

# Summary Statistic Based Inference in Population Genetics

Andreas Futschik

Universität Wien

Population genetics provides an exciting field for statisticians with new challenges arising as data are becoming more and more easily available. We will talk about our recent work and focus on Watterson's theta, one of the most widely used summary statistics in this area.

We will first show that Watterson's theta is inadmissible and how an improved version of this estimate can be obtained. (Futschik and Gach (2008)). Then we will look at NGS (next generation sequencing experiments) and show how Watterson's and other estimates can be computed in the context of cost saving pooling experimental designs. (Futschik and Schlötterer (2010)).

Finally we will look at the role summary statistics play in ABC (Approximate Bayesian Computation). ABC has become very popular in population genetics as it permits to carry out Bayesian inference in situations where the likelihood is computationally intractable. Careful tuning of the influence of different summary statistics is important in order to make the method work efficiently, and we investigate how cross-validation performs in this situation. (Futschik and Bertl, ongoing work).