概率论系列报告

报告题目(Title)： Maximum likelihood implementation of an isolation-with-migration model for three species （最大似然法框架下的多物种隔离移民模型研究）

报告人(Speaker)： 朱天琪 博士 中科院数学与系统科学院

时间(Time)： 5 月 15 日(周一)下午 3：00-4：00

地点(Venue)： 北京大学理科一号楼 1303

摘要(Abstract)： We develop a maximum likelihood (ML) method for estimating migration rates between species using genomic sequence data. A species tree is used to accommodate the phylogenetic relationships among three species, allowing for migration between the two sister species, while the third species is used as an out-group. A Markov chain characterization of the genealogical process of coalescence andmigrationis used tointegrate out themigration histories at eachlocus analytically, whereas Gaussian quadrature is used to integrate over the coalescent times on each genealogical tree numerically. Our implementation can accommodate tens of thousands of loci, making it feasible to analyze genome-scale data sets to test for gene flow. We calculate the posterior probabilities of gene trees at individual loci to identify genomic regions that are likely to have been transferred between species due to gene flow. We conduct a simulation study to examine the statistical properties of the likelihood ratio test for gene flow between the two in-group species and of the ML estimates of model parameters such as the migration rate. Inclusion of data from a third out-group species is found to increase dramatically the power of the test and the precision of parameter estimation. We compiled and analyzed several genomic data sets from the Drosophila fruit flies. We discuss the utility of the multispecies coalescent model for species tree estimation, accounting for incomplete lineage sorting and migration. [IM model, maximum likelihood, multispecies coalescent, migration, speciation.]

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