

Hapl-o-Mat - Getting Started

Please also see the README.

Hapl-o-Mat

Hapl-o-Mat is software for HLA haplotype inference coded in C++. Besides estimating haplotype frequencies via an expectation-maximization algorithm, it is capable of processing HLA genotype population data. This includes translation of alleles between various typing resolutions and resolving allelic and genotypic ambiguities. Both common formats for recording HLA genotypes, multiple allele (NMDP) codes and genotype list strings, are supported.

This guide explains how to use Hapl-o-Mat under Linux. For more information refer to our publications on Hapl-o-Mat:

Journal article to come

C. Schaefer, A.H. Schmidt, J. Sauter: Hapl-O-mat: A Versatile Software for Haplotype Frequency Estimation. HLA (2016), 87, 236-320

Getting Started

This guide is an introduction on how to use Hapl-o-Mat. In order to follow this guide, you need a Linux system and a C++ compiler supporting C++11. In this tutorial, we use Ubuntu 14.04.4 LTS and GNU compiler collection (GCC) version 4.8.4. If you are a seasoned Linux-User, feel free to refer to the shorter version of this guide, [gettingStarted](#).

After successfully downloading Hapl-o-Mat, start a terminal and browse to the location where Hapl-o-Mat is stored. Enter the folder Hapl-o-Mat by typing “`cd Hapl-o-Mat`”. Check what is inside by typing “`ls`”. You should see the following:



```
cschaefer@tuesrhla03: ~/Hapl-o-Mat
File Edit View Terminal Help
cschaefer@tuesrhla03:~$ cd Hapl-o-Mat/
cschaefer@tuesrhla03:~/Hapl-o-Mat$ ls
ChangePreamble.py      examplePopulations  Makefile            parametersMA        README
COPYING                gettingStarted      parametersGL        parametersREAD     src
detailedGettingStarted.pdf include            parametersGLC       prepareData        systemTest
cschaefer@tuesrhla03:~/Hapl-o-Mat$
```

You see folders in blue ink and files in black ink. We give you some information on the files you find. Files which are important for using Hapl-o-Mat are marked as bold:

File name	Description
ChangePreamble.py	A python script to adapt the preamble in all files. You are not going to use it.
COPYING	The GNU General Public License.
detailedGettingStarted	This guide
examplePopulations	Some genotype population data we are going to work with in the section Tutorials.
gettingStarted	A shorter form of this tutorial
include	A part of Hapl-o-Mat's source code. If you do not want to change code, do not touch it
Makefile	Instructions for building Hapl-o-Mat. You might need to adapt it, if you use another compiler than GCC
parametersGL, parametersGLC, parametersMA, parametersMA	Parameter files for Hapl-O-mat. We are going to discuss this in section Parameters
prepareData	Here is everything to create the data required by Hapl-o-Mat
README	Read me
src	A part of Hapl-o-Mat's source code. If you do not want to change code, do not touch it
systemTest	Run the system test after changing code to check, if you broke something.

To estimate haplotype frequencies we only need to consider the folder prepareData and the files Makefile, parametersGL, parametersGLC, parametersMA, and parametersREAD. To finish this tutorial we need the folder examplePopulations, too.

Install Hapl-o-Mat

We compile Hapl-o-Mat with GCC using a Makefile. Just type "make" to create the executable "haplomat" and "make clean" to clean up. Type again "ls" to find a new file, haplomat (indicated in green in the figure below).

```
cschaefer@tuesrhla03: ~/Hapl-o-Mat
File Edit View Terminal Help
cschaefer@tuesrhla03:~$ cd Hapl-o-Mat/
cschaefer@tuesrhla03:~/Hapl-o-Mat$ ls
ChangePreamble.py      examplePopulations  Makefile            parametersMA        README
COPYING               gettingStarted      parametersGL         parametersREAD      src
detailedGettingStarted.pdf include             parametersGLC        prepareData         systemTest
cschaefer@tuesrhla03:~/Hapl-o-Mat$ make
g++ -Wall -march=native -Ofast -std=c++11 -Iinclude -c -o src/Allele.o src/Allele.cc
g++ -Wall -march=native -Ofast -std=c++11 -Iinclude -c -o src/DataProcessing.o src/DataProcessing.cc
g++ -Wall -march=native -Ofast -std=c++11 -Iinclude -c -o src/File.o src/File.cc
g++ -Wall -march=native -Ofast -std=c++11 -Iinclude -c -o src/Genotypes.o src/Genotypes.cc
g++ -Wall -march=native -Ofast -std=c++11 -Iinclude -c -o src/Glid.o src/Glid.cc
g++ -Wall -march=native -Ofast -std=c++11 -Iinclude -c -o src/Haplotype.o src/Haplotype.cc
g++ -Wall -march=native -Ofast -std=c++11 -Iinclude -c -o src/Locus.o src/Locus.cc
g++ -Wall -march=native -Ofast -std=c++11 -Iinclude -c -o src/Main.o src/Main.cc
g++ -Wall -march=native -Ofast -std=c++11 -Iinclude -c -o src/Parameters.o src/Parameters.cc
g++ -Wall -march=native -Ofast -std=c++11 -Iinclude -c -o src/Phenotype.o src/Phenotype.cc
g++ -Wall -march=native -Ofast -std=c++11 -Iinclude -c -o src/Report.o src/Report.cc
g++ -Wall -march=native -Ofast -std=c++11 -Iinclude -c -o src/Utility.o src/Utility.cc
g++ -Wall -march=native -Ofast -std=c++11 -Iinclude -o haplomat src/Allele.o src/DataProcessing.o sr
c/File.o src/Genotypes.o src/Glid.o src/Haplotype.o src/Locus.o src/Main.o src/Parameters.o src/
Phenotype.o src/Report.o src/Utility.o
cschaefer@tuesrhla03:~/Hapl-o-Mat$ make clean
rm -f -f src/*.o *.d
cschaefer@tuesrhla03:~/Hapl-o-Mat$ ls
ChangePreamble.py      examplePopulations  include             parametersGLC        prepareData  systemTest
COPYING               gettingStarted      Makefile            parametersMA         README
detailedGettingStarted.pdf haplomat            parametersGL         parametersREAD      src
cschaefer@tuesrhla03:~/Hapl-o-Mat$
```

Data Preparation

Hapl-o-Mat relies on information on the HLA nomenclature. This information is provided by data files, which we are going to create. As the HLA nomenclature evolves over time, e.g. by finding new alleles or adding new NMDP codes, it is important to update data from time to time. Hapl-o-Mat relies on the following files, which must be placed in the folder “Hapl-o-Mat/data” (we create the folder “data” later):

File name	Description
AllAllelesExpanded.txt	A list of relevant existing HLA alleles with their enclosed more-digit typing resolutions
AlleleList.txt	If your input data in GL format includes a missing single-locus genotype, it can be replaced by combining all alleles of the same locus from this file
Ambiguity.txt	Data basis for the ambiguity filter
LargeG.txt	A list of G-groups with their enclosed alleles in 8-digit resolution
MultipleAlleleCodes.txt	A list of multiple allele codes and their translation to alleles
P.txt	A list of P-groups with their enclosed alleles in 8-digit resolution
Smallg.txt	A list of g-groups with their enclosed alleles in 8-digit resolution

In the following we are going to create these data files.

Download Data

Go to the folder “prepareData” by typing “cd prepareData” and check its content by typing “ls”.

Allele Code List in Alphabetical Order

https://bioinformatics.bethematchclinical.org/hla-resources/allele-codes/allele-code-lists/allele-code-list-in-alphabetical-order/

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Allele Codes

Allele Code Nomenclature

Allele Code Lists

Allele Code List in Numerical Order

Allele Code List in Alphabetical Order

Non-Common and Well Documented Alleles

Allele Code Mailing List

HLA Resources > Allele Codes > Allele Code Lists > Allele Code List in Alphabetical Order

Allele Code List in Alphabetical Order

Example:
AA 01/02/03/05
AB 01/02
AC 01/03

The allele code list in alphabetical order is provided in a variety of formats:

HTML Format (.html)

This format is recommended if you simply want to view the allele code list online.

- [Alphabetical Allele Code List \(HTML\) \(new nomenclature\)](#)
Note: New window will open.
- [Alphabetical Allele Code List \(HTML\) \(old nomenclature\)](#)
Note: New window will open.

Text Format (.txt)

Download a zip compressed file. Once extracted, the text file will be called "alpha.txt."

- [Alphabetical Allele Code List \(ZIP\) \(new nomenclature\)](#)
Note: Extraction requires a data compression program such as WinZip.
- [Alphabetical Allele Code List \(ZIP\) \(old nomenclature\)](#)
Note: Extraction requires a data compression program such as WinZip.

The self-extracting executable file has been removed as of 10/21/03. The allele code lists will no longer be available for download in this format. Please mail new-allelecodes@nmdp.org with any questions or concerns regarding this change.

Enter the folder "Input data" and type "unzip alpha.v3.txt" to extract the archive. You can remove the archive "alpha.v3.zip" afterwards.

```
cschaefer@tuesrhla03: ~/InputData
File Edit View Terminal Help
cschaefer@tuesrhla03:~/InputData$ ls
alpha.v3.zip hla_nom.g.txt hla_nom.p.txt
cschaefer@tuesrhla03:~/InputData$ unzip alpha.v3.zip
Archive:  alpha.v3.zip
  inflating: alpha.v3.txt
cschaefer@tuesrhla03:~/InputData$ ls
alpha.v3.txt alpha.v3.zip hla_nom.g.txt hla_nom.p.txt
cschaefer@tuesrhla03:~/InputData$ rm alpha.v3.zip
cschaefer@tuesrhla03:~/InputData$ ls
alpha.v3.txt hla_nom.g.txt hla_nom.p.txt
cschaefer@tuesrhla03:~/InputData$
```

- Go to the website <https://www.ebi.ac.uk/ipd/imgt/hla/ambig.html>. Click on "Download Excel" for the wanted release (usually the latest) and save ambiguity_v<>.xls (replace <> by version).

Ambiguous allele combination

← → ↻ <https://www.ebi.ac.uk/ipd/imgt/hla/ambig.html>

<https://www.surveymonkey.co.uk/r/F5GHVGF>

Ambiguous Allele Combinations Search Tool (Beta)

This search tool provides an alternative method of viewing the ambiguous combinations currently detailed in the downloads.

STEP 1 - Enter the allele you wish to search for

Query allele:

STEP 2 - Search

[Search Now](#)

Download Ambiguous Allele Combinations files

The IPD-IMGT/HLA Ambiguous Allele Combinations files are available in XML and Microsoft Excel formats for the current release. The PDF versions of the files are no longer being made available from this website because the number of combinations increases rapidly with the release of novel alleles. For this reason, we would encourage our users to use the XML and Microsoft Excel formats where possible. Please note that Microsoft Office 2010 or later is required to view the files.

Older releases are also available in PDF format, as well as XML and Microsoft Excel.

Release	Date	PDF File	Excel File	XML File
3.24.0	2016-04-15	-	Pending	View XML
3.23.0	2016-01-19	-	Download Excel	View XML
3.22.0	2015-10-10	-	Download Excel	View XML
3.21.0	2015-07-06	-	Download Excel	View XML
3.20.0	2015-04-19	-	Download Excel	View XML
3.19.0	2015-01-19	-	Download Excel	View XML
3.18.0	2014-10-10	-	Download Excel	View XML
3.17.0.1	2014-08-21	-	Download Excel	View XML
3.17.0	2014-07-17	-	Download Excel	View XML
3.16.0	2014-04-14	-	Download Excel	View XML

Next we extract the information from the Excel sheet. Open ambiguity_v<>.xls in Excel and save as ambiguity_v<>.xslm to run macros.

ambiguity_v3230.xls [Kompatibilitätsmodus] - Microsoft Excel

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[Öffnen](#)
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Informationen zu ambiguity_v3230

\\tuesma02\users\cschaefer\Desktop\InputData\ambiguity_v3230.xls

Kompatibilitätsmodus
Einige neue Features sind deaktiviert, um Probleme beim Arbeiten mit früheren Versionen von Office zu verhindern. Die Konvertierung dieser Datei aktiviert diese Features, kann jedoch zu Layoutänderungen führen.

Berechtigungen
Jeder kann diese Arbeitsmappe öffnen und beliebige Teile kopieren und ändern.

Für die Freigabe vorbereiten
Bevor Sie diese Datei freigeben, machen Sie sich bewusst, dass sie Folgendes enthält:

- Dokumenteigenschaften und Name des Autors
- Ausgeblendete Zellen
- Inhalte, die aufgrund des aktuellen Dateityps nicht auf Probleme bei der Barrierefreiheit geprüft werden können

Versionen
Es sind keine früheren Versionen dieser Datei vorhanden.

Eigenschaften

Größe 29,1MB
 Titel Titel hinzufügen
 Kategorien Tag hinzufügen
 Kategorien Kategorie hinzufügen

Verwandte Datumsangaben

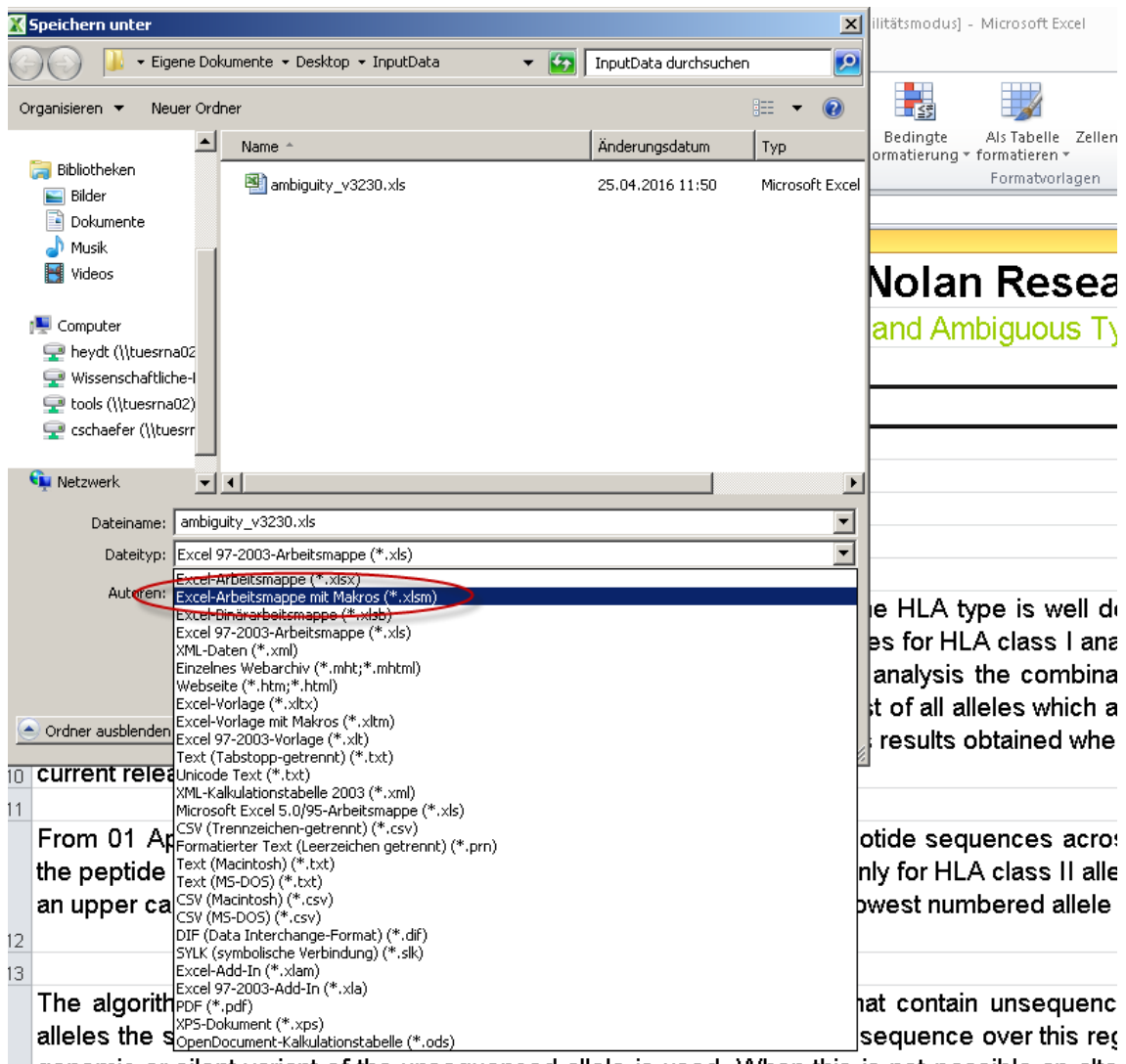
Letzte Änderung 19.01.2016 14:40
 Erstellt 18.01.2016 12:36
 Zuletzt gedruckt Nie

Verwandte Personen

Autor James Robinson
 Autor hinzufügen
 Zuletzt geändert von Anup Raushan Soormally

Verwandte Dokumente

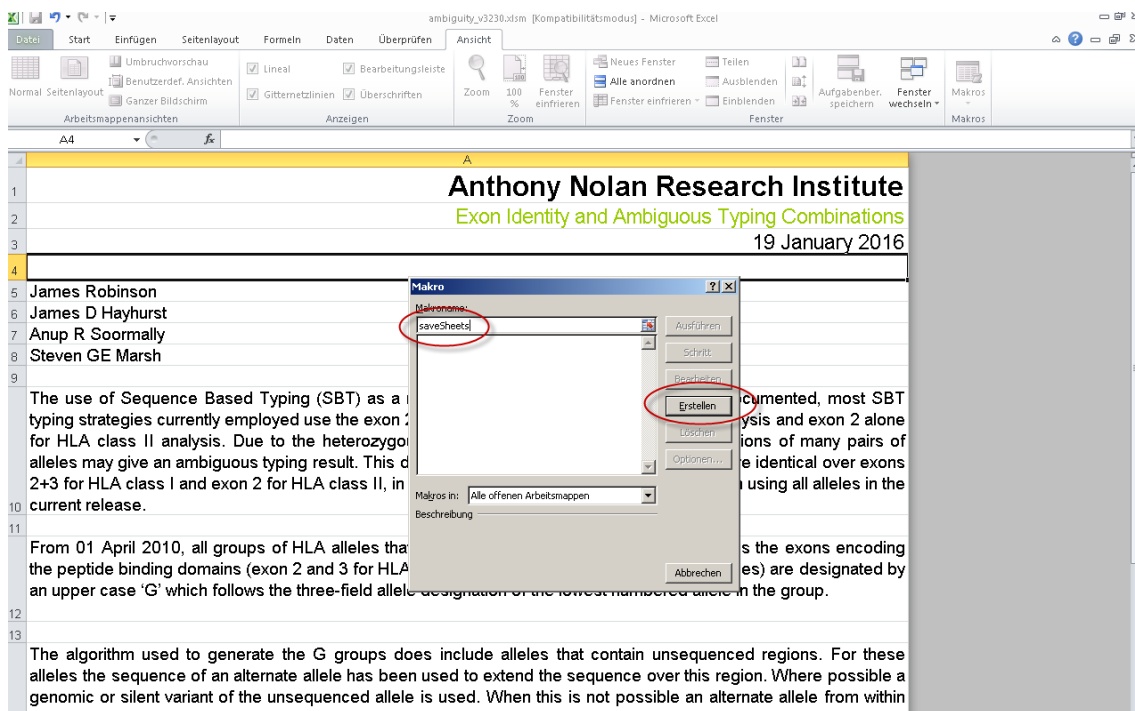
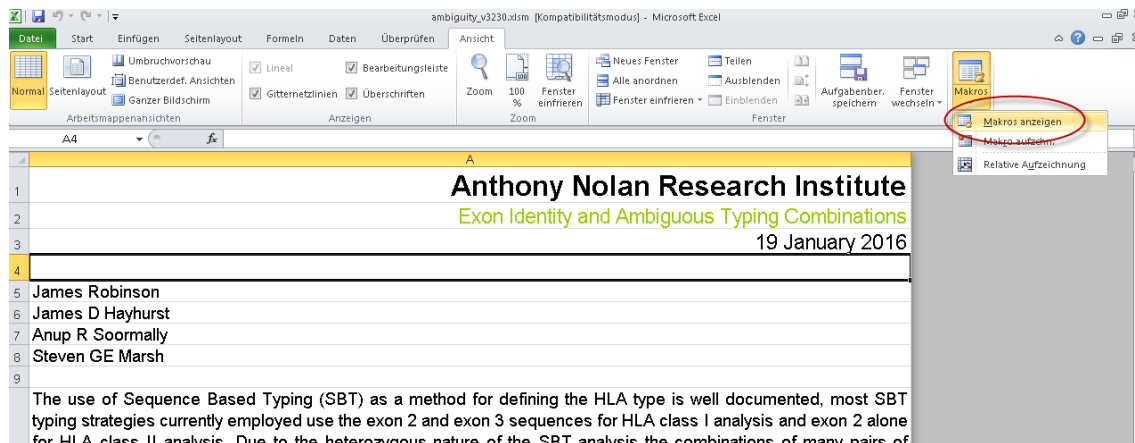
☐ Dateispeicherort öffnen
[Alle Eigenschaften anzeigen](#)

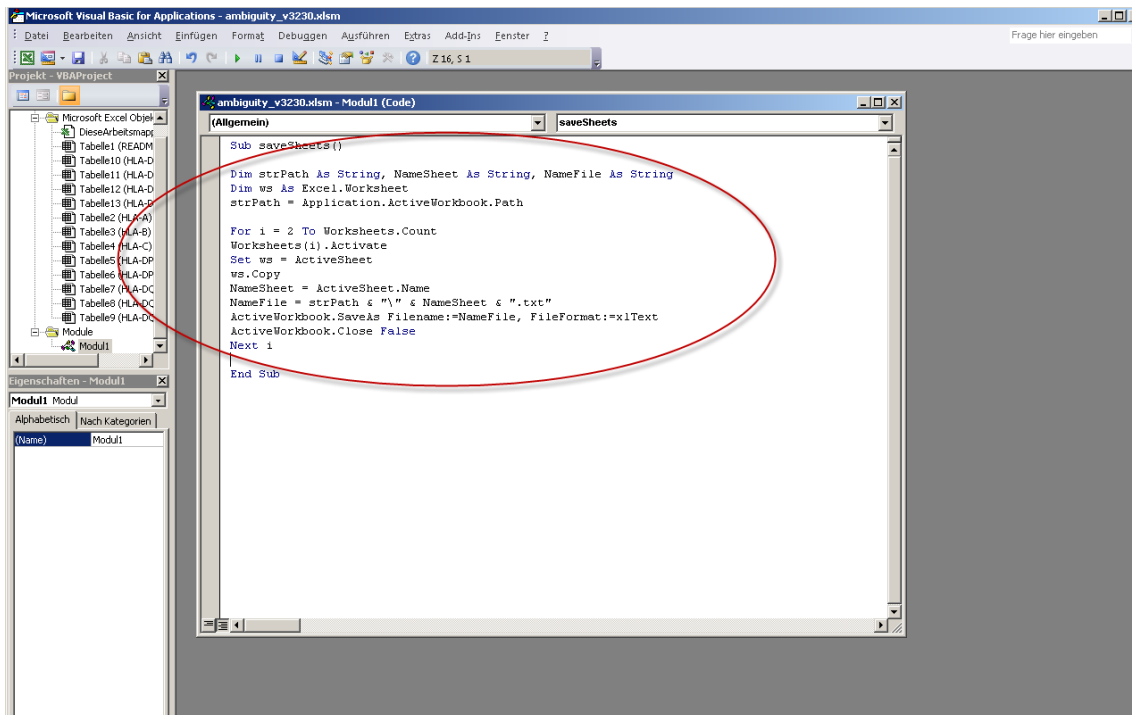


Now insert the following macro, which saves relevant information from the Excelsheets as text files:

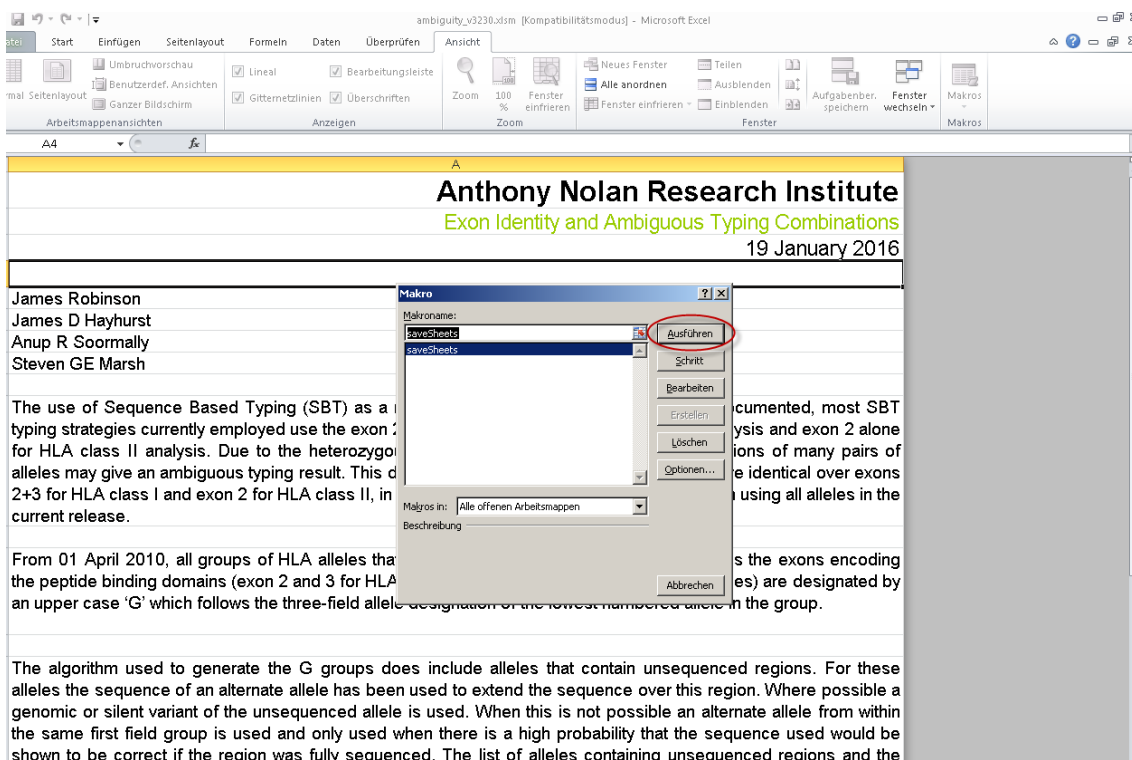
```
Sub saveSheets()
    Dim strPath As String, NameSheet As String, NameFile As String
    Dim ws As Excel.Worksheet
    strPath = Application.ActiveWorkbook.Path

    For i = 2 To Worksheets.Count
        Worksheets(i).Activate
        Set ws = ActiveSheet
        ws.Copy
        NameSheet = ActiveSheet.name
        NameFile = strPath & "\" & NameSheet & ".txt"
        ActiveWorkbook.SaveAs Filename:=NameFile, FileFormat:=xlText
        ActiveWorkbook.Close False
    Next i
End Sub
```





Close the window and execute the macro:



Some new text files should have appeared in your folder „inputData“. Afterwards you can remove the Excel file.

Build Data for Hapl-o-Mat

Enter the folder InputData via “cd InputData” and copy all files via “cp * ../prepareData” to the folder “prepareData”. Then enter folder “prepareData” via “cd ../prepareData” and check what is there via typing “ls”. Next, create the data required for Hapl-o-Mat by running the bash script via “bash

BuildData.sh". It automatically calls the python scripts and moves the created files to the folder "data". Check for the created files by going one folder back typing "cd .." and typing "ls data".

```

cschaefer@tuesrhla03: ~/Hapl-o-Mat
File Edit View Terminal Help
cschaefer@tuesrhla03:~/Hapl-o-Mat$ cd InputData/
cschaefer@tuesrhla03:~/Hapl-o-Mat/InputData$ cp * ../prepareData/
cschaefer@tuesrhla03:~/Hapl-o-Mat/InputData$ cd ../prepareData/
cschaefer@tuesrhla03:~/Hapl-o-Mat/prepareData$ ls
AddAllelesMissingIngCode.py      BuildAmbiguity.py      HLA-C.txt              HLA-DRB3.txt
AddAllelesMissingIngCode.py~     BuildData.sh           HLA-DPA1.txt           HLA-DRB4.txt
AddGToAmbiguity.py              BuildLargeG.py         HLA-DPB1.txt           HLA-DRB5.txt
alpha.v3.txt                    BuildP.py              HLA-DQA1.txt           hla_nom_g.txt
BuildAllAllelesExpanded.py       BuildSmallg.py         HLA-DQA.txt            hla_nom_p.txt
BuildAllAllelesFrom_hla_nom_g.py HLA-A.txt              HLA-DQB1.txt           README
BuildAlleleList.py              HLA-B.txt              HLA-DRB1.txt           TransferAlphaToMultipleAlleleCodes.py
cschaefer@tuesrhla03:~/Hapl-o-Mat/prepareData$ bash BuildData.sh
cschaefer@tuesrhla03:~/Hapl-o-Mat/prepareData$ cd ..
cschaefer@tuesrhla03:~/Hapl-o-Mat$ ls data/
AllAllelesExpanded.txt  Ambiguity.txt  LargeG.txt  MultipleAlleleCodes.txt  P.txt  Smallg.txt
cschaefer@tuesrhla03:~/Hapl-o-Mat$

```

Input Genotype Data

Hapl-o-Mat infers haplotypes from population genotype data. It supports different formats of recording genotype data. To use Hapl-o-Mat your data should be in one of the following data formats:

Data format	Description
MA	Ambiguities are encoded by multiple allele (MA) codes. Except for the first line, input files hold an individual's identification number and genotype per line. Genotypes are saved allele by allele without locus name. Identification number and alleles are TAB-separated. The first line of the file is a header file indicating the name of the first column and the loci of the other columns. Same loci must be placed next to each other. For an example refer to "examplePopulations/populationData_a.dat".
GLC	Genotypes with or without ambiguities are saved by genotype list strings. Input files hold an individual's identification number and genotype per line. Identification number and single-locus genotypes are TAB-separated. For an example refer to "examplePopulations/populationData_b.dat"
GL	Genotypes with or without ambiguities are saved by genotype list (GL) strings. Population data is saved in two files. The pull-file contains an individual's identification number and a list of integer numbers, GL-ids, referring to its single-locus genotype. The GL-ids are separated from the identification number via ";" and from each other via ":". The second file, the glid-file, contains a translation from GL-ids starting with "1" to actual single-locus genotypes. GL-id and genotype are separated via ";". A GL-id of "0" is interpreted as a missing typing at the corresponding locus and does not require a translation in the glid-file. For an example refer to

	"examplePopulations/populationData_c.pull" and "examplePopulations/populationData_c.glid".
READ	Ambiguities are completely resolved and alleles are already translated to the wanted typing resolutions. The input data is of the format as Hapl-o-Mat records processed genotype data. This allows for easily repeating a run without the need to resolve genotype data again.

Parameters

Each input format for genotype data requires a different set of parameters. The parameters are saved in the corresponding files "parametersMA", "parametersGLC", "parametersGL", and "parametersREAD". All input formats have the following parameters in common:

Parameter	Description
FILENAME_HAPLOTYPES	Name of the file which temporarily saves haplotype names
FILENAME_GENOTYPES	Name of the file which saves resolved genotypes.
FILENAME_HAPLOTYPEFREQUENCIES	Name of the file which saves haplotypes and estimated haplotype frequencies.
FILENAME_EPSILON_LOGL	Name of the file which saves stopping criterion and log-likelihood per iteration.
INITIALIZATION_HAPLOTYPEFREQUENCIES	Initialization routine for haplotype frequencies. It takes the following values: <ul style="list-style-type: none"> • "equal": All haplotype frequencies are initialized with the same frequency • "numberOccurrence": Haplotype frequencies are initialized according to the initial number of occurrence of the haplotype • "random": Haplotype frequencies are initialized randomly • "perturbation": Haplotype frequencies are initialized as in numberOccurrence and then randomly modified by a small (<10%) positive or negative offset
EPSILON	Value for the stopping criterion, i.e. the maximal change between consecutive haplotype frequency estimations is smaller than the assigned value.
CUT_HAPLOTYPEFREQUENCIES	Estimated haplotype frequencies smaller than this value are removed from the output
RENORMALIZE_HAPLOTYPEFREQUENCIES	Takes values "true" and "false". If "true", normalize estimated haplotype frequencies to sum to one. Within machine precision, this becomes necessary, if estimated haplotypes are removed, e.g. via the option CUT_HAPLOTYPEFREQUENCIES
SEED	Set the seed of the used pseudo random number generator. If set to "0", the seed is initialized by the system time.

Depending on the input format (indicated in brackets), additional parameters are:

Parameter	Input format	Description
FILENAME_INPUT	MA, GLC, READ	The file name of the input population data
FILENAME_PULL	GL	The file name of the pull-file
FILENAME_GLID	GL	The file name of the glid-file
LOCI_AND_RESOLUTIONS	MA, GL, GLC	Loci included into analysis and desired typing resolution per locus. The list is separated by "," and contains the locus name followed by ":" and the desired typing resolution, e.g. A:g,B:4d,C:g. Supported typing resolutions and their abbreviations are g-groups (g), P-groups (P), G-groups (G), 2-digit fields (2d), 4-digit fields (4d), 6-digit fields (6d), and 8-digit fields (8d). Alleles are not translated via the option asItIs (applying the ambiguity filter includes an intrinsic translation to G-groups)
LOCIORDER	GL	Specify the order of loci the individual's GL-ids correspond to. Loci are separated via ",".
RESOLVE_MISSING_GENOTYPES	GL	Takes values "true" and "false". If set to true, a missing typing is replaced by a combination of all alleles from AlleleList.txt at the locus. Else, individuals with a missing typing are discarded from analysis
MINIMAL_FREQUENCY_GENOTYPES	MA, GL, GLC	Genotypes which split into more genotypes than the inverse of this number are discarded from analysis
DO_AMBIGUITYFILTER	MA, GL, GLC	Takes values "true" and "false". The option "true" activates the ambiguity filter
EXPAND_LINES_AMBIGUITYFILTER	MA, GL, GLC	Takes values "true" and "false". If set to "true", matching lines with additional genotype pairs in the ambiguity filter are considered

Whenever specifying a file name including folders, you have to create the folders before running Hapl-o-Mat.

Tutorials

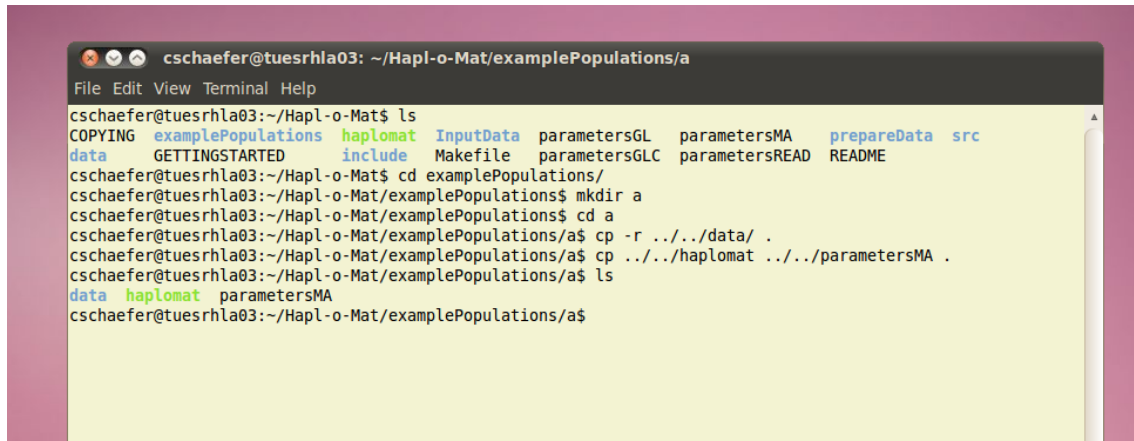
We have everything ready to use Hapl-o-Mat. In the following we estimate haplotype frequencies from some included genotype data recorded in different input formats.

Input Format MA

You find the relevant population data in "examplePopulations/populationData_a.dat". As ambiguities are recorded as multiple allele codes, the input format is MA. We are going to infer three locus (A, B, DRB1) haplotypes from this data. Alleles at loci A and B shall be translated to typing resolution g and alleles at locus DRB1 to 4-digits typing resolution.

Preparations

Enter the folder “examplePopulations” by typing “cd examplePopulations”, create a folder named “a” by typing “mkdir a”, and enter the folder by typing “cd a”. Then provide the data required by Hapl-o-Mat by copying the folder data to “a”, “cp -r ../../data .”. Additionally, copy the executable “haplomat” and the file “parametersMA” to folder “a”, “cp ../../haplomat ../../parametersMA .”. Check that everything is there by typing “ls”.

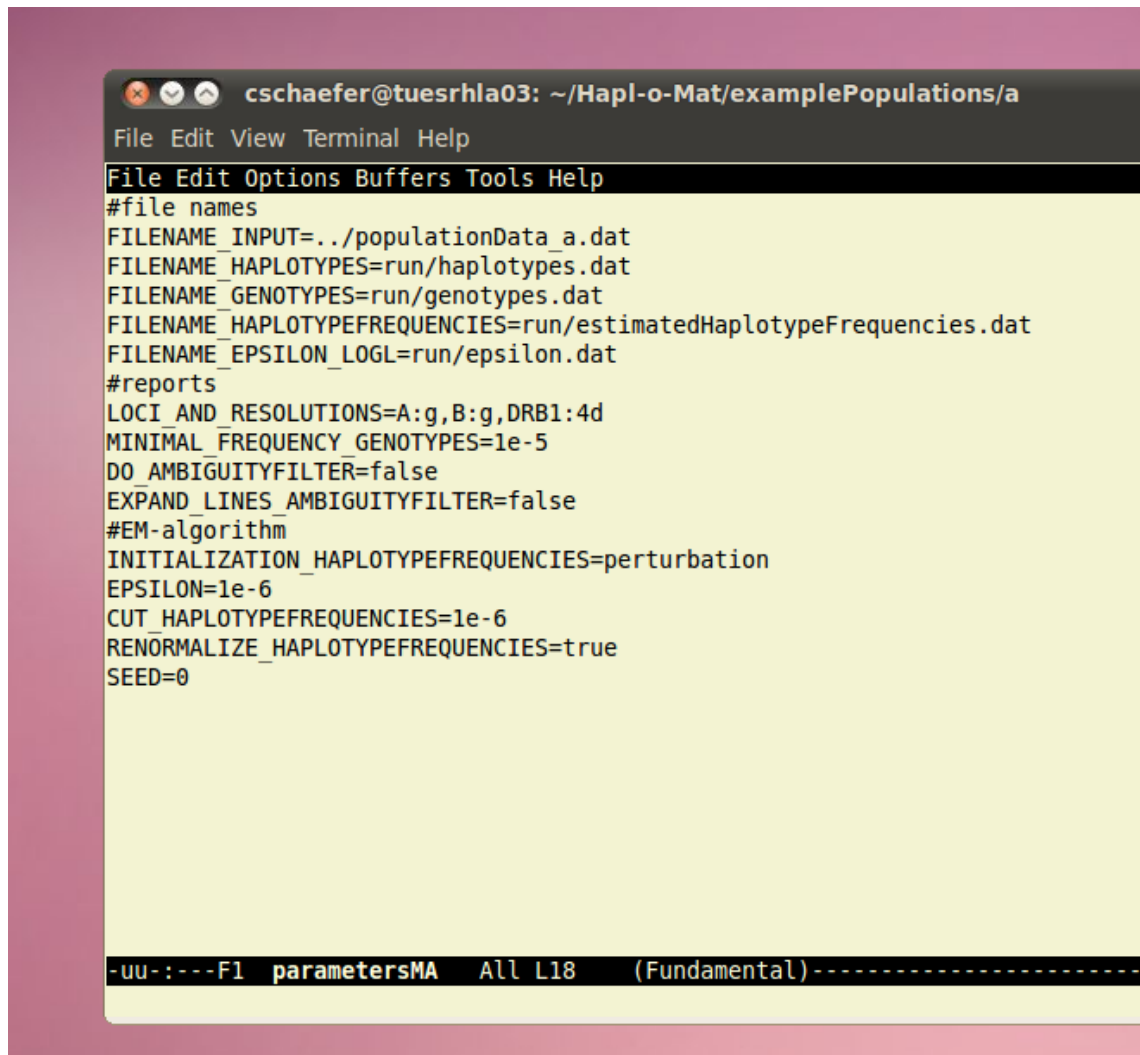


```
cschaefer@tuesrhla03: ~/Hapl-o-Mat/examplePopulations/a
File Edit View Terminal Help
cschaefer@tuesrhla03:~/Hapl-o-Mat$ ls
COPYING  examplePopulations  haplomat  InputData  parametersGL  parametersMA  prepareData  src
data     GETTINGSTARTED      include   Makefile   parametersGLC  parametersREAD  README
cschaefer@tuesrhla03:~/Hapl-o-Mat$ cd examplePopulations/
cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations$ mkdir a
cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations$ cd a
cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations/a$ cp -r ../../data/ .
cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations/a$ cp ../../haplomat ../../parametersMA .
cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations/a$ ls
data  haplomat  parametersMA
cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations/a$
```

Parameters

According to the format of the input genotype data we use the parameter file “parametersMA”. Open it in a text editor of your choice and set the following values:

```
#file names
FILENAME_INPUT=../populationData_a.dat
FILENAME_HAPLOTYPES=run/haplotypes.dat
FILENAME_GENOTYPES=run/genotypes.dat
FILENAME_HAPLOTYPEFREQUENCIES=run/hfs.dat
FILENAME_EPSILON_LOGL=run/epsilon.dat
#reports
LOCI_AND_RESOLUTIONS=A:g,B:g,DRB1:4d
MINIMAL_FREQUENCY_GENOTYPES=1e-5
DO_AMBIGUITYFILTER=false
EXPAND_LINES_AMBIGUITYFILTER=false
#EM-algorithm
INITIALIZATION_HAPLOTYPEFREQUENCIES=perturbation
EPSILON=1e-6
CUT_HAPLOTYPEFREQUENCIES=1e-6
RENORMALIZE_HAPLOTYPEFREQUENCIES=true
SEED=1000
```

A screenshot of a terminal window with a dark title bar and a light yellow background. The title bar shows the user 'cschaefer@tuesrhla03' and the directory '~/Hapl-o-Mat/examplePopulations/a'. The terminal displays the contents of a configuration file with various parameters for Hapl-o-Mat, including file names, reports, and algorithm settings. At the bottom, a status bar shows '-uu-:---F1 parametersMA All L18 (Fundamental)-----'.

```
cschaefer@tuesrhla03: ~/Hapl-o-Mat/examplePopulations/a
File Edit View Terminal Help
File Edit Options Buffers Tools Help
#file names
FILENAME_INPUT=./populationData_a.dat
FILENAME_HAPLOTYPES=run/haplotypes.dat
FILENAME_GENOTYPES=run/genotypes.dat
FILENAME_HAPLOTYPEFREQUENCIES=run/estimatedHaplotypeFrequencies.dat
FILENAME_EPSILON_LOGL=run/epsilon.dat
#reports
LOCI_AND_RESOLUTIONS=A:g,B:g,DRB1:4d
MINIMAL_FREQUENCY_GENOTYPES=1e-5
DO_AMBIGUITYFILTER=false
EXPAND_LINES_AMBIGUITYFILTER=false
#EM-algorithm
INITIALIZATION_HAPLOTYPEFREQUENCIES=perturbation
EPSILON=1e-6
CUT_HAPLOTYPEFREQUENCIES=1e-6
RENORMALIZE_HAPLOTYPEFREQUENCIES=true
SEED=0

-uu-:---F1 parametersMA All L18 (Fundamental)-----
```

Do not forget to create the folder “run” by typing “mkdir run”.

Run Hapl-o-Mat

Compute haplotype frequencies from the genotype input data by running Hapl-o-Mat. If you are not already there, go to folder “a” and run Hapl-o-Mat via

```
./haplomat MA
```

It produces some output on the screen including your chosen parameters, statistics on the resolved genotype data and the expectation-maximization algorithm, and the run time. You can easily write this output to an extra file by starting Hapl-o-Mat with

```
./haplomat MA > Log.dat
```

```

cschaefer@tuesrhla03: ~/Hapl-o-Mat/examplePopulations/a
File Edit View Terminal Help
cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations/a$ ls
data haplomat parametersMA parametersMA~
cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations/a$ mkdir run
cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations/a$ ./haplomat MA

Hapl-o-Mat
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#####Initialization
MA format
#####Parameters I/O
Input: ../populationData a.dat
Output haplotypes: run/haplotypes.dat
Output genotypes: run/genotypes.dat
Output estimated haplotype frequencies: run/estimatedHaplotypeFrequencies.dat
Output epsilon and log(L): run/epsilon.dat
#####Parameters resolving genotypes
Minimal frequency of genotypes: 1e-05
Loci with target allele resolutions:
A : g
B : g
DRB1 : 4d
Apply ambiguity filter: no
#####Parameters EM algorithm
Haplotype frequency initialization: perturbation
Epsilon: 1e-06
Cut haplotype frequencies: 1e-06
Renormalize haplotype frequencies
Zero: 1e-14

```

Results

Now let's examine the results produced by Hapl-o-Mat. We first look into the file with the resolved genotypes, "run/genotypes.dat".

```

cschaefer@tuesrhla03: ~/Hapl-o-Mat/examplePopulations/a
File Edit View Terminal Help
File Edit Options Buffers Tools Help
1 NNN 1 A*26:04+A*29:67^B*07:218+B*54:16^DRB1*11:182+DRB1*13:14
2 III 0.098765432098765 A*02:570+A*24:02g^B*13:07N+B*14:01^DRB1*12:01+DRB1*14:23
2 III 0.012345679012346 A*02:570+A*24:50^B*13:07N+B*14:01^DRB1*12:01+DRB1*14:23
2 III 0.098765432098765 A*02:570+A*24:02g^B*13:07N+B*14:14^DRB1*12:01+DRB1*14:23
2 III 0.012345679012346 A*02:570+A*24:50^B*13:07N+B*14:14^DRB1*12:01+DRB1*14:23
2 III 0.098765432098765 A*02:570+A*24:02g^B*13:07N+B*14:19^DRB1*12:01+DRB1*14:23
2 III 0.012345679012346 A*02:570+A*24:50^B*13:07N+B*14:19^DRB1*12:01+DRB1*14:23
2 III 0.098765432098765 A*02:570+A*24:02g^B*13:07N+B*14:01^DRB1*12:06+DRB1*14:23
2 III 0.012345679012346 A*02:570+A*24:50^B*13:07N+B*14:01^DRB1*12:06+DRB1*14:23
2 III 0.098765432098765 A*02:570+A*24:02g^B*13:07N+B*14:14^DRB1*12:06+DRB1*14:23
2 III 0.012345679012346 A*02:570+A*24:50^B*13:07N+B*14:14^DRB1*12:06+DRB1*14:23
2 III 0.098765432098765 A*02:570+A*24:02g^B*13:07N+B*14:19^DRB1*12:06+DRB1*14:23
2 III 0.012345679012346 A*02:570+A*24:50^B*13:07N+B*14:19^DRB1*12:06+DRB1*14:23
2 III 0.098765432098765 A*02:570+A*24:02g^B*13:07N+B*14:01^DRB1*12:10+DRB1*14:23
2 III 0.012345679012346 A*02:570+A*24:50^B*13:07N+B*14:01^DRB1*12:10+DRB1*14:23
2 III 0.098765432098765 A*02:570+A*24:02g^B*13:07N+B*14:14^DRB1*12:10+DRB1*14:23
2 III 0.098765432098765 A*02:570+A*24:02g^B*13:07N+B*14:19^DRB1*12:10+DRB1*14:23
2 III 0.012345679012346 A*02:570+A*24:50^B*13:07N+B*14:19^DRB1*12:10+DRB1*14:23
3 NNN 1 A*02:570+A*29:67^B*13:07N+B*35:54^DRB1*13:121+DRB1*14:23
4 NIN 0.333333333333333 A*02:77+A*66:10^B*14:01+B*15:154^DRB1*16:30+DRB1*16:30
4 NIN 0.333333333333333 A*02:77+A*66:10^B*14:14+B*15:154^DRB1*16:30+DRB1*16:30
4 NIN 0.333333333333333 A*02:77+A*66:10^B*14:19+B*15:154^DRB1*16:30+DRB1*16:30
5 NNN 1 A*03:217+A*29:36^B*15:01g+B*35:54^DRB1*11:95+DRB1*14:23
6 NNN 1 A*02:454+A*03:93^B*15:316+B*35:54^DRB1*04:52+DRB1*08:18
7 NNN 1 A*24:02g+A*30:13^B*18:19+B*39:27^DRB1*13:116+DRB1*14:23
--uu:---F1 genotypes.dat Top L1 (Fundamental)-----
For information about GNU Emacs and the GNU system, type C-h C-a.

```

The first column corresponds to the individual's identification number. The second column indicates how ambiguities per single-locus genotypes have been resolved. If no ambiguity occurred or no additional genotypes are formed, the type is N. If an ambiguity occurred and was resolved via building all possible allele combinations, the type is I. Activating the ambiguity filter gives additional types: A, if one matching line in the ambiguity file was found, and M if multiple matching lines were

found. The third column gives the frequency of the genotype and the fourth column the genotype itself. The genotype is saved in the GL format. If an individual's genotype splits into a set of genotypes, each genotype is written to one line starting with the same identification number. The corresponding frequencies become non-integer and sum to one.

The evolution of the stopping criterion and log-likelihood while iterating expectation and maximization steps is written to "run/epsilon.dat". The first column is the stopping criterion and the second one the not normalized log-likelihood.

```

cschaefer@tuesrhla03: ~/Hapl-o-Mat/examplePopulations/a
File Edit View Terminal Help
File Edit Options Buffers Tools Help
1.65047053136533e-02 -8.45323844078806e+02
6.73697608887705e-03 -7.98275484097206e+02
2.48854943275664e-03 -7.93699085510797e+02
2.83776634798794e-04 -7.93419184742460e+02
6.14023927099406e-04 -7.93131275957098e+02
1.15924990646807e-03 -7.92320740770168e+02
1.14108919896940e-03 -7.91065507474409e+02
1.20046020216511e-03 -7.89697944953104e+02
1.08446159199447e-03 -7.88278106693153e+02
1.13270509109496e-03 -7.87196632003306e+02
8.83993295265539e-04 -7.86688434128350e+02
2.46787483501847e-04 -7.86579300896777e+02
2.78024575360233e-05 -7.86573568427811e+02
2.51291424789510e-05 -7.86573303976139e+02
2.28460671790852e-05 -7.86573089939133e+02
2.08784871108154e-05 -7.86572904974493e+02
1.91690622885106e-05 -7.86572743885267e+02
1.76731517783704e-05 -7.86572602607060e+02
1.63555412094479e-05 -7.86572477920655e+02
1.51881219918049e-05 -7.86572367247058e+02
1.41482165502537e-05 -7.86572268498743e+02
1.32173505523608e-05 -7.86572179970059e+02
1.23803400403719e-05 -7.86572100255358e+02
1.16246037398324e-05 -7.86572028187064e+02
1.09396388762832e-05 -7.86571962788290e+02
1.03166172280358e-05 -7.86571903236191e+02
-uu-:---F1 epsilon.dat Top L1 (Fundamental)-----
For information about GNU Emacs and the GNU system, type C-h C-a.

```

The inferred haplotypes including estimated frequencies are listed in "run/hfs.dat". Haplotypes are saved in the GL format. This is the file you were aiming at. It is sorted by descending frequency and already normalized if you activated the corresponding option (we did in this tutorial).


```

cschaefer@tuesrhla03: ~/Hapl-o-Mat/examplePopulations/a
File Edit View Terminal Help
File Edit Options Buffers Tools Help
A*29:25-B*15:101-DRB1*16:30 0.0600000000000000
A*11:01g-B*40:01g-DRB1*07:56 0.0400000000000000
A*24:02g-B*15:27-DRB1*14:85 0.0300000000000000
A*68:70-B*37:19-DRB1*13:52 0.0300000000000000
A*11:01g-B*15:316-DRB1*11:182 0.0300000000000000
A*30:13-B*18:12-DRB1*11:147 0.0250000000000000
A*32:33-B*54:16-DRB1*11:182 0.0250000000000000
A*03:02g-B*35:32-DRB1*09:02 0.0250000000000000
A*30:73N-B*14:08-DRB1*14:01 0.02013379227088
A*26:04-B*54:16-DRB1*11:182 0.0200000000000000
A*03:217-B*35:51-DRB1*14:85 0.0200000000000000
A*03:93-B*35:54-DRB1*04:52 0.0200000000000000
A*02:454-B*15:316-DRB1*08:18 0.0200000000000000
A*03:217-B*15:01g-DRB1*11:95 0.0200000000000000
A*02:570-B*13:07N-DRB1*14:23 0.0200000000000000
A*66:10-B*15:154-DRB1*16:30 0.0150000000000000
A*68:70-B*35:32-DRB1*13:66 0.0150000000000000
A*03:217-B*52:49N-DRB1*08:30 0.0150000000000000
A*32:73-B*51:114-DRB1*07:56 0.0150000000000000
A*29:67-B*35:54-DRB1*13:121 0.0150000000000000
A*03:239-B*27:98-DRB1*03:103 0.0150000000000000
A*02:258-B*42:14-DRB1*13:121 0.0150000000000000
A*68:94N-B*39:27-DRB1*03:103 0.0150000000000000
A*66:10-B*51:01g-DRB1*04:52 0.0150000000000000
A*02:163-B*37:28-DRB1*16:30 0.0150000000000000
A*23:06-B*08:145-DRB1*16:30 0.0150000000000000
-UU-:---F1 estimatedHaplotypeFrequencies.dat Top L1 (Fundamental)-----
For information about GNU Emacs and the GNU system, type C-h C-a.

```

Input Format GLC

This time ambiguities in the genotypic population data are recorded via genotype list strings. The file with the population data is called "populationData_b.glc". As all the information is in one file, the input format is GLC. Running Hapl-o-Mat works exactly as in the first tutorial. You just use the parameter file "parametersGLC" instead of "parametersMA" and make the appropriate changes. Run Hapl-o-Mat in folder "b" with

./haplomat GLC

```

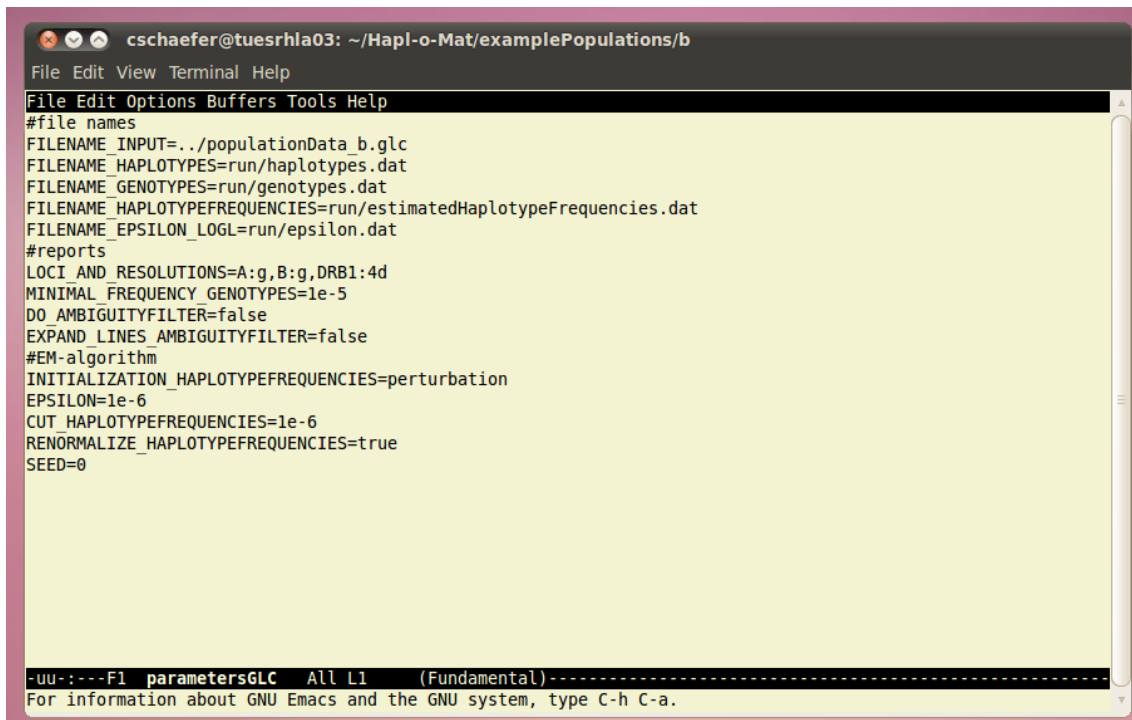
cschaefer@tuesrhla03: ~/Hapl-o-Mat/examplePopulations/b
File Edit View Terminal Help

cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations$ ls
a populationData a.dat populationData b.glc populationData c.glid populationData c.pull
cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations$ mkdir b
cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations$ cd b/
cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations/b$ cp -r ../data/ ../haplomat ../parametersGLC
.
cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations/b$ ls
data haplomat parametersGLC
cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations/b$ e parametersGLC
cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations/b$ mkdir run
cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations/b$ ./haplomat GLC

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#####Initialization
GLC format
#####Parameters I/O
Input: ../populationData b.glc
Output haplotypes: run/haplotypes.dat
Output genotypes: run/genotypes.dat
Output estimated haplotype frequencies: run/estimatedHaplotypeFrequencies.dat
Output epsilon and log(L): run/epsilon.dat
#####Parameters resolving genotypes
Minimal frequency of genotypes: 1e-05
Loci with target allele resolutions:
A : g

```



```
cschaefer@tuesrhla03: ~/Hapl-o-Mat/examplePopulations/b
File Edit View Terminal Help
File Edit Options Buffers Tools Help
#file names
FILENAME_INPUT=../populationData_b.glc
FILENAME_HAPLOTYPES=run/haplotypes.dat
FILENAME_GENOTYPES=run/genotypes.dat
FILENAME_HAPLOTYPEFREQUENCIES=run/estimatedHaplotypeFrequencies.dat
FILENAME_EPSILON_LOGL=run/epsilon.dat
#reports
LOCI_AND_RESOLUTIONS=A:g,B:g,DRB1:4d
MINIMAL_FREQUENCY_GENOTYPES=1e-5
DO_AMBIGUITYFILTER=false
EXPAND_LINES_AMBIGUITYFILTER=false
#EM-algorithm
INITIALIZATION_HAPLOTYPEFREQUENCIES=perturbation
EPSILON=1e-6
CUT_HAPLOTYPEFREQUENCIES=1e-6
RENORMALIZE_HAPLOTYPEFREQUENCIES=true
SEED=0

-uu:---F1 parametersGLC All L1 (Fundamental)-----
For information about GNU Emacs and the GNU system, type C-h C-a.
```

Input Format GL

Again, ambiguities in the genotypic population data are recorded via genotype list strings. Since the data is saved in two different files, the input format is GL. Follow the steps from tutorial a), but use the parameter file "parametersGL". The file names for the population data are "populationData_c.pull" and "populationData_c.glid". I guess, you can figure out the matching positions in the parameter file. GL input format requires the order of loci as input, which can be obtained by looking in the pull- and glid-file. The first individual from "populationData_c.pull" has GL-ids 1, 2, 3, 4, 5, and 6. We know from "populationData_c.pull" that they correspond to loci B, A, DPB1, DRB1, C, and DQB1, respectively. Because of that we set `LOCIORDER=B,A,DPB1,DRB1,C,DQB1`. Finally, set the additional option `RESOLVE_MISSING_GENOTYPE` to "false". Run Hapl-o-Mat in folder "c" with

```
./haplomat GL
```

```
cschaefer@tuesrhla03: ~/Hapl-o-Mat/examplePopulations/c
File Edit View Terminal Help

cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations$ mkdir c
cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations$ cd c/
cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations/c$ cp -r ../../data/ ../../haplomat ../../parametersGL
.
cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations/c$ e parametersGL
cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations/c$ mkdir run
cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations/c$ ./haplomat GL

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#####Initialization
GL format
#####Parameters I/O
Input pull file: ../populationData_c.pull
Input GL-id file: ../populationData_c.glid
Output haplotypes: run/haplotypes.dat
Output genotypes: run/genotypes.dat
Output estimated haplotype frequencies: run/estimatedHaplotypeFrequencies.dat
Output epsilon and log(L): run/epsilon.dat
#####Parameters resolving genotypes
Minimal frequency of genotypes: 1e-05
Loci with target allele resolutions:
A : g
B : g
DRB1 : 4d
Resolve missing genotypes: no
```

```
cschaefer@tuesrhla03: ~/Hapl-o-Mat/examplePopulations/c
File Edit View Terminal Help
File Edit Options Buffers Tools Help
#file names
FILENAME_PULL=../populationData_c.pull
FILENAME_GLID=../populationData_c.glid
FILENAME_HAPLOTYPES=run/haplotypes.dat
FILENAME_GENOTYPES=run/genotypes.dat
FILENAME_HAPLOTYEPFREQUENCIES=run/estimatedHaplotypeFrequencies.dat
FILENAME_EPSILON_LOGL=run/epsilon.dat
#reports
LOCIORDER=B,A,DPB1,DRB1,C,DQB1
LOCI_AND_RESOLUTIONS=A:g,B:g,DRB1:4d
MINIMAL_FREQUENCY_GENOTYPES=1e-5
DO_AMBIGUITYFILTER=false
EXPAND_LINES_AMBIGUITYFILTER=false
RESOLVE_MISSING_GENOTYPES=false
#EM-algorithm
INITIALIZATION_HAPLOTYEPFREQUENCIES=perturbation
EPSILON=1e-6
CUT_HAPLOTYEPFREQUENCIES=1e-6
RENORMALIZE_HAPLOTYEPFREQUENCIES=true
SEED=0

-uu-:--F1 parametersGL All L1 (Fundamental)-----
For information about GNU Emacs and the GNU system, type C-h C-a.
```

Input Format READ

Finally, we test the input format READ. Create a folder "d" and copy one file with resolved genotypes, say "a/run/genotypes.dat" there. Add "haplomat" and "parametersREAD" to this folder. Using the input format READ, Hapl-o-Mat does not resolve ambiguities or translates alleles, but reads in already resolved genotype data. Because of that the folder "data" is not required and the parameter file "parameterREADS" misses some options. Just adjust the file names and set parameters for the haplotype frequency estimation. Run Hapl-o-Mat in folder "d" via

```
./haplomat READ
```

```
cschaefer@tuesrhla03: ~/Hapl-o-Mat/examplePopulations/d
File Edit View Terminal Help
cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations$ ls
a b c populationData a.dat populationData_b.glc populationData_c.glid populationData_c.pull
cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations$ mkdir d
cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations$ cd d/
cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations/d$ cp ../a/run/genotypes.dat .
cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations/d$ cp ../../haplomat ../../parametersREAD .
cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations/d$ e parametersREAD
cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations/d$ mkdir run
cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations/d$ ls
genotypes.dat haplomat parametersREAD parametersREAD~ run
cschaefer@tuesrhla03:~/Hapl-o-Mat/examplePopulations/d$ ./haplomat READ

Hapl-o-Mat
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#####Initialization
Readin format
#####Parameters I/O
Input: genotypes.dat
Output haplotypes: run/haplotypes.dat
Output estimated haplotype frequencies: run/estimatedHaplotypeFrequencies.dat
Output epsilon and log(L): run/epsilon.dat
#####Parameters EM algorithm
Haplotype frequency initialization: perturbation
Epsilon: 1e-06
Cut haplotype frequencies: 1e-06
Renormalize haplotype frequencies
Zero: 1e-14
Seed: 1461593514120206388
```

```
cschaefer@tuesrhla03: ~/Hapl-o-Mat/examplePopulations/d
File Edit View Terminal Help
File Edit Options Buffers Tools Help
#file names
FILENAME_INPUT=genotypes.dat
FILENAME_HAPLOTYPES=run/haplotypes.dat
FILENAME_HAPLOTTYPEFREQUENCIES=run/estimatedHaplotypeFrequencies.dat
FILENAME_EPSILON_LOGL=run/epsilon.dat
#EM-algorithm
INITIALIZATION_HAPLOTTYPEFREQUENCIES=perturbation
EPSILON=1e-6
CUT_HAPLOTTYPEFREQUENCIES=1e-6
RENORMALIZE_HAPLOTTYPEFREQUENCIES=true
SEED=0

-uu-:---F1 parametersREAD All L1 (Fundamental)-----
For information about GNU Emacs and the GNU system, type C-h C-a.
```

Quick Guide

The following overview gives you a small reminder on how to use Hapl-o-Mat:

- 1) Build the executable “haplomat” via make.
- 2) Update the data comprising information on the HLA nomenclature following the instructions under Data Preparation or in the file “prepareData/README”.
- 3) Prepare the genotype population data you want to study. Identify how genotyping ambiguities are recorded (NMDP codes or GL strings) and choose the input format

accordingly. Adapt the format of your data, e.g. include the header line or make alleles TAB separated.

- 4) Set the parameters in the parameter file corresponding to your input format.
- 5) Copy the executable “haplomat”, the folder “data”, the parameter file, and your input population data into one folder. Create any folders you specified in the parameter file. You do not need all the other files to run Hapl-o-Mat. Run Hapl-o-Mat.