

**Wiener Biometrische Sektion
der Internationalen Biometrischen Gesellschaft
Region Österreich – Schweiz**

<http://www.meduniwien.ac.at/wbs/>

Einladung zum

BIOMETRISCHEN KOLLOQUIUM

am Mittwoch, 13. Jänner 2016 um 13:00 Uhr

in der Informatik-Bibliothek (Ebene 3, Raum 88.03.806) des
Zentrums für Medizinische Statistik, Informatik und Intelligente Systeme (CeMSIIS)
der Medizinischen Universität Wien, Spitalgasse 23, 1090 Wien
(Plan siehe <http://www.muw.ac.at/cemsiis/allgemeines/anschrift/>)

Vortragender:

ANDREAS FUTSCHIK

Johannes Kepler Universität Linz

**ON THE INADMISSIBILITY OF COMMON POPULATION GENETIC
ESTIMATES AND THEIR IMPROVEMENT BY USING SHRINKAGE**

Wir freuen uns auf zahlreichen Besuch.

Franz König
Präsident

Stephan Lehr
Sekretär

ON THE INADMISSIBILITY OF COMMON POPULATION GENETIC ESTIMATES AND THEIR IMPROVEMENT BY USING SHRINKAGE

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Abstract:

Two key parameters in population genetics are the scaled mutation parameter θ and the scaled recombination rate ρ . Estimates of these parameters have been obtained either from suitable summary statistics, or via more sophisticated methods such as maximum (composite) likelihood. We show that there is often room for uniform improvement of these estimates. We first explain why the popular Ewens-Watterson estimate of θ is inadmissible in terms of the mean squared error under the classical Wright-Fisher model and how it can be uniformly improved. Also other estimates of θ such as the MLE can be improved, although to a smaller extent. Then we look at estimating the scaled recombination rate ρ , and explore possible gains that can be obtained for composite likelihood estimates. Also here, it turns out that there is often still room for uniform improvement.

Both for Watterson's estimate and when estimating recombination, the improvement can be achieved without a lot of computational effort. However, as no explicit formulas for bias and variance are available when estimating ρ , the coefficients turning up in the improvement need to be estimated from simulations. The talk will start with a short introduction into population genetics, the Wright-Fisher-Model and the other mentioned statistical methods.