**You are cordially invited to a** **Computational Genomics Seminar**

**Dr. Elior Rahmani**

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*"Robust identification of systematic genomic variation at the single-cell level"*

Wednesday **December 28**, at 11:15

**Check Point** building, room **420**

**Abstract:** A major limitation in single-cell genomics is a lack of ability to conduct cost-effective population-level studies. As a result, much of the current research in single-cell genomics focuses on biological processes that are broadly conserved across individuals, such as cellular organization and tissue development. This limitation prevents us from reliably studying the etiology of experimental or clinical conditions that may be inconsistent across individuals and datasets owing to molecular variation and a wide range of effects in the population. In this presentation, I will describe several novel computational methods for addressing the above limitation, and I will show how these methods dramatically improve the robustness and replicability of common downstream analysis tasks in single-cell genomics.

Host: Prof. Ron Shamir, School of Computer Science, TAU