An Integrated Genetic Analysis Package Using R

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1 Introduction

This package was designed to integrate some C/Fortran/SAS programs I have written or used over the years. As such, it would rather be a long-term project, but an immediate benefit would be something complementary to other packages currently available in R, e.g. **genetics**, **hwde**, **haplo.score**, etc. I hope eventually this will be part of a bigger effort to fulfill most of the requirements foreseen by many, e.g. Guo and Lange (2000), within the portable environment of R for data management, analysis, graphics and object-oriented programming.

So far the number of functions is quite limited and experimental, but I already feel enormous advantage by shifting to R and would like sooner rather than later to share my work with others. I will not claim this work is exclusively done by me, but would like to invite others to join me and enlarge the collections and improve them.

2 Implementation

The following, extracted from the package INDEX, shows the data and functions currently available.

```
aldh2                   ALDH2 markers and Alcoholism
apoeapoc                APOE/APOC1 markers and Schizophrenia
bt                      Bradley-Terry model for contingency table
chow.test               Chow's test for heterogeneity
fbsize                  Sample size for family-based linkage and association design
fsnps                   A case-control data involving four SNPs for missing genotype
gc.em                   Gene counting for haplotype analysis
gcontrol                Genomic control
genecounting            Gene counting for haplotype analysis
gif                     Kinship coefficient and genetic index of familiality
```

```
hap                     Haplotype reconstruction
hap.em                  Gene counting for haplotype analysis
hap.score               Score Statistics for Association of Traits with haplotypes
hla                     HLA markers and Schizophrenia
hwe                     Hardy-Weinberg equilibrium test
hwe.hardy               Hardy-Weinberg equilibrium test using MCMC
htr                     Haplotype trend regression (with permutation)
kbyl                    LD statistics for two multiallelic loci
kin.morgan              kinship matrix for simple pedigree
makeped                 A function to prepare post-MAKEPED format file
mia                     Multiple imputation analysis for hap
mtdt                    Transmission/disequilibrium test of a multiallelic marker
muvar                   Means and variances under 1- and 2- locus QTL model
pbsize                  Sample size for population-based association desgin
pfc                     Probability of familial clustering of disease
pgc                     Preparing frequency weight for GENECOUNTING
s2k                     Statistics for 2 by K table
tbyt                    LD statistics for two SNPs
whscore                 Whittemore-Halpern scores for allele-sharing
```

Assuming proper installation, you will be able to obtain the list by typing *library(help=gap)* or view the list within a web browser via *help.start()*.

You can cut and paste examples at end of each function's documentation.

Both *genecounting* and *hap* are able to handle SNPs and multiallelic markers, with the former be flexible enough to include features such as X-linked data (not incorporated yet) and the later being able to handle large number of SNPs, an advantage over algorithms in **haplo.score**. But the latter is able to recode allele labels automatically, so functions *gc.em* and *hap.em* are in **haplo.score**'s *haplo.em* format and used by a modified function *hap.score* in association testing.

It is notable that multilocus data are handled differently from that in **hwde** and elegant definitions of basic genetic data can be found in **genetics** package.

Incidentally, I found my mixed-radixed sorting routine in C (Zhao & Sham 2003) is much faster than R's internal function.

With exceptions such as function *pfc* which is very computer-intensive, most functions in the package can easily be adapted for analysis of large datasets involving either SNPs or multiallelic markers. Some are utility functions, e.g. *muvar* and *whscore*, which will be part of the other analysis routines in the future.

For users, all functions have unified format. For developers, it is able to incorporate their C/C++ programs more easily and avoid repetitive work such as preparing own routines for matrix algebra and linear models. Further advantage can be taken from packages in **Bioconductor**, which are designed and written to deal with large number of genes.

3 Examples

Examples can be found from most function documentations. You can also try several simple examples via *demo*:

```
> library(gap)
> demo(gap.demo)
```

4 Known bugs

Unaware of any bug after hwe.hardy was fixed.

5 References

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