

Wiener Biometrische Sektion der Internationalen Biometrischen Gesellschaft Region Österreich – Schweiz



Please join the Biometric Colloquium

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COMMON ATOMS MIXTURE MODELS IN SOME

BIOSTATISTICAL INFERENCE PROBLEMS

May 28th, 2025 at 9:15 am

Seminarraum Center for Medical Data Science (previously CeMSIIS), Spitalgasse 23, Room 88.03.513 Medical University of Vienna, 1090 Wien Host: Martin Posch

Abstract:

We consider several examples of statistical inference for two or more related populations. In one example we characterize two patient populations that are relevant in the construction of a clinical study design, and propose a method to adjust for detected differences. Another example is about comparative immune profiling under two biologic conditions of interest when we identify shared versus condition-specific homogeneous cell subpopulations. In a third example we model spatially aligned cell subpopulations for spatial transcriptomics data.

Bayesian inference in all three applications requires prior probability models for two or more related distributions. We build on extensive literature on such models based on Dirichlet process priors. Related models are commonly known as dependent Dirichlet processes (DDP), with many variations and extensions beyond the Dirichlet process model. One special feature in all three motivating applications is the focus on understanding the nature of the dependence across the related populations. In one application we aim to adjust for differences in population heterogeneity, in another we aim to identify and understand homogeneous subpopulations that are characteristic for one or the other condition.