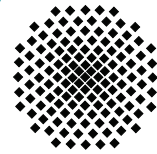


Stuttgarter Physikalisches Kolloquium

Max-Planck-Institut für Festkörperforschung
Max-Planck-Institut für Intelligente Systeme
Fachbereich Physik, Universität Stuttgart

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Dienstag, 22. April 2014

17.15 Uhr

Hörsaal 2 D5

Stuttgarter Max-Planck-Institute, Heisenbergstraße 1, 70569 Stuttgart-Büsnau

Using the Neandertal Genome to learn about our distant past

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Abstract

The genomes of humans and apes consists of over 3 billion nucleotides that make up the DNA. The majority of the nucleotide-differences that can be observed between genome sequences of human individuals or between a human and an ape are of no functional consequence. Due to the neutral nature of most differences between genome sequences, the accumulation of differences is expected to proceed linearly with time. This clock-like property of differences allows us to gain insight into the relationship of organisms by comparing their genome sequences.

Until recently, closely related human forms inhabited the planet simultaneously with us modern humans. By studying pieces of DNA that are preserved in remains of Neandertals and other ancient humans, we are now able to reconstruct the relationship to our extinct relatives and answer the question what happened when humans met these ancient forms. The talk will present the latest results from the analyses of the high-quality genome sequence of a Neandertal and its comparison to modern humans and Denisovans, an extinct hominin group most closely related to Neandertals that was found in Siberia.