

Date/Time :	Th, 26 February 2015 15:00 – 16:00
Venue :	Meeting Room C016, Level C, Lab 1
Speaker:	Katarzyna Bozek, Ph.D.
Title:	CAS-MPG Partner Institute for Computational Biology Machine learning and comparative methods in the study

Title: Machine learning and comparative methods in the study of HIV and human evolution

Abstract:

The talk will consist of two parts. In the first part I will present a method for prediction of HIV tropism - mechanism of the virus cell entry. The method is based on a combination of machine learning approaches and encodes physicochemical properties of the HIV envelope protein. The results show improved prediction accuracy compared to sequence-based methods, and provide additional insights into the physicochemical properties of the HIV envelope protein that determine its entry mechanism into the host cell (Bozek et al., Plos Comp Bio, 2013). In the second part I will present a comparative study of human metabolome. Based on metabolome and gene expression measurements of a rich collection of tissue samples from three brain regions and two non-neural tissues of humans, chimpanzees, macaque monkeys, and mice, we performed analysis of evolutionary dynamics of metabolites - small molecules with a weight of less than 1,500 Daltons. While chimpanzee, macague, and mouse metabolomes diverge following the genetic distances among species, we detected a remarkable acceleration of metabolome evolution in human prefrontal cortex and skeletal muscle affecting neural and energy metabolism pathways. We further conducted muscle strength tests in humans, chimpanzees, and macagues. The results suggest that, while humans are characterized by superior cognition, their muscular performance is markedly inferior to that of chimpanzees and macaque monkeys (Bozek et al., Plos Bio, 2014).