

Pedigree Analysis Programme GTree 1.2 and Its Application

Daisuke Ogino¹

ogino@matsys.org

Masato Nose³

masanose@m.ehime-u.ac.jp

Shiro Mori²

siromori@mail.cc.tohoku.ac.jp

Hideki Sawada⁴

sawada@matsys.org

¹ Department of Pathology, Institute of Development, Aging and Cancer, Tohoku University, Sendai 980-8575, Japan

² Department of Oral Medicine and Surgery, Graduate School of Dentistry, Tohoku University, Sendai 980-8575, Japan

³ Department of Pathology, School of Medicine, Ehime University, Ehime 791-0295, Japan

⁴ Department of Mathematical Sciences, Faculty of Science, Yamagata University, Yamagata 990-8560, Japan

Keywords: correlation, scatter plot, pedigree analysis, GTree

1 Introduction

A pedigree analysis is one of the methods to search genotype frequency and gene frequency. It is very important to find the intergenerational changes from the visual angle in case where one cannot apply methods of molecular genetics. In this version GTree 1.2¹ we have developed our programme for finding out strict characteristics of a given strain data by correlation coefficient as well as scatter plot.

In this poster we first introduce three cases on correlations of pedigree data in Section 2, and show the scatter plot and correlation coefficient of a given strain data from certain mice in Section 3.

2 Correlations in Pedigree

Now we should like to explain various correlations on pedigree data. For a general reference on the terminologies in population genetics see [1].

GTree 1.2 calculates correlation coefficients, according to the following 3 cases. Let N be the number of total generations of a given pedigree.

(i) Generation [command: corrg]

In this case it calculates the correlation coefficient on j -th generation ($1 \leq j \leq N$) to find correlation of statistics of sample1 and sample2 on the generation. If we calculate it in each generation, that will show us characteristics of intergenerational changes of a relationship between sample1 and sample2.

(ii) Sex or Disease [command: corrs, corrd]

In this case GTree 1.2 calculates the correlation coefficient separately according to sex and the disease in order to finding out characteristics of the disease with respect to sex.

¹It is a C-language programme on LINUX which analyze pedigrees. [2, 3]

(iii) Statistics of total sample1 and sample2 [command: corrt]

In this case it calculates the correlation coefficient on all pairs, to find relations of statistics of total sample1 and sample2 through the generations.

This classification suggests us that the correlation of statistics of sample1 and sample2 should be parameterized by generation, sex and the disease.

3 Scatter Plot and Correlation Coefficient

In this section of the poster we should like to show scatter plots and correlations from the pedigree of certain mice.

We represent the each mouse's or object's information as a row. A data of matrix consists of ten columns (identity number, breeding diary + or -, their father's number, their mother's number, sex, generation, disease + or -, statistic of sample1, statistic of sample2 and date of birth). The next table is a row of the input data.

identity number	breeding diary + or -	father's number	mother's number	sex	genera- tion	disease + or -	statistic of sample1	statistic of sample2	date of birth
-----------------	-----------------------	-----------------	-----------------	-----	--------------	----------------	----------------------	----------------------	---------------

3.1 Commands of GTree 1.2

This is the table of commands of GTree 1.2. We use the standard symbols of pedigree (see, e.g., [1]).

Command	Classification	Output
all, id	CUI	The data matrix, Individual data
corrg, corrs	CUI	Correlation coefficient of statistics of sample1 and sample2
corrd, corrt	CUI	Correlation coefficient of statistics of sample1 and sample2
fchld, mchld	CUI	Children of father, Children of mother
fmly, pts	CUI	The pedigree, Parents
fr, mr	CUI	Father's side, Mother's side
gw1, gws	CUI	Statistic of sample1 or sample2 for each generation
w1, ws	CUI	Statistic of sample1 or sample2 for the total generations
xchld, xfmly	GUI	children, pedigree
xfmly5, Xfmly	GUI	pedigree(5 generations), pedigree(10 generations)
xgwls	GUI	Scatter diagram statistics of sample1, 2 for each generation
xw1, xws	GUI	Bar graph statistic of sample1 or sample2 for the total generations
xwls	GUI	Scatter diagram statistics of samples for each generation

In our recent paper [2] sample1 is weight of axillary lymphndns and sample2 is weight of spleen.

References

- [1] Crow, J.F., *Genetics Notes*, 8th edition, Burgess Publishing Company, 1983.
- [2] Ogino, D., Mori, S., Nose, M., and Sawada, H., Complexity and application of pedigree analysis programme GTree, *Proc. IEEE Computer Society Bioinformatics Conference*, 333–335, 2002.
- [3] Ogino, D., Mori, S., Nose, M., and Sawada, H., Pedigree analysis programme GTree 1.0, *Genome Informatics*, 13:246–247, 2002.