第 24 回　葉山セミナー / The 24th Hayama Seminar

2025. Aug. 5th (15:00 – 16:30) (at: Room 310, Hybrid Style)

Powerful inference of admixture using joint genealogies of ancient and modern humans

Leo Speidel （シュパイデル玲雄）

RIKEN ECL Research Unit Leader, Mathematical Genomics RIKEN ECL Research Unit, Division of Fundamental Mathematical Science, RIKEN Center for Interdisciplinary Theoretical and Mathematical Sciences (iTHEMS)
理研 数理創造研究センター (iTHEMS) 数理基礎部門 数理遺伝学理研 ECL 研究ユニット 理研 ECL 研究ユニットリーダー

Abstract:

Over the past decade, ancient DNA has opened a unique window into our shared genetic past, allowing us to directly study genomic change in ancient human groups. Additionally, we are now able to build the joint genetic trees that relate individuals, modern and ancient, through their shared ancestors back in time. In this talk, I will present two new methods, Twigstats and Ghostbuster. These can reveal previously hidden events implicated by these genetic trees, ranging from events in the deeper human past to fine-scale ancestry transformations in a nation's recent past. Twigstats boosts f-statistics to enable robust fine-scale admixture inference. Applied to >1000 available ancient genomes focussed on Northern Europe, we reveal waves of mobility during the early historical period in Europe. Ghostbuster identifies different patterns of coalescences with other human groups and models individuals as mixtures of these ancestral components. This allows us to pinpoint older mixtures involving potentially unsampled ancestries along the genome.

(Host: Prof. Innan)