Chapter 1

Linear Mixed Model Implementation

The LMM implementation is available as C source code. It depends on the standard C libraries CHOLMOD (Davis, 2008) and GSL (Galassi et al., 2009). It can be found at `http://www.mcw.edu/biostatistics/Research/Software`

1.1 Data Preparation

A program has been provided for typical data preparation: `onetime.c` . It depends on two header files. The first `gsl_cholmod.h` defines two C preprocessor (cpp) macros that allow GSL to read and write to CHOLMOD matrices present in memory. `MAT(A, B)` is used for matrices and `VEC(A, B)` is used for vectors. They both take two parameters.

`A`: A pointer to an already existing matrix created by CHOLMOD.

`B`: The name of a GSL object to create. No new memory will be allocated since `A` already has memory allocated to it. Therefore, you will not need to \free" the memory associated with `B`; that will be taken care of when you \free" `A` instead. The new `B` object will need

Table 1.1: The definitions of the values found in `onetime.h`.

Variable	Definition
`p`	the dimension of the fixed parameters β
`q1`	the number of primary clusters (hospitals)
`q2`	the number of secondary clusters (surgeons)
`q`	the number of total clusters
`N`	the number of subjects (patients)

to be operated on as a memory location. For example, if the second parameter is `X`

Table 1.2: List of input/output files for `onetime.c` and their definitions.

Filename:	content definition
`Y.mtx`	the input file for the outcome vector $\boldsymbol{y}$
`uX.mtx`	the input file for the \uncentered" covariates $\boldsymbol{X}$
`X.mtx`	the output file for the \centered" covariates $\boldsymbol{X}$
`XtX.mtx`	the output file for $\boldsymbol{X}^{\prime}\boldsymbol{X}$ where $\boldsymbol{X}$ has been \centered"
`XtY.mtx`	the output file for $\boldsymbol{X}^{\prime}\boldsymbol{y}$ where $\boldsymbol{X}$ has been \centered"
`uZ.mtx`	the input file for the \unordered" $\boldsymbol{Z}$
`ZtZ.mtx`	the output file for $\boldsymbol{Z}^{\prime}\boldsymbol{Z}$
`ZtX.mtx`	the output file for $\boldsymbol{Z}^{\prime}\boldsymbol{X}$ where $\boldsymbol{X}$ has been \centered"
`ZtY.mtx`	the output file for $\boldsymbol{Z}^{\prime}\boldsymbol{y}$
`P.mtx`	the output file for the permutation $\boldsymbol{P}$
`u1mask.mtx`	An output file for a vector of 1s and 0s. The 1s represent the locations of re-ordered hospitals in $\boldsymbol{\alpha}$; the 0s, re-ordered surgeons.
`D1.mtx`	A similar definition to `u1mask.mtx` . It is the hospital portion of $\boldsymbol{D}$ with the surgeon portion zeroed out.
`D2.mtx`	A similar definition to `D1.mtx` . It is the surgeon portion of $\boldsymbol{D}$ with the hospital portion zeroed out.

Table 1.3: The definitions of the values found in `Normal.h`.

Variable	Definition
`p`	the dimension of the fixed parameters β
`q1`	the number of primary clusters (hospitals)
`q2`	the number of secondary clusters (surgeons)
`q`	the number of total clusters
`N`	the number of subjects (patients)
`M`	the number of Gibbs samples to perform
`a1`	the 1st posterior parameter to the Gamma distribution for $_1$
`b1`	the 2nd prior parameter to the Gamma distribution for $_1$
`a2`	the 1st posterior parameter to the Gamma distribution for $_2$
`b2`	the 2nd prior parameter to the Gamma distribution for $_2$
`ae`	the 1st posterior parameter to the Gamma distribution for
`be`	the 2nd prior parameter to the Gamma distribution for
`am`	the prior mean for
`bm`	the prior precision for
`yty`	$\boldsymbol{y}^0\boldsymbol{y}$
`mu`	the initial value of
`taue`	the initial value of
`tau1`	the initial value of $_1$
`tau2`	the initial value of $_2$
`beta`	the initial value of β

Table 1.4: List of input files for `Normal.c` and their definitions.

Filename:	content definition
`C.mtx`	the prior precision of β
`Cc.mtx`	the prior mean of β
`XtX.mtx`	$X'X$ where X has been \centered"
`XtY.mtx`	$X'Y$ where X has been \centered"
`ZtZ.mtx`	$Z'Z$
`ZtX.mtx`	$Z'X$ where X has been \centered"
`ZtY.mtx`	$Z'Y$
`u1mask.mtx`	A vector of 1s and 0s. The 1s represent the locations of re-ordered hospitals in u; the 0s, re-ordered surgeons.
`D1.mtx`	A similar definition to `u1mask.mtx` . It is the hospital portion of D with the surgeon portion zeroed out.
`D2.mtx`	A similar definition to `D1.mtx` . It is the surgeon portion of D with the hospital portion zeroed out.

1.3 Noninformative Prior

The Noninformative prior version of the program, `Normal-Uniform.c`, is very similar to the conjugate prior version. The header file is now named `Normal-Uniform.h`. The definition of the parameters is the same except for those associated with $_1$ and $_2$: a1, b1, a2 and b2. For example, for the XS Scenario, the file looks like Figure 1.3.

```
const int p=4, q1=5, q2=25, q=q1+q2, N=2500, M=20000;
const double a1=(q1-1)/2.,  b1=0.01,
             a2=(q2-1)/2.,  b2=0.01,
             ae=(N+0.1)/2., be=0.1,
             am=0.,         bm=0.001,
             yty=43137.609891;
double mu=0., taue=1., tau1=1., tau2=1.;
```

Chapter 2

Logistic Mixed Model Implementation

The Logistic Mixed Model implementation is available as C source code. It depends on the standard C libraries CHOLMOD (Davis, 2008) and GSL (Galassi et al., 2009). It can be found at `http://www.mcw.edu/biostatistics/Research/Software`

Although, there are fewer one-time calculations for the Logistic Mixed Model, you

After compiling `Logistic.c` into `Logistic.out` (or whatever you are calling your executable), then running `Logistic.out` produces an R source file `Logistic.R` containing the Gibbs samples for β, , $_1$ and

Bibliography

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