**Proportional Method**

1. Installation

*R CMD SHLIB McCOIL\_prop\_code.c llfunction.c*

2. Input format

Assuming there are *n* individuals and *k* loci, SNP information is stored in two *n* × *k* matrices *A1* and *A2*, representing the intensity of two alleles in the SNP assay, respectively. Each element in the matrices, *A1ij* or *A2ij ,* represents the intensity of allele 1 or allele 2 at locus *j* of individual *i*, and missing data is set to -1.

3. Run

See test\_R\_code.R for an example.

**Usage**

McCOIL\_proportional(dataA1, dataA2, ...)

**Arguments**

|  |  |
| --- | --- |
| dataA1, dataA2 | An **R** data frame. The intensity of signals of allele 1 and allele 2 from the SNP assay. Row names are names of samples and column names are names of assays. |
| maxCOI | Upper bound for COI. The default is 25. |
| totalrun | The total number of MCMC iterations. The default is 10000. |
| burnin | The total number of burnin iterations. The default is 1000. |
| M0 | Initial COI. The default is 15. |
| epsilon | The level of measurement error (*εest*). The default is 0.2. |
| path | The default is the current directory. |
| output | The name of output file. The default is “output.txt”. |
| err\_method | The default is 1.  1: use pre-specified epsilon and treat as constant.  3: epsilon is estimated with COI and allele frequencies. |