



Institute colloquium

Institute Colloquium: Why there is more to gene evolution than protein function: splicing

Laurence Hurst

University of Bath

Host:

There is considerable variation in the rate at which different genes evolve. Why is this? Classically it has been considered that the density of functionally important sites must predict rates of protein evolution.

Likewise, amino acid choice is usually assumed to reflect optimal protein function and codon choice is random. Here I briefly review evidence suggesting that this view is too simplistic. In particular I concentrate on how selection acting during the protein's production history can also affect gene evolutionary rates as well as amino acid and codon choice.

Exploring the role of selection at the DNA and RNA level, I specifically address how the need 1) to specify exonic splice enhancer motifs in pre-mRNA and 2) to ensure nucleosome positioning on DNA, impacts amino acid choice, codon choice and rates of evolution at both synonymous and non-synonymous sites.

Monday, April 23, 2012 04:30pm - 05:30pm

Raiffeisen Lecture Hall, Central Building



This invitation is valid as a ticket for the ISTA Shuttle from and to Heiligenstadt Station. Please find a schedule of the ISTA Shuttle on our webpage: <https://ista.ac.at/en/campus/how-to-get-here/> The ISTA Shuttle bus is marked ISTA Shuttle (#142) and has the Institute Logo printed on the side.