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Easy-HLA : an online software suite to reveal the full details of HLA typing for genetic analyses.

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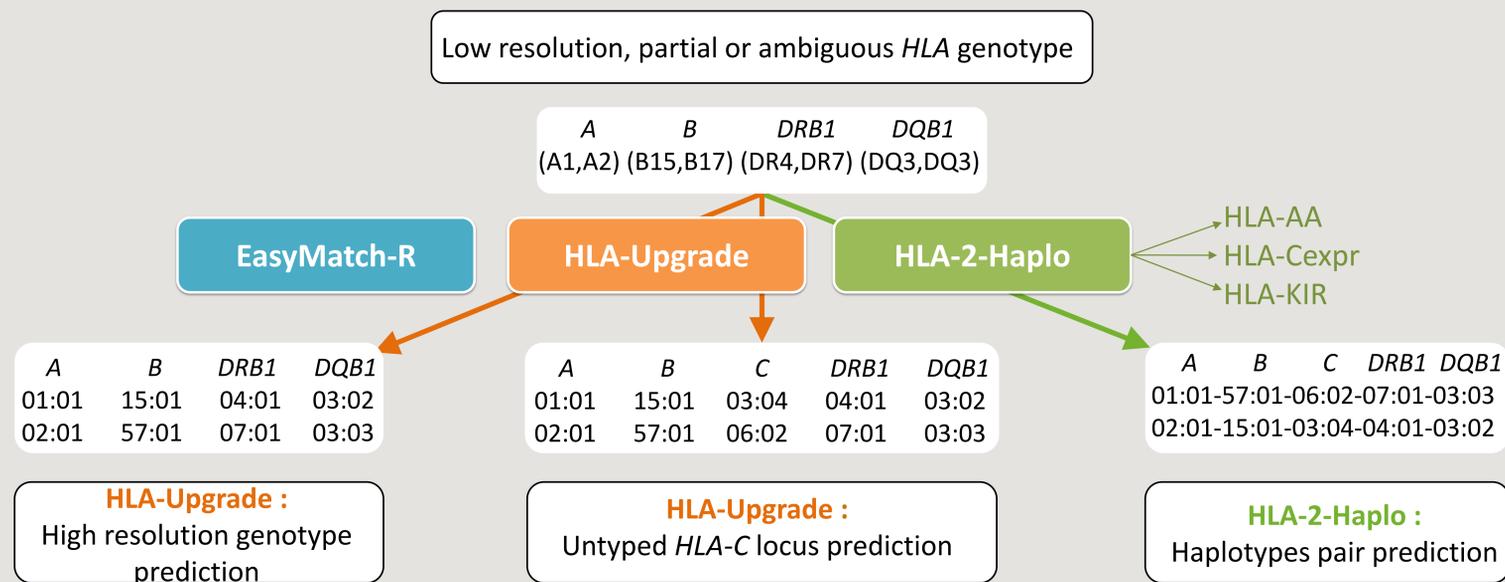
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Easy-HLA presentation

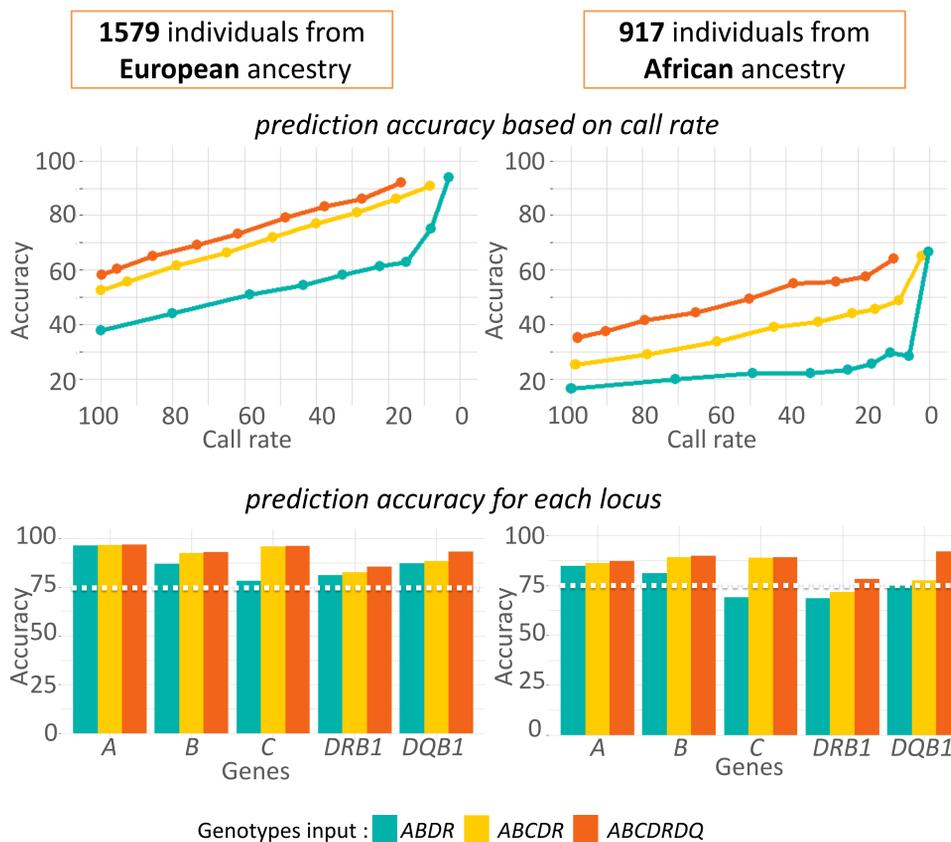
The HLA has a pivotal role between clinic and research. The determination of HLA alleles of an individual is required in transplantation. Moreover the HLA is described as associated with countless immune pathologies described by association studies. As the HLA system is the most polymorphic one, both nomenclature and methods constantly refined since the discovery of HLA antigens, leading to difficulties to use old archived typings. We developed a web application called Easy-HLA to facilitate the comprehension of HLA typing. Easy-HLA is based on validated and published HLA haplotypes frequencies. HLA haplotypes frequencies are used to solve typing ambiguities, predict HLA typing of loci (HLA-Upgrade) as well as haplotypes pairs (HLA-2-Haplo) or search for matched HSCT donors (EasyMatch-R). It provides new functional immunogenomics parameters: HLA-Cexpr imputes HLA-C expression, HLA-AA provides amino acid equivalence of HLA alleles and HLA-KIRlig gives KIR ligand classification of HLA alleles.



In this example, a given HLA serological typing ($HLA-A\sim B\sim DRB1\sim DQB1$) is processed by Easy-HLA. HLA-Upgrade statistically predicts high resolution typing by leveling-up the HLA genotype and also predict an untyped locus such as HLA-C. HLA-2-Haplo imputes the corresponding haplotypes pair.

HLA-Upgrade validation

- 2 datasets with high-resolution HLA typing downgraded to low resolution



HLA-Upgrade can predict successfully $HLA-A\sim B\sim C\sim DRB1\sim DQB1$ high resolution typing in different populations from low resolution/partially known HLA typing. The accuracy of the most probable prediction increases as the call rate is reduced. The prediction accuracy by locus is on average 10% above for European compared to African-American.

HLA-2-Haplo validation

- Prediction compared to familial determined haplotypes
- 273 individuals from European ancestry and 116 from African ancestry



HLA-2-Haplo imputes haplotypes pairs with high confidence: >70% of haplotypes pairs correctly predicted. There is no significant difference of prediction accuracy between population.

HLA-2-Haplo accuracy relies on the number of haplotypes in the database, it performs haplotyping one sample at a time regardless of the input sample size.

Easy-HLA conclusion

Our results validate the haplotypes efficiency in predicting high resolution HLA typing and determining haplotypes pairs. Our tools can be used in multiple conditions both in clinic and research to: update cohorts, help HSCT donor matching search, bring new parameters for association studies. Both HLA-Upgrade and HLA-2-Haplo show good performance in term of accuracy.

Easy-HLA is tuned to deliver updated HLA information from all HLA typing resolution. These predictions are all done in silico and as such do not require additional typing in the laboratory. Our software will continue improving as we will update our database with additional HLA haplotypes.