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

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*"Statistical* *challenge*s and methods for studying disease heterogeneity in epidemiologic research*"*

Wednesday **December 7**, at 11:15

**Check Point** building, room **180**

**Abstract:** A common goal in molecular pathological epidemiology studies is to evaluate whether the effects of risk factors on disease incidence vary across different disease subtypes.  A popular approach implements either a multinomial regression model or a cause-specific Cox model in which each of the non-zero values (or “causes”) corresponds to a bona fide disease subtype. Then, heterogeneity in the exposure effects across subtypes is examined by comparing the coefficients of the exposure between the different subtypes. Consider for example high-level microsatellite instability (MSI), a well-established feature observed in approximately 15% of the colorectal cancer cases. The association between cigarette smoking and colorectal cancer was found to be stronger for MSI-high subtype than for non-MSI-high subtype.

In this talk, I will survey the commonly used statistical methods to answer these heterogeneity questions and present a variety of challenges we have been tackling over the past several years, including missing subtype data and subtype misclassification. In addition, I will explain why the common approaches do not recover causal effects, even when all confounders are measured, and briefly discuss our proposed solution.

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