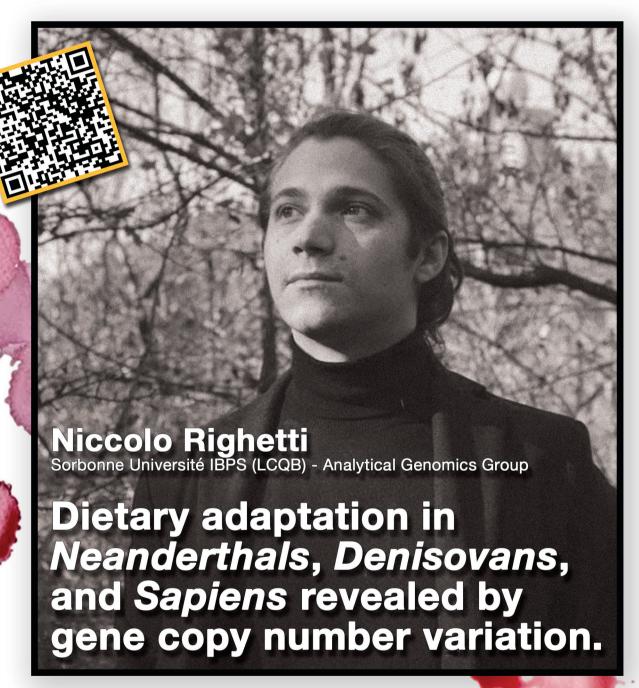
Venerdì 14 Giugno

17:00 - 18:00

Sala Lauree



Dietary adaptation involves developing an efficient **digestive system suited to the available food** in an ecosystem. Traditional reconstructions of ancient human diets rely on isotopic analysis of remains and faunal findings at archaeological sites, supplemented by recent metagenomic studies of dental plaque. We propose a **novel computational method** to uncover the genetic basis of human dietary adaptation. Analyzing 15 genomes from Neandertals, Denisovans, and early *Homo sapiens*, we identify 23 genes - including six gene clusters - with **discernible copy number variation trends at the population level**. The genomic variation shows how metabolic pathways for lipid, brown fat, protein or carbohydrate metabolism adapt to metabolize food from animal or plant sources in archaic humans. Our findings suggest *Homo sapiens* **possessed evolutionary advantages in adapting to cold and temperate ecosystems** compared to *Neandertals* and *Denisovans*.



