Metafounders

MiX99 course on genomic prediction

COURSE DAY 1, March 9th, 2026

Contents

- Theory: what is the idea
- How to make Gamma file, using Bpop
- Metafounders in Pedigree
- Metafounders in RelaX2
- Metafounders in CLIM

Theory and estimating Γ

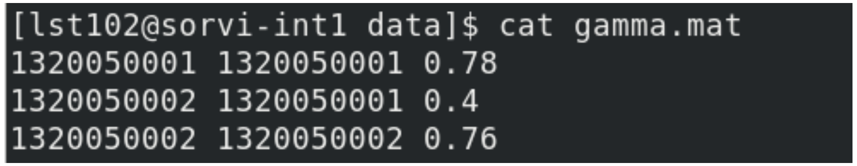
Using Γ with MiX99 and tools

Metafounders in pedigree file

NOTE: MF groups and gamma matrix are made for illustration purposes only.

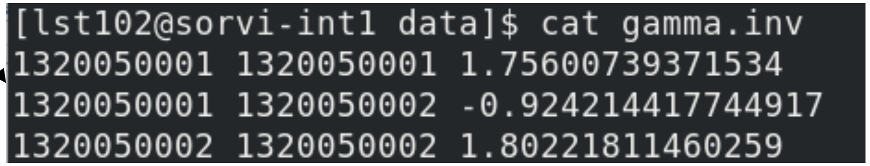
- MF group codes are **positive integer numbers**, not negative like for UPG
- Integer codes must match to the codes in gamma and inverse of gamma files!
- Make sure MF codes do not overlap with animal codes!

Γ



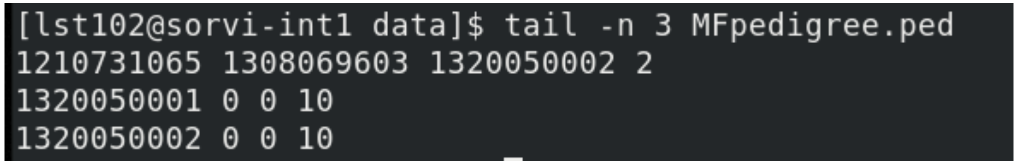
```
[lst102@sorvi-int1 data]$ cat gamma.mat
1320050001 1320050001 0.78
1320050002 1320050001 0.4
1320050002 1320050002 0.76
```

Γ^{-1}



```
[lst102@sorvi-int1 data]$ cat gamma.inv
1320050001 1320050001 1.75600739371534
1320050001 1320050002 -0.924214417744917
1320050002 1320050002 1.80221811460259
```

- Sire and dam for MF group are set to 0
- Use large block code for MF



```
[lst102@sorvi-int1 data]$ tail -n 3 MFpedigree.ped
1210731065 1308069603 1320050002 2
1320050001 0 0 10
1320050002 0 0 10
```

Calculating inbreeding coefficients with RelaX2

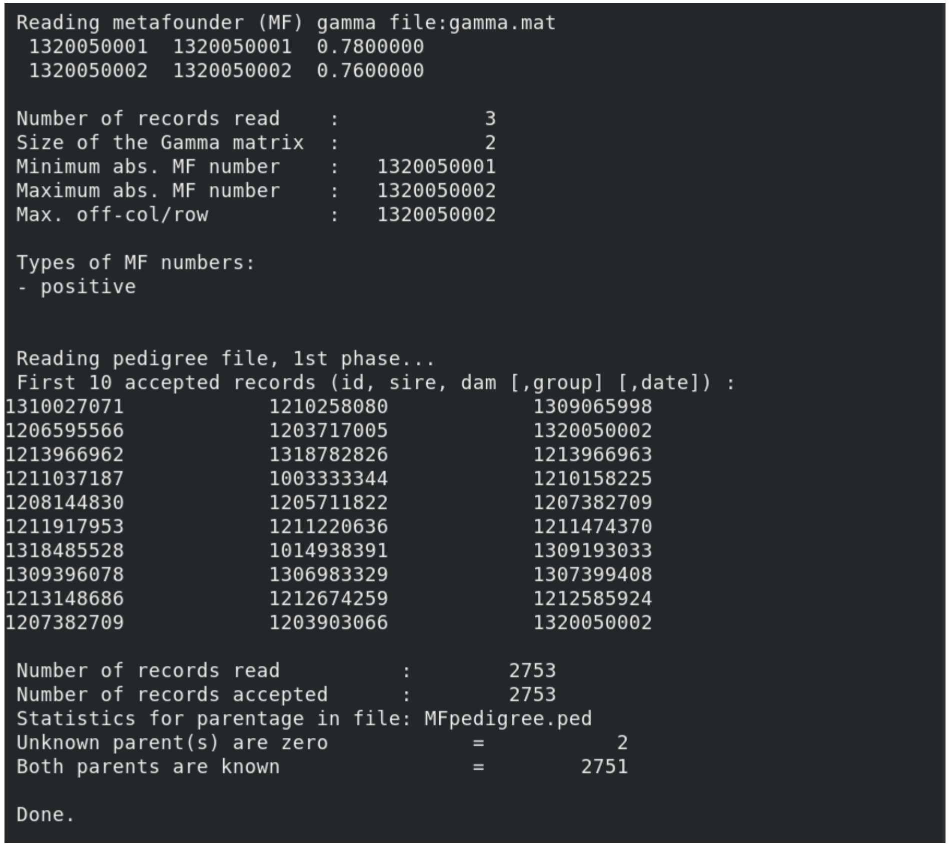
```
# Calculate inbreeding using MF
input pedigree
  file  MFpedigree.ped
  record id sire  dam

# Define gamma file
input gamma
  file gamma.mat

output overwrite inbreeding inbreeding.dat
```

← Pedigree with metafounders

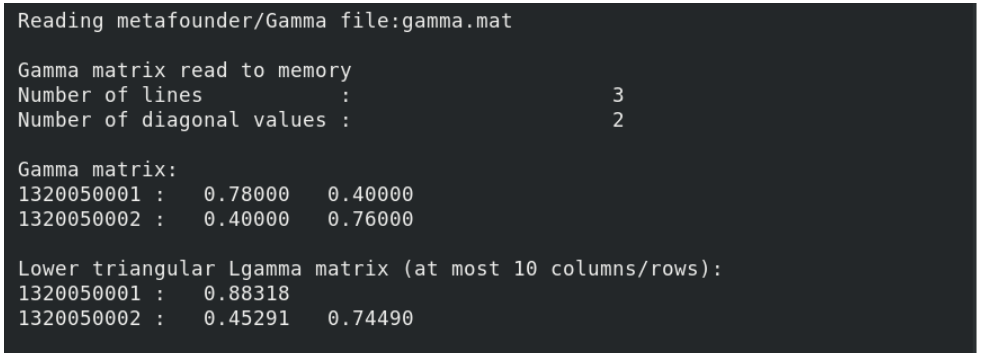
← Gamma in ijval format

← Output inbreedings to inbreeding.dat

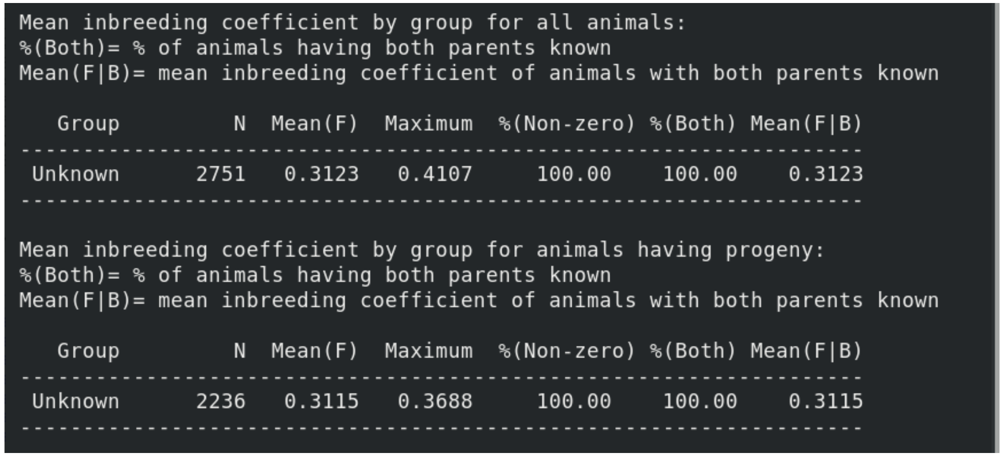
Selected RelaX2 output



```
Reading metafounder (MF) gamma file:gamma.mat
 1320050001  1320050001  0.7800000
 1320050002  1320050002  0.7600000

Number of records read    :            3
Size of the Gamma matrix  :            2
Minimum abs. MF number    :   1320050001
Maximum abs. MF number    :   1320050002
Max. off-col/row          :   1320050002

Types of MF numbers:
- positive


Reading pedigree file, 1st phase...
First 10 accepted records (id, sire, dam [,group] [,date]) :
1310027071            1210258080            1309065998
1206595566            1203717005            1320050002
1213966962            1318782826            1213966963
1211037187            1003333344            1210158225
1208144830            1205711822            1207382709
1211917953            1211220636            1211474370
1318485528            1014938391            1309193033
1309396078            1306983329            1307399408
1213148686            1212674259            1212585924
1207382709            1203903066            1320050002

Number of records read          :        2753
Number of records accepted      :        2753
Statistics for parentage in file: MFpedigree.ped
Unknown parent(s) are zero            =           2
Both parents are known                =        2751

Done.
```



```
Reading metafounder/Gamma file:gamma.mat

Gamma matrix read to memory
Number of lines            :                      3
Number of diagonal values :                       2

Gamma matrix:
1320050001 :   0.78000   0.40000
1320050002 :   0.40000   0.76000

Lower triangular Lgamma matrix (at most 10 columns/rows):
1320050001 :   0.88318
1320050002 :   0.45291   0.74490
```



```
Mean inbreeding coefficient by group for all animals:
%(Both)= % of animals having both parents known
Mean(F|B)= mean inbreeding coefficient of animals with both parents known

   Group         N  Mean(F)  Maximum  %(Non-zero) %(Both) Mean(F|B)
-------------------------------------------------------------------
 Unknown      2751   0.3123   0.4107     100.00    100.00    0.3123
-------------------------------------------------------------------

Mean inbreeding coefficient by group for animals having progeny:
%(Both)= % of animals having both parents known
Mean(F|B)= mean inbreeding coefficient of animals with both parents known

   Group         N  Mean(F)  Maximum  %(Non-zero) %(Both) Mean(F|B)
-------------------------------------------------------------------
 Unknown      2236   0.3115   0.3688     100.00    100.00    0.3115
-------------------------------------------------------------------
```

Calculating A_{22} matrix that uses metafounder information

```
#Calculate A22 matrix for genotyped animals
input pedigree
  file  MFpedigree.ped
  record id sire  dam

input gamma
  file gamma.mat

input animals
 file genotyped.id
 record id
output overwrite amatrix A22.dat
```

← Pedigree with metafounders

← Gamma in ijval format

← Ids for genotyped animals

← Output A22

Lower triangle dense format by: `output overwrite lower amatrix A22L.dat`

Defining Metafounders in CLIM file

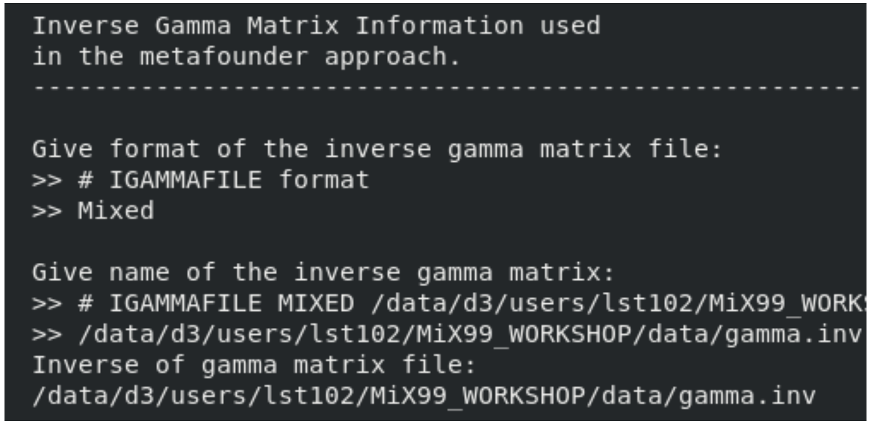
- CLIM needs inverse of gamma and inbreeding

```
IGAMMAFILE MIXED gamma.inv
INBRFILE   inbreeding.dat
INBREEDING PEDIGREECODE=1  FINBR=3
```

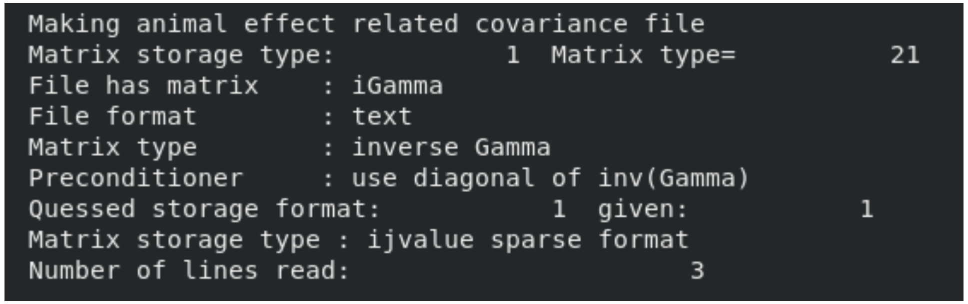
- DO NOT SPECIFY UNKOWN PARENT GROUPS

~~PEDIGREE g am+p 0.333~~ #WRONG!!!!!!

PEDIGREE g am #CORRECT



```
Inverse Gamma Matrix Information used
in the metafounder approach.
-----------------------------------------------

Give format of the inverse gamma matrix file:
>> # IGAMMAFILE format
>> Mixed

Give name of the inverse gamma matrix:
>> # IGAMMAFILE MIXED /data/d3/users/lst102/MiX99_WORK
>> /data/d3/users/lst102/MiX99_WORKSHOP/data/gamma.inv
Inverse of gamma matrix file:
/data/d3/users/lst102/MiX99_WORKSHOP/data/gamma.inv
```

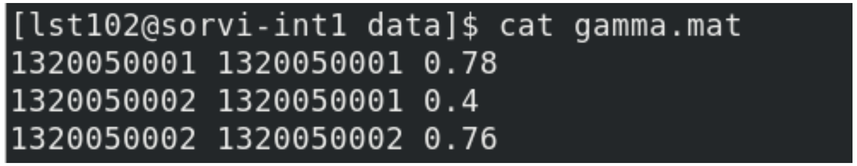


```
Making animal effect related covariance file
Matrix storage type:           1  Matrix type=         21
File has matrix    : iGamma
File format        : text
Matrix type        : inverse Gamma
Preconditioner     : use diagonal of inv(Gamma)
Quessed storage format:          1  given:           1
Matrix storage type : ijvalue sparse format
Number of lines read:                      3
```

Conclusions, using metafounders

- PEDIGREE
  - MF group codes are **positive integer numbers**,
  - Sire and dam for MF group are set to 0

- Gamma and its inverse needed
  - Use i j val format to store matrices



```
[lst102@sorvi-int1 data]$ cat gamma.mat
1320050001 1320050001 0.78
1320050002 1320050001 0.4
1320050002 1320050002 0.76
```

RelaX2 requires Γ :

```
input gamma

  file gamma.mat
```

CLIM requires Γ^{-1}

```
IGAMMAFILE MIXED gamma.inv
INBRFILE   inbreeding.dat
INBREEDING PEDIGREECODE=1 FINBR=3
PEDIGREE g am    # NO +p!
```

Thank you!

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