells in the tissue section.

Credit: KTH The Royal Institute of Technology

Researchers in Sweden have shown how data-driven AI could contribute to a better understanding of how prostate cancer develops, and even improve clinical diagnosis and treatment of the disease.

Every [cancer tumor](#) is unique, with characteristics that change over time. This so-called heterogeneity is due to competing clones within a given tumor, as well as acquired mutations that increase the likelihood of metastases.

Researchers at Sweden's Science for Life Laboratory have demonstrated how data-driven AI methodology has the potential to contribute to a better understanding of these major events regarding heterogeneity in [prostate tumors](#) and in the surrounding micro environment. The research team from KTH and Karolinska Institutet, led by Joakim Lundeberg, Professor of Molecular Biology at KTH, used data obtained from nearly 6,750 [tissue](#) samples with spatial transcriptomics – a method that combines histology (tissue) with quantitative analysis of the active genes, which has been developed by KTH and Karolinska Institutet at SciLifeLab. The results were presented in the scientific journal *Nature Communications*.

The use of spatial information makes a big contribution, Lundeberg says. Analysis of prostate tumor gene activity in a tissue section dramatically increases the granularity, compared to conventional tumor analysis. "We have demonstrated that sampling different parts of the same prostate tumor shows remarkable differences on the [gene activity](#) level of the cancer cells at each site as well as the surrounding non-tumor cells, such as cells related to inflammation response likely to be linked to outcome of the patient," he says.

This rich source of information enables unattended AI methods to identify genetic patterns that cannot be seen by the naked eye, he says. Thus, this massive tissue genetic analysis can serve as a basis for an AI-based clinical evaluation of cancerous tissues and provide insight into gene expression in the [tumor](#)'s micro environment.

"AI simply helps us to create a computerized tissue anatomy," he says.

Further insights into the mechanisms underlying cancer are crucial for understanding the progression of tumors and how patients respond to treatment, he says.

Molecular data has been used successfully in the treatment of other forms of epithelial cancers, such as breast cancer. Co-author, Emelie Berglund, a doctoral student at KTH, says that recent studies show that it can help with [prostate cancer](#) too. "Early remedy of primary [prostate cancer](#) is efficient, however differentiating those that will progress to aggressive cases and who will benefit from what treatment is still problematic," Berglund says. "We hope that this study makes a significant contribution to these aspects."

More information: Emelie Berglund et al. Spatial maps of prostate cancer transcriptomes reveal an unexplored landscape of heterogeneity, *Nature Communications* (2018). [DOI: 10.1038/s41467-018-04724-5](https://doi.org/10.1038/s41467-018-04724-5)

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