*THE REAL McCOIL* is a Markov chain Monte Carlo method that estimates complexity of infection and population allele frequencies using SNP data obtained from Sequenom or similar types of SNP assays.

We used the data in two ways: 1) *categorical method*, in which we considered SNP to be heterozygous or homozygous, and 2) *proportional method*, in which the relative signal intensity for each allele is used.

The codes can be run on both Mac and Windows. After compiling, you can run the code using the function ***McCOIL\_categorical*** (categorical) or ***McCOIL\_proportional*** (proportional) in R.

The instructions of how to compile the codes can be found in README.docx in the folders of categorical method and proportional method. You can also find example R codes that show how to use R functions as well as example input and output files in those folders (example R code: *test\_R\_code.R*; input files: *input\_test.txt* [categorical], *dataA1\_test.txt* and *dataA2\_test.txt* [proportional]; output files: *output\_test.txt* and *output\_test.txt\_summary.txt*). Please note that it is important to check the convergence of MCMC and it is recommended to run the codes multiple times and check consistency between them.

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01-31-2017: *THE REAL McCOIL v2* includes the function of estimating parameters of measurement error with COI and allele frequencies.