

Starting Genetic Imaging Analyses with SOLAR-Eclipse

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SCHOOL OF MEDICINE



TEXAS BIOMEDICAL
RESEARCH INSTITUTE

FORMERLY THE SOUTHWEST FOUNDATION FOR BIOMEDICAL RESEARCH

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



SOLAR-Eclipse

- Extension of SOLAR for imaging genetics
- Developed for multiplatform (pc/mac/linux)
 - Genetic analysis of discreet 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/
 - 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
 - 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?

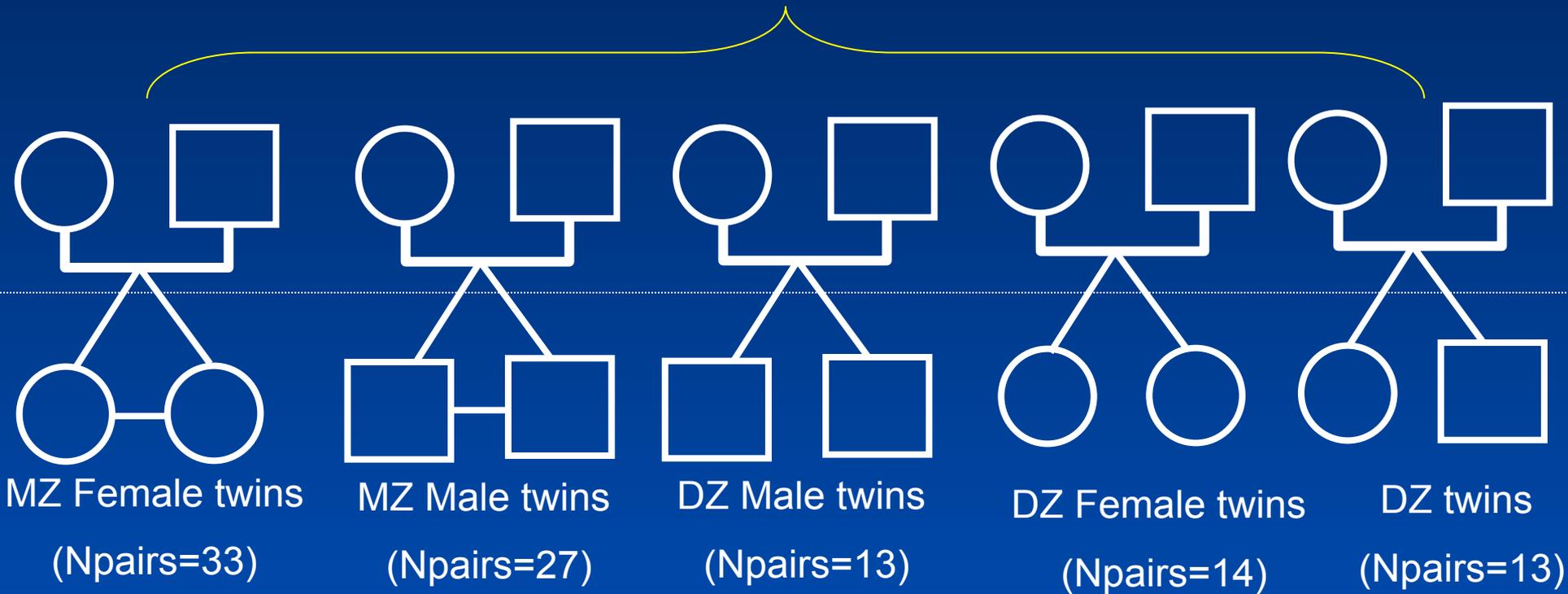
- Approach

- 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

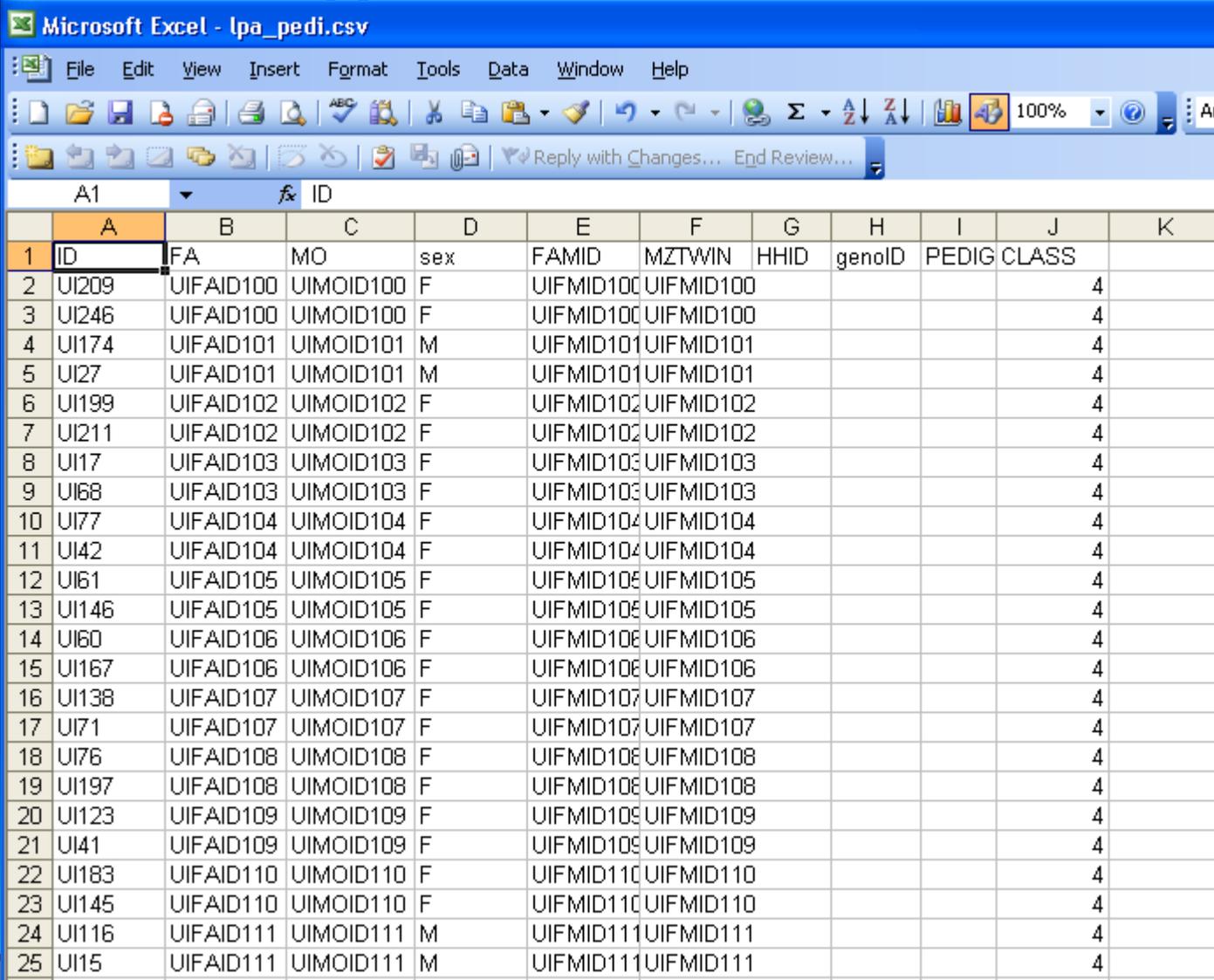
- A very important step.
- Pedigree contains “genetic information” based on relatives.
 - Expressed as kinship matrix
 - MZ twins share 100% genetic variance
 - DZ twins share 50% of genetic variance
- SOLAR pedigree must have “founders”
 - Founders are the basis of the pedigree and are assumed unrelated
 - 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	genolD	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	UIF MID100	UIF MID100					4
3	UI246	UIFAID100	UIMOID100	F	UIF MID100	UIF MID100					4
4	UI174	UIFAID101	UIMOID101	M	UIF MID101	UIF MID101					4
5	UI27	UIFAID101	UIMOID101	M	UIF MID101	UIF MID101					4
6	UI199	UIFAID102	UIMOID102	F	UIF MID102	UIF MID102					4
7	UI211	UIFAID102	UIMOID102	F	UIF MID102	UIF MID102					4
8	UI17	UIFAID103	UIMOID103	F	UIF MID103	UIF MID103					4
9	UI68	UIFAID103	UIMOID103	F	UIF MID103	UIF MID103					4
10	UI77	UIFAID104	UIMOID104	F	UIF MID104	UIF MID104					4
11	UI42	UIFAID104	UIMOID104	F	UIF MID104	UIF MID104					4
12	UI61	UIFAID105	UIMOID105	F	UIF MID105	UIF MID105					4
13	UI146	UIFAID105	UIMOID105	F	UIF MID105	UIF MID105					4
14	UI60	UIFAID106	UIMOID106	F	UIF MID106	UIF MID106					4
15	UI167	UIFAID106	UIMOID106	F	UIF MID106	UIF MID106					4
16	UI138	UIFAID107	UIMOID107	F	UIF MID107	UIF MID107					4
17	UI71	UIFAID107	UIMOID107	F	UIF MID107	UIF MID107					4
18	UI76	UIFAID108	UIMOID108	F	UIF MID108	UIF MID108					4
19	UI197	UIFAID108	UIMOID108	F	UIF MID108	UIF MID108					4
20	UI123	UIFAID109	UIMOID109	F	UIF MID109	UIF MID109					4
21	UI41	UIFAID109	UIMOID109	F	UIF MID109	UIF MID109					4
22	UI183	UIFAID110	UIMOID110	F	UIF MID110	UIF MID110					4
23	UI145	UIFAID110	UIMOID110	F	UIF MID110	UIF MID110					4
24	UI116	UIFAID111	UIMOID111	M	UIF MID111	UIF MID111					4
25	UI15	UIFAID111	UIMOID111	M	UIF MID111	UIF MID111					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

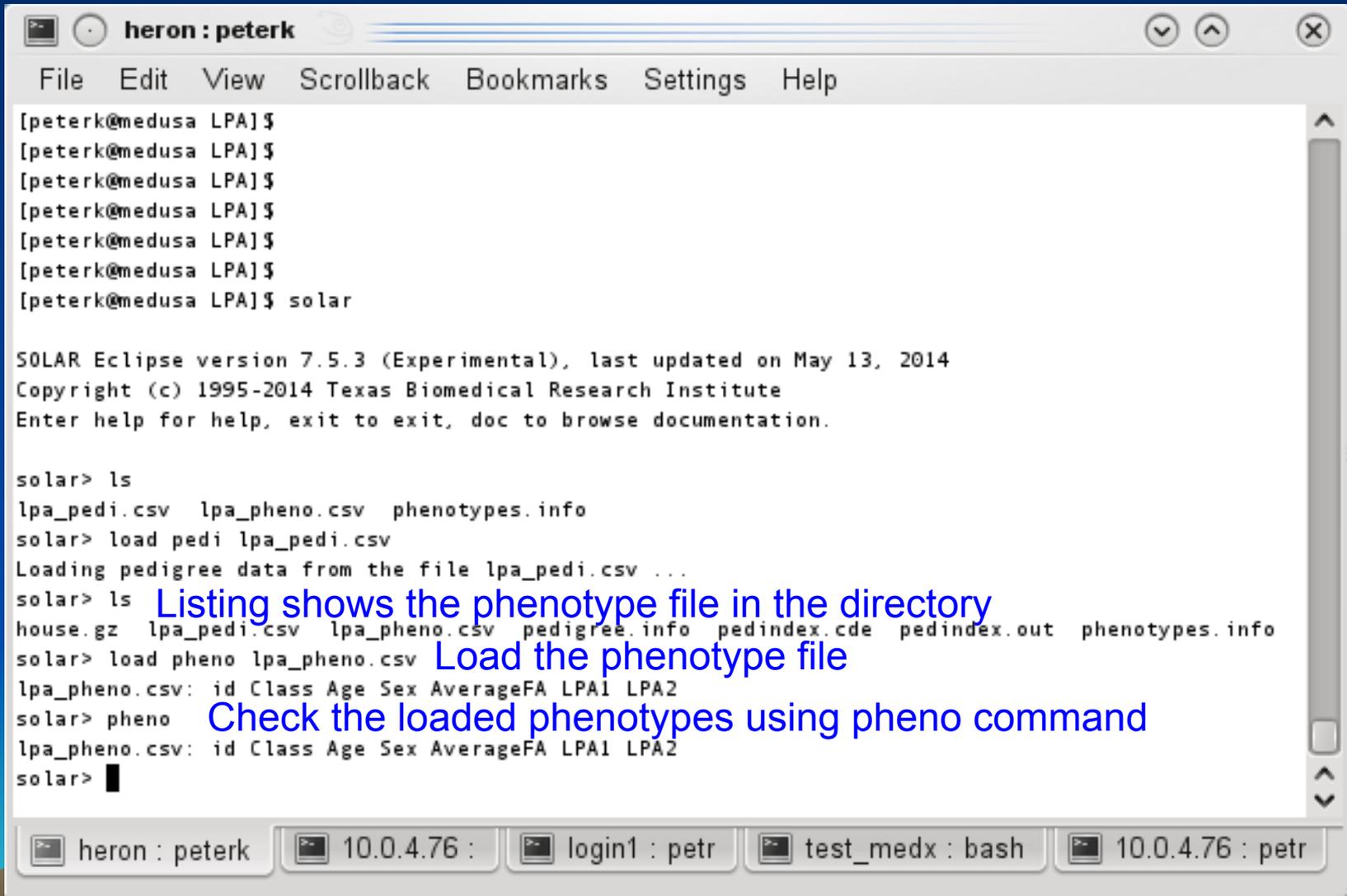
- Phenotypes are stored in a simple csv format
- Subject ID should match IDs in pedigree file
- Multiple phenotypes files can be loaded at once and merged in memory
 - Convenient for storing fixed factors such as sex and age for the entire pedigree
- Load phenotype command is
 - “load pheno file_name.csv”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



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

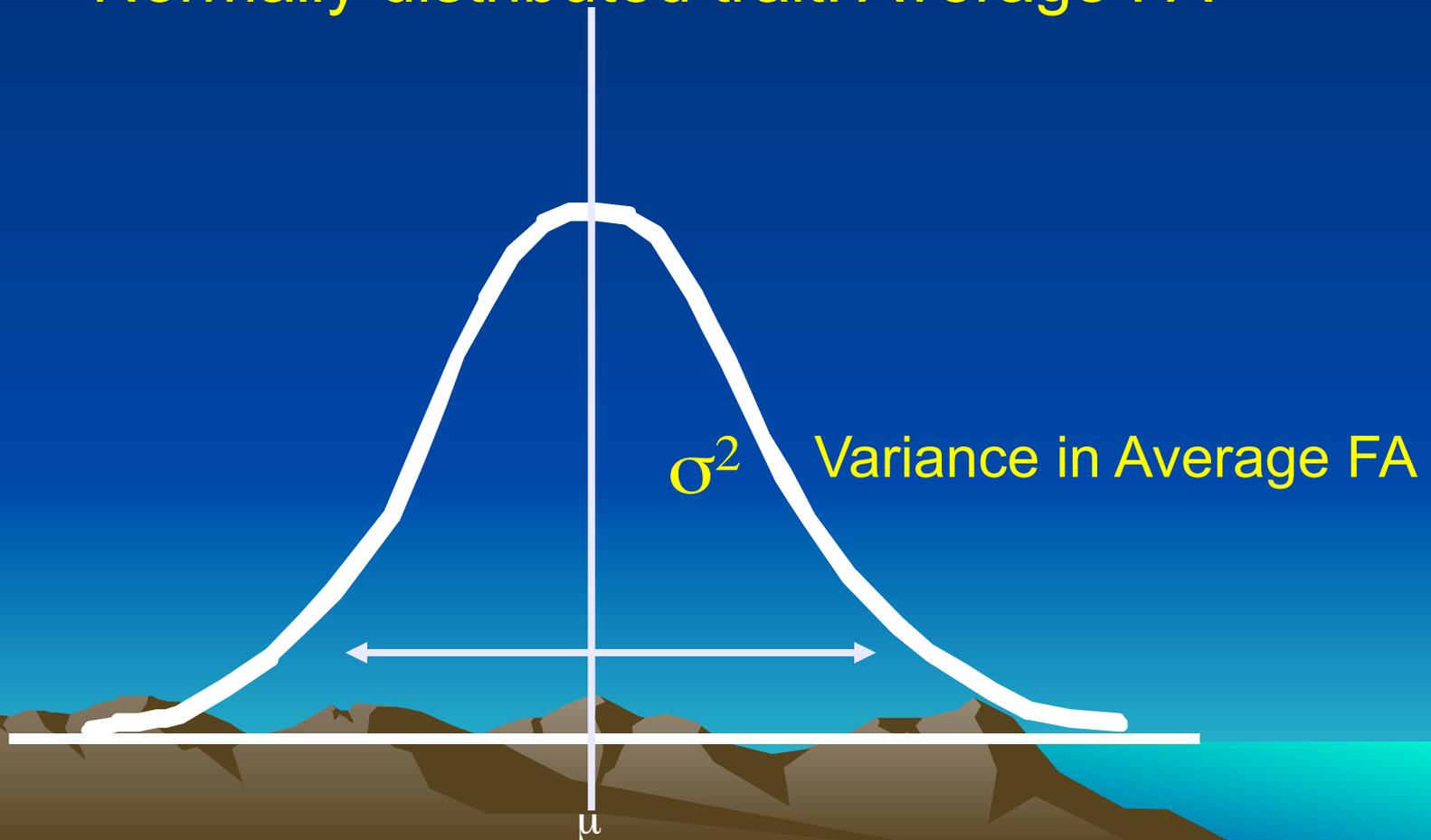
solar> ls
lpa_pedi.csv lpa_pheno.csv phenotypes.info
solar> load pedi lpa_pedi.csv
Loading pedigree data from the file lpa_pedi.csv ...
solar> ls Listing shows the phenotype file in the directory
house.gz lpa_pedi.csv lpa_pheno.csv pedigree.info pedindex.cde pedindex.out phenotypes.info
solar> load pheno lpa_pheno.csv Load the phenotype file
lpa_pheno.csv: id Class Age Sex AverageFA LPA1 LPA2
solar> pheno Check the loaded phenotypes using pheno command
lpa_pheno.csv: id Class Age Sex AverageFA LPA1 LPA2
solar> █
```

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

Calculating heritability

- What is heritability?

Normally distributed trait: Average FA



Variance Decomposition

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

σ_p^2 = Total phenotypic variance

σ_g^2 = Variance due to genetic sources

σ_e^2 = Variance due to environmental source

Genetic variance is due to

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

σ_a^2 = Additive genetic variance

σ_d^2 = Dominance variance



Additive genetic effect

Homozygote allele

Heterozygote

Homozygote allele

AA

AB

BB



Mean-a

Mean

Mean+a

heterozygote is half way between the two homozygotes,

Homozygote allele

Heterozygote

Homozygote allele

AA

AB

BB



Mean-a

Mean

Mean+a

Dominant genetic effect: A dominates B

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

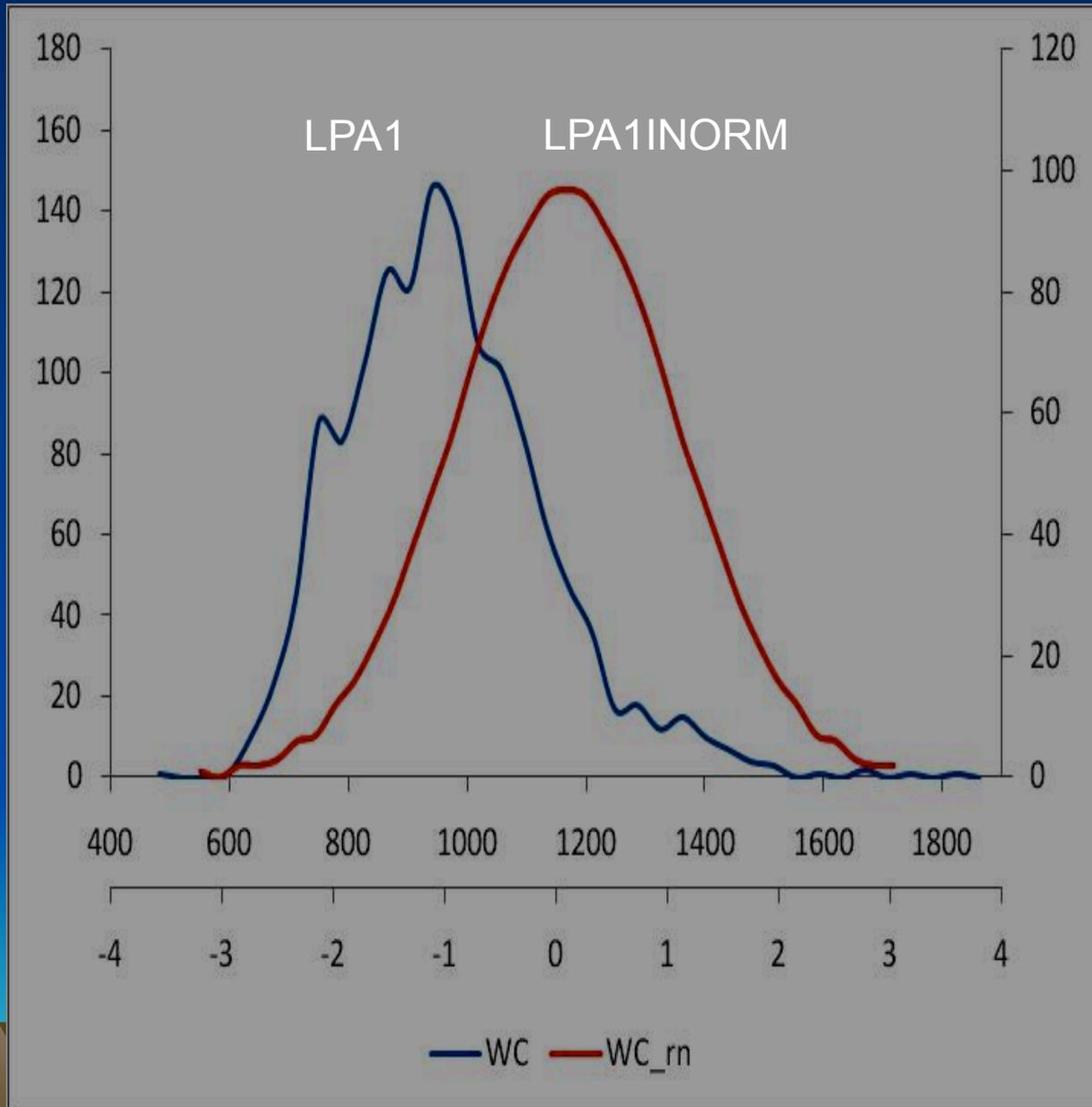


What to do about it?

- 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 (ρ_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 ρ_G and ρ_E
- ρ_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^{1,2}#sex
 - Covaries effects of age, age², 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>

The screenshot shows a web browser window with the URL `https://hcpx-demo.humanconnectome.org/app/template/UnivariatePolygenic.vm`. The page header includes the "CONNECTOME db" logo and navigation links for "Dashboard" and "Published Subject Keys". A search bar is visible on the right.

A yellow warning icon with the text "Plugin Required!" is displayed. To its right, a message states: "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 he...".

The main content area shows a form with the following fields:

- Trait: FABody (selected in a dropdown)
- Covariates: age sex
- Inverse normalization?:
- Submit button

Below the form, the text "Logged in as: kochur" is visible.

The analysis results are displayed in a monospaced font, enclosed in a box with asterisks at the top and bottom. The results include:

- 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/SolarEcl...
- Summary results are in /home/xnat/data/user/resources/SolarEclipse-8fa0dc8bea32/...
- 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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