

# 2019년 제 7회 통계세미나

통계연구소에서는 다음과 같이 통계 세미나를 개최하오니 많은 참여 바랍니다.

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## Bayesian Inference of Evolutionary Histories from Genomic Data

<Abstract>

The evolutionary history of a group of organisms explains the process of their genetic variation over time. Due to recent sequencing and computing advances, statistical inference has played an important role in the study of evolutionary history from genomic data. However, typical analyses are either limited to a small amount of data or fail to estimate complex and diverse evolutionary models. In this talk, I will present a new Bayesian method for estimating population/species-level history including population sizes, splitting time of two populations, and migration rates. The new method resolves statistical limitations and overcomes major roadblocks to analyze genome-scale data. Using importance sampling and a Markov chain representation of genealogy, the new method scales to genomic data without mixing difficulty in a Markov chain Monte Carlo simulation. I will demonstrate the new method with simulated data and real DNA sequences.

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