Genetic Relationships

LRS

CGIL

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Pedigrees

Step 1. Chronological Order

Animal	Sire	Dam	Generation Number
BF	DD	HE	1
DD	GA	EC	1
GA			1
EC	GA	FB	1
FB			1
AG	BF	EC	1
HE	DD	FB	1

Pedigrees
Step 1. Chronological Order

Animal	Sire	Dam	Generation Number	
BF	DD	HE	1	
DD	GA	EC	1	2
GA			1	
EC	GA	FB	1	
FB			1	
AG	BF	EC	1	
HE	DD	FB	1	2

Pedigrees
Step 1. Chronological Order

Animal	Sire	Dam	Generation Number	
BF	DD	HE	1	
DD	GA	EC	1	2
GA			1	3
EC	GA	FB	1	3
FB			1	
AG	BF	EC	1	
HE	DD	FB	1	2

Pedigrees
Step 1. Chronological Order

Animal	Sire	Dam	Generation Number	
BF	DD	HE	1	
DD	GA	EC	1	2
GA			1	4
EC	GA	FB	1	3
FB			1	4
AG	BF	EC	1	
HE	DD	FB	1	2

Pedigrees
Step 1. Chronological Order

Animal	Sire	Dam	Generation Number		
BF	DD	HE	1	2	2
DD	GA	EC	1	3	4
GA			1	4	5
EC	GA	FB	1	3	4
FB			1	4	5
AG	BF	EC	1	1	1
HE	DD	FB	1	2	3

Pedigrees
Step 1. Chronological Order

Animal	Sire	Dam	Generation Number			
BF	DD	HE	1	2	2	2
DD	GA	EC	1	3	4	4
GA			1	4	5	6
EC	GA	FB	1	3	4	5
FB			1	4	5	6
AG	BF	EC	1	1	1	1
HE	DD	FB	1	2	3	3

Pedigrees
Step 2. Sort in order

Animal	Sire	Dam	Generation Number
GA			6
FB			6
EC	GA	FB	5
DD	GA	EC	4
HE	DD	FB	3
BF	DD	HE	2
AG	BF	EC	1

R function

```
border=function(anm,sir,dam){
maxloop=1000
changes = 1
count = 0
mam=length(anm)
old = rep(1,mam)
new = old
while(changes>0){
for (j in 1:mam){
  ks = sir[j]
  kd = dam[j]
  gen = new[j]+1
 if(ks != "NA"){
   js = match(ks,anm)
   if(gen > new[js]){new[js] = gen}
   }
```

R function

```
   if(kd != "NA"){
     jd = match(kd,anm)
     if(gen > new[jd]){new[jd] = gen}
     }
 }   # for loop
 changes = sum(new - old)
 old = new
 count = count + 1
 if(count > maxloop){changes=0}
 }   # while loop
return(new)
 }  # function loop
```

Usage

```
animal=c("bf","dd","ga","ec","fb","ag","he")
sire=c("dd","ga","NA","ga","NA","bf","dd")
dams=c("he","ec","NA","fb","NA","ec","fb")
gg=border(animal,sire,dams)
 ka = order(-gg)
 oanm=animal[ka]
 osir=sire[ka]
 odam=dams[ka]
 cbind(oanm,osir,odam)
```

Tabular Method

Wright's Coefficient of Relationship

$$w_{ij} = \frac{Cov(a_i, a_j)}{(Var(a_i)Var(a_j))^{.5}}$$

$Cov(a_i, a_j)$ from 0 to 2, numerator relationship.
$Var(a_i)$ from 1 to 2
w_{ij} from 0 to 1
Coefficient of Kinship $= \frac{1}{2}Cov(a_i, a_j)$, used in plant breeding.
Henderson presented Tabular Method to get $Cov(a_i, a_j)$

Tabular Method

	-,- GA	-,- FB	GA,FB EC	GA,EC DD	DD,FB HE	DD,HE BF	BF,EC AG
GA	1	0					
FB	0	1					
EC			1				
DD				1			
HE					1		
BF						1	
AG							1

Tabular Method

	-,- GA	-,- FB	GA,FB EC	GA,EC DD	DD,FB HE	DD,HE BF	BF,EC AG
GA	1	0	1/2	3/4	3/8	9/16	17/32
FB	0	1					
EC	1/2		1				
DD	3/4			1			
HE	3/8				1		
BF	9/16					1	
AG	17/32						1

Tabular Method

	-,- GA	-,- FB	GA,FB EC	GA,EC DD	DD,FB HE	DD,HE BF	BF,EC AG
GA	1	0	1/2	3/4	3/8	9/16	17/32
FB	0	1	1/2	1/4	5/8	7/16	15/32
EC	1/2	1/2	1				
DD	3/4	1/4		1			
HE	3/8	5/8			1		
BF	9/16	7/16				1	
AG	17/32	15/32					1

Tabular Method

	-,- GA	-,- FB	GA,FB EC	GA,EC DD	DD,FB HE	DD,HE BF	BF,EC AG
GA	1	0	1/2	3/4	3/8	9/16	17/32
FB	0	1	1/2	1/4	5/8	7/16	15/32
EC	1/2	1/2	1	3/4	5/8	11/16	27/32
DD	3/4	1/4	3/4	5/4	3/4	1	7/8
HE	3/8	5/8	5/8	3/4	9/8	15/16	25/32
BF	9/16	7/16	11/16	1	15/16	11/8	33/32
AG	17/32	15/32	27/32	7/8	25/32	33/32	43/32

$$w_{BF,AG} = \frac{33/32}{((11/8)(43/32))^{.5}} = 0.75867$$

R function

```
numer8 = function(sid,did){
  N = length(sid)+1
  ss = sid + 1  # increase id's by 1
  dd = did + 1  # no 0's in ids
  ss = c(0,ss)
  dd = c(0,dd)
  A = diag(c(1:N))
  A[1,1]=0
```

R function

```
for(i in 2:N){  # row by row
for(j in i:N){  # col within row
  ks=ss[j]
  kd = dd[j]
  if( i == j){
    A[i,j] = 1 + 0.5*A[ks,kd] } else
  { A[i,j] = 0.5*(A[i,ks]+A[i,kd]
      A[j,i] = A[i,j] }
 } }
 ka = c(2:N)
 B = A[ka,ka]  # original animals
 return(B)   }
```

Usage

```
# letters converted to numbers
# 1=GA, 2=FB, 3=EC, 4=DD, 5=HE, 6=BF, 7=AG
sid = c(0,0,1,1,4,4,6)
did = c(0,0,2,3,2,5,3)
A = numer8(sid,did)*32
     [,1] [,2] [,3] [,4] [,5] [,6] [,7]
[1,]   32    0   16   24   12   18   17
[2,]    0   32   16    8   20   14   15
[3,]   16   16   32   24   20   22   27
[4,]   24    8   24   40   24   32   28
[5,]   12   20   20   24   36   30   25
[6,]   18   14   22   32   30   44   33
[7,]   17   15   27   28   25   33   43
```

Activity

- Add KK with parents GA and HE
- Apply Tabular Method
- Calculate $w_{GA,KK}$
- Use R function to verify

Inverse of A

- **A** has order equal to number of animals
- Direct inverse not practical
- Henderson(1975) major discovery

Discovery

$$
\begin{aligned}
\mathbf{A} &= \begin{pmatrix} 1 & 0 & \frac{1}{2} \\ 0 & 1 & \frac{1}{2} \\ \frac{1}{2} & \frac{1}{2} & 1 \end{pmatrix} \\
&= \mathbf{LL}' \\
&= \begin{pmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ \frac{1}{2} & \frac{1}{2} & (\frac{1}{2})^{.5} \end{pmatrix} \begin{pmatrix} 1 & 0 & \frac{1}{2} \\ 0 & 1 & \frac{1}{2} \\ 0 & 0 & (\frac{1}{2})^{.5} \end{pmatrix} \\
\mathbf{L} &= \mathbf{TD} \\
&= \begin{pmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ \frac{1}{2} & \frac{1}{2} & 1 \end{pmatrix} \begin{pmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & (\frac{1}{2})^{.5} \end{pmatrix} \\
\mathbf{A} &= \mathbf{T}(\mathbf{DD}')\mathbf{T}' = \mathbf{TD}^2\mathbf{T}'
\end{aligned}
$$

More Discovery

$$
\begin{aligned}
\mathbf{A} &= \mathbf{T}\mathbf{D}^2\mathbf{T}' = \mathbf{T}\mathbf{B}\mathbf{T}' \\
\mathbf{A}^{-1} &= \mathbf{T}'^{-1}\mathbf{B}^{-1}\mathbf{T}^{-1} \\
\mathbf{T}'^{-1} &= \begin{pmatrix} 1 & 0 & -\frac{1}{2} \\ 0 & 1 & -\frac{1}{2} \\ 0 & 0 & 1 \end{pmatrix} \\
\mathbf{A}^{-1} &= \sum_{i=1}^{n} \mathbf{T}'^{-1}_{i}\mathbf{B}^{-1}_{ii}\mathbf{T}^{-1}_{i} \\
&= \begin{pmatrix} 1 \\ 0 \\ 0 \end{pmatrix} (1) \begin{pmatrix} 1 & 0 & 0 \end{pmatrix} + \begin{pmatrix} 0 \\ 1 \\ 0 \end{pmatrix} (1) \begin{pmatrix} 0 & 1 & 0 \end{pmatrix} \\
&\quad + \begin{pmatrix} -\frac{1}{2} \\ -\frac{1}{2} \\ 1 \end{pmatrix} (2) \begin{pmatrix} -\frac{1}{2} & -\frac{1}{2} & 1 \end{pmatrix}
\end{aligned}
$$

More Discovery

$$\mathbf{A}^{-1} = \begin{pmatrix} 1 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} + \begin{pmatrix} 0 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 0 \end{pmatrix} + \begin{pmatrix} .5 & .5 & -1 \\ .5 & .5 & -1 \\ -1 & -1 & 2 \end{pmatrix}$$
$$= \begin{pmatrix} 1.5 & .5 & -1 \\ .5 & 1.5 & -1 \\ -1 & -1 & 2 \end{pmatrix}$$

Inverse of **A** can be written from list of pedigrees and $\mathbf{B}_{ii}^{-1}$ values. For inbred animals b_{ii} is less than 0.5. Meuwissen and Luo (1996) method for determining inbreeding.

$$b_{ii} = (0.50 - 0.25 \times (F_s + F_d))$$

F_s, F_d are inbreeding coefficients of sire and dam of animal i.

Meuwissen and Luo Method

- Process animals in chronological order
- Find a row of $\mathbf{T}$ for animal i
- Find diagonal of $\mathbf{B}$ for animal i
- Multiply to find diagonal of $\mathbf{A}$
- Subtract 1 to get F_i

Earlier Example

Animal	Sire	Dam	F_i	b_{ii}
GA			0	1
FB			0	1
EC	GA	FB	0	1/2
DD	GA	EC		

ID vector	T-row	b_i
DD	1	$(.5 - .25(0+0))=1/2$
GA	.5	1
EC	.5	1/2
GA	.25	1
FB	.25	1

Example continued

ID vector	T-row	b_i
DD	1	(.5 - .25(0+0))=1/2
GA	.5+.25	1
EC	.5	1/2
FB	.25	1

$$
\begin{aligned}
a_{DD} &= 1^2(1/2) + (3/4)^2(1) + (1/2)^2(1/2) + (1/4)^2(1) \\
&= (8 \ + \ 9 \ + \ 2 \ + \ 1)/16 \\
&= 1 + (1/4) \\
F_{DD} &= 1/4
\end{aligned}
$$

Next animal, HE

ID vector	T-row	b_i
HE	1	$(.5 - .25(.25 + 0)) = 7/16$
DD	.5	$1/2$
FB	.5	1
GA	.25	1
EC	.25	$1/2$
GA	.125	1
FB	.125	1

Next animal, HE

ID vector	T-row	b_i
HE	1	7/16
DD	.5	1/2
FB	5/8	1
GA	3/8	1
EC	.25	1/2

$$
\begin{aligned}
a_{HE} &= 1^2(7/16) + (1/2)^2(1/2) + (5/8)^2(1) + (3/8)^2(1) + (1/4)^2(1/2) \\
&= (28 \ + \ 8 \ + \ 25 \ + \ 9 \ + \ 2)/64 \\
&= 1 + (1/8) \\
F_{HE} &= 1/8
\end{aligned}
$$

Earlier Example

Animal	Sire	Dam	F_i	b_{ii}
GA			0	1
FB			0	1
EC	GA	FB	0	1/2
DD	GA	EC	1/4	1/2
HE	DD	FB	1/8	7/16
BF	DD	HE	3/8	13/32
AG	BF	EC	11/32	13/32

Writing $\mathbf{A}^{-1}$

Henderson's Rules

Let $\delta = 1/b_{ii}$, then add

	Animal	Sire	Dam
Animal	δ	$-.5\delta$	$-.5\delta$
Sire	$-.5\delta$	$.25\delta$	$.25\delta$
Dam	$-.5\delta$	$.25\delta$	$.25\delta$

Writing $\mathbf{A}^{-1}$

	-,- GA	-,- FB	GA,FB EC	GA,EC DD	DD,FB HE	DD,HE BF	BF,EC AG
GA							
FB							
EC							
DD							
HE							
BF							
AG							

Animal GA, $b_{ii} = 1$ so $\delta = 1$, parents unknown

Writing $\mathbf{A}^{-1}$

	-,- GA	-,- FB	GA,FB EC	GA,EC DD	DD,FB HE	DD,HE BF	BF,EC AG
GA	1						
FB							
EC							
DD							
HE							
BF							
AG							

Animal FB, $b_{ii} = 1$ so $\delta = 1$, parents unknown

Writing $\mathbf{A}^{-1}$

	-,- GA	-,- FB	GA,FB EC	GA,EC DD	DD,FB HE	DD,HE BF	BF,EC AG
GA	1						
FB		1					
EC							
DD							
HE							
BF							
AG							

Animal EC, $b_{ii} = 1/2$ so $\delta = 2$, parents known

Writing $\mathbf{A}^{-1}$

	-,- GA	-,- FB	GA,FB EC	GA,EC DD	DD,FB HE	DD,HE BF	BF,EC AG
GA	1.5	.5	-1				
FB	.5	1.5	-1				
EC	-1	-1	2				
DD							
HE							
BF							
AG							

Animal DD, $b_{ii} = 1/2$ so $\delta = 2$, parents known

Writing $\mathbf{A}^{-1}$

	-,- GA	-,- FB	GA,FB EC	GA,EC DD	DD,FB HE	DD,HE BF	BF,EC AG
GA	2	.5	-.5	-1			
FB	.5	1.5	-1				
EC	-.5	-1	2.5	-1			
DD	-1		-1	2			
HE							
BF							
AG							

Animal HE, $b_{ii} = 7/16$ so $\delta = 16/7$, parents known

Writing $\mathbf{A}^{-1}$

	-,- GA	-,- FB	GA,FB EC	GA,EC DD	DD,FB HE	DD,HE BF	BF,EC AG
GA	2	.5	-.5	-1			
FB	.5	1.5+4/7	-1	4/7	-8/7		
EC	-.5	-1	2.5	-1			
DD	-1	4/7	-1	2+4/7	-8/7		
HE		-8/7		-8/7	16/7		
BF							
AG							

Animal BF, $b_{ii} = 13/32$ so $\delta = 32/13$, parents known

Writing $\mathbf{A}^{-1}$

	-,- GA	-,- FB	GA,FB EC	GA,EC DD	DD,FB HE	DD,HE BF	BF,EC AG
GA	2	.5	-.5	-1			
FB	.5	1.5+4/7	-1	4/7	-8/7		
EC	-.5	-1	2.5	-1			
DD	-1	4/7	-1	$2+\frac{4}{7}+\frac{8}{13}$	$-\frac{8}{7}+\frac{8}{13}$	-16/13	
HE		-8/7		$-\frac{8}{7}+\frac{8}{13}$	$\frac{16}{7}+\frac{8}{13}$	-16/13	
BF				-16/32	-16/13	32/13	
AG							

Animal AG, $b_{ii} = 13/32$ so $\delta = 32/13$, parents known

Writing $\mathbf{A}^{-1}$

	-,- GA	-,- FB	GA,FB EC	GA,EC DD	DD,FB HE	DD,HE BF	BF,EC AG
GA	2	.5	-.5	-1			
FB	.5	$1.5+\frac{4}{7}$	-1	$\frac{4}{7}$	$-\frac{8}{7}$		
EC	-.5	-1	$2.5+\frac{8}{13}$	-1		$\frac{8}{13}$	$-\frac{16}{13}$
DD	-1	$\frac{4}{7}$	-1	$2+\frac{4}{7}+\frac{8}{13}$	$-\frac{8}{7}+\frac{8}{13}$	$-\frac{16}{13}$	
HE		$-\frac{8}{7}$		$-\frac{8}{7}+\frac{8}{13}$	$\frac{16}{7}+\frac{8}{13}$	$-\frac{16}{13}$	
BF			$\frac{8}{13}$	$-\frac{16}{32}$	$-\frac{16}{13}$	$\frac{40}{13}$	$-\frac{16}{13}$
AG			$-\frac{16}{13}$			$-\frac{16}{13}$	$\frac{32}{13}$

DONE! Fill in empty spaces with 0.

Bill's Routines

C language routines "wrapped" into R functions.

```
xpdinit(nam)       # initialize pedigree
xpdadd(sire,dam)   # add a new animal
xpdd(animal)       # returns  bi value
xpdf(animal)       # returns  f  value
xpdfree()          # frees up memory after
           all inbreeding computed

zzlib = file.choose()  #  find  rclib.dll
dyn.load(zzlib)
zbill = file.choose()  #  find  Bills.R
source(zbill)
```

Compute Inbreeding

```
animals numbered in chronological order, 1 to nam
sid       # a string of sire numbers, 1 to nam
did       # a string of dam numbers,  1 to nam
xpdint(nam)  # initialize functions
inbc = rep(0,nam)
inbb = rep(0,nam)

for(i in 1:nam){
  inbc[i] = xpdadd(sid[i],did[i])
  inbb[i] = xpdd(i)
  }
```

A-inverse Function

```
AINV = function(sid,did,bi){
rules=matrix(data=c(1,-.5,-.5,-.5,0.25,0.25,-.5,.25,.25
   byrow=TRUE,nrow=3)
 nam = length(sid);  np = nam + 1
 ss = sid+1;         dd = did + 1
 LAI = matrix(data=c(0),nrow=np,ncol=np)
 for( i in 1:nam){
    ip = i + 1;      X = 1/bi[i]
    k = cbind(ip,ss[i],dd[i])
    LAI[k,k] = LAI[k,k] + rules*X
    }
  k = c(2:np);       C = LAI[k,k]
  return(C)  }

AI = AINV(sid,did,inbb)
```

Sire-MGS Relationships

What would be the rules if

$$\mathbf{A} = \begin{pmatrix} 1 & 0 & \frac{1}{2} \\ 0 & 1 & \frac{1}{4} \\ \frac{1}{2} & \frac{1}{4} & 1 \end{pmatrix}$$

- Apply Cholesky decomposition
- Form $\mathbf{TD}^2\mathbf{T}'$
- Invert $\mathbf{T}$
- Deduce the rules. Try it.

Sire-MGS

Henderson's Rules

Let $\delta = 16/11$, then if both ancestors known add

	Animal	Sire	MGS
Animal	δ	$-.5\delta$	$-.25\delta$
Sire	$-.5\delta$	$.25\delta$	$.125\delta$
MGS	$-.25\delta$	$.125\delta$	$.0625\delta$

If MGS unknown, $\delta = 4/3$.
If Sire unknown, $\delta = 16/15$.

Sire Models

$$y_{ijk...} = Fixed + Random + s_k + e_{ijk...}$$

- Genetic part through sire, records on progeny, half-sibs.
- Each progeny assumed to have one record, first lactations.
- Each progeny from a different, random dam, equal genetic quality.
- Progeny distributed randomly across other effects in the model.
- Sire estimates were Transmitting Abilities, ETA.
- Sires related, **A** based on Sire-MGS relationships, no inbreeding.
- 1970's

Sire-MGS Models

$$y_{ijk...} = Fixed + Random + s_k + .5\ s_l + e_{ijk...}$$

- Dams assumed to be random female progeny of the MGS.
- All progeny of a sire are half-sibs.
- One record per progeny.
- One progeny per dam, dams from different genetic levels as indicated by MGS.
- ETA obtained.
- **A** based on Sire-MGS relationships, no inbreeding.
- Progeny distributed randomly across other effects in the model.

Sire-Dam Models

$$y_{ijk...} = Fixed + Random + s_k + d_l + e_{ijk...}$$

- Dams can have more than one progeny, full-sibs allowed.
- Dams can have different genetic potential.
- Dams not randomly mated to sires.
- Dams can be mated to different sires.
- Dam effects might include maternal effects.
- One record per progeny.
- ETA obtained.
- Progeny distributed randomly across other effects in the model.
- **A** may be based on Sire-Dam relationships or Sire-MGS relationships, no inbreeding.

Animal Models

$$y_{ijk...} = Fixed + Random + a_k + pe_l + e_{ijk...}$$

- One or more records per animal, but all animals must have a first record.
- PE effects if more than one record included.
- **A** based on Sires-Dams, takes into account non-random matings, all additive relationships and inbreeding.
- Animals are random progeny from sire-dam matings, i.e. not selected.
- Animals distributed randomly among other factors in the model.
- EBV obtained, the combined additive effect of all loci in the genome.