

## JWORKS AND KWORKS

Once you have downloaded the zip file for your FTDNA account, extract the files to one folder. Then go to DNAGedcom, Autosomal Tools tab, select JWorks – Autosomal Grouping Tool. Download the Excel or Macintosh program and put in the same folder with your source csv files. Open JWorks, enable editing and enable content. In the box that comes up enter the kit #. If you get an error the first time you run it, close the error box and click on Click me to Run JWorks and enter the kit number again. Usually the second time will run.

Enter Kit no.: OK

Cancel

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123456

Click OK, another box will come up to enter the minimum cM threshold. The default is 6, but you may want to increase it. Click OK. The program will run and give you a results file showing the possible triangulation groups and who is ICW by adding “x” s. KWorks instructions can be found here on page 7. [http://www.dnagedcom.com/JWorks/Jworks\\_Kworks.pdf](http://www.dnagedcom.com/JWorks/Jworks_Kworks.pdf) . Please read the Common Errors with JWorks on the next page if you have problems.

					Devin	Anthony	Beverly	Carl	Leon
Devin	1	2514775	8673178	13.57	x	x	x	x	
Anthony	1	3034041	5600362	7.96	x		x	x	
Beverly	1	3034041	10881522	16.73	x	x		x	x
Carl	1	3034041	10881522	16.73	x	x	x		x
Leon	1	4090545	9016716	9.87	x		x	x	

These programs, JWorks and KWorks, can sometimes fail. The most common reason is user error. There are both directions and troubleshooting help on DNAGedcom.com, under the Autosomal Tools Tab where you download these programs. Please use them! I have made most of these mistakes myself over the months.

When we first had these programmers written there were far fewer test results. We are now sometimes having program failures because of more data. As I mentioned, the complete directions for these are on the page where you download the program.

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## COMMON JWORKS ERRORS

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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.

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## EXPLANATION OF JWORKS PROBLEM WITH SEGMENT PILE-UPS

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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 1<sup>st</sup> 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.

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## WHAT DOES JWORKS DO?

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The JWorks program does the triangulations for you from the files you just extracted.



There are a few points I will mention here:

- Use JWorks if you have Excel. You can use KWorks no matter what spreadsheet software you have.
- You MUST save JWorks to the same folder or directory where you have saved the three files you just extracted from your downloads.

- Click on the JWorks that is in that directory or folder on your PC and it will open in Excel. You probably have to OK running macros (enable editing and enable content) in your Excel.
- **The first time you run it, it may give you an error. Close the error box and enter your kit number again. Often the second attempt works.**
- Then put the kit number of your data into the blank on JWorks. In Jon’s case his files are B55089\_chromosomebrowser.csv and B55089\_ICW.csv so the kit number is B55089.
- Run JWorks and the output will be a file that is sorted by overlapping DNA segment sets. To the right of these sets is a matrix with X’s in it. The file is called Results.xls.

						Carol Cluff	Daniel Whitehead	Robin Starr Midkiff
Carol Cluff	1	87606031	101159333	12.42	Carol Cluff			
Daniel Whitehead	1	87904968	101534706	12.27	Daniel Whitehead	x		
Robin Starr Midkiff	1	99636054	114104489	15.27	Robin Starr Midkiff			

The red arrow is pointing to the intersection of the row for Whitehead and the column for Cluff. The X means they are ICW.

JWorks produces an extensive spreadsheet with many sets of overlapping DNA and matrices.

**HINT:** To protect your original **Results** document, save a copy with the name **Working Results** spreadsheet and work on that from now on.

I color-code mine using one color for over-12 cM segments to 25 cM segments, a second color for 26 cM – 40 cM, a third for 41 cM - 60 cM and a 4th color for over-61 cMs. This way I can more easily pick out the two or three longest segments in each set.

Start looking for matches with people who preferably have trees and who have the longest DNA segments and who are ICW with each other.

If you have difficulty running this program, see **Common JWorks Errors** above.