The proposed research aligns closely with the mandate of the Institute of Genetics (IG). Our research will focus on the computational and statistical aspects of genome wide association studies, especially regarding the burden of multiple testing correction. We wish to evaluate and validate a methodology for correction which is gaining traction in the community, stratified FDR. Our findings in this study will have direct applications to GWAS studies and and other techniques which draw information from GWAS studies, such as polygenic risk scoring. In this way, our research will assess the performance of sFDR and develop guidelines for its use based on genomic information and dependencies. We will assess the mathematical and statistical validity of using this approach, and should it be altered, we will work together with the original developer to improve its use.

Should this research be funded, it will involve the simulation of human genomes and development of a bioinformatics pipeline for the permutative evaluation of multiple testing accuracy and reliability, both important questions in the field of genetics and statistical genetics.