FGID

Forensic DNA Analysis System

FGID kinship software

User Manual: V1.0

Date: 2024/11/01
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1. Purpose

This document provides the standard operating procedures for using and maintaining the FGID kinship software. It ensures that the software is utilized effectively, consistently, and securely by all employees.

2. Scope

This user manual applies to all employees who have access to use the FGID kinship software. It covers the installation, configuration, usage, troubleshooting of the software.

# 3. Installation and Setup

3.1 Prerequisites

Before installing FGID kinship software, ensure the following prerequisites are met:

- Windows 10 or later.
- Strawberry Perl Microsoft Installer Package (MSI).

3.2 Installation Procedure

1. Download the installer package from github: https://github.com/gaosjlucky/FGID-kinship.
2. Extract the zip package to an appropriate directory. It is recommended to use Bandizip.
3. After installation, double-click **FGI-20230414-English.exe** to launch the program for **Kinship analysis**.
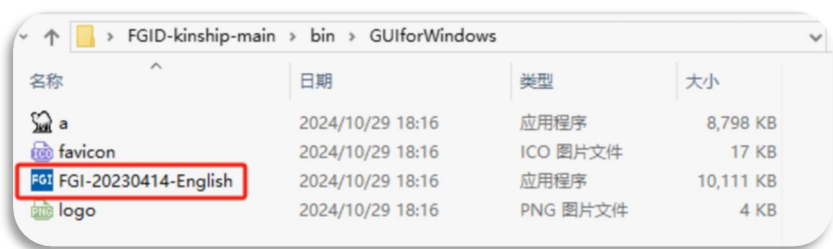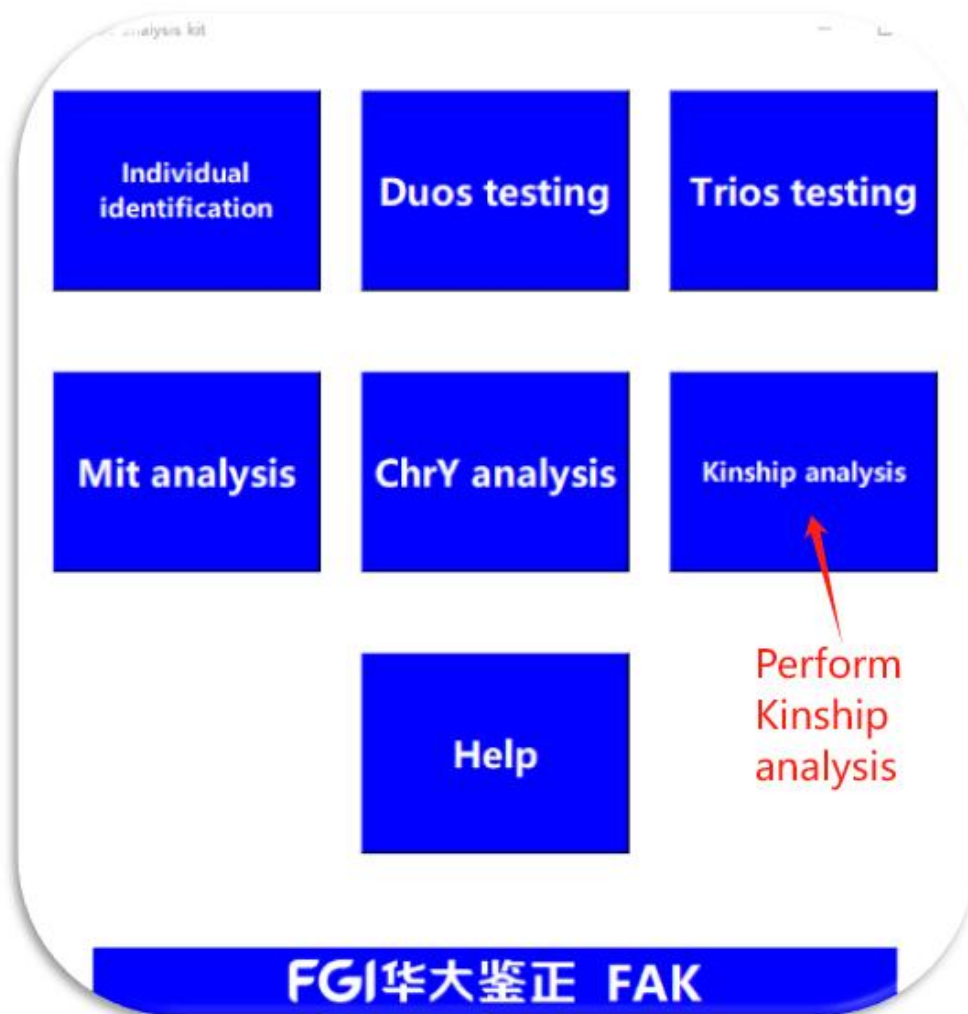
3.3 Configuration

1. Frequency File for **Frequency**: This file should contain three columns of information: MH loci name, allele combination, and allele combination frequency. You could find the frequency file for Chinese Han Population in the folder: example.

2. Sample Genotyping File for **Case**: This file should include four columns of information: sample name, MH loci name, allele combination 1, and allele combination 2. You could find the example file generated from real pedigree genotyping data in the same folder.

3. Sample Genotyping File for **Data**: This file should include four columns of information: sample name, MH loci name, allele combination 1, and allele combination 2. You could find the example file generated from real pedigree genotyping data in the same folder.

4. Perform kinship analysis using the example data to ensure all configurations are correct.

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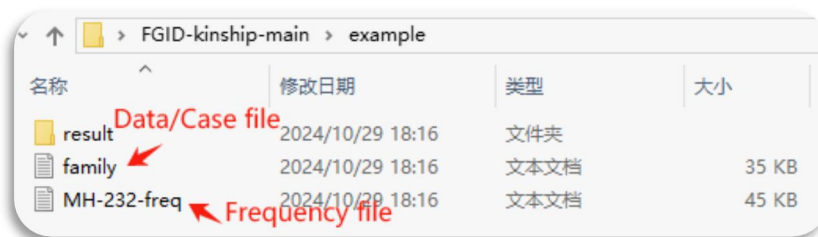
4. Usage Guidelines

4.1 Basic Usage.

- **Performing Tasks:**
  Ensure you follow the workflow and use features appropriately.

- The configuration files should be well-formatted. The columns within these files should be separated by tabs, and there must be no headers or any supplementary information.

- File paths must not contain spaces, parentheses, or other special characters.
- Sample Genotyping File for Case and Sample Genotyping File for Data may contain identical samples.
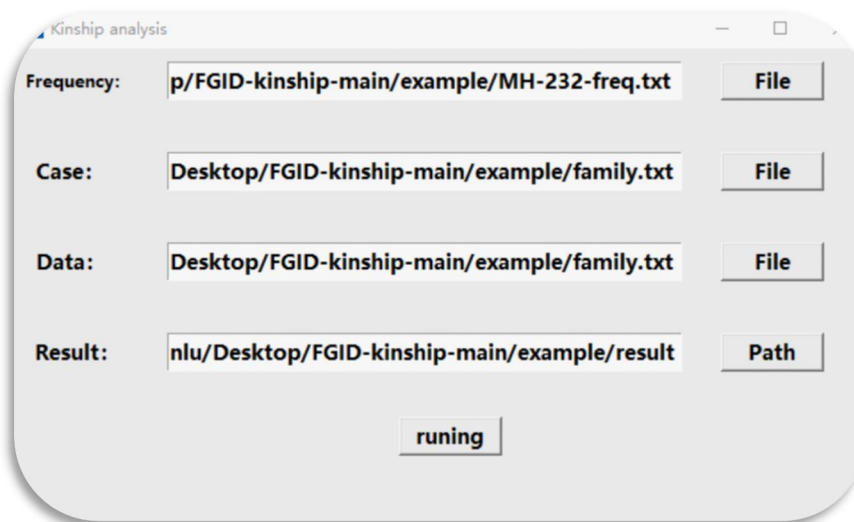
- After specifying the file paths to import relevant files, click on running to perform kinship analysis. You could find the result files in the specified Result path

4.2 Troubleshooting

- **Issue 1:** No result files generated
  Solution: 1. Ensure your system meets the minimum requirements. 2. Check your configuration files. The columns within these files should be separated by tabs. 3. Check your file path. File paths must not contain spaces, parentheses, or other special characters.

- **Issue 2:** The software is running slow
  Solution: 1. Close any unnecessary applications and restart the software. 2. If you need to handle large data sets, we recommend you to use the Linux version for the FGID kinship software.

5. Troubleshooting and Support

For assistance, please contact the author through the following methods:

- **Email:** gaoshengjie@genomics.cn

All incidents and issues should be reported, and users should provide detailed descriptions of the problem to assist in quicker resolution.

6. Version Control and Document History

Version	Date	Description	Author
V1.0	2024-11-01	Describe installation, configuration, usage, troubleshooting of the software.	Yunlu Gao