

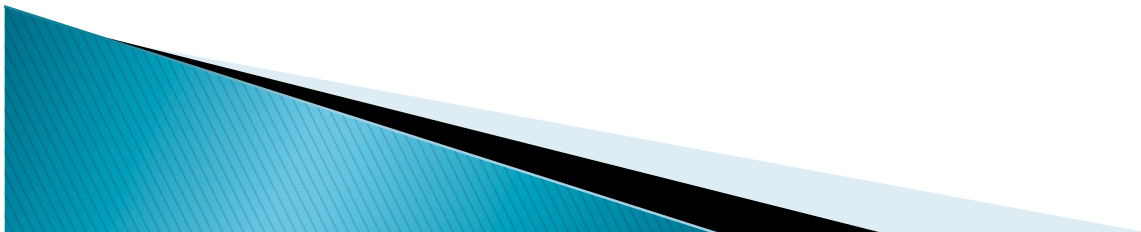
PedStats Introduction

Pedstats software

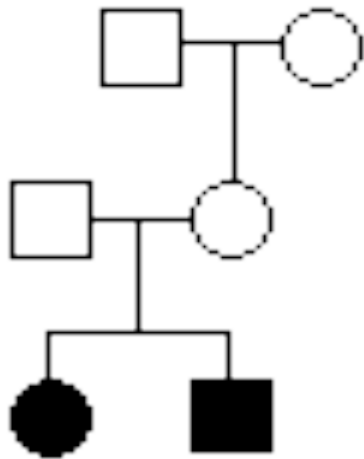
- ▶ Pedigree statistics
- ▶ produce graphical output in PDF format
- ▶ General option
Pedstats -d Simulated_Trait.dat -p
Simulated_Trait.ped
- ▶ Useful options
--pair, --byFamily, **--bySex**, --pdf

Input Files

- ▶ Pedigree File
 - Relationships
 - Genotype data (optional)
 - Phenotype data
- ▶ Data File
 - Describes contents of pedigree file



Describing Relationships



FAMILY	PERSON	FATHER	MOTHER	SEX
example	granpa	unknown	unknown	m
example	granny	unknown	unknown	f
example	father	unknown	unknown	m
example	mother	granny	granpa	f
example	sister	mother	father	f
example	brother	mother	father	m

Example Pedigree File

<contents of example.ped>

```
1 1 0 0 1 1 x 3 3 x x
1 2 0 0 2 1 x 4 4 x x
1 3 0 0 1 1 x 1 2 x x
1 4 1 2 2 1 x 4 3 x x
1 5 3 4 2 2 1.234 1 3 2 2
1 6 3 4 1 2 4.321 2 4 2 2
```

<end of example.ped>

Encodes family relationships, marker and phenotype information

Data File Field Codes

Code	Description
M	Marker Genotype
A	Affection Status.
T	Quantitative Trait.
C	Covariate.
Z	Zygoty (Twins).
S[n]	Skip n columns.

Example Data File

<contents of example.dat>

T some_trait_of_interest

M some_marker

M another_marker

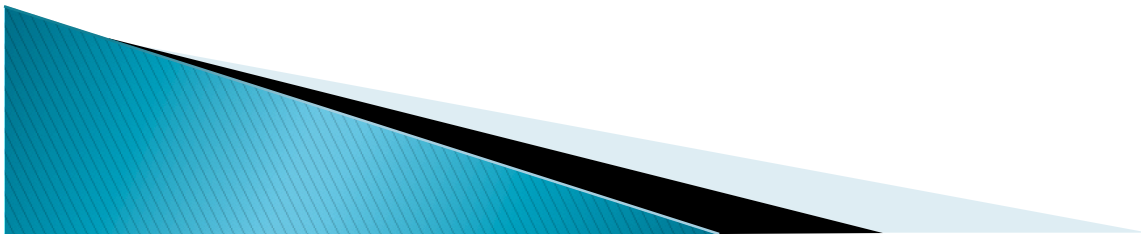
<end of example.dat>

Provides information necessary to decode
pedigree file

Files

`Simulated_Trait.ped`

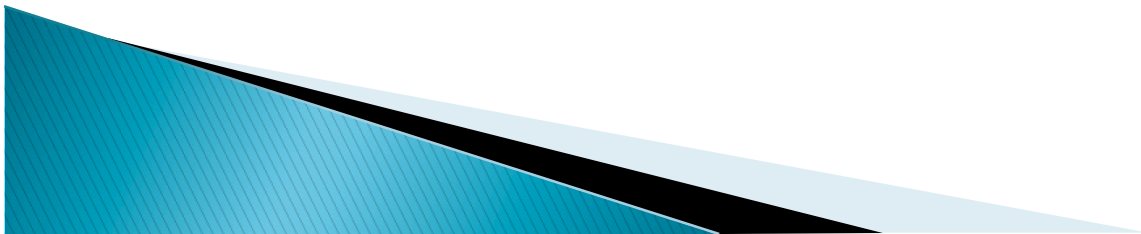
`Simulated_Trait.dat`



.dat file

T qpheno

E END-OF-DATA



Pedstats

- ▶ Copy the files to a folder
- ▶ Open MS-DOS prompt or Mac OS / Linux Terminal - go to the folder where the files are

- ▶ Type

```
pedstats -d Simulated_Trait.dat -p  
    Simulated_Trait.ped
```

- ✓ “pedstats” for Linux or Mac OS
- ✓ “pedstats.exe” for Windows

Output (part)

PEDIGREE STRUCTURE

=====

Individuals: 32000

Founders: 10000 founders, 22000 nonfounders

Gender: 18000 females, 14000 males

Families: 2000

Family Sizes

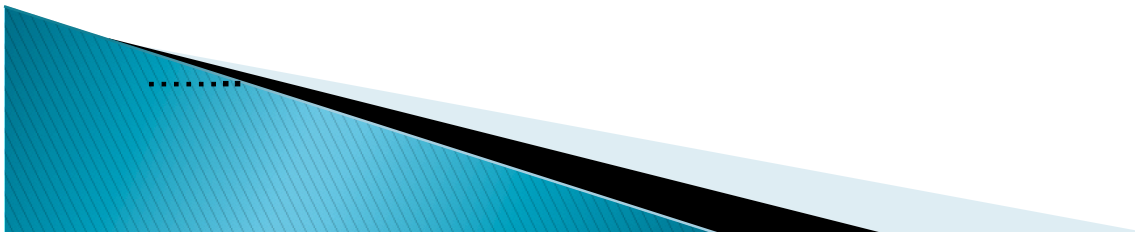
Average: 16.00 (16 to 16)

Distribution: 16 (100.0%), 0 (0.0%) and 1 (0.0%)

Generations

Average: 3.00 (3 to 3)

Distribution: 3 (100.0%), 0 (0.0%) and 1 (0.0%)



Exercise (Pedstats)

- ▶ What are the fullsib, halfsib, parent–offspring, grandparent–grandchild, etc., correlation for the phenotype?
- ▶ Provide an estimate of heritability from the correlation between relatives.
- ▶ What assumptions did you make regarding the genetic model for your heritability estimate?

Exercise (Pedstats)

- ▶ Try `--bySex`, and compare with previous results.
- ▶ Can use options such as `--pdf`, `--pairs`, and `--bySex` together

```
pedstats -d Simulated_Trait.dat -p  
    Simulated_Trait.ped --bySex --pairs --pdf
```