JWorks(v0.512) and KWorks for FTDNA, 23andMe and Gedmatch Data:
Automated Chromosome Browser Tools

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DNAGedcom wishes to offer special thanks to the volunteer programmers of these two valuable tools, Jay Pizarro (JWorks) and Kitty Munson Cooper (KWorks). Their hard work will save you hours of data analysis! If you find them valuable in your research, please consider making a donation. All donations are used to support the development and hosting of new tools.

Note: These utilities work with your Family Tree DNA (FTDNA), 23andMe results and Gedmatch Tier 1 segment and triangulation uploads.

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JWorks and KWorks are two automated tools that do the same thing. They organize your FTDNA match data so that you can quickly discover shared common ancestors (" The Methodology"). Both tools do the sorting, grouping and matrix-building necessary for you to work with your most promising matches.

Either tool automatically completes the first two items below – the criteria for identifying the common ancestor of your matches. You'll be ready to work with GEDCOMs in a matter of minutes.

1. They have to share overlapping DNA segments.
2. At least two members in a set have to have ICW status.
3. Those ICW members have to have a family tree or GEDCOM available.

The difference between the two tools is that JWorks is for users of Microsoft Excel, there is also a Mac version, and KWorks is for those using other spreadsheet software:

JWorks v0512: JWorks is a macro-enabled Excel spreadsheet. If you have Microsoft Excel, JWorks will automatically run and generate a new spreadsheet that groups overlapping segment matches into sets and creates an ICW ("in common with") matrix for each set.

KWorks: If you don't have Excel on your PC, KWorks will generate the data on a server and create a *.csv file for you to download. This type of file is in a text-based format that can be opened by many free apps such as Google Spreadsheets, Open Office or a CSV reader so that you can easily view the data.

To use either tool, you first have to generate the FTDNA data files each tool will use to sort your matches (Step A). Once you have completed Step A, determine which tool you will use.

- If you have Excel, go to the instructions for JWorks in Step B.

- If you have other spreadsheet software, skip down to Step C for instructions for using KWorks.

- Step D contains troubleshooting tips.

A. Download your FTDNA and/or 23andMe Data Files from DNAGedcom.com

When FTDNA blocked the ICW and myTrees files in early February 2017, Rob programmed a new DNAGedcom Client V2 capable of downloading all 3 files from FTDNA, as well as Ancestry and 23andme files. The FTDNA and 23andme files can be synced to the DNAGedcom website. The Ancestry files can be loaded to GWorks, the tree/gedcom comparison tool on DNAGedcom. This app, version 1.9.7.4, is different than the current Client, version 1.5.1.3. You will need to be a subscriber to the client. Currently it is for Windows PC users only. It is still in Beta and has not been released so we would appreciate your feedback. A Mac version is in development and should be available soon.

You can download the PC installation file here: http://www.dnagedcom.com/app2/DNAGedcomClientv2.htm

The basic instructions (still being updated) can be found here:
http://www.dnagedcom.com/docs/Welcome_to_the_New_DNAGedcom_Client.pdf

Note: The files you can run in JWorks will be in the Export Folder specified on the Options page of the Client. In order to run JWorks, the program, JWorks_v0512.xls, must be in the same folder as your files.

B. Instructions for Using JWorks

1. Download JWorks from DNAGedcom.com. http://dnagedcom.com/JWorks/Jworks_v0512.xls The link to JWorks is also located under the Tools menu on DNAAdoption.com.
2. Save JWorks to the same directory as the three files you downloaded and expanded in Step A. Open the file JWorks_v0512.xls
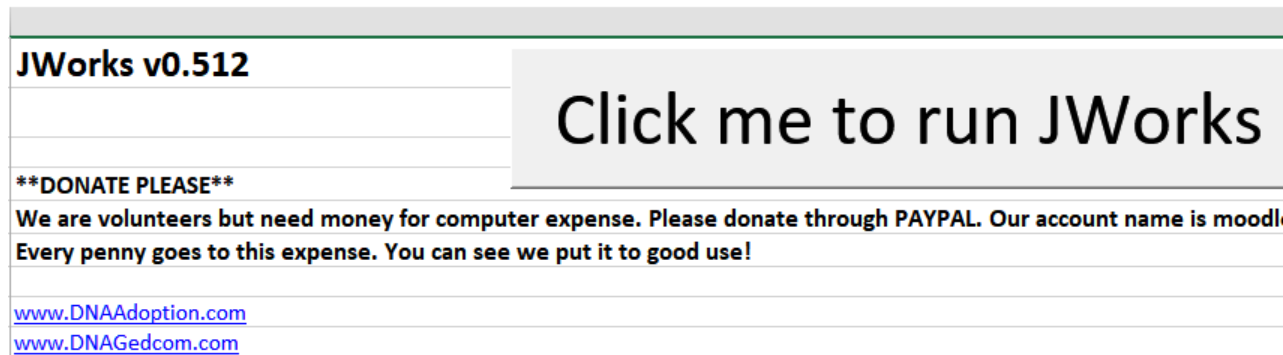

JWorks v0.512

Click me to run JWorks

DONATE PLEASE
We are volunteers but need money for computer expense. Please donate through PAYPAL. Our account name is moodl
Every penny goes to this expense. You can see we put it to good use!

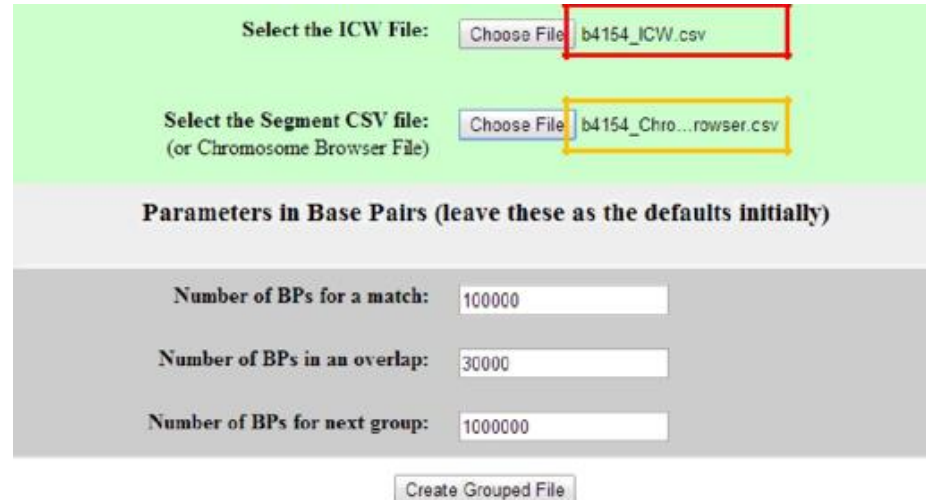www.DNAAdoption.com
www.DNAGedcom.com

Figure 6 JWorks

4. Click the gray button to run JWorks. (Figure 6).

   a. The file may open in Protected View. Be sure to click "**Enable Editing**" at the top of the screen.
   b. If you get a Security Warning, be sure to click "**Enable Content**" at the top of the screen.
5. Enter your FTDNA kit number in the pop-up window and click "OK."

6. Enter the minimum amount of cMs to include. The default is 6. If you have a large list of matches you may need to run

the minimum cMs at 10. Note: It is generally not recommended to go below 5 cM.

7. This process may take a few minutes to run and generates data in several phases. You can see the progress indicator on the bottom left-hand corner of the Excel window. Once completed, a window pops up with the message "Process complete. Have fun!"

8. A prompt will ask you if you want to run another kit. Enter the kit number of the next kit or click "Cancel."

9. The organized chromosome browser opens in a new spreadsheet window and is automatically saved in the same directory as JWorks and the FTDNA Matches, Chromosome Browser and ICW files.

10. Your ICW matches will appear in a matrix for each group of overlapping segments.

11. The file name is *yourkitnumber_*results.xls.

12. Common JWorks errors are on page 8.

C. Alternate Instructions for Using KWorks

1. Open your internet browser and go to http://kittymunson.com/dna/MakeSegmentGroups.php.

2. Locate the directory on your PC where you downloaded and unzipped the three FTDNA files from DNAGedcom.com (Figure 2).

Figure 3 KWorks

3. Click "Choose File" and browse to FTDNA ICW file in the appropriate directory on your PC and double-click (Figure 3, outlined in red).

4. Click "Choose File" and browse to the FTDNA Chromosome Browser file and double-click.

   Note: Both files must be entered to generate the data (Figure 3, outlined in orange).

5. Click "Create Grouped File."

6. Once the server has generated the file, a link will appear at the bottom of the screen. (Figure 4).

```
>>> There are 44 names for chr 1 ... Chromosome 1 is completed ... at May 4, 2014 - 12:11 PM CDT
>>> There are 24 names for chr 2 ... Chromosome 2 is completed ... at May 4, 2014 - 12:11 PM CDT
>>> There are 14 names for chr 3 ... Chromosome 3 is completed ... at May 4, 2014 - 12:11 PM CDT
>>> There are 27 names for chr 4 ... Chromosome 4 is completed ... at May 4, 2014 - 12:11 PM CDT
>>> There are 39 names for chr 5 ... Chromosome 5 is completed ... at May 4, 2014 - 12:11 PM CDT
>>> There are 27 names for chr 6 ... Chromosome 6 is completed ... at May 4, 2014 - 12:11 PM CDT
>>> There are 22 names for chr 7 ... Chromosome 7 is completed ... at May 4, 2014 - 12:11 PM CDT
>>> There are 29 names for chr 8 ... Chromosome 8 is completed ... at May 4, 2014 - 12:11 PM CDT
>>> There are 24 names for chr 9 ... Chromosome 9 is completed ... at May 4, 2014 - 12:11 PM CDT
>>> There are 31 names for chr 10 ... Chromosome 10 is completed ... at May 4, 2014 - 12:11 PM CDT
>>> There are 8 names for chr 11 ... Chromosome 11 is completed ... at May 4, 2014 - 12:11 PM CDT
>>> There are 28 names for chr 12 ... Chromosome 12 is completed ... at May 4, 2014 - 12:11 PM CDT
>>> There are 11 names for chr 13 ... Chromosome 13 is completed ... at May 4, 2014 - 12:11 PM CDT
>>> There are 7 names for chr 14 ... Chromosome 14 is completed ... at May 4, 2014 - 12:11 PM CDT
>>> There are 18 names for chr 15 ... Chromosome 15 is completed ... at May 4, 2014 - 12:11 PM CDT
>>> There are 7 names for chr 16 ... Chromosome 16 is completed ... at May 4, 2014 - 12:11 PM CDT
>>> There are 10 names for chr 17 ... Chromosome 17 is completed ... at May 4, 2014 - 12:11 PM CDT
>>> There are 30 names for chr 18 ... Chromosome 18 is completed ... at May 4, 2014 - 12:11 PM CDT
>>> There are 13 names for chr 19 ... Chromosome 19 is completed ... at May 4, 2014 - 12:11 PM CDT
>>> There are 21 names for chr 20 ... Chromosome 20 is completed ... at May 4, 2014 - 12:11 PM CDT
>>> There are 11 names for chr 21 ... Chromosome 21 is completed ... at May 4, 2014 - 12:11 PM CDT
>>> There are 22 names for chr 22 ... Chromosome 22 is completed ... at May 4, 2014 - 12:11 PM CDT
>>> There are 8 names for chr X ... Chromosome X is completed ... at May 4, 2014 - 12:11 PM CDT
Click here to download the CSV file
```

Figure 4 KWorks Download Link

7. Click the link. The file will automatically download to your internet browser's default download directory and will be named *yourkitname* _ChromsomeBrowser_GRP.csv.

8. Open the file in a spreadsheet application or CSV reader to see your ICW matches in a matrix for each group of overlapping segments. The "F" indicates that the match is from Family Tree DNA.

9. If you have created a combined chromosome browser file to replace the file downloaded from then you must be sure that the column headings for the file are as follows: THEY ARE CASE SENSITIVE!
    i. Column 1 Source

ii. Column 2 Profile Name

iii. Column 3 Match Name

iv. Column 4 Chr

v. Column 5 Start

vi. Column 6 End

vii. Column 1 cMs

D. Troubleshooting

1. Family Tree File Downloads from DNAGedcom.com

    If you are still having trouble after trying the above remedies, email DNAGedcom.com for support. Please note that support is provided by volunteers using their own time and resources which may cause a delay in response.

2. KWorks

    1 Be sure you uploaded the correct FTDNA files to the server. These files download to the default directory of your internet browser. The first file is the ICW file, and the second is the Chromosome Browser.

    2 Check to see if you unzipped (extracted) the FTDNA *.zip file from DNAGedcom.com.

    3 Make sure the files have the names as shown in Figure 2 (beginning with your FTDNA kit number and ending in *.csv) haven't changed.

    4 Check that the column names are correct as listed above using the correct case

    5 The name in the ICW field (both Column 1 and Column 2) must exactly match the name in the chromosome file for it to match in the ICW matrix. Margo Louise Wells does not match Margo Wells or Margo L Wells, it only matches Margo Louise Wells.

    6 If you still have difficulty, please contact the developer at http://kittymunson.com/index.php?page=contact-us. Please note that support is provided by volunteers using their own time and resources which may cause a delay in response.

JWorks - If you have problems running the JWorks app, please check the following:

COMMON JWORKS ERRORS

We get lots of support requests on using JWorks, and almost every single one is user error. Please check list below carefully if you have a problem running it. Here are some of the most common JWorks Errors:

- You must have an Excel program (Version 2003 or later) for JWorks to function.

- No headers on Line 1 for the CB and/or the ICW csv files.

- The JWorks program is NOT in the same directory as the CB and ICW .csv files. It must be.

- Changes in the name of the CB and/or ICW files. Do not change any part of the name after the kit #.
  You can change the beginning of the name, such as adding a letter to the kit (example: #123456A_ChromosomeBrowser.csv) if you want to differentiate from other files you have. I normally just create a new directory and call it "123456 3-20-15" showing the date. But if you do change the first part of the file name and run those in JWorks, the kit # to enter would be 123456A. *If you change the name by adding a letter, you must change both the CB and the ICW names as well.*

- Trying to run JWorks using ".xls" or ".xlsx" files. Make sure they are ".csv" files and not ".xls" or ".xlsx" files that you use for JWorks.

- Corresponding ICW names are not being manually input correctly into the ICW file. If you have to manually enter names to the ICW list and, let's say, John matches Mary, you must also add Mary to Col A and John to Col B, as well as having John in Col A and Mary in Col B.

- Mac users of JWorks seem to have more issues than those working with the PC version. We are not sure why. Running those files on the PC version of JWorks works better.

- Lack of patience... always seems to be an issue. Many files need time to run and complete, one took 1/2 hour.

- Once you download JWorks, enable editing and/or enable content. The first time you run it, it may give you an error. Close the error box and try running it again. Often the second attempt works.

- Segment Pile-ups. See Explanation below.

EXPLANATION OF JWORKS PROBLEM WITH SEGMENT PILE-UPS

As the CB/ICW data grows and becomes larger, these files may not run in JWorks at the default minimum cMs of 6. Change to a larger minimum at the start of the program after you enter the kit number. Try 10 cMs ,15cMs or even 20 cMs. This is because of pile-ups, or sticky segments, which make the number of matching segments exceed 165.

These pile-ups can also be caused by having other close relatives in your list of matches (parents, siblings). "Pile-up" segments (also referred to as "clumping" or "sticky segments") of DNA are not shared among all of the matches because of mutually shared recent ancestry, but are shared due to one or more other factors. A shared segment of DNA, if it appears at a significantly high frequency in the database, is much more likely to be IBS than IBD, even if it is a large segment. Similarly, a shared segment of DNA that is less frequent in the database is much more likely to be IBD than IBS, even if it is a very small segment.

For now, you may have to eliminate some of these matches by trial and error while still leaving those that are especially pertinent to your search. For example, if you have very close relatives (parents, siblings, aunts/uncles or 1st cousins) who also tested and are showing as matches in your chromosome browser and they are not on the lines you are searching for...

Or say you are looking for your maternal grandmother, and you have your father or a paternal uncle tested; remove your father/uncle completely from the CB data, as he probably is not going to help with your maternal-side search. You can also remove them from the ICW.csv but usually that is not necessary. Also remove a full sibling who might be redundant to your own DNA; in that case I would run two separate JWorks, one removing your sibling from your CB and then a second one using your sibling's data and removing yourself.