

microTyper

genotyping microhaplotypes

Mainly focused on genotyping using reads from amplicon sequencing.

Reads bam files using the bamtools API (Barnett et al. 2011, <https://doi.org/10.1093/bioinformatics/btr174>), which is bundled with the microTyper code for ease of install.

Installation and example

First, we unpack and compile

```
tar -xzf microTyper.tar.gz
cd microTyper/
cmake .
make
```

Now, navigate to the example folder

```
cd example/
```

Here, there are three samples, a position file, and a reference file. We then calculate log-likelihoods for each genotype and sample

```
../mtype -f *.bam -p examplePositionFile.txt -r exampleReference.fasta
```

Then, we call genotypes using a minimum posterior probability of .99 and a minimum number of reads that perfectly match one of the alleles in the genotype of 10

```
../genoCaller -f microtyper_llh.mhgenos -c .99 -m 10
```

If we don't want to save the intermediate output file with log-likelihoods, we can pipe the output from one to the other (`-o -` specifies writing output to stdout, and `-f -` specifies reading from stdin):

```
../mtype -f *.bam -p examplePositionFile.txt -r exampleReference.fasta -o - |
../genoCaller -f - -c .99 -m 10
```

Manual

microTyper is intended to genotype individual samples for microhaplotypes using aligned reads from amplicon sequencing. The goal is to provide a straightforward program that takes reasonable inputs, outputs genotypes and related information (log-likelihoods) in a format that is easy to use as input for downstream analyses and is amenable to the level of automation required by high-throughput genotyping projects.

microTyper optionally uses the openMP library for parallel processing. If the openMP library is NOT detected during compilation, the microTyper will still compile and function, but will be limited to one thread.

microTyper has two steps, the first calculates log-likelihoods of each genotype and the second calls genotypes based on posterior probability and an optional depth filter.

The first step (calculating log-likelihoods):

```
mtype -f sample.bam -p positionFile.txt -r reference.fasta
```

Required arguments

- `-f` space separated list of input bam files. For example:
 - `-f sample1.bam`
 - `-f sample1.bam sample2.bam`
 - `-f ./bamfiles/*.bam`
- `-p` the "position file" giving information about the microhaplotypes to genotype (see below for details)
- `-r` a fasta file with the reference sequences that reads were mapped to. Each reference sequence is assumed to be one locus (one microhaplotype).

Optional arguments

- `-o` the name to give the output file (default: `microtyper_llh.mhgenos`).
 - To write output to stdout, use `-o -`
- `-eps_S` the probability of an incorrect base being present in a read prior to sequencing error (error due to PCR error during amplification, index hopping, etc.) (default: 0.01)
- `-eps_I` the probability of an indel error in a read (default: 0.01)
- `-b` the "batch size" to use when multithreading. in order to control memory usage, individuals are genotyped in batches and then results written out. Larger batches make processing quicker but use more memory. (default: 100)
- `-t` the number of threads to use. Ignored if openMP was not found during compilation. (default: 1)
- `--manySNPs` If your loci have a very, very large number of SNPs in them, it is imaginable that without this option, log-likelihoods will not all be able to be calculated by the normal routine. This will result in "nan" being present in the output file where the log-likelihood should be. If that is the case, using this option will calculate the log-likelihoods, but will be slower than otherwise.
- `--version` print the version of microTyper being used and exit

The second step (calculating posterior probabilities and calling genotypes):

```
genoCaller -f microtyper_llh.mhgenos
```

Required arguments

- `-f` the file containing log-likelihoods that was output during step 1. The order of the lines in this file is important, so do not reorder any lines after running step 1. To read from stdin, use `-f -`

Optional arguments

- `-o` the name to give the output file (default: mh_genotypes.txt)
- `-p` a file specifying the priors to use, see below for format. (default: uniform priors)
- `-c` the minimum posterior probability the most probable genotype must have (for a given individual and locus) to be accepted (default: 0.95)
- `-m` the minimum number of reads that match one of the alleles in the most probable genotype at all SNPs for that genotype to be accepted (default: 0)
- `--version` print the version of microTyper being used and exit

The position file

The position file gives information about the SNPs within each locus. It is a tab-delimited file with a REQUIRED header row (actual text in header row is not important). Each line defines a SNP. The columns are, in order,

Locus RefPos Type ValidAlt

- Locus: the name of the reference sequence for the locus containing this SNP
- RefPos: the position of the SNP in the reference sequence
- Type: the type of SNP, relative to the reference. One of "S", "I", or "D" for substitution, insertion, or deletion, respectively
- ValidAlt:
 - for substitution SNPs, a comma separated list of alternative bases to look for in the read (A,C,T, or G). Bases must be capitalized. The reference base is pulled automatically from the reference fasta file.
 - for insertion SNPs, a character (not "D") to use in the output when an insertion is found. The reference allele is automatically designated as "D".
 - for deletion SNPs, a character (not "I") to use in the output when a deletion is found. The reference allele is automatically designated as "I".

The prior file

The prior gives the prior probability for each genotype of each locus. It is a tab-delimited file with a REQUIRED header row (actual text in header row is not important). Each line describes a genotype. The columns are, in order,

Locus Allele1 Allele2 Prior

- Locus: the name of the reference sequence for the locus
- Allele1: the first allele in this genotype
- Allele2: the second allele in this genotype
- Prior: The prior probability

After being read, the priors are normalized within each locus, and so these may be relative probabilities. Priors must not be zero, but can be very small. Priors can be expressed using exponential notation (i.e. 1e-20).

The entries for Allele1 and Allele2 must match exactly the entries present in the output file created by step 1 (with the log-likelihoods for each genotype). **The easiest way to make this file is to run the first step with one input bam file, then delete the "Indiv", "A1_perfect_count", and "A2_perfect_count" columns, and then replace**

the LLH values with your prior values. There is an example prior input file in the "examples" directory.

Output file formats

The output of the first step is a file containing the log-likelihood of each genotype for each locus in each individual. It also has two columns containing the counts of reads that are "perfect matches" for each allele of each genotype. The "A1_perfect_count" column has the number of reads that match Allele1 at all SNPs in the locus. If the genotype is a homozygous genotype, the "A2_perfect_count" column is 0. Otherwise, the "A2_perfect_count" column has the number of reads that match Allele2 at all SNPs in the locus. This file is mainly used as the input for the second step, but is output for users who may want to use the likelihoods or perfect match read counts directly. If a user wants to examine the number of reads that are perfect matches for each allele, this can be extracted by using the values in "A1_perfect_count" for all homozygous genotypes.

The output of the second step contains one line for each individual and each locus. If the most probable genotype for a locus in a given individual passes the filters (-c and -m), it is included in the output in the "Allele1" and "Allele2" columns. If it does not pass the filters, those two columns are blank. Regardless of whether it passed the filters or not, the posterior probability of the most probable genotype is in the "Pr_geno" column. The "A1_perfect" column has the number of reads that match Allele1 at all SNPs in the locus. If the genotype is a homozygous genotype, the "A2_perfect" column is 0. Otherwise, the "A2_perfect" column has the number of reads that match Allele2 at all SNPs in the locus.