Speaker: Stef Baas (MRC Biostatistics Unit, Cambridge)

Date: 26/06/2026 at 11:00 in 4 West 4.8

Title: Design-optimal e-values: An investigation and application to multi-stage single-arm trials

Abstract:
The e-value is gaining traction as a robust alternative to p-values and Bayes factors for quantifying statistical evidence. e-values are a promising method for adaptive clinical trials due to their anytime-validity: e-values ensure type I error rate control at any stopping time, facilitating repeated interim analyses, complex stopping rules, and valid inference under protocol deviations. In this presentation, I will introduce the concept of an e-value, position it against what is already there in the adaptive design literature, and will present a method to "optimize the e-value with respect to a clinical trial design" using (constrained) dynamic programming based on the betting interpretation underlying an e-value, resulting in what we denote a "design-optimal e-value". I will focus on an application to single-arm multi-stage clinical trials with binary data, which we explored as a starting point in `https://arxiv.org/abs/2605.28653`. Using exact calculations, we showed that, next to robustness, e-value-based designs can provide competitive operating characteristics to standard (non-)adaptive designs with and without futility stopping and outperform, standard, growth-rate-optimal e-values in finite samples. In addition, design-optimal e-values automatically indicate trial when continuation is futile, e.g., an e-value (capital) of zero indicates the impossibility of an efficacy conclusion (automatic curtailment). This all seems like a free lunch, and the last part of this presentation will discuss where this comes from and where the cost may lie.