

## DEVELOPMENT OF AN R-BASED GUI FOR VISUALISATION AND STATISTICAL ANALYSIS OF COMBINED KIR AND HLA GENETIC DATA IN HUMAN GALLBLADDER CANCERS

Natural killer (NK) cells are immune cells important in the defense against viruses and tumors. The function of these cells is regulated by their surface expression of inhibitory and activating receptors. One such family of receptors is the killer cell immunoglobulin-like receptor (KIR) family. KIRs represent a polymorphic and polygenic family of activating and inhibitory receptors that recognize distinct human leukocyte antigen (HLA) class I alleles. NK cells are the main KIR-expressing immune cells, and KIR expression on NK cells is variegated, seemingly to ensure broad specificity and capacity to sense the presence or absence of single HLA class I alleles. The genetic presence or absence of certain KIR receptors and their related HLA class I ligands have been extensively characterized in immunogenetic studies and multiple associations between KIRs, HLA, and human disease, including occurrence of several cancers, have been revealed.

We have over the last 10 years collected DNA-material from a unique cohort of 160 patients with gallbladder cancer (GBC). GBC is a severe cancer type with few treatment options and dismal prognosis. These individuals have been KIR and HLA-genotyped. Except for this novel cohort, we also have access to ten other cohorts of healthy or diseased humans, including more than 1000 individuals, where we have collected genetic data regarding the presence or absence of KIR and HLA genes of interest.

The primary aim of this Master thesis project is to compare KIR-HLA gene associations in GBC to healthy humans and explore if unique combinations of these genes are associated with development of GBC. A second aim is to develop a new comprehensive analysis tool for the broad scientific community. More specifically the tasks will be to generate original visualization tools and combined statistics using online scientific databases as prior knowledge, as well as designing an interactive graphical user interface (GUI) tool.

For this purpose, the applicant should have (i) good skills in coding and developing scripts in R including graphical customized items, (ii) good statistical knowledge including various multivariate analysis and prediction models, (iii) bioinformatics skills for online databases interactions.

### References:

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<http://www.allelefreqencies.net>  
<https://www.ebi.ac.uk/jpd/kir/>

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