A program to estimate nucleotide diversity from AFLP data

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The source code written in C is named pi_AFLP.c.
First, compile it:

        >> gcc pi_AFLP.c -o pi -lm

which creates a complied program named "pi".
Then, run it:

        >> ./pi

It will ask for the following information, so please type them.
Here is an example from Table 1 in Innan et al. (1999).

For the first primer pair in the table, AG/CAG, input six values from your
observation, then, the program provides an estimate of nucleotide diversity (d).
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Number of selective bases (EcoRI-primer): 2
Number of selective bases (MseI-primer): 3
Lmin: 20
Lmax: 500
Average number of bands (m): 45.5
Proportion of shared bands (F): 0.902

d = 0.006530
Press RETURN to quit the program.
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I suppose that you have AFLP data from multiple primer pairs, which should
have been scored from different gels. It is very important to note the calculation
should be done for each gel (primer pair). Never pool the data from more than
one gel! m and F should be computed for each primer pair.