



# Biological Colloquium

## Gene expression memory: a family story

**Prof. Dr. David Suter**

Associate Professor  
Institute of Bioengineering  
Ecole Polytechnique Federale de  
Lausanne (EPFL) Switzerland



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Assigning single cell transcriptomes to cellular lineage trees has transformed our understanding of differentiation during development, regeneration, and disease. However, lineage identification is technically demanding and most single cell (sc) RNA-seq datasets are devoid of lineage information. In this talk I will describe Gene Expression Memory-based Lineage Inference (GEMLI), a computational tool allowing to robustly determine cell lineages solely from scRNA-seq datasets. GEMLI allows to study heritable gene expression, to discriminate symmetric and asymmetric cell fate decisions and to reconstruct individual multicellular structures from pooled scRNA-seq datasets. In human breast cancer biopsies, GEMLI revealed previously unknown gene expression changes at the onset of cancer invasiveness. The universal applicability of GEMLI allows studying the role of cell lineage trees in a wide range of physiological and pathological contexts. GEMLI is available as an R package on GitHub (<https://github.com/UPSUTER/GEMLI>).

**Hosts:**

**Prof. Dr. Nils Johnsson, Institute of Molecular Genetics and Cell Biology  
& Prof. Dr. Christof Gebhardt, Institute of Biophysics**

**Students and colleagues are all welcome!**