

HOWTO: Loading Genotype Data

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April 21, 2009

1 Introduction

This document demonstrates how to use the *GeneticsBase* package to generate marker summary tables for studies with a small number of markers. It is written as a step-by-step tutorial. For additional details on each of the R functions utilized, please see the individual help pages

Note: The textual displays described here are not suitable for large numbers of markers. They are intended for reviewing detailed information on a small number of markers, such as those in candidate gene studies, or a small set of markers achieving a 'quality' or 'significance' cutoff from a larger set.

2 Example

2.1 Prepare phenotype data

The first step is to prepare the phenotype data. It may be in the form of a SAS dataset, SAS export file, comma-delimited text file (CSV), tab-delimited text file (TSV), or Microsoft Excel spreadsheet file (XLS). It should have one row per observation and one column per variable, and must contain a subject identifier variable that can be used to match observations with the corresponding genotype data.

2.2 Prepare genotype data

You also need to store the genetic call data in a file that can be read into R. *GeneticsBase* package accepts genotype data in a variety of formats:

- standard pedigree (ped) format.

a2m	apoe						
50103	5010004	5090005	5090004	2	2	1	
2	3	4					
50103	5010005	5090005	5090004	2	2	1	
1	3	4					
50105	5010049	5090021	5090022	2	2	1	
1	4	4					
50105	5010070	5090020	5090019	1	2	1	
1	3	4					


```
> PfizerExample <- readGenes.pfizer("PfizerExample.txt", format = "Listing")
```

- Perlegen data format

```
> PerlegenExample <- readGenes("PerlegenExample.txt", gformat = "perlegen")
```