

Graphical user interface for the haplotype frequency estimation software Hapl-o-Mat

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Motivation

Population-specific human leukocyte antigen (HLA) haplotype frequencies are the fundament of advanced search algorithms for donor selection in the field of unrelated hematopoietic stem cell transplantation. In 2017, we introduced Hapl-o-Mat, a versatile tool for haplotype frequency estimation based on an expectation-maximization (EM) algorithm.

To make Hapl-o-Mat accessible to a wider range of users, we complemented the command-line interface (CLI)-based software with a new, optional graphical user interface (GUI) that facilitates routine use and eases user interaction.

Hapl-o-Mat

- Tool for haplotype frequency estimation
- Applicable to
 - ✓ multi-allelic genes
 - ✓ arbitrary number of diploid loci
 - ✓ inhomogeneous and ambiguous typing data
 - ✓ complex HLA nomenclature
- C++ implementation
- Publicly available on GitHub

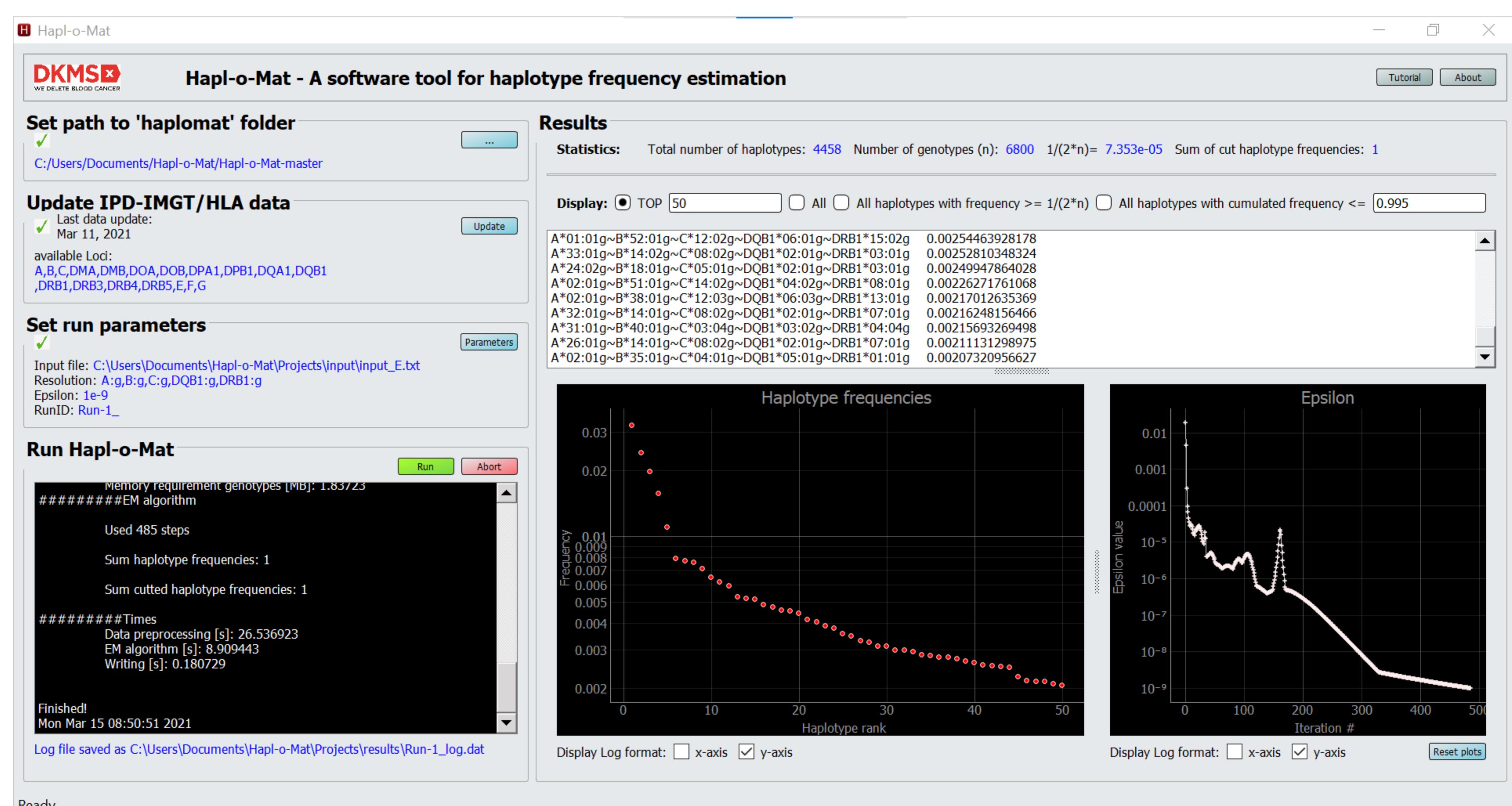
GUI features

Update IPD-IMGT/HLA data

- Easy update to the latest IPD-IMGT/HLA nomenclature
- Time of last update indicated
- Shows genes available for frequency estimation

Set run parameters

- Overview of active parameters
- Files for logs, parameters and results feature a common identifier (run-ID)
- Dialog for parameter settings concerning:
 - ✓ Run definition: considered loci, typing resolution, filter settings
 - ✓ EM algorithm settings: frequency initialization, convergence criterion, minimal genotype frequency
 - ✓ Paths to input and output files



Results

- Graphical display of the convergence criterion (Epsilon) during run time
- Display of haplotype frequency results as list and diagram
- Indication of major run statistics: Total number of haplotypes, number of genotypes, cumulated frequency sum
- ASCII result files from Hapl-o-Mat

Software implementation

- Coded in Python3 and PyQt5
- OS: Windows and Linux
- Open source code
- Windows binary version of Hapl-o-Mat including the GUI without dependency on other pre-installed software
- Publicly available on GitHub
- Independent GUI package enables parallel use of Hapl-o-Mat via CLI and GUI

Download

Source code

<https://github.com/DKMS/hapl-o-Mat>

GUI source code

https://github.com/DKMS/hapl-o-Mat_GUI

Windows binary version

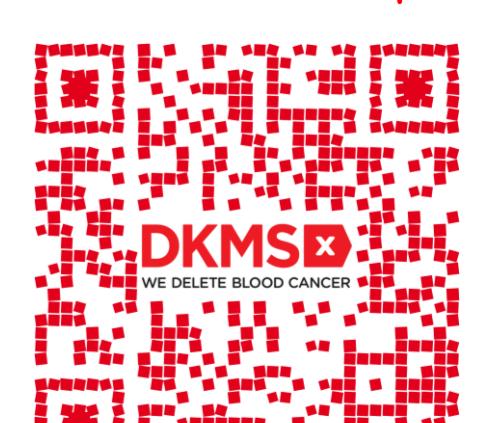
https://github.com/DKMS/hapl-o-Mat_WinBin

Reference: Schäfer C, Schmidt AH, Sauter J. Hapl-o-Mat: open-source software for HLA haplotype frequency estimation from ambiguous and heterogeneous data. BMC Bioinformatics. 2017 May 30;18(1):284.

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