Inception G5 candidates

Sara Ballouz
Sara Ballouz did her undergraduate studies at the University of New South Wales, receiving a Bachelor in Engineering (Bioinformatics) and a Bachelor of Science (Genetics) with Honors first class in 2008. Her honors project was on modeling the evolution and clustering of gene operons in bacteria. She continued her graduate studies under the supervision of Drs Merridee A Wouters and Bruno Gaeta at the University of New South Wales in conjunction with the Victor Chang Cardiac Research Institute, receiving her PhD in Bioinformatics in 2013. There she looked at uncovering the genetic basis of complex diseases using genome wide association studies data and implementing a disease candidate gene prediction system. She joined the Gillis lab as a post-doctoral fellow early in 2013, shifting her work slightly to gene function and the establishment of "gold standard" data sets for more context specific work. With a current focus on co-expression networks, she is hoping to be able to elucidate rules, pathways, interactions and complexes that help define function in a general way. Downstream application to diseases, with a particular focus on cognitive and X-linked disorders, will hopefully lead to the discovery of common rules and features that can be applied even more broadly to genotype-phenotype relationships.

Florence Cavalli
Dr Cavalli obtained her PhD from the EMBL-European Bioinformatics Institute and the University of Cambridge studying transcriptional regulation. During her postdoctoral research, in Dr Taylor's laboratory at the Hospital for Sick Children (Toronto), she uncovered the full molecular heterogeneity of the most common pediatric malignant brain tumor and described different degrees of intra-tumoral heterogeneity in Medulloblastoma. She then joined the SU2C Canadian Cancer Stem Cell dream team, as a bioinformatics project leader, focused on multi-faceted approaches to characterize and target brain tumour stem cells.

Rayan Chikhi
Rayan Chikhi is a bioinformatics researcher with a background in computer science, and interests ranging from theory to biological applications. He was a student and PhD student at ENS Cachan antenne de Bretagne, then a postdoc at Pennsylvania State University. He joined CNRS at Université of Lille as a junior researcher in 2014. His area of interest is DNA sequencing data analysis. He has previously worked on methods and tools related to reference-free analysis of genomes and metagenomes (e.g. Minia, KmerGenie, GATB tools). He collaborated with biological teams on the giraffe genome assembly, and the gorilla Y chromosome assembly. His current work focuses on methods applied to metagenomics, third-generation sequencing, and hypothesis-free variant detection. web page: http://rayan.chikhi.name

Marco Galardini
The high plasticity of bacterial genomes and its relationship with changes in phenotypes form the core of my past and future research. My main contribution to this area has come from my work on genotype-to-phenotype models in the Escherichia coli strain collection I have assembled during my post-doc. In particular I have demonstrated how it is possible to combine the predicted impact of genetic variants with extant knowledge in gene function to deliver conditional growth predictions across strains. Understanding the influence of the accessory genome and of the genetic background on phenotype is the logic continuation of my research.

Edoardo Pasolli
Dr. Edoardo Pasolli is a Marie Skłodowska-Curie Individual investigator in the Laboratory of Computational Metagenomics at University of Trento, Italy. With a training in machine learning,

his current research is focused on developing computational tools for the analysis of the human microbiome from shotgun metagenomic data.

Marc Vaudel
I currently work as a scientist at the KG Jebsen Center for Diabetes Research, Department of Clinical Science, University of Bergen, and at the Center for Medical Genetics and Molecular Medicine, Haukeland University Hospital, both in Bergen, Norway. My main research focus is the development of bioinformatics solutions for the integrative analysis of genomics and proteomics data to improve patient care. The outcome is (1) bioinformatics methods and tools that can be used in a wide variety of contexts, (2) improved understanding of the interplay between genetic architecture and disease mechanisms, and (3) novel approaches for patient stratification and therapy guidance.