

Linear Mixed Models in QTL analysis

Variance Components

Andrey Ziyatdinov

Unit of Genetics of Complex Diseases (UGCD), Sant Pau, Barcelona @ 5 Mar 2014

About this presentation

In UGCD we are working on

- Family-based sample (GAIT1 and GAIT2 projects)
- Targeted to search for Quantitative Trait Loci (QTLs)
- Heavily ~~abused~~ used **SOLAR** tool

Objective of this presentation is to talk more about linear mixed models

- write down some maths
- look at other examples rather than those polygenic ones
- discuss the issues related to QTL analysis

About this presentation

Expected profit

- be sure we use **SOLAR** in a proper way
- be able to run its standard and, perhaps, advanced features
- and ... estimate the cost to go away from **SOLAR** one day ~~some contradiction has been detected here~~

The way to make use of this presentation

- Be aware of 'maths overload'
- Focus on examples
- Come back to the maths someday

Agenda

- General linear models
- Mixed linear models
 - Examples
- Models in SOLAR
- Discussion

Timeline

- Sir Ronald Fisher introduced random effect model to study the trait correlations between relatives in 1918.
- Charles Roy Henderson derived best linear unbiased estimates (BLUE) for fixed effects and best linear unbiased predictions (BLUP) for random effects in the 1950s.

It took some time to overcome the computation demands and make practical tools.

- SOLAR: Sequential Oligogenic Linkage Analysis Routines ([Blangero & Almasy, 1996](#)).
- A commercial program [ASReml](#) by Gilmour and his colleges in 1999.
- R package `nlme` since 1999 and [lme4](#) since 2002 by Douglas Bates and his colleges.
- R package [MCMCglmm](#): MCMC Generalised Linear Mixed Models ([Hadfield, 2010](#)).

Sources: [Wikipedia](#), [github.com/lme4/BIRS](#)

Quick and dirty start from SOLAR

A model in which n QTLs and polygenes influence a quantitative trait ([Almasy & Blangero, 1998](#)):

$$y_j = \mu + x_j\beta + g_j + \sum_{i=1}^n q_{ij} + e_j$$

- y_j : quantitative trait of the j -th individual
- μ : the grand trait mean
- x_j : vector of covariates of the j -th individual
- g_i : additive polygenic effect of the j -th individual
- q_{ij} : the i -th QTL effect of the j -th individual
- e_j : random environmental deviation of the j -th individual

General Linear Models

General Linear Model

$$y = X\beta + e$$

with

$$e \sim (0, \sigma_e^2 R)$$

- y : vector of n observations
- X : the design or incidence $n \times p$ matrix
- e : vector of a residual error with covariance matrix $\sigma_e^2 R$,
 - off-diagonal elements of R indicate the lack of independence, while the diagonal elements indicate the heteroscedasticity

Note that

- y and X are observed data, while β is a vector of parameters
- $E(y) = X\beta$
- $\text{Var}(y) = \text{Var}(e) = \sigma_e^2 R$

Ordinary Least Squares (OLS)

The assumption is that the residual errors e are uncorrelated and have equal variances (homoscedasticity).

- $\sigma^2(e_i) = \sigma_e^2$
- $\sigma(e_i, e_j) = 0$ for $i \neq j$

In a matrix form it has the form $e \sim (0, \sigma_e^2 I)$.

The OLS estimate of β is a vector b that minimizes the residual sum of squares

$$\sum_{i=1}^n \hat{e}_i^2 = \hat{e}^T \hat{e} = (y - Xb)^T (y - Xb) \rightarrow b = (X^T X)^{-1} X^T y$$

Note that

- If $e \sim \text{MVN}(0, \sigma_e^2 I)$, then the OLS estimate is also the maximum-likelihood estimate.
- If $X^T X$ is singular, b still hold when a generalized inverse is used.

Gauss–Markov theorem

The OLS estimator is the best linear unbiased estimator (BLUE) of the coefficients β for linear models in which the errors are uncorrelated and have equal variances.

- best: it minimizes the sampling variance
- linear: it is a linear function of the observed data y
- unbiased: $E(\hat{\beta}_{\text{BLUE}}) = \beta$

Note that the errors don't need to be normal, independent nor identically distributed

Gauss–Markov theorem

The theorem was extended by Aitken to the general linear model in the case the errors have non-scalar covariance matrix.

The BLUE in this case is

$$\hat{\beta} = (X^T R^{-1} X)^{-1} X^T R^{-1} y$$

Derivation is hacked by multiplying both sides of the model equation by $R^{1/2}$. See ([Lynch & Walsh, 1998](#)), Appendix 3, pp. 842.

Summary on General Linear Models

- Modeling a quantitative trait assumes working in terms of both **mean** and **variance**.
- The best linear unbiased estimator (BLUE) provides estimation of the model parameters (coefficients β).

Linear Mixed Models

Mixed Model (in Genetics)

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

- Consider a vector y of the phenotype measured in n individuals.
- We assume that these observations are described adequately by a linear model with
 - $p \times 1$ vector of fixed effects (β)
 - and $q \times 1$ vector of random effects (u).
- The first element of the vector β is typically the population mean.
- Other elements of the vector β may be gender, location, year of birth, experimental treatment, etc.
- The elements of the vector u are usually genetic effects such as additive genetic values.

See ([Lynch & Walsh, 1998](#)), Chapter 26, pp. 746. Example 1 on page 746 is a must (this comes in a few slides).

Mixed Model (matrix form)

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

- X : $n \times p$ incidence or design matrix
- Z : $n \times q$ incidence matrix
- e : $n \times 1$ vector of residual deviations

Note that

- e assumed to be distributed independently of the random genetic effects (thus, we can sum up variances).
- Usually, all elements of Z matrix are either 0 or 1.

Example 1

Suppose that three sires are chosen at random from a population, and each mated to a randomly chosen dam. Two offspring from each mating are evaluated, some in environment 1 and some in environment 2. The model assumes no sire \times environment interaction.

Let y_{ijk} denote the phenotypic value of the k th offspring of sire i in environment j . The model is then

$$y_{ijk} = \beta_j + u_i + e_{ijk}$$

The model has three random effects, which measure the contribution from each sire.

$$\mathbf{u} = \begin{pmatrix} u_1 \\ u_2 \\ u_3 \end{pmatrix}$$

The model also has two fixed effects, which describe the influence of the two environments.

$$\mathbf{u} = \begin{pmatrix} \beta_1 \\ \beta_2 \end{pmatrix}$$

Example 1 with simulated data

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

$$y = \begin{pmatrix} y_{1,1,1} \\ y_{1,2,1} \\ y_{2,1,1} \\ y_{2,1,2} \\ y_{3,1,1} \\ y_{3,2,1} \end{pmatrix} = \begin{pmatrix} 9 \\ 12 \\ 11 \\ 6 \\ 7 \\ 14 \end{pmatrix}$$

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

Mixed Model vs. General Linear model

General linear model

$$y = X\beta + e^* \text{ where } e^* \sim (0, V) \text{ implying } y \sim (X\beta, V)$$

Mixed model partitions the residual effect into two components, with $e^* = Zu + e$, giving

$$y = X\beta + Zu + e \text{ where } u \sim (0, G) \text{ and } e \sim (0, R)$$

$$\text{implying } y \sim (X\beta, V) = (X\beta, ZGZ^T + R)$$

Note that

- Both formulations yield the same estimate of the fixed effects β , when analyzed in the appropriate way.
- The mixed-model formulation further allows estimates of the random effects u .

BLUE and BLUP

BLUE of β is just the generalized least-squares estimator

$$\hat{\beta} = (X^T V^{-1} X)^{-1} X^T V^{-1} y$$

Henderson showed that the BLUP of u is

$$\hat{u} = (GZ^T V^{-1})(y - X\hat{\beta})$$

Summary on Mixed Models

- y, X, Z are observed
- β, u, R, G are unknown
- The covariance matrices R and G typically are functions of a few unknown parameters (σ -parameters)
- Analysis involves two complementary tasks:
 1. estimation of the covariance matrices G and R
 2. estimation of the fixed and random effects, β and u (BLUE and BLUP)

Maximum likelihood (ML) and Restricted Maximum likelihood (REML) are the methods for variance-component estimation. It could be the topic of another presentation. This presentation has been already saturated with maths. See ([Lynch & Walsh, 1998](#)), Chapter 27.

Example 1 to be finished

What are the BLUP values for the sire effects (u_1, u_2, u_3)?

Some assumptions are needed:

- We assume that the residual variances within both environments are the same (σ_e^2), so $R = \sigma_e^2 I$, where I is the 6×6 identity matrix.
- We assume that all three sires are unrelated and drawn from the same population, $G = \sigma_s^2 I$, where I is the 3×3 identity matrix.

Imagine the the step 1 (see the previous slide) is completed, and we know $\sigma_e^2 = 6$ and $\sigma_s^2 = 2$. Thus, the covariance matrix V is given by $ZGZ^T + R$.

$$V = 2 \begin{pmatrix} 1 & 0 & 0 \\ 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \\ 0 & 0 & 1 \end{pmatrix} I_{3 \times 3} \begin{pmatrix} 1 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 1 \end{pmatrix} + 6I_{6 \times 6}$$

Example 1 last shot

$$V = \begin{pmatrix} 8 & 2 & 0 & 0 & 0 & 0 \\ 2 & 8 & 0 & 0 & 0 & 0 \\ 0 & 0 & 8 & 2 & 0 & 0 \\ 0 & 0 & 2 & 8 & 0 & 0 \\ 0 & 0 & 0 & 0 & 8 & 2 \\ 0 & 0 & 0 & 0 & 2 & 8 \end{pmatrix}$$

A few simple matrix calculations are left.

$$\hat{\beta} = \begin{pmatrix} \hat{\beta}_1 \\ \hat{\beta}_2 \end{pmatrix} = (X^T V^{-1} X)^{-1} X^T V^{-1} y = \frac{1}{18} \begin{pmatrix} 148 \\ 235 \end{pmatrix}$$

$$\hat{u} = \begin{pmatrix} \hat{u}_1 \\ \hat{u}_2 \\ \hat{u}_3 \end{pmatrix} = (GZ^T V^{-1})(y - X\hat{\beta}) = \frac{1}{18} \begin{pmatrix} -1 \\ 2 \\ -1 \end{pmatrix}$$

Now try to compare the effects knowing that

$$y = (9, 12, 11, 6, 7, 14)$$

Examples

Genetics Mixed Models and others

Mixed Model for GAIT1 sample (398 individuals in 21 families)

- 398 random effects (length of the vector u)
- Z incidence matrix is the identity matrix $I_{398 \times 398}$
- the random effects are distributed as $(0, A_{398 \times 398})$, where A is $2 \times$ kinship matrix

General-case examples are rather different from those in the genetics.

- random effects are applied to both intercepts and slopes
- covariance matrix of the random effect is the identity matrix

Example 2: Penicillin data

Description:

Six samples of penicillin were tested using the `_B. subtilis_` plate method on each of 24 plates. The response is the diameter (mm) of the zone of inhibition of growth of the organism.

Format:

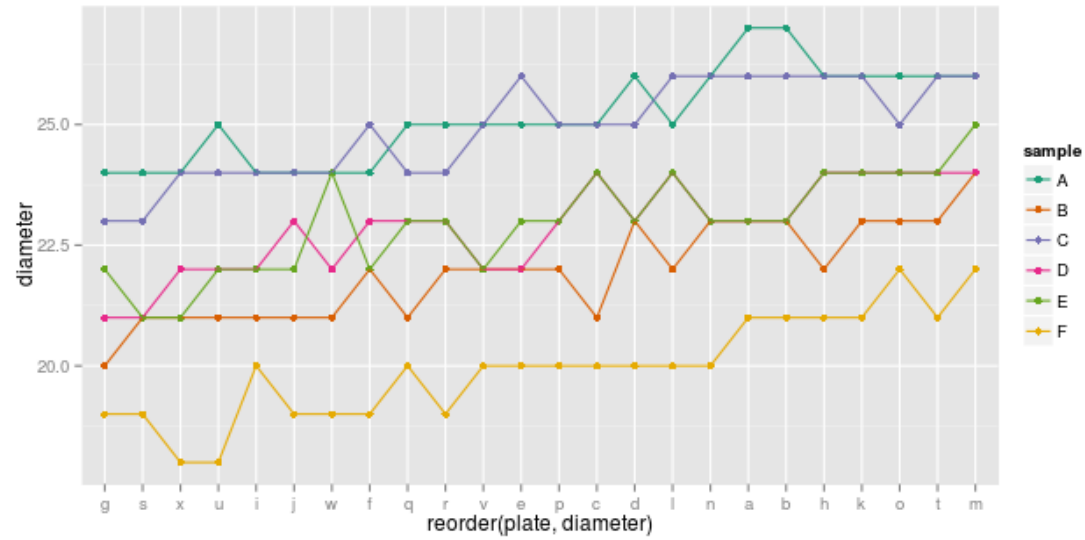
A data frame with 144 observations on the following 3 variables.

`'diameter'` diameter (mm) of the zone of inhibition of the growth of the organism.

`'plate'` assay plate. A factor with levels `'a'` to `'x'`.

`'sample'` penicillin sample. A factor with levels `'A'` to `'F'`.

Penicillin data



```
library(lme4)
data(Penicillin)
lmer(diameter ~ (1|plate) + (1|sample), Penicillin)
```

Linear mixed model fit by REML ['lmerMod']
Formula: diameter ~ (1 | plate) + (1 | sample)
Data: Penicillin

REML criterion at convergence: 330.9

Random effects:

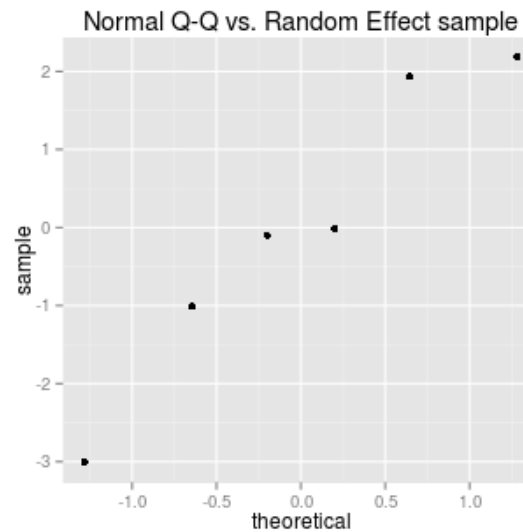
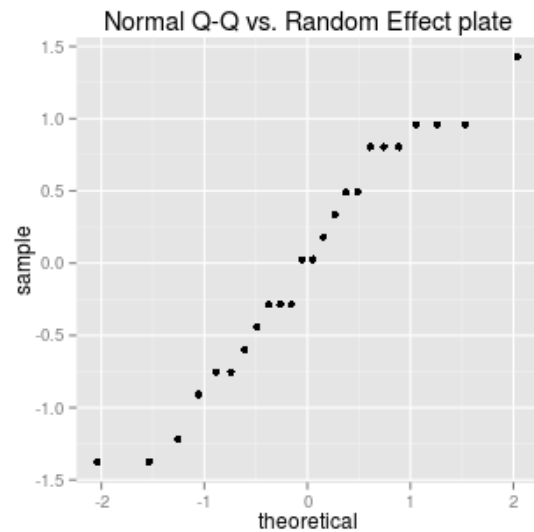
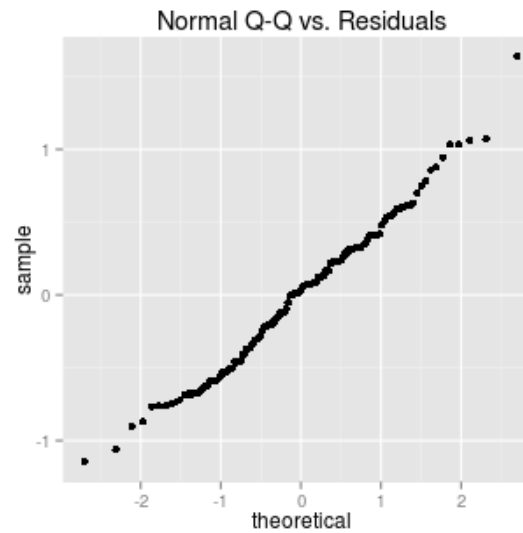
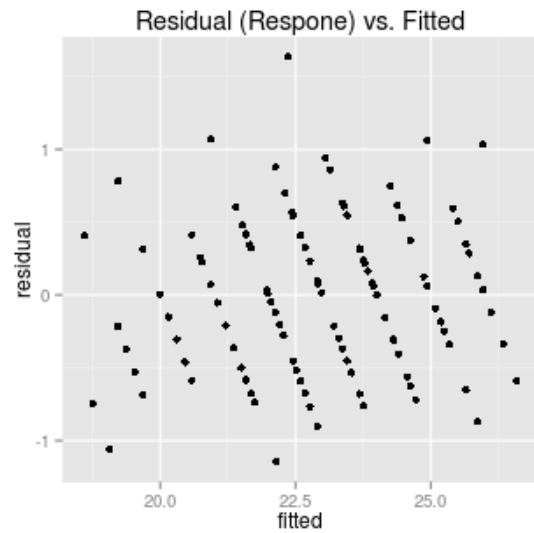
Groups	Name	Variance	Std.Dev.
plate	(Intercept)	0.717	0.847
sample	(Intercept)	3.731	1.932
Residual		0.302	0.550

Number of obs: 144, groups: plate, 24; sample, 6

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	22.972	0.809	28.4

Penicillin model diagnostics



Example 3: sleepstudy data

Description:

The average reaction `time` per `day` for subjects `in` a sleep deprivation study. `On day 0` the subjects had their normal amount of sleep. Starting that night they were restricted to `3` hours of sleep per night. The observations represent the average reaction `time` on a series of tests given each `day` to each subject.

Format:

A data frame with `180` observations on the following `3` variables.

'Reaction' Average reaction `time` (ms)

'Days' Number of days of sleep deprivation

'Subject' Subject number `on` which the observation was made.

```
lmer(Reaction ~ Days + (Days|Subject), sleepstudy)
```

Linear mixed model fit by REML ['lmerMod']

Formula: Reaction ~ Days + (Days | Subject)

Data: sleepstudy

REML criterion at convergence: 1744

Random effects:

Groups	Name	Variance	Std.Dev.	Corr
Subject	(Intercept)	612.1	24.74	
	Days	35.1	5.92	0.07
Residual		654.9	25.59	

Number of obs: 180, groups: Subject, 18

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	251.41	6.82	36.8
Days	10.47	1.55	6.8

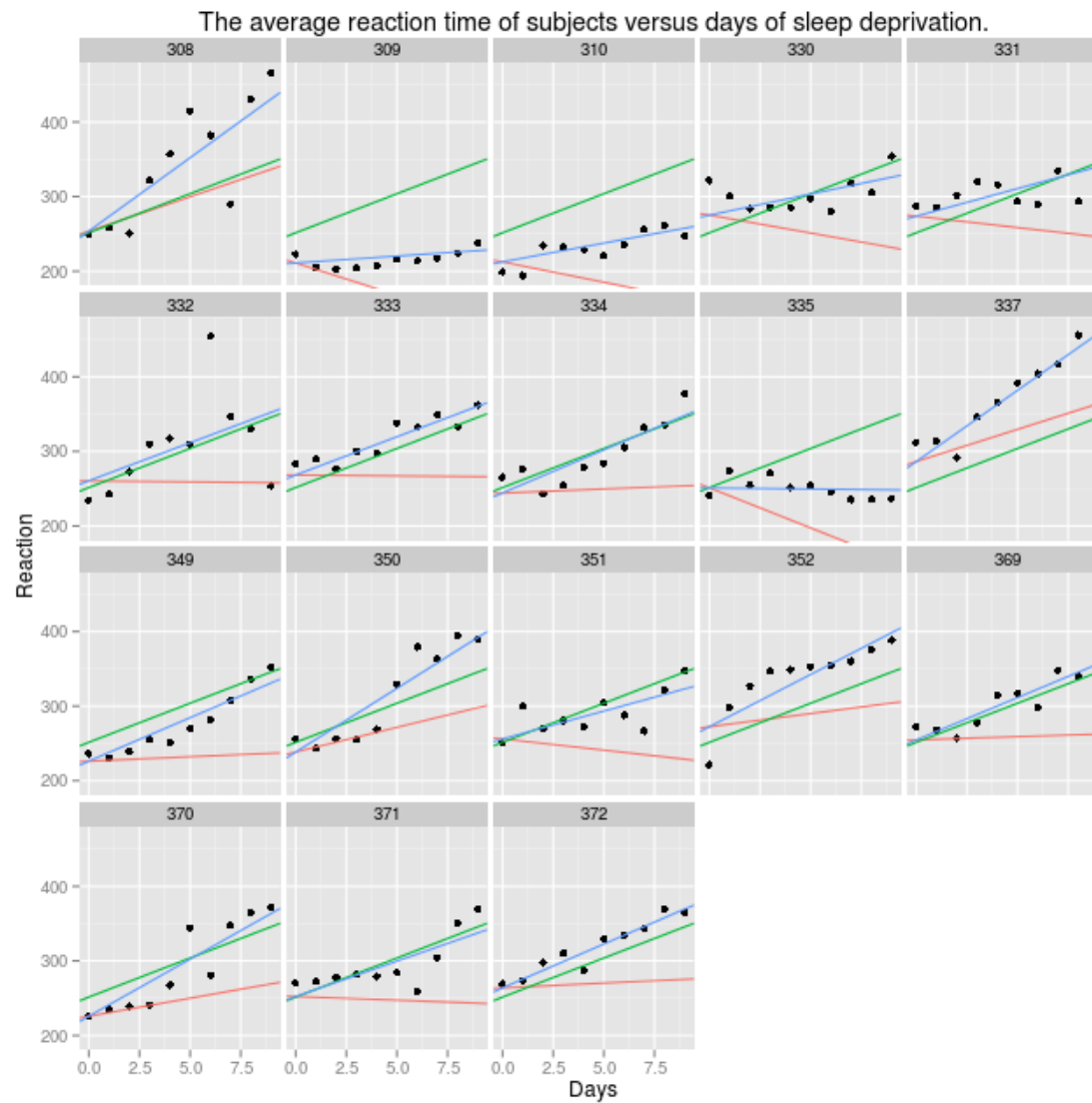
Correlation of Fixed Effects:

(Intr)

Days -0.138

Random and Fixed Effects

total effect = fixed effect + random effect



Comparison of Models

```
m2 <- lmer(Reaction ~ Days + (Days|Subject), sleepstudy)
m2.uncorr <- lmer(Reaction ~ Days + (1|Subject) + (0+Days|Subject), sleepstudy)
anova(m2, m2.uncorr)
```

Data: sleepstudy

Models:

m2.uncorr: Reaction ~ Days + (1 | Subject) + (0 + Days | Subject)

m2: Reaction ~ Days + (Days | Subject)

	Df	AIC	BIC	logLik	deviance	Chisq	Chi	Df	Pr(>Chisq)
m2.uncorr	5	1762.0	1778.0	-876.00	1752.0				
m2	6	1763.9	1783.1	-875.97	1751.9	0.0639		1	0.8004

Summary on Examples

- The definition of a random effect can be implemented either via Z matrix or G matrix.
- Currently, the `lme4` package allows only the Z -based parametrization.
- Rönnegård and Carlborg have shown a statistically equivalent definition of G matrix via an incidence matrix Z ([Rönnegård & Carlborg, 2007](#)). See also [hglm](#) R package.

SOLAR Models

Polygenic (Univariate) Model

$$y = X\beta + g + Hc + e$$

where $g \sim (0, \sigma_g^2 A)$ and $c \sim (0, \sigma_c^2 I)$ and $e \sim (0, \sigma_e^2 I)$

implying $y \sim (X\beta, V) = (X\beta, \sigma_g^2 A + \sigma_c^2 I + \sigma_e^2 I)$

Heritability: $h = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_c^2 + \sigma_e^2}$.

Likelihood Ratio Test (LRT):

MODEL	FREE PARAMETERS	RESTRICTED PARAMETERS
No polygenic effect	σ_c^2, σ_e^2	$\sigma_g^2 = 0$

Bivariate (correlation) Model

$$\begin{pmatrix} y_1 \\ y_2 \end{pmatrix}_{nk \times 1} = \begin{pmatrix} X_1 & 0 \\ 0 & X_2 \end{pmatrix}_{nk \times nk} \begin{pmatrix} \beta_1 \\ \beta_2 \end{pmatrix}_{nk \times 1} + \begin{pmatrix} g_1 \\ g_2 \end{pmatrix}_{nk \times 1} + \begin{pmatrix} e_1 \\ e_2 \end{pmatrix}_{nk \times 1}$$

$$G_{nk \times nk} = C_{k \times k} \otimes A_{n \times n} = \begin{pmatrix} c_{11} A & c_{12} A \\ c_{21} A & c_{21} A \end{pmatrix} = \begin{pmatrix} \sigma_1^2 A & \rho \sigma_1 \sigma_2 A \\ \rho \sigma_1 \sigma_2 A & \sigma_2^2 A \end{pmatrix}_g$$

$$R_{nk \times nk} = E_{k \times k} \otimes I_{n \times n} = \begin{pmatrix} e_{11} I & e_{12} I \\ e_{21} I & e_{21} I \end{pmatrix} = \begin{pmatrix} \sigma_1^2 I & \rho \sigma_1 \sigma_2 I \\ \rho \sigma_1 \sigma_2 I & \sigma_2^2 I \end{pmatrix}_e$$

Likelihood Ratio Test (LRT):

MODEL	FREE PARAMETERS	RESTRICTED PARAMETERS
No genetic correlation	$(\sigma_1^2, \sigma_2^2)_g, (\sigma_1^2, \sigma_2^2, \rho)_e$	$\rho_g = 0$
No pleiotropy	$(\sigma_1^2, \sigma_2^2)_g, (\sigma_1^2, \sigma_2^2, \rho)_e$	$\rho_g = 1$
No environmental correlation	$(\sigma_1^2, \sigma_2^2, \rho)_g, (\sigma_1^2, \sigma_2^2)_e$	$\rho_e = 0$

Weight is a covariate for model of Height

Table 1 Variance components and heritability for horn length in unicorns estimated under models of differing fixed effects.

Model	Fixed effects	V_A	V_R	V_P	h^2	$V_{P(obs)}$	$V_A/V_{P(obs)}$
1a	Mean	0.361 (0.115)	3.117 (0.138)	3.478 (0.115)	0.116 (0.040)	3.466	0.104
1b	Mean + age + sex	0.362 (0.052)	0.653 (0.039)	1.014 (0.038)	0.554 (0.106)	3.466	0.104
1c	Mean + age + sex + age:sex	0.351 (0.049)	0.599 (0.036)	0.950 (0.035)	0.585 (0.110)	3.466	0.101
2a	Mean + weight	0.239 (0.097)	3.042 (0.129)	3.281 (0.1074)	0.078 (0.034)	3.466	0.069
2b	Mean + age + sex + weight	0.234 (0.039)	0.601 (0.033)	0.836 (0.030)	0.389 (0.080)	3.466	0.068
2c	Mean + age + sex + age:sex + weight	0.228 (0.036)	0.546 (0.029)	0.774 (0.028)	0.418 (0.083)	3.466	0.066

Phenotypic variance V_P is determined as the sum of V_A and V_R , and h^2 as the ratio of V_A to V_P . Also shown is the observed phenotypic variance estimated directly from the data [$V_{P(obs)}$] and the heritability calculated using $V_{P(obs)}$ [i.e. $V_A/V_{P(obs)}$].

([Wilson, 2008](#))

Comparing models 2a–c with models 1a–c shows that including weight yields lower estimates of V_A , with concomitant declines in the >heritability. This is because the structure of the **G** matrix used to simulate the phenotypes was such that a positive genetic >correlation exists between weight and horn length. Thus, accounting for differences among individuals in the weight actually removes a >portion of additive variance for the horn length. Thus, the estimates of V_A (and heritability) under models 2a–c are conditioned on the second trait of weight.

Linkage (Univariate) Model

$$y = X\beta + g + Hc + q + e$$

where $g \sim (0, \sigma_g^2 A)$ and $c \sim (0, \sigma_c^2 I)$ and $p \sim (0, \sigma_q^2 IBD)$ and $e \sim (0, \sigma_e^2 I)$

implying $y \sim (X\beta, V) = (X\beta, \sigma_g^2 A + \sigma_c^2 I + \sigma_q^2 IBD + \sigma_e^2 I)$

Likelihood Ratio Test (LRT):

MODEL	FREE PARAMETERS	RESTRICTED PARAMETERS
No linkage	$\sigma_g^2, \sigma_c^2, \sigma_e^2$	$\sigma_q^2 = 0$

Assosiation Model

$$y = X\beta + \beta_{\text{SNP}} * \text{SNP} + g + Hc + e$$

where $g \sim (0, \sigma_g^2 A)$ and $c \sim (0, \sigma_c^2 I)$ and $e \sim (0, \sigma_e^2 I)$

implying $y \sim (X\beta, V) = (X\beta, \sigma_g^2 A + \sigma_c^2 I + \sigma_e^2 I)$

Likelihood Ratio Test (LRT):

MODEL	FREE PARAMETERS	RESTRICTED PARAMETERS
No association	$\sigma_g^2, \sigma_c^2, \sigma_e^2$	$\beta_{\text{SNP}} = 0$

Summary on SOLAR Models

What SOLAR topics should have also been here?

- Bivariate Linkage Model
- Sex-Specific Model
- Parent-Of-Origin Model (available in SOLAR?)
- Derivation and testing the phenotypic correlation
- Definition of the LOD score and its correction methods

Discussion

My long way of learning things

1. Manual of SOLAR
2. Papers of SOLAR
3. Tutorials on the animal model
4. Book ([Lynch & Walsh, 1998](#)), Chapters 26 and 27
5. Writing my own code github.com/variiani/solaris
6. Watching project of other people and trying to contribute to github.com/variiani/lme4

Next Candidate Topics

- Mixed models in application to other type of genetic data? Our data are family-based GAIT!
- Multivariate variance-based methods to fix the family effect?
- Review pro y contra family-based clinical studies
- Improve polygenic model by adding diet and/or treatment as random variable

Are we ready for GAIT2?

Are we ready for GAIT2?

Workflow 'Linkage > Fine-Mapping > Gene Candidates'

- Linkage maps based on SNPs and further linkage analysis
- Use of gene expression data to confirm a gene-candidate
- Association with haplotypes
- Simultaneous linkage and association (rare variants?)
- Multi-loci association
- Association with imputed SNPS

Are we ready for GAIT2?

Storage and sharing knowledge at github.com/ugcd

- Do some planning about methods/tools we are going to use
- Work hard to deliver the phenotypic information about GAIT2
- Invite partners to contribute (UPC, Genebra, etc) and share their ideas
- Store the material of publications by the group

References

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Credits

- [slidify, io2012](#)
- [knitr](#)
- [knitcitations](#)

Thank you