Anexo Homework 4

Gerardo Mamani

10/13/2017

Question 1

```
pedigree<-read.table(header=T, text = 'ID sire dam gener
                                Lord_Raglan 0 0 1
                                Mistletoe Lord_Raglan 0 2
                                Champion_of_England 0 0 3
                                Duchess_of_Gloster Lord_Raglan 0 2
                                The_Czar Lord_Raglan 0 2
                                Mimulus Champion_of_England Mistletoe 3
                                Grand_Duke_Gloster Champion_of_England Duchess_of_Gloster 3
                                Carmine The_Czar 0 3
                                Royal_Duke_Gloster Grand_Duke_Gloster Mimulus 4
                                Princess_Royal Champion_of_England Carmine 4
                                Roan_Gauntlet Royal_Duke_Gloster Princess_Royal 5 ')

pedigree
```

```
                   ID                 sire                dam gener
1          Lord_Raglan                    0                  0     1
2            Mistletoe          Lord_Raglan                  0     2
3  Champion_of_England                    0                  0     3
4   Duchess_of_Gloster          Lord_Raglan                  0     2
5              The_Czar          Lord_Raglan                  0     2
6               Mimulus Champion_of_England          Mistletoe     3
7   Grand_Duke_Gloster Champion_of_England Duchess_of_Gloster     3
8               Carmine             The_Czar                  0     3
9   Royal_Duke_Gloster  Grand_Duke_Gloster            Mimulus     4
10      Princess_Royal Champion_of_England            Carmine     4
11       Roan_Gauntlet  Royal_Duke_Gloster     Princess_Royal     5
```

Recoding the pedigree names by numbers

Id	code
Lord Raglan	1
Mistletoe	2
Champion of England	3
Duchess of Gloster	4
The Czar	5
Mimulus	6
Grand Duke Gloster	7
Carmine	8
Royal Duke Gloster	9
Princess Royal	10
Roan Gauntlet	11

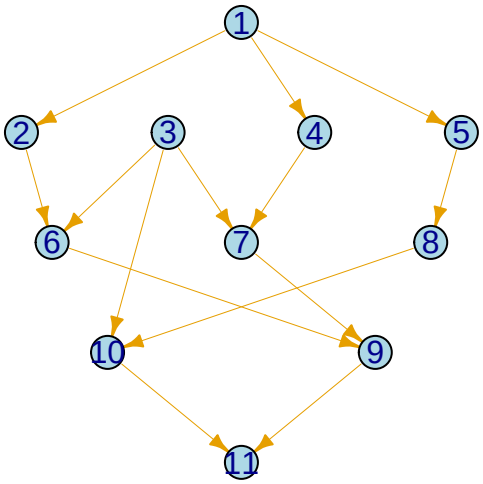
Working with pedigree recoded

```
pedigree<-read.table(header=T, text = 'Id sire dam gen
                                       1    0   0   1
                                       2    1   0   2
                                       3    0   0   2
                                       4    1   0   2
                                       5    1   0   2
                                       6    3   2   3
                                       7    3   4   3
                                       8    5   0   3
                                       9    7   6   4
                                       10   3   8   4
                                       11   9   10 5 ')
```

Using synbreed package

```
library(synbreed)
pedigree <- create.pedigree(pedigree$Id,pedigree$sire,pedigree$dam,pedigree$gen,unknown=c('Id','0'))
```

```
plot(pedigree)
```




```
IGRAPH c9f22d5 DN-- 11 14 --
+ attr: name (v/c), Par1 (v/c), Par2 (v/c), gener (v/n)
+ edges from c9f22d5 (vertex names):
 [1] 1 ->2  1 ->4  1 ->5  3 ->6  3 ->7  5 ->8  3 ->10 7 ->9  9 ->11 2 ->6
[11] 4 ->7  8 ->10 6 ->9  10->11
```

```r
A <- kin(pedigree,ret="add")
round(A,5)
```

```
        1      2   3      4      5       6       7       8      10       9
1  1.0000 0.5000 0.0 0.5000 0.5000 0.25000 0.25000 0.25000 0.12500 0.25000
2  0.5000 1.0000 0.0 0.2500 0.2500 0.50000 0.12500 0.12500 0.06250 0.31250
3  0.0000 0.0000 1.0 0.0000 0.0000 0.50000 0.50000 0.00000 0.50000 0.50000
4  0.5000 0.2500 0.0 1.0000 0.2500 0.12500 0.50000 0.12500 0.06250 0.31250
5  0.5000 0.2500 0.0 0.2500 1.0000 0.12500 0.12500 0.50000 0.25000 0.12500
6  0.2500 0.5000 0.5 0.1250 0.1250 1.00000 0.31250 0.06250 0.28125 0.65625
7  0.2500 0.1250 0.5 0.5000 0.1250 0.31250 1.00000 0.06250 0.28125 0.65625
8  0.2500 0.1250 0.0 0.1250 0.5000 0.06250 0.06250 1.00000 0.50000 0.06250
10 0.1250 0.0625 0.5 0.0625 0.2500 0.28125 0.28125 0.50000 1.00000 0.28125
9  0.2500 0.3125 0.5 0.3125 0.1250 0.65625 0.65625 0.06250 0.28125 1.15625
11 0.1875 0.1875 0.5 0.1875 0.1875 0.46875 0.46875 0.28125 0.64062 0.71875
        11
1  0.18750
2  0.18750
3  0.50000
4  0.18750
5  0.18750
6  0.46875
7  0.46875
8  0.28125
10 0.64062
9  0.71875
11 1.14062
attr(,"info")
[1] "This relationshipMatrix was calculated by synbreed version 0.12-6"
attr(,"type")
[1] "add"
attr(,"class")
[1] "relationshipMatrix" "matrix"
```

Question 3

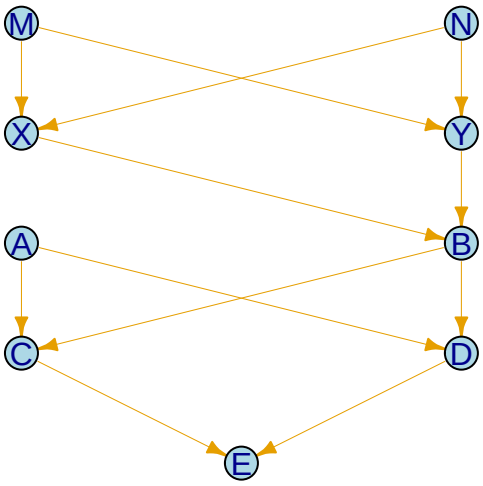
First case, when parents of individual B are full-siblings relative

```
ped3a<-read.table(header=T, text = 'Id sire dam ger
                                    M  0   0   1
                                    N  0 0 1
                                    X  M   N   2
                                    Y  M   N   2
                                    A  0   0   3
                                    B  X   Y   3
                                    C  A   B   4
                                    D  A   B   4
                                    E  C   D   5 ')
```

```
library(synbreed)
ped3a <- create.pedigree(ped3a$Id,ped3a$sire,ped3a$dam,ped3a$ger,unknown=c('Id','0'))
ped3a
```

```
  ID Par1 Par2 gener
1  M    0    0      1
2  N    0    0      1
3  X    M    N      2
4  Y    M    N      2
5  A    0    0      3
6  B    X    Y      3
7  C    A    B      4
8  D    A    B      4
9  E    C    D      5
```

```
plot(ped3a)
```




```
IGRAPH 8d32f7f DN-- 9 12 --
+ attr: name (v/c), Par1 (v/c), Par2 (v/c), gener (v/n)
+ edges from 8d32f7f (vertex names):
 [1] M->X M->Y X->B A->C A->D C->E N->X N->Y Y->B B->C B->D D->E
```

```
A3a <- kin(ped3a,ret="add")
round(A3a,5)
```

```
     M    N     X     Y   A     B       C       D       E
M 1.00 0.00 0.500 0.500 0.0 0.500 0.25000 0.25000 0.25000
N 0.00 1.00 0.500 0.500 0.0 0.500 0.25000 0.25000 0.25000
X 0.50 0.50 1.000 0.500 0.0 0.750 0.37500 0.37500 0.37500
Y 0.50 0.50 0.500 1.000 0.0 0.750 0.37500 0.37500 0.37500
A 0.00 0.00 0.000 0.000 1.0 0.000 0.50000 0.50000 0.50000
B 0.50 0.50 0.750 0.750 0.0 1.250 0.62500 0.62500 0.62500
C 0.25 0.25 0.375 0.375 0.5 0.625 1.00000 0.56250 0.78125
D 0.25 0.25 0.375 0.375 0.5 0.625 0.56250 1.00000 0.78125
E 0.25 0.25 0.375 0.375 0.5 0.625 0.78125 0.78125 1.28125
attr(,"info")
[1] "This relationshipMatrix was calculated by synbreed version 0.12-6"
attr(,"type")
[1] "add"
attr(,"class")
[1] "relationshipMatrix" "matrix"
```

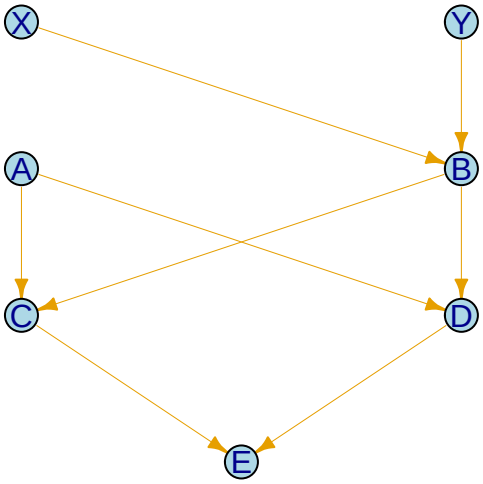
Second case, when the parents of B are unrelated

```
ped3b<-read.table(header=T, text = 'Id sire dam ger
                                    X  0   0   1
                                    Y  0   0   1
                                    B  X   Y   2
                                    A  0   0   2
                                    C  A   B   3
                                    D  A   B   3
                                    E  C   D   4')
```

```
library(synbreed)
ped3b <- create.pedigree(ped3b$Id,ped3b$sire,ped3b$dam,ped3b$ger,unknown=c('Id','0'))
ped3b
```

```
  ID Par1 Par2 gener
1  X    0    0     1
2  Y    0    0     1
4  A    0    0     2
3  B    X    Y     2
5  C    A    B     3
6  D    A    B     3
7  E    C    D     4
```

```
plot(ped3b)
```




```
IGRAPH babd15a DN-- 7 8 --
+ attr: name (v/c), Par1 (v/c), Par2 (v/c), gener (v/n)
+ edges from babd15a (vertex names):
[1] X->B A->C A->D C->E Y->B B->C B->D D->E
```

```
A3b <- kin(ped3b,ret="add")
round(A3b,5)
```

```
     X    Y   A   B    C    D    E
X 1.00 0.00 0.0 0.5 0.25 0.25 0.25
Y 0.00 1.00 0.0 0.5 0.25 0.25 0.25
A 0.00 0.00 1.0 0.0 0.50 0.50 0.50
B 0.50 0.50 0.0 1.0 0.50 0.50 0.50
C 0.25 0.25 0.5 0.5 1.00 0.50 0.75
D 0.25 0.25 0.5 0.5 0.50 1.00 0.75
E 0.25 0.25 0.5 0.5 0.75 0.75 1.25
attr(,"info")
[1] "This relationshipMatrix was calculated by synbreed version 0.12-6"
attr(,"type")
[1] "add"
attr(,"class")
[1] "relationshipMatrix" "matrix"
```