

# Longitudinal Association Analysis of Quantitative Traits

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## 1 Overview

This document describes a R package to implement the models of association mapping to analyze population longitudinal data. The document contains three files: `Age_Sex_Geno_Trait_data.csv`, `simulation_log-mu_web_example.R`, and `simulation_log-mu_codes_for_Age_Sex_Geno_Trait_data.R`. The first one is a dataset used in `simulation_log-mu_web_example.R`, and the third one generates datasets and implements codes to run the models of Fan et al. (2012). Notice that you may generate a dataset `Age_Sex_Geno_Trait_data.csv` by running `simulation_log-mu_codes_for_Age_Sex_Geno_Trait_data.R`.

Section 2 briefly describes the installation of the program of `Longitudinal_qtl_popu_web.zip`. Section 3 explains how to run the program using one example.

The theoretical basis for this program is given in our research paper in **Reference**. Please refer to the reference if you use the program in any published work. In case of suggestions and questions and/or problems, you can contact us via e-mail ([fanr@mail.nih.gov](mailto:fanr@mail.nih.gov)).

## 2 Download and Installation

The package is written in R. Download the package `Longitudinal_qtl_popu_web.zip`. Put the three files in one directory.

## 3 How to Run the Program

On an R Console in a PC, open the file `simulation_log-mu_codes_for_Age_Sex_Geno_Trait_data.R` or `simulation_log-mu_web_example.R`. Change the paths leading to the directory of the package. Then, you may run the program.

## 4 References

1. Fan RZ, Zhang YW, Albert PS, Liu AY, Wang YJ, and Xiong MM (2012) Longitudinal association analysis of quantitative traits. *Genetic Epidemiology* **36**:856-869.