# Why some commonly population genetic estimates are inadmissible and how to improve them by shrinkage

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An important goal in population genetics is to infer key parameters describing the population history based on a sample of DNA sequences. Two such key parameters are the scaled mutation parameter $\theta$ and the scaled recombination rate $\rho$. Historically, estimates of these parameters have been obtained from suitable summary statistics. Unbiasedness has been considered to be an important property of such estimates. More recently, likelihood and Bayesian methods became popular, although they tend to be computationally much more demanding.

In our talk, we will explore how shrinkage can be used to improve population genetic estimates. We will first present previous work by Futschik and Gach (2008) showing that the popular Ewens-Watterson estimate of q is inadmissible under the classical Wright-Fisher model and can be improved uniformly by shrinkage. We will then explore, whether other estimates of q such as the MLE can also be improved. We will also explain why shrinkage is helpful in this context involving Poisson processes observed over intervals of random lengths. Then we will look at estimates for other parameters such as the scaled recombination rate r, and explore possible gains that can be obtained by shrinkage in this context. Finally, we will investigate how shrinkage can be applied with estimates obtained from next generation sequencing data, where sequencing errors play a role and pooling designs are often used as a strategy to save cost.