UNIVERSITÀ DI TRENTO
Dipartimento di
Biologia Cellulare, Computazionale e Integrata - CIBIO

4 APRIL
AT 11.30 P.M.
ROOM B109 | POVO 2

OPEN ST: HIGH-RESOLUTION SPATIAL TRANSCRIPTOMICS IN 3D

GIUSEPPE MACINO

UNIVERSITY OF ROME "LA SAPIENZA"

Spatial transcriptomics (ST) methods have been developed to unlock molecular mechanisms underlying tissue development, homeostasis, or disease. However, there is a need for easy-to-use, high-resolution, cost-efficient, and 3D-scalable methods. Here, we report Open-ST, a sequencing-based, open-source experimental and computational resource to address these challenges and to study the molecular organization of tissues in 3D. In mouse brain, Open-ST captured transcripts at subcellular resolution and reconstructed cell types. In primary tumor and patient-matched healthy/metastatic lymph nodes, Open-ST captured the diversity of immune, stromal and tumor populations in space. Distinct cell states were organized around cell-cell communication hotspots in the tumor, but not the metastasis. Strikingly, the 3D reconstruction and multimodal analysis of the metastatic lymph node revealed spatially contiguous structures not visible in 2D and potential biomarkers precisely at the 3D tumor/lymph node boundary. We anticipate Open-ST to accelerate the identification of spatial molecular mechanisms in 2D and 3D.

DEPARTMENT OF CELLULAR, COMPUTATIONAL AND INTEGRATIVE BIOLOGY - CIBIO
VIA SOMMARIVE, 9
38123 - POVO (TN)
COMUNICAZIONE.CIBIO@UNITN.IT