Instituto de Biología Funcional y Genómica

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Beatriz Rosón

Grupo de Medicina Reproductiva
Instituto Investigación Sanitaria del Hospital Clínico de Valencia, INCLIVA
Valencia

Unravelling pathological mechanisms through single-cell transcriptomic maps

Abstract: *Single-cell atlases provide high-quality reference maps of gene expression patterns for the different cell types within a specific tissue. The Human Cell Atlas initiative currently promotes the acquisition of these datasets, which will serve as reference data repositories for further biomedical studies. As part of this initiative, the Human Uterus Cell Atlas (HUTER) project aimed to create a transcriptomic single-cell reference map of the human uterus, not only in health but also in disease and across women's lifespan.*

Here, I will present two relevant disease reference maps derived from the HUTER project. First, the disease atlas of Asherman's Syndrome depicting specific fibrotic-inflammatory niche interactions within the endometrium. Second, the myometrial atlas serving as a proxy for understanding contractile uterine dysfunction associated with aging.

Expanding computational biology applications to atlas comparative analysis has enabled the detection of disease-associated perturbations in cellular composition and intra-tissue communications. This research field has the potential to unravel the complexity of biological processes such as fibrosis, tissue regeneration, and cellular niche interactions, translating this knowledge into clinical assets and driving drug discovery innovations.

Viernes 28 Junio 2024

Hora: 12:00 pm
Lugar: Salón de actos del IBFG
Web: https://ibfg.usal-csic.es/semext.php
Contacto: Olga Calvo (ocalvo@usal.es)

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