

We will be working in qualtrics :

https://qimr.az1.qualtrics.com/jfe/form/SV_bjXq3wCxYVR0SEu

We will be using the script TrioGCTA_Practical_2024.R

You will need to copy simulated data into your folder:

Create a directory to hold today's work

```
mkdir day4_triogcta
```

Move into that directory, and then copy over my folder

```
cd day4_triogcta
```

```
cp -r /home/ziada/2024/day4_triogcta/TrioGCTA_practical* ./
```

```
#####  
##  
# STEP 2: Compute GRM (genetic relatedness matrix) #  
#####  
##  
  
A = GRM(dat) #create a genetic relatedness matrix
```

NB!! this GRM becomes
computationally intensive when working
with larger data sets < 60,000 trios

in that case we would recommend
using the programming language Julia
which is known for its speed in high
performance computing

Contact Espen Eilertsen
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scripts

```
#####  
# STEP 3: Subset GRM into blocks  
#####
```

```
mid = 1:1000  
pid = 1001:2000  
oid = 2001:3000  
Amm = A[mid, mid]  
App = A[pid, pid]  
Aoo = A[oid, oid]  
Dpm = A[pid, mid] + A[mid, pid]  
Dom = A[oid, mid] + A[mid, oid]  
Dop = A[oid, pid] + A[pid, oid]
```

These blocks define the correlation structure of each family members effects i.e., direct indirect covariance

The implied structure of the model can be described by these blocks alone

```
#####
##
# STEP 4: Define the trio model in open mx
#####
##
# set up model
yX = cbind(dat@ped$pheno[oid], 1) # create a matrix
including phenotype data and a column of ones
colnames(yX) = c("y", "x")
K = 1000 # Number of trios
```

Here we specify the owner of the phenotype, this will influence how we interpret the parameters

$$\sigma_m^2 \quad \sigma_p^2 \quad \sigma_o^2$$

Bonus script questions?

Table 2 Parameter estimates and standard errors from the fitted models

From: Direct and Indirect Effects of Maternal, Paternal, and Offspring Genotypes: Trio-GCTA

Parameter
σ_m^2
σ_p^2
σ_o^2
σ_{om}
σ_{op}
σ_{pm}
σ_e^2

BW offspring birth weight, RS maternal relationship satisfaction six months after birth, BMI paternal body mass index

Model	Variance decomposition
Full	$\sigma_c^2 + \sigma_p^2 + \sigma_m^2 + \sigma_{om} + \sigma_{op} + \sigma_e^2$
No Covariance	$\sigma_c^2 + \sigma_p^2 + \sigma_m^2 + \sigma_e^2$
Direct Only	$\sigma_c^2 + \sigma_e^2$
Null	σ_e^2

For a more detailed analysis it would be preferable to fit alternative nested models as seen above and compare whether simpler models are equally supported by the data.