



Joint Seminar on Computer Science and Applied Mathematics  
Mathematical Institute of the Serbian Academy of Sciences and Arts  
IEEE Chapter Computer Science (CO-16)  
Belgrade, Republic of Serbia

### **Genetic analysis of individual's origin: Y chromosome, mitochondrial genes and HLA**

Vladimir Brusica, Ph.D.

Position: Principal Associate in Medicine

Institution: Dana-Farber Cancer Institute

Department: Medicine

Division: Oncology

Address: Dana Farber Cancer Institute, Med Onc /HIM 401, 44 Binney St ,  
Boston, MA 02115, USA



27. December 2012, 18:30

Mathematical Institute of the Serbian Academy of Sciences and Arts  
Knez Mihailova 36, room 301f

#### **Abstract**

Present-day Pacific islanders are thought to be the descendants of Neolithic agriculturalists who expanded from island Southeast Asia several thousand years ago. They speak languages belonging to the Austronesian language family, spoken today in an area spanning half the circumference of the world, from Madagascar to Easter Island, and from Taiwan to New Zealand. To investigate the genetic affinities of the Austronesian-speaking peoples, we analysed mitochondrial DNA, HLA and Y chromosome polymorphisms in individuals from eight geographical locations in Asia and the Pacific (China, Taiwan, Java, New Guinea highlands, New Guinea coast, Trobriand Islands, New Britain and Western Samoa). Our results show that the demographic expansion of the Austronesians has left a genetic footprint. However, there is no simple correlation between languages and genes in the Pacific. So, let us see how it is with Balkans and Dinaroids.

#### **About the Speaker:**

##### **Vladimir Brusica, Ph.D, MBA, Director of Bioinformatics**

Dr Brusica is the Director of the Cancer Vaccine Center Bioinformatics Core at Dana-Farber Cancer Institute. He works on the development and application of computational methods in immunology and computer-aided development of vaccines. He has contributed a number of pioneering studies in computational immunology and immunoinformatics. He introduced the use of several advanced machine learning techniques and developed novel algorithms for identification of T-cell epitopes and selection of vaccine targets. His current work includes development of computational solutions for the study of B-cell epitopes and integrative approaches to vaccine formulations. His research interests span the fields of biological databases, data mining, computational models of biological systems, simulation of molecular interactions, and biological discovery using simulation of laboratory experiments. He holds degrees in Engineering, Information Technology, Computer Science, and Business Administration. Before joining CVC, Dr Brusica worked at the Walter and Eliza Hall Institute, Melbourne, Australia; Institute for Infocomm Research, Singapore; and University of Queensland, Brisbane, Australia. Dr Brusica is responsible for bioinformatics research and support at the CVC, which includes the integration of diverse cancer-related and immunology data, their analysis, and development of novel computational solutions for the advancement of cancer vaccine research. He works closely with the CVC researchers and the directors of core facilities supporting discovery, therapeutic, and clinical trial activities at CVC.