Typeloader2: Automated submission of full-length HLA, KIR and MIC alleles to IPD databases

Bianca Schöne[1], Markus Fuhrmann[1] , Vineeth Surendranath[1], Alexander H Schmidt[1,2], Vinzenz Lange[1], Gerhard Schöfl[1]

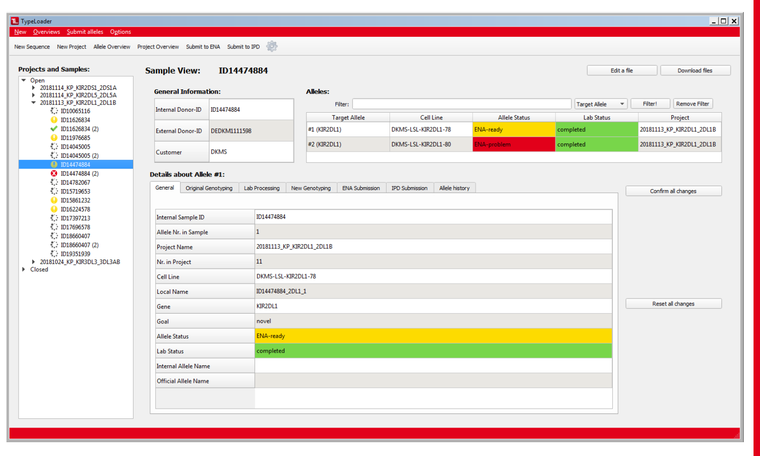
[1]DKMS Life Science Lab, St. Petersburger Str. 2, 01069 Dresden, Germany;

[2]DKMS, Kressbach 1, 72072 Tübingen, Germany

Introduction

The IPD databases provide global, curated repositories for allelic sequence information of genes of the immune system. In order to extend partially described alleles or to characterize and submit new alleles in full length, we developed Typeloader2, a standalone application for Windows and Linux PCs for the automated submission of HLA, KIR and MIC alleles to the IPD-IMGT/HLA and IPD-KIR databases. The intuitive GUI with its underlying SQLite database stores a wide range of metadata about each target allele and allows the user to survey the status of projects and target alleles easily in various specialized views.

Typeloader2 is ready to serve as a lab‘s central information platform for the annotation, curation and submission of full-length allele sequences.



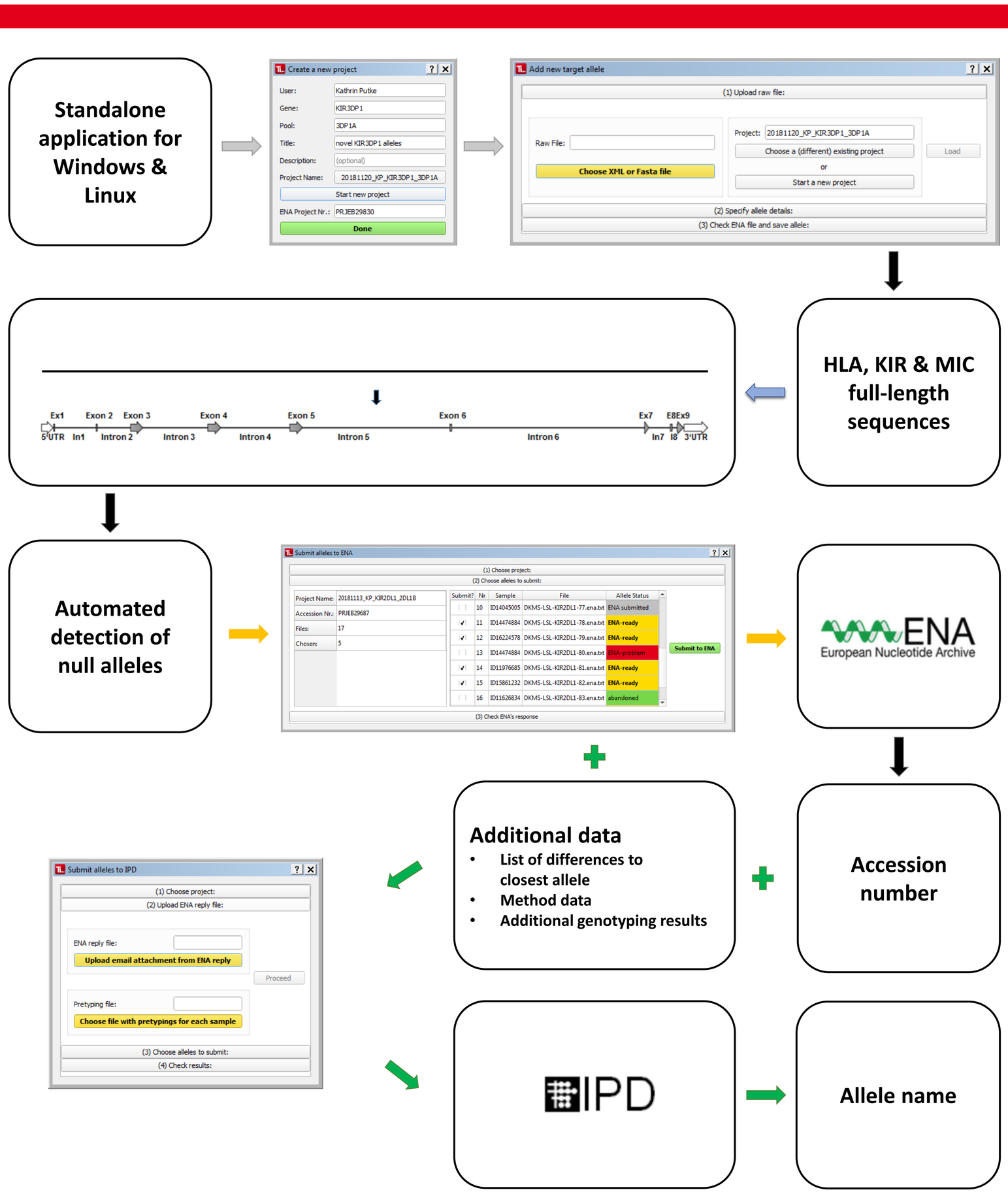
Workflow of Typeloader2

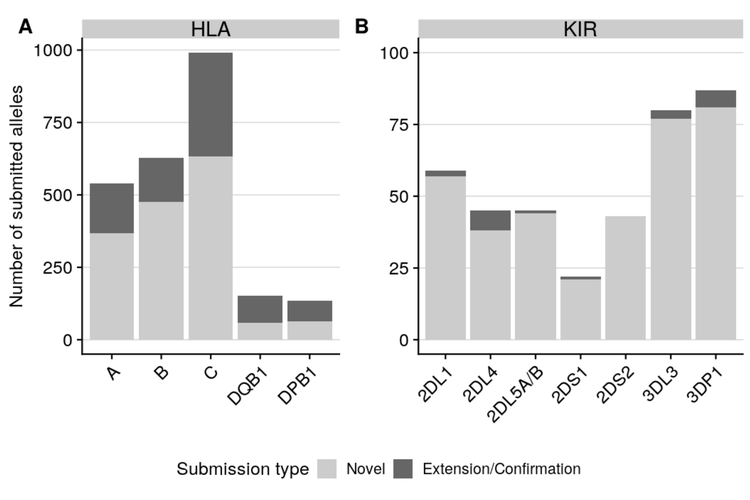
- Create a project structure
- Load HLA, KIR or MIC sequence files in FASTA or GenDx NGSengine XML format into project

- Typeloader2 searches for reference alleles in IPD-IMGT/HLA and IPD-KIR database and provides exon-intron boundaries of novel sequences
- Annotated sequences are formatted for submission to EMBL-ENA

- Automated detection of null alleles generated by premature stop codons or frameshift mutations
- Choose alleles to submit
- Submit ENA-ready files directly to EMBL-ENA server, see ENA server response immediately

- Receive EMBL-ENA accession number and assign to target allele
- Take accession number, annotated sequence data and additional metadata to submit samples to the appropriate IPD database
- IPD processes the submitted alleles and assigns allele names





Conclusion

Typeloader2 is the first tool which can handle full-length HLA, KIR and MIC sequences for automated allele submission. Through its GUI design, we implemented a highly comfortable way to maintain projects and work on a bulk of alleles simultaneously.

So far, we have successfully submitted 2,827 full-length alleles to IPD, including 381 KIR alleles. These numbers show Typeloader2‘s capability to handle large throughput with minimal user interaction. Enabled by this easy to use submission interface, we hope other laboratories will also submit their discovered novel MIC and KIR sequences to extend the IDP databases, so that the understanding of these gene systems can catch up to that of HLA in the near future.

DKMS Life Science Lab

GitHub *Download from GitHub:* *https://github.com/DKMS-LSL*

DKMS Life Science Lab

St. Petersburger Str. 2 • 01069 Dresden • www.dkms-lab.de

Get this poster:

Get in touch:
schoene@dkms-lab.de