Workshop VII
Can physics be useful to human genetics?

March 20, Tuesday, Danciger B building, seminar room, 2.00 pm (20.03.18 at 14.00)

Refreshments 14.00 – 14.15
3. 15.35 – 16.25 Prof. Liran Carmel: Reconstructing ancient epigenomes: what Neanderthals teach us about ourselves?

All interested, including students, are welcomed.

Refreshments will be in the lobby of Danciger B building, from 14.00

M. Ya. Amusia, APS Fellow

Abstract of Prof. Doron Behar talk:
Previous Y-chromosome studies demonstrate that approximately two thirds of all Ashkenazi Levites, members of the paternally inherited Jewish priestly caste, descend on their
direct male lines from a single common ancestor found within Y-chromosome haplogroup R1a. Recently, whole Y-chromosome data indicated a geographic source of the R1a Levite founder lineage in the Near East and its likely presence among pre-Diaspora Hebrews. However, paucity of data at the whole Y-chromosome level prevented explicit conclusions regarding the lineage’s geographic origin, route and date of entering Europe, or its expansion and spread within it. The presentation will summarize the analysis of 504 whole Y-chromosomes meant to define the variation within the R1a Levite clade, its relations to non-Levite Jewish or non-Jewish R1a samples, and its cladistic characteristics as compared to other haplogroups prevalent among Ashkenazi Jews.

Abstract of Prof. Liran Carmel talk:
Recent technological advances enable the reading of the DNA sequence of individuals who died even tens of thousands of years ago. This provides means to directly compare the genetics of modern humans to that of other human groups like Neanderthals and Denisovans, and to understand the unique features that characterize *Homo sapiens*. However, the sequences themselves bear little information on the physiological differences between these humans, as many of these differences are thought to be attributed to changes in the level of gene activity rather than to the gene sequence. But how ancient DNA sequences can teach us how genes actually worked in these long-dead individuals?

In the talk, I will present a novel method developed in my lab to reconstruct pre-mortem patterns of gene activity in ancient individuals and extinct human groups. The method is based on harnessing asymmetries in DNA decay patterns. I observe hundreds of genes that had changed the way they work since we split from our closest relatives. I will show how these changes are related to present-day human speech capabilities, morphology and cognition.