



Geppetto – Population Synthesis Software



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Geppetto is a population synthesis tool. It offers numerous features such as creating populations from different ancestral origins, creating admixed individuals, and finally also a pedigree creation feature. Compatible with the HapMap genome data format, as well as capable of handling its own, simpler format, this tool can prove useful in meeting research needs that deal with populations, pedigrees and mapping by admixture linkage disequilibrium (MALD).

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Geppetto Overview

Geppetto is population synthesis software. It can “create” genomes of individuals, according to genotype data provided by the user – it creates the genomes by assigning an allele to each marker in the genotype data. The genotype data input defines probabilities for each allele in each marker, and Geppetto assigns the alleles according to the alleles’ probabilities.

Population Creation

There are several methods of population creation. Geppetto supports 6 population creation scenarios, which are detailed in [Population Creation Scenarios](#) section.

In Geppetto, there are essentially 3 ways of creating a population: The first is non-admixed population creation, where each person genome from the population is created straight from the genotype data. The second is admixed population creation – each person is a result of different types of populations (or ancestries) that their mating (or mixing) over time yielded genomes of mixed ancestries. Geppetto simulates that scenario – it creates the genomes of the founders (people that their genomes are originated in one population) and actually mates them, while considering recombination points, to produce mixed genomes. The third population creation way is done through creating an entire pedigree – given a pedigree, Geppetto creates all the genomes of the pedigree’s individuals, while taking into account all the relations between them.

Geppetto also has the ability to create individuals within the created population who possess a certain trait, or sickness, that is described by the user (a [disease model](#)).

Project Aims

Geppetto Aims are to provide an extensible tool, which can create diverse populations in different scenarios, with sick and healthy individuals to a certain genetic sickness. That can be of many uses:

- Help research of a genetic disease: through inspection of the created individual’s genomes, one can assess whether a disease is linked to a certain population, or a certain marker within diverse population, etc.
- Test labeling programs (AncestryMap Software n.d.): simulating the labeling software on created populations to verify their correctness.
- Help to design a genetic panel microarray experiments: By testing the selected genetic panel (a group of alleles which is supposed to be used in microarray gene hunting) on synthesized populations first, one can save a lot of time and money, before issuing the final panel.

General Information

Geppetto is written in Java. Due to the size of the genotype data, the size of the output (each person’s genome is a collection of text files), and different population scenarios, Geppetto uses large amounts of CPU time and memory, uses the hard drive, and its execution time may vary

between few seconds to several minutes (depending on the type of population creation and the genotype data). In order to keep track of Geppetto execution, you can see the console logs throughout the execution (Tip: use the [trace](#) verbosity level).

The admixed population creation scenarios, which define sick people to create are most prone to lengthy execution times – Geppetto tries to create a sick person, and then according to the disease model, determines if indeed the created person is sick. If the person is not sick, Geppetto tries again, and that can result in long execution time. Therefore, the execution time is dependent on the disease model and the complexity of the created population (when admixed population creation methods are the most complex).

Geppetto is highly configurable – the user can define an extensive [disease model](#), define the [rate of genetic recombination](#) in the pedigree, define number of [sick and healthy people](#) to produce, define the number of generation of admixture that the created population underwent (see the admixed population creation scenarios for more info: [HI](#), [CGF](#) and [Straight Admixed](#)), and more.

Authors and Contacts

Geppetto was written by Amit Zur and Daniel Anvar, as an undergraduate project in the department of bioinformatics, Technion, Israel, under the guidance of Prof. Dan Geiger and Sivan Bercovici.

Run the Geppetto program

The Geppetto program must be executed with an input file. The input file defines all the parameters for the program execution, and you can find its structure and some examples in this section.

Executing Geppetto

From a console line, run “Java Geppetto <input file path>” with your input file (which complies with the Geppetto input file format).

Tip: to run Java with more memory, use the flag “-mx1000m” for virtualizing 1000 mega of Java heap memory.

There are 6 population creation methods (or scenarios): [Plain](#), [Stratification](#), [Create from Pedigree](#), [Hybrid Isolated](#), [Continuous Gene Flow](#), and [Straight Admixed](#). See explanations about each population creation scenario in the [Population Creation Scenarios](#) section.

Geppetto Input File Format

The input file is a simple text file. Each of the parameters is defined with a “#” sign following by the parameter name, and after a “=” sign the parameter value:

```
#<parameter name> = <parameter value>
```

The parameters are case-insensitive.

All the lines in the input file which don’t correspond to a valid parameter name are ignored.

Input File Parameters List

The following table lists all the parameters that can be defined in the Geppetto input file. Some parameters are common to all population creation scenarios, and are marked as **bold** (they are also explained in detail in the Common Geppetto [Parameters](#) section).

Name	Description
#Creation Method	The population creation scenario method
#Genotype	Genotype data
#Output Folder	Path of the program output folder
#Seed	Seed of the program’s random operations
#ChrLoadersBinaries	Path of the chromosome binaries folder
#Recombination Rate	Recombination Rate function
#Disease Model File	Disease Model file path

#pedigree file	Pedigree PedFile path
#healthy people	Number of healthy people to produce
#sick people	Number of sick people to produce
#generations	Number of generations of created population admixture
#number of populations	Number of populations (ancestries) involved in the created population
#populations fractions	Fractions of the ancestry population in the created population
#Lambda	Lambda parameter (simulates number of generations in the created admixed populations)
#Trace	Trace verbosity flag
#Use Garbage Collection	Call Java's Garbage Collector flag

Geppetto Parameters

The Geppetto program operates according to user input parameters, which are defined in the [Geppetto Input File](#).

There are common input parameters, shared by all the population creation scenarios, and there are some parameters which are used under different scenarios. You can find extensive information about input parameters of each scenario under each population creation scenario section.

Common Input Parameters

All population creation scenarios of the Geppetto program share some common input parameters, some are required and some are optional.

The following table lists the list of common program parameters.

Chromosome Loaders	<p>The chromosome loaders hold the genotype data which the program will create the population's genomes by.</p> <p>They hold information about the markers that represents the genome. The program will create, according to the population creation scenario and in a randomly fashion, populations' genomes by assigning values to each marker.</p> <p>See more information about the different types of loaders, how to use them in the program and more in the Chromosome Loaders section.</p>
Seed (optional)	<p>The program's random operations seed. The program uses random objects to create the population in a pseudo-randomly fashion. The seed specified is the source for all the pseudo-random actions that the program takes. Meaning, every time the program runs with the same seed it produces equal results.</p> <p>If this parameter is not set, the seed will be randomly created and will be reported to the user, so a reproduction is possible.</p> <p>Set in the input file:</p> <div data-bbox="472 1507 1377 1640" style="border: 2px solid black; padding: 5px; text-align: center;"><code>#Seed = <number of type long></code></div>
Output folder (optional)	<p>A path of a folder on the file system, which the output of the program will be plotted to. See each of the population creation scenarios sections for mode details on their output.</p> <p>If this parameter is not set, the default output folder will be "<i><folder of the input file >\Output></i>"</p>

	<p>Set in the input file:</p> <div data-bbox="472 260 1382 394" style="border: 3px double black; padding: 5px; text-align: center;"><code>#output file= <output folder's path></code></div>
Trace (Optional)	<p>Flag that controls the verbosity level of the program's output to the console line. If this flag is set and its value is "True", then the program's verbosity is enhanced.</p> <p>The default value is False, meaning that the program produces less trace lines in the console.</p> <p>Set in the input file:</p> <div data-bbox="472 751 1382 886" style="border: 3px double black; padding: 5px; text-align: center;"><code>#trace = <true / false></code></div>
Use Garbage Collection (Optional)	<p>Flag that controls the Java Garbage Collector calling schedule.</p> <p>The Java Garbage Collection is fired in order to free up memory for the program to use. Since the Geppetto program uses large amounts of memory, when creating big populations or handling big chromosome loaders, there might be a memory shortage issue.</p> <p>Use this flag in order to call the garbage collector more often (by setting it to "true"), and by that freeing up memory as the program progresses, and enable the program to complete. You must note that the performance of the program might be reduced.</p> <p>The default value is False, meaning that the program will not call Java Garbage Collection intentionally.</p> <p>Set in the input file:</p> <div data-bbox="472 1545 1382 1680" style="border: 3px double black; padding: 5px; text-align: center;"><code>#use garbage collection = <true / false></code></div>

Chromosome Loaders

The chromosome loaders are objects that the program uses to hold the genotype data which the program will create the population's genomes by, for a given chromosome.

They hold information about the markers that represents the chromosome. The program will create, according to the population creation scenario and in a randomly fashion, populations' genomes by assigning values to each marker at each chromosome.

The chromosome loaders obtain their data from [genotype data](#). The genotype data can be given to Geppetto using the currently supported genotype data format: [HapMap genotype data](#), and [Geppetto genotype data](#). See those sections for more details.

Loading Genotype Data

You can load genotype data for several chromosomes, by specifying in the input file

```
#genotype = <path to genotype data file(s)>
```

See more information in the [Genotype Data](#) section.

Binary Chromosome Loaders

The genotype data files are parsed by the Geppetto program into the chromosome loaders objects, which are the data structure the program uses. Parsing of the genotype text files is a long and memory consuming operation. Therefore, the Geppetto program, after parsing the text files, saves the created chromosome loaders as binary files. The chromosome loaders binary files are saved under the *<output folder>\ChrLoaders* folder.

You can use those binary chromosome loaders as input to the Geppetto program. Using them will speed up the program execution (parsing of the text files are not necessary), and it is recommended.

How to Use Binary Chromosome Loaders

In order to run Geppetto with binary chromosome loaders files, specify in the input file the following: Just specify a path to the folder that holds those binaries. Each file in that folder (that was created in a previous run of the program) has a filename of "ChrLoader??.bin" name. Specify the binaries folder in the following way in the input file:

```
#ChrLoadersBinaries = <ChrLoaders folder path>
```

Example:

Say we already ran the program with text genotype data, and the output folder was set as "c:\output". Then from that run, a folder "c:\output\ChrLoaders" was created. In the next execution of Geppetto, we can define the following line:

```
#ChrLoadersBinaries = D:\output\ChrLoaders
```

Disease Model

The Disease Model entity defines the model, on top of which a person from a created population will be marked as “sick” (or will possess a certain trait. For the simplicity of the discussion, we will refer to “sickness”). In Geppetto, a person will be created, and then, if he is supposed to be sick, his genome will be checked against the disease model, to determine his sickness status.

The Geppetto Disease Model enables defining genetic diseases – diseases that are characterized by a specific allele of a specific marker, or combination of such markers. This in fact, lets you define disease that it is linked to certain markers in the genome.

For example, say we have a disease that is linked to a certain VNTR (marker) allele, in 95% of the cases. Then you can define the Disease Model to reflect that: specify the RS number of the marker (or VNTR), its “infected” allele, and 0.95 as the probability of a person that possesses this marker to be sick with that disease.

The Geppetto Disease Model also lets you define several combinations of markers and alleles that are linked to the disease, with different probabilities. For example, you can define that the disease is linked to 2 joined markers with the probability of 0.3, and to another 3 markers with probability of 0.9. When creating the population you can check amongst the sick people, which of the markers sequence are more linked to the disease, in the created population.

Disease Model File Format

The Disease Model file must have a header line, which defines the used markers’ RS numbers in the different marker sequences. Each token of the header must be in the “rsXXX” format, and the RS number should be defined in the chromosome loaders (meaning in the genotype data given to the program), otherwise the marker will be ignored.

Example of a header line:

```
rs32130 rs4328 rs3129
```

The above line defines 3 RS numbers that may be used in the disease model.

The next lines, define each a sequence of alleles from the chromosome pair of the defined RS numbers, and the probability of being sick when possessing that sequence of alleles, as the last token. Each allele pair token is correlated with the matching RS number token defines in the header line.

If you want to define a sequence with less markers than in the header line, just enter -1/-1 as the alleles’ values of the redundant markers.

The disease model format also enables you to define only one allele value for a marker, when the value of the other allele is not important. Set the unimportant allele value as -1.

Example of a sequence line:

```
a/c g/a t/t 0.9
```

The above line sets, that when a person has the alleles “a” and “c” at RS number rs32130 (from both chromosomes), “g” and “a” at rs4328, and “t” and “t” at rs3129, that person has 0.9 probability of being sick.

Example of an entire Disease Model file:

```
rs32130 rs4328 rs3129
a/a      a/a      t/t      0.9
-1/-1    -1/-1    c/-1     0.3
```

Here there are 2 possible “causes” to the disease:

- The first alleles sequence involves all the 3 markers defined in the header line, and it causes the disease with probability of 0.9,
- The second alleles sequence involves only 1 marker (the redundant markers in this sequence are marked as having -1/-1 alleles), and the marker has only one allele that is enough to cause sickness (if the genome contain the allele “c” in the marker rs3129, while the other allele can have any value), and it causes the disease with probability of 0.3.

Pedigree File – PedFile

[The PedFile file format](#) is a format used to describe a pedigree. A PedFile file describes all the individuals in the pedigree (their sex, affected (sickness) status, etc.) and the family relations between them – parenting relations, sibyl relations and etc.

The PedFile format Geppetto uses is adapted from the [Superlink](#)(SuperLink Genetic Linkage Analysis Project n.d.) PedFile format, which is adapted from the [Linkage PedFile format](#)(Ped files format n.d.) , with a minor addition that will be described.

PedFile Format

[In this format](#), each individual in the pedigree is defined in a single line of text. The whole pedigree is composed of individuals’ descriptions.

Each line has at least 10 fields. The mandatory fields:

In short:

```
Column 1: Pedigree number
```

Column 2: Individual number
 Column 3: Number of father
 Column 4: Number of mother
 Column 5: Number of first child
 Column 6: Number of next sibling with same father
 Column 7: Number of next sibling with same mother
 Column 8: Sex - (1 = Male, 2 = female)
 Column 9: ignored (the value must be 0)
 Column 10: affected status - 1 is healthy, 2 is sick.

More detailed information:

1. Pedigree number. The pedigree number (ID) that the person is related to. There can only be one pedigree in a PedFile.
2. Individual number. The person's unique ID in the defined pedigree.
3. Father's ID. The number of the person's father in the pedigree. If the person does not have a father in the defined pedigree, we consider the person as an "ancestor" of the pedigree.
4. Mother's ID. The number of the person's mother in the pedigree. If the person does not have a mother in the defined pedigree, we consider the person as an "ancestor" of the pedigree.
5. Must exist, but the value is Ignored by the Geppetto program.
6. Must exist, but the value is Ignored by the Geppetto program.
7. Must exist, but the value is Ignored by the Geppetto program.
8. Sex. The person's sex – set it to 1 if the person is a male, or 2 if female.
9. Must be of value 0.
10. Affected status: The person affected status determines if the person possesses the sickness (or trait). Set it to 1 if the person is healthy (doesn't possess the trait), 2 if the person is sick (does possess the trait), or 0 if its condition is unknown (at this case, the person will be treated as healthy).

Optional field supported in the Geppetto program is at field number 11 – The person's ancestry. To set the person's ancestry, add to the person line in the PedFile the field "Pop:<ancestry>" when <ancestry> is A, B, If this value is not set, then the program will treat the person as it is from the "A" population by default.

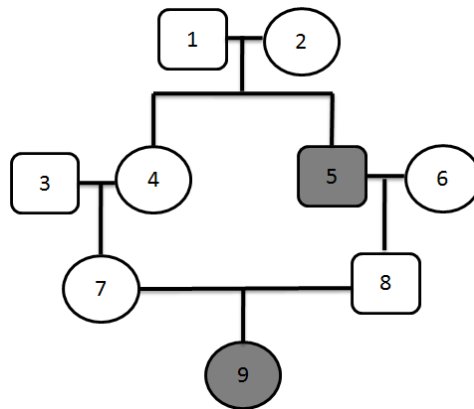
PedFile Example

The following is a PedFile which describes a pedigree with ID 2.

2	1	0	0	0	0	0	1	0	1	Pop:A
2	2	0	0	0	0	0	2	0	1	Pop:A
2	3	0	0	0	0	0	1	0	1	Pop:A

2	4	1	2	0	0	0	2	0	1	Pop:A
2	5	1	2	0	0	0	1	0	2	Pop:A
2	6	0	0	0	0	0	2	0	1	Pop:A
2	7	3	4	0	0	0	2	0	1	Pop:A
2	8	5	6	0	0	0	1	0	1	Pop:A
2	9	8	7	0	0	0	2	0	2	Pop:A

This PedFile describes the pedigree (male #5 and female #9 are sick, the pedigree if from ancestry "A"):



Recombination Rate Producer

Geppetto uses chromosome mixing as a way to simulate individual creation. In the process of mixing, one chromosome naturally comes from the father and one from the mother. Before they are transferred to the offspring, these chromosomes undergo the process of meiosis. Geppetto simulates meiosis by simulating recombination events. [According to Haldane](#), the number of recombination events is a Poisson occurrence, distributed with a certain parameter which is called the recombination rate parameter [\(Haldane 1919\)](#).

In order to reach high randomness, Geppetto uses a different recombination rate parameter for every individual it produces. The way this is done is by raffling a different recombination rate parameter each time. The distribution from which this parameter is taken depends on the user's input. Geppetto supplies a Normal distribution parameter producer, so the user can specify the mean and variance of the normal distribution in the input file (see input sections of the different scenarios for more information).

Geppetto offers the user an option to choose its own "meta-distribution" of the parameter. Should they choose to do so, the users should implement the

IRecombinationRateProducer interface in package *Geppetto.metaRecombinationDistribution*, and add it to the Geppetto class files when running the program. There are 3 methods to implement:

1. `int ProduceRecombinationRate()` – this is the main method, in here you can implement whatever distribution (or constant...) you wish for the recombination rate parameter.
2. `boolean QueryInterface(String descriptionLine)` – This method queries whether or not your interface matches the wanted parameters specified in the input file. The parameter `descriptionLine` should be in the format: `<Function> : <Parameters>` i.e. “Normal: 3, 0.5” for a Normal distribution with mean 3 and variance 0.5. Other than that, you can name your interface whatever you want.
3. `IRecombinationRateProducer CreateInstance(String descriptionLine, long seed)` – This method assumes that “QueryInterface” was called and succeeded. It should initialize your object with the correct parameters according to the `descriptionLine` accepted as a parameter. The seed parameter is used in case your class uses a Random number generator as a member, so you can initialize it with the seed.

For further help on how to implement this feature, we advise you to check out the Geppetto source code and examine the implementation of the `NormalRecombinationRateProducer` class.

Genotype Data

Genotype data holds information about each marker:

- ID number (or, RS number): unique marker identifier
- Position in the genome: chromosome number, physical and genetic positions
- Alleles: each marker can have as many alleles as it have, and the frequency of each allele. The alleles can be SNPs (the DNA bases, A/C/G/T), VNTR numbers, or other types of alleles. They must be either A/C/G/T or an integer number.

The alleles' information can be set for any number of populations, and in that case and with dependence on the population creation scenario, the created populations may have genomes which are a mix of genomes from the populations. Meaning, each population has a different set of probabilities for each allele.

For example, say we have a SNP with 2 possible alleles: T and G. in population A the frequency of allele T is 0.9 and G has 0.1 frequency, while in population B the frequency of allele T is 0.3 and the frequency of allele G is 0.7. Instead T and G we can define the alleles as 12 VNTRs (variable number tandem repeats) and 3.

The genotype data is given to the program in text files. Currently, the program supports two formats of genotype data: HapMap format, and Geppetto Genotype format. See the different format later on.

Each chromosome's markers are given in their own file. You can choose only one of the formats for each chromosome (you cannot mix the two formats for the same chromosome loader).

In the following sections you can find information about each format and how to use it as an input to the Geppetto program.

HapMap Genotype Data

From www.hapmap.org:

"The goal of the International HapMap Project is to develop a haplotype map of the human genome, the HapMap, which will describe the common patterns of human DNA sequence variation."

HapMap project contains data about markers of the human genome, from various populations, from places such as Nigeria (Yoruba), Japan, China and the U.S. (residents with ancestry from Northern and Western Europe, collected in 1980 by the Centre d'Etude du Polymorphisme Humain (CEPH) and used for other human genetic maps).

HapMap genotype data dump file is a file that contains information about markers (usually SNPs) in a specific chromosome, where every marker has exactly 2 alleles, and the file is

population specific. That is, you can find genotype data about a chromosome for a specific population.

The chromosome loaders accept HapMap genotype data dump (NOT the frequency or LD data dump!) as the genotype data. You can obtain those files from the [HapMap website](http://www.hapmap.org/genotypes/), for example: <http://www.hapmap.org/genotypes/?N=D>. You can specify several genotype data files, one for each population. The chromosome loader must get also a genetic map, that maps the physical positions of each marker to its genetic position on the chromosome (the HapMap genotype data dump only contain information about the physical positions). This data also is accessible from the [HapMap website](http://www.hapmap.org/), and you can also find it here: https://mathgen.stats.ox.ac.uk/wtccc-software/recombination_rates/. The program will match genetic positions from that map to the HapMap genotype files, and will complete missing genetic distances when it can (by means of simple interpolation).

HapMap Genotype File Format

In this file format, every line corresponds to a SNP – a marker with 2 alleles, and each file represents one chromosome of a single population.

The line format (only describing the fields relevant to the Geppetto program):

- 1st field: marker ID, its RS number.
- 2nd field: chromosome number (“chr#” where # is between 1-22, or “chrX” for the X chromosome, and “chrY” for the Y chromosomes – or “chr23” and “chr24” respectively).
- 3rd field: physical position of the marker on the chromosome. The position should be of “long” type, meaning an positive integer number.
- 11th field: first allele value. The allele value is one of A/C/G/T.
- 12th field: first allele frequency.
- 14th field: second allele value.
- 15th field: second allele frequency. The frequencies should sum to 1, otherwise the marker will be ignored by the chromosome loader.

You can read more about the HapMap genotype format in any of HapMap genotype data READMEs, for example: http://www.hapmap.org/genotypes/latest_ncbi_build36/00README.txt

Note:

HapMap genotype files contain exactly 2 alleles per marker. So if you need more alleles per marker, you might want to use the Geppetto genotype format.

Example:

Look at the following line from a chromosome 22 HapMap genotype file:

```
rs915674 chr22 14433624 + ncbi_b35 perlegen  
urn:lsid:perlegen.hapmap.org:Protocol:Genotyping_1.0.0:2
```

urn:lsid:perlegen.hapmap.org:Assay:25760.6201814:1

urn:lsid:dcc.hapmap.org:Panel:CEPH-30-trios:1 QC+ G 0.871 101 A 0.129 15 116

The above line defines a marker (more specifically, a SNP) with RS number *rs915674* on physical position *14433624* at chromosome 22, with two alleles: G with frequency of 0.871 and A with frequency 0.129.

How to Use HapMap Genotype Files

In order to run Geppetto with HapMap genotype files specify in the input file the following: For each chromosome loader in the HapMap format, enter a line in the input file at the following format:

#Genotype = <chrNumber>, <HapMap Genotype file path of population 1> < HapMap Genotype file path of population 2>, <...>, <HapMap Genotype file path of population n>, <Genetic Map>

- *<chrNumber>* is the chromosome number, an integer between 1..24 (23 is the X chromosome, 24 is the Y chromosome),
- There must be at least one HapMap genotype file, and the last file specified must be a genetic map file (as explained earlier).

Example:

```
#Genotype = 1, D:\Geppetto\ChrLoaders\allele_freqs_chr1_CEU_r21a_nr_fwd.txt,
D:\Geppetto\ChrLoaders\allele_freqs_chr1_YRI_r21a_nr_fwd.txt,
D:\Geppetto\ChrLoaders\genetic_map_chr1.txt
#Genotype = 22, D:\Geppetto\ChrLoaders\allele_freqs_chr22_CEU_r21a_nr_fwd.txt,
D:\Geppetto\ChrLoaders\allele_freqs_chr22_YRI_r21a_nr_fwd.txt,
D:\Geppetto\ChrLoaders\genetic_map_chr22.txt
```

The 2 lines above specify 2 chromosome loaders for the 1 and 22 chromosomes. There are 2 populations: CEU (Utah residents with ancestry from Northern and Western Europe) and YRI (Yoruban in Ibadan, Nigeria (West Africa)).

Geppetto Genotype Data

In order to address HapMap genotype data downfalls, such as redundant fields for population synthesis programs, lack of genetic distance data, its cumbersomeness, and the need to have many files to describe markers of several ancestries, we defined a new genotype data format, “Geppetto Genotype Data” format.

Geppetto genotype files are text files, where each marker is represented on a different, single line of text.

It enables defining several alleles per marker, and several populations in a single file.

Geppetto Genotype File Format

Each line represents a marker. The line is separated into tokens, or fields, where each field is separated by a space character(s) – series of single white spaces or tabs.

- 1st field: marker ID, its RS number.
- 2nd field: chromosome number (“chr#” where # is between 1-22, or “chrX” for the X chromosome, and “chrY” for the Y chromosomes – or “chr23” and “chr24” respectively).
- 3rd field: physical position of the marker on the chromosome. The position should be of “long” type, meaning a positive integer.
- 4th field: genetic position of the marker on the chromosome. The genetic position should be of “double” type, meaning a positive fraction.
- From the 5th field: here the different alleles of the marker are declared. All markers must have the same number of alleles (if a marker has only one allele, or less alleles than it should then enter bogus alleles to fill the fields, and set their frequencies to 0). Each allele can be of type integer (useful for alleles of VNTR types for example), or a genetic base, such as A/C/G/T.

Say we want to define n alleles at most per marker, then for each marker we will have n fields for the alleles, we will mark them as a_1, a_2, \dots, a_n .

- The next fields are the frequencies fields. Here are defined the frequencies of each allele of the marker, per population.

If we have n alleles per marker, and p populations, then there must be $n * p$ frequencies fields.

Each population defines n frequencies, which match the alleles of the marker. The i^{th} population, will define the following allele frequencies: $\text{freq}_i(a_1), \text{freq}_i(a_2), \dots, \text{freq}_i(a_n)$.

The alleles' frequencies for each population must sum up to 1.0.

See the example for another explanation.

Each frequency should be of type double, a number between 0.0 and 1.0, where you must use “1.0” and “0.0” for 1 and 0, respectfully, in order to differentiate the frequencies from the allele's values.

Example:

Look at the following line from a Geppetto genotype file:

rs23 chr4 100 2.0; A G C; 0.2 0.7 0.1; 0.1 0.9 0.0; 0.0 0.0 1.0

The above line defines a marker in the Geppetto format. The marker RS number is 23, it is on chromosome 4, in physical position 100, and genetic position 2.0. There are 3 alleles for the marker: A, G and C, and there are 3 different populations defined.

In population 1 the frequency of allele A is 0.2, for G is 0.7, and for C is 0.1.

In population 2 the frequency of allele A is 0.1, for G is 0.9, and for C is 0.0 (This allele doesn't exist in population 2).

In population 3 the frequency of allele A is 0.0, for G is 0.0, and for C is 1.0 (in population 3, only the C allele exists).

How to Use Geppetto Genotype Files

In order to run Geppetto with Geppetto genotype files specify in the input file the following: For each chromosome loader in the Geppetto format, enter a line in the input file at the following format:

#Genotype = <chrNumber>, <Geppetto Genotype file path>

- *<chrNumber>* is the chromosome number, an integer between 1..24 (23 is the X chromosome, 24 is the Y chromosome),

Example:

#Genotype = 1, D:\Geppetto\ChrLoaders\Chromosome1Loader.txt

#Genotype = 17, D:\Geppetto\ChrLoaders\Chromosome17Loader.txt

The above specify 2 chromosome loaders for the 1 and 17 chromosomes.

Population Creation Scenarios

There are 6 population creation scenarios that Geppetto supports. Each of them is explained in details in its section, and each has its set of input parameters.

The following table describes briefly the meaning of each scenario and what to specify in the input file in order to create a population with that creation method.

Plain	#Creation Method = Plain	Create a non-admixed population of single ancestry
Stratification	#Creation Method = Stratification	Create a non-admixed population of several ancestries
Create the pedigree's genomes	#Creation Method = Create from Pedigree	Create the genomes of the given pedigree
Admixed - Continuous Gene Flow (CGF)	#Creation Method = Continuous Gene Flow -or- #Creation Method = CGF	Create an admixed population that is derived from the CGF model
Admixed – Hybrid Isolated (HI)	#Creation Method = Hybrid Isolated -or- #Creation Method = HI	Create an admixed population that is derived from the HI model
Admixed – Straight Admixed	#Creation Method = Straight Admixed	Create an admixed population that is derived from admixture at a certain point in time

Create from Pedigree Scenario

The Create from Pedigree scenario is the scenario where, given a pedigree where each individual is marked as sick or healthy, and a disease model, the program creates the genomes of each individual in the pedigree.

Use it when you need to create the genomes of an entire family, that the family is described in a Pedfile.

Input

Pedigree	<p>The pedigree is given in a PedFile format. It describes the pedigree from which the people's genomes will be created.</p> <p>Each individual is marked as healthy (1), sick (2), or unknown (0, will be treated as healthy) in the 11th column of the PEDFILE.</p> <p>The founders of the pedigree have in the 11th column of the PEDFILE their ancestry, which should correspond to the ancestries provided in the Chromosome Loaders. If the ancestry is not set, the program will set as a default the first ancestry.</p> <p>Set in the input file:</p> <pre>#pedigree file = <path to the PEDFILE></pre>
Recombination Rate Parameters	<p>See Recombination Rate Parameters explanation section.</p> <p>Set in the input file:</p> <pre>#Recombination Rate = function = <function name>; parameters = < list of comma-separated parameters ></pre>
Disease Model	<p>The disease model is given as a path to a file which holds the disease model . The disease model is used to figure out whether the created individual is sick according to this model, when creating its genome.</p> <p>Set in the input file:</p>

	#Disease Model File = <path to a disease model file>
Chromosome Loaders	See Chromosome Loaders Section

Output

Each individual genome will reside in the output folder specified, under a folder with the created population ID and there under a folder with the person ID, its sickness status (healthy or sick) and its gender (male or female). The genome of the individual is represented by a text file of each chromosome of the created individual. The chromosomes are those who have matching chromosomes loaders as input.

For each individual in the pedigree, the program will produce it's genome in text files.

Each individual genome will reside in the output folder specified, under a folder with the pedigree ID and there under a folder with the person ID in the pedigree, its sickness status (healthy or sick) and its gender (male or female). The genome of the individual is represented by a text file of each chromosome of the created individual. The chromosomes are those who have matching chromosomes loaders as input.

Example:

For a healthy male individual whose ID is 5, in the pedigree whose ID is 3, with the 4 and 17 chromosomes loaders, the individual's created genome will be represented by the following files:

Both 3 chromosomes: <Output Folder>\pedigree003\005_Healthy_Male\chr3a.txt

<Output Folder>\pedigree003\005_Healthy_Male\chr3b.txt

Both 17 chromosomes: <Output Folder>\pedigree003\005_Healthy_Male\chr17a.txt

<Output Folder>\pedigree003\005_Healthy_Male\chr17b.txt

Overview – How it works

Flow:

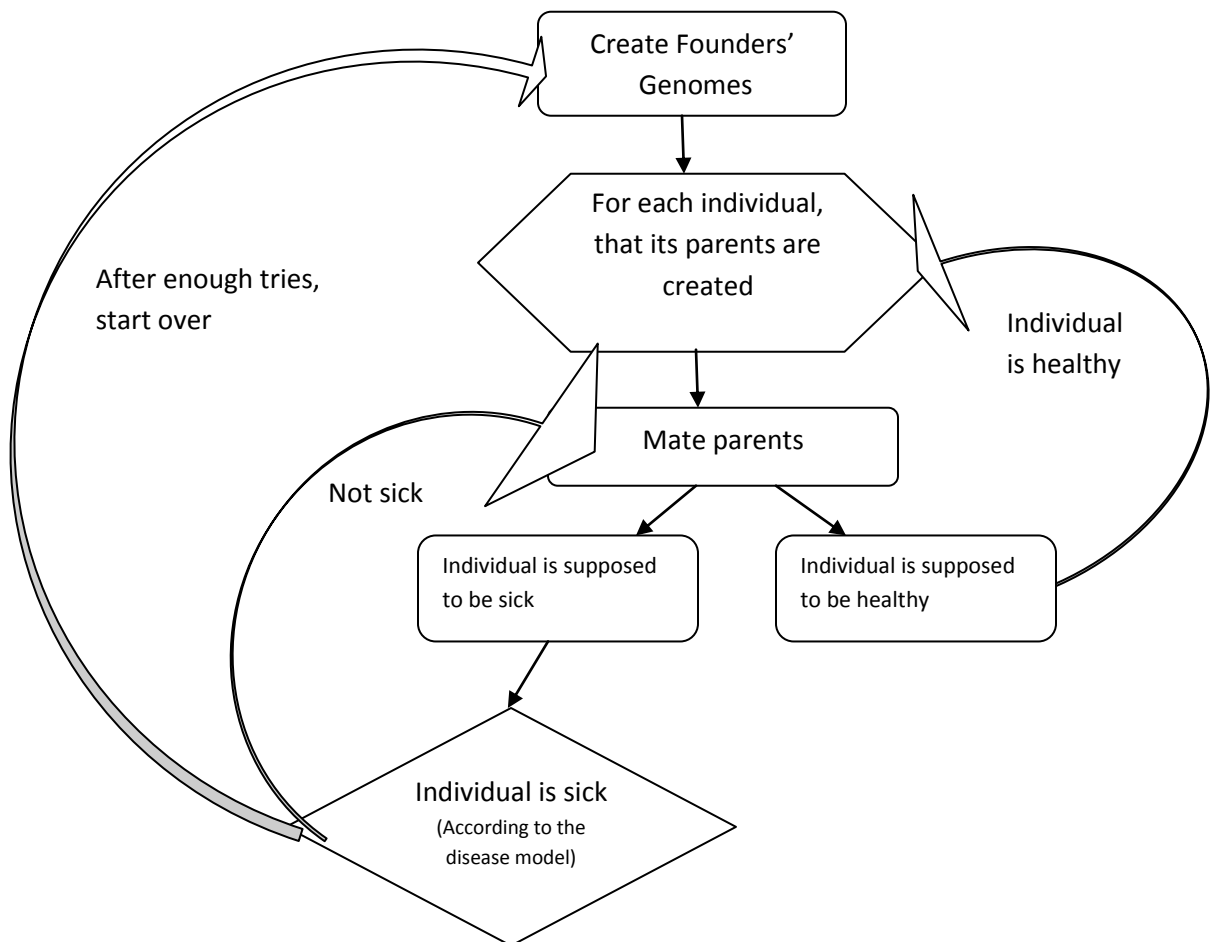
1. Load the pedigree from the PEDFILE:

- a. Parse each line of the PEDFILE, and create the pedigree structure.
 - b. Each node in the pedigree graph represents an individual in the pedigree.
2. Creating the genomes of each individual in the pedigree:
- a. First, create the genomes of the founders.

Create each of the founder's chromosomes, by assigning markers from the markers data, according to his ancestry
 - b. For each two parents who their genomes are created, mate them to create their child - mix their chromosomes, and create their child genome.

If their child should be sick, using the disease model, check whether the child's assigned genome has sick alleles. Try to mix the parents until the child's genome indicates a sickness according to the disease model. Do those until a certain threshold – if it doesn't work, return to step 1 for another try of creating a pedigree that complies with the pedigree individuals' status.

Create population from pedigree; Flow Diagram



Plain Scenario

This population creation scenario produces a non-admixed single population, where all individuals in the created population are from the same ancestry – meaning, the created population is a “pure population” – all individuals’ genome is of that ancestry.

Given number of sick and healthy people to produce, and a disease model, the program creates a population of that content whom all the individuals are from the same ancestry, and each person’s genome is created.

Input

Number of Healthy People	<p>Specifies the number of healthy people that the created population will have. Each created individual is considered healthy, unless it is checked against the disease model.</p> <p>Set in the input file:</p> <pre>#healthy people = <number of healthy people, non-negative integer></pre>
Number of Sick People	<p>Specifies the number of sick people that the created population will have. The sickness status is decided upon the disease model given.</p> <p>Set in the input file:</p> <pre>#sick people = <number of sick people, non-negative integer></pre>
Disease Model	<p>The disease model is given as a path to a file which holds the disease model . The disease model is used to figure out whether the created individual is sick according to this model, when creating its genome.</p> <p>It must be set if there are sick people to produce.</p> <p>Set in the input file:</p> <pre>#Disease Model File = <path to a disease model file></pre>

Output

For each individual in the created population, the program will produce its genome in text files.

Each individual genome will reside in the output folder specified, under a folder with the created population ID and there under a folder with the person ID, its sickness status (healthy or sick) and its gender (male or female). The genome of the individual is represented by a text file of each chromosome of the created individual. The chromosomes are those who have matching chromosomes loaders as input.

Example:

For a male individual whose ID is 5, in the population whose ID is 3, with the 4 and 17 chromosomes loaders, the individual's created genome will be represented by the following files:

Both 3 chromosomes: <Output Folder>\population003\005_Healthy_Male\chr3a.txt
<Output Folder>\population003\005_Healthy_Male\chr3b.txt

Both 17 chromosomes: <Output Folder>\population003\005_Healthy_Male\chr17a.txt
<Output Folder>\population003\005_Healthy_Male\chr17b.txt

Overview – How it works

Flow:

This scenario is a simple subset of the stratification scenario.

1. Create folder that will store the created population's genomes.
 - a. The folder will reside in the output folder of the program. Its name will be the next population index (relative to the previously created population in the output folder).
2. Create genomes of the healthy individuals in the population.

For each healthy individual:

 - a. Decide its ancestry:

According to the number of populations, and the given fraction from each population, raffle the individual's ancestry.
 - b. Decide its sex:

Chance that's it's a male is 49%.
 - c. Create the individual's genome:

Create each of the chromosomes, by assigning markers from the markers data, according to the individual's ancestry. Each individual has one ancestry, so whole the genome will be derived from one ancestry in the chromosome loaders data (or, each chromosome will be "pure ancestry" chromosome, as opposed to the admixed scenarios).
The sex chromosomes are created according the individual's sex.

3. Create genomes of the sick individuals in the population.

For each sick individual:

a. Decide its ancestry:

According to the number of populations, and the given fraction from each population, raffle the individual's ancestry.

b. Decide its sex:

Chance that's it's a male is 49%.

c. Create the individual's genome:

Create each of the chromosomes, by assigning markers from the markers data, according to the individual's ancestry. Each individual has one ancestry, so whole the genome will be derived from one ancestry in the chromosome loaders data (or, each chromosome will be "pure ancestry" chromosome, as opposed to the admixed scenarios).

The sex chromosomes are created according the individual's sex.

d. Check if the created genome is sick according to the disease model:

Using the disease model, check whether the individual's assigned genome has sick alleles.

If it does, continue to create the next individual.

Else, try to create another individual, to replace current one. Do this until a threshold of tries was achieved.

Stratification Scenario

This population creation scenario produces a non-admixed population, where each person is of different ancestry (the ancestries are user-defined) – meaning, of a different “pure population”, and his entire genome is of that ancestry (or, “pure population” person).

Given number of sick and healthy people to produce, the fraction of each ancestry in the created population, and a disease model, the program creates a population, in which the number of people from each ancestry complies with the given population fraction, and each person’s genome is created.

Use it when you need to create several people, each from several ancestries – might be useful for genotype labeling testing – create a population of different ancestries and test whether the labeling program labeled the genotype correctly.

It may be interesting to define a disease model, and then observed which of the ancestries are most matched to the defined disease model – Say that there are 2 populations, A and B, and the fraction of each population is 50%, and 90% of the created sick individuals are originated in population A, then we can fairly deduct that the disease model is depicting a population A related disease.

Input

<p>Number of Populations</p>	<p>Specifies the number of populations that the created population’s individuals are composed from. Meaning, each original population will be treated as an ancestry, and the first population will be marked as ancestry of type “A”, the second will be marked as “B” and so on. The ancestries marking should comply with the ancestries given in the chromosome loaders files.</p> <p>Each created individual from the created population will have a genome that is composed solely of one ancestry.</p> <p>Set in the input file:</p> <div style="border: 2px solid black; padding: 5px; margin: 10px 0;"><pre>#Number of populations= <number of populations, non-negative integer></pre></div>
<p>Fraction of Each Population</p>	<p>Specifies the fractions of each original population representation in the created population. The number of fractions must be the same of the number of population specified (see above parameter), and must sum up to one - as each created individual has origin from exactly one original population.</p>

	<p>For example, to create a population that is comprised from 2 different populations (or ancestries), that is comprised of 80% individuals from the first original population, set the population fractions to 0.8; 0.2</p> <p>Set in the input file:</p> <div style="border: 2px solid black; padding: 5px; margin: 10px 0;"> <pre>#PopFreq = <semi-colon delimited list of fractions that sum to 1></pre> </div>
<p>Number of Healthy People</p>	<p>Specifies the number of healthy people that the created population will have. Each created individual is considered healthy, unless it is checked against the disease model.</p> <p>The healthy people can be of any of the original ancestries.</p> <p>Set in the input file:</p> <div style="border: 2px solid black; padding: 5px; margin: 10px 0;"> <pre>#healthy people = <number of healthy people, non-negative integer></pre> </div>
<p>Number of Sick People</p>	<p>Specifies the number of sick people that the created population will have. The sickness status is decided upon the disease model given.</p> <p>The sick people can be of any of the original ancestries. This may be interesting to test the relevance and connection of a certain disease model to an original population.</p> <p>Set in the input file:</p> <div style="border: 2px solid black; padding: 5px; margin: 10px 0;"> <pre>#sick people = <number of sick people, non-negative integer></pre> </div>
<p>Disease Model</p>	<p>The disease model is given as a path to a file which holds the disease model . The disease model is used to figure out whether the created individual is sick according to this model, when creating its genome.</p> <p>It must be set if there are sick people to produce.</p> <p>Set in the input file:</p>

	<i>#Disease Model File = <path to a disease model file></i>
--	---

Output

For each individual in the created population, the program will produce its genome in text files.

Each individual genome will reside in the output folder specified, under a folder with the created population ID and there under a folder with the person ID, its sickness status (healthy or sick) and its gender (male or female). The genome of the individual is represented by a text file of each chromosome of the created individual. The chromosomes are those who have matching chromosomes loaders as input.

Example:

For a healthy male individual whose ID is 5, in the population whose ID is 3, with the 4 and 17 chromosomes loaders, the individual's created genome will be represented by the following files:

Both 3 chromosomes: *<Output Folder>\population003\005_Healthy_Male\chr3a.txt*
<Output Folder>\population003\005_Healthy_Male\chr3b.txt

Both 17 chromosomes: *<Output Folder>\population003\005_Healthy_Male\chr17a.txt*
<Output Folder>\population003\005_Healthy_Male\chr17b.txt

Overview – How it works

Flow:

1. Create folder that will store the created population's genomes.
 - a. The folder will reside in the output folder of the program. Its name will be the next population index (relative to the previously created population in the output folder).
2. Create genomes of the healthy individuals in the population.

For each healthy individual:

 - a. Decide its ancestry:

According to the number of populations, and the given fraction from each population, raffle the individual's ancestry.
 - b. Decide its sex:

Chance that's it's a male is 49%.
 - c. Create the individual's genome:

Create each of the chromosomes, by assigning markers from the markers data, according to the individual's ancestry. Each individual has

one ancestry, so whole the genome will be derived from one ancestry in the chromosome loaders data (or, each chromosome will be “pure ancestry” chromosome, as opposed to the admixed scenarios).

The sex chromosomes are created according the individual’s sex.

3. Create genomes of the sick individuals in the population.

For each sick individual:

a. Decide its ancestry:

According to the number of populations, and the given fraction from each population, raffle the individual’s ancestry.

b. Decide its sex:

Chance that’s it’s a male is 49%.

c. Create the individual’s genome:

Create each of the chromosomes, by assigning markers from the markers data, according to the individual’s ancestry. Each individual has one ancestry, so whole the genome will be derived from one ancestry in the chromosome loaders data (or, each chromosome will be “pure ancestry” chromosome, as opposed to the admixed scenarios).

The sex chromosomes are created according the individual’s sex.

d. Check if the created genome is sick according to the disease model:

Using the disease model, check whether the individual’s assigned genome has sick alleles.

If it does, continue to create the next individual.

Else, try to create another individual, to replace current one. Do this until a threshold of tries was achieved.

Admixed Populations Scenarios

These population creation scenarios produce populations of admixed individuals. An admixed individual is a person whose ancestral origin relies on more than one pure ancestry. For example, African Americans are the consequence of an admixture of two “pure” populations – Europeans and Africans.

Geppetto population synthesis program currently supports 3 admixed population creation scenarios:

[Hybrid Isolated](#), [Continuous Gene Flow](#) and [Straight Admixed](#).

Hybrid Isolated Scenario

In this model of admixture (Pfaff, et al. 2001), the populations are assumed to have mixed at some point in history, and blended into one another in a way that mating was free between individuals from different populations. Hence, the mixture occurs over a span of one generation, and the next generation consists of admixed individuals, who have large ancestral segments of DNA in their chromosomes, and breed among themselves. As the generations advance and time elapses, the segments of ancestral DNA in the chromosome become shorter until they reach a point where the information extracted from this data does not contribute what is expected from MALD. Therefore, we recommend the user not to create a population in this model with an admixture that occurred over 15 generations ago.

Input

Number of Healthy People	<p>Specifies the number of healthy people that the created population will have. Each created individual is considered healthy, unless it is checked against the disease model.</p> <p>Set in the input file:</p> <pre>#healthy people = <number of healthy people, non-negative integer></pre>
Number of Sick People	<p>Specifies the number of sick people that the created population will have. The sickness status is decided upon the disease model given.</p> <p>Set in the input file:</p> <pre>#sick people = <number of sick people, non-negative integer></pre>
Disease Model	<p>The disease model is given as a path to a file which holds the disease model. The disease model is used to figure out whether the created individual is sick according to this model, when creating its genome.</p> <p>It must be set if there are sick people to produce.</p> <p>Set in the input file:</p> <pre>#Disease Model File = <path to a disease model file></pre>

<p>Number of Generations</p>	<p>The number of generations that passed since the populations were first introduced.</p> <p>Set in the input file:</p> <div style="border: 1px solid black; padding: 5px; margin: 10px 0;"> <pre>#Generations = <number of generations, non-negative integer></pre> </div>
<p>Number of Populations</p>	<p>The number of populations that admixed together. See the part on "<i>How Does the number of populations blend in?</i>" for further information.</p> <p>Set in the input file:</p> <div style="border: 1px solid black; padding: 5px; margin: 10px 0;"> <pre>#number of populations = <number of populations, non-negative integer></pre> </div>
<p>Populations Fractions</p>	<p>The fractions of each of the populations in the genome of the admixed individual. The number of values supplied must be equal to the number of populations specified. In addition, the fractions must sum to 1. In CGF, the first value will be the fraction of the main population. See the part on "<i>How Does the number of populations blend in?</i>" for further information.</p> <p>Set in the input file:</p> <div style="border: 1px solid black; padding: 5px; margin: 10px 0;"> <pre>#populations fractions = <fraction> ; <fraction> ; <fraction> ; ...</pre> </div> <p>For example:</p> <div style="border: 1px solid black; padding: 5px; margin: 10px 0;"> <pre>#populations fractions = 0.5 ; 0.3 ; 0.1 ; 0.1</pre> </div>
<p>Recombination Rate Parameters</p>	<p>See Recombination Rate Parameters explanation section.</p> <p>Set in the input file:</p>

```
#Recombination Rate =  
function = <function name>;  
parameters = < list of comma-separated parameters >
```

Output

For each individual in the created population, the program will produce its genome in text files.

Each individual genome will reside in the output folder specified, under a folder with the created population ID and there under a folder with the person ID, its sickness status (healthy or sick) and its gender (male or female). The genome of the individual is represented by a text file of each chromosome of the created individual. The chromosomes are those who have matching chromosomes loaders as input.

Inside the person's folder you will also find a PedFile that describes the pedigree that created that individual, and a folder named "Ancestors" that lists the chromosomes of the people in the pedigree (who are that person's ancestors). **An interesting point** is examining the chromosomes of the people in the pedigree from the top level to the bottom and seeing how the ancestral segments become a more and more delicate partition of the chromosome.

Example:

For a healthy male individual whose ID is 5, in the population whose ID is 3, with the 4 and 17 chromosomes loaders, the individual's created genome will be represented by the following files:

Both 3 chromosomes: <Output Folder>\population003\005_Healthy_Male\chr3a.txt
<Output Folder>\population003\005_Healthy_Male \chr3b.txt
Both 17 chromosomes: <Output Folder>\population003\005_Healthy_Male \chr17a.txt
<Output Folder>\population003\005_Healthy_Male \chr17b.txt
Ped file: <Output Folder>\population003\005_Healthy_Male \ancestors.ped

Ancestors' chromosome files (example for ancestor number 4, female):

<Output Folder>\population003\005_Healthy_Male \Ancestors\004_Healthy_Female.txt

Overview – How It Works

The method of creating each individual is by simulating the pedigree that created him/her. Given the parameters listed above, a person from the admixed population has a pedigree that is

predicted by the program, and, starting from the founders of the pedigree, mating is simulated to form the final offspring, who is the admixed individual.

How does the number of populations blend in?

For each individual there is a pedigree that creates him/her. In this model of admixture, the pedigree is an inverse full tree, with the founders all at the top level. They are assigned populations randomly according to the population fractions from the input file.

Flow:

1. Create folder that will store the created population's genomes.
 - a. The folder will reside in the output folder of the program. Its name will be the next population index (relative to the previously created population in the output folder).
2. Create genomes of the healthy individuals in the population.

For each individual:

- a. Decide its sex:
Chance that's it's a male is 49%.
- b. Raffle the **pedigree** that creates him/her:
According to the admixture model, gender, number of populations, and the given fraction from each population. **For sick people, create the pedigree such that the offspring of the pedigree will have a sick status.**
- c. Create the individual's genome:
Assign the people in the pedigree their genomes. **Pay attention, that for each of the people in the pedigree, the chromosomes will only contain the ancestral segments.** Making use of the chromosome loader files will only take place for creating the actual individual that belongs to the population.

Continuous Gene Flow Scenario

In this model (Pfaff, et al. 2001), there is one dominant population that is breeding among itself. At a certain point in time, other populations (possibly more than one) started mingling with this population, to insert a certain amount of genetic information into the population. In every generation, a fixed average percentage, α , of foreign DNA is assumed to have been “injected” into the population. With time, the percentage of the injected population’s DNA will increase within the admixed population’s individuals’ chromosomes.

Input

Number of Healthy People	<p>Specifies the number of healthy people that the created population will have. Each created individual is considered healthy, unless it is checked against the disease model.</p> <p>Set in the input file:</p> <pre>#healthy people = <number of healthy people, non-negative integer></pre>
Number of Sick People	<p>Specifies the number of sick people that the created population will have. The sickness status is decided upon the disease model given.</p> <p>Set in the input file:</p> <pre>#sick people = <number of sick people, non-negative integer></pre>
Disease Model	<p>The disease model is given as a path to a file which holds the disease model. The disease model is used to figure out whether the created individual is sick according to this model, when creating its genome.</p> <p>It must be set if there are sick people to produce.</p> <p>Set in the input file:</p> <pre>#Disease Model File = <path to a disease model file></pre>
Number of Generations	<p>The number of generations that passed since the populations were first introduced.</p>

	<p>Set in the input file:</p> <pre>#Generations = <number of generations, non-negative integer></pre>
<p>Number of Populations</p>	<p>The number of populations that admixed together. See the part on "How Does the number of populations blend in?" for further information.</p> <p>Set in the input file:</p> <pre>#number of populations = <number of populations, non-negative integer></pre>
<p>Populations Fractions</p>	<p>The fractions of each of the populations in the genome of the admixed individual. The number of values supplied must be equal to the number of populations specified. In addition, the fractions must sum to 1. In CGF, the first value will be the fraction of the main population. See the part on "How Does the number of populations blend in?" for further information.</p> <p>Set in the input file:</p> <pre>#populations fractions = <fraction> ; <fraction> ; <fraction> ; ...</pre> <p>For example:</p> <pre>#populations fractions = 0.5 ; 0.3 ; 0.1 ; 0.1</pre>
<p>Recombination Rate Parameters</p>	<p>See Recombination Rate Parameters explanation section.</p> <p>Set in the input file:</p> <pre>#Recombination Rate = function = <function name>; parameters = < list of comma-separated parameters ></pre>

Output

For each individual in the created population, the program will produce its genome in text files.

Each individual genome will reside in the output folder specified, under a folder with the created population ID and there under a folder with the person ID, its sickness status (healthy or sick) and its gender (male or female). The genome of the individual is represented by a text file of each chromosome of the created individual. The chromosomes are those who have matching chromosomes loaders as input.

Inside the person's folder you will also find a PedFile that describes the pedigree that created that individual, and a folder named "Ancestors" that lists the chromosomes of the people in the pedigree (who are that person's ancestors). **An interesting point** is examining the chromosomes of the people in the pedigree from the top level to the bottom and seeing how the ancestral segments become a more and more delicate partition of the chromosome.

Example:

For a healthy male individual whose ID is 5, in the population whose ID is 3, with the 4 and 17 chromosomes loaders, the individual's created genome will be represented by the following files:

Both 3 chromosomes: <Output Folder>\population003\005_Healthy_Male\chr3a.txt
<Output Folder>\population003\005_Healthy_Male \chr3b.txt
Both 17 chromosomes: <Output Folder>\population003\005_Healthy_Male \chr17a.txt
<Output Folder>\population003\005_Healthy_Male \chr17b.txt
Ped file: <Output Folder>\population003\005_Healthy_Male \ancestors.ped

Ancestors' chromosome files (example for ancestor number 4, female):

<Output Folder>\population003\005_Healthy_Male \Ancestors\004_Healthy_Female.txt

Overview – How It Works

The method of creating each individual is by simulating the pedigree that created him/her. Given the parameters listed above, a person from the admixed population has a pedigree that is predicted by the program, and, starting from the founders of the pedigree, mating is simulated to form the final offspring, who is the admixed individual.

How Does the number of populations blend in?

For each individual there is a pedigree that creates him/her. In this model of admixture, the pedigree is created dynamically, from offspring to founders. According to population fractions and the number of generations, the pedigree is created. The founders located at the top level

will be from the main population, and every founder that arrived later will have an ancestry of one of the co-populations. The main population is always considered “population A”, so in the population fractions part in the input file, the first value should be the fraction of the main population, and the rest of the values will be the fractions of the co-populations.

Flow:

3. Create folder that will store the created population’s genomes.
 - a. The folder will reside in the output folder of the program. Its name will be the next population index (relative to the previously created population in the output folder).
4. Create genomes of the healthy individuals in the population.

For each individual:

 - a. Decide its sex:

Chance that’s it’s a male is 49%.
 - b. Raffle the **pedigree** that creates him/her:

According to the admixture model, gender, number of populations, and the given fraction from each population. **For sick people, create the pedigree such that the offspring of the pedigree will have a sick status.**
 - c. Create the individual’s genome:

Assign the people in the pedigree their genomes. **Pay attention, that for each of the people in the pedigree, the chromosomes will only contain the ancestral segments.** Making use of the chromosome loader files will only take place for creating the actual individual that belongs to the population.

Straight Admixed Scenario

This population creation scenario produces a population of admixed individuals. An admixed individual is a person whose ancestral origin relies on more than one pure ancestry. For example, African Americans are the consequence of an admixture of two “pure” populations – Europeans and Africans.

This scenario provides an additional method to create admixed populations. It will be interesting for the user to create several populations using the different scenarios and models of admixture and examine the differences in the created individuals (interesting parameters: size of segments, their distribution, the ancestral distribution of segments, the ancestry at the disease locus which cause for the sickness status, etc.).

The method of creation for this scenario is as the name implies. In contradiction to the previous scenario, in which the individual was created by simulating the actual admixture of its ancestors, in this scenario the person is created in a straight forward way by creating its admixed chromosomes. The creation of admixed chromosomes is done as a simulation according to parameters that describe the admixture pattern of the populations [\(Patterson, et al. 2004\)](#).

There are two important parameters which influence the outcome of an admixed chromosome creation:

1. Lambda parameter: this parameter simulates the number of generations that passed since admixture. The higher it gets, the more delicate will be the partition of the chromosome to ancestral segments, i.e. there will be more segments and they will be shorter.

In our program, this parameter is believed to be distributed with Gamma distribution [\(Patterson, et al. 2004\)](#) across individuals in the population. Therefore, in the input file, the user must supply a mean and variance for this parameter, and for each individual there will be a randomization of the specific lambda parameter according to the parameters supplied.

How this parameter is used:

Actually, ancestral segments in the chromosome are the result of recombination events that occur in meiosis. Recombination rate is often modeled as a Poisson process, which means that the number of recombination events is Poissonly distributed. In addition, as a general property of Poisson processes, the length of the segments is distributed exponentially. So the lambda parameter is used as the parameter of an Exponential distribution in randomizing segment lengths.

2. Populations Fractions: this parameter indicates what the fraction of each population is in the genome of the created individual. For example, a common fraction is used is for African Americans, who are believed to be composed of 0.8 African ancestry and 0.2 European Ancestry.

Input

Number of Healthy People	<p>Specifies the number of healthy people that the created population will have. Each created individual is considered healthy, unless it is checked against the disease model.</p> <p>Set in the input file:</p> <div data-bbox="472 527 1370 653" style="border: 2px solid black; padding: 5px;"><pre>#healthy people = <number of healthy people, non-negative integer></pre></div>
Number of Sick People	<p>Specifies the number of sick people that the created population will have. The sickness status is decided upon the disease model given.</p> <p>Set in the input file:</p> <div data-bbox="472 867 1370 993" style="border: 2px solid black; padding: 5px;"><pre>#sick people = <number of sick people, non-negative integer></pre></div>
Disease Model	<p>The disease model is given as a path to a file which holds the disease model. The disease model is used to figure out whether the created individual is sick according to this model, when creating its genome.</p> <p>It must be set if there are sick people to produce.</p> <p>Set in the input file:</p> <div data-bbox="472 1318 1370 1444" style="border: 2px solid black; padding: 5px;"><pre>#Disease Model File = <path to a disease model file></pre></div>
Lambda parameter	<p>The lambda parameter's mean and variance. See the paragraph on "<i>Lambda parameter</i>" for further information.</p> <p>Set in the input file:</p> <div data-bbox="472 1665 1370 1791" style="border: 2px solid black; padding: 5px;"><pre>#Lambda = <mean> ; <Variance></pre></div>
Number of	<p>The number of populations that admixed together.</p>

Populations	<p>Set in the input file:</p> <pre>#number of populations = <number of populations, non-negative integer></pre>
Populations Fractions	<p>The fractions of each of the populations in the genome of the admixed individual. The number of values supplied must be equal to the number of populations specified. In addition, the fractions must sum to 1.</p> <p>Set in the input file:</p> <pre>#populations fractions = <fraction> ; <fraction> ; <fraction>; ...</pre> <p>For example:</p> <pre>#populations fractions = 0.5 ; 0.3 ; 0.1 ; 0.1</pre>
Recombination Rate Parameters	<p>See Recombination Rate Parameters explanation section.</p> <p>Set in the input file:</p> <pre>#Recombination Rate = function = <function name>; parameters = < list of comma-separated parameters ></pre>

Output

For each individual in the created population, the program will produce it's genome in text files.

Each individual genome will reside in the output folder specified, under a folder with the created population ID and there under a folder with the person ID, its sickness status (healthy or sick) and its gender (male or female). The genome of the individual is represented by a text file of each chromosome of the created individual. The chromosomes are those who have matching chromosomes loaders as input.

Example:

For a healthy male individual whose ID is 5, in the population whose ID is 3, with the 4 and 17 chromosomes loaders, the individual's created genome will be represented by the following files:

Both 3 chromosomes: `<Output Folder>\population003\005_Healthy_Male\chr3a.txt`
`<Output Folder>\population003\005_Healthy_Male \chr3b.txt`

Both 17 chromosomes: `<Output Folder>\population003\005_Healthy_Male \chr17a.txt`
`<Output Folder>\population003\005_Healthy_Male \chr17b.txt`

Overview – How It Works

Flow:

1. Create folder that will store the created population's genomes.
 - a. The folder will reside in the output folder of the program. Its name will be the next population index (relative to the previously created population in the output folder).
2. Create genomes of the healthy individuals in the population.

For each healthy individual:

 - a. Decide its sex:

Chance that's it's a male is 49%.
 - b. Divide its chromosome to segments
According to the lambda parameter, creates a partition of the chromosome to segments. Each segment is decided its ancestral origin randomly in accordance with the population fractions parameter.
 - c. Create the individual's genome:
Each marker is given its allele value according to the ancestry of the segment in which it relies, and to the frequencies of alleles specified in the chromosome loader file.

For each sick individual:

 - a. Decide its sex:

Chance that's it's a male is 49%.
 - b. Divide its chromosome to segments
According to the lambda parameter, creates a partition of the chromosome to segments. Each segment is decided its ancestral origin randomly in accordance with the population fractions parameter.
 - c. Create the individual's genome:
Each marker is given its allele value according to the ancestry of the segment in which it relies, and to the frequencies of alleles specified in the chromosome loader file.
 - d. Check if the created genome is sick according to the disease model:
Using the disease model, check whether the individual's assigned genome has sick alleles.

If it does, continue to create the next individual.

Else, try to create another individual, to replace current one. Do this until a threshold of tries was achieved.

References

HapMap Project:

Home: <http://www.hapmap.org/>.

Genotype data files: <http://www.hapmap.org/genotypes/?N=D>

Genetic Maps: https://mathgen.stats.ox.ac.uk/wtccc-software/recombination_rates/

README: http://www.hapmap.org/genotypes/latest_ncbi_build36/00README.txt

SuperLink Software: <http://cbl-fog.cs.technion.ac.il/superlink/>.

Ped File Format: <http://linkage.rockefeller.edu/soft/linkage/sec2.7.html>.

AncestryMap Software: <http://genepath.med.harvard.edu/~reich/Software.htm>.

Haldane, J.B.S. "The combination of Linkage values and the calculation of distances between the loci of linked factors." *Journal of Genetics* 8 (1919): 299-309.

Patterson, N, et al. "Methods for high-density admixture mapping of disease genes." *American Journal of Human Genetics* 74, no. 5 (May 2004): 1001-1013.

Pfaff, C. L., et al. "Population Structure in Admixed Populations: Effect of Admixture." *American Journal of Human Genetics*, no. 68 (2001): 198-207.