Running MENDEL

- Written by Ken Lange
- Very wide range of analyses

Parametric and nonparametric linkage

IBD estimation

Haplotyping

Individual or family based association

Ethnicity estimation

http://www.genetics.ucla.edu/software

MENDEL: most analyses
SIMWALK2: for larger pedigrees

Genetic Association with MENDEL

- Transmission-disequilibrium test
- Gamete competition model
- Generalized linear model association
- Association given linkage (permutation test)
- Association in pedigrees (polygenic background)

Genetic Association with MENDEL

- Can infer/impute genotypes in relatives of genotyped individuals: increases power
- Some simulation-based P-values
- Genetic association for survival data

“SNP” Haplotypes

- Very general: families or individuals
- Allows for linkage disequilibrium
- Limited in maximum number of SNPs per haplotype
- Can limit haplotype number by frequency
- Need to specify control file and “SNP file”

Creating data files

These can be created using Sib-pair:

- Pedigree file
- Locus file
- Map file
- Control file
- “Var” quantitative trait list file
- SNP file

Association analysis using FBAT

- Transmission-disequilibrium type testing allowing for missing parental data
- Binary, continuous and survival traits
- Monte-Carlo P-values
- Haplotype association
- Deals with population admixture
- Association in the presence of linkage

Preparing files for FBAT

- Pedigree file: pedigree data plus genotype data
- Phenotype data file (similar to SOLAR)

```
load ped
load phe
trait
fbat –e
hbat -e
```