

PRELIMINARY PROGRAM

GENOMIC COMPLEXITY

Satellite Meeting to ECCS 2012

Thursday, September 6, 2012

Organisers: Yannis Almirantis, Wentian Li & Astero Provata

Time	Speaker	Title
8:50-9:00	<i>Opening by Organisers</i>	
9:00-9:40	Peter F. Arndt	The complexity of neutrally evolving genomes
9:40-10:20	Hanspeter Herzel	Circadian rhythms in gene expression
10:20-10:40	Pedro Carpena	On the complex distribution of relevant words in the human genome
10:40-11:00	<i>COFFEE BREAK</i>	
11:00-11:40	Benjamin Audit	Multi-scale analysis of the mammalian replication programme - Relation to large-scale chromatin folding
11:40-12:00	Pietro Lio	Genome complexity versus metabolic constrains
12:00-12:20	Wentian Li	Can we understand the parameter values in human genome?
12:20-13:30	<i>LUNCH</i>	
13:30-14:10	Pedro Bernaola-Galvan	Very-large-scale compositional organization of the human genome
14:10-14:30	Marco Jose	A novel indicator of GC content reflects the evolution of primate species
14:30-14:50	Eugene Korotkov, Maria Korotkova and Yulia Suvorova	Pair change points of the triplet periodicity in genes
14:50-15:10	Pedro Miramontes	Nonlinear dynamics and genome analysis
15:10-15:30	Michael Sadovsky	Island periodicity in genomes
15:30-15:50	Vikram Singh	Universal spectral features of genomic DNA sequences
15:50-16:10	<i>COFFEE BREAK</i>	

16:10-16:50	Ivo Grosse	Dependencies within CTCF binding sites
16:50-17:10	Philipp Benner	Bayesian nonparametrics for motif estimation of transcription factor binding sites
17:10-17:30	Rudolf Hanel	Self-organized systemic interdependence of the makeup of genetic regulatory systems and variations of molecular decay rates
17:30-17:50	Marcin Zagorski	Emergence of motifs in model gene regulatory networks
17:50-18:10	Irina A. Roznovat	Modelling the genetic and epigenetic signals in colon cancer using a bayesian network
18:10-18:30	Sang Hoon Lee	The organization of human cancer-related protein complexes
18:30	<i>Closing by Organisers</i>	
POSTERS		
09:00-18:00	Hugo Hernandez-Saldaña	Analytical distribution for the short range distances in DNA sequences