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**Day 1- 25.6, Session II- 15:00-16:30**

## **Modeling the effects of early life adversity on DNA methylation**

Abstract:

Life course epidemiology provides a useful conceptual framework for studying the role of time-varying exposures. Moving beyond crude comparisons of those ever exposed versus never exposed to early life adversity, we can now test life course hypotheses regarding whether the effects of exposure vary based on the timing, duration, or recency of exposure. A new statistical approach – called the structured life course modeling approach (SLCMA) – allows researchers to simultaneously compare these different life course theoretical hypotheses and select the hypothesis best supported by data. Recently, we applied the SLCMA to assess how the developmental timing of exposure to childhood adversity was associated with genome-wide DNA methylation patterns. In this talk, I will summarize results from a set of simulations comparing five statistical inference methods that can be used in the SLCMA. I will also showcase applications of these methods in a study of epigenetic mechanisms of early life adversity. Results indicate that the five methods performed differently in an epigenome-wide analysis with respect to their Type I error control, statistical power, and confidence interval coverage, allowing us to make recommendations for new users of the SLCMA. The SLCMA is a promising approach to identify epigenetic and other omic biomarkers and understand the biological consequences of time-varying exposures.