

Familytreemap User Guide

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<https://github.com/yogischogi/familytreemap/>

November 4, 2015

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1 Introduction

For the lost ones.

Familytreemap calculates population frequencies (relative or absolute) from Family Tree DNA projects.

It's main purpose is to create heat maps of project members.

2 Command Line Options

Familytreemap is a command line program. It is invoked by

familytreemap <options>

Options may be given in arbitrary order.

-help Prints available program options.

-tin Input file (testers is) contains the total number of testers for each country.

-in Input file contains a table with Family Tree DNA project data in CSV format.

-col Number of the column that contains the country names.

-out Output file contains population frequencies in CSV format.

-relative If **-relative=false** the absolute number of testers belonging to a group is calculated. Default value is **-relative=true**.

3 Installation

3.1 Linux Mint

1. Make sure that the Go programming language is installed. You can install it by typing
`sudo apt-get install golang`
2. Read the Go [Getting Started](#) guide. Make sure to set your *GOPATH* variable and include it in your *PATH* so that Go programs can be found.
3. Fetch the familytreemap program with
`go get github.com/yogischogi/familytreemap`
4. Install the program with
`go install github.com/yogischogi/familytreemap`

3.2 Windows, FreeBSD, Mac OS X

1. Read the Go [Getting Started](#) guide and install the Go programming language. Make sure to set your *GOPATH* variable and include it in your *PATH* so that Go programs can be found.

2. Fetch the familytreemap program with
`go get github.com/yogischogi/familytreemap`
3. Install the program with
`go install github.com/yogischogi/familytreemap`

4 First Usage

1. Go to a Family Tree DNA project on the web and open the page containing the DNA results in a web browser.
2. Copy the results into a spreadsheet and save it in CSV (Comma Separated Values) format. For this example name it *projectdata.csv*.
3. Open a command line interpreter and go to the directory where your files are.
4. Determine the number of the column which contains the countries. Often this is 3, familytreemap's default value.
5. Issue a command to test if the program works:
`familytreemap -in projectdata.csv -out result.csv -col 3`
The program should be working and prompt you to use the `-tin` option to provide the number of total testers for each country. Without the `-tin` option it is not possible to calculate an accurate relative distribution. Instead the program uses build in example data.

5 The -tin Option

To calculate a relative distribution of project members it is necessary to provide a number for each country which denotes the total number of testers from that country.

This is done by using the `-tin` option and providing a file in JSON format that contains country names and the total number of testers. A very simple example file for just three countries looks like this:

```
{"Belarus":1000,  
"Belgium":2000,  
"Brazil":100}
```

A good way to get the number of testers for each country is to sign into Family Tree DNA and go to *Ancestral Origins*. If you have completed your `-tin` file, you can name it for example `totals.json` and provide it to the program like this:

```
familytreemap -tin totals.json -in projectdata.csv -out result.csv  
-col 3
```

The program should be fully working now.

6 How to Create a Heat Map

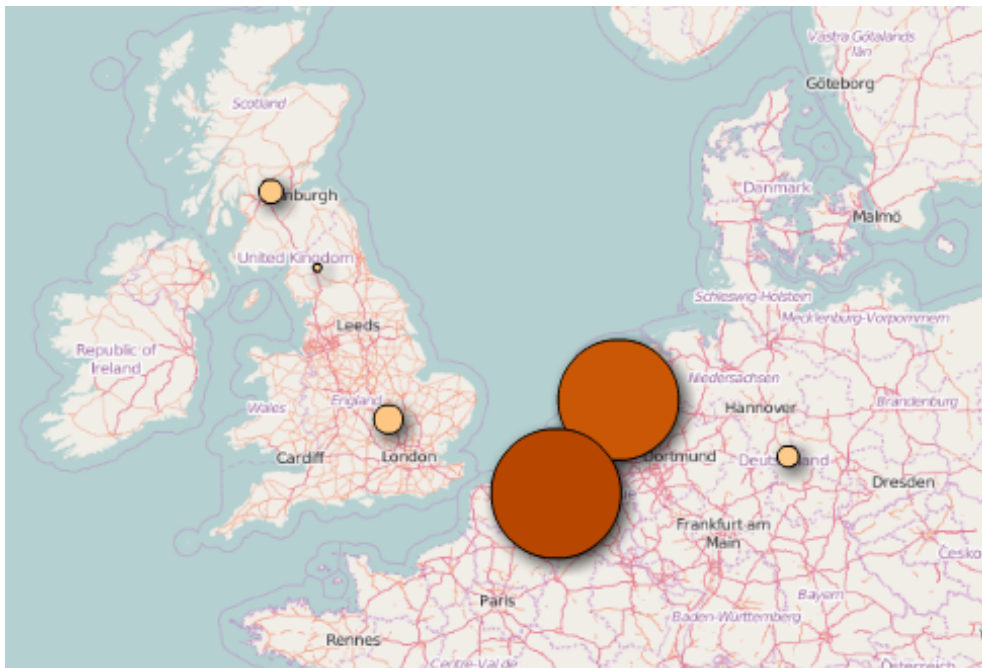


Figure 1: Geographical distribution of persons belonging to a haplogroup. Created with [OpenHeatMap](http://www.openheatmap.com).

1. Run the familytreemap program:

```
familytreemap -tin totals.json -in projectdata.csv -out result.csv  
-col 3
```
2. Open your web browser and go to <http://www.openheatmap.com>.
 - (a) Click on *Create your map*.

- (b) *Excel or CSV file.*
 - (c) *Upload* your results file, in this example *result.csv*.
 - (d) *View your map* and adjust the settings until you like it.
 - (e) *Save & view*
3. You are done! You can share your map via social networks or take a screenshot of it.