



Abdelouahab Dehimat, PhD, is an Associate Professor and researcher in the Department of Natural and Life Sciences, Faculty of Sciences, University of M'sila, Algeria. He is a computational cancer biologist working at the interface of computational biology, transcriptomics, and experimental cancer research. His current research focuses on single-cell and spatial transcriptomics in colorectal cancer, including tumor microenvironment heterogeneity, cellular states, molecular interactions, and tumor-associated programs. He is experienced in R and Python-based analysis, machine learning, genomic and transcriptomic analysis, pathway analysis, and computational modelling, with a strong biological background that enables computational findings to be interpreted in the context of cancer mechanisms and experimental validation. His work also encompasses computational drug discovery, including integrative QSAR/3D-QSAR modelling, machine learning-based virtual screening, molecular docking, molecular dynamics simulations, binding free energy calculations, and network pharmacology. He is particularly interested in developing integrative approaches that combine transcriptomic, metabolomic, and immunological data to understand cancer biology and therapeutic response, with a focus on multitarget anticancer drug discovery and structural biophysics. His recent work has been accepted for oral presentation at CancersScape: Spatial Biology of the Tumor Ecosystem (2025), and he has contributed to multiple peer-reviewed publications and international conferences.