LIGHT ON THE DARK SIDE OF THE GENOME

15-16 September 2016, Ugent – PAC Zuid (Woodrow Wilsonplein, 9000 Gent)

ABSTRACT

The human genome encodes the blueprint of life using only 2% of its nearly three billion bases to code for approximately 20,000 genes. The remaining portion is often referred to as "junk" DNA. Over the past decade, advances in genomic technologies and initiatives like the ENCODE and the Roadmap Epigenomics projects, revealed that these regions encrypt a regulatory code accommodating numerous key elements (e.g. enhancers, non-coding RNA,…) necessary to orchestrate the regulatory complexity of gene expression patterns. Moreover, progress has been made in mapping the interaction between these regulatory elements and genes resulting in locus-centric long-range interactions and the identification of large, megabase-sized genome-wide local chromatin interaction domains, termed topologically associated domains.

Together with the identification of new regulatory elements, an increasing number of studies emphasize the importance of non-coding variation in the etiology of both monogenic and complex genetic disorders including cancer. With the explosion of publicly available data and with the improved access to whole genome sequencing, the number of studies dealing with the non-coding portion of the genome in human genetics rapidly increase.

Overall, this two-day workshop will provide new insights into the organization and regulation of our genes and genome, and into the impact of variations or dysregulation of regulatory elements on human disease. Besides providing an overview of the dark matter of the genome, speakers will discuss state-of-the-art technologies and present case-studies of non-coding defects in monogenic and complex disease, and in cancer. Apart from invited lectures, participants will have the opportunity to give short oral presentations.

The workshop will end with a practical session demonstrating several bioinformatics tools, allowing the participants to implement the gained knowledge in their own research.

CONFIRMED INVITED SPEAKERS AND TOPICS:

- **Stein Aerts**, Leuven University, Belgium - *cis*-regulatory control of transcription
- **Axel Visel**, Lawrence Berkeley National Lab, USA – enhancers
- **Pieter Mestdagh**, Ghent University, Belgium – non-coding RNAs
- **Ramin Shiekhattar**, University of Miami, USA – enhancer RNAs
- **Wim Vanden Berghe**, University of Antwerp & Ghent University, Belgium - epigenetic plasticity of health & disease
- **Wouter Meuleman**, Broad Institute, USA – Roadmap Epigenomics
- **Josée Dostie**, McGill University, Canada – long-range interactions
- **Jesse Dixon**, Ludwig Institute for Cancer Research, USA – topologically associated domains
- **Malte Spielmann**, Max Planck Institute, Germany - disruptions of topological chromatin domains
- **Laura Lettice**, MRC Human Genetics Unit, UK - non-coding mutations in monogenic disease
- **Marc Mansour**, UCL Cancer Institute, UK – oncogenic super-enhancers
- **Carl Herrmann**, German Cancer Research Center (DKFZ), Heidelberg, Germany - cancer gene regulation
- **Morgane Thomas-Chollier**, IBENS, Paris, France, Regulatory Sequence Analysis Tools (RSAT)
- To be confirmed - non-coding variation in complex disease