

Technique for Segment Triangulation when GEDmatch Tool not Available

Notebook: Lesson 2
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Technique for Segment Triangulation when GEDmatch Tool not Available

8/28/2014

7 Comments

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Those of us who are heavy users of [GEDmatch](#) are sorely missing the wonderful segment triangulation tool, which hasn't yet been restored since the relocation of GEDmatch to new servers. In order to be able to continue identifying triangulated groups with DNA matches, I'm using a workaround, by expanding what I previously did for the X-chromosome (Chr 23 in the figure below), which isn't included in the segment triangulation tool. In addition, segment triangulation on GEDmatch is limited to the highest 200 matches, so this method can also be used for lower level matches, even when the segment triangulation tool is back.

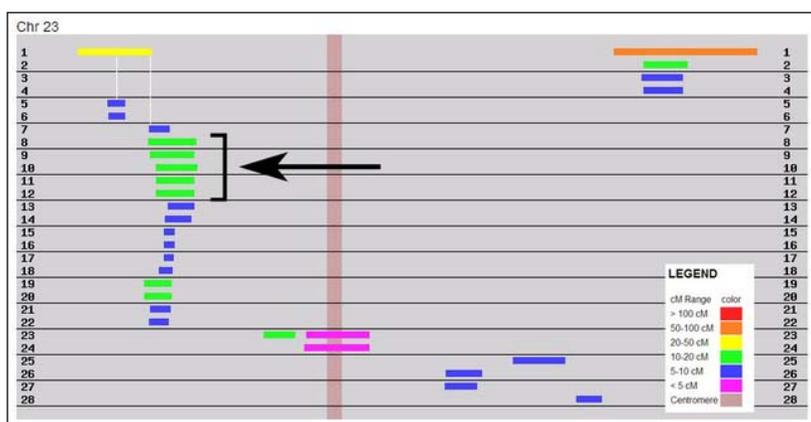


Figure 1: Segment Triangulation using GEDmatch Chromosome Browser

Steps:

- Use "one-to-many" to create a match list.
- In the 4th column, click on the first 200 matches or so (#1 in Figure 2 – obvious

DNA matches to Kit F340000.

These matches are calculated from DNA test data files submitted by users. Results are based on the default parameters for the GEDmatch Autosomal comparison software. These results are for comparison only and will likely be somewhat different from those shown by your testing company.

Default parameters (and results) may change periodically based on feedback from users, and from any research results.

Click on 'I' for list of matches for that person.
Click on 'A' for details on Autosomal comparison (Detail data may take up to a minute to process).
Click on 'N' for details on X-DNA comparison.

Select 2 or more from Subject column, and **2** button for a Chromosome Browser comparison.

Author



My name is Sue Griffith and I live in California, but I was brought up in the UK. Over the last few years I've become a total genealogy junkie and, more recently, a genetic genealogy junkie! I'm also a bit of a supplier to anyone who shows a hint of an interest in family history and am encouraging as many relatives as possible to have their DNA

tested for genealogical purposes.

p.s. I'm not one of those fuddy-duddies I had the (wrong) impression that all genealogists are.

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duplicates across multiple sites can be ignored). This is a little tedious to do (!), but it is a means to an end. I tried clicking on more boxes, but it won't run if too many are selected. Then click on Chr-Browse (#2 in Figure 2).

- When the almost blank page appears, click on "HERE" to display the Chromosome Browser (Figure 1).

Select 2 or more from Select column, and click this button for an Autosomal Match comparison.
[Autos] ✓

Select 2 or more from Select column, and click this button for a Generational Match comparison.
[Generative] ✓

Select 2 or more from Select column, and click this button for an X-DNA Match comparison.
[X-DNA] ✓

* Add cM column has an adjustment applied to compare 1 cM differences in X-Chromosome.

Intensity of GREEN background indicates how recent (within last 30 days) a match is.

To qualify as a 'match' in the genealogical sense, results must have a largest Autosomal segment that has at least 700 SNPs and be at least 7 cM. It must have BOTH. Results with the largest segment less than 7 cM are highlighted in pink. To check the number of SNPs, click on the 'A' on the

Kit #	Type	Sex	Surname	M1	M2	Y	Autosomal			X-DNA				
							Detail	Total cM	largest cM	Chrom	Detail	Total cM	largest cM	
F3	F	L	W	F	H	Set	6	42.4	33.2	4.2	X	0	0	0
F10	F	L	W	U	H	RY	6	22.8	17.7	4.8	X	0	0	0
M6	M	L	W	F	H		6	21.6	16.3	4.7	X	0	0	0
M10	M	L	W	M	J	cd	6	20.6	15.2	4.7	X	0	0	0
A74	F	L	W	M			6	20.5	14.5	4.7	X	0	0	0
M2	M	L	W	F	H		6	20.2	14.1	4.7	X	0	0	0
M3	M	L	W	F			6	19.9	13.2	4.7	X	0	0	0

Figure 2: DNA Matches on "One-to-Many"

- I then SAVE the resulting Chromosome Segment Matching webpage, so I can access it at any time, in part so I don't have to repeat the same 200 clicks, but in part so I can access it even when GEDmatch is unavailable (or when I'm off-line). To do this, press Ctrl + S (for Windows) or Command + S (for MacOS), or File then Save on the browser menu. The default filename would be "chrom_match_4c.php.htm", but I change this and include the kit number and, for example, "Matches 1-200", the latter because I may repeat the whole procedure for Matches 201-400, 401-600, etc. In addition to the htm file, a folder with the same name and containing 23 gif files (one for each chromosome) will also be saved. You can go back and use the htm file at any time, even when GEDmatch is "down" – just click on the htm file and it will open in your default browser.
- Scroll down the chromosome plots, looking for potential triangulated groups (TGs) – for example at the black arrow in Figure 1, which shows a potential TG on the X-chromosome (Chr 23) of segments >10 cM. Make a note of the kit numbers of the individuals in this group (Lines 8-12 in the example shown – these Match IDs are found in the table above each chromosome segment plot) and the approximate location of this group on the chromosome (~18.4-28.6 Mb in this example – table not shown). Using "one-to-one" (or X one-to-one, if applicable, as in this example), compare each member of the group with the others in the group, and either include or exclude the individual from the TG, as appropriate.

X-Chromosome Segment Triangulation

Even with GEDmatch's segment triangulation tool, this does not include the X-chromosome. If I'm only interested in doing X-chromosome segment triangulation, I firstly change the order of my matches in Figure 2, sorting on largest cM in the last X-DNA column, so the X-chromosome matches are grouped together. To do this, click on the little blue triangle shown by the blue arrow in Figure 2, which will turn red once sorted, then click on boxes shown at Figure 2, #1 for anyone with X-chromosome matches. As above, click on Chr-Browse – everything can be ignored for Chromosomes 1-22, so just go down to "Chromosome 23" at the bottom, to assess the X-chromosome, then start triangulating.

Final Comments:

- Yes, this method is a bit tedious compared with using GEDmatch's segment triangulation tool, but I have found it useful during these months when the tool hasn't been available, and it is my Number 1 method for the X-chromosome (I manage far too many kits to have time to create and maintain GEDmatch segment spreadsheets for everyone).
- If you haven't ever made a donation to GEDmatch, or you haven't made one recently, please consider doing so, to help support the costs for additional servers and to minimize the chances of outages in the future. THANK YOU! *There's a Paypal Donate icon at the foot of the GEDmatch Home page once you've logged in, allowing one-off or recurring (monthly) payments.*

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Teresa

9/24/2014 16:41:44

Sue, thank you for sharing this. One question: You say to use one-to-one compare to include or exclude a match re: the TG. I'm not clear on what criteria you're using to compare and then include/exclude. How do you decide?

Reply

Sue Griffith

9/25/2014 00:20:43

Hi Teresa:

I tend to just use GEDmatch's defaults (700 SNPs, 7 cM), so if GEDmatch indicates a match with one-to-one I just accept that. You have to remember that you inherit 2 chromosomes and that a group of your matches could match you on one chromosome (from your father) and a group could match on the other chromosome (from your mother). So some of your matches only match some of the others and others of your matches match other people. There is only a triangulated group (TG) when those matches not only match you but also match each other. So for your matches, you may be able to break them out into 2 separate groups (one on your maternal side and the other on your paternal) -- but they may be all on the same side (and you may not know which side that is, although they all match each other and are therefore a TG).

Sue.

Reply

Joel

12/5/2014 16:26:38

I am doing an X chromosome comparison right now and had to lower the threshold as I am getting almost no matches otherwise. Right now I am using 500 snps and 5 cMs. I had a list of about 50 in an X segment all above 11 cM matches and none were matching at the Gedmatch default threshold for some reason.

Sue Griffith

12/5/2014 21:25:50

@Joel (I couldn't post a reply to your message on my own blog -- not sure why but hope you notice this):

I've sometimes noticed issues similar to yours with GEDmatch. Also the "opposite", where there were "matches" shown on One-to-Many and yet when I checked One-to-One, there was no matching DNA unless I lowered the thresholds well below the defaults. This type of thing makes me a little uncomfortable -- but I hate to criticize GEDmatch because of everything they do!

Ann

9/26/2014 13:50:22

Hello, I have a question. I'm new to Gedmatch.com, what does it mean when a kit number matches your kit number and it have some weird numbers/letters under Mt or Y Haplogroup or both?

Reply

Sue Griffith

9/26/2014 19:29:06

Hello Ann:

The letters and/or numbers under Mt or Y Haplogroup are what the tester has entered when they uploaded their kit to GEDmatch, and in general, these haplogroups do not provide any useful information. With very few exceptions, you can ignore these when you are reviewing your matches. The DNA results that are uploaded to GEDmatch are for autosomal DNA, which cover all branches of your family tree, and this is what is compared to give you your match list under the "one-to-many" comparison.

The DNA that is tested for Mt or Y Haplogroups is mitochondrial DNA and Y-chromosome DNA.

respectively. No matching is done for Mt or Y DNA on GEDmatch. Everyone has Mt-DNA and both males and females inherit this from their mother. This type of DNA is passed down the mother's mother's mother's (etc.) line virtually unchanged for tens of thousands of years, so it only covers that one branch of your family tree (the so-called matriline). Only males have Y-chromosome DNA and this is passed down the father's father's father's father's (etc.) line virtually unchanged for tens of thousands of years, so it only covers that one branch of your family tree (the so-called patriline). If you know your Mt DNA results (or Y-DNA results from your father/brother/uncle or from you if you are male), then having these results for a match on

GEDmatch can EXCLUDE someone from matching you on the patriline or matriline, so all you know is that the match is one of your other branches on your family tree.

If you have tested at 23andMe, as well as your autosomal DNA results, you will also be shown high level (not very specific) Mt Haplogroup (and Y Haplogroup if you are male) and so individuals who have tested at 23andMe can add these details when they upload to GEDmatch and you will see them if they are on your match list. The Family Finder (autosomal DNA) test at Family Tree DNA does not provide haplogroup information, although very specific tests for Mt and Y-DNA are run at Family Tree DNA, so a tester may have haplogroup results available from testing there. AncestryDNA only tests autosomal DNA, although in the past did run Mt and Y-DNA tests, so the vast majority of people with AncestryDNA tests will not have haplogroup information unless they have also tested elsewhere.

Bottom line is that you can generally ignore Mt and Y Haplogroup information, although there may be occasional situations where it can help you, but only if you know your own haplogroup(s). Sometimes I look at the haplogroups of 2 or more matches when they are each matching me over the same segment for the same length, as it may give me a quick idea whether they are likely to be related (e.g., father/son, maternal/paternal cousins, siblings) when they show different e-mail addresses, although if I want to obtain a better idea of their relationship, I run a one-to-one comparison of these 2 matches with each other.

This is probably more than you needed to know, but if you have other questions, send me an e-mail (click on the envelope icon) or a message via the Contact link.

Sue.

Reply

Dan Stone

10/19/2014 16:10:01

I wanted to say thank you very much for this fantastic alternative to the triangulation tool. I am sharing this method as part of my blog series on using GEDmatch (<http://stonefamilytree.wordpress.com/2014/10/19/introduction-to-using-gedmatch-part-5-alternate-to-triangulation-tool/>). In addition, in case you are unaware, the programmer of Genome Mate has just added a new import option to take advantage of your method (<https://www.facebook.com/GenomeMate> and <http://genealogypuzzlesdna.blogspot.com/2014/05/getting-started-with-genome-mate-using.html>). Keep up the great work!

Reply

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