GENETICS, SOFTWARE

NEW LD MEASURE

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There is a new way to calculate LD that may overcome the limitations of D’ and R^2 that are not easily generalizable to multiallelic markers (or haplotypes) and depend on the distribution of SNPs (or haplotypes).
The paper is at BMC, the sources at the authors’ website. I have slightly modified the program to allow input and output file names on the command line before compiling it. Use at your own risk, yea, yea.

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