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 <u>BMC</u>, the sources at the <u>authors' website</u>. I have slightly modified the program to allow input and output file names on the command line before <u>compiling</u> it. Use at your own risk, yea, yea.

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