Getting started FamiliasPedigreeCreator

This is a brief getting started help on how to use the software **FamiliasPedigreeCreator**, freely available at http://www.familias.no. For a nice introduction video, please visit the following link (narrator Thore Egeland).

Description

FamiliasPedigreeCreator is a simple tool to generate pedigree plots for multiple **Familias** projects at once. This is performed via the free software R (https://cran.r-project.org/bin/windows/base/). R is a powerful tool for general plotting and provides some excellent libraries to plot pedigrees. The plots are saved as .png files where the **Familias** projects are located and can later be displayed in the software itself. Make sure you have write priviligies in the directory where the **Familias** projects are located.

Download and install

The software is found at http://www.familias.no and head to *Downloads*. Simply download and install the software, a desktop shortcut should appear.
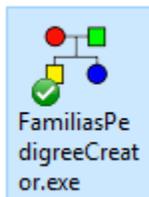
Running the software

Open the software by clicking the desktop shortcut. The window below should appear.
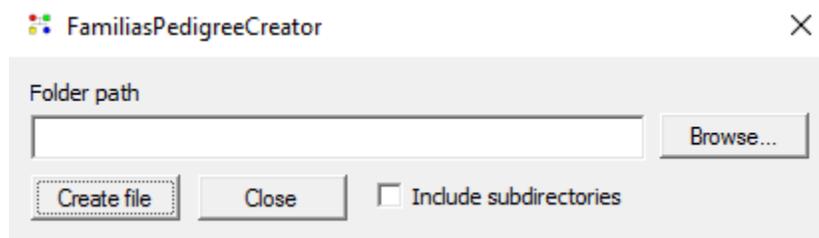
Press *Browse* to open a dialog to choose a directory/folder on your computer (locally or on the network). Press *Select folder* once you have located your folder, it should now appear as below.

FamiliasPedigreeCreator ✕

Folder path

D:\Dropbox   Browse...

Create file   Close   ☐ Include subdirectories
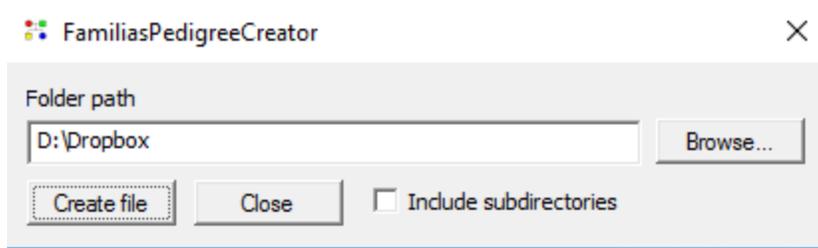
Press *Create file* to start the process outlined below. To also include all the subdirectories (subfolders) of the specified directory, tick the indicated button.

1. The user will be asked to give a file name. This is the file that will contain the output from the software.
2. The software will scan the directory (and subdirectory) looking for **Familias** projects, either in the .fam format or in the older .txt format.
3. A list with all files will be generated and for each file the following will be done,
   a. Open and verify the contents.
   b. If pedigrees exist, generate a text.
   c. The text is inserted into the file mentioned in 1.
4. The software will now try to open the file (see 1.). The contents should be a long list with instructions for the software R (https://cran.r-project.org/bin/windows/base/). If you get a message stating that the file could not be opened, you may just ignore it. Instead, use the options described in 5.
5. Either use the *Source* option in R or copy the contents of the file (see 1.) into the R command window. This will start the process that will generate pictures/plots for all the pedigrees in all the **Familias** projects in the directory you selected. Currently persons without any relations will be removed in the plots and therefore will not be displayed.
6. In the latest version of **Familias** (3.2 and above), use the *Pedigree* plot button in the *Pedigrees* window to view the generated plots.