BAMily required input:

-L/-list FILE BAMily takes in a plain text file as input containting the path to each individual's sequence data (BAM format). For each individual, a carrier status MUST be assigned (1 carrier, 0 non-carrier). For a nuclear family, in which a father and a child are suspected of sharing a variant of interest not present in either the mother or the other child, the file would be as follows:

```
/path/to/data/father.sorted.bam:1
/path/to/data/mother.sorted.bam:0
/path/to/data/child1.sorted.bam:1
/path/to/data/child2.sort.bam:0
```

-R/-reference FILE BAMily requires a reference sequence in FASTA format.

BAMily optional input:

-O/-output NAME Provide a name for your output VCF file [results]

-P/-prior DOUBLE Set prior for the detection of a variant in a single individual [0.001]

-Q/-minquality DOUBLE Provide a minimum quality cutoff threshold [0.2]

-I/-IndAlleles INT Set the number of independent alleles [number of samples*2]

Example:

java -Xmx1024m -jar /path/to/BAMily.jar -L FamilyB.list -R Sapiens.HG19.fasta -O FamilyB