

# Starting Genetic Imaging Analyses with SOLAR-Eclipse

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# To participate in the demo

- Please register and get HCP account
- <http://hcpx-demo.humanconnectome.org>
- The univariate demo
  - <http://tinyurl.com/mvyxcmq>
  - or
  - <https://hcpx-demo.humanconnectome.org/app/template/UnivariatePolygenic.vm>
- The bivariate demo
  - <http://tinyurl.com/ltqf8sj>
  - or
  - <https://hcpx-demo.humanconnectome.org/app/template/GeneticCorrelation.vm>



# Introduction


- What is SOLAR-Eclipse
- Downloading and installing SOLAR-Eclipse
- Creating a solar analysis directory
  - Pedigree file
  - Phenotype file
- Common analyses types
  - Heritability
  - Genetic Correlations
    - Get this file: [www.mdbrain.org/personalpages/peter/lpa.tar](http://www.mdbrain.org/personalpages/peter/lpa.tar)



# SOLAR-Eclipse

- Extension of SOLAR for imaging genetics
- Developed for multiplatform (pc/mac/linux)
  - Genetic analysis of discrete and continuous traits
  - Supports All Common Genetic Analyses for Continuous and Discrete traits.
    - Heritability
    - Genetic Correlation
    - Quantitative trait Linkage
    - GWAS analyses in related and unrelated samples
  - Supports uni-and-multivariate analyses
  - Supports discrete and continuous covariates

Main Strength – Genetic Analysis in Family and Twin Samples



# Downloading/Installing SOLAR

- Get it from NITRC website
  - [http://www.nitrc.org/projects/se\\_linux/](http://www.nitrc.org/projects/se_linux/)
  - Use the linux version for most of the features
    - Latest Apple/PC versions are compiled at request
- Email your user name to get the registration code.
  - [solar@txbiomedgenetics.org](mailto:solar@txbiomedgenetics.org)
  - This code will work on any machine with the same user name
  - Registering for a specific domain is also available
- Manual/Instructional videos at <http://www.mdbrain.org/solareclipse/>

# Develop Analysis Plan

- Background

- Lipo-Protein A (LPA) stimulates lipid metabolism.
- Specific polymorphisms may influence LPA1/2 levels measured in blood

- Questions

- Are LPA1/2 concentrations in blood influenced by additive genetic effects?
- To what extent is white matter integrity measured through DTI-FA determined by additive genetic effects?
- What extent are the same genetic factors influencing both white matter integrity and LPA levels?

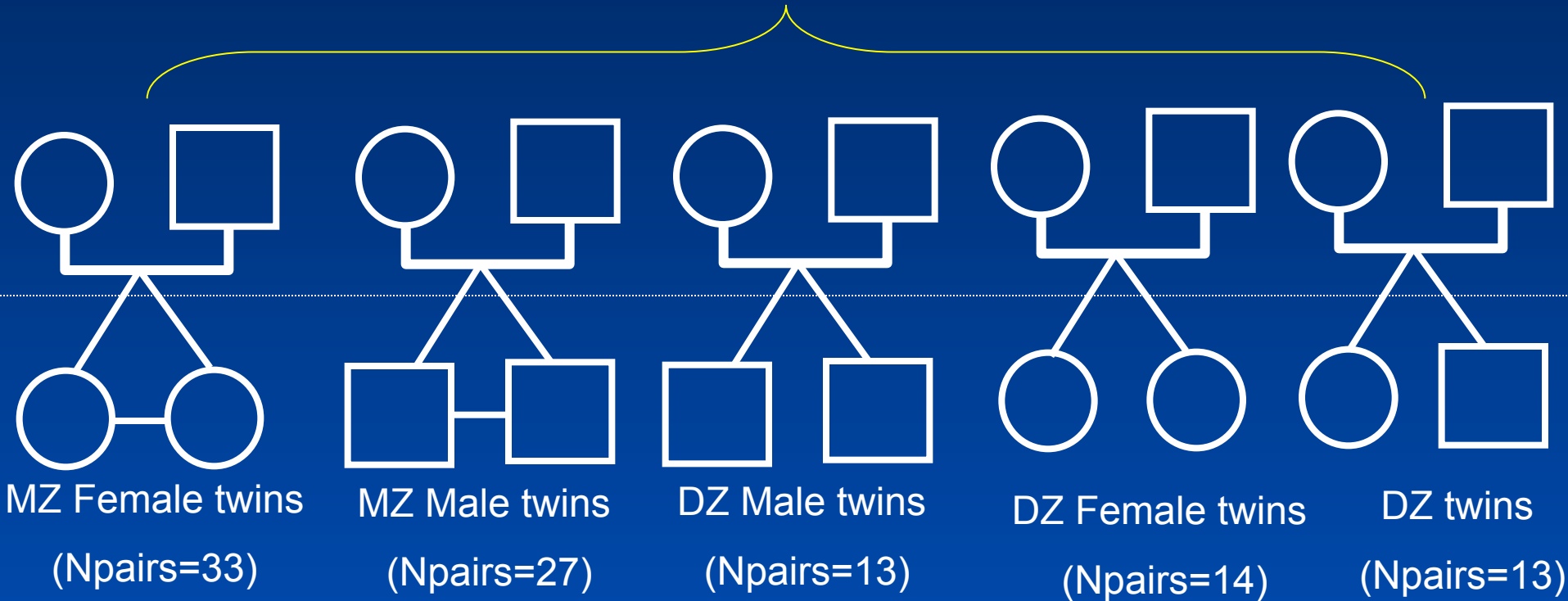
- Approach

- Measure DTI-FA and [LPA1/2] in blood in N=60/50 MZ/DZ twin pairs.
- Measure heritability of average FA values
- Measure heritability of [LPA]
- Calculate pleiotropy between two traits!



# Our Twin Pedigree

Founders



Subjects

# Making a pedigree

- A very important step.
- Pedigree contains “genetic information” based on relatives.
  - Expressed as kinship matrix
  - MZ twins share 100% genetic variance
  - DZ twins share 50% of genetic variance
- SOLAR pedigree must have “founders”
  - Founders are the basis of the pedigree and are assumed unrelated
  - Founder only pedigrees can be used for GWAS analysis of unrelated individuals.



# Actually is a very simple process

ID	FA	MO	sex	FAMID	MZTWIN	HHID	genID	PEDIGREE NUMBER	CLAS
UI209	UIFAID100	UIMOID100	F	UIFMID100	UIFMID100				
UI246	UIFAID100	UIMOID100	F	UIFMID100	UIFMID100				

- Best done in Excel
- Start coding one subject per line.
- ID – subject id (your choice)
- FA/MO are IDs for parents
  - will have to be included as founders even if they don't have phenotypes
- FAMID – optional family id
- MZTWIN – identifier for MZ twins. A twin pair is defined as subjects with same identifier.

# Pedigree file in excel

Microsoft Excel - lpa\_pedi.csv

File Edit View Insert Format Tools Data Window Help

100%

Reply with Changes... End Review...

	A	B	C	D	E	F	G	H	I	J	K
1	ID	FA	MO	sex	FAMID	MZTWIN	HHID	genoID	PEDIG	CLASS	
2	UI209	UIFAID100	UIMOID100	F	UIFMID100	UIFMID100				4	
3	UI246	UIFAID100	UIMOID100	F	UIFMID100	UIFMID100				4	
4	UI174	UIFAID101	UIMOID101	M	UIFMID101	UIFMID101				4	
5	UI27	UIFAID101	UIMOID101	M	UIFMID101	UIFMID101				4	
6	UI199	UIFAID102	UIMOID102	F	UIFMID102	UIFMID102				4	
7	UI211	UIFAID102	UIMOID102	F	UIFMID102	UIFMID102				4	
8	UI17	UIFAID103	UIMOID103	F	UIFMID103	UIFMID103				4	
9	UI68	UIFAID103	UIMOID103	F	UIFMID103	UIFMID103				4	
10	UI77	UIFAID104	UIMOID104	F	UIFMID104	UIFMID104				4	
11	UI42	UIFAID104	UIMOID104	F	UIFMID104	UIFMID104				4	
12	UI61	UIFAID105	UIMOID105	F	UIFMID105	UIFMID105				4	
13	UI146	UIFAID105	UIMOID105	F	UIFMID105	UIFMID105				4	
14	UI60	UIFAID106	UIMOID106	F	UIFMID106	UIFMID106				4	
15	UI167	UIFAID106	UIMOID106	F	UIFMID106	UIFMID106				4	
16	UI138	UIFAID107	UIMOID107	F	UIFMID107	UIFMID107				4	
17	UI71	UIFAID107	UIMOID107	F	UIFMID107	UIFMID107				4	
18	UI76	UIFAID108	UIMOID108	F	UIFMID108	UIFMID108				4	
19	UI197	UIFAID108	UIMOID108	F	UIFMID108	UIFMID108				4	
20	UI123	UIFAID109	UIMOID109	F	UIFMID109	UIFMID109				4	
21	UI41	UIFAID109	UIMOID109	F	UIFMID109	UIFMID109				4	
22	UI183	UIFAID110	UIMOID110	F	UIFMID110	UIFMID110				4	
23	UI145	UIFAID110	UIMOID110	F	UIFMID110	UIFMID110				4	
24	UI116	UIFAID111	UIMOID111	M	UIFMID111	UIFMID111				4	
25	UI15	UIFAID111	UIMOID111	M	UIFMID111	UIFMID111				4	

Lpa\_pedi.csv. CSV stands for comma separated value file format

# Continued

ID	FA	MO	sex	FAMID	MZTWIN	HHID	genoID	PEDIGREE NUMBER	CLASS
UI209	UIFAID100	UIMOID100	F	UIFMID100	UIFMID100				4
UI246	UIFAID100	UIMOID100	F	UIFMID100	UIFMID100				4

- HHID
  - Household id. Use for study of household effects
  - Use it if you have twins living in different households
- genoID
  - Is not commonly used
- Pedigree Number
  - Is not commonly used in humans
- CLASS
  - Important for mega-genetic analysis. Covariates and other normalizations are performed per class
  - If you plan to combine multiple studies assign them non-overlapping class values

# Code founders like this

ID	FA	MO	sex	FAMID	MZTWIN	HHID	genoID	PEDIGREE	CLASS
UIFAID1			M	UIFMID1					4
UIFAID2			M	UIFMID2					4

- Founders are identified as “orphaned” subjects.
  - Make sure you have the right gender
- Save the file in the .csv format.
  - On the mac use “Windows CSV” option
  - Otherwise, “^L” is used to identify end of line



# Fire up solar-eclipse

```
[peterk@medusa LPA]$  
[peterk@medusa LPA]$  
[peterk@medusa LPA]$  
[peterk@medusa LPA]$ solar
```

Solar command starts the tcl shell with R-like interface

```
SOLAR Eclipse version 7.5.3 (Experimental), last updated on May 13, 2014  
Copyright (c) 1995-2014 Texas Biomedical Research Institute  
Enter help for help, exit to exit, doc to browse documentation.
```

```
solar> ls
```

Solar inherits all bash commands, so “ls” gives listing of directory

```
lpa_pedi.csv  lpa_pheno.csv  
solar> █
```

Lpa\_pedi is the file we just created. Lpa\_pheno doesn't exist yet!

heron : peterk    10.0.4.76 :    login1 : petr    test\_medx : bash    10.0.4.76 : petr

# Load your pedigree

```
[peterk@medusa LPA]$  
[peterk@medusa LPA]$  
[peterk@medusa LPA]$  
[peterk@medusa LPA]$ solar  
  
SOLAR Eclipse version 7.5.3 (Experimental), last updated on May 13, 2014  
Copyright (c) 1995-2014 Texas Biomedical Research Institute  
Enter help for help, exit to exit, doc to browse documentation.  
  
solar> ls  
lpa_pedi.csv  lpa_pheno.csv  phenotypes.info  
solar> load pedi lpa_pedi.csv  "Load pedi" command with the name of the file  
Loading pedigree data from the file lpa_pedi.csv ...  
solar> ls  Several new files will be created  
house.gz  lpa_pedi.csv  lpa_pheno.csv  pedigree.info  pedindex.cde  pedindex.out  phenotypes.info  phi2.gz  
solar> █
```

heron : peterk    10.0.4.76 :    login1 : petr    test\_medx : bash    10.0.4.76 : petr

SOLAR creates several internal files that re-arrange pedigree in computation friendly format

Hint – phi2.gz is the kinship matrix in text format that can be used for other packages

# Obtaining phenotypes

- DTI-FA values we calculated using ENIGMA-DTI pipeline
  - <http://enigma.ini.usc.edu/protocols/dti-protocols/>
  - Average whole brain FA values were used
- LPA 1 and 2 levels were obtain from blood
  - 12 hour fasting
  - Measured using Cardio IQ™ Ion Mobility assay
    - Unknown to me and hence presumed very accurate



# Lets make a phenotype file

- Phenotypes are stored in a simple csv format
- Subject ID should match IDs in pedigree file
- Multiple phenotypes files can be loaded at once and merged in memory
  - Convenient for storing fixed factors such as sex and age for the entire pedigree
- Load phenotype command is
  - “load pheno file\_name.csv”
  - [http://www.mdbrain.org//solareclipse/solar\\_commd.html](http://www.mdbrain.org//solareclipse/solar_commd.html)
  - Type “pheno” to check that phenotypes were loaded

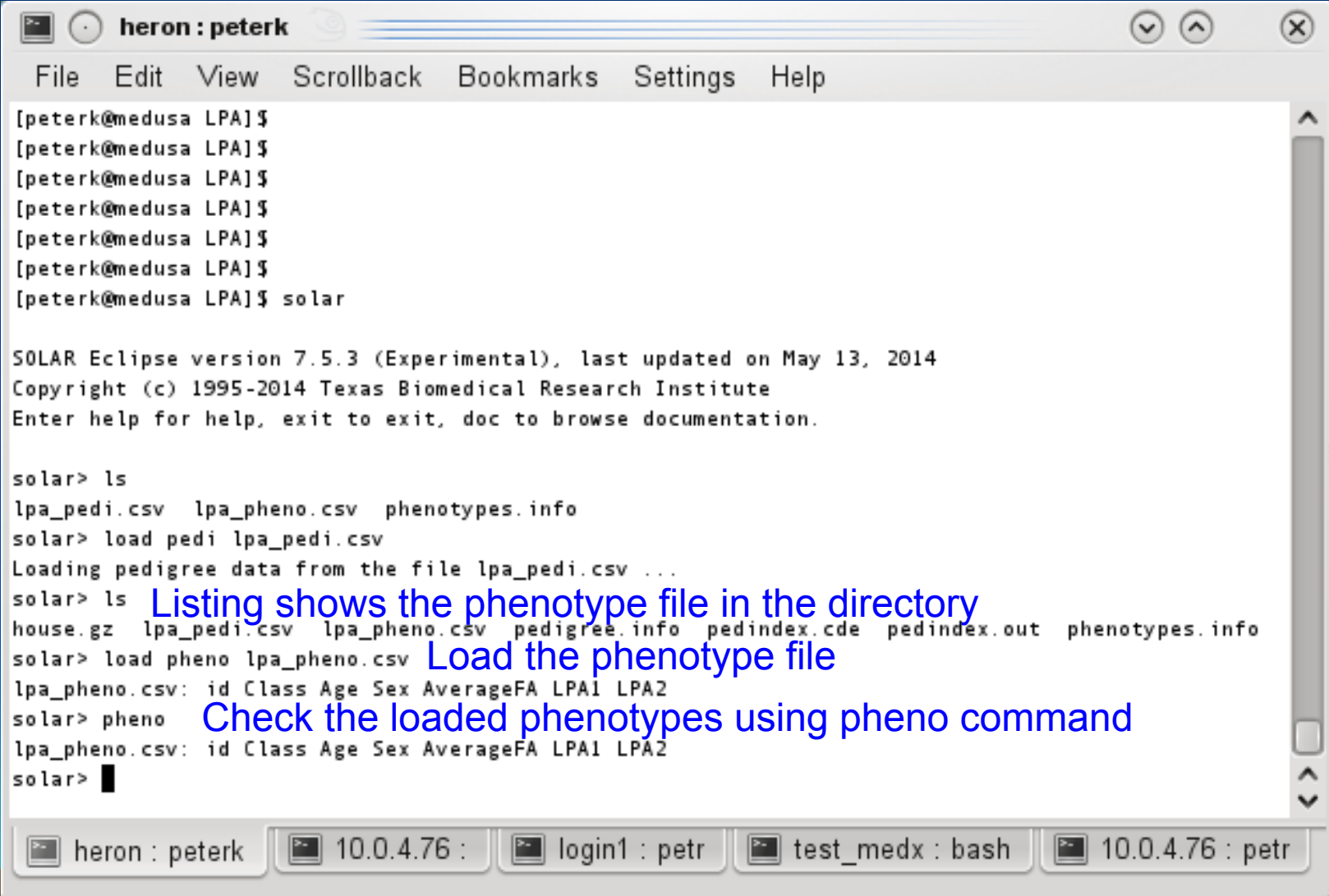


# Phenotype file

- Let put average FA values measured from DTI
- Blood-levels of two LPA proteins LPA1 and LPA2
- Add sex and gender
- Simple CSV format.

id	Age	Sex	AverageFA	LPA1	LPA2
UI101	38	F	0.489995	6.27615	1.191184
UI102	38	F	0.486044	5.73763	1.05002
UI103	45	F	0.475386	6.42397	1.13037
UI10	35	F	0.455976	5.40412	1.11781
UI104	19	F	0.493612	6.20166	1.01562
UI105	56	F	0.457284	6.03059	1.14993
UI106	35	F	0.471036	1.96892	1.05707
UI107	36	F	0.498711	6.31608	1.17105
UI108	32	F	0.485737	6.12398	1.07816

# Load the phenotype file



The screenshot shows a terminal window titled "heron : peterk". The user is in a shell session on a machine named "peterk@medusa LPA". They type the command "solar", which starts the SOLAR Eclipse version 7.5.3. The user then runs "ls" and "load pedi lpa\_pedi.csv". After running "ls" again, they see the file "lpa\_pheno.csv" in the directory. They then run "load pheno lpa\_pheno.csv" and "pheno" to check the loaded phenotypes. The terminal output shows the file listing and the command execution results.

```
[peterk@medusa LPA]$  
[peterk@medusa LPA]$  
[peterk@medusa LPA]$  
[peterk@medusa LPA]$  
[peterk@medusa LPA]$  
[peterk@medusa LPA]$  
[peterk@medusa LPA]$ solar  
  
SOLAR Eclipse version 7.5.3 (Experimental), last updated on May 13, 2014  
Copyright (c) 1995-2014 Texas Biomedical Research Institute  
Enter help for help, exit to exit, doc to browse documentation.  
  
solar> ls  
lpa_pedi.csv  lpa_pheno.csv  phenotypes.info  
solar> load pedi lpa_pedi.csv  
Loading pedigree data from the file lpa_pedi.csv ...  
solar> ls  
house.gz  lpa_pedi.csv  lpa_pheno.csv  pedigree.info  pedindex.cde  pedindex.out  phenotypes.info  
solar> load pheno lpa_pheno.csv  
lpa_pheno.csv: id Class Age Sex AverageFA LPA1 LPA2  
solar> pheno  
lpa_pheno.csv: id Class Age Sex AverageFA LPA1 LPA2  
solar>
```

Listing shows the phenotype file in the directory

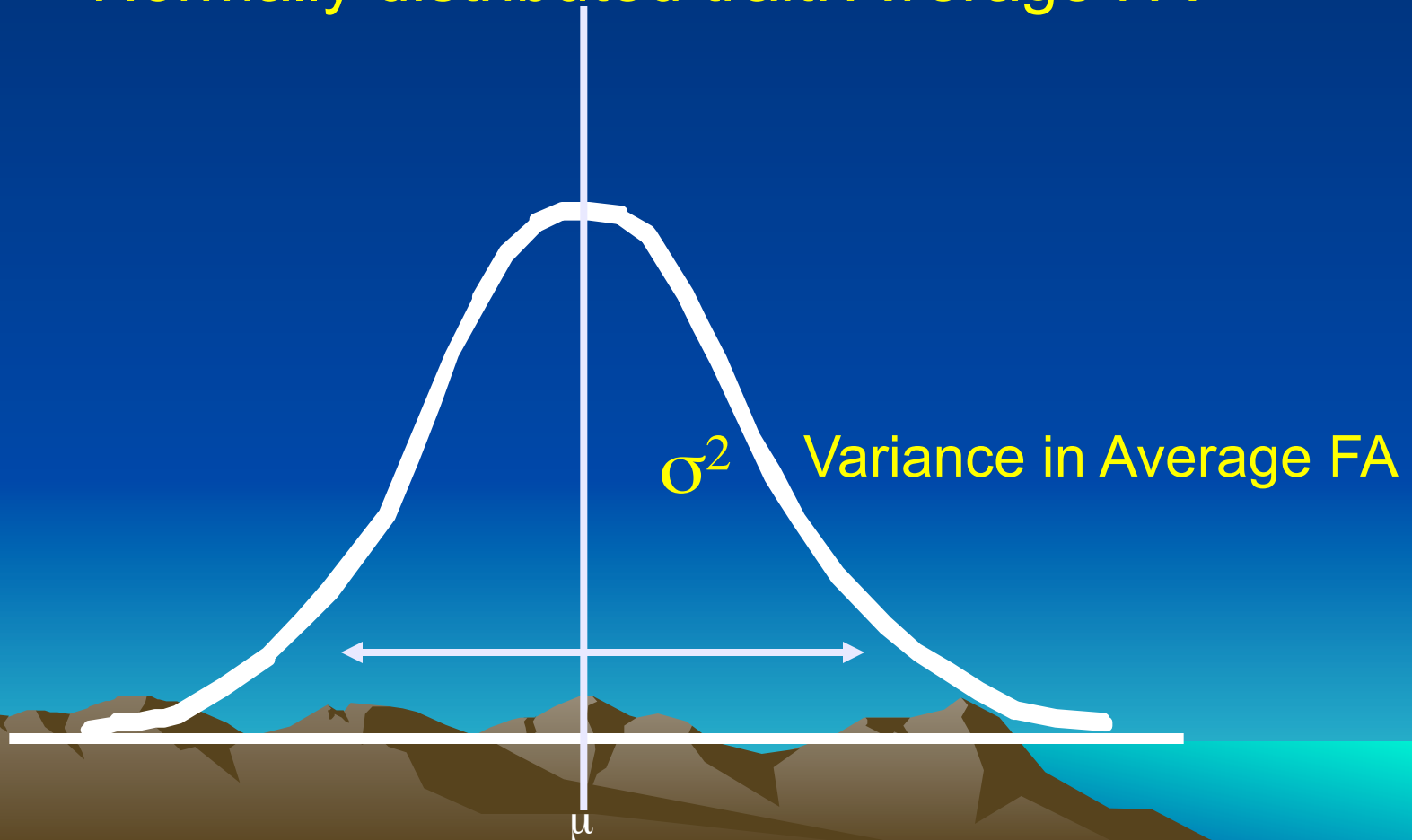
Load the phenotype file

Check the loaded phenotypes using pheno command

# Calculating heritability

- What is heritability?

Normally distributed trait: Average FA



# Variance Decomposition

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

$\sigma_p^2$  = Total phenotypic variance

$\sigma_g^2$  = Variance due to genetic sources

$\sigma_e^2$  = Variance due to environmental source



Genetic variance is due to

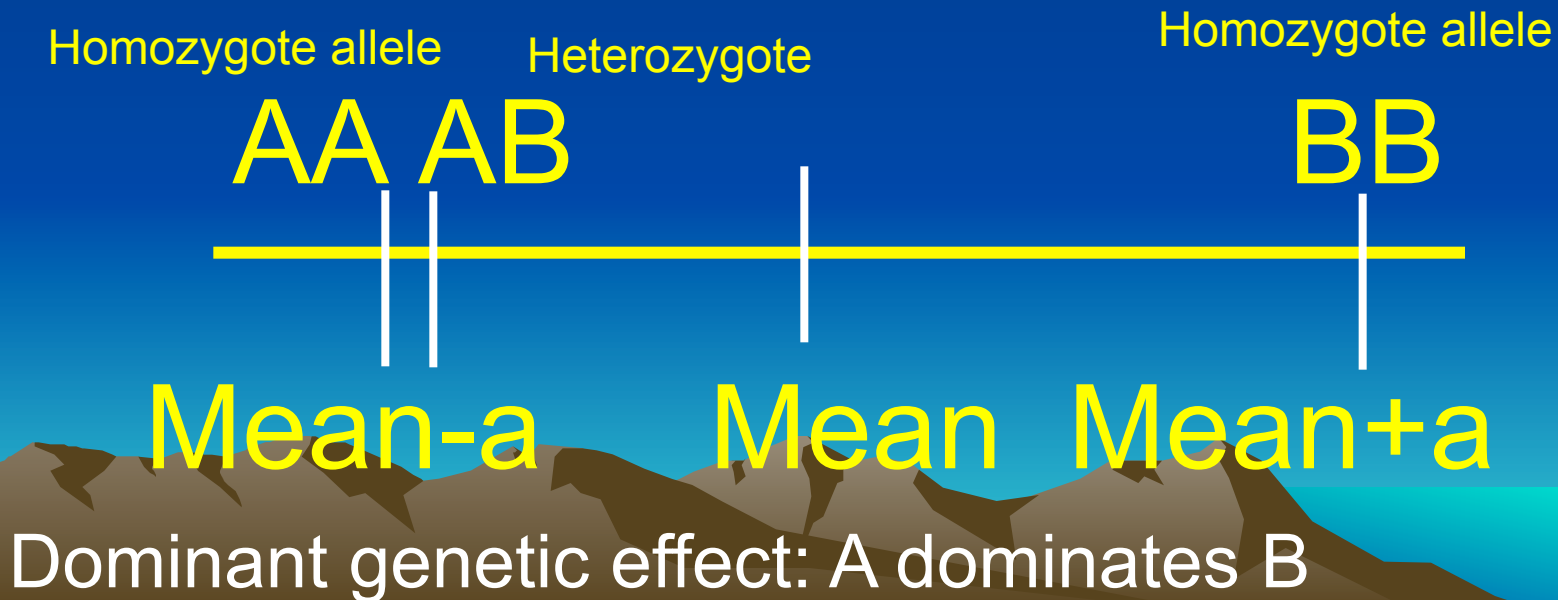
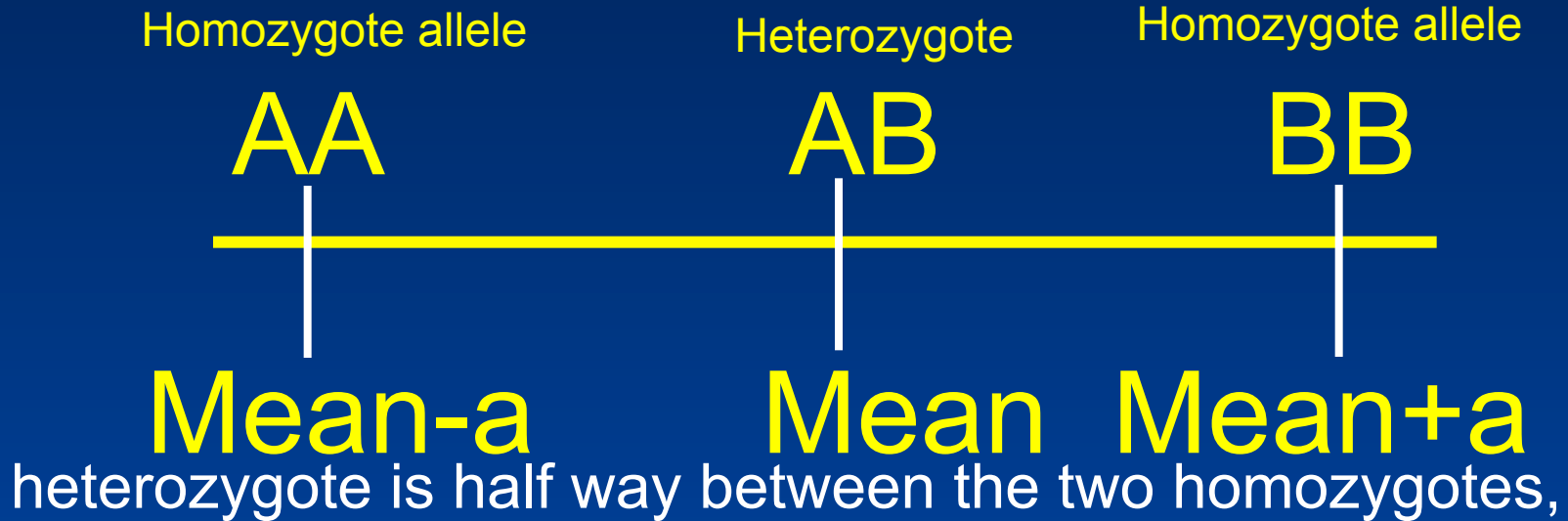
$$\sigma_g^2 = \sigma_a^2 + \sigma_d^2$$

$\sigma_a^2$  = Additive genetic variance

$\sigma_d^2$  = Dominance variance



# Additive genetic effect



# Additive genetic (narrow sense) heritability

$$h^2 = \frac{\sigma_a^2}{\sigma_p^2}$$

Fraction of the total variance in a trait explained by additive genetic variance



# How to calculate it?

```
solar> trait AverageFA Identify the trait
solar> covar Age Sex Age*Sex Identify the covariates
solar> polygen Run polygenic command
*****
* Maximize sporadic model Calculating sporadic model – just covariates
*****

*** Loglikelihood of sporadic model is 959.844031

*****
* Maximize polygenic model Calculating polygenic model –covariates + kinship
```

heron : peterk 10.0.4.76 : login1 : petr test\_medx : bash 10.0.4.7 <

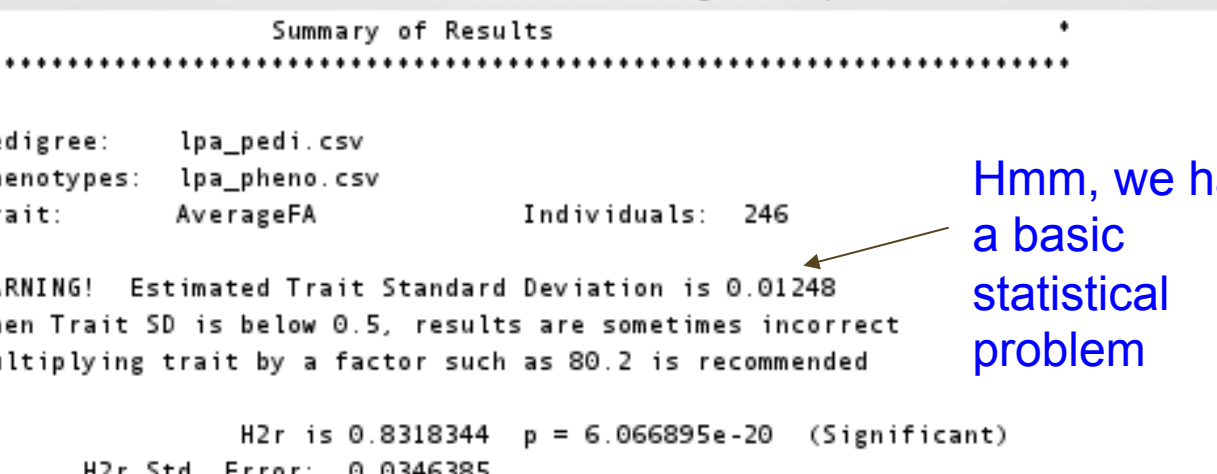
Polygenic function tests two GLM models based on their log-likelihood values

Sporadic model assumes no genetic effects (unitary kinship matrix)

Polygenic model assumes genetic effects (non-unitary kinship matrix)



# Output



```
heron : peterk
File Edit View Scrollback Bookmarks Settings Help
*
Summary of Results
*
Pedigree: lpa_pedi.csv
Phenotypes: lpa_pheno.csv
Trait: AverageFA Individuals: 246

WARNING! Estimated Trait Standard Deviation is 0.01248
When Trait SD is below 0.5, results are sometimes incorrect
Multiplying trait by a factor such as 80.2 is recommended

H2r is 0.8318344 p = 6.066895e-20 (Significant)
H2r Std. Error: 0.0346385

Proportion of Variance Due to All Final Covariates Is
0.1987657

Output files and models are in directory AverageFA/
Summary results are in AverageFA/polygenic.out
Loglikelihoods and chi's are in AverageFA/polygenic.logs.out
Best model is named poly and null0 (currently loaded)
Final models are named poly, spor, nocovar

Residual Kurtosis is -0.0206, within normal range
solar>
```

Hmm, we have a basic statistical problem

# Do the same to LPA1

```
heron : peterk
File Edit View Scrollback Bookmarks Settings Help

*** Trait SD in model with covariates is 0.5956513
*** Trait SD in model without covariates is 0.6180166
*** Proportion of variance explained by covariates is 0.0710681

.....
*                               Summary of Results                               *
.....

Pedigree:      lpa_pedi.csv
Phenotypes:    lpa_pheno.csv
Trait:         LPA1                      Individuals: 246

                H2r is 0.4463829  p = 0.0000065  (Significant)
                H2r Std. Error: 0.0862146

Proportion of Variance Due to All Final Covariates Is
                0.0710681

Output files and models are in directory LPA1/
Summary results are in LPA1/polygenic.out
Loglikelihoods and chi's are in LPA1/polygenic.logs.out
Best model is named poly and null0 (currently loaded)
Final models are named poly, spor, nocovar

Warning! Residual Kurtosis is 12.1259 which is too high.
See note 5 in "help polygenic".

solar> 
```

Another basic statistical problem

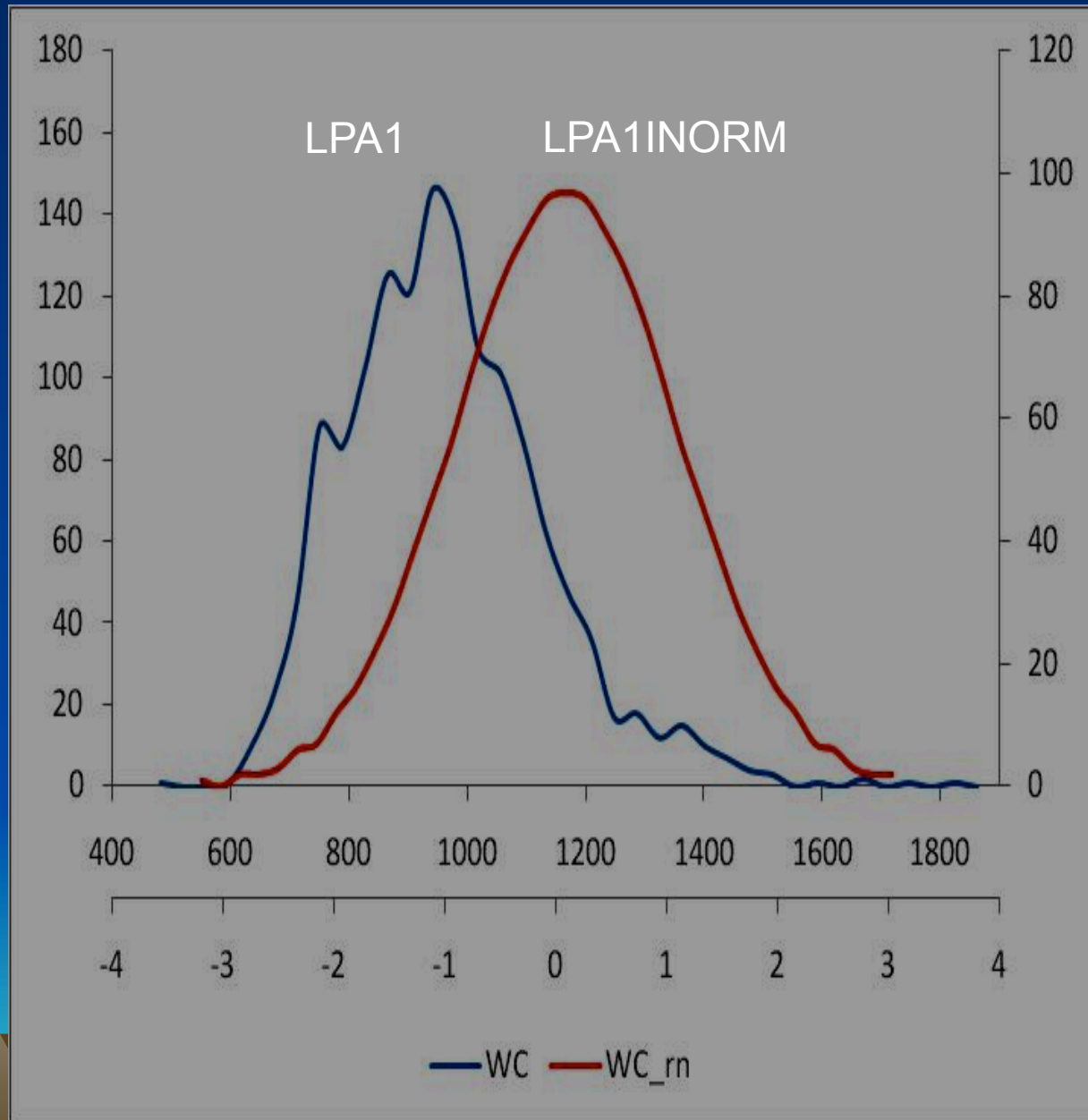
```
heron : peterk  10.0.4.76 :  login1 : petr  test_medx : bash  10.0.4.76 : petr
```

# What to do about it?

- Both problems infer lack of normal distribution
- Normality of the distribution has to be enforced for validity of measurements
- Inorm function in solar does it
  - $\text{AverageFAINOR} = \text{inorm\_AverageFA}$
  - $\text{LPA1INORM} = \text{inorm\_LPA1}$
- Lets repeat!



## Forcing normal distribution via inverse Gaussian transform.



# A-ha, inorm did the trick!

```
heron : peterk
File Edit View Scrollback Bookmarks Settings Help
*****
*** Trait SD in model with covariates is 0.9545215
*** Trait SD in model without covariates is 0.9814815
*** Proportion of variance explained by covariates is 0.0541830
*****
*                               Summary of Results                               *
*****

Pedigree:    lpa_pedi.csv
Phenotypes:  lpa_pheno.csv
Trait:       LPA1INORM           Individuals:  246

                H2r is 0.6109886  p = 3.6882665e-10  (Significant)
                H2r Std. Error:  0.0688235

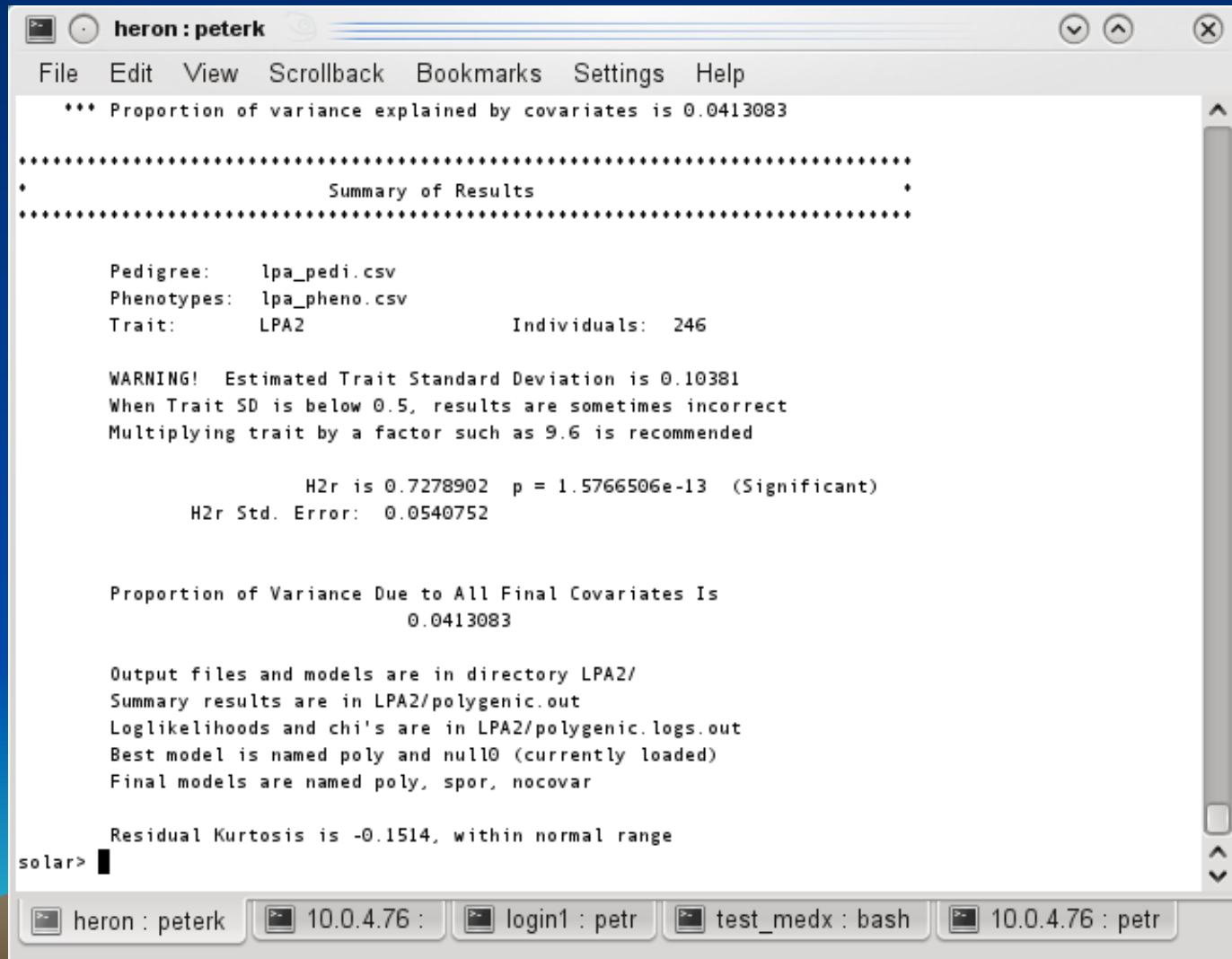
Proportion of Variance Due to All Final Covariates Is
                0.0541830

Output files and models are in directory LPA1INORM/
Summary results are in LPA1INORM/polygenic.out
Loglikelihoods and chi's are in LPA1INORM/polygenic.logs.out
Best model is named poly and null0 (currently loaded)
Final models are named poly, spor, nocovar

Residual Kurtosis is -0.2515, within normal range
solar> 
```

heron : peterk   10.0.4.76 :   login1 : petr   test\_medx : bash   10.0.4.76 : petr

# Do the same for LPA2



```
heron : peterk
File Edit View Scrollback Bookmarks Settings Help

*** Proportion of variance explained by covariates is 0.0413083

.....
*                               Summary of Results                               *
.....

Pedigree:    lpa_pedi.csv
Phenotypes:  lpa_pheno.csv
Trait:       LPA2                      Individuals:  246

WARNING! Estimated Trait Standard Deviation is 0.10381
When Trait SD is below 0.5, results are sometimes incorrect
Multiplying trait by a factor such as 9.6 is recommended

                H2r is 0.7278902  p = 1.5766506e-13  (Significant)
                H2r Std. Error:  0.0540752

Proportion of Variance Due to All Final Covariates Is
                0.0413083

Output files and models are in directory LPA2/
Summary results are in LPA2/polygenic.out
Loglikelihoods and chi's are in LPA2/polygenic.logs.out
Best model is named poly and null0 (currently loaded)
Final models are named poly, spor, nocovar

Residual Kurtosis is -0.1514, within normal range
solar> 
```

heron : peterk 10.0.4.76 : login1 : petr test\_medx : bash 10.0.4.76 : petr

# What do we have

Additive genetic variance explains

- 82% of FA variance
- 61% of the variance in LPA1 protein
- 72% of the variance in LPA2 protein

Now the important part.

- Is that variance shared between traits?
  - This would suggest common genetic or environmental cause



# Perform genetic correlation

- Use genetic correlation ( $\rho_G$ )

$$r = \sqrt{h_A^2} \sqrt{h_B^2} \cdot \rho_G + \sqrt{1 - h_A^2} \sqrt{1 - h_B^2} \cdot \rho_E$$

- Pearson's  $r$  decomposed into  $\rho_G$  and  $\rho_E$
- $\rho_G$  is the proportion of variability due to shared genetic effects
  - To calculate degree of shared genetic variance



# Multivariate Analysis in Solar

- Simply use more than one trait
  - trait AverageFAINORM LPA1INORM
  - covar age<sup>1,2</sup>#sex
    - Covaries effects of age, age<sup>2</sup>, sex and age by sex
  - Polygen –testrhoe –testrhog –testrhop
    - –testrhoe calculates significance of genetic correlation
    - –testrhog calculates significance of environmental correlation
    - –testrhop calculate significance of the phenotypic (combined) correlation
      - Useful for calculating correlations in family samples

# Results for FA and LPA1

```
heron : peterk
File Edit View Scrollback Bookmarks Settings Help
*****
Pedigree:    lpa_pedi.csv
Phenotypes:  lpa_pheno.csv
Trait:       AverageFAINORM LPA1INORM  Individuals:  246

                H2r(AverageFAINORM) is 0.8372909
                H2r(AverageFAINORM) Std. Error: 0.0337385

                H2r(LPA1INORM) is 0.6124907
                H2r(LPA1INORM) Std. Error: 0.0679538

                RhoE is 0.4158286  p = 0.0002559
                RhoE Std. Error: 0.0990957

                RhoG is 0.3832307
                RhoG Std. Error: 0.0934102

                RhoG different from zero  p = 0.0003428
                RhoG different from 1.0   p = 4.3069417e-10
                Derived Estimate of RhoP is 0.3788552
                RhoP different from zero  p = 2.9122759e-86

Output files and models are in directory AverageFAINORM.LPA1INORM/
Summary results are in AverageFAINORM.LPA1INORM/polygenic.out
Loglikelihoods and chi's are in
    AverageFAINORM.LPA1INORM/polygenic.logs.out
Best model is named poly and null0 (currently loaded)

heron : peterk  10.0.4.76 :  login1 : petr  test_medx : bash  10.0.4.76 : petr
```

Environmental correlation = 0.42

Genetic correlation = 0.38

Phenotypic correlation = 0.38

# Results for FA and LPA2

```
heron : peterk
File Edit View Scrollback Bookmarks Settings Help
Pedigree: lpa_pedi.csv
Phenotypes: lpa_pheno.csv
Trait: AverageFAINORM LPA2INORM Individuals: 246

H2r(AverageFAINORM) is 0.8377282
H2r(AverageFAINORM) Std. Error: 0.0335613

H2r(LPA2INORM) is 0.7238363
H2r(LPA2INORM) Std. Error: 0.0537367

RhoE is 0.0229742 p = 0.8503605
RhoE Std. Error: 0.1218340

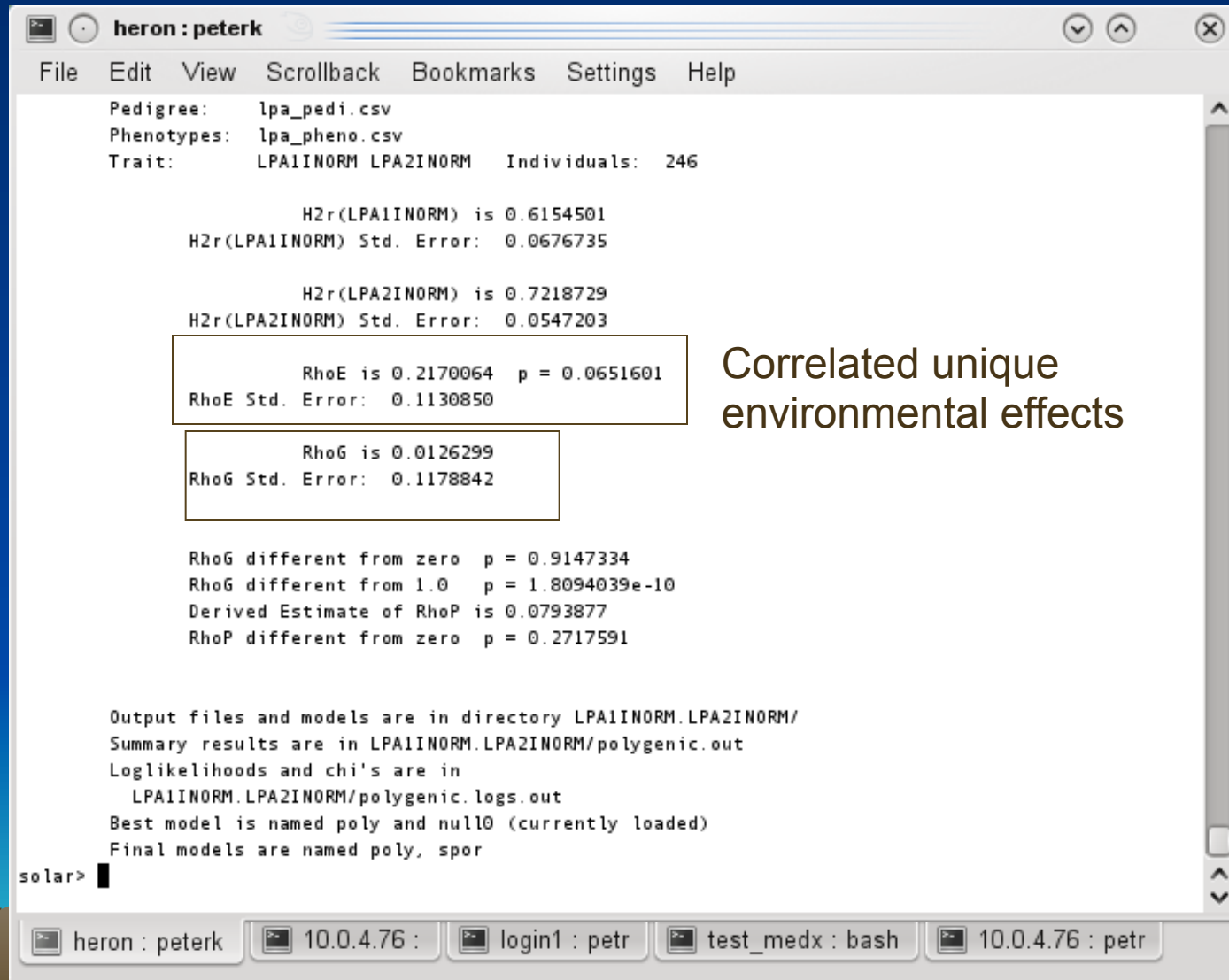
RhoG is 0.3942780
RhoG Std. Error: 0.0885505

RhoG different from zero p = 0.0000626
RhoG different from 1.0 p = 1.2884383e-11
Derived Estimate of RhoP is 0.3118888
RhoP different from zero p = 1.2143532e-33

Output files and models are in directory AverageFAINORM.LPA2INORM/
Summary results are in AverageFAINORM.LPA2INORM/polygenic.out
Loglikelihoods and chi's are in
AverageFAINORM.LPA2INORM/polygenic.logs.out
Best model is named poly and null0 (currently loaded)
Final models are named poly, spor
solar>
```

heron : peterk 10.0.4.76 : login1 : petr test\_medx : bash 10.0.4.76 : petr

# What about LPA1 and LPA2



```
heron : peterk
File Edit View Scrollback Bookmarks Settings Help
Pedigree: lpa_pedi.csv
Phenotypes: lpa_pheno.csv
Trait: LPA1INORM LPA2INORM Individuals: 246

H2r(LPA1INORM) is 0.6154501
H2r(LPA1INORM) Std. Error: 0.0676735

H2r(LPA2INORM) is 0.7218729
H2r(LPA2INORM) Std. Error: 0.0547203

RhoE is 0.2170064 p = 0.0651601
RhoE Std. Error: 0.1130850

RhoG is 0.0126299
RhoG Std. Error: 0.1178842

RhoG different from zero p = 0.9147334
RhoG different from 1.0 p = 1.8094039e-10
Derived Estimate of RhoP is 0.0793877
RhoP different from zero p = 0.2717591

Output files and models are in directory LPA1INORM.LPA2INORM/
Summary results are in LPA1INORM.LPA2INORM/polygenic.out
Loglikelihoods and chi's are in
LPA1INORM.LPA2INORM/polygenic.logs.out
Best model is named poly and null0 (currently loaded)
Final models are named poly, spor

solar>
```

Correlated unique  
environmental effects

# What have we learned?

- FA has shared genetic variance with blood volumes of two lipid messenger/receptors
- FA shows shared environmental variance
  - Caused by factors like stress or diet
- The two LPA molecules are genetically independent
  - Encoded by different genes
  - But show some common environmental variance




# Contact (pkochunov@gmail.com)

- HCP researchers are running SOLAR-Eclipse as a part of their analysis service
- <https://hcpx-demo.humanconnectome.org/app/template/UnivariatePolygenic.vm>  
<https://hcpx-demo.humanconnectome.org/app/template/GeneticCorrelation.vm>
- Visit SOLAR-Eclipse workshop at Imaging Genetic Conference
  - <http://www.imaginggenetics.uci.edu/>
  - 1/19-20, 2015/ Irvine California
  - To learn how to use SE
    - Voxel-wise genetic analysis
    - Mega and Meta genetic analysis
    - Linkage and GWAS

# Human Connectome Web SE

<https://hcpx-demo.humanconnectome.org/app/template/UnivariatePolygenic.vm>

 Dashboard Published Subject Keys Search

**⚠ Plugin Required!**

A browser check indicates that you do not have the Aspera Connect plug  
Project is using an Aspera server to dramatically boost data transfer speed  
using any of ConnectomeDB's services, including downloading. ([Need help?](#))

Logged in as: [kochur](#)

Trait

Covariates

Inverse normalization? ☒

\*\*\*\*\*  
\* Summary of Results \*  
\*\*\*\*\*

Pedigree: hcp\_pedi.csv  
Phenotypes: combined\_data.csv  
Trait: FABodyINORM Individuals: 214

H2r is 0.8458364 p = 1.5415431e-10 (Significant)  
H2r Std. Error: 0.0522210

age p = 0.9970146 (Not Sig., but fixed)  
sex p = 0.0007807 (Significant)

Proportion of Variance Due to All Final Covariates Is  
0.0623123

Output files and models are in directory /home/xnat/data/user/resources/SolarEclipse-8fa0dc8bea32/  
Summary results are in /home/xnat/data/user/resources/SolarEclipse-8fa0dc8bea32/polygenic.log  
Loglikelihoods and chi's are in  
/home/xnat/data/user/resources/SolarEclipse-8fa0dc8bea32/polygenic.logs.out  
Best model is named poly and null0 (currently loaded)  
Final models are named poly, spor, nocovar  
Constrained covariate models are named no

Residual Kurtosis is -0.4497, within normal range

# Human Connectome Web SE





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