C++ Programming for Animal Breeding

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Construction of Normal Equations

- Normal equations
  - Left and Right hand sides
- Ones and zeros
- One-way model
- Two-way model
- Covariates

Normal equations

$$\boldsymbol{y} = \boldsymbol{X}\boldsymbol{\beta} + \boldsymbol{e}$$

- $\boldsymbol{y}$: $n \times 1$ vector
- $\boldsymbol{X}$: $n \times p$ matrix of rank r
- $\boldsymbol{\beta}$: $p \times 1$ vector
- $\boldsymbol{e} \sim \mathrm{N}(\boldsymbol{0}, \boldsymbol{I}\sigma^2)$: $n \times 1$ vector

$$(\boldsymbol{X}'\boldsymbol{X})\widehat{\boldsymbol{\beta}} = \boldsymbol{X}'\boldsymbol{y}$$

- Left hand side ($\boldsymbol{LHS}$) of the normal equations

$$\boldsymbol{X}'\boldsymbol{X}$$

  - p^2 elements

$$\boldsymbol{LHS}_{ij} = \sum_{k=1}^{n} x_{ki}x_{kj}$$

  - np^2 multiplications

- Right hand side ($\boldsymbol{RHS}$) of the normal equations
  - np multiplications

One-way Model

$$y_{ij} = \mu + \alpha_i + e_{ij}$$

Trt	y
1	1.0
1	1.5
2	2.0
2	2.5

$$\boldsymbol{X} = \begin{pmatrix} 1 & 1 & 0 \\ 1 & 1 & 0 \\ 1 & 0 & 1 \\ 1 & 0 & 1 \end{pmatrix}$$

$$\begin{aligned} \boldsymbol{LHS}_{23} &= 1*0+1*0+0*1+0*1 \\ &= 0 \end{aligned}$$

- Perhaps there is a better way!

- $\boldsymbol{LHS}_{ij} = \sum_{k=1}^{n} x_{ki} x_{kj}$
- Think in terms of observations

$$\boldsymbol{X} = \begin{pmatrix} \boldsymbol{x}_1' \\ \boldsymbol{x}_2' \\ \vdots \\ \boldsymbol{x}_n' \end{pmatrix}$$

- $\boldsymbol{LHS}$

$$\boldsymbol{LHS} = \sum_{i=1}^{n} \boldsymbol{x}_i \times \boldsymbol{x}_i'$$

- Series of updates

$$\boldsymbol{LHS}_1 = \boldsymbol{x}_1\boldsymbol{x}_1'$$
$$\boldsymbol{LHS}_2 = \boldsymbol{LHS}_1 + \boldsymbol{x}_2\boldsymbol{x}_2'$$
$$\vdots$$
$$\boldsymbol{LHS} = \boldsymbol{LHS}_n = \boldsymbol{LHS}_{n-1} + \boldsymbol{x}_n\boldsymbol{x}_n'$$
$$\boldsymbol{RHS} = \boldsymbol{RHS}_n = \boldsymbol{RHS}_{n-1} + \boldsymbol{x}_n\boldsymbol{y}_n$$

- Individual update

$$\boldsymbol{x}_1\boldsymbol{x}_1' = \begin{pmatrix}1\\1\\0\end{pmatrix}\begin{pmatrix}1 & 1 & 0\end{pmatrix}$$

$$= \begin{array}{c} \\ 1 \\ 1 \\ 0 \end{array}\begin{array}{c}\begin{array}{ccc}1 & 1 & 0\end{array}\\ \begin{pmatrix}1 & 1 & 0\\ 1 & 1 & 0\\ 0 & 0 & 0\end{pmatrix}\end{array}$$

- Non-zero elements

Row	Column	Value
1	1	1
1	Trt+1	1
Trt+1	1	1
Trt+1	Trt+1	1
1	$\boldsymbol{RHS}$	y_i
Trt+1	$\boldsymbol{RHS}$	y_i

- C++
  - Zero indexed

$$\begin{pmatrix} \{0,0\} & \{0,1\} & \{0,2\} \\ \{1,0\} & \{1,1\} & \{1,2\} \\ \{2,0\} & \{2,1\} & \{2,2\} \end{pmatrix}$$

Header

```
#include <fstream>     //Input/Output header files
#include <iostream>
#include <iomanip>

#include <matvec/doublematrix.h>  // doubleMatrix class
#include <matvec/vector.h>        // vectors class
#include <matvec/session.h>       // matvec housekeeping

using namespace std;              // use standard C++ functions
```

Setup

```
int main() {
        try {
                matvec::SESSION.initialize("matvec_trash");
                matvec::doubleMatrix mme;  // LHS
                matvec::Vector<double> rhs, sol;
                unsigned J[2];
                char* filename = "Data/oneway.dat";
                ifstream datafile;
                datafile.open(filename);
                if(!datafile) {
                        cerr << "Couldn't open " << filename << endl;
                        exit (-1);
```



```
                int n = 3;
                mme.resize(n,n,0.0);
                rhs.resize(n,0.0);
                unsigned trt;
```

Build the normal equations

```
while (datafile >> trt >> y){
                        J[0] = 0;      //Location of nonzeros
                        J[1] = trt;
                        for (unsigned i=0; i<2; i++){
                                unsigned ii = J[i];
                                rhs[ii] += y;
                                for (unsigned j = 0;j<2;j++){
                                        unsigned jj = J[j];
                                        mme[ii][jj] += 1;
                                }
                        }
                }
```


Write results

```
cout <<"\n The lhs ..... \n\n";
for (unsigned i = 0;i<n;i++){
        for (unsigned j = 0;j<n;j++){
                cout << setw(5) << mme[i][j] <<" ";
        }
        cout << endl;
}
cout << endl;
cout <<" The rhs ..... \n\n";
```

Results

```
The lhs .......

   4     2     2
   2     2     0
   2     0     2

The rhs .......

     7
   2.5
   4.5
```


Two-way Model

$$y_{ijk} = \mu + \alpha_i + \beta_j + e_{ijk}$$

TrtA	TrtB	Y
1	1	7.0
1	1	8.0
1	2	15.0
1	2	16.7
2	1	29.0
2	2	30.1

$$\boldsymbol{\beta} = \begin{matrix} 0 \\ 1 \\ 2 \\ 2+1=3 \\ 2+2=4 \end{matrix} \begin{pmatrix} \mu \\ \alpha_1 \\ \alpha_2 \\ \beta_1 \\ \beta_2 \end{pmatrix}$$

- μ at position 0
- α_i at position i
- β_j at position $j+2$

$$\boldsymbol{x}_1\boldsymbol{x}_1' = \begin{pmatrix} 1 & 1 & 0 & 1 & 0 \end{pmatrix} \begin{pmatrix} 1 \\ 1 \\ 0 \\ 1 \\ 0 \end{pmatrix}$$

$$= \begin{pmatrix} 1 & 1 & 0 & 1 & 0 \\ 1 & 1 & 0 & 1 & 0 \\ 1 & 1 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix} \begin{pmatrix} 1 \\ 1 \\ 0 \\ 1 \\ 0 \end{pmatrix}$$

Changes

```
matvec::SESSION.initialize("matvec_trash");
matvec::doubleMatrix mme;
matvec::Vector<double> rhs, sol;
unsigned J[3];
char* filename = "Data/twoway.datc";
ifstream datafile;
datafile.open(filename);
if(!datafile) {
        cerr << "Couldn't open " << filename << endl;
        exit (-1);
}
```



```
mme.resize(n,n,0.0);
rhs.resize(n,0.0);
unsigned trtA, trtB;
double y;
while (datafile >> trtA >> trtB >> y){
        J[0] = 0;
        J[1] = trtA;
        J[2] = 2 + trtB;
        for (unsigned i=0; i<3; i++){
                unsigned ii = J[i];
                rhs[ii] += y;
                for (unsigned j = 0;j<3;j++){
                        unsigned jj = J[j];
                        mme[ii][jj] += 1;
                }
        }
}
```

Results

```
The lhs .......

   6     4     2     3     3
   4     4     0     2     2
   2     0     2     1     1
   3     2     1     3     0
   3     2     1     0     3

The rhs .......

 105.8
  46.7
  59.1
    44
```


Models with Covariates

$$y_{ij} = \mu + \alpha_i + b\, cov_{ij} + e_{ij}$$

TrtA	X	Y
1	1.0	1.0
1	1.5	2.0
2	2.0	3.0
2	2.5	4.0

$$\boldsymbol{\beta} = \begin{matrix} 0 \\ 1 \\ 2 \\ 2+1=3 \end{matrix} \begin{pmatrix} \mu \\ \alpha_1 \\ \alpha_2 \\ b \end{pmatrix}$$

- μ at position 0
- α_i at position i
- b at position $1+2$

$$\boldsymbol{x}_2\boldsymbol{x}_2' = \begin{pmatrix} 1 & 1 & 0 & 1.5 \end{pmatrix} \begin{pmatrix} 1 \\ 1 \\ 0 \\ 1 \\ 1.5 \end{pmatrix}$$

$$= \begin{pmatrix} 1 & 1 & 0 & 1.5 \\ 1 & 1 & 0 & 1.5 \\ 1 & 1 & 0 & 1.5 \\ 0 & 0 & 0 & 0 \\ 1.5 & 1.5 & 0 & 1.5 * 1.5 = 2.25 \end{pmatrix} \begin{pmatrix} 1 \\ 1 \\ 0 \\ 1.5 \end{pmatrix}$$

Changes

- Multiplier vector `V`

$$v = \begin{pmatrix} 1 & 1 & cov_i \end{pmatrix}$$

- Position vector `J[2]=2+1`
- dimension `n`
- `rhs[ii]+=y*V[i]`
- `mme[ii][jj] += V[i]*V[j];`

A C++ class (Recoder)

- Recoding
- Templates and Classes
- Interactions

Recoding

- Assumed the levels for factor A were coded 1...a.
- However, this is rarely the case

A	B	Y
A1	B1	7.0
A1	B1	8.0
A1	B2	15.0
A1	B2	16.7
A2	B1	29.0
A2	B2	30.1

A	A level
A1	1
A1	1
A1	1
A1	1
A2	2
A2	2

- Build a map that takes a "label" and returns a value
- Start with an empty map $\mathcal{M} = \{\}$ with $n = 0$ elements
- Read a record from the data
  - Check to see if the current level α is in $\mathcal{M}$
  - If it's not
    * assign it next value and add it the map

$$\mathcal{M} = \mathcal{M} \cap \{\alpha \Rightarrow n + 1\}$$
$$n = n + 1$$

A	map	count	A level
	$\{\}$	0	
A1	$\{\} + \{A1 = 0 + 1\}$	0+1	1
A1	$\{A1 = 1\}$	1	1
A1	$\{A1 = 1\}$	1	1
A1	$\{A1 = 1\}$	1	1
A2	$\{A1 = 1\} + \{A2 = 1 + 1\}$	1+1	2
A2	$\{A1 = 1, A2 = 2\}$	2	2
A1	$\{A1 = 1, A2 = 2\}$	2	1

Recoder class

```
Recoder<string> ARecoder;
```

- `Recoder`: Recoder class
- `<string>`: It's a Recoder class that works with strings
- `ARecoder`: ARecorder is an object of the Recoder class that works with strings


```
template <class T>
class Recoder : public map<T,unsigned> {
  unsigned count;
 public:
  Recoder(void){count=0;}
  unsigned code(T s){
    typename map<T,unsigned>::iterator mapit = find(s);
    if(mapit == end()){
      (*this)[s] = ++count;
      return count;
    }
    else {
      return (*mapit).second;
    }
```

```
  void display_codes(ostream & os = cout){
    typename Recoder::iterator it;
    for (it=begin(); it!=end();it++){
      os << (*it).first << " " << (*it).second << endl;
    }
  }
};
```

- Perhaps, we should need to spend some time on this.

Building on existing classes

- Frequently someone has done much of the work for you
- Standard Template Library
  - map class
  - Key⇒Value

```
map<string, int> Months;
Months["January"]=1;
Months["June"]=6;
cout << Months["January"] << endl;
```

$$\mathcal{M} = \{January \Rightarrow 1, June \Rightarrow 6\}$$

  - size()

- Iterator

```
map<string,int>::iterator it;
for(it=Months.begin();it!=Months.end();it++){
    cout << it->first << "->" << it->second<<endl;
}
```

- find(Key)
  - pointer to element whose key is Key
  - or end() if not found

A simple example

```
#include <map>
int main() {
  unsigned Value=0;
  string Key;
  map<string, unsigned> mymap;
  map<string, unsigned>::iterator it;
  while(cin >> Key ){
    if(mymap.find(Key)==mymap.end()) mymap[Key]=++Value;
  }
  for(it=mymap.begin();it!=mymap.end();it++){
    cout << setw(9) << setiosflags(ios_base::left) << it->first  <<" -> "
    << resetiosflags(ios_base::left) << setw(2)<< it->second << endl;
  }
}
```

```
January         April     ->  4
February        August    ->  8
March           December  -> 12
April           February  ->  2
May             January   ->  1
June            July      ->  7
July            June      ->  6
August          March     ->  3
September       May       ->  5
October         November  -> 11
November        October   -> 10
December        September ->  9
```


- Return to the Recoder class
- Recorder can use a variety of Key types and is a descendant of `map`
- `count` will be a private variable
- Now we will start the public section and define a constructor which will initialize `count`

```
template <class T>
class Recoder : public map<T,unsigned> {
  unsigned count;
 public:
  Recoder(void){count=0;}
```

- Define a code function

  The code function will return the value associated with key s. If key s is not in the map, then it will be added.

```
unsigned code(T s){
  typename map<T,unsigned>::iterator mapit = find(s);
  if(mapit == end()){
    (*this)[s] = ++count;
    return count;
  }
  else {
    return (*mapit).second;
  }
```


- Define a display_codes function

```
void display_codes(ostream & os = cout){
  typename Recoder::iterator it;
  for (it=begin(); it!=end();it++){
    os << (*it).first << " " << (*it).second << endl;
  }
 }
};
```

The Program

- The Declarations

```
#include <fstream>
#include <iostream>
#include <iomanip>
...
#include <map>
#include <matvec/doublematrix.h>
#include <matvec/vector.h>
#include <matvec/session.h>
#include "util.h"

using namespace std;
```



```
int main() {
        try{
                matvec::SESSION.initialize("matvec_trash");
                Recoder<string> ARecoder;
                matvec::doubleMatrix mme;
                matvec::Vector<double> rhs, sol;
                char *filename     = "Data/twoway.dat";
                char* outfile_name = "Data/twoway.dat.coded";
                string AString, BString;
                double y;
                unsigned J[2], ALevel;
                {ifstream datafile;
                        datafile.open(filename);
                        if(!datafile) {
                                cerr << "Couldn't open " << filename << endl;
                                exit (-1);
                        }
```

```
ofstream outfile;
  outfile.open(outfile_name,ios::trunc);
  if(!outfile) {
          cerr << "Couldn't open " << outfile_name << endl;
          exit (-1);
  }
  outfile.setf(ios::fixed);
```


- Recode and output the recoded values

```
        while (datafile >> AString >> BString >> y){
                ALevel = ARecoder.code(AString);
                outfile << setw(5) << ALevel <<" " << y << endl;
          }
          datafile.close();
          outfile.close();
}
```

- Dimensions of the normal equations are determined from the data.

```
{ifstream datafile;
          datafile.open(outfile_name);
          unsigned nlevelsA= ARecoder.size();
          unsigned n = nlevelsA + 1;
          mme.resize(n,n,0.0);
          rhs.resize(n,0.0);
          J[0] = 0;
          while (datafile >> ALevel >> y){
                  J[1] = ALevel;
                  for (unsigned i = 0;i<2;i++){
                          unsigned ii = J[i];
                          rhs[ii] += y;
                          for (unsigned j = 0;j<2;j++){
                                  unsigned jj = J[j];
                                  mme[ii][jj] += 1;
                          }
```



```
                  }
          }
          for (unsigned i = 0;i<n;i++){
                  for (unsigned j = 0;j<n;j++){
                          cout << setw(5) << mme[i][j] <<" ";
                  }
                  cout << endl;
          }
          cout << endl;
```

- Solve the normal equations

```
                cout << rhs << endl;
                sol = mme.ginv0()*rhs;
                cout << sol << endl;
                ARecoder.display_codes();
                datafile.close();
            }
        }
        catch (matvec::exception &ex) {
            cerr << ex.what() << endl;
            exit(1);
        }
        catch (...) {
            cerr << "other exceptions were caught"<<endl;
            exit(1);
        }
}
```


Results

```
   6     2     4
   2     2     0
   4     0     4

  105.8
   59.1
   46.7

 13.7417
 15.8083
-2.06667

A1 1
A2 2
```

Interactions

$$y_{ijk} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + e_{ijk}$$

- A×B interaction term can be constructed by combining the A and B labels

A	B	AB
A1	B1	A1xB1
A1	B1	A1xB1
A1	B2	A1xB2
A1	B2	A1xB2
A2	B1	A2xB1
A2	B2	A2xB2

- Combine the Labels

```
AString+"x"+BString
```

- Code the levels

```
ABLevel = ABRecoder.code(AString+"x"+BString);
```

Random Effects

- Mixed Model Equations
- $D = I\sigma^2$
- A^{-1}
  - Pedigree
  - Inbreeding
  - Non-zero elements

Mixed Model Equations

$$y = X\beta + Zu + e$$

$$\begin{pmatrix} u \\ e \end{pmatrix} \sim \mathrm{N}\left[\begin{pmatrix} 0 \\ 0 \end{pmatrix}, \begin{pmatrix} D & 0 \\ 0 & R \end{pmatrix}\right]$$

$$\begin{pmatrix} X'R^{-1}X & X'R^{-1}Z \\ Z'R^{-1}X & Z'R^{-1}Z + D^{-1} \end{pmatrix} \begin{pmatrix} \widehat{\beta} \\ \widehat{u} \end{pmatrix} = \begin{pmatrix} X'R^{-1}y \\ Z'R^{-1}y \end{pmatrix}$$

- Which can be simplified if $\boldsymbol{R} = \boldsymbol{I}\sigma_0^2$

$$\begin{pmatrix} \boldsymbol{X}'\boldsymbol{X} & \boldsymbol{X}'\boldsymbol{Z} \\ \boldsymbol{Z}'\boldsymbol{X} & \boldsymbol{Z}'\boldsymbol{Z} + \boldsymbol{D}^{-1}\sigma_0^2 \end{pmatrix} \begin{pmatrix} \widehat{\boldsymbol{\beta}} \\ \widehat{\boldsymbol{u}} \end{pmatrix} = \begin{pmatrix} \boldsymbol{X}'\boldsymbol{y} \\ \boldsymbol{Z}'\boldsymbol{y} \end{pmatrix}$$

- Letting $\boldsymbol{W} = (\boldsymbol{X} \quad \boldsymbol{Z})$ and $\boldsymbol{\theta}' = (\boldsymbol{\beta}' \quad \boldsymbol{u}')$

$$\left[\boldsymbol{W}'\boldsymbol{W} + \begin{pmatrix} \boldsymbol{0} & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{D}^{-1}\sigma_0^2 \end{pmatrix}\right] \left(\widehat{\boldsymbol{\theta}}\right) = \boldsymbol{W}'\boldsymbol{y}$$

addGinv

$$\begin{aligned} \boldsymbol{y}_{ijk} &= \mu + \alpha_i + b_j + e_{ijk} \\ \boldsymbol{b} &\sim \mathrm{N}(\boldsymbol{0}, \boldsymbol{I}\sigma_b^2) \\ \boldsymbol{e} &\sim \mathrm{N}(\boldsymbol{0}, \boldsymbol{I}\sigma_e^2) \\ \lambda &= \sigma_e^2/\sigma_b^2 \\ i &= 1 \ldots a \\ j &= 1 \ldots b \\ k &= 1 \ldots n_{ij} \end{aligned}$$

- Want to add b λ's to the diagonal of the left hand sides starting at the `nlevelsA+1` diagonal element.
- Define a function which adds the value ratio to the n diagonal elements starting at the start element.

```
void addGinv(matvec::doubleMatrix& lhs, unsigned start,
             unsigned n, double ratio){
               for(unsigned i=0;i<=n;i++){
                 unsigned ii=start+i;
                   lhs[ii][ii]+=ratio;
               }
 }
```



```
while (datafile >> ALevel >> BLevel >> ABLevel >>  y){
        J[1] = ALevel;
        J[2] = nlevelsA + BLevel;
        J[3] = nlevelsA + nlevelsB + ABLevel;
        for (unsigned i = 0;i<4;i++){
                ....
                 }
        }
}
addGinv(mme,nlevelsA + nlevelsB+1,nlevelsAB,ratio);
for (unsigned i = 0;i<n;i++){
        for (unsigned j = 0;j<n;j++){
                cout << setw(5) << mme[i][j] <<" ";
        }
        cout << endl;
}
cout << endl;
```

Calculation A^{-1}

- Offspring i with Parents s and d
- s and d known

$$d = \frac{4}{2 - f_s - f_d}$$

- Only s known

$$d = \frac{4}{3 - f_s}$$

- Both unknown

$$d = 1$$

For known animals and typical elements

$$A^{ii} += [-1/2]^0 \, d = d$$

$$A^{is} += [-1/2]^1 \, d = \frac{-d}{2}$$

$$A^{id} += [-1/2]^1 \, d = \frac{-d}{2}$$

$$A^{ss} += [-1/2]^2 \, d = \frac{d}{4}$$

$$A^{sd} += [-1/2]^2 \, d = \frac{d}{4}$$

$$A^{dd} += [-1/2]^2 \, d = \frac{d}{4}$$

```
void Pedigree::addAinv(matvec::doubleMatrix& lhs, unsigned startRow,
                       unsigned startCol, double ratio){
        double q[3];
        double d,fs,fd;
        unsigned pos[3];
        vector<PNode*>::iterator it;
        for (it=pedVector.begin();it!=pedVector.end();it++){
                pos[0] = (*it)->sire;
                pos[1] = (*it)->dam;
                pos[2] = (*it)->ind;
                if((*it)->sire && (*it)->dam){
                        q[0] = -0.5;
                        q[1] = -0.5;
                        q[2] =  1.0;
                        fs = pedVector[pos[0]-1]->f;
                        fd = pedVector[pos[1]-1]->f;
                        d = 4.0/(2 - fs - fd);
                }
```



```
                else if((*it)->sire){
                        q[0] = -0.5;
                        q[1] =  0.0;
                        q[2] =  1.0;
                        fs = pedVector[pos[0]-1]->f;
                        d = 4.0/(3-fs);
                }
                else if((*it)->dam){
                        q[0] =  0.0;
                        q[1] = -0.5;
                        q[2] =  1.0;
                        fd = pedVector[pos[1]-1]->f;
                        d = 4.0/(3-fd);
                }
```

```
        else{
                q[0] =  0.0;
                q[1] =  0.0;
                q[2] =  1.0;
                d = 1.0;
        }
```



```
for (unsigned i=0;i<3;i++){
        if(pos[i]){
                unsigned ii = startRow + pos[i] - 1;
                for (unsigned j=0;j<3;j++){
                        if(pos[j]) {
                                unsigned jj = startCol + pos[j] - 1;
                                lhs[ii][jj] += ratio*q[i]*d*q[j];
                        }
                    }
                }
         }
    }
}
```

Inbreeding

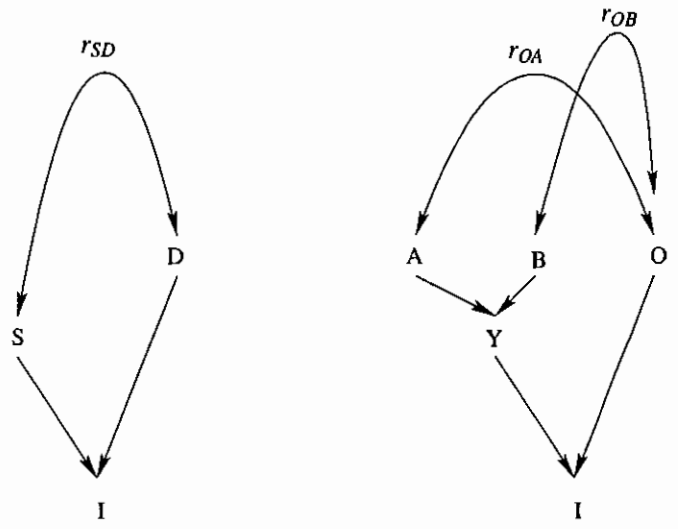
- Malecot's coefficient of coancestry between the sire and the dam

$$f_i = r_{sd}$$

- If r_{sd} is unknown, then

$$r_{sd} = .5[r_{oa} + r_{ob}]$$

where o is the oldest of the s and d, and a and b are the sire and dam of the youngest.



$C = \{r_{ij}\}$ Coancestry matrix

- Only need some of the values
- Symmetric
- map<idx,double>

```
class SparseCij {
 map<const idx , double> C;
public:
  double retrieve_cij(const unsigned i, const unsigned j);
  void   put_cij(const unsigned i, const unsigned j, double cij);
  void   clear(void){C.clear();}
};
```



```
class idx {
public:
  unsigned i,j;
  bool operator<(const idx y) const
    {
      if (i < y.i) { return 1; }
      if (i > y.i) { return 0; }
      else { if (j < y.j) { return 1; }
             else { return 0; }
           }
    }
};
```

$$\begin{pmatrix} & < & \\ < & ij & \not< \\ & \not< & \end{pmatrix}$$

- Retrieve an entry or return a -1
- Symmetric (Store Upper Triangle$\Rightarrow$ $i \leq j$)

```
double SparseCij::retrieve_cij(const unsigned i, const unsigned j){
  idx ind;
  unsigned ii,jj;
  ii = i; jj = j;
  if (i>j) { ii = j; jj = i; }
  ind.i = ii;
  ind.j = jj;
  map<const idx , double>::iterator cit = C.find(ind);
  if (cit != C.end()) { return cit->second; }
  else                { return -1.0; }
}
```


- $f_i = r_{sd}$

```
void Pedigree::calc_inbreeding(void){
        vector <PNode*>::iterator it;
        unsigned rec = 0, rec1 = 0, non_rec = 0;
        cout << "calculating inbreeding \n";
        for (it=pedVector.begin();it!=pedVector.end();it++){
                (*it)->f = get_rij((*it)->sire,(*it)->dam);
        }
}
```

- If the r_{sd} exists, then return the stored value
- Otherwise, calculate it using

$$r_{sd} = .5[r_{oa} + r_{ob}]$$


```
double Pedigree::get_rij(int i, int j){
        if (i==0||j==0){ return 0.0; }
        double x = SpCij.retrieve_cij(i,j);
        if(x != -1.0) { return x; }
        int old, young;
        if(i < j){ old = i; young = j; }
        else if(j < i){ old = j; young = i; }
        else{  double f = pedVector[i-1]->f;
               x = 0.5*(1 + f);
               SpCij.put_cij(i,j,x);
               return x; }
        int y_sire = pedVector[young-1]->sire;
        int y_dam  = pedVector[young-1]->dam;
        x = (get_rij(old,y_sire)+get_rij(old,y_dam))/2.0;
        SpCij.put_cij(i,j,x);
        return x;
}
```

Pedigree Object

- Gather pedigree information
  - Vector of individual pedigree information
    `vector <PNode*> pedVector;`
  - Individual ID map
    `Recoder<string> coder;`
  - Coancestry matrix
    `SparseCij SpCij;`
- Variety of pedigree operators


```
class Pedigree : public map<string,PNode*> {
public:
  unsigned COUNT;
  SparseCij SpCij;
  vector <PNode*> pedVector;
  Recoder<string> coder;
  void inputPed(char* fname);
  void displayPed(void);
  void generateEntriesforParents(void);
  void codePed();
  void code(PNode *ptr);
  void calc_inbreeding(void);
  void makePedVector(void);
  void fillCoder(void);
  double get_rij(int i, int j);
  void output(char* ped);
  void addAinv(matvec::doubleMatrix& lhs, ...,  double ratio);
};
```

Pedigree Node

- Gather an individual's pedigree information
  - Alphanumeric id's
  - Coded id's
  - Inbreeding coefficients

```
class PNode {
public:
   int     ind, sire, dam;
  double    f;
  string ind_str, sire_str, dam_str;
  ...
```


- ...
- Initialize with missing values

```
PNode(string indstr, string damstr, string sirestr){
    ind = -1;
    sire = -1;
    dam = -1;
    f = -1.0;
    ind_str  = indstr;
    sire_str = sirestr;
    dam_str  = damstr;
  }
};
```

Input Pedigree

- Read pedigree data into a pedVector
- Add missing parents to pedVector
- Work our way through pedVector to generate coded id's
  1. Code parents
  2. Code individual
- Calculate inbreeding
- Fill Pedigree Recoder with coded id's

Read pedigree data into a pedVector

```
void Pedigree::inputPed(char* fname){
        ...
        PNode *ptr;
        while (datafile>>indstr>>damstr>>sirestr){
                ptr = new PNode(indstr, damstr, sirestr);
                (*this)[indstr] = ptr;
        }
        datafile.close();
        generateEntriesforParents();
        codePed();
        makePedVector();
        calc_inbreeding();
        fillCoder();
}
```

Work our way through pedVector to generate coded id's

```
void Pedigree::codePed(){
        Pedigree::iterator it;
        COUNT = 0;
        unsigned rec = 0, rec1 = 0;
        for(it=begin();it!=end();it++){
                PNode *ptr =(*it).second;
                code(ptr);
        }
}
```



```
void Pedigree::code(PNode *ptr){
        if(ptr->ind != -1) { // already coded
                return;
        }
        .
        .
        .
        }
        else{
                PNode* sire_ptr = (*this)[ptr->sire_str];
                if (sire_ptr->ind == -1) { code(sire_ptr); }
                PNode*  dam_ptr = (*this)[ptr->dam_str ];
                if ( dam_ptr->ind == -1) { code(dam_ptr ); }
                ptr->ind = ++COUNT;
                ptr->sire = sire_ptr->ind;
                ptr->dam  = dam_ptr->ind;
        }
}
```

Fill Pedigree Recoder with coded id's

- Fill pedVector young to old

```
void Pedigree::makePedVector(void){
        Pedigree::iterator it;
        pedVector.resize(size());
        for(it=begin();it!=end();it++){
                PNode *ptr = (*it).second;
                unsigned i = ptr->ind - 1;
                pedVector[i] = ptr;
        }
}
```


- Build pedigree from young to old

```
void Pedigree::fillCoder(void){
    vector<PNode *>::iterator it;
    for(it=pedVector.begin();it!=pedVector.end();it++)
            coder.code((*it)->ind_str);
}
```

Adding A^{-1} to the mixed model equations

- Read in Pedigree
- Recode data using the pedigree recoder for additive effects
- Build $\boldsymbol{W}'\boldsymbol{W}$ and $\boldsymbol{W}'\boldsymbol{y}$
- Add $\boldsymbol{A}^{-1}\lambda$

Maternal Effects and Multi-trait Models

- Maternal effects
  - Correlated random effects
- Multiple Trait Models

Maternal effects

- Two additive genetic effects
  - Direct genetic effect $\boldsymbol{a} \sim \mathrm{N}(\boldsymbol{0}, \boldsymbol{A}\sigma_a^2)$
  - Maternal genetic effect $\boldsymbol{m} \sim \mathrm{N}(\boldsymbol{0}, \boldsymbol{A}\sigma_{am}^2)$

$$\boldsymbol{y} = \boldsymbol{X}\boldsymbol{\beta} + \boldsymbol{Z}_d\boldsymbol{a} + \boldsymbol{Z}_m\boldsymbol{m} + \boldsymbol{e}$$

- Correlated random effects $\mathrm{cov}(\boldsymbol{a}, \boldsymbol{m}) = \boldsymbol{A}\sigma_{am}$

$$\boldsymbol{u} = \begin{pmatrix} \boldsymbol{a} \\ \boldsymbol{m} \end{pmatrix} \sim \mathrm{N}\left[\boldsymbol{0}, \boldsymbol{D} = \boldsymbol{A} \otimes \boldsymbol{G}\right]$$

Mixed Model Equations

$$\left[\boldsymbol{W}'\boldsymbol{R}^{-1}\boldsymbol{W} + \begin{pmatrix} \boldsymbol{0} & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{D}^{-1} \end{pmatrix}\right]\left(\widehat{\boldsymbol{\theta}}\right) = \boldsymbol{W}'\boldsymbol{R}^{-1}\boldsymbol{y}$$

$$\boldsymbol{D} = \boldsymbol{A} \otimes \boldsymbol{G}$$

$$\boldsymbol{D} = \begin{pmatrix} \boldsymbol{A}\sigma_a^2 & \boldsymbol{A}\sigma_{am} \\ \boldsymbol{A}\sigma_{am} & \boldsymbol{A}\sigma_m^2 \end{pmatrix}$$

$$\boldsymbol{D}^{-1} = \boldsymbol{A}^{-1} \otimes \boldsymbol{G}^{-1}$$

- One additional effect to $\boldsymbol{W'R^{-1}W}$ and $\boldsymbol{W'R^{-1}y}$
- Add $\boldsymbol{A^{-1}}\lambda_i$ to the direct and maternal sections of the left hand sides
- Add $\boldsymbol{A^{-1}}\lambda_{am}$ to direct and maternal intersection of the left hand sides

$$\begin{pmatrix} \lambda_a & \lambda_{am} \\ \lambda_{am} & \lambda_m \end{pmatrix} = \boldsymbol{G^{-1}}$$

Example

Data

Animal	Dam	Y
CC2	AA1	5.7
DDD	CC2	7.0
CC1	AA3	5.0

Pedigree

Animal	Dam	Sire
AA1	0	0
DDD	CC2	BB1
AA2	0	0
BB1	AA1	0
BB2	0	AA2
CC1	AA3	AA4
CC2	AA1	BB2

- Input the pedigree
  - Pedigree Recoder
  - Calculate Inbreeding coefficients

Uncoded		
Animal	Dam	Sire
AA1	0	0
DDD	CC2	BB1
AA2	0	0
BB1	AA1	0
BB2	0	AA2
CC1	AA3	AA4
CC2	AA1	BB2

Coded				
Individual	Ind.	Sire	Dam	F
AA1	1	0	0	0
AA2	2	0	0	0
AA3	3	0	0	0
AA4	4	0	0	0
BB1	5	0	1	0
BB2	6	2	0	0
CC1	7	4	3	0
CC2	8	6	1	0
DDD	9	5	8	0.125

Program

```
Pedigree ped;
ped.inputPed("Data/additive.ped");
ped.displayPed();
```

- Defines the recoder that will be used for both the direct and maternal effects.

```
ped.coder
```

Recode the data

```
while (datafile >> strId >> strIdDam >> y){
        directLevel = ped.coder.code(strId);
        maternalLevel = ped.coder.code(strIdDam);
        outfile << setw(5) << directLevel << " " <<
                                maternalLevel << " " << y << "\n";
}
datafile.close();
outfile.close();
```

- Use pedigree coder for additive genetic effects.

Build $W'R^{-1}W$ and $W'R^{-1}y$

- Addition of $R^{-1} = \text{Diag}\, I\sigma_0^2$

$$W'W = \sum_{i=1}^{n} w_i w_i'$$

$$W'R^{-1}W = \sum_{i=1}^{n} \frac{w_i w_i'}{\sigma_0^2}$$

$$W'R^{-1}y = \sum_{i=1}^{n} \frac{w_i y_i}{\sigma_0^2}$$

```
for(unsigned i=0;i<n;i++) maxw=max(maxw,labels[i].length());
mme.resize(n,n,0.0);
rhs.resize(n,0.0);
J[0] = 0;
while (datafile >> directLevel >> maternalLevel >> y){
        J[1] = directLevel;
        J[2] = nlevelsDirect + maternalLevel;
        for (unsigned i = 0;i<3;i++){
                unsigned ii = J[i];
                rhs[ii] += y*resVarInv;
                for (unsigned j = 0;j<3;j++){
                        unsigned jj = J[j];
                        mme[ii][jj] += 1.*resVarInv;
                }
        }
}
```


Addition of $A^{-1} \otimes G^{-1}$

```
unsigned startRow, startCol;
matvec::doubleMatrix G;
G.resize(2,2);
G(1,1) = 1.0; G(1,2) = 0.5; G(2,1) = 0.5; G(2,2)=2.0;
matvec::doubleMatrix Gi = G.inv();
startRow = 1;                       startCol = 1;
ped.addAinv(mme,startRow,startCol,Gi(1,1));
startRow = 1;                       startCol = nlevelsDirect + 1;
ped.addAinv(mme,startRow,startCol,Gi(1,2));
startRow = nlevelsDirect + 1;       startCol = 1;
ped.addAinv(mme,startRow,startCol,Gi(2,1));
startRow = nlevelsDirect + 1;       startCol = nlevelsDirect + 1;
ped.addAinv(mme,startRow,startCol,Gi(2,2));
```

Multiple Traits

- Still have a linear mixed model

$$\boldsymbol{y} = \boldsymbol{W}\boldsymbol{\beta} + \boldsymbol{Z}\boldsymbol{u} + \boldsymbol{e}$$

$$\begin{pmatrix} \boldsymbol{u} \\ \boldsymbol{e} \end{pmatrix} \sim \mathrm{N}\left[\begin{pmatrix} \boldsymbol{0} \\ \boldsymbol{0} \end{pmatrix}, \begin{pmatrix} \boldsymbol{D} & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{R} \end{pmatrix} \right]$$

- $\boldsymbol{R}$ is no longer a diagonal matrix

- For trait t and individual i, the model equation is

$$y_{it} = \boldsymbol{w}'_{i1}\boldsymbol{\theta}_i + e_{it}$$

- Group the observations by individual into a vector

$$\begin{pmatrix} y_{i1} \\ y_{i2} \end{pmatrix} = \begin{pmatrix} \boldsymbol{w}'_{i1} & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{w}'_{i2} \end{pmatrix} \begin{pmatrix} \boldsymbol{\theta}_1 \\ \boldsymbol{\theta}_2 \end{pmatrix} + \begin{pmatrix} e_{i1} \\ e_{i2} \end{pmatrix}$$

$$\boldsymbol{y}_i = \boldsymbol{W}'_i\boldsymbol{\theta} + \boldsymbol{e}_i$$

Construction of $W'R^{-1}W$

$$W = \begin{pmatrix} W_1' \\ \vdots \\ W_N' \end{pmatrix}$$

$$R^{-1} = \bigotimes R_i^{-1}$$

$$W'R^{-1}W = \sum_{i=1}^{N} W_i R_i^{-1} W_i'$$

$$W_i R_i^{-1} W_i' = \begin{pmatrix} w_{i1} & 0 \\ 0 & w_{i2} \end{pmatrix} \begin{pmatrix} r^{11} & r^{12} \\ r^{21} & r^{22} \end{pmatrix} \begin{pmatrix} w_{i1}' & 0 \\ 0 & w_{i2}' \end{pmatrix}$$

$$= \begin{pmatrix} w_{i1} r^{11} w_{i1}' & w_{i1} r^{12} w_{i2}' \\ w_{i2} r^{21} w_{i1}' & w_{i2} r^{22} w_{i2}' \end{pmatrix}$$

Construction of $W'R^{-1}y$

$$y = \begin{pmatrix} y_1 \\ \vdots \\ y_N \end{pmatrix}$$

$$R^{-1} = \bigotimes R_i^{-1}$$

$$W'R^{-1}y = \sum_{i=1}^{N} W_i R_i^{-1} y_i$$

$$W_i R_i^{-1} y_i = \begin{pmatrix} w_{i1} & 0 \\ 0 & w_{i2} \end{pmatrix} \begin{pmatrix} r^{11} & r^{12} \\ r^{21} & r^{22} \end{pmatrix} \begin{pmatrix} y_{i1} \\ y_{i2} \end{pmatrix}$$

$$= \begin{pmatrix} w_{i1}(r^{11} y_{i1} + r^{12} y_{i2}) \\ w_{i2}(r^{21} y_{i1} + r^{22} y_{i2}) \end{pmatrix}$$

Two trait additive example

$$y_{it} = \mu_i + a_{it} + e_{it}$$

$$\boldsymbol{\theta} = \begin{pmatrix} \mu_1 \\ \boldsymbol{a}_1 \\ \mu_2 \\ \boldsymbol{a}_2 \end{pmatrix}$$

$$\begin{pmatrix} 0 \\ (1 \ldots n_d) \\ n_d + 1 \\ (n_d + 2 \ldots 2 * n_d + 2) \end{pmatrix}$$

Implementation

- Build $\boldsymbol{R}^{-1}$

```
matvec::doubleMatrix R, Ri;
R.resize(2,2);
R(1,1) = 1.0;
R(1,2) = 0.5;
R(2,1) = R(1,2);
R(2,2) = 2.0;
Ri = R.inv();
```

- Initialize

```
unsigned nlevelsDirect   = ped.coder.size();
unsigned n = 1 + nlevelsDirect + 1 + nlevelsDirect;
mme.resize(n,n,0.0);
rhs.resize(n,0.0);
Tr[0] = 1;  // μ1 ⇒ Trait 1
Tr[1] = 1;  // a1 ⇒ Trait 1
Tr[2] = 2;  // μ2 ⇒ Trait 2
Tr[3] = 2;  // a2 ⇒ Trait 2
```


- Build $\boldsymbol{W}'\boldsymbol{R}^{-1}\boldsymbol{W}$ and $\boldsymbol{W}'\boldsymbol{R}^{-1}\boldsymbol{y}$

```
J[0] = 0;
J[2] = 1 + nlevelsDirect;double y[2];
while (datafile >> directLevel >> y[0] >> y[1]){
        J[1] = directLevel;
        J[3] = nlevelsDirect + 1 + directLevel;
        for (unsigned i = 0;i<4;i++){
                unsigned ii = J[i];
                unsigned ti = Tr[i];
                for (unsigned k=0;k<2;k++){
                        rhs[ii] += Ri(ti,k+1)*y[k];
                }
                for (unsigned j = 0;j<4;j++){
                        unsigned jj = J[j];
                        unsigned tj = Tr[j];
                        mme[ii][jj] += Ri(ti,tj);
                }
```

- Add $A^{-1} \otimes G^{-1}$

```
matvec::doubleMatrix G;
G.resize(2,2);
G(1,1) = 1.0; G(1,2) = 0.5; G(2,1) = 0.5; G(2,2)=2.0;
matvec::doubleMatrix Gi = G.inv();
unsigned startRow, startCol;
startRow = startCol = 1;
ped.addAinv(mme,startRow,startCol,Gi(1,1));
startRow = 1;
startCol = 1 + nlevelsDirect + 1
ped.addAinv(mme,startRow,startCol,Gi(1,2));
startRow = 1 + nlevelsDirect + 1;
startCol = 1;
ped.addAinv(mme,startRow,startCol,Gi(2,1));
startRow = 1 + nlevelsDirect + 1;
startCol = 1 + nlevelsDirect + 1;
ped.addAinv(mme,startRow,startCol,Gi(2,2));
```


Matvec classes for GLMM

- GLMM
- Matvec Program
- Matvec Class Library
  - Data Prep
  - Model Specification
  - Estimation and Testing

GLMM

- Linear Mixed Model

$$\boldsymbol{y}_i|\boldsymbol{u} \sim \text{ ind. } \mathrm{N}(\boldsymbol{X}_i\boldsymbol{\beta} + \boldsymbol{Z}_i\boldsymbol{u}, \boldsymbol{R}_i)$$
$$\boldsymbol{u} \sim \mathrm{N}(\boldsymbol{0}, \boldsymbol{D})$$

  - $\boldsymbol{\mu}_i = \mathrm{E}(\boldsymbol{y}_i|\boldsymbol{u})$ is a linear function of $\boldsymbol{\theta}$
  - $\mathrm{var}(\boldsymbol{y}_i|\boldsymbol{u})$ doesn't depend on $\boldsymbol{\mu}_i$
  - Data is normally distributed

- Generalized Linear Mixed Model
  - Conditional Independence
  - Linear predictor

$$\boldsymbol{\eta}_i = \boldsymbol{X}_i\boldsymbol{\beta} + \boldsymbol{Z}_i\boldsymbol{u}$$

  - $\boldsymbol{\mu}_i = h(\boldsymbol{\eta}_i)$ is a function of $\boldsymbol{\eta}_i$.
    - Inverse link function: $\boldsymbol{\eta}_i \rightarrow \boldsymbol{\mu}_i$
    - Link function: $\boldsymbol{\eta}_i \leftarrow \boldsymbol{\mu}_i$
  - Variance function: $\mathrm{var}(\boldsymbol{y}_i|\boldsymbol{u}) = \nu(\boldsymbol{\mu}_i, \psi)$
    - Scale parameters: ψ

- Posterior mode estimates of the fixed and random effects

$$\begin{pmatrix} X'H'R^{-1}HX & X'H'R^{-1}HZ \\ Z'H'R^{-1}HX & Z'H'R^{-1}HZ \end{pmatrix} \begin{pmatrix} \widehat{\beta} \\ \widehat{u} \end{pmatrix} = \begin{pmatrix} X'H'R^{-1}y^* \\ Z'H'R^{-1}y^* \end{pmatrix}$$

- Which involves a number of derivatives and other fun things
- `matvec::GLMM` call is a C++ class for working with generalized linear mixed models

Matvec Program

- The GLMM class has been incorporated into the Matvec program
- Structure is very similar to a C++ program
  - Data Prep
  - Model Specification
  - Estimation and Testing

Threshold example from Gianola and Foulley (1983)[1]

- Calving Difficulty: 0–2 (Easy–Difficult)
- Fixed Effects: Herd-Year, Age of Sam, Sex of Calf
- Random Effect: Sire $\mathrm{N}(0, \sigma_s^2 = 1/19)$
- $\Pr(0|\eta_i) = \Phi(\eta_i)$
- $\Pr(1|\eta_i) = \Phi(\eta_i + \tau_1) - \Phi(\eta_i)$
- $\Pr(2|\eta_i) = 1 - \Phi(\eta_i + \tau_1)$

[1]Gianola, D. and J. L. Foulley. (1983) Sire evaluation for ordered categorical traits with a threshold model. *Génét. Sél. Evol.*,**15**:201-224;


```
D=Data();
D.input("../data/calve.dat","HY age sex $ sire n score");
M=Model();
M.equation("score=HY age sex sire,score=intercept");
M.variance("sire",1/19*identity(2,2));
M.variance("residual",identity(2,2));
M.weight("n");
M.link("thresh",0);
M.param(1);
M.fitdata(D);
M.glim();
M.contrast("HY",[1,0,-1]);
M.save("calve_g.out");
M.vce_aireml(40,0);
M.contrast("HY",[1,0,-1]);
M.save("calve.out");
```

```
              RESULTS FROM CONTRAST(S)
 ------------------------------------------------------------
  Contrast MME_addr    K_coef   Raw_data_code
  ------------------------------------------
   1          1            1   score:HY:1
   1          3           -1   score:HY:2
         estimated value (K'b-M) = 0.297455 +- 0.495004
            Prob(|t| > 0.600915) = 0.547965 (p_value)
 ------------------------------------------------------------

Original  Residual Log Likelihood:-28.2167

 Iteration 1.0 Res Log Like -27.9195 Change 0.29719
 Iteration 2.0 Res Log Like -27.9348 Change -0.0153321
     ...
 Iteration 23.0 Res Log Like -27.9465 Change -1.42109e-14
 Iteration 24.0 Res Log Like -27.9465 Change -7.10543e-15
```



```
 Iteration 24 Converged
 Final Estimates
0.269984
       0
0.0526316
 Last Change
-3.17624e-14
       0
       0
 Unscaled Last Change
-3.17624e-14
       0
       0
 Residual log likelihood -27.9465
 Asy Covariance Matrix
 0.202462        0        0
        0        0        0
        0        0        0
```

```
          RESULTS FROM CONTRAST(S)
-----------------------------------------------------------
 Contrast MME_addr    K_coef   Raw_data_code
 ------------------------------------------------
  1          1            1   score:HY:1
  1          3           -1   score:HY:2
        estimated value (K'b-M) = 0.504178 +- 0.525854
           Prob(|t| > 0.958778) = 0.3378 (p_value)
           1794.11 (Error degrees of freedom)
-----------------------------------------------------------
```


Matvec Class Library

- Same basic structure
- Need to use `matvec::Model M;`
- Instead of `M=Model();`

Header Section

```
#include <fstream>
#include <iostream>
#include <iomanip>
#include <string>
#include <sstream>
#include <matvec/statdist.h>
#include <matvec/doublematrix.h>
#include <matvec/model.h>
#include <matvec/data.h>
#include <matvec/glmm.h>
#include <matvec/session.h>
#include "link.h"

using namespace std;
```


Basic structure

```
int main() {
        try{
            .........
        }
        catch (matvec::exception &ex) {
                cerr << ex.what() << "\n";
                exit(1);
        }
        catch (...) {
                cerr << "other exceptions were caught\n";
                exit(1);
        }
}
```

Data Prep

```
matvec::SESSION.initialize("matvec_trash");
matvec::Data D;
matvec::GLMM M;
matvec::doubleMatrix V;
matvec::Vector<void *> param(1);
D.input("Data/calve.dat","HY age sex $ sire n score");
```


void matvec::Data::input(const std::string & *fname*, const std::string & *recfmt*)

- Reads in data from the file *fname* using record format *recfmt*
- Record format
  - String of variable names
  - Alphanumeric variables are denoted with $

Model Specification

```
M.equation("score=HY age sex sire,score=intercept");
M.variance("sire",(1./19.)*V.identity(2,2));
M.variance("residual",V.identity(2,2));
M.weight("n");
matvec::link_map("thresh","None",&M,0);
double type=1;
param(1)=(void *)&type;
M.Param(param.begin());
M.fitdata(D);
```


int matvec::GLMM::equation(const std::string & *modelspecs*)

- Equation for the linear predictor
  - intercept is an automatic variable
  - A(B) factor A is nested within factor B
  - A*B two-way interaction between A and B
- Return value = 1 for a valid model and 0 for an invalid model
- Covariates are defined using `void matvec::Model::covariate ( const std::string &` *covariate_names*)

void matvec::Model::variance (const std::string &*termname*, const doubleMatrix &*v*)

- *termname* is model term for the random effect
  - "residual" is used to identify the residual
- *v* is the covariance matrix
- void matvec::Model::variance (const std::string &*termname*, Pedigree &*P*, const doubleMatrix &*v*)

  Additive effects

std::string matvec::link_map(std::string *link*, std::string *varfn*,GLMM *M, int *nvc*);

- *link* link function
- *varfn* variance function "None"
- *M* Model object
- *nvc* number of residual variance components

Function	Distribution	Link	Inverse Link	$v(\mu)$
`normal`	Multi. Normal	Identity	η	$R = \{\sigma_{ij}\}$
`normal log`	Multi. Normal	Identity	η	$R = \exp(\{\sigma_{ij}\})$
`logit`	Binomial/n	Logit	$e^{\eta}/(1+e^{\eta})$	$\mu(1-\mu)/n$
`probit`		Probit	$\Phi(\eta)$	
`cloglog`		Complementary log-log	$1-\exp(-\exp(\eta))$	
`thresh`	Multinomial	Threshold	$\Pr(\eta+\tau_{i-1} < Z \leq \eta+\tau_i)$	$\text{Diag}(\mu) - \mu\mu'$
`poisson`	Poisson	Log	e^{η}	μ
`weibull`	Weibull			
`richards`	Richards Function		$\eta_1(1 \pm e^{-\eta_3(t-t\eta_2)})^{\eta_4}$	σ^2

Model Specification Parameters

- Many link functions define a family of link functions and model specification parameters identify a specific link function.
  - `thresh` link function includes both the probit and logit inverse links
    - Probit:1
    - Logit:0

void matvec::Model::fitdata (Data & D)

- Closes the model specification section
- Identifies the Data object

Estimation and Testing

```
M.glim();
matvec::doubleMatrix Kprime(1,3);
matvec::Vector<double> M0(1);
Kprime(1,1)=1; Kprime(1,3)=-1;
M.contrast("HY",Kprime,M0);
M.save("calve_g.out");
matvec::doubleMatrix Results;
Results=M.AI_REML(40,0);
cout << "sigma^2_s="<<Results(1,1)<<" +- " << sqrt(Results(1,2))<< endl;
```

Vector<double> * matvec::GLMM::glim (int *iterations* = 10)

- Obtain the posterior model estimates of the fixed and random effects
- *iterations* number of iterations
- returns the vector of solutions

double matvec::GLMM::contrast (const std::string & *termname*, const doubleMatrix & Kp, const Vector<double> & M)

- $H_0 : \boldsymbol{K}'\boldsymbol{\theta} = \boldsymbol{M}$
- *termname* identifies the starting term for $\boldsymbol{K}'$
- Returns the p-value for the test

doubleMatrix matvec::GLMM::AI_REML (int *numiter* = 10, double *tol* = 1.e-4,)

- Find the penalized quasi-likelihood estimates of the variance components using AIREML
- *numiter* number of iterations
- *tol* stopping criteria
  - $tol > 0$ don't allow the PQL to increase
  - *tol* use session ϵ as tolerance
  - $tol < 0$ allow the PQL to increase

void matvec::GLMM::GLMM::save (const std::string & *fname*, const int *io_mode* = ios::out|ios::noreplace)

- Save the results to the file *fname*
- Covariance matrix and solutions

```
h2=4.*Results(1,1)/(1.+Results(1,1));
double part,sd;
part=(4.-h2)/(1.+Results(1,1));
sd=part*sqrt(Results(1,2));
cout << "h^2_a="<< h2<<" +- " << sd << endl;
M.contrast("HY",Kprime,M0);
M.save("calve.out");
```


Pedigree

- Pedigree

```
#include <matvec/pedigree.h>
....
matvec::Pedigree P;
P.input("Data/calve.txt","individual father mother");
D.input("Data/calve.txt","calf $ sire $ dam $ HY age sex $ score");
```

- Additive Genetic effects

```
M.equation("score=HY age sex calf,score=intercept");
M.variance("calf",P,(1./4.)*V.identity(2,2));
```