Inferring complex tumor states in lung cancer using cfDNA methylation from liquid biopsies

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This presentation will explore the use of cell-free DNA (cfDNA) methylation profiling as a powerful tool to uncover complex tumor states, especially lung cancer, offering insights beyond traditional genomic approaches. The development and optimization of methods suitable for clinical implementation, including analytical validation and workflow standardization, will be discussed. Emphasis will be placed on how these approaches enable biomarker-driven clinical trials and support the design of precision oncology strategies. Finally, the importance of building robust, reproducible biomarkers to ensure clinical utility and impact patient care will be highlighted.