

DiSCourse Seminar

The Digital Science Center and the Department of Molecular Biology would like to invite you to the following presentation:

Francesca Finotello
University of Innsbruck

Charting Tissue Complexity Through Transcriptomics Deconvolution

The investigation of the cellular organization of tissues is key to understand mechanisms that underlie tissue function and its disruption during disease. *Deconvolution* is a computational technique for the quantification of the cellular composition of tissues profiled with transcriptomics technologies. Recent deconvolution methods can be trained using single-cell transcriptomics data to learn the transcriptional “fingerprints” of any cell type, thereby possibly extending deconvolution to any tissue, disease context, and organism of interest. These approaches can be now also applied to spatial transcriptomics data, revealing the architecture of tissues and the spatial distribution of their cellular constituents. In this talk, I will show how different types of transcriptomics data can be jointly analyzed with deconvolution techniques to chart the tissue organization in health and disease. A major focus will be on methodologies to characterize the tumor microenvironment and especially tumor-infiltrating immune cells, which are our inner line of defense against cancer.

About the speaker

[Francesca Finotello](#) is an Assistant Professor at the Department of Molecular Biology and Digital Science Center (DiSC), where she leads the Computational Biomedicine Group. Her research focuses on the bioinformatic analysis of bulk and single-cell multiomics data and on the development of computational methods to inform precision and personalized medicine.

Date, Time, Place:

Friday, 5 May 2023, 12:00 (CEST), hybrid

Participants are invited to join the event at the Digital Science Center, Innrain 15, Open Space Area (1st floor) *or* online via [Big Blue Button](#).