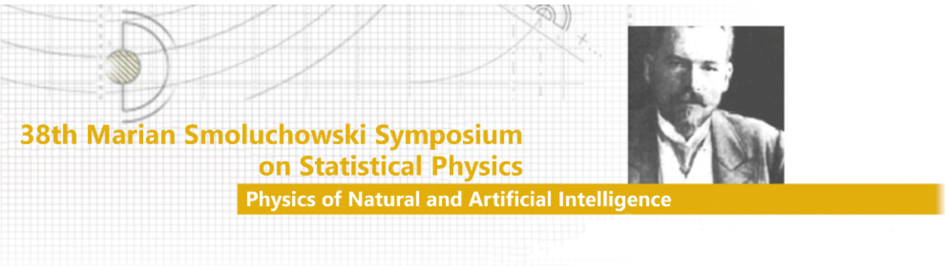

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Type: **Invited talk**

The Hidden Language of Cancer Genomes

Monday, 15 September 2025 15:00 (30 minutes)

Whole genome sequencing is playing an increasingly central role in modern oncology, offering detailed insights that support the development of individualized treatment strategies, especially when combined with machine learning techniques. Traditional approaches that concentrate solely on identifying key driver mutations face limitations due to both the restricted sensitivity of current technologies and the still-evolving understanding of cancer biology. Notably, different alterations can trigger similar disease phenotypes, complicating straightforward interpretations. For this reason, growing emphasis is being placed on integrative methods that not only identify driver mutations but also evaluate their broader effects on genome integrity. The resulting mutational signatures — patterns that reflect underlying biological processes — are proving to be powerful tools in guiding therapeutic decisions.

In this presentation, I will discuss the main obstacles in constructing reliable genomic classifiers and share examples of effective solutions grounded in mutational pattern analysis. I will also illustrate how studying these patterns in cancer genomes can reveal fundamental mechanisms at work even in healthy cells.

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