

CCR – IMPROMPTU

Friday, January 30th 2026, 12:00 PM

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From Molecular Complexity to Evidence-Driven Therapy Prioritization

Tumors typically harbor several co-occurring driver alterations that influence oncogenic pathways in interconnected ways. This complexity poses a major challenge for treatment selection, particularly when multiple potential therapeutic targets or resistance mechanisms coexist within the same tumor. Clinical data indicate substantial variability in expert recommendations, with reports showing 40–63% concordance across molecular tumor boards evaluating identical input profiles. These findings highlight the need for reproducible, systematic approaches capable of integrating heterogeneous molecular evidence. Digital Drug Assignment (DDA) is a computational reasoning framework designed to analyze the full molecular profile of an individual tumor. DDA aggregates and weighs published functional, preclinical, and clinical evidence to generate an ordered list of potential targeted therapies based on the totality of available molecular information. The method has been evaluated using large experimental datasets, clinical trial cohorts, and real-world molecular profiles, where it has demonstrated associations with improved response rates and treatment outcomes. These studies support the utility of algorithmic treatment ranking as a complementary tool for NGS-based clinical decision-making in oncology.

Venue: Lecture Hall B2, Borschkegasse 4a

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Host: Gergely Szakacs



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