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**GFESD.cpp**

This C++ program, written by Takahiro Maruki, estimates allele and genotype frequencies from simulated sequence-read data of multiple diploid individuals from a population by a maximum-likelihood (ML) method. To compile this program, type the following command:

g++ GFESD.cpp -o GFESD –lm

Then, to run the program, type the following command,

./GFESD N e n reps P Q out\_file\_name

In the above command, the meanings of the arguments are as follows:

N: number of sampled individuals

e: error rate

n: mean depth of coverage

reps: number of simulation replications

P: major-homozygote frequency

Q: minor-homozygote frequency

out\_file\_name: name of the output file

For example, to run 10,000 simulation replications with N = 100, e = 0.01, n = 3, P = 0.9, Q = 0.1, and output the results in a file named GFESD\_N100e0.01n3P0.9Q0.1.txt, type the following:

./GFESD 100 0.01 3 10000 0.9 0.1 GFESD\_N100e0.01n3P0.9Q0.1.txt