

## Einladung zum Biometrischen Kolloquium

### SATOSHI MORITA

Department of Biomedical Statistics and Bioinformatics, Kyoto  
University Graduate School of Medicine, Kyoto, Japan

**18. Oktober 2019, 10:30h**

Informatikbibliothek 888.03.806

Medizinischen Universität Wien, Spitalgasse 23, 1090 Wien

**Host:** Martin Posch

### **BAYESIAN POPULATION FINDING WITH BIOMARKERS IN A RANDOMIZED CLINICAL TRIAL**

The identification of good predictive biomarkers allows investigators to optimize the target population for a new treatment. We propose a novel utility-based Bayesian population finding (BaPoFi) method to analyze data from a randomized clinical trial with the aim of finding a sensitive patient population. Our approach is based on casting the population finding process as a formal decision problem together with a flexible probability model, Bayesian additive regression trees (BART), to summarize observed data. The proposed method evaluates enhanced treatment effects in patient subpopulations based on counter-factual modeling of responses to new treatment and control for each patient. In extensive simulation studies, we examine the operating characteristics of the proposed method. We compare with a Bayesian regression-based method that implements shrinkage estimates of subgroup-specific treatment effects. For illustration, we apply the proposed method to data from a randomized clinical trial.