

Double Match Triangulator Version 5.2.1, 12 Jul 2023

www.doublematchtriangulator.com

Double Match Triangulator (DMT) is an autosomal DNA analysis tool for Windows. DMT automates the analysis of two or more segment match files with common ancestor information you supply. DMT uses data available from [Family Tree DNA](#), [23andMe](#), [MyHeritage DNA](#) or [GEDmatch](#).

DMT finds all triangulating segments that two people share with some third person. The user adds known Most Recent Common Ancestors (MRCAs) and DMT uses those to determine ancestral paths for each segment and to put the people into ancestral clusters. The results are given to you in Excel files with details for each match, and a summary of all people. You also can have DMT produce a file containing ancestral paths that can be uploaded to [DNA Painter](#).

Double Match Triangulator was imagined and developed by Louis Kessler (Behold Genealogy). The concept of double matching to determine triangulation groups enabled DMT to place 3rd in the Innovator Showdown at RootsTech 2017 in Salt Lake City.

This document is available in PDF format at: www.doublematchtriangulator.com/DMTHelpFile.pdf

The Purpose of DMT

Our goal as genealogists is to extend our family tree. We take DNA tests to try to find relatives who may share common ancestors with us. We know how we're related to some of the people our DNA matches to. But for most of our DNA matches, we don't know that. If we can figure out how we're related to the other people our DNA matches, we'll have new branches we can add to our tree.

Double Match Triangulator (DMT) is an autosomal DNA analysis tool to help you find how the people you DNA match with may be related.

DMT combines segment match data of two or more people to find all the double matches and triangulating segments they share. Using known common ancestors of known relatives, DMT determines ancestral paths to indicate the common line that the DNA passed through and it organizes these into triangulation groups for you. DNA relatives who match in any particular triangulation group may have a common ancestor along or beyond the ancestral path who passed this segment to all the people in the group. The assignment of ancestral paths to segments of your DNA is known as **Chromosome Mapping** or **DNA Painting**.

Over the past five years Tim Janzen and Jim Bartlett have developed various manual techniques for chromosome mapping. They are leaders in this field and have both been able to determine the triangulation groups that cover almost all their DNA. This work deals with a lot of data and they have done this manually in spreadsheets, taking a lot of their time and effort. Double Match Triangulator has been developed to automate this process, and to make this type of chromosome mapping possible for anyone.

Double Match Triangulator will produce the following output for you:

1. Every one of your matches is presented visually in an Excel spreadsheet. Every triangulation that is possible from the segment match data is shown. You will see how the segments overlap with each other. The ancestral line, if one can be determined, is shown for each segment. The segment matches are then organized into **Triangulation Groups**. Segment match data is shown on the Chromosome Map pages.
2. Summary information for every person is provided in an Excel spreadsheet. It includes the ancestral lines that are determined for every match for each person. DMT assesses the ancestral lines to assign a primary ancestral line to each person. The people are organized for you by ancestral line, which in effect is doing a **DNA Clustering** of your matches for you. Person summary information is shown on the People page or file.

3. Ancestral path data for input to the **DNA Painter** website is optionally provided in a .csv file. You can take this file and upload it to DNA Painter to add your ancestral paths from DMT to an existing or a new DNA Painter profile.

4. Log files are created after every run that give detailed information about the results, including number of people, number of segments, double matches and triangulations, parent and sibling information, persons A and B's matching segments, errors in the input files, as well as progress information about the run. Combined runs also include a segment size summary.

With DMT, you can skip the long and involved steps of looking for matching segments, identifying triangulations, identifying the ancestral path of each segment, and determining triangulation groups. Instead you'll be able to jump right ahead to using the results to help you identify how your DNA matches are related and extend your family tree.

Segment Match Data

DMT uses segment match data that is available from Family Tree DNA, 23andMe, MyHeritage DNA, or GEDmatch. These are the only companies that provide you with all your segment match data. AncestryDNA does not give you access to your segment match data. To use your AncestryDNA results you have to upload your DNA raw data to Family Tree DNA, MyHeritage DNA or GEDmatch and then download your segment match data from there. GEDmatch requires a Tier 1 subscription (\$10 to \$15 for a month) to access the utility to download segment match data from their site.

Segment match data differs between companies. You cannot compare segment match data from one company with segment match data from another company. The main reason is that matches need to compare to the same person in both files, but the same person often didn't test at different companies and when they did may have used different display names at the different companies. To a computer, John Smith is not the same as J. Smith or John D. Smith or JS. An additional reason is that each company uses their own proprietary algorithm to determine whether two people match over a segment and where the start and the end of a match is. Using two files from the same company eliminates differences due to matching algorithms.

Although DMT will accept just one segment match file, you cannot determine triangulating segments from just one file. So you really will want to use two or more segment match files from a single company to get full value from DMT's analysis.

Your own segment match file contains all the segments of all the people you match to. You'll want segment match files from some of the people you match to that you can compare with.

Here are some of the people you would like segment match files for:

1. **Cousins whose relationships you know.** If you know your common ancestors with your cousin, then most of your segments in common with that cousin should match through those common ancestors.
2. **Aunts/Uncles, half siblings.** They will match one of your parents and both your grandparents on that parent's side, helping you partition your father's matches from your mother's.
3. **Parents.** Matching with a parent is what I call parental filtering. If a parent doesn't match on the same segment that you match someone, then that match is either on your other parent, or it is a false match. DMT gives you additional information for parent matches. If you have both your parent match files, then any of your matches that neither parent matches will be shown by DMT as likely being a false by-chance match.
4. **Siblings.** They are tricky, because you can match them on both parents at the same time. But they are still very useful for double matching and, are quite usable for triangulations and Missing A-B and Missing B-C matching. In addition siblings are excellent for inferred matching, which is where your sibling matches someone but you don't.

5. **Nephews/nieces.** They only get one chromosome from your sibling, so they won't match on both your parents at the same time. They should match to many of your relatives on both your father and mother's sides.
6. **Children/grandchildren.** Although they can only match on segments that you match, they still are very useful for triangulations since the child effectively phases the parent to one set of alleles which then match a third person.
7. **Someone who you know is related but don't know how.** The cluster that these people are put into may be able to help you identify your common ancestor with this person.
8. **Children of matches.** They may allow you to triangulate with their parent.
9. **Anyone else who matches you.** You never know what might be revealed.

Important Concepts

Autosomal DNA

Each of us have 23 pairs of chromosomes, one of each pair from our father and one from our mother. The 23rd pair are two X chromosomes for a woman, and an X and a Y chromosome for a man. The Y chromosome is not included as part of autosomal DNA, so a man will only have a single X in the 23rd position for the purpose of autosomal DNA analysis.



Above is an example showing the 45 autosomal chromosomes for a man drawn with DNAPainter. The chromosome pairs are numbered 1 to 23, with number 23 known to be X. The top chromosome of each pair is from the person's father and the bottom of each pair is from the person's mother. The single X chromosome for a man is from his mother.

Recombination and Crossovers

Each parent passes you 23 chromosomes. Like you, your parent has 2 of each of their chromosomes, and in the process of giving you yours, they recombine each of their pairs into one for you. It is done in a simple manner, by taking the first bit from one parent, the next from the other, back to the first, etc. Each chromosome normally "crosses over" only a few times. So parts of the chromosome are from one grandparent, and parts are from the other. It is possible for a chromosome not to crossover, and in that case, the whole chromosome will be from one grandparent. The above diagram shows light and dark green segments of DNA that are likely from the person's paternal grandmother and blue segments that are likely from the person's paternal grandfather.

Ancestral Paths

Each little bit of DNA comes down some ancestral path. You get it from either your father or mother. Your father or mother gets it from their father or mother, etc. DMT will use "F" for father and "M" for mother to denote an ancestral path. So FMF comes from your father's mother's father, i.e. your great-grandfather. **This Ancestral Path helps you to figure out how a relative may be related to you.** If a person matches you on, say, an FMF segment, then they may be related to you on your father's mother's father's side. Using that information, you can look for records that may show your connection through that ancestral path.

Most Recent Common Ancestor (MRCA)

When two people are related, they share common ancestors. The Most Recent Common Ancestors of Person A and Person C are those who are the closest two ancestors who may have passed a segment to both A and C. For example, if A and C are second cousins, then they share a pair of great-grandparents. You will need to assign the MRCA to Person C and save it in DMT's People File so that DMT can use it. The MRCA is similar in construction to an ancestral path, but it usually ends in an "R" to represent a pair of ancestors, e.g. your great-grandfather and great-grandmother. So an MRCA for your 2nd cousin might be: FMFR, indicating that your father's mother's father's parents are also your cousin's great-grandparents. DMT uses the MRCA information you supply to create ancestral paths for each segment. So DMT can only go back as far back as the MRCAs you supply to it.

Segment Match Data

The data from each company that DMT uses is different from each other, but generally includes the following information:

Name	Match Name	Chromosome	Start Location	End Location	Centimorgans	Matching SNPs
Louis Kessler,			1,48986234	53343247	1.04256	600
Louis Kessler,			3,17642886	20434306	2.14899	500
Louis Kessler,			19,17027981	19668340	1.74167	600
Louis Kessler,			20,30561521	33256820	2.12609	500
Louis Kessler,			8,83933847	87383874	1.26132	500
Louis Kessler,			17,42708188	45012823	1.31185	500
Louis Kessler,			1,220908712	223882258	2.05058	700
Louis Kessler,			4,16776906	24991881	10.11568	1983
Louis Kessler,			11.48014889	55878633	1.00213	500

1. The name of the DNA tester, we'll call Person A
2. The name of another DNA tester who Person A matches to, we'll call Person C.
3. The chromosome they match on.
4. The starting position on the chromosome of the match, in **base pairs (bp)**.
5. The ending position on the chromosome of the match, in base pairs (bp).
6. The genetic distance of the match in **centimorgans (cM)**.
7. The number of tested **Single Nucleotide Polymorphisms (SNPs)** on that segment.

Each company tests the DNA at their own set of SNP locations. They each use their own proprietary method for determining what they will call a segment match between two people.

Single Matching

The information in one segment match file gives all of a person's single matches. There are two values at each SNP, one for the father and one for the mother. The DNA test results cannot differentiate which value at each SNP is the father's and which is the mother's. As a result, the testing companies compare both of Person A's values at a SNP to both of Person C's values at each SNP. If either of A's values match either of C's values, then that SNP is called a match. The more SNPs that match on this basis that you have in a row, the more likely it is that one chromosome on A is matching one chromosome on C. Once you reach a certain number of SNPs, often thought to be about 3000, equivalent to about 15 cM, then the likelihood of **a match by chance** or **false match**, where either chromosome of A is matching either chromosome of C, becomes very small. If this is not a match by chance, then you can be fairly certain that one of Person A's parents matches one of Person C's parents over the majority of the segment. Assigning matches to one parent is called **phasing**. Two phased matches are often **Identical by Descent (IBD)** where a common ancestor has passed the segment down to both Persons A and C. If you know how Persons A and C are related, then you may know who their common ancestors are, and you can map this segment to the ancestral path leading to these common ancestors. This ancestral path can be given a color and "painted" onto the segment with a program like DNA Painter. The important thing to remember about overlapping single matches is that some may be

on dad's side and some on mom's. Just because they overlap, you cannot assume they are on the same side without additional information.

Double Matching

When you have segment match data for a second DNA tester, we'll call Person B, then you can compare Person A's matches with every Person C to Person B's matches with every Person C. If Person A and Person B both match the same Person C on the same chromosome and the start and end locations match or overlap each other, then the overlapping part will be a **double match**. A double match by itself does not mean much by itself. It needs a bit more.

Triangulating Segment

When you have three people, Person A, B and C, and Person A matches Person C, Person B matches Person C, and Person A matches Person B, all on the same chromosome and their start and end locations all overlap, then the common overlapping segment is called a **triangulating segment**. Because you now have 3 people in pairs all matching each other, it takes fewer SNPs to make the a match by chance unlikely. Only about 1400 SNPs or 7 cM are now needed to be fairly certain that one of each of Person A, B and C's parents all match each other over the overlapping part of the match. The other thing about three people who triangulate on a segment is that the three people generally will match on the same chromosome, either your father's or your mother's. (There are a few exceptions to this, e.g. two or more of the people being siblings, people related more than one way, or triangulations on opposite parents). A triangulating segment will often (but not always) have been passed down to Persons A, B and C from a common ancestor of the three.

Triangulation Groups

When Person A, Person B and Person C triangulate on a segment, then they form a triangulation group. If other people also match Person A, Person B and Person C on the same segment, then they are also part of the triangulation group. In actuality, every person in the triangulation group must match each other. But in practice some may not if their total shared matches did not reach the company's minimum or if one person's match file was downloaded before the other's test results came in. A matching segment between two or more people has three possibilities:

1. It could be part of a triangulation group on the father's chromosome and indicates a common ancestor on the father's side,
2. It could be part of a triangulation group on the mother's chromosome and indicates a common ancestor on the mother's side, or
3. It is simply a match by chance and does not indicate a common ancestor.

The segments in a triangulation group will often (but not always) have been passed down to all people in the triangulation group from a common ancestor of them all.

Double Match Triangulation

Double Match Triangulator works by using two match files of Person A and Person B. It finds all double matches that A has with C and B has with C on the same segment. Person A's match file also has matches with Person B (as does Person B's with Person A) and now it is a simple matter to see if Person A and Person B match on the same segment. If they do, we have a segment triangulation. Double Match Triangulator thus can easily find **all** the segments and people that Person A and Person B triangulate with. The discovery of this led to the development of DMT.

Identical By Descent (IBD)

If a segment is passed down to two or more people, that segment match is called Identical By Descent (IBD). This also means that when two or more people share an IBD segment, they share a common ancestor who passed that segment down to them. If the segment data is correct, then every person that shares the same IBD segment should triangulate on that segment. The reverse is not always true, as triangulation does not always mean IBD (see A Few Caveats, below).

In Common With (ICW)

When two related people, Person A and Person B, both share DNA with a Person C, they are said to be sharing DNA In Common With Person C. This does not necessarily mean that they share overlapping segments or triangulate anywhere. But it does mean that Person A and Person C are likely related, and that Person B and Person C are likely related. All DNA companies provide a list of In Common With people. Ancestry DNA does not provide segment matching data, but does provide ICW people that can be used with various clustering techniques (see Clusters, below).

Missing AB, Missing BC

In Common With information is very important in Double Match Triangulator. When you have a double match where Person A matches C on a segment and Person B matches C on the same segment, it is very important that they all share data with each other somewhere, i.e. that they are ICW each other. So on that double match, if Person A also matches Person B on that same segment, we have a triangulating segment. But if Person A and B don't match each other on that segment, but do match each other elsewhere, we then have what we call a Missing AB match. Similarly, if Person A matches C on a segment, Person A matches B on that segment, Person B does not match C on that segment, and A, B and C are ICW, then we have what we call a Missing BC match. DMT shows all Missing AB and Missing BC matches in its analysis.

Inferred Matches

An inferred match is where Person B matches Person C on a segment but Person A does not match Person C on the same segment. Persons A, B and C must be ICW each other. If you know how Person A and B are related, and how Person A and C are related, then the segment where Person B matches Person C might tell you what A's segment's ancestral path cannot be. DMT finds all possible inferred matches and displays and uses them in its analysis.

Clusters

You can group people into clusters from lists of ICW people using techniques such as the Leeds Method and clustering programs based on it. Clustering people is very useful. When the relationships of a few people in a cluster are known, they can be indicative of what the ancestral path might be for all people in the cluster. DMT puts people into clusters as well, but rather than using ICW information at a person level it instead uses the ancestral paths of the segment matches of the person. Different clustering tools provide different resulting clusters, and DMT provides its own cluster results for you to make use of.

A Few Caveats

Three or more overlapping IBD segments should triangulate with each other. However, sometimes they may not because:

- One person doesn't meet a company's total cM matching threshold required for them to be considered a match with the other.
- The particular segment match is does not hae a cM large enough to meet a company's individual segment match requirement.
- One person's match file was downloaded before the other person tested, therefore the other person is not in the match file.
- A company did not consider that segment to be a match because of some algorithm or imputation that they use.
- The raw data over that match may have some read errors causing the segment to not match.
- One of the people may have had a few mutations that could have caused the segment not to match.

In other words, **if your data does not show a triangulation, there still might be one.**

Triangulation does not necessarily mean IBD, because:

- One of the segments may match by chance to the other two, expecially if small (e.g. under 7 cM)
- Three triangulating segments may match each other each on opposite parent chromosomes, e.g. (1) paternal A matches maternal B, (2) paternal B matches maternal C, and (3) paternal C matches maternal A. In this case, there are three different common ancestors each passed down a segment to two of A, B and C.
- The company's algorithm, imputation, read errors or mutations, may result in a triangulation where there really is not one.

In other words, **if you have a triangulation, don't assume it is IBD.**

But, **because an IBD segment shared by 3 or more people must triangulate, a segment that triangulates passes the first test that it might be IBD.**

Nothing Is Guaranteed

DMT must listen to what the data is telling it. It has to assume that the segment matches it is given are correct. If the data says that 3 segment matches don't triangulate, then DMT has to accept that. Due to the caveats specified above, some of the data DMT makes use of could be incorrect. Some of the incorrect data may affect the results.

You will be entering into DMT, the common ancestor information for your DNA matches whose relationships you know. Most of the segments you match with a person will likely be along the MRCA you specified. Some segments, however, may come from other lines if that relative is related more distantly on some other line. Or maybe you're from an endogamous population and some segment matches come from who-knows-where. These segments that are not from MRCAs you specify will therefore be incorrectly assigned by DMT. There will be some matching segments through closer relationships and others through more distant relationships. DMT uses "majority rules" as its resolution technique, and will accept the ancestral path that the most matches agree on. The correct relationships in theory should outnumber the incorrect relationships.

But not always. Be very aware that some results from DMT may not be correct. As you add more match data and more MRCAs that you know, DMT's segment assignments will improve.

DMT automates the analysis of more data than you'll ever be able to analyze by hand yourself. Just remember, as Blaine Bettinger said at MyHeritageLive 2019: "Automation does not give you the answer. It gives you a suggestion." Use DMT's suggestions wisely.

DMT's Method of Chromosome Mapping

Double Match Triangulator tries to get the most information possible out of your DNA segment matches. It uses techniques that include **DNA painting** as done at Jonny Perl's website dnapainter.com and **clustering** as started by Dana Leeds and enhanced by others. DMT includes the ideas and concepts of Tim Janzen and Jim Bartlett who use **triangulation groups** to map chromosomes to ancestors. Tim and Jim did this manually for years. Tim often presents his techniques at genealogy conferences and online. Jim created a website www.segmentology.org that described his methods.

Double Match Triangulator does the work to automate these methods the way a person would manually do it if they had all the data and enough time and patience.

DMT uses a primary person whose DNA is of most interest, a second person whose matches are compared to the primary person, and the results will include the matches of all the people who the primary person matches to.

- **Person A** is the person of interest whose chromosomes you are mapping.
- **Person B** is the person who you have a match file for who is really only useful if they match Person A somewhere. It is helpful to know the common ancestor between Person A and Person B, but that is not necessary.
- **Person C** refers to any of the people who Person A matches to. Knowing the common ancestor of some of the C people is what will allow you to map your chromosomes to your ancestors.

Double Match Triangulator can be run without knowing any common ancestors. In that case, all mappings will be to "U" (unknown), but you will still be shown all the triangulations that Person A and B share, plus other double matches and single matches of Person A.

These are the elements of chromosome mapping as done by Double Match Triangulator:

- **Triangulations:** provide additional information to map additional segments using the fact that there are only two triangulation groups (one paternal, one maternal) at any one position on a chromosome, and that one triangulation group must come from a single ancestral path. Triangulations also allow the use of smaller segments than single matches, which [according to Jim Bartlett](#) allow you to have confidence down to at least 7 cM and maybe even 5 cM, compared to the 15 cM reliability level for single matches.
- **Missing A-B matches:** This is where Person A matches Person C, and Person B matches Person C on the same segment, but Person A does not match Person B on that segment. This is not a triangulation and indicates that Person B is most likely matching Person C through a different relationship than Person A has with Person C.
- **Missing B-C matches:** This is where Person A matches Person C, and Person A matches Person B on the same segment, but Person B does not match Person C on that segment. This is not much better than a single A-C match, except that it does indicate that Person A matches Person B, so Person B is most likely matching A on the opposite parent that Person C is matching.
- **Single A-C matches:** If neither B matches C, nor A matches B on this segment, then no additional information is available from this match. If the match is above a user threshold (the default being 15 cM) then the match will still be included in the analysis because it is most likely a real match. It will be assumed to not be matching the chromosome of the parent that has triangulations on that segment.
- **Inferred matches:** Information may be available when Person B matches Person C on a segment that Person A does not match Person C. In some cases, [a technique named "Inferred Matching"](#) by Jonny Perl can be used. Inferred matching requires that both the common ancestor between Person A and Person B and the common ancestor between Person A and Person C are known. It tells you that the segment where Person B matches Person C cannot be from a specific common ancestor. Because if it was, then Person A and Person C would match as well.
- **MRCAs and Ancestral Paths:** DMT uses a notation to represent the Most Recent Common Ancestor (MRCA) of Person C with Person A and almost the same notation for ancestral paths. The notation is simply a string of "F"s and "M"s. So an ancestral path through Person A's father's mother's mother would be FMM. The only difference in notation

is that an MRCA can end with an "R" which represents a pair of parents who both Person A and Person C share. The common ancestor is always from Person A's point of view. If Person C is a second cousin through Person A's father's mother's parents, then the MRCA would be FMR. There would be two possible ancestral paths shared with the cousin: FMM and FMF. Siblings, nephews, nieces and children of Person A will all have an MRCA of just R. Half-relatives would need to go up one level to get to the R, for example, a half-sibling would be either FR or MR depending on whether the common parent is father or mother.

How DMT Does It

Double Match Triangulator automates the steps a person would take using double matching to map their chromosomes. These are the steps DMT follows.

1. **Eliminate Small Segments** - Double Match Triangulator uses the "Min Triang" value to exclude small segments from analysis. The DMT default is 7 cM. Triangulations less than 7 cM might be matches by chance (matching on more than one chromosome) and thus be false triangulations. Jim Bartlett believes this number might be as low as 5 cM.
2. **Double Matches** - All the matches in Person A's file and Person B's file are compared. Every Person C who matches both Person A and Person B on an overlapping segment on the same chromosome is a double match. It's called a double match because there is both an A-C match and a B-C match.
3. **Triangulating Segments** - Every double match is checked to see if there is also an A-B match on the same segment. This will find all triangulating segments that Person A and Person B have with any Person C. Double Match Triangulator finds and displays every triangulating segment that is contained in the segment data after the small segments are removed. For each triangulating segment where the MRCA of Person C is supplied, that MRCA is "painted" onto the chromosome for that parent. It is painted for the entire length of the A-C match while marking which sections have triangulations.
4. **Missing AB Matches** - If there is no A-B match on the double match, then it is called a Missing AB match. This is not a triangulation which usually indicates that this was not a segment passed down from a common ancestor to Persons A, B and C. We are saying specifically here, that A does not match B on the segment. We want to be sure, so the A-C match must be at least the Min Single value (default 15 cM) to ensure that we are not dealing with a possible false match. For each Missing AB match where the MRCA of Person C is supplied, that MRCA is "painted" onto the chromosome for that parent for the length of the A-C match less 1.5 Mbp on either end to allow for a bit of random matching.
5. **Missing BC Matches** - If there is no double match, but A matches B on the segment, then it is called a Missing BC match. This is also not a triangulation. However, if B is in common with C on other segments, then B and C are confirmed not to match on this segment. Like Missing AB matches, the A-C match must be at least the Min Single value. For each Missing BC match where the MRCA of Person C is supplied, that MRCA is "painted" onto the chromosome for the parent for the length of the A-C match less 1.5 Mbp on either end to allow for a bit of random matching.
6. **Inferred Matches** - When Person B matches Person C on a segment, but Person A does not match Person C on that segment, then it may be possible to infer something about Person A's ancestral line along the same segment. Depending on how Person A is related to Person B, the fact that B is matching may indicate that A cannot match along some related ancestral line. To infer anything, you must know both Person A's MRCA with Person B and MRCA with Person C. This technique works very well when Person B or C is a sibling or niece/nephew, because you can often eliminate a whole grandparent from Person A's possible ancestral lines on a segment, meaning Person A's ancestral line must go through the other grandparent on that segment. I wrote [a blog post about Inferred Segment Matches](#) in March 2019. Since then, I determined all the ways that inferred matches can give results. Anyone descended from both of Person A's parents are able to refute a grandparent. For other people, the refutation is 2 generations beyond the closer MRCA up the line of the further MRCA, meaning one MRCA must be at least 2 generations past the other. Double Match Triangulator finds, displays and makes use of every inferred match that is at least of Min Single size that is contained in the segment data.

7. Single Matches - Any A-C matches that did not triangulate and were not Missing A-B or Missing B-C matches are now considered. DMT will "paint" the MRCA of any match with centimorgans of at least "Min Single" (default 15 cM) onto the parental chromosome and will be designated as "Single AC". If the single match has less cM than "Min Single" but more than "Min Triang", DMT will call it "Small AC" and will display it in an "Unassigned" section to emphasize that this segment doesn't triangulate and may be by chance.

8. Ancestral Paths for Every Mbp - DMT next takes the "paintings" done above, and comes up with a consensus for the ancestral path at every **Mega Base Pair (Mbp)** for each parent along each chromosome. Inferred matches are taken into account and sometimes will determine the ancestral path when the MRCAs themselves do not. A "majority rules" type of consensus is used to first determine the grandparent, then the great-grandparent, etc., until we've reached the limit of the MRCAs that have been assigned.

9. Triangulation Groups - Triangulation group boundaries are determined for the father and mother chromosomes based on the number of matches that start and stop at each Mbp. All segments assigned to a parent, whether triangulating or not, are then assigned a triangulation group based on the boundaries that will contain them.

10. Grandparent Extensions - All Mbp within each triangulation groups should come from the same grandparent. If a grandparent is assigned to some but not all Mbp in a triangulation group, then the same grandparent can be assigned to the other Mbp in the group. If both grandparents are each assigned to some Mbp in a triangulation group, then the grandparent with the most assignments is used and the others are overwritten.

11. Ancestral Paths for Every Segment Match - DMT next assigns an ancestral path to every segment. It first sees if it can determine the parental chromosome of the segment. If there were triangulations painted on the Mbp making up the segment, then DMT sees which parent the triangulations were painted on. If they were painted on just one parent, then triangulations must be on that parent and other matches (Missing AB, Missing BC and Single Matches) must be on the other parent. If triangulations were painted on both parents (which can validly occur if Person B matches Person A on both parents as often happens with siblings), then the parental side is not known. If the parental side of the segment is not known but the person has an MRCA assigned, then then the parental side of the MRCA is used. If a parental side is determined, then the ancestral path at each Mbp for that parent is found, and a consensus is determined and assigned to the segment match. When no parental side is determined, then the segment is put into the "U" (unassigned) group..

12. Clustering People - Each person now has all their segments assigned. Most of one person's segments are often on one ancestral path, but they still might have some segments on different paths or on unassigned paths. They may be related through both of Person A's parents and match on both father's side and mother's side. DMT now goes through each person and determines what the majority of the ancestral paths agree on. The resulting path will be assigned as that person's Cluster. This cluster is likely the ancestral path through which this person is most closely related to Person A.

13. This completes the chromosome mapping process for two segment match files between Person A and one Person B. DMT produces an Excel file with two pages containing the results. The Chromosome Map page lists all the A-C matches along with information about each match ordered by triangulation group. The People page lists all the people who match Person A ordered by cluster along with information about that person's segment matches. A log file summarizes the run, and a comma delimited csv file is optionally created with triangulation group information in a format suitable for upload to DNA Painter.

14. If the "Folder B" option was selected, then steps 1 through 13 will be done for File A against each match file in Folder B.

15. If the "Combine all results" option was selected, then steps 1 through 13 will be done for File A against each match file in Folder B, and then the results will be combined. DMT produces 23 Chromosome files and creates or updates Person A's People file. A log file summarizes the run, and a comma delimited csv file is optionally created with triangulation group information in a format suitable for upload to DNA Painter.

Downloading Segment Match Data

DMT uses segment match data. Each company has different methods of providing you with that data.

On the next pages are instructions on how to download segment match data from Family Tree DNA, 23andMe, MyHeritage DNA and GEDmatch.

Important Note: DNA companies change the format of their segment match data and download procedures from time to time. If DMT is not working as prescribed, please contact me and I'll look at the issue.

Whose segment match files should you download? Try to download any people whose direct relationship you know. You will be assigning the Most Recent Common Ancestor (MRCA) to these people and DMT will be able to compute ancestral lines from them. At GEDmatch, you can download anyone's match file if you subscribe to their Tier 1 services. At the other companies, you only have access to the testers you administer, so you would have to contact the people whose tests you don't have access to, and ask them to download the match data and send it to you.

Here's what's good and bad about the segment match data you can get from each company:

Family Tree DNA:

Good:

- Allows you to download a person's segment matches with a single click.
- All of the segment matches for all matching people are downloaded.
- You get all single matches down to 6 cM.
- The download at FTDNA usually takes at most a couple of minutes.

Bad:

- The segment match data does not include the tester's name, so you must add the testers name to cell G1 in the match data file.
- The segment match data does not contain a unique ID number, so if two people have the same name, e.g. both being John Smith, their results will be mixed together. DMT does its best to detect, inform you of this, and eliminate duplicate matches where possible.
- You can only download segment match data for the kits you administer. To get the segment match data from other DNA relatives, you will have to contact and ask them to download their segment match data and send it to you.

23andMe

Good:

- Allows you to download a person's segment matches with a single click.
- You get all single matches down to 5 cM.

Good and Bad:

- You can only download segment match data for the kits you administer. To get the segment match data from other DNA relatives, you will have to contact them and ask them to download their segment match data and send it to you. But there is an alternative. The program [DNAGedcom](#) can download your segment match data of people in your match list without you contacting them. DNAGedcom charges \$5 for a month usage of their program.

Bad:

- You are limited to the segment matches of the 1500 closest people you match with plus any others you've "connected" with. For \$39 a year, you can subscribe to 23andMe+ and get 5000 matches.
- The segment match data does not contain a unique ID number, so if two people have the same name, e.g. both being John Smith, their results will be mixed together. DMT does its best to detect, inform you of this, and eliminate duplicate matches where possible.

MyHeritage DNA

Good:

- Allows you to request a person's segment matches with a single click which will send the file to you a few minutes later as an attachment to an email.
- You get all single matches down to 6 cM.
- Uses a Match ID number, so each kit is identifiable, even if two people's names are the same. DMT appends part of the Match ID number to the name to ensure uniqueness of the name.

- The file is grouped by person, with a blank line between people so you can see all the matches of each person together. The people are ordered by highest total shared cM down to lowest.
- The file gets emailed to you when it is ready, so you don't have to wait online for it to complete.

Bad:

- MyHeritage's segment match data does not include matches on the X chromosome.
- MyHeritage uses imputation and stitching techniques to derive their segment matches. As a result, they tend to have larger false segments than other companies. You may want to raise DMT's Minimum Single match limit from 15 cm to 20 or 25 cM.
- The MyHeritage segment file name depends on what your Windows language is.
- You can only download segment match data for the kits you administer. To get the segment match data from other DNA relatives, you will have to contact them and ask them to download their segment match data and send it to you.

GEDmatch

Good:

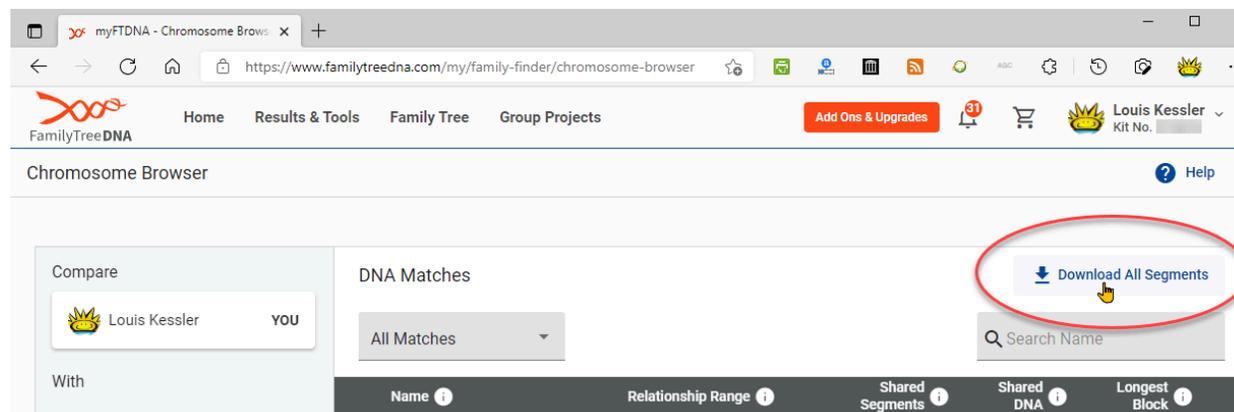
- Allows you to download a person's segment matches with a single click.
- Uses a GEDmatch ID number, so each kit is identifiable, even if two people's names are the same. DMT appends the kit number to the name to ensure uniqueness of the name.
- Includes people who have tested at different companies and all their segment data have been converted to GEDmatch's chromosome mappings so the segment data can be compared.
- You can download any person's segment matches. You need not be an administrator of their data and do not need to contact the other person to download their data.

Bad:

- The segment match data does not include the tester's name, but it does include the ID number of the tester. The download is always named csvsegmatch_.csv and does not contain the name of the person or ID number. DMT has to retrieve the name of the tester from other match files.
- Their segment match report excludes matches between people sharing more than 2100 cM. That means that all parents, children and siblings, and some uncles, aunts, nephews and nieces will be excluded from the match data. You definitely do want these people included. To get around this, DMT includes a "Save GEDmatch 1-1" button so that you can retrieve data via the GEDmatch one-to-one report to get parent, children and sibling match data. It's an extra small pain that GEDmatch shouldn't have to make you do.
- You are limited to the segment matches of the 10,000 closest people you match with. The default supplied is 1,000 and you have to change it every download if you want 10,000.
- You need Tier 1 services from GEDmatch to download segment match data. Tier 1 services currently cost \$15 a month with a minimum one-month signup or \$100 a year.

Family Tree DNA

From Family Tree DNA's home page, under Autosomal DNA Results & Tool, click on "Chromosome Browser" to go to their Chromosome Browser page. From there, click on the link that is named: "Download All Segments" that is shown by the hand pointer circled in red below.



Click on the link once and wait. You should get a wait indication symbol in your browser indicating that FTDNA is processing your request. Now you have to be patient but it shouldn't take more than a few minutes. Unfortunately FTDNA does not provide any feedback about their processing until the file has been generated.

This will download a special file named: `nnnnnn_Chromosome_Browser_Results_yyyymmdd.csv` where:

- nnnnnn is your Family Tree DNA kit number,
- yyymmdd is the date of your download, and
- .csv indicates this is a comma delimited file which can be read by Excel and other programs.

Do not rename the "nnnnn_Chromosome_Browser_Results" part of the segment match file names or change their ".csv" extension. DMT looks for that to find segment match files and will not accept files not following that structure. However, to help identify whose file it is, you may change the filename by adding the name of the person between the "Results" and the date, e.g:

`nnnnnn_Chromosome_Browser_Results_JohnSmith_yyyymmdd.csv`

DMT will then use "nnnnnn_JohnSmith" as part of the output file names so you can identify who the output files are for.

When loaded into Excel, the file can be seen to contain all the segment matches:

	A	B	C	D	E	F	G	H
1	Match Name	Chromosome	Start Location	End Location	Centimorgans	Matching SNPs		
2	Rc	1	203910220	209092631	7.594626	1460		
3	En	1	92106637	99956910	6.9060063	2297		
4	Ra	1	15197909	18550683	6.313448	1184		
5	Sil	1	205813672	216787802	13.588031	3661		
6	Ba	1	204359597	209722581	7.599839	1469		
7	Fr	1	21541735	26516022	6.3713923	1342		
8	Nc	1	209728590	216942781	8.544905	1859		
9	M	1	244390564	249208153	9.02795	1215		
10	jo	1	14407802	18460526	7.7983937	1218		
11	Le	1	977780	4012010	7.0244875	760		
12	Le	1	223647537	230436932	6.500096	1742		
13	Rc	1	204115477	208974597	6.780189	1366		
14	Do	1	12828498	18689252	11.389936	1609		
15	Aa	1	101123278	108015234	6.5845413	1738		
16	He	1	100292878	107919409	6.7073445	1796		
17		1	221868406	229738236	7.4391837	1929		
18	Je	1	31113232	37427336	8.434372	1513		
19	Xr	1	168474310	177610393	8.562908	2272		
20	Ar	1	201164691	208974597	6.678179	1350		

Column A (Match Name) is the person who matches. The file lists match names in alphabetical order, so blank names are first.

Column B (Chromosome), C (Start Location) and D (End Location) is the chromosome number with the start and end locations of the matching segment on that chromosome.

Columns E (Centimorgans) and F (Matching SNPs) is the distance in Centimorgans (cM) and number of SNPs for the matching segment.

Adding the Name of the Tester to cell G1

Important: In July 2021, Family Tree DNA changed the format of this file and removed the name of the tester which used to be in Column A before the Match Name. This is unfortunate, as now there is no way for Double Match Triangulator to know the name of the tester from the file itself.

As a result, you must now add the name of the tester into cell G1 to include this needed information.

Open the file with Excel, add the name of the tester into cell G1, and save the file.

Make sure you use the tester's name exactly as Family Tree DNA refers to it in other Chromosome Browser Results files. Make sure the capitalization, spaces, special characters and any punctuation is correct. The easiest way to ensure you have the tester's name correct is to find the tester in the Match Name column (column A) of someone else's Chromosome Browser Results file, and copy it into column G1 of the tester's Chromosome Browser Results file.

e.g.: If this is the name of the tester in someone else's Chromosome Browser Results file:

334	Marius Saines	1	203910220	209092631	7.594626	1460		
335	N. Smith (Proxy name 1)	1	241110180	245121226	9.231564	1128		
336	Joshua Lerner-Lew	1	12828498	18689252	11.389936	1609		

Then copy the name in cell A335 to cell G1 of that person's file and save the file:

	A	B	C	D	E	F	G	H
1	Match Name	Chromosome	Start Location	End Location	Centimorgans	Matching SNPs	N. Smith (Proxy name 1)	
2	Rn	1	203910220	209092631	7.594626	1460		

If you still have older FTDNA files (prior to July 2021), don't add the name of the tester to cell G1, because the tester's name is already there in column A.

New Files versus Old Files

You may have a mix of new Chromosome Browser Results files (July 2021 or later) or old Chromosome Browser Results files (prior to July 2021). Double Match Triangulator will allow them to be used with each other.

However, Family Tree DNA also changed their matching algorithm, so their segment matches between any two people have changed.

Also remember, if someone tested after the old file was created, they will not be in that file.

Best practice would be to use old files with old files and new files with new files if possible.

23andMe

At 23andMe, go to the bottom of your DNA Relatives page and select "Request DNA Relatives Data Download" that is shown below enclosed in a red square and pointed to by the red arrow:

The screenshot shows the 23andMe website interface. At the top, there is a navigation bar with the 23andMe logo and menu items: HOME, ANCESTRY, HEALTH & TRAITS, RESEARCH, and FAMILY & FRIENDS. Below this is a sub-menu with 'List', 'Family Tree', 'Map', and 'Frequently Asked Questions'. The main heading is 'DNA Relatives' with a sub-heading 'Get started with your predicted relationships, then connect and message to learn more.' There is a search bar and a 'Sort by' dropdown set to 'Strength of Relationship'. A list of relatives is shown, including '1st Cousin, Once Removed' and '2nd Cousin'. A blue banner at the bottom of the list says 'Help us improve this tool! Answer a survey'. A red arrow points to a blue button labeled 'Request DNA Relatives Data Download' which is enclosed in a red square. A help tooltip is visible over the button, stating: 'Download shared DNA segments and profile data for your DNA Relatives as a .csv file. The information about each relative is dependent on their personal privacy settings and sharing level. The data download can sometimes take up to 12 hours to prepare. You will receive a notification when the data download is ready.'

Despite the help button saying that it may take up to 12 hours to prepare, it likely will take at most a minute or two. You'll know it is completed when the blue request button changes to a black "Download DNA Relatives Data button":

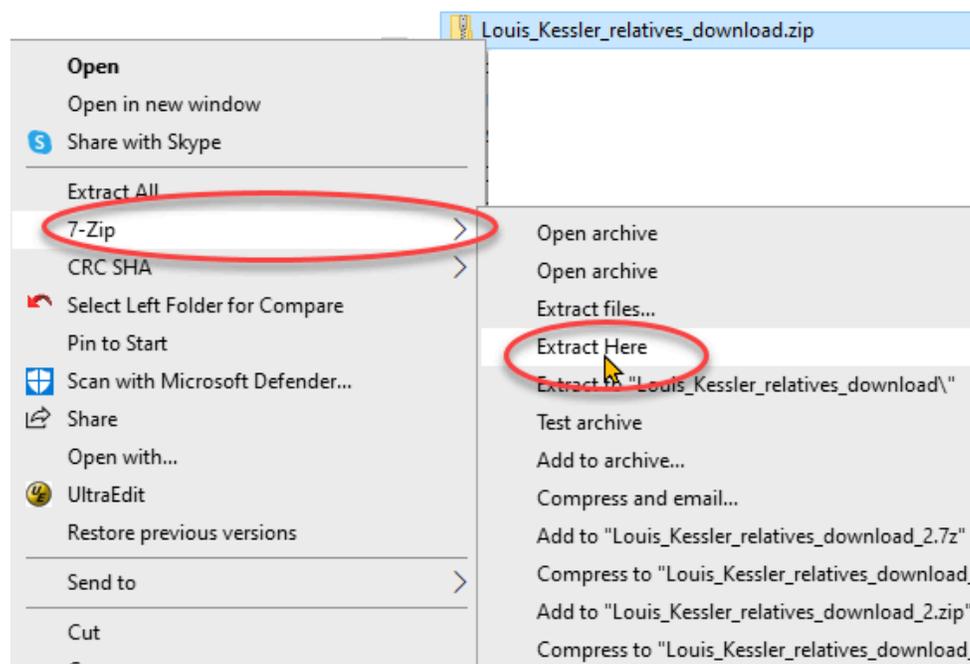
Download DNA Relatives Data

You'll also get an email telling you your file is ready, but if you've waited and it changed, then you don't need the email.

Clicking the download button will download a special file named: `nnnnnn_relatives_download.zip` where:

- `nnnnnn` is your name (with underscores instead of spaces)
- `.zip` indicates this is a compressed file

Then open Windows Explorer in the directory you saved the file, and right-click on it and use the Windows 7-Zip utility to "Extract Here" (or use another unzipping program of your choice).



You will get a file named: `nnnnnn_relatives_download.zip` which has the same file name but a `.csv` extension. `.csv` indicates this is a comma delimited file which can be read by Excel and other programs.

This `.csv` file is the file you use with DMT.

Important note: 23andMe does not include the name of the tester in the file. The `nnnnnn` in the filename is the only indication of who the tester is. DMT will use the name in the filename replacing underscores with spaces as the name of the tester. If that name is not found in other people's match files, then you won't match. If you find this happening, you will need to change the filename to match how the person is named in other people's match files.

Do not rename the `"_relatives_download"` part of the segment match file names or change their `.csv` extension. DMT looks for that to find segment match files and will not accept files not following that structure. However, you may change the filename after the word `download`. I often add the date so that I can compare with my previous download to see what new matches have been added, e.g:

`nnnnnn_relatives_download_yyyymmdd.csv`

When loaded into Excel, the file can be seen to contain all the chromosome segment matches, as well as a lot of other information in columns to the right that DMT does not use:

	A	B	C	D	E	F	G	H	I
1	Display Name	Surname	Chromosom	Chromosome Start Point	Chromosome End Point	Genetic Distance	# SNPs	Full IBD	Link to Profile Page
2			1	7775335	18387310	19.8441906	2018		https://you.23andme.com/profil
3			1	60373500	164573864	90.69423676	15480		https://you.23andme.com/profil
4			1	223469313	237852141	22.19107056	3362		https://you.23andme.com/profil
5			1	244652123	248263145	7.079162598	902		https://you.23andme.com/profil
6			2	119601872	134637112	16.75276184	2547		https://you.23andme.com/profil
7			2	215931905	238811902	37.97213745	5158		https://you.23andme.com/profil
8			3	1	6021637	15.74513245	2016		https://you.23andme.com/profil
9			3	76055157	94523335	6.401756287	2033		https://you.23andme.com/profil
10			4	102641265	170560139	61.65801239	11438		https://you.23andme.com/profil
11			5	1	5772527	14.7580452	1583		https://you.23andme.com/profil
12			5	135479348	172492449	46.37104797	7976		https://you.23andme.com/profil
13			6	117779402	137532751	19.5396347	4098		https://you.23andme.com/profil
14			8	134524839	146274708	18.63891602	2765		https://you.23andme.com/profil
15			10	1	4769379	10.15937042	1389		https://you.23andme.com/profil
16			11	19100736	34682767	20.62195778	3419		https://you.23andme.com/profil
17			11	78963697	92722761	11.18399048	3042		https://you.23andme.com/profil
18			11	123395470	133093579	19.2170105	2703		https://you.23andme.com/profil

Column A (Display Name) is the full name of the person who matches.

Column B (Surname) is the surname of the person who matches.

Column C (Chromosome Number), D (Chromosome Start Point) and E (Chromosome End Point) is the chromosome number with the start and end locations of the matching segment on that chromosome.

Columns F (Genetic Distance) and G (# SNPs) is the distance in Centimorgans (cM) and number of SNPs for the matching segment.

Columns H through AD contain additional data including: Full IBD, Link to Profile Page, Sex, Birth Year, Set Relationship, Predicted Relationship, Relative Range, Percent DNA Shared, # Segments Shared, Maternal Side, Paternal Side, Maternal Haplogroup, Paternal Haplogroup, Family Surnames, Family Locations, Maternal Grandmother Birth Country, Maternal Grandfather Birth Country, Paternal Grandmother Birth Country, Paternal Grandfather Birth Country, Notes, Sharing Status, Showing Ancestry Results, Family Tree URL. - These fields are not used by DMT.

Using DNAGedcom

You can use the DNAGedcom Client program to download other people's segment match information if they are in your match list. This is a Windows program available from <https://www.dnagedcom.com>. They charge \$5 a month to use the program.

After you download and login to the program, then you go to the Gather page and Select 23andMe. On that page, you then enter your 23andMe login information and press Login. Select your Profile. Then press "Gather Matches". Once you've done that, you'll see in the dropdown under "Choose ICW to Gather" will be a list of all your 23andMe matches. You can select any of them and then press the "Gather ICW" button.

The screenshot shows the 23andMe website interface. At the top, there is a navigation bar with the DNAged.com logo and links for Home, Gather, Autosoma, People, and Data. The 'Gather' link is highlighted. Below the navigation bar, there is a '23andMe Login' section with input fields for 'E-Mail / Username' (containing 'lkessler@lkessler.com') and 'Password' (masked with dots), and a 'LOGIN' button. A 'Remember Me' checkbox is also present. Below the login section, there is a green message: 'Finished Gathering Shares.' Underneath, there is a 'Profile:' dropdown menu showing 'Louis Kessler' and a 'Gather Matches' button. At the bottom, there is a 'Choose ICW to Gather' section with a dropdown menu showing options: 'Gather Matches that Overlap each other', 'Gather ALL Matches', and 'Louis Kessler'. There are 'Gather ICW' and 'Cancel' buttons. A mouse cursor is pointing at the 'Gather ALL Matches' option in the dropdown menu.

Although they are calling this ICW (In Common With), you are actually getting all the individual segment matches with the people you match to, which is exactly what DMT uses.

This will download a file named: nnnnnn_23andMe_FIA.csv, where:

nnnnnn is your match's name

.csv indicates this is a comma delimited file which can be read by Excel and other programs.

The file will be put in the folder where your DNAGedcom database is located. (In DNAGedcom, the DB Folder is set in Home->Settings)

Do not rename the "23andMe_FIA" part of the segment match file names or change their ".csv" extension. DMT looks for that to find DNAGedcom-produced segment match files for 23andMe and will not accept files not following that structure. However, you may change the filename after the word FIA. I often add the date so that I can compare with my previous download to see what new matches have been added, e.g:

nnnnnn_23andMe_FIA_yyyymmdd.csv

When loaded into Excel, the file can be seen to contain all the chromosome segment matches, as well as information in columns to the right that DMT does not use:

	A	B	C	D	E	F	G	H	I	J
1	Person1	Person2	Chromosc	StartPoint	EndPoint	GeneticDistance	SNPs	ShareID1	ShareID2	
2			1	101315934	107918319	6.044433594	1099	b	10	
3			1	107648423	111736672	6.307281494	887	b	10	
4			1	108018847	111959983	5.671264648	898	b	10	
5			1	108018847	112240694	6.117869854	989	b	10	
6			1	108018847	114773981	9.173609734	1541	b	10	
7			1	108018847	115798513	9.977127075	1717	b	10	
8			1	108021506	111546531	5.106414795	780	b	10	
9			1	108021506	111960807	5.662139893	896	b	10	
10			1	108021506	116776787	11.29893494	1928	b	10	
11			1	108037997	116764781	11.28501892	1915	b	10	
12			1	108355778	112032347	5.401794434	801	b	10	
13			1	108527281	114079822	7.677154541	1227	b	10	
14			1	108711268	114447034	7.558898926	1211	b	10	
15			1	109161046	116828702	10.87454033	1719	b	10	
16			1	109513497	116776787	9.858539581	1614	b	10	
17			1	111202710	116707890	6.408910864	1222	b	10	

Column A (Person 1) is the full name of the DNA Tester.

Column B (Person 2) is the full name of the person who matches.

Column C (Chromosome), D (StartPoint) and E (EndPoint) is the chromosome number with the start and end locations of the matching segment on that chromosome.

Columns F (GeneticDistance) and G (SNPs) is the distance in Centimorgans (cM) and number of SNPs for the matching segment.

Columns H and I are the 23andMe ID numbers of Person 1 and Person 2.

Note that this file does include the DNA Tester's name in the first column.

DMT accepts both the 23andMe relatives download file and the DNAGedcom 23andMe FIA file as valid 23andMe segment match files.

DMT does not accept the DNAGedcom Overlap_23andMe_FIA file from their "Gather Matches that Overlap each other" dropdown option, nor does it accept the Combined_23andMe_FIA file from their "Gather ALL Matches" dropdown option.

DNAGedcom selects many of the same set of people for the segment matches that 23andMe selects, but there are some people each include that the other doesn't. You can compare DNAGedcom FIA files with 23andMe relative_download files, but you'll get more people common if you just compare FIA with FIA or 23andMe with 23andMe than if you mix them.

MyHeritage DNA

At MyHeritage DNA, go to the DNA Matches page. Select the 3 vertical dots on the right and you'll get a dropdown. From that select "Export shared DNA segment info for all DNA Matches".

The screenshot shows the MyHeritage DNA interface. At the top, the user is identified as Louis Kessler. The main navigation includes Overview, Ethnicity Estimate, DNA Matches (selected), and DNA Tools. A dropdown menu is open on the right side, showing options: 'Export entire DNA Matches list', 'Export shared DNA segment info for all DNA Matches' (highlighted with a red circle and a mouse cursor), and 'What are DNA Matches?'. The background shows a match card for an 'Uncle' with details on estimated relationship, DNA match quality (28.1% shared DNA), and shared segments (52).

You will be emailed a file with your segment matches named: nnnnnn DNA Matches shared segments dddddd-MH-xxxxxx.zip

where:

nnnnnn is your name

dddddd is the date,

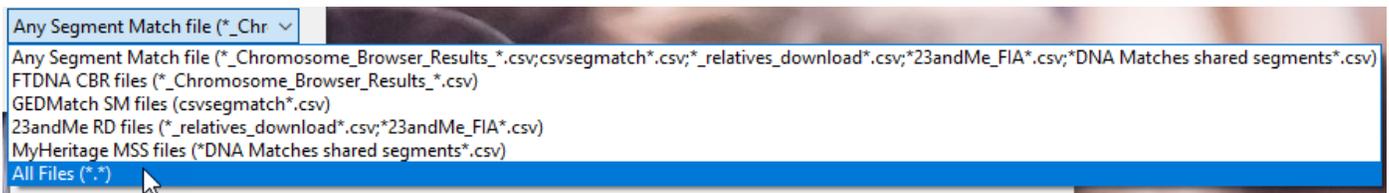
xxxxxx are some hexadecimal numbers, and

.zip indicates this is a compressed file which needs to be unzipped

Note: People in non-English countries or using a non-English version of Windows may have a different filename with words translated.

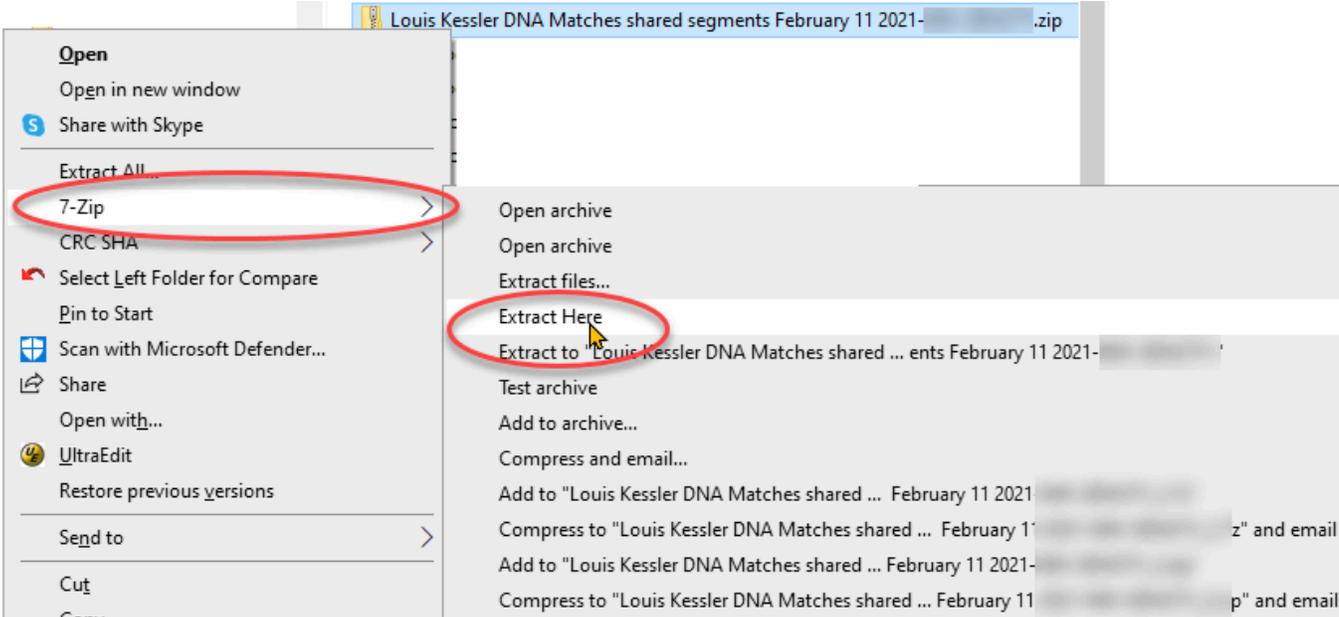
e.g. Hungarian: nnnnnn DNS-egyezés lista 2019. január 2.-MH-xxxxxx.zip

When Selecting a MyHeritage File in DMT, the dialog box will only display MyHeritage Matches Shared Segment files in English. To find MyHeritage MSS files that have non-English names, either select "All Files(*.*)" in the dropdown of the Select box, or enter *.* into the File Name field.



Save that file.

Then open Windows Explorer in the directory you saved the file, and right-click on it and use the Windows 7-Zip utility to "Extract Here" (or use another unzipping program of your choice).



The file will be expanded and you will get a file with the same name but with a .csv extension on the end. .csv indicates this is a comma delimited file which can be read by Excel and other programs.

You can rename the file, but ensure that there is a "DN" somewhere in the filename and don't change the ".csv" extension. DMT looks for that to find segment match files and will not accept files with filenames not following that format.

When loaded into Excel, the file can be seen to contain all the chromosome segment matches, as well as a some other information:

	A	B	C	D	E	F	G	H	I	J	K
1	DNA Match ID	Name	Match name	Chromosome	Start Location	End Location	Start RSID	End RSID	Centimorgans	SNPs	
45		Louis Kessler		17	1389	32332830	rs62053747	rs8081899	53.1	16640	
46		Louis Kessler		17	73110279	81151539	rs1531564	rs35284141	20	5503	
47		Louis Kessler		18	5229653	56778826	rs9959662	rs77692916	62.3	26368	
48		Louis Kessler		19	247265	44161618	rs143370410	rs4251944	69.1	21632	
49		Louis Kessler		19	52228759	59097933	rs3794977	rs117625253	20	5247	
50		Louis Kessler		20	49709468	62960292	rs8122541	rs11698187	33.6	9727	
51		Louis Kessler		21	18457656	48100155	rs73200830	rs10483083	52.9	19199	
52		Louis Kessler		22	22710758	37619021	rs17578409	rs9610672	28.1	9600	
53		Louis Kessler		22	44817955	51214796	rs135957	rs190639024	19.1	5631	
54											
55		Louis Kessler		3	124642835	179368498	rs9859266	rs9860298	54.3	26496	
56		Louis Kessler		7	153216346	155693442	rs4626512	rs12533675	8.7	1920	
57		Louis Kessler		11	70655927	77680235	rs76079118	rs145922587	6.1	3200	
58		Louis Kessler		13	26767833	30667136	rs117949812	rs35221920	7.8	2560	
59		Louis Kessler		13	105585505	108115473	rs1409462	rs149108835	7	1920	
60		Louis Kessler		15	67433946	71778812	rs79738232	rs80278457	6.4	2432	
61		Louis Kessler		16	82473366	85959438	rs34522318	rs880366	13.6	3968	
62		Louis Kessler		19	3586543	6402648	rs8113232	rs6510896	7	1664	
63		Louis Kessler		20	31240778	53183424	rs116951392	rs7268501	30.5	12288	
64											
65		Louis Kessler		1	13176463	17296882	rs28488227	rs41303881	8.3	2176	
66		Louis Kessler		3	76917552	100085556	rs7433861	rs277641	7.7	7040	
67		Louis Kessler		4	82644011	91775468	rs13132246	rs17248761	9.6	4352	
68		Louis Kessler		6	41497096	44572155	rs114832539	rs1283946	6.7	1920	
69		Louis Kessler		7	79295257	88736883	rs12535032	rs4728798	8.2	4736	
70		Louis Kessler		7	155360511	158170263	rs11772335	rs117975324	6.6	2048	

Column A (DNA Match ID) contains a string containing the ID of the tester and the ID of his match.

Column B (Name) is the name of the tester.

Column C (Match name) is the name of the person who matches.

Column D (Chromosome), E (Start Location) and F (End Location) is the chromosome number with the start and end locations of the matching segment on that chromosome.

Columns G (Start RSID) and H (End RSID) are the Reference SNP identification (i.e. the names for) the starting and ending SNPs. DMT does not use these.

Columns I (Centimorgans) and J (SNPs) is the distance in Centimorgans (cM) and number of SNPs for the matching segment.

Note: People in non-English countries or using a non-English version of Windows may have a different header line (Line 1):

e.g. Hungarian: "DNS-egyezési azonosító",Név,"Az egyezés neve",Kromoszóma,Startpozíció,Végpozíció,"RSID kezdet","RSID vége",Centimorgan,SNP-k

Also Note: MyHeritage's DNA Matches List file has a similar name to the DNA Matches Shared Segment file. If you download a Matches List file to the same directory as your segment matches files and pick a Matches List file in DMT by mistake, DMT will show the message **** MH Not Shared Segm** to warn you that this is not a Shared Segment file.

GEDmatch

Note: GEDmatch has two interfaces: "New" and "Classic". It does not matter which one you use. They both have the same functionality. They just look a bit different. The documentation below is for the "Classic" interface.

At GEDmatch, you need to pay for Tier 1 services to get access to a report to display your match data. Tier 1 services currently cost \$10 to \$15 a month with a minimum one-month signup.

With Tier 1 services enabled, click on Tier 1 -> Segment Search. Enter your Kit Number. All the defaults should be okay. You will want to increase the number of closest matches from 1000 to 10000 to get as many of your segment matches as can. Then press the Submit button. It could take anywhere from a few minutes to an hour for the report to run, depending on the server load at GEDmatch at the time.

GEDmatch[®] DNA Segment Search

This utility allows you to find other kits with matching chromosome segments. (Note that matches closer than 2100 cm's are skipped to save resources.)

Kit Number:

Max number of closest matches to consider: Max Kits

Build to Display (Choose just one): B36 B37 B38

SNP count minimum threshold to be considered a matching segment
(Leave blank for dynamically-calculated value (200 - 400))

Minimum segment cM size to be included in total:
(Leave blank for default value = 7)

Prevent Hard Breaks (default is to create hard breaks when
distance between SNP's exceeds 500,000 base positions):

Chromosome to scan (or all)

Optional segment start to match:
(Only use if a specific chromosome is specified)

Optional segment end to match:
(Only use if a specific chromosome is specified)

Show graphic bar for Chromosome? Yes No

Once the report completes, you will get something looking like this:

GEDmatch[®] Matching Segment Search - V1.0

Software Version Jan 13 2021 10:18:21
Kit: [redacted] (Louis Kessler) [6 Companies Combined]

Minimum segment threshold size to be included in total = SNPs
Minimum segment cM to be included in total = 7 cM
To conserve system resources, matches closer than 2100 cM will not be shown.
Comparison Finished (10000 kits)

Submit selected items to Multi-Kit-Analysis
 Multi-Kit-Analysis Select 2 or more from column

Click [HERE](#) to download segment match csv data to a comma-separated CSV file.

Kit	✓	Chr	B37 Start Posn	B37 End Posn	cM	SNPs	Name	Sex	Email
Chromosome 1									
[redacted]	<input type="checkbox"/>	1	752721	5042941	13.1	986	[redacted]	M	[redacted]
[redacted]	<input type="checkbox"/>	1	752721	4973107	13	1131	[redacted]	F	[redacted]
[redacted]	<input type="checkbox"/>	1	752721	4723046	12.4	865	[redacted]	F	[redacted]
[redacted]	<input type="checkbox"/>	1	752721	4384773	11.4	977	[redacted]	F	[redacted]
[redacted]	<input type="checkbox"/>	1	752721	4208542	10.9	801	[redacted]	F	[redacted]
[redacted]	<input type="checkbox"/>	1	752721	4120311	10.7	872	[redacted]	M	[redacted]
[redacted]	<input type="checkbox"/>	1	752721	4120311	10.7	719	[redacted]	F	[redacted]
[redacted]	<input type="checkbox"/>	1	752721	4113096	10.7	864	[redacted]	F	[redacted]
[redacted]	<input type="checkbox"/>	1	752721	4061608	10.5	849	[redacted]	M	[redacted]

Click on the "HERE" to download the segment match file, named: csvsegmatch_.csv
where:
.csv indicates this is a comma delimited file which can be read by Excel and other programs.

The file always downloads as csvsegmatch_.csv, so if you download the file for a different person, it may overwrite the earlier download. So you should rename the file. DMT uses the "csvsegmatch" text at the beginning of the filename to identify GEDmatch segment match files, so don't change that. I like to put in the person's name and GEDmatch ID number between the "csvsegmatch_" and the ".csv", e.g.:
csvsegmatch_Louis_Kessler_A123456.csv

The output files that DMT creates will include whatever you added after the "csvsegmatch" as part of their filename.

When loaded into Excel, the file has the segment matches, as well some additional information not used by DMT:

	A	B	C	D	E	F	G	H	I	J
1	PrimaryKit	MatchedKit	chr	B37Start	B37End	Segment cM	SNPs	MatchedName	Matched Sex	MatchedEmail
2			1	752721	5042941	13.1	986		M	
3			1	752721	4973107	13	1131		F	
4			1	752721	4723046	12.4	865		F	
5			1	752721	4384773	11.4	977		F	
6			1	752721	4208542	10.9	801		F	
7			1	752721	4120311	10.7	872		M	
8			1	752721	4120311	10.7	719		F	
9			1	752721	4113096	10.7	864		F	
10			1	752721	4061608	10.5	849		M	
11			1	752721	4057488	10.5	741		M	
12			1	752721	4057488	10.5	661		F	
13			1	752721	4037665	10.5	656		F	
14			1	752721	4037665	10.5	657		F	
15			1	752721	4010743	10.4	827		M	
16			1	752721	4009793	10.4	685		F	
17			1	752721	4002958	10.4	688		M	
18			1	752721	3787379	9.7	780		F	
19			1	752721	3769760	9.6	615		F	
20			1	752721	3613067	9.2	579		M	
21			1	752721	3513067	9.2	578		F	

Column A (PrimaryKit) is the kit number of the tester, which defines the tester uniquely

Column B (MatchedKit) is the kit number of the person matching, which defines the match uniquely

Column C (chr), D (B37start) and E (B37end) is the chromosome number with the start and end locations of the matching segment on that chromosome.

Columns F (segment cM) and G (SNPs) is the distance in Centimorgans (cM) and number of SNPs for the matching segment.

Column H is the name of the person matching.

Columns I and J are the sex and email of the person matching, which are not used by DMT.

Note: In November 2020, GEDmatch changed the format of their csvsegmatch file and it no longer includes the name of the primary kit owner. DMT now warns you about this in the log file with the message:

** Person A's name is not available in Person A's segment match file. DMT will look for it when other match files are processed.

Then in that same run, DMT waits until it processes a File B that contains Person A, and will then inform you in the log file with the message: "File B contains Person A's name: nnnnnnn"

GEDmatch[®]

Matching Segment Search - V1.0

Software Version Jan 13 2021 10:18:21

Kit: [REDACTED] (Louis Kessler) [6 Companies Combined]

Minimum segment threshold size to be included in total = SNPs

Minimum segment cM to be included in total = / cM

To conserve system resources, matches closer than 2100 cM will not be shown.

Comparison Finished (10000 kits)

The GEDmatch Segment Search screenshot above the statement: "To conserve system resources, matches closer than 2100 cM will not be shown." This is unfortunate. Your match file from GEDmatch will not include parents, children, siblings, and it's possible that a few of your aunts, uncles, nephews, nieces, grandparents, grandchildren or half siblings could be left out of it.

For every segment match file you download, you should run the "GEDmatch One-to-many Comparison Result" to see who you have as matches above 2100 cM:



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When you contact a potential match, you should include in your email your kit number and the kit number you think you match with. Many people manage multiple kits, and they have no other way of confirming the match you think you have.

It is generally considered to be bad form to send out emails to large numbers of names on your results list, without first reviewing those results in some detail. This falls into the category of 'Spam' email.

'Overlap' is the number of positions that exist in common between both kits, without regard to whether they match or not. The amount of overlap, along with the largest cM amount, is usually a good indication of the relative quality of the match.

Matches with low overlap have that field highlighted with a pink or red background, depending on the overlap value. Matches with very low overlap are not shown.

[Here](#) is a link to a useful YouTube video on how to use One To Many.

Kit: [redacted] (Louis Kessler) [6 Companies Combined]

For [Visualization Options] select 3 or more from column '✓'

Kit	✓ 1:1	Name	Email	Largest Seg	Total cM	Gen	Overlap	Date Compared	Testing Company
[redacted]	<input type="checkbox"/>	[redacted]	[redacted]	81.4	1917.8	1.5	319176	2019-06-13	Migration - F2 - T
[redacted]	<input type="checkbox"/>	[redacted]	[redacted]	86.4	958.4	2.0	245178	2020-03-28	Ancestry
[redacted]	<input type="checkbox"/>	[redacted]	[redacted]	50.8	432.9	1.5	203043	2019-06-13	Migration - F2 - A
[redacted]	<input type="checkbox"/>	[redacted]	[redacted]	22.5	93.8	3.6	235815	2019-06-13	Migration - V4 - M
[redacted]	<input type="checkbox"/>	[redacted]	[redacted]	22.5	92.0	3.6	311420	2019-06-13	Migration - F2 - T
[redacted]	<input type="checkbox"/>	[redacted]	[redacted]	17.8	86.7	3.7	313779	2019-06-13	Migration - F2 - F
[redacted]	<input type="checkbox"/>	[redacted]	[redacted]	15.8	86.6	3.7	243700	2019-06-13	23andMe
[redacted]	<input type="checkbox"/>	[redacted]	[redacted]	20.4	84.4	3.7	305164	2020-03-20	FTDNA
[redacted]	<input type="checkbox"/>	[redacted]	[redacted]	26.8	84.1	3.7	314596	2019-06-13	FTDNA
[redacted]	<input type="checkbox"/>	[redacted]	[redacted]	16.9	83.8	3.7	317865	2020-05-05	23andMe
[redacted]	<input type="checkbox"/>	[redacted]	[redacted]	12.7	80.3	3.7	309408	2019-06-13	AncestryDNA V1
[redacted]	<input type="checkbox"/>	[redacted]	[redacted]	12.7	80.3	3.7	305241	2019-06-13	Migration - F2 - A

The report will be sorted by highest Total cM. Look for any people with more than 2100 Total cM. My report above doesn't have any. But let's say the first two were over 2100.

For each person over the 2100, You'll need to run two reports:

1. One-to-One Autosomal DNA Comparison, and
2. One-to-One X-DNA Comparison

Enter the Kit number of the tester as Kit Number 1, and the Kit Number of the person the tester matches as Kit Number 2.

Leave the default values for everything else.

The resulting report should look something like this:

GEDmatch® Autosomal One-to-One Comparison

Software Version Oct 6 2022 01 43 10

[Here](#) is a link to a useful YouTube video on using the One to One DNA comparison tool.

Individual marker indications:

Base Pairs with Full Match	
Base Pairs with Half Match	
Match with Phased data	
Base Pairs with No Match	

Validity of segments:

SNP Density 0 to 0.5. Darker blue means higher density.	
Large gap between adjacent SNPs	
No Match	

Comparing Kit [redacted] (Louis Kessler) [6 Companies Combined] and [redacted] [Migration - F2 - T]

Segment threshold size will be adjusted dynamically with an average of 200 SNPs. About 2/3 will occur between 185 and 214 SNPs.

Minimum segment cM to be included in total = 7.0 cM

Mismatch-bunching Limit will be adjusted to 60 percent of the segment threshold size for any given segment.

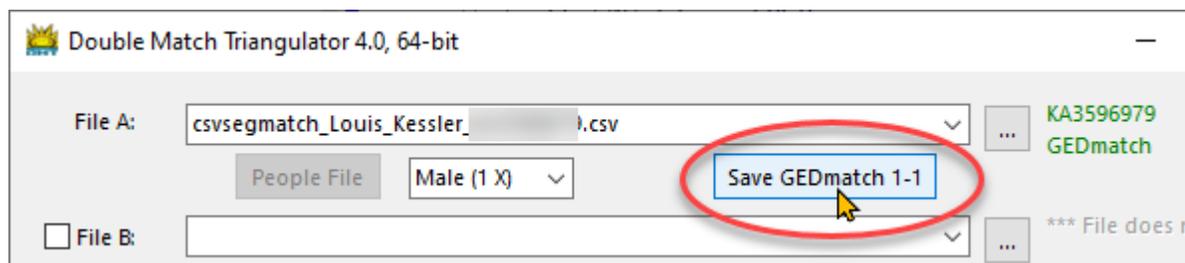
Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs	Segment threshold	Bunch limit	SNP Density Ratio
1	752,566	13,176,463	29.1	3,196	211	126	0.44
1	18,461,490	61,264,038	51.4	9,543	211	126	0.48
1	86,939,130	120,526,982	32.8	7,687	224	134	0.48
1	149,815,536	201,125,326	52.5	11,005	205	123	0.47
1	206,293,116	222,519,003	18.9	3,929	217	130	0.46
1	241,000,790	245,655,241	12.9	1,275	187	112	0.45

Chr 1



Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs	Segment threshold	Bunch limit	SNP Density Ratio
2	18,674	8,776,102	19.7	2,582	190	114	0.46

Unfortunately GEDmatch does not have a link to let you download the output from these programs. So there is a button in DMT to let you save the data:



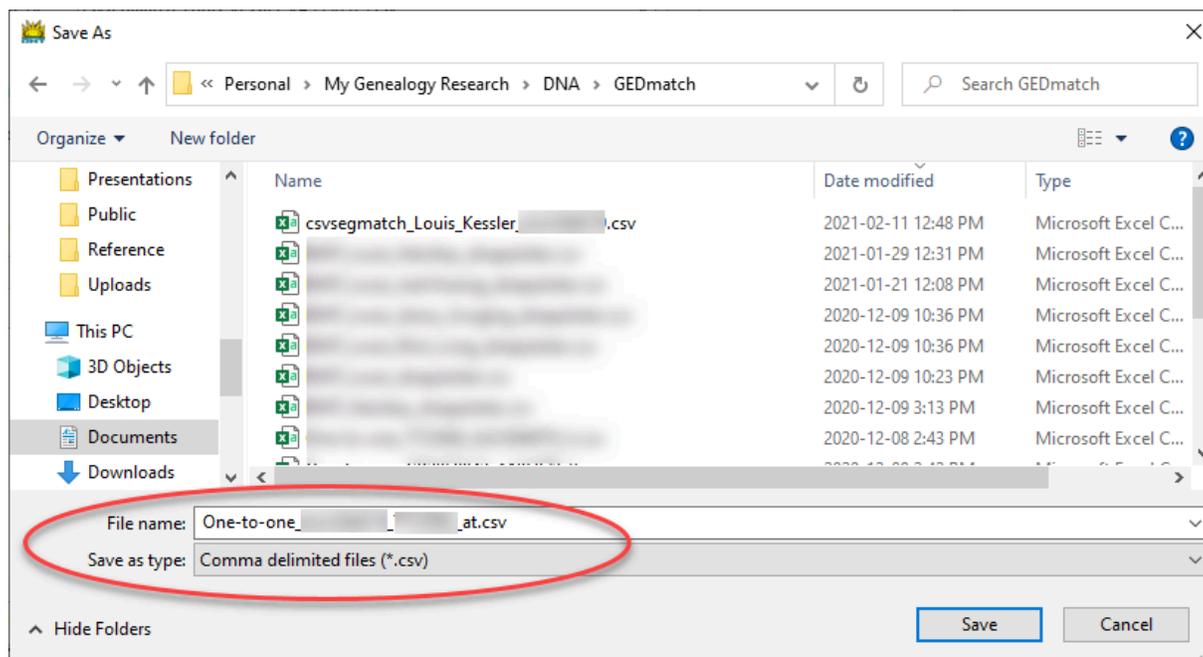
Run each of the two GEDmatch reports for every person over 2100 cM. After each run, use your web browser to select everything from the GEDmatch page and copy it to the clipboard. Depending on your web browser, you can do this one of 3 ways:

1. From the menu: Edit->Select all,
2. With your mouse right-click and pick "Select all", or
3. With the keyboard type Ctrl+A (i.e. while holding down the Ctrl key, type "A").

Then copy the selection to the clipboard one of these 3 ways:

1. From the menu: Edit->Copy,
2. With your mouse right-click and pick "Copy", or
3. With the keyboard type Ctrl+C (i.e. while holding down the Ctrl key, type "C").

Then go to DMT and click on the "Save GEDmatch 1-1" button. If the One-to-one data has been properly copied to the clipboard, you should see the following dialog so that you can save that data as a file:



DMT will assign the filename for you as: One-to-one_aaaaaa_bbbbbbb_ss.csv

where:

aaaaaa is the kit number of the first kit in the One-to-one

bbbbbbb is the kit number of the second kit in the One-to-one

_ss indicates whether this was the Autosomal comparison (at) or if it was the X-DNA comparison (X)

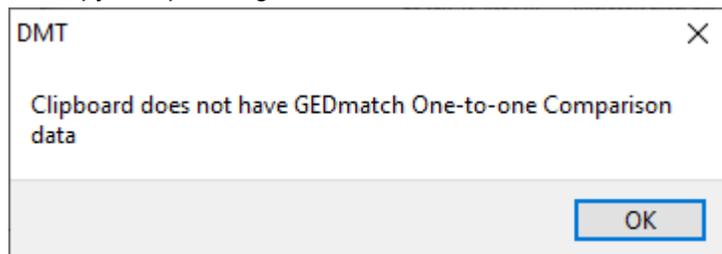
.csv indicates this is a comma delimited file which can be read by Excel and other programs.

The best place to save this file is to same folder where your segment match file for person with kit aaaaaa is.

You don't have to download the file if the reverse file for bbbbbbb as the first kit and aaaaaa as the second kit is already in the folder. For person with kit aaaaaa, DMT will first include all the One-to-one's with aaaaaa in the first position, and then will add any others with aaaaaa in the second position. It will use the first one it finds.

You also don't have to download the X file if you have no X matches with the person.

If the clipboard does not contain One-to-one data, then you'll get the following message. If you get this message, try the copy and paste again:



DMT will also look for any and all GEDmatch one-to-one files that are in:

1. The folder containing File A
2. If "File B" is selected, then the folder containing File B
3. if "Folder B" is selected, then Folder B and if "include subfolders" is selected, then additionally all subfolders of Folder B.

You can use a One-to-one file to add any match whether they share more than 2100 cM or not.

If the person is already in the segment match file, they will not be included a second time.

File B segment match files will only include the One-to-one file if the person is in File A or was added to File A by a One-to-one file.

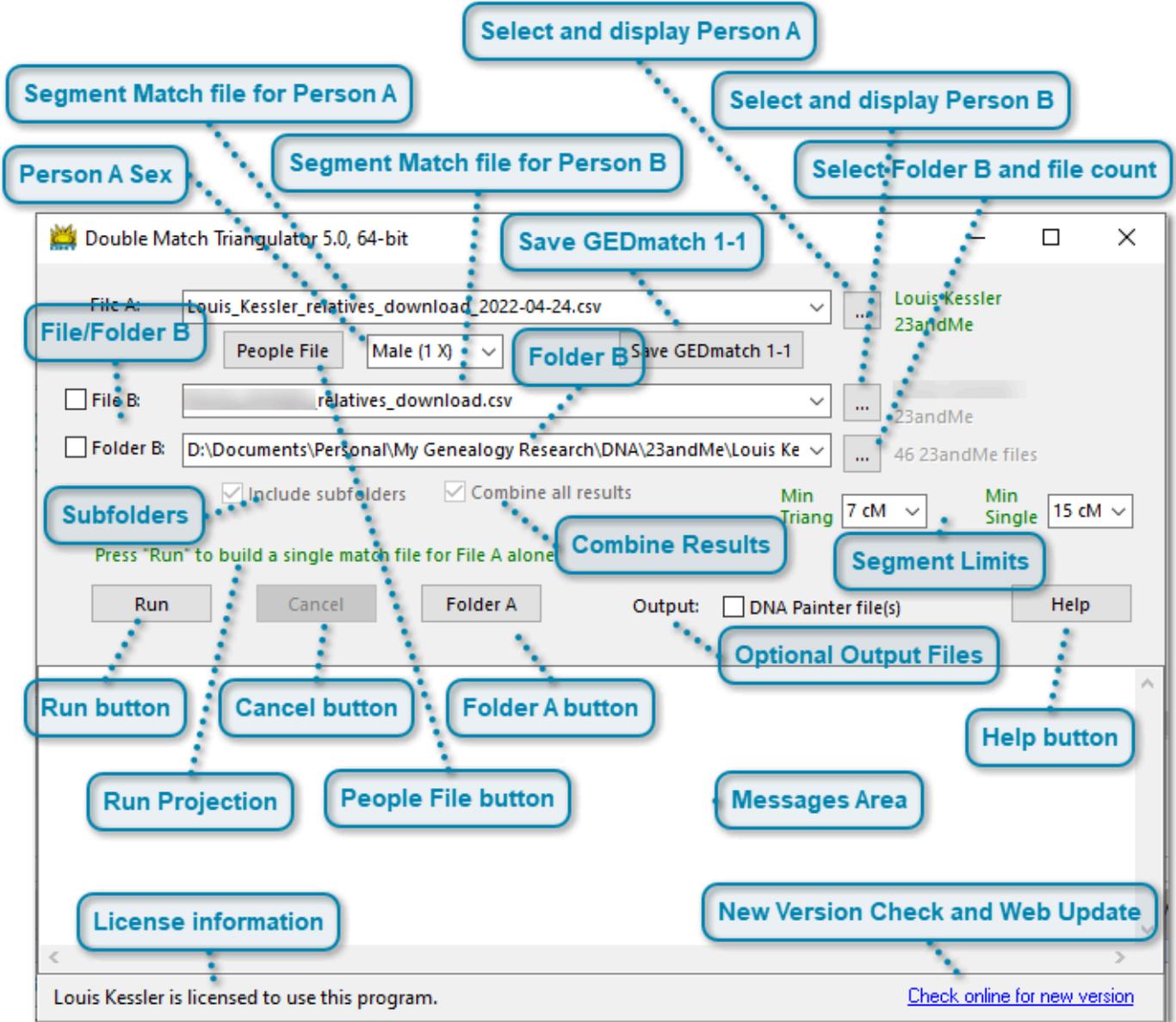
The log file created for the run will indicate which One-to-one files were included with each segment match file.

How to Use Double Match Triangulator

Follow through the pages in this section.

First, you'll familiarize yourself with the Double Match Triangulator Main Window.

Getting Started with DMT, DMT's Main Window



Getting Started with Double Match Triangulator:

DMT has a single window that performs all its functionality. Messages are written on the window itself. Green text is good. Red text is not good.

When you press the Run button, the Messages Area will show you the status of the run and tell you when the run is complete

Segment Match file for Person A

Louis_Kessler_relatives_download_2022-04-24.csv

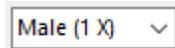
The segment match file for Person A is shown here. There is a dropdown at the right that allows fast selection of previously used files. Person A is normally the person you are interested in, often yourself, or someone whose ancestors you want to find.

Select and display Person A



Pressing the  button will bring up a file dialog that allows you to select the Person A file. When a Person A file is selected, the first few lines of the file are read and the name of Person A and the DNA company is obtained and displayed here to make it easy for you to verify that it is the correct file. **The name is shown in green if this is a valid segment match file. A message is shown in red if this is not a valid segment match file.**

Person A Sex



You can select Male (1 X) or Female (2 X). If you select Male, then DMT will display one X chromosome, otherwise it will display 2 X chromosomes. The Male/Female designation is stored in the People file.

Segment Match file for Person B



The segment match file for Person B is shown here. There is a dropdown at the right that allows fast selection of previously used files. Person B people is the person whose matches will be compared to Person A when you select the File B check box.

Select and display Person B



Pressing the  button will bring up a file dialog that allows you to select the Person B file. When a Person B file is selected, the first few lines of the file are read and the name of Person B and the DNA company is obtained and displayed here to make it easy for you to verify that it is the correct file. **The name is shown in green if File B is selected and this file is valid and will be used in the DMT run. If the file is not a valid segment match file, a message in red will be shown.** This is shown in grey if File B is not selected.

Save GEDmatch 1-1



The Tier 1 Matching Segment Search results at GEDmatch do not include matches with close relatives who share 2100 cM or more. So the segment match files from GEDmatch will not include parents, children, siblings, and some aunts, uncles, nephews, nieces, grandparents, grandchildren or half siblings could be left out of it. To obtain them, you'll have to run a One-to-one report at GEDmatch. Once you do, you copy the resulting report to your clipboard and then press this "Save GEDmatch 1-1" button and DMT will create a One-to-one file that it will use to include with the segment matches. For full instructions on obtaining and downloading the GEDmatch 1-1 files, see: [Downloading Segment Match Data: GEDmatch](#).

File/Folder B

File B:

Folder B:

There are actually 3 choices here:

1. Check only File B to use the Person B selection and to compare Person A with just Person B.
2. Check only Folder B to use every segment match file that is in Folder B and compare Person A with all the people represented by the segment match files in Folder B.
3. Leave both File B and Folder B unchecked. This will run File A alone in order to obtain just the single matches or to initially create the People file.

Folder B

D:\Documents\Personal\My Genealogy Research\DNA\23andMe\Louis Ke ▾

The folder containing the segment match files to be matched with Person A is shown here. There is a dropdown at the right that allows fast selection of previously used folders.

Select Folder B and file count

... 46 23andMe files

Displays the number of segment match files in Folder B (and subfolders if that is selected). This is shown in green if Folder B is selected and the files in this folder (and subfolders if selected) will be used in the DMT run. This is shown in red if there are no segment match files in the folder. This is shown in grey if Folder B is not selected.

Subfolders

Include subfolders

If checked, then the files in Folder B and all its subfolders will be used and the count of files will include the subfolders. If not checked, then only files in Folder B will be used.

Combine Results

Combine all results

If Folder B is selected and this box is unchecked, then a DMT Excel file will be created for Person A run individually against each Person B in Folder B (and optionally the subfolders).

If Folder B is selected and this box is checked, then the results of Person A with each Person B in Folder B (and optionally the subfolders) are combined together. Since the combined file could become very large, there is one DMT file produced for each of 23 chromosomes and a separate People file.

Segment Limits

Min Triang 7 cM ▾ Min Single 15 cM ▾

These are two important settings.

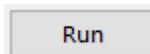
1. **Min Triang** is the smallest triangulating or double matching segment that will be included in the analysis. This is to exclude by chance matches that can occur for small segments in triangulations. The default is 7 cM and you'll see that the dropdown contains lines on either side of the 7 cM selection to remind you that it is the

suggested value. "Min Triang" will be shown in green if you selected 7 cM or more. It will be shown in grey if 5 cM or 6 cM is selected. It will be shown in red if 4 cM or less is selected, but DMT will still run.

2. **Min Single** is the smallest single matching segment that will be assumed to be valid. This is to exclude by chance matches that can occur for small segments in single matches. Non-triangulating A-C matches that are smaller than this value will still be included in the results, but will be placed in an "X" (eXcluded) section and given the status "Small AC" or "Small Inferred". The default is 15 cM and you'll see that the dropdown contains lines on either side of the 15 cM selection to remind you that it is the suggested value. "Min Single" will be shown in green if you selected 15 cM or more. It will be shown in grey if 10 cM or 12 cM is selected, where up to 40% of your matches might be by-chance. It will be shown in red if 8 cM or less is selected, but DMT will still run. Many to most of your small matches might be by-chance.

DMT will not allow you to enter a value of Min Triang that is larger than Min Single.

Run button



Press this button to run File A against File B or the Folder B files and build the resulting DMT Excel files.

Cancel button



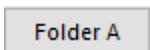
This will cancel the building of the DMT Excel files after the current DMT Excel file that is being worked on is completed.

Run Projection

Press "Run" to build a single match file for File A alone.

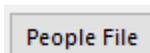
Displays a message stating the number of Double Match Triangulator (DMT) Excel files that will be created when the run button is pressed. When File B is selected, then only the one DMT Excel file will be produced. When Folder B is selected, then multiple DMT Excel files will be produced as specified. The number is shown in green if the Run will result in at least 1 DMT Excel file, A message will be shown in red if the A and B selections will not result in any DMT Excel files. Person A's file will not be run against itself so its segment match file will not be included in the count.

Folder A button



All the DMT Excel files produced for a run, as well as the log file for the run and the People file, are put in Folder A, the folder where Person A's segment match file is. Press this button to open a Windows Explorer window to the folder so you can then view the files produced. This button is very convenient to get you to your data. I use it all the time.

People File button



Press this button to open the People File for Person A in Excel. This button is very convenient to allow you to open your People file to add or modify your MRCAs. I use it all the time.

Optional Output Files

Output: DNA Painter file(s)

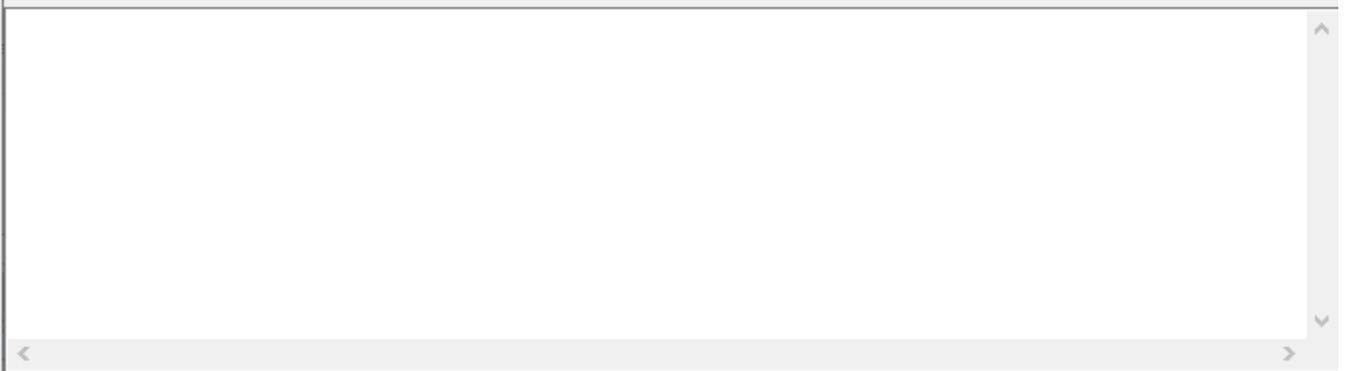
Select the DNA Painter file(s) box to have a DNA Painter file produced. See [DNA Painter File](#) for more information about this file.

Help button

Help

This button will open the DMT Help file.

Messages Area



This is where runtime messages are displayed so that you can monitor the progress of your DMT runs. Most of these messages are also included in the log file that is produced. See [Log File](#) for more detail about the messages.

License information

Louis Kessler is licensed to use this program.

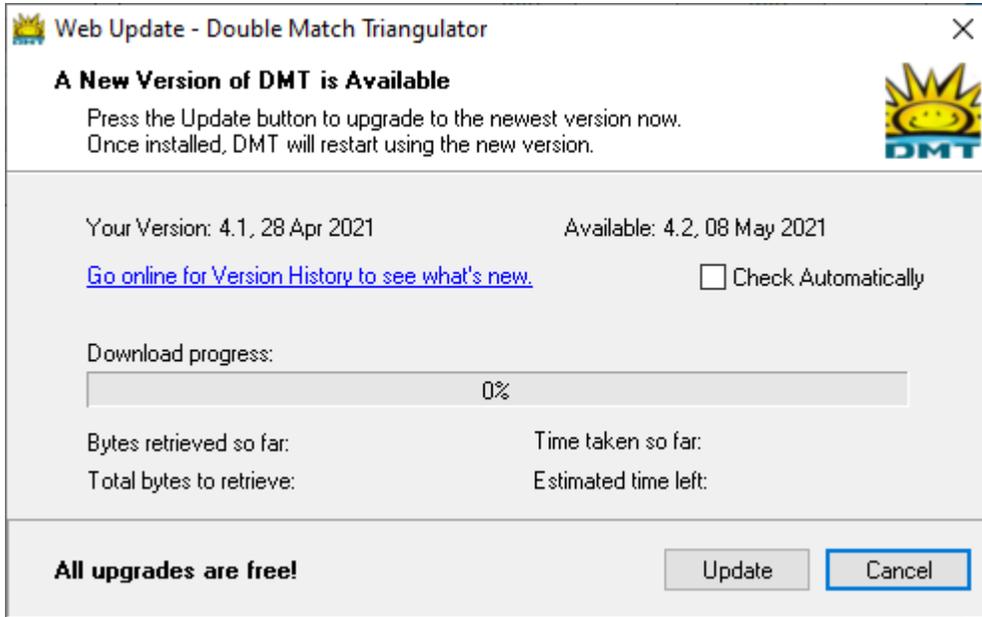
This area shows who purchased the license to be the user of this program. If the program is not licensed, then a registration area appears instead, allowing you to enter your license information.

New Version Check and Web Update

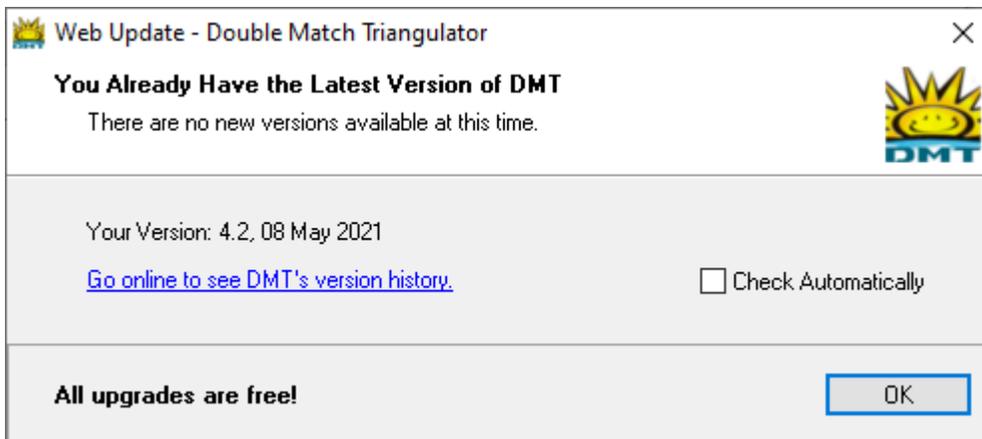
[Check online for new version](#)

Click on this link and DMT will check online if there is a new version available and will open up a new window that will tell you if there is.

If there is a new version, you will get a window like this and be able to do a quick and easy web update to install the new version.



If there is not a newer version than the one you already have, you will get a window like this:



You can check the "Check Automatically" box Check Automatically to have DMT check online for a new version each time you start the program. Doing that will display either "New Version Available" or "You Have the Latest Version" instead of "Check online for new version".

Note that to check for a new version, DMT needs to read a small file on the DMT website that has the latest version number in it. DMT will never attempt to go to the internet unless you give it permission to by either clicking the "Check online for new version" link or by checking the "Check Automatically" box. Reading the small file with the version is the only thing DMT will do. It will not transmit or receive any other information other than getting the DMT installation file when you do an update.

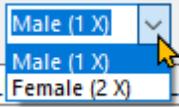
1. Set Up Your People File and MRCAs

Person A is the person whose chromosomes you want to map. Every Person A will have their own "People file".

The People file has the same filename as the Person A's segment match file, except that "_people.xlsx" is at the end of its name instead of ".csv". DMT looks for the People file in the same folder as Person A's segment match file.

If you don't have a People file for Person A yet, do the following to create or update your file:

1. Ensure your segment match file for Person A is listed in the File A box. Find it with the  button.
2. Set the selection box below the File A box to Male (1 X) or Female (2 X) to designate whether Person A should be built with one or two X chromosomes.



DMT will write your selection into cell A1 of the people file so that it will remember your selection the next time you pick this segment match file as Person A.

3. Leave both File B: and Folder B: unchecked, and press the  button.

4. When the run completes, you should see that the  button becomes activated. Press the button to open your People file.

The People File will initially look like this:

	A	B	C	D	E	F	G	H	I	J	K	L	M	
1	NAME-A (1X)	NAME-C	MRCA-C	CLUSTER	STATUS	TRISEG	INFSEG	NUMAC	TOTAC	MAXAC	XTOTAC	AC1	AC2	AC3
2	ca	vi		U	Only AC matches	0	0	22	3384.5	267.2	0	u	u	u
3	ca	S		U	Only AC matches	0	0	23	3384.3	267.2	195.9	u	u	u
4	ca	V		U	Only AC matches	0	0	51	2709.9	182.5	108.3	u: u,u,u, u: x,u,u, u: u		
5	ca	A		U	Only AC matches	0	0	54	1711	124.2	65	u: u,u,u, u: x,u	u: u	
6	ca	E		U	Only AC matches	0	0	54	1708.2	124.2	65	u: u,u,u, u: x,u	u: u	
7	ca	H		U	Only AC matches	0	0	22	483.7	77.6	0	u: x,u,u, u: u,x	u	
8	ca	A		U	Only AC matches	0	0	23	439.1	64.9	0	u	u: x,x,u,u,x	
9	ca	C		U	Only AC matches	0	0	16	307	41.9	0	u	u: x,x,u,u,x	
10	ca	Ji		U	Only AC matches	0	0	4	80.8	22.9	0			
11	ca	M		U	Only AC matches	0	0	8	79.2	16.9	0			x
12	ca			U	Only AC matches	0	0	8	69.3	15.1	0		x	x
13	ca	D		U	Only AC matches	0	0	6	67.2	15.8	0	x	u	x
14	ca	R		U	Only AC matches	0	0	5	66.5	18.9	0	u	u	
15	ca	S		U	Only AC matches	0	0	6	65.1	17.2	0		u	
16	ca	A		U	Only AC matches	0	0	6	63.8	19.7	0			
17	ca	R	ij	U	Only AC matches	0	0	5	58.7	23.8	0	x		u: x
18	ca	M		U	Only AC matches	0	0	5	57.6	18.5	0		x	u: x
19	ca	D		U	Only AC matches	0	0	5	56.4	16	0		x	
20	ca	A		U	Only AC matches	0	0	4	56.3	20.4	0	x		
21	ca	K		U	Only AC matches	0	0	5	55.1	19.9	0			u
22	ca	E		U	Only AC matches	0	0	4	54.7	17.4	0			x
23	ca	w		U	Only AC matches	0	0	6	53.2	15.7	0	x		
24	ca	C		U	Only AC matches	0	0	3	52.6	31.6	0	x		
25	ca	C		U	Only AC matches	0	0	3	52.4	29	0			
26	ca	S		U	Only AC matches	0	0	5	52.4	17.3	0		x	
27	ca	D		U	Only AC matches	0	0	4	52.2	15.4	0			u
28	ca	K		U	Only AC matches	0	0	6	52	17.8	7.6			
29	ca	E		U	Only AC matches	0	0	4	51.8	22	0			
30	ca	J		U	Only AC matches	0	0	5	51.6	18.4	0		x: x,x	
31	ca	K		U	Only AC matches	0	0	3	51.3	28.8	0			u

The NAME-C column contains all the people who match Person A, ordered by cluster in the CLUSTER column which initially is all "U" for Unknown, and then by Total cM in the TOTAC column. Also shown are the number of segments matching (TOTAC), the largest segment match (MAXAC) and the total X match (XTOTAC).

5. **What's important to do now is to fill in the MRCA-C column** that is shown above by the red box. This column contains the Most Recent Common Ancestor (MRCA) between A and C expressed from A's point of view up to the ancestor. There is a simple notation developed for you so that you can enter that information.

- Use "F" for the Father's line
- Use "M" for the Mother's line
- Use "R" to represent the pair of ancestors who are the MRCAs.

For example. If person C is person A's 2nd cousin on their Father's Mother's side, then the MRCA should be entered as: **FMR**

Here's some guidelines and you'll get the hang of it quick:

R - use for all descendants of Person A's parents. This includes Person A's children, grandchildren, siblings, nieces, nephews, great-nieces, etc.

FR - use for all descendants of Person A's father's parents. This includes Person A's father, aunts, uncles, 1st cousins, descendants of 1st cousins, etc.

MR - same as FR but on Person A's mother's side.

FFR - use for all descendants of Person A's father's father's parents. This includes Person A's grandfather, great-uncles/aunts, 2nd cousins, descendants of 2nd cousins, etc.

FMR, MFR, MMR - Same as for FFR except for father's mother's parents, mother's father's parents, and mother's mother's parents.

FMMMFFFFMMFMR - You can extend this to any level if you know your ancestry back that far.

But remember, we want the "Most Recent" common ancestral line which is the line that likely supplied most of the matching segments.

For half-relatives, e.g., half-siblings or half-uncles/aunts, go up to the level at which you share both ancestors, e.g.

FR - half sibling sharing father

FFR - half uncle/aunt sharing grandfather

Only enter MRCAs that you are fairly certain about.

If a person is equally related on through both parents, e.g. a first cousin of both your father and your mother, enter them as **R**. The MRCA overrules the cluster assignment and will prevent this person from influencing the ancestral path assigned to the segments.

Any person whose MRCA is assigned **R** and who shares from 2300 to 3300 cM will be assumed to be a sibling, and a line will be added into the log file for each sibling assumption. Siblings matches have to be handled by DMT in a custom manner because they match on both parents about 25% of the time. Currently, you cannot override DMT's assumption about siblings. If DMT is incorrectly assuming siblings, then remove the **R** from that person's MRCA or change it if it was wrong.

An **R** at the end of an MRCA indicates you know the MRCA exactly.

An MRCA without an **R** at the end, which is called a **Partial MRCA**, may be entered to indicate that you only know part of the line up to the MRCA, e.g.

MF - You know someone is on your mother's father's side but don't know after that (may be MFF... or MFM...)

Partial MRCAs not ending in **R** are a good way to enter partial lines that you might get from DNA clustering tools that use the Leeds Method or something similar.

Partial MRCAs will not overrule DMT's cluster assignment and DMT may extend or reduce or change the Partial MRCA when assigning the cluster to the person.

If a person is related more than one way, e.g., **MFFR** and **MMMR**, then you may enter a partial MRCA for them up to the point in common, e.g. in this example **M**.

Partial MRCAs are not used in inferences, since inferences need exact MRCAs.

DMT can only attempt to calculate ancestral lines as deep as the MRCAs you enter, so try to enter MRCAs for as many people on different ancestral lines that you know. However, avoid entering MRCAs that are very deep

such as 6 or more generations unless you are certain that this person is not related through other ancestral lines.

6. Normally, you'll know most of the MRCA of your closer matches but fewer from your more distant matches. After you've entered your MRCAs, you should have something that looks like this:

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	NAME-A (1X)	NAME-C	MRCA-C	CLUSTER	STATUS	TRISEG	INFSEG	NUMAC	TOTAC	MAXAC	XTOTAC	AC1	AC2	AC3
2	ca	vi	FR	U	Only AC matches	0	0	22	3384.5	267.2	0	u	u	u
3	ca	SI	MR	U	Only AC matches	0	0	23	3384.3	267.2	195.9	u	u	u
4	ca	Vi	R	U	Only AC matches	0	0	51	2709.9	182.5	108.3	u: u,u,u, u: x,u,u, u: u		
5	ca	Ar	MR	U	Only AC matches	0	0	54	1711	124.2	65	u: u,u,u, u: x,u	u: u	
6	ca	El	MR	U	Only AC matches	0	0	54	1708.2	124.2	65	u: u,u,u, u: x,u	u: u	
7	ca	H.	FMR	U	Only AC matches	0	0	22	483.7	77.6	0	u: x,u,u, u: u,x	u	
8	ca	Al	MFR	U	Only AC matches	0	0	23	433.1	64.9	0	u	u: x,x,u,u,x	
9	ca	G	MFR	U	Only AC matches	0	0	16	307	41.9	0	u	u: x,x,u,u,x	
10	ca	JL		U	Only AC matches	0	0	4	80.8	22.9	0			
11	ca	M		U	Only AC matches	0	0	8	79.2	16.9	0			x
12	ca			U	Only AC matches	0	0	8	69.3	15.1	0		x	x
13	ca	D		U	Only AC matches	0	0	6	67.2	15.8	0	x	u	x
14	ca	R.	MMFR	U	Only AC matches	0	0	5	66.5	18.9	0	u	u	
15	ca	Si		U	Only AC matches	0	0	6	65.1	17.2	0		u	
16	ca	Al		U	Only AC matches	0	0	6	63.8	19.7	0			
17	ca	Ri		U	Only AC matches	0	0	5	58.7	23.8	0	x		u: x
18	ca	M		U	Only AC matches	0	0	5	57.6	18.5	0		x	u: x
19	ca	D.		U	Only AC matches	0	0	5	56.4	16	0		x	
20	ca	Al		U	Only AC matches	0	0	4	56.3	20.4	0	x		
21	ca	K.		U	Only AC matches	0	0	5	55.1	19.9	0			u
22	ca	Er		U	Only AC matches	0	0	4	54.7	17.4	0			x
23	ca	W		U	Only AC matches	0	0	6	53.2	15.7	0	x		
24	ca	G		U	Only AC matches	0	0	3	52.6	31.6	0	x		
25	ca	C.		U	Only AC matches	0	0	3	52.4	29	0			
26	ca	S.		U	Only AC matches	0	0	5	52.4	17.3	0		x	
27	ca	D.		U	Only AC matches	0	0	4	52.2	15.4	0			u
28	ca	Ki		U	Only AC matches	0	0	6	52	17.8	7.6			
29	ca	El		U	Only AC matches	0	0	4	51.8	22	0			
30	ca	Ja		U	Only AC matches	0	0	5	51.6	18.4	0		x: x,x	
31	ca	Ki		U	Only AC matches	0	0	3	51.3	28.8	0			u
32	ca	S.		U	Only AC matches	0	0	4	51	15.6	0	x		

As you enter the MRCAs, their background will get a shade that DMT associates with that parent or grandparent line. DMT adds conditional formats to these cells so that the shading will occur.

In the above screenshot, for example:

The two people sharing 3384 cM could either be parents or children. In this case, they are parents. The mother was given **MR**. The father was given **FR**. There are not any children here, but if there were, they should be assigned **R**. Since DMT makes special use of parent information, it is very important that the parents be given the correct MRCA. You should only have at most one person more than about 3300 cM assigned **FR** and at most one assigned **MR**. Unfortunately, many of us do not have the benefit of having one or both of our parents tested.

The person sharing 2709.9 cM is a sibling and is assigned **R**.
The people sharing 1711 cM and 1708.2 cM are both siblings of Person A's mother, so they are assigned **MR**.

The people sharing 307 cM to 483 cM are all 1C1Rs (1C of Person A's parent). There's a 2C1R sharing 66.5 cM.

The screenshot above only goes down to 51 cM, but don't forget to look through the people with lower match totals, as some may be known relatives who can be assigned an MRCA.

7. Now save the People file.

DMT will read the MRCAs from this People file every time this Person A is selected.

Each Person A has their own People file and the MRCAs are from their own point of view.

Note: You can change the MRCAs in the People file in between runs. DMT starts every run by reading all the MRCAs in the People file, and will write the same MRCAs back into it if it recreates the file.

If you already have a People file but download a new segment match file for Person A and give it a different name, you can copy or rename your current People file to match the new Person A file name (but with "_people.xlsx" at the end of its name instead of .csv). That way, you won't have to add all your MRCA information again.

The format of the People file is the same as the People page. To understand what the People file contains, see: [DMT Excel File - People Page](#)

The People file will be created during a run if it doesn't exist.

It will be updated for any Combine All Results run to contain the people information for that run. The MRCAs you entered will be retained in the file.

It will be updated during any run where the number of Person A matches is different than the number in the People file. This may happen if you download a new segment match file for Person A or if you download new One-to-one files from GEDmatch for Person A.

If you want to force a rebuild of the Person A file, a sneaky trick is to delete a few people who don't have MRCAs from the People file and then do any run.

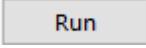
2. Running Single Matches

Single matching is what most people are used to doing. One segment match file contains all the segment matches for one person.

The general technique for single match painting is to find the people you know the MRCAs for, and to "paint" those ancestors onto those segments. Tools like DNA Painter are usually used to do the painting.

DMT can give you the information about the segments that can be painted. It can also produce a summarized file that DNA Painter can load with your ancestor's segments.

To run single matches with DMT, do the following:

1. Ensure your segment match file for Person A is listed in the File A box. Find it with the  button.
2. Ensure your MRCAs are already set up in your People File. See [Step 1. Set Up Your People File and MRCAs](#).
3. Optionally select **Output:** **DNA Painter file(s)** if you want a DNA Painter file produced.
4. Leave both **File B:** and **Folder B:** unchecked, and press the  button.

You can press the  button to take you to the directory where the Person A segment match file is, which is also where the result will be.

DMT will produce a results file in Excel format that contains a Chromosome Map page and a People page, a Log file in text format, and optionally a DNA Painter file in comma delimited format. The name of the result files identify Person A for you.

Name	Date modified	Type	Size
 DMT_ [redacted] _single.xlsx	2022-05-01 2:57 PM	Microsoft Excel Worksheet	1,242 KB
 DMT_ [redacted] _single_dnapainter.csv	2022-05-01 2:57 PM	Microsoft Excel Comma Separated Values File	3 KB
 DMT_ [redacted] _single_log.txt	2022-05-01 2:57 PM	Text Document	2 KB

The **Chromosome Map page** will look like this:

The top section with blue, green, orange and yellow shades are all the people with MRCAs or clusters assigned. They are followed by everyone else with cluster U (unassigned) or X (people with all matches smaller than the Min Single cM limit).

The People file [that you set up earlier](#) will not be updated unless the people have changed.

For details about this page, see [DMT Excel File - People Page](#).

Also produced will be a [Log File](#).and an optional [DNA Painter File](#).

3. Running Person A with Person B

Using two people's segment match files together is what I call **double matching**. Person A is the person you're interested in. Person B is someone whose matches you want to compare to Person A's matches.

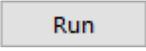
If Person A matches Person C on a segment, and Person B matches Person C on at least part of the same segment, then they **double match** on that segment. If person A also matches Person B on that double match, then that segment match **triangulates**.

The double matching technique will find ALL the triangulating segments between two people, A and B, that are contained in the match data. This is the main function Double Match Triangulator was originally developed to do, i.e. find all the triangulating segments so that you don't have to look for them yourself.

Segments that triangulate are important for two reasons:

1. It is an indicator that the segment might be Identical By Descent (IBD), i.e. passed down from a common ancestor.
2. It considerably reduces the likelihood that the segment might match by chance, thus segments down to 7 cM are not likely to be by chance rather than the 15 cM threshold for single matches.

To run double matching with DMT, do the following:

1. Ensure your segment match file for Person A is listed in the File A box. Find it with the  button.
2. Ensure your MRCAs are already set up in your People File. See [Step 1. Set Up Your People File and MRCAs](#).
3. Ensure your segment match file for Person B is listed in the File B box. Find it with the  button.
4. Optionally select **Output:** **DNA Painter file(s)** if you want a DNA Painter file to be produced.
5. Ensure that **File B:** is checked and press the  button.

You can press the  button to take you to the directory where the Person A segment match file is, which is also where the results will be.

DMT will produce a results file in Excel format that contains a Chromosome Map page and a People page, a Log file in text format, and optionally a DNA Painter file in comma delimited format. The names of the result files identify Person A and Person B for you.

Name	Date modified	Type	Size
 DMT_..._..._... .xlsx	2022-05-01 4:05 PM	Microsoft Excel Worksheet	1,485 KB
 DMT_..._..._..._dnapainter.csv	2022-05-01 4:05 PM	Microsoft Excel Comma Separated Values File	4 KB
 DMT_..._..._..._log.txt	2022-05-01 4:05 PM	Text Document	7 KB

The **Chromosome Map page** will look like this:

4. Running Person A with each Person B

If you have a good number of segment match files, you don't want to have to match each of them to Person A one by one. Instead, DMT can do them all for you.

To run double matching of Person A with each of many segment match files, do the following:

1. Ensure your segment match file for Person A is listed in the File A box. Find it with the  button.
2. Ensure your MRCAs are already set up in your People File. See [Step 1. Set Up Your People File and MRCAs](#).
3. Ensure all the segment match files for each Person B that you want to match are in a folder on your computer, or a folder and some subfolders.
4. Find the folder containing the Person B match files with the  button.
5. Ensure that **Folder B:** is checked. If you want subfolders as well then check **Include subfolders**.
6. Optionally select **Output:** **DNA Painter file(s)** if you want DNA Painter files to be produced for each A versus B run.
7. Ensure that **Combine all results** is not checked and press the  button.

DMT will produce a results file in Excel format that contains a Chromosome Map page and a People page and optionally a DNA Painter file in comma delimited format for Person A in combination with each Person B. It will also produce a Log file in text format.

You can press the  button to take you to the directory where the Person A segment match file is, which is also where the result will be.

For example, running a Person A using a folder containing 10 Person B segment match files will produce 10 result files, 1 log file, and optionally 10 DNA Painter files:

4. Running Person A with each Person B

Name	Date modified	Type	Size
DMT_..._244...xlsx	2022-05-01 4:20 PM	Microsoft Excel Worksheet	1,555 KB
DMT_..._244..._dnainter.csv	2022-05-01 4:20 PM	Microsoft Excel Comma Separated Values File	3 KB
DMT_...all_doubles_log.txt	2022-05-01 4:20 PM	Text Document	54 KB
DMT_..._244...2.xlsx	2022-05-01 4:20 PM	Microsoft Excel Worksheet	1,531 KB
DMT_..._244...2_dainter.csv	2022-05-01 4:20 PM	Microsoft Excel Comma Separated Values File	3 KB
DMT_..._279...3.xlsx	2022-05-01 4:19 PM	Microsoft Excel Worksheet	1,352 KB
DMT_..._279...3_dainter.csv	2022-05-01 4:19 PM	Microsoft Excel Comma Separated Values File	3 KB
DMT_..._294...0.xlsx	2022-05-01 4:19 PM	Microsoft Excel Worksheet	1,333 KB
DMT_..._294...0_dainter.csv	2022-05-01 4:19 PM	Microsoft Excel Comma Separated Values File	3 KB
DMT_..._297...3.xlsx	2022-05-01 4:19 PM	Microsoft Excel Worksheet	1,314 KB
DMT_..._297...3_dainter.csv	2022-05-01 4:19 PM	Microsoft Excel Comma Separated Values File	3 KB
DMT_..._305...0.xlsx	2022-05-01 4:19 PM	Microsoft Excel Worksheet	1,369 KB
DMT_..._305...0_dainter.csv	2022-05-01 4:19 PM	Microsoft Excel Comma Separated Values File	4 KB
DMT_..._308...3.xlsx	2022-05-01 4:19 PM	Microsoft Excel Worksheet	1,346 KB
DMT_..._308...3_dainter.csv	2022-05-01 4:19 PM	Microsoft Excel Comma Separated Values File	3 KB
DMT_..._386...3.xlsx	2022-05-01 4:19 PM	Microsoft Excel Worksheet	1,381 KB
DMT_..._386...3_dainter.csv	2022-05-01 4:19 PM	Microsoft Excel Comma Separated Values File	4 KB
DMT_..._599...xlsx	2022-05-01 4:19 PM	Microsoft Excel Worksheet	1,485 KB
DMT_..._599..._dainter.csv	2022-05-01 4:19 PM	Microsoft Excel Comma Separated Values File	4 KB
DMT_..._599...xlsx	2022-05-01 4:19 PM	Microsoft Excel Worksheet	1,367 KB
DMT_..._599..._dainter.csv	2022-05-01 4:19 PM	Microsoft Excel Comma Separated Values File	4 KB

The names of the result files and DNA Painter files identify Person A and Person B for you.

5. Combine All Results

It is very useful to run Person A with different Person B people. Each Person B gives different match results about different parts of Person A's DNA. Each Person B suggests triangulation groups on Person B's side of the family and indicates other triangulation groups through Person A's other parent.

By combining all the results of each A versus B comparison, you can build up much more of each chromosome and develop triangulation groups for many different ancestral lines.

Often, suggested ancestral lines for a match conflict for different B people. That can happen because even though a relative is known to be, say, a second cousin on mother's father's side, some individual matches of that second cousin may be through a different ancestral line because that cousin is related more distantly in another way. Double Match Triangulator uses a method of consensus, meaning majority rules, and if more matches say one ancestral line than the other, then that ancestral line is the one assigned to the match. In general, this would usually lead to the most logical conclusion. That doesn't mean it is always correct.

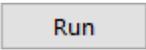
This result of combining all files gives the best estimate of the ancestral lines and triangulation groups of Person A. It suggests how other people who match might be related. Those suggestions might hint at an ancestral line that you, as the genealogist, can research and hopefully find the connection. If a connection is found, the MRCA of that person can be added to the people file and the combined results can be run again.

Once enough MRCAs are known, a combined results run should successfully map the majority of Person A's DNA to ancestral lines and triangulations groups.

Doing a combine all results run is very similar to doing a Person A with each Person B run. The only difference is that

Combine all results

is checked. The procedure is:

1. Ensure your segment match file for Person A is listed in the File A box. Find it with the  button.
2. Ensure your MRCAs are already set up in your People File. See [Step 1. Set Up Your People File and MRCAs](#).
3. Ensure all the segment match files for each Person B that you want to match are in a folder on your computer, or a folder and some subfolders.
4. Find the folder containing the Person B match files with the  button.
5. Ensure that Folder B: is checked. If you want subfolders as well then check Include subfolders.
6. Optionally select **Output:** DNA Painter file(s) if you want a DNA Painter file to be produced for the combined results.
7. Ensure that Combine all results is checked and press the  button.

You can press the  button to take you to the directory where the Person A segment match file is, which is also where the result will be.

DMT will produce 23 results files in Excel format that each contain a Chromosome Map page for one Chromosome. It splits the results into chromosomes simply because a combined results file can get too large for Excel to handle efficiently. DMT will also update the People file, produce a Log file in text format, and will optionally create a DNA Painter file in comma delimited format for Person A. The names of the result files identify Person A for you.

Below are the files that you will have following a combine all results run:

Name	Date modified	Type	Size
DMT_..._Chromosome_1.xlsx	2022-05-01 4:40 PM	Microsoft Excel Worksheet	153 KB
DMT_..._Chromosome_2.xlsx	2022-05-01 4:40 PM	Microsoft Excel Worksheet	276 KB
DMT_..._Chromosome_3.xlsx	2022-05-01 4:40 PM	Microsoft Excel Worksheet	118 KB
DMT_..._Chromosome_4.xlsx	2022-05-01 4:40 PM	Microsoft Excel Worksheet	106 KB
DMT_..._Chromosome_5.xlsx	2022-05-01 4:40 PM	Microsoft Excel Worksheet	107 KB
DMT_..._Chromosome_6.xlsx	2022-05-01 4:40 PM	Microsoft Excel Worksheet	131 KB
DMT_..._Chromosome_7.xlsx	2022-05-01 4:40 PM	Microsoft Excel Worksheet	186 KB
DMT_..._Chromosome_8.xlsx	2022-05-01 4:40 PM	Microsoft Excel Worksheet	106 KB
DMT_..._Chromosome_9.xlsx	2022-05-01 4:40 PM	Microsoft Excel Worksheet	110 KB
DMT_..._Chromosome_10.xlsx	2022-05-01 4:40 PM	Microsoft Excel Worksheet	157 KB
DMT_..._Chromosome_11.xlsx	2022-05-01 4:40 PM	Microsoft Excel Worksheet	105 KB
DMT_..._Chromosome_12.xlsx	2022-05-01 4:40 PM	Microsoft Excel Worksheet	187 KB
DMT_..._Chromosome_13.xlsx	2022-05-01 4:40 PM	Microsoft Excel Worksheet	78 KB
DMT_..._Chromosome_14.xlsx	2022-05-01 4:40 PM	Microsoft Excel Worksheet	64 KB
DMT_..._Chromosome_15.xlsx	2022-05-01 4:40 PM	Microsoft Excel Worksheet	96 KB
DMT_..._Chromosome_16.xlsx	2022-05-01 4:40 PM	Microsoft Excel Worksheet	130 KB
DMT_..._Chromosome_17.xlsx	2022-05-01 4:40 PM	Microsoft Excel Worksheet	59 KB
DMT_..._Chromosome_18.xlsx	2022-05-01 4:40 PM	Microsoft Excel Worksheet	123 KB
DMT_..._Chromosome_19.xlsx	2022-05-01 4:40 PM	Microsoft Excel Worksheet	78 KB
DMT_..._Chromosome_20.xlsx	2022-05-01 4:40 PM	Microsoft Excel Worksheet	107 KB
DMT_..._Chromosome_21.xlsx	2022-05-01 4:40 PM	Microsoft Excel Worksheet	44 KB
DMT_..._Chromosome_22.xlsx	2022-05-01 4:40 PM	Microsoft Excel Worksheet	48 KB
DMT_..._Chromosome_23.xlsx	2022-05-01 4:40 PM	Microsoft Excel Worksheet	80 KB
DMT_..._combined_log.txt	2022-05-01 4:40 PM	Text Document	43 KB
DMT_..._dnainter.csv	2022-05-01 4:40 PM	Microsoft Excel Comma Separated Values File	5 KB
DMT_..._people.xlsx	2022-05-01 4:40 PM	Microsoft Excel Worksheet	454 KB

The People file will be overwritten with the combined results. All the MRCAs you've added to it will be retained.

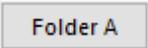
DMT Output Files

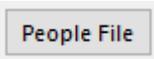
DMT produces a number of different output files.

Most are in Excel format and the filename ends with the .xlsx suffix. These can be read by Excel or any other spreadsheet program.

The Log file records the details of every run you make. It lists all the problems encountered in your match files and has a lot of summary information about your matches that you may find useful.

The DNA Painter File is an optional output file that is in comma delimited format and the filename has the .csv suffix. This is the format DNA Painter uses for input.

You can press the  button to take you to the directory where the Person A segment match file is, which is also where DMT puts its output files.

You can press the  button to open the People File associated with Person A that will be in Folder A.

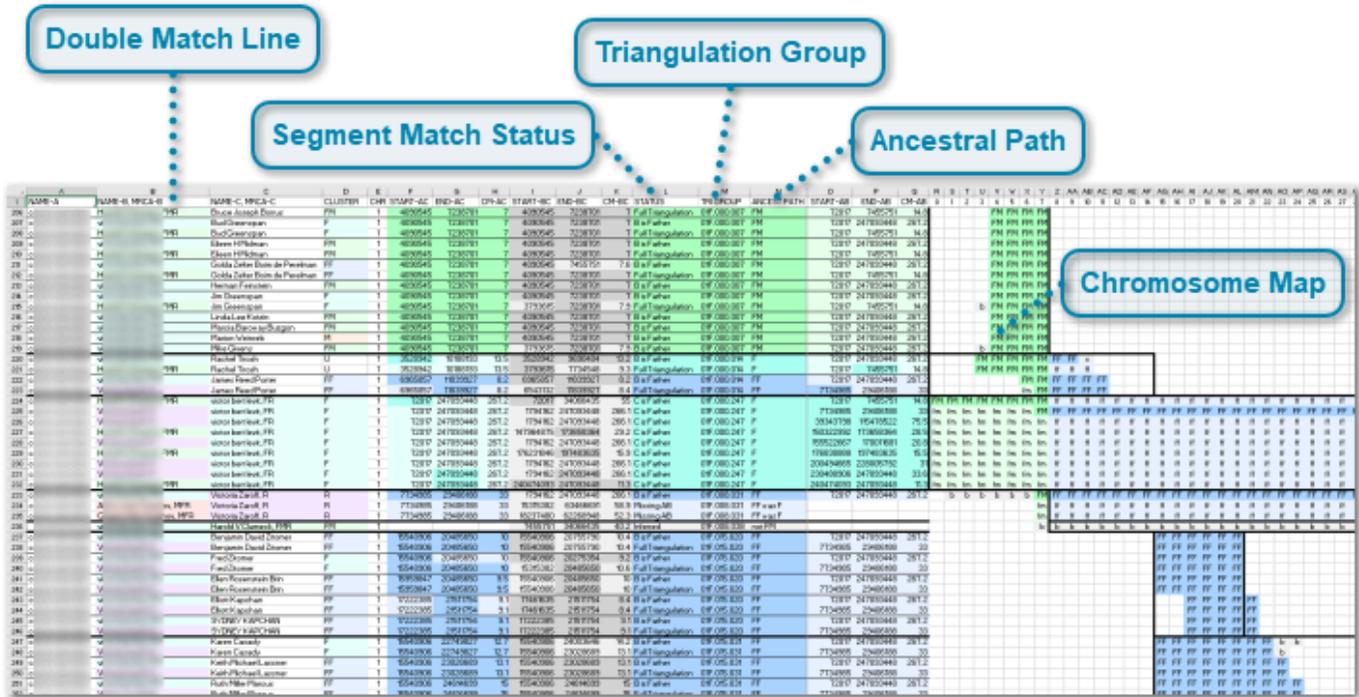
See the next pages for details of each type of output file.

DMT Excel File - Chromosome Map Page

When **comparing two files** the output of the DMT program is an Excel file that has two pages. The first page is the Chromosome Map page and shows all Chromosomes 1 to 23 on the page, one after another.

When **combining all files** the output of the DMT program includes 23 Excel files, with one Chromosome Map page for each chromosome.

The two Chromosome Map pages are very similar and both are described here. The example shown below is from Chromosome 1 and is generated by combining all files.



Double Match Line

1	NAME-A	NAME-B, MRCA-B	NAME-C, MRCA-C	CLUSTER	CHR	START-AC	END-AC	CM-AC	START-BC	END-BC	CM-BC	STATUS	TRI GROUP	ANCESTRAL PATH	START-AB	END-AB	CM-AB	
206	o	H	*MR	Bruce Joseph Borrus	FM	1	4090545	7238701	7	4090545	7238701	7	Full Triangulation	01F 000.007	FM	72017	7455751	14.8
207	o	vi		Bud Greenspan	F	1	4090545	7238701	7	4090545	7238701	7	Bi-Father	01F 000.007	FM	72017	247093448	267.2
208	o	H	*MR	Bud Greenspan	F	1	4090545	7238701	7	4090545	7238701	7	Full Triangulation	01F 000.007	FM	72017	7455751	14.8

Column A (NAME-A) is Person A, the person you are interested in whose ancestors you want to find. Column A is not shown for inferred matches to indicate that Person A does not match.

Column B (NAME-B, MRCA-B) is Person B, the person whose segment match file is compared and double matched with Person A. If Person B has a MRCA, the MRCA is shown following the name and a comma. The background shade is based on the MRCA. Person B is not shown for A-C matches or Missing B-C matches to indicate that Person B does not match.

Column C (NAME-C, MRCA-C) is Person C, who is always one of the people who Person A matches. Only people Person A matches to are included in Person A's analysis. If Person C has an MRCA, the MRCA is shown following the name and a comma. The background shade is based on the MRCA.

Column D (CLUSTER) is the cluster that was determined for Person C. It is determined from the most common ancestral line of the segment matches between Person A and Person C. See [the People Page](#) for more information about the cluster. The background shade is based on the cluster.

Column E (CHR) is the chromosome the match is on. When comparing two files, all chromosomes are shown in order in the one file. Chromosome X is included last. When combining all files, each chromosome is in their own file.

Columns F (START-AC) and G (END-AC) give the start and end base addresses of the Person A match with Person C. The background shade is based on the ancestral path in column N. It is a darker shade if the address coincides with the start or end of the triangulating region. The AC matches are what you see in a chromosome browser from Person A's point of view.

Column H (CM-AC) gives the number of Centimorgans (cM) of the match between Person A and Person C. The background shade is that same as for Columns F and G. It is a darker shade if START-AC and END-AC both coincide with the start and end of the triangulating region, meaning it is also the length of the triangulation.

Columns I (START-BC) and J (END-BC) give the start and end base addresses of the Person B match with Person C. They are shown in a background shade of grey to illustrate that this is not a Person A match. It is a darker shade if the the address coincides with the start or end of the triangulating region.

Column K (CM-BC) gives the number of centimorgans (cM) of the match between Person B and Person C. The background shade is grey. It is a darker shade if START-BC and END-BC both coincide with the start and end of the triangulating region. meaning it is also the length of the triangulation. This value can help identify whether Person A or Person B is related more closely to the C person. In general, close relationships will have longer BC matches than more distant relationships. Also, BC matches that are longer than the AC match indicate a possible closer relationship of B to C than of A to C. Shorter matches indicate a possible farther relationship. This may provide clues as to the relationship between Persons A, B and C and who their common ancestor might be.

Column L (STATUS) is described in its own section below: Segment Match Status

Column M (TRIGROUP) is described in its own section below: Triangulation Group

Column N (ANCEST PATH) is described in its own section below: Ancestral Path

Columns O (START-AB) and P (END-AB) give the start and end base addresses of the Person A match with Person B. The background shade is based on the ancestral path in column N. It is a darker shade if the address coincides with the start or end of the triangulating region. Triangulations can only occur where A matches B. The "Freeze Pages" property is set to Column N, so scrolling right will hide columns O, P and Q.

Column Q (CM-AB) gives the number of centimorgans (cM) of the match between Person A and Person B. The background shade is that same as for Columns O and P. It is a darker shade if START-AC and END-AC both coincide with the start and end of the triangulating region, meaning it is also the length of the triangulation.

Segment Match Status

L
STATUS
Full Triangulation
B is Father
Full Triangulation
B is Father
Full Triangulation

These are the possible status values for each segment match:

Full Triangulation **Full Triangulation** means that Person A matches Person C, Person B matches Person C, and Person A matches Person B on at least some part of this segment. Triangulations often indicate that the segment may have come from a common ancestor. The tricky part for you is to genealogically figure out who that ancestor was. In the Chromosome Map area of this page, the triangulating segments are denoted with capital letters and a dark shaded background.

MRCAs Differ These are full triangulations where the parent of the MRCA of A-B differs from the parent of the MRCA of A-C. Because the parents differ, the MRCAs are not likely the same and there may be a triangulation only because A-B, A-C and B-C are each matching on differing parents, i.e. opposite chromosomes. DMT treats these like Single A-C matches (see below). For more information about this situation, see my blog post: [Triangulation does NOT mean IBD](#). If there are any MRCAs that differ, then the number of them is given in the log file to alert you, and you can use the Excel "find" to search for them in the Status column.

B is Father or **B is Mother** or **C is Father** or **C is Mother** indicates that Person A is matching their parent on the segment and that Person A and their parent are triangulating on that segment with the other person. This is a full triangulation but it is special because the parent effectively "phases" the match to that parent's chromosome. If the parent's match is smaller than Person A's match, then the extra bits of the A-C match are marked as false and will be shown with *

Missing BC A **Missing B-C Match** is where Person A matches Person C and Person A matches Person B, but Person B does not match Person C on this segment. Person B and Person C must be in-common-with each other, i.e. they must match somewhere, but not here. These matches are very useful, because if they in fact are not a triangulation, then they cannot occur on the same parental chromosome as any triangulations that are at that location. They would then have to be A-C matches that are on the other parent's chromosome. Thus, even though a Person B may be related on one parent's side, information is available for both parents' chromosomes.

Missing AB A **Missing A-B Match** is where Person A matches Person C and Person B matches Person C, i.e. a double match, but Person A does not match Person B on the segment so it is not a triangulation. This works the same as a Missing B-C match.

Inferred An **Inferred** match is where Person B matches Person C but Person A does not match Person C on the same segment. When the MRCA of Person A with both Person B and Person C are known, in some cases the B-C match may be able to tell you what the A-C match cannot be. Inferred matches are shown in a grey shade because to indicate that they are not an A-C match. The ancestral path of an inferred match will always start with "not ", e.g. **not MF**. The ancestral path that this match refutes is the one given.

Single AC A **Single A-C** match is an A-C match that does not triangulate, is also not a missing B-C or missing A-B match, and is at least as large as the Min Single cM limit. Being larger than the Min Single limit assumes that this match is large enough to not be a match by chance and likely was passed down from a common ancestor. If the MRCA for person C was assigned, then the MRCA's parental side will be used, unless there are also overlapping triangulations on that parental side which indicate a conflict. If the MRCA is not assigned and there were triangulations on that segment then the segment will be assigned to the opposite parent. In case of a conflict or no MRCA and no triangulations, then this match is placed into the "U" unknown parent section.

MRCA Bad on X - if you see this status, then you may have a Person C matching on the X chromosome whose MRCA is on Person A's father and Person A is male. That can't happen since a male only receives an X chromosome from his mother. DMT only includes a mother-side X chromosome when Person A is male. Or you may have a Person C matching on the X chromosome whose MRCA includes "FF". That can't happen because an X chromosome doesn't pass down from a male to a male.

Small AC A **Small A-C** match is a single match that does not reach the Min Single cM limit. These matches might be by chance matches that do not come from a common ancestor. They are included in DMT's output so that you can still see all of Person A's matches, but they are put into the "X" excluded section so that you will know what A-C segments were not used in the analysis.

Small Inferred A **Small Inferred** match is an inferred match that does not reach the Min Single cM limit. These matches might be by chance B-C matches that do not come from a common ancestor of B and C.

They are included in DMT's output so that you can still see all the inferred matches, but they are put into the "X" excluded section so that you will know what inferred segments were not used in the analysis.

Triangulation Group

M
TRI GROUP
01F.000.007

The triangulation group containing the segment is specified with an 11 character notation based on a similar notation designed by Jim Bartlett.

The first two characters is the chromosome number, "01" to "23", where "23" represents the X chromosome.

The 3rd character is either "F" for father's chromosome, "M" for mother's chromosome, "U" for unknown whether father or mother, or "X" for exclude from analysis. The latter group is used for small single segments and small inferred segments.

Then are two sets of 3 digit numbers with a period separating them for readability. The 3 digit numbers are the starting and ending base positions of the triangulation group given in Mbp (mega base pairs = 1,000,000 of them). They are truncated to the nearest Mbp which is good enough for accuracy since there is usually extra matching at the ends of each segment.

DMT bases the start and end of of triangulation groups on the positions where triangulations start and end. Each segment will be assigned to the smallest triangulation group that contains the segment.

In the "U" unknown parent section and "X" excluded section, only one group is used on each chromosome with the start and end positions covering the entire chromosome.

For example, 01F.003.007 refers to the triangulation group that is on father's chromosome 1, starts at a base address of 3 Mbp and goes up to and includes the 9 Mbp column, i.e. 10 Mbp starts a new triangulation group.

Ancestral Path

N
ANCEST PATH
FM

The ancestral path is determined where possible for each segment match. MRCA's are needed to calculate ancestral paths, and the notations of the two are similar.

Ancestral paths are comprised of "F" and "M" characters, so an FMF ancestral path states that the segment may come from Person A's father's mother's father. Ancestral paths never contain the trailing "R" that MRCA's do.

The right section of the Chromosome Map page in the Excel file, from columns O to JB, provides a simple visual representation of the matches.

The numbers at the top (Row 1) represent the base pair addresses in millions (Mbp). So, for example, 14 would represent base pair addresses between 14000000 and 14999999.

FM FM FM FM - Capital letters with dark shaded backgrounds represent triangulations. The capital letters indicate the ancestral path up to the grandparent that was determined for each Mbp. So the possibilities are F, FF, FM, M, MF, MM. The color used is based on the parent or grandparent. You can also have triangulations where the parental side is unknown. **U U U**

fm fm fm fm - Small letters with light shaded backgrounds are segment matches which are not triangulations. The letters also indicated the ancestral path up to the grandparent, but there may also be **b b** for B-C matches of inferences or extra B-C matching before or after the A-C match starts and ends, e.g: **b FM FM**. You can have matches that are not triangulations where the parent is unknown **u u u**, and matches that are excluded from analysis: **x x x**

The dark vertical and horizontal lines separate triangulation groups.

Some segments may seem to span two ancestral lines, such as the segments shown here that start as FM and end as FF:

	b	FM	FM	FM	FM					
	FM	FM	FM	FM	FM	FF	FF	x		
	FM	FM	FM	FM	FM	ff	ff	ff		
				FM	FM	FF	FF	FF	FF	
				fm	FM	FF	FF	FF	FF	

Technically, ancestors can change over one segment but they should not normally change grandparents. DMT extends grandparents to triangulation group boundaries so within a triangulation, if grandparents change then it will be at a triangulation boundary.

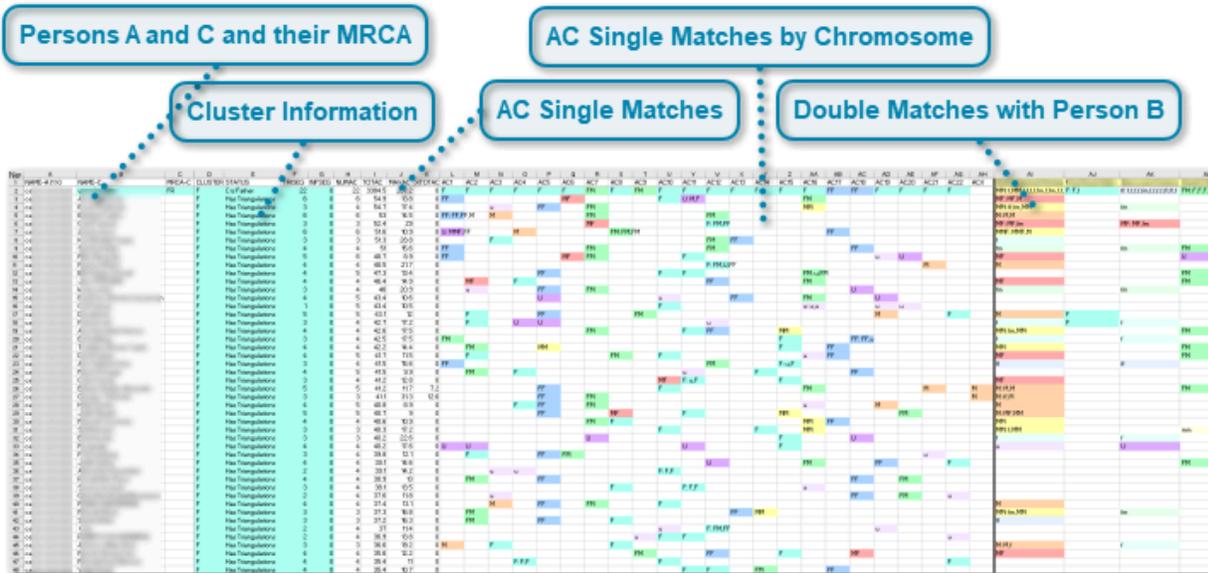
DMT Excel File - People Page

This page is an index of the people matching Person A. It lists every Person C who matches Person A.

When comparing two files, this page is the second page of the produced Excel file, following the Chromosome Map page which is the first page.

When combining all results, this page is a separate Excel file for Person A and it is called the People file. This is the file that you update the MRCAs you know for Person A's relatives. See: [Set Up Your People File and MRCAs](#). The People page and People file have exactly the same format.

The illustration below shows a combine all results People file that shows only the first 5 lines in each cluster.



Persons A and C and their MRCA

A	B	C
NAME-A (1X)	NAME-C	MRCA-C
CE	V	FR
CE	A	
CE	E	
CE	E	
CE	C	

Column A (NAME-A) is the name of Person A. The column name in cell A1 will be NAME-A (1 X) if Person A is male, i.e. has 1 X chromosome, and it will be NAME-A (2 X) if Person A is female, i.e. has 2 X chromosomes. To change this value, use the Person A Sex dropdown on [Double Match Triangulator's Main Window](#).

Column B (NAME-C) are the names of all the C people who match Person A. Person C names beginning with ## have overlapping matches, which indicate there likely are two or more indistinguishable people having the same name. The ## warns you that their matches have been combined under that one name. Unless you know that all the people with ## have the same MRCA, you should not assign them an MRCA so that they will not improperly influence the ancestral path assignments.

Column C (MRCA-C) contains your entries of any Most Recent Common Ancestors (MRCA) for Person A and Person C that you know. See [Set Up Your People File and MRCAs](#) for more info on how to enter your MRCAs. If the MRCA has been entered, then columns B and C will be given a background shade based on what the MRCA is.

Cluster Information

D	E	F	G	M
CLUSTER	STATUS	TRISEG	INFSEG	
F	C is Father	22	0	
F	Has Triangulations	6	0	
F	Has Triangulations	3	0	
F	Has Triangulations	6	0	
F	Has Triangulations	3	0	
F	Has Triangulations	6	0	
F	Has Triangulations	3	0	

Column D (CLUSTER) contains the cluster that DMT assigns to Person C. The Cluster is the ancestral path from Person A that is expected to lead to Person C. Clusters help classify the side of the family that each person may belong to. The people page is grouped by cluster. They will allow you to genealogically focus on that line to try to find how Person C is actually related to Person A. When you determine their actual relationship, then you can fill in this person's MRCA in column C of Person A's people file and run the whole shebang again.

The cluster will be calculated based on the most common agreed upon ancestral path on chromosomes 1 to 23. For example if a Person C has just two chromosomes with ancestral paths assigned of **FF** and **FMF**, then the cluster for Person C will be **F**.

R Cluster **R** is for people whose MRCA is **R**, meaning they share both parents with Person A, i.e. Person A's children, grandchildren, siblings, nephews and nieces.

U Cluster **U** is for people whose parental side did not cannot be determined, or people whose chromosomes are equally represented with ancestral paths on both parents.

X Cluster **X** is for people that only have excluded matches.

For people who have a known MRCA (with an **R** at the end), that MRCA will always be used as the cluster (less the trailing **R**).

The background shade of the cluster is based on the first two letters of the cluster. A darker shade is used if the person has triangulations and a lighter shade is used if not.

Column E (STATUS) indicates the nature of the matches between Persons A, B and C:

C is Father or **C is Mother** indicates Person C is a parent of Person A. The MRCA of Person C must have been specified as **FR** or **MR**.

Has Triangulations indicates that Person A, B and C triangulate on at least one segment.

In Common With B indicates that Person A and Person B both match Person C, but they do not triangulate anywhere.

Only AC matches indicates that Person A matches Person C, but person B does not match Person C.

Column F (TRISEG) gives the total number of triangulating segments between Person A, any of the B people, and Person C.

Column G (INFSEG) gives the number of inferred segments that any of the B people have with Person C.

AC Single Matches

H	I	J	K
NUMAC	TOTAC	MAXAC	XTOTAC
22	3384.5	267.2	0
6	54.9	13.8	0
4	54.7	17.4	0
6	53	14.5	0
3	52.4	29	0
6	51.6	10.9	0
3	51.3	28.8	0

Columns H (NUMAC), I (TOTAC), J (MAXAC) and K (XTOTAC) give the number of segments matching between Person A and Person C, their total match length in cM, the largest matching segment length in cM, and the total match length on the X chromosome in cM.

Note that the TOTAC includes only segments that at least as large as the MinTriang segment limit that you have set. The default is 7 cM. Each company has their own limit as to what they include in their total, so their total cM may be different. TOTAC also excludes X chromosome segments.

Within clusters, the people on the Chromosome Map page are sorted by highest total match length (TOTAC) so that the presumably closer relatives of Person A in each cluster will be listed first.

BC Single Matches

When comparing two files with each other (Person A with Person B), there will be four additional columns included in the people file following the XTOTAC column:

L	M	N	O
NUMBC	TOTBC	MAXBC	XTOTBC
36	996.7	81.9	0
1	8.9	8.9	0
2	16.7	9.5	0
1	9.5	9.5	0

NUMBC, TOTBC, MAXBC AND XTOTBC, which is the same information but for the matches of Person B with Person C rather than Person A with Person C.

AC Single Matches by Chromosome

L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	AD	AE	AF	AG	AH
AC1	AC2	AC3	AC4	AC5	AC6	AC7	AC8	AC9	AC10	AC11	AC12	AC13	AC14	AC15	AC16	AC17	AC18	AC19	AC20	AC21	AC22	ACX
F	F	F	F	F	F	FM	F	FM	F	F	F	F	F	F	F	FF	FF	F	F	F	F	
FF					MF				F	U:MF					FM							
FF:FF,FF,M		u		FF		FM					FM				MM							
						FM					F:FM,FF											
U:MMF,FF			M					FM:FM,FM														

The next 23 columns (L ... AH) show for every chromosome, the ancestral lines assigned to each match between Person A and Person C on that chromosome. Triangulations are in uppercase. Non-triangulations are in lower case. If the ancestral line is an unknown parent, then it is "U" or "u". Inferreds are shown as "i".

If there is more than one single match on the chromosome, a consensus ancestral path is determined and shown as the first path in the list followed by a colon. Triangulations take precedence in determining the ancestral path. Unknown parents and inferreds make no contribution to the consensus path.

e.g. **FM:m,FM,u** shows that there are three single A-C matches on the chromosome. The first A-C match has ancestral path **m**, which is non-triangulating on Person A's mother's side. The second A-C match is a triangulating **FM** match on Person A's father's mother's side. The third match is a **u** unknown parent match. In this example, the consensus is the triangulating **FM** match, so the consensus **FM:** is added before the other three. The background shade is based on the consensus match.

Double Matches with Person B

	AI	AJ	AK	AL
		: F		
MM: f,MM,f,f,f,f,fm,f,fm,f,f, F: F,f			ff: f,f,f,f,fm,f,f,f,f,ff,f	FM: F,F,F,F
MF: MF,M				
MM: ff,fm,MM			fm	
M: M,M				
MF: MF,fm			MF: MF,fm	
MMF: MMF,M				
f				

These are only included when combining all files. One column is added for every Person B that was used. Person B's name is listed in row 2. These columns will give you information about which C people are triangulating or otherwise interacting or not interacting with each B person.

Under each B person's name are the ancestral paths of matches between Person A and Person C that overlap with a match of Person B and Person C, or overlap with a match of Person A and Person B. Where there is more than one ancestral path, a consensus ancestral path is determined and shown as the first path in the list followed by a colon. The consensus ancestral path is determined the same as described in AC Single Matches by Chromosome above. The background shade is based on the consensus match.

Since these are double matches, they will triangulate and be shown in uppercase if the third leg (A-B or B-C) also matches on the segment. If the third leg does not match on the segment, they will not triangulate and will be shown in lowercase.

DNA Painter File

DMT optionally can produce files that can be input into Jonny Perl's [DNA Painter](#) website.

The file DMT creates is a comma delimited file with the name: DMT_nnnnnn_dnapainter.csv where nnnnnn identifies the person (for a combine all run) or the two people (for a compare files run).

If you open the file in Excel or a text editor, you can see the contents:

	A	B	C	D	E	F	G	H	I	J	K
1	Chr	Start	End	cM	SNPs	Match	Conf	Group	Side	Notes	Colour
2	1	0	10000000			FTDNA c... and 11 people		FMF	paternal		#9FDFAF
3	1	12000000	15000000			FTDNA c... and 11 people		FMF	paternal		#9FDFAF
4	1	15000000	39000000			FTDNA c... and 11 people		FF	paternal		#AAD5FF
5	1	43000000	200000000			FTDNA c... and 11 people		FMF	paternal		#9FDFAF
6	1	202000000	213000000			FTDNA c... and 11 people		FF	paternal		#AAD5FF
7	1	214000000	248000000			FTDNA c... and 11 people		FMF	paternal		#9FDFAF
8	1	0	16000000			FTDNA c... and 11 people		MMFM	maternal		#BFBF40
9	1	1000000	39000000			FTDNA c... and 11 people		MM	maternal		#FFFFAA
10	1	39000000	116000000			FTDNA c... and 11 people		MF	maternal		#FAAAAA
11	2	7000000	12000000			FTDNA c... and 11 people		FMF	paternal		#9FDFAF
12	2	123000000	165000000			FTDNA c... and 11 people		FMF	paternal		#9FDFAF
13	2	234000000	243000000			FTDNA c... and 11 people		FMF	paternal		#9FDFAF
14	2	0	8000000			FTDNA c... and 11 people		MF	maternal		#FAAAAA
15	2	8000000	30000000			FTDNA c... and 11 people		MMMM	maternal		#FFFF00
16	2	30000000	66000000			FTDNA c... and 11 people		MMFM	maternal		#BFBF40
17	2	66000000	235000000			FTDNA c... and 11 people		MF	maternal		#FAAAAA
18	2	194000000	217000000			FTDNA c... and 11 people		MFFF	maternal		#9F6060
19	3	0	200000000			FTDNA c... and 11 people		FMF	paternal		#9FDFAF
20	3	0	200000000			FTDNA c... and 11 people		MM	maternal		#FFFFAA
21	4	0	187000000			FTDNA c... and 11 people		FF	paternal		#AAD5FF

Columns A (Chr), B (Start), C (End) and I (Side) contain the chromosome, start position and end position of each segment as well as the parental side of the segment (paternal or maternal)

Column F (Match) identifies the DMT run this data is from. It is the same in every line.

Column H (Group) contains the ancestral group for that segment, using DMT's notation (F=father, M=mother). This will be used as the DNA Painter group. You'll notice that all segments on the paternal side will have its group start with F and all on the maternal side will have its group start with M.

Only segments with ancestral paths of at least two generations (to the grandparents) will be included. There is really no need to include segments only known to be **F** or to be **M** because you already know the whole paternal chromosome is F and the whole maternal chromosome is M.

Column K (Colour) will be displayed in DNA Painter as the same grandparent colors used in DMT, with different shades of those colors used to give additional differentiation right up to the 4th generation, giving 16 possible different colors.

The cM, SNPs, Conf and Notes fields are not known by DMT and are not filled in.

Loading the file into DNA Painter

1. Either create a new profile in DMT, or open one of your existing profiles if you want to add to it.
2. Click on the gear and select the Action: "Import segment data"

The screenshot shows the DNA Painter web interface. At the top, there is a navigation bar with 'DNA PAINTER', 'Dashboard', 'Tools', and 'Help'. On the right, a user profile for 'Louis Kessler' is visible. The main content area features a profile for 'Example Load from DMT' with a 'Male' gender indicator and a progress bar showing '~ 0% / 0 segments painted'. A 'PAINT A NEW MATCH' button is present. Below this is a search bar with a tooltip: 'To reposition the key, click 'edit key' and drag it; extend its width by clicking and dragging on the right edge'. A menu is open, showing 'Import Tools' (highlighted with a red arrow), 'Actions', 'Options', and 'Reports'. The 'Import Tools' section includes 'Import segment data', 'Import 23andme ancestry composition', and 'Import mat/pat info from ftDNA'. The 'Options' section has several checkboxes for display preferences. The 'Reports' section includes 'All segment data', 'Inline segment editor', and 'All matches'.

3. On DNA Painter's import screen, use the "Choose File" button to locate the DMT dnainter.csv file to upload. You can leave DNA Painters' cM settings as they are.
4. Press the "Import this File" button.
5. Congrats. You've done it. Here is an example of what the above file gives in DNA Painter:



Example Load from DMT

Male

~ 79% / 84 segments painted

Switch chromosome map

PAINT A NEW MATCH

Click to add a description

To reposition the key, click 'edit key' and drag it; extend its width by clicking and dragging on the right edge

Import complete!
84 new segments over 10cM (or with no cM value set) imported for 1 match.
Note: If you retain the threshold and match names as imported, DNA Painter will automatically skip these matches when you next import the data. To force the importing of duplicates, uncheck the 'Skip matches that seem to have been imported already' option.



MFFF
MMMM
MF
MM
MMFM
FF
FMF

ALL NONE PATERNAL MATERNAL

Help with this page

Log File

Every time you press the Run button, the DMT program displays progress information about the run in the "Messages" area of DMT's main window.

DMT also creates a log file that documents the above progress information. The log file summarizes the run and includes the details of any errors encountered and the processing that has taken place.

Log files are not needed by Double Match Triangulator. They are created by DMT to provide you more information about your results. Feel free to delete the log files if you feel you have too many of them or if they are getting in your way.

Log files are saved in Folder A along with the DMT Excel Output files.

For single runs, the log file is named: DMT_aaaaaa_single_log.txt
 For A vs B runs, the log file is named: DMT_aaaaaa_bbbbbbb_log.txt
 For A vs all B runs, the log file is named: DMT_aaaaaa_all_doubles_log.txt
 For combined runs, the log file is named: DMT_aaaaaa_combined_log.txt
 where:

aaaaaa - is the identifier for Person A
 bbbbbbb - is the identifier for Person B

The DMT log file will be overwritten with new results when the same run is done again.

DMT log files can be viewed in Notepad or any other text editor. Here is how the beginning of a log file looks when opened in Notepad:

```

DMT_..._combined_log.txt - Notepad
File Edit Format View Help
Double Match Triangulator 5.0, 64-bit, by Louis Kessler: www.doublematchtriangulator.com
Louis Kessler is licensed to use this program.
This log file was saved as: DMT_..._combined_log.txt in D:\Documents\Personal\My Genealog
Segment limits used: Min Triang = 7 cM, Min Single = 15 cM.

Person A: ...
File A: D:\Documents\Personal\My Genealogy Research\DNA\Family Tree DNA\...
File A has 7013 people with 142136 segment matches. Smallest 1 cM. Largest 267.2 cM.
Using 7013 people and their 13304 segment matches that are at least 7 cM
*** Found 7 people with the same name as someone else and cannot be identified uniquely. Their name w

People File: D:\Documents\Personal\My Genealogy Research\DNA\Family Tree DNA\...
The People file has 9 MRCAs that DMT will use out of 7013 people.
Found the mother of Person A: ... sharing 3384.3 cM
Found the father of Person A: ... sharing 3384.5 cM

Comparing and then combining with up to 20 FTDNA segment match files in the folder: D:\Documents\Pers
Match 1 with: ... in file: D:\Documents\Personal\My Genealogy Research\DNA\Family Tree
Match 2 with: ... in file: D:\Documents\Personal\My Genealogy Research\DNA\Family Tree
Ln 1, Col 1 50% Windows (CRLF) UTF-8 with BOM
  
```

Below are details of the sections of information in the order that they are presented:

Header Section

```
Double Match Triangulator 5.0, 64-bit, by Louis Kessler: www.doublematchtriangulator.com
Louis Kessler is licensed to use this program.
This log file was saved as: DMT_..._combined_log.txt in D:\Documents\Personal\My Genealog
Segment limits used: Min Triang = 7 cM, Min Single = 15 cM.
```

The log file starts with the program version, licensee, the file it was saved to and the segment limits used for the run.

Person A Information

```
Person A: ...
File A: D:\Documents\Personal\My Genealogy Research\DNA\Family Tree DNA\...
File A has 7013 people with 142136 segment matches. Smallest 1 cM. Largest 267.2 cM.
Using 7013 people and their 13304 segment matches that are at least 7 cM
*** Found 7 people with the same name as someone else and cannot be identified uniquely. Their name w
```

Information about Person A's segment file, including the file path, the number of people and segment matches, and how many are being used with the segment size limit that was set. Any data problems to note are preceded by three asterisks ***.

The People File and MRCAs

```
People File: D:\Documents\Personal\My Genealogy Research\DNA\Family Tree DNA\...
The People file has 9 MRCAs that DMT will use out of 7013 people.
Found the mother of Person A: ... sharing 3384.3 cM
Found the father of Person A: ... sharing 3384.5 cM
```

The people file for Person A is read. The number of valid MRCAs you specified in the file will be shown. Illegal MRCAs that will not be used will be listed. If you have specified one or both of Person A's parents in the file using MRCAs of FR and/or MR, then DMT will confirm here that they were found.

The Processing DMT will do

```
Comparing and then combining with up to 20 FTDNA segment match files in the folder: D:\Documents\Pers
Match 1 with: ... in file: D:\Documents\Personal\My Genealogy Research\DNA\Family Tree
Match 2 with: ... in file: D:\Documents\Personal\My Genealogy Research\DNA\Family Tree
Match 3 with: ... in file: D:\Documents\Personal\My Genealogy Research\DNA\Family Tree DN
Match 4 with: ... in file: D:\Documents\Personal\My Genealogy Research\DNA\Family Tr
*** No match with: ..., file: D:\Documents\Personal\My Genealogy Research\DNA\Family Tre
Match 5 with: ...; in file: D:\Documents\Personal\My Genealogy Research\DNA\Family Tree D
Match 6 with: ... in file: D:\Documents\Personal\My Genealogy Research\DNA\Family Tree DNA\Ar
*** No match with: ..., file: D:\Documents\Personal\My Genealogy Research\DNA\Family
*** No match with: ..., file: D:\Documents\Personal\My Genealogy Research\DNA\Family Tree DNA
*** No match with: ..., file: D:\Documents\Personal\My Genealogy Research\DNA\Famil
Match 7 with: ... in file: D:\Documents\Personal\My Genealogy Research\DNA\Family T
Already found ... so skipping file: D:\Documents\Personal\My Genealogy Research\DNA
Match 8 with: ... in file: D:\Documents\Personal\My Genealogy Research\DNA\Family Tree D
*** No match with: ..., file: D:\Documents\Personal\My Genealogy Research\DNA\Family Tree D
Match 9 with: ... in file: D:\Documents\Personal\My Genealogy Research\DNA\Family Tre
*** No match with: ..., file: D:\Documents\Personal\My Genealogy Research\DNA\Family Tree D
*** No match with: ..., file: D:\Documents\Personal\My Genealogy Research\DNA\Family
Match 10 with: ... in file: D:\Documents\Personal\My Genealogy Research\DNA\Family Tr
Match 11 with: ... in file: D:\Documents\Personal\My Genealogy Research\DNA\Family
Already found ... so skipping file: D:\Documents\Personal\My Genealogy Research\DN
Found and will try to use 11 files of different people who match Person A
```

The files DMT will process are listed. If Folder B is selected, then all the files to be processed will be listed.

For a combine all run (shown above), each file B s checked to see if that person matches Person A somewhere. If not, they will not be included since all people must match Person A in a combined run. Also, if DMT detects more than one segment match file for a Person B, it will use the newest file and skip the others.

Match File Processing Information for Each Pair of Files

```

Person B: ██████████
File B: D:\Documents\Personal\My Genealogy Research\DNA\Family Tree DNA\██████████
File B has 8459 people with 202070 segment matches. Smallest 1 cM. Largest 55.3 cM.
Using 4275 people and their 9763 segment matches that are at least 7 cM where Person C is also a match
*** Found another 4 people with the same name as someone else and cannot be identified uniquely. Their
The MRCA of Person A and B is: MMFR
These are Person A's matching segments with Person B:
Person B's matches with Person A are the same as Person A's matches with Person B.
Persons A and B match each other on 5 segments, 66.5 cM total, 18.9 cM largest
Checking parent matches against each of Person A's matches with Person B:
Ch 1, 3265009 to 12148559, 18.4 cM, with mother only, start increased to 3528942
Ch 2, 38858709 to 56855610, 18.9 cM, with mother only, end decreased to 55747932
Ch 9, 14002596 to 24282583, 12.5 cM, with mother only
Ch 11, 117096794 to 121763566, 8.5 cM, with father only
Ch 16, 780770 to 5633477, 8.2 cM, with mother only
Father of A matches alone on 1 segment. Mother of A matches alone on 4 segments.
Both Father and Mother of A match on 0 segments. Neither Father nor Mother of A match on 0 segments.
Persons A and B are in common with 4274 people on 8576 segments with A and 9758 segments with B.
Persons A and B triangulate with 93 people on 103 segments containing 103 triangulations.
Persons A and B have Missing AB matches with 7 people on 16 segments.
Persons A and B have Missing BC matches with 0 people on 0 segments.
Person A has single matches of at least 15 cM with 479 people on 650 segments that do not double match
Person A has small single matches from 7 up to 15 cM with 6832 people on 12530 segments that do not double
Merging matches from file 1 of 11

```

Every run of File A with File B has its own processing summary. This will include a summary of what is in Person B's match file. Up to the first 100 data problems are displayed and well as a summary of them. The MRCA and matching segments between Person A and Person B are shown. If one or both parents are in Person A's match file, then additional parent processing is shown. A summary of the matches between Person A and Person B is provided.

Output File summary

```

DMT Chromosome file: DMT_██████████_Chromosome_1.xlsx
The map page will have 1022 lines
Time taken to build this DMT result file: 0.26 sec

```

Each output file will be listed.

DNA Painter File summary

```

61 lines written to DNA Painter file: DMT_██████████_dnainter.csv
Grandparents Mbp assigned: 1336 (43.8%) paternal; 1272 (41.7%) maternal

```

If a DNA Painter output file was desired, the DNA Painter filename and path is shown. It also displays the total Mbp and percentage of each parents DNA that have been mapped back to at least grandparents.

Extra Information in a Combine All Results run

Segment Size Summary

```

At least 25 cM: 87 F, 105 M, 26 U, 0 X, 218 total, 0.0% excluded, 28 Inferred
24-24.99 cM: 2 F, 4 M, 0 U, 0 X, 6 total, 0.0% excluded, 1 Inferred
23-23.99 cM: 5 F, 9 M, 1 U, 0 X, 15 total, 0.0% excluded, 1 Inferred
22-22.99 cM: 9 F, 6 M, 3 U, 0 X, 18 total, 0.0% excluded, 7 Inferred
21-21.99 cM: 8 F, 7 M, 0 U, 0 X, 15 total, 0.0% excluded, 0 Inferred
20-20.99 cM: 16 F, 10 M, 1 U, 0 X, 27 total, 0.0% excluded, 1 Inferred
19-19.99 cM: 16 F, 12 M, 5 U, 0 X, 33 total, 0.0% excluded, 1 Inferred
18-18.99 cM: 21 F, 20 M, 2 U, 0 X, 43 total, 0.0% excluded, 2 Inferred
17-17.99 cM: 38 F, 32 M, 6 U, 0 X, 76 total, 0.0% excluded, 0 Inferred
16-16.99 cM: 86 F, 33 M, 5 U, 0 X, 124 total, 0.0% excluded, 0 Inferred
15-15.99 cM: 125 F, 43 M, 7 U, 0 X, 175 total, 0.0% excluded, 2 Inferred
14-14.99 cM: 139 F, 70 M, 12 U, 0 X, 221 total, 0.0% excluded, 1 Inferred
13-13.99 cM: 239 F, 112 M, 21 U, 0 X, 372 total, 0.0% excluded, 1 Inferred
12-12.99 cM: 245 F, 160 M, 33 U, 0 X, 438 total, 0.0% excluded, 7 Inferred
11-11.99 cM: 453 F, 302 M, 73 U, 0 X, 828 total, 0.0% excluded, 8 Inferred
10-10.99 cM: 657 F, 368 M, 135 U, 0 X, 1160 total, 0.0% excluded, 3 Inferred
9-9.99 cM: 1061 F, 921 M, 362 U, 0 X, 2344 total, 0.0% excluded, 6 Inferred
8-8.99 cM: 1637 F, 1086 M, 737 U, 0 X, 3460 total, 0.0% excluded, 7 Inferred
7-7.99 cM: 1399 F, 982 M, 1530 U, 0 X, 3911 total, 0.0% excluded, 10 Inferred
Total: 6243 F, 4282 M, 2959 U, 0 X, 13484 total, 0.0% excluded, 114 Inferred (28 without cM)

```

A Combine All Results will summarize the F (father), M (mother), U (unknown), and X (excluded) segment matches of Person A, give the percentage excluded (X), and the number inferred, all by segment size.

People File summary

```

Created the DMT People file for Person A: DMT_██████████.people.xlsx
People with Clusters assigned: 5423
Time taken to build this People file: 0.50 sec

```

Tells you if the People File was updated. The MRCAs you had previously entered into the People File will be retained.

Completion Line

```

Completed processing for 11 FTDNA Person B files. Total time taken: 17.38 sec.

```

If the run completes normally, there should be a final processing summary line.

Ideas, Tips and Tricks

What DMT Can Give You

Double Match Triangulator will provide you with ALL triangulations that Person A has with Person B down to the "Min Triang" limit that you specify.

Double Match Triangulator will also provide you with ALL inferred matches that Person A has with Person B down to the "Min Single" limit. Inferred matches can only be determined from a Person B and Person C who both have their MRCAs assigned.

Double Match Triangulator will also take your known MRCAs and automate the DNA Painting procedure that you would do if you had the time and patience to paint thousands of segments. It will include the use of triangulation information which most DNA Painting methods do not consider. And it will optionally produce DNA Painter output file that can be uploaded to [Jonny Perl's Dna Painter tool](#).

Double Match Triangulator will organize the people into Clusters that correspond to your MRCAs, providing different and additional information from other clustering tools.

Interpreting Results

Double Match Triangulator is designed to help you extract information from your DNA matches. It automates a lot of the work of comparing segments and assigning ancestral paths that you would want to do.

The results are only as good as the segment data and your MRCA assignments. Generally segment data is more "correct" than "incorrect" and the same hopefully can be said for your MRCA assignments. What that means is that DMT's results should generally be good, but are definitely subject to error. You should check any results you use to see that they seem logical and make sense to you.

Think of DMT like a clustering algorithm that does its best job to put people together into clusters that make them most similar. That in no means gives you perfect results. It just gives a best-possible algorithmic estimate of what the most likely results are. That is good information that can help you to place your DNA relatives into your family tree.

Incorrect Results

If you assign an MRCA to a person, but the person is also related another way, then the segments through the other relationship will be assigned an incorrect ancestral path. Since DMT uses a consensus-based decision as to what the ancestral path of a segment is, hopefully in most cases, correct assignments will outnumber incorrect assignments and the final mapping will be correct. But not always.

If a segment match is a match by chance or false match, the MRCA will be assigned if the match is included. You can manipulate the segments that will or will not be triangulated and included with the Min Triang and Min Segment settings.

Using Older Segment Match Files

Any segment match file can only include people who tested before you downloaded the file. A newer file will have people who tested that the older file did not. Obviously, you would like the newest file possible, but maybe you got the segment match file a while ago from someone else and have no way of updating it. Can you still use that file?

If you compare a newer file as File A with an older file as File B, the newer File A may match Person C, but the older File B may not because Person C did not test yet. That match could actually be a triangulation, but would then only

show up as a single A-C match. If Person A has any triangulations with other people on the segment, then the A-C match will be incorrectly assigned to the opposite parent.

If you compare an older file as File A with a newer file as File B, then the Person A file will not contain any newer matches and there should be no problems with triangulations.

So the general rule if you have a choice, is use a File A that is older than any of your File B's. If that's not possible, then just be aware that for C people who tested after B tested may have some segments assigned by DMT to the opposite parent when they should be triangulations.

Organize Your Match Files

I create a DNA folder for all my DNA analysis.

Under that, I have a folder for FTDNA, one for 23andMe, one for MyHeritage and one for GEDmatch.

Under those, I have a folder for each person who I got the match files from. My own files and the files of people I administer are in a folder called "Louis Kessler". For GEDmatch, you can download files yourself, so you could put them all in the GEDmatch folder if you want.

Then, I can run myself (or anyone else) as File A against all the files I got from a specific person, or all my matches by specifying the DNA company folder and checking **Include subfolders**

One Company At a Time

DMT only can compare same to same. i.e. FTDNA to FTDNA, 23andMe to 23andMe, MyHeritage to MyHeritage, and GEDmatch to GEDmatch. That is mainly because the same people at different companies very often have different names.

If you have data for a Person A from multiple companies, then what you can do is use is set up DMT to do a Combine all Results run and do that once for each company. Each company will have a different People file for Person A, and you'll have to enter Person A's MRCAs into each of them. But then you'll be able to compare the result files between the companies yourself, or create DNA Painter files and load them into DNA Painter and use the DNA Painter tools to compare them.

Which company? All of them that you have data for, of course. Every one will give different information because you match to different people at the different companies. Ancestry DNA unfortunately doesn't supply its users with their match data, so the only way to include an Ancestry DNA tester is if they've uploaded one of the other companies.

MRCAs Rule!

If you don't know any of your DNA match's MRCAs, then DMT won't be able to calculate any ancestral paths for you. The ancestral paths can only be calculated as deep as your most distant MRCA is. So if you only know a second cousin, e.g. whose MRCA is **MFR**, then usually the best DMT can do for you is to separate out MF from MM. The more MRCAs you know exactly, the better.

However, do realize that an MRCA very deep, e.g. **MMFFFMR**, might be a common ancestor, but it might not be the only common ancestor and it might not be the Most Recent Common Ancestor. Even so, it is definitely worth trying it. If that person is only related through that ancestral path, then you got it right.

To test if your deep path might be likely the best, try a run leaving its MRCA blank. See what ancestral paths DMT assigns its segments and what cluster the person is put into. If the cluster and most of the segments agree with the deep path, then you are likely safe to use that deep path.

Partial MRCAs

If you don't know the full MRCA of a DNA match, you can leave it blank and DMT will do its best to assign ancestral paths to all the segment matches without that information.

But if you do know the match is along a specific line somewhere, feel free to enter the known part of the MRCA in the people file. Partial MRCAs are indicated by not having a trailing **R**. That means the true MRCA is at least as long and may be longer than what is given but the rest is unknown. e.g. you can use **MM** if you know the person is related somehow through your Mother's Mother's line. The Leeds Method and various clustering tools may help you assign partial MRCAs to some of your matches, especially at the grandparent level.

DMT will use full or partial MRCAs to be each segment's assumed starting ancestral path.

If you have a relative you know is related more than one way, then some segments will come from one MRCA and some will come from another. You can only pick one MRCA, so segments from the other will be assigned incorrectly. You can leave the MRCA blank, or you can use an partial MRCA (one without an "R" at the end) if the two MRCAs start along the same path.

The X Chromosome

A male only has one chromosome 23 (aka X) that is passed from his mother. DMT uses the sex you enter for Person A. If Person A is a male, DMT will calculate all ancestral paths on his X chromosome as coming only from his mother.

Any X matches with someone who has **FF** as part of their MRCA will be considered false. The X chromosome does not pass through two males.

Triangulation Groups

Double Match Triangulator bases its triangulation groups boundaries on Mbp that have a local minimum number of triangulations running through that location. This means that there are some triangulations that end before this point and others that start after this point. This indicates a possible subdivision point that divides a triangulation group for a closer MRCA into two triangulation groups of more distant MRCAs.

The starting and ending locations of triangulation groups cannot be determined exactly because there can be by-chance matching at both the start and end of any real match. So the best that can be done are approximate boundaries between triangulation groups. DMT rounds triangulation group boundaries to the nearest Mbp, and even so, you'll see matches often extending a few Mbp past their boundary.

A key to interpreting matches and triangulation groups is that the start and end of any match is due to a recombination that occurred somewhere down from the Most Recent Common Ancestor, and that could have happened on the way down to Person A, down to Person B, or down to Person C. The Start-AC, End-AC, Start-BC and End-BC positions on the Chromosome Map page can help you identify whose line "owns" the endpoint. If that endpoint was owned by Person A, then the segment on the other side of the endpoint would have come from a different ancestor.

Small Segments

Be very careful on interpreting small segments. Single matches less than 15 cM might be matches by chance. Triangulations under 7 cM might be matches by chance.

Generally, you should leave the DMT defaults at these 7 cM and 15 cM levels:

The image shows two dropdown menus. The first is labeled 'Min Triang' and has '7 cM' selected. The second is labeled 'Min Single' and has '15 cM' selected.

You're much better off trying to figure out new MRCAs to add, or getting other people's match files, than lowering these limits.

What To Do When Results are Wrong

DMT has to use the data it is given. It uses all the matches from the segment match files filtered down to the Min Triang level and it uses the MRCAs that you provide. Often the data conflicts, e.g. a segment triangulates with someone on your father's father's side and someone else on your father's mother's side.

There are many possible reasons for these type of seemingly impossible results. Segment data isn't perfect. Company matching algorithms aren't perfect. A match may be by chance. A smaller segment may be filtered out. Your MRCA may not be correct. Your relative may be related more than one way. A triangulation may be through opposite parents. One person may triangulate with everyone else because their two chromosomes match with the one segment. Two different people might have the same name.

DMT attempts to take every assertion that your data makes and combine it into a consensus-based best estimate of what's going on. It uses human-like logic to "paint" the segments, assign ancestral paths, and cluster your matches. It does what you would want to do with the data, but does it in seconds rather than years.

One method you can use for analyzing segments matches and resolving conflicts is to produce both a "Combine all results" run and then uncheck it and produce all the individual one-to-one runs. First look through the combined results for anything that looks strange, Then check the relevant one-to-one runs to determine the details. You might want to look at the specific segment match files to see the raw data that was used. Almost always, you'll find that there is conflicting data, and the program is really doing the best it can with what it has.

If there is a specific person who is problematic, you can remove their MRCA, or use a partial MRCA, e.g. remove the "R" or reduce the MRCA to just "F" or "M" without an "R" at the end and let DMT tell you what it suggests as the ancestral path of the person's segments and the cluster of the person.

You may also have some slightly-larger-than-small false segments. You may want to try increasing Min Triang and/or Min Single by a few cM.

Try the other tools, including DNA Painter, Leeds Method, Clustering, etc. and compare results.

The best ways to improve overall results is to find out how you're related to more people and add their MRCA. You can also get more segment match files for some of your matches, especially second, third and fourth cousins who will help identify the ancestral paths along their lines. At GEDmatch and 23andMe with DNAGedcom, you can obtain segment match files yourself for any of your matches. At Family Tree DNA, MyHeritage or 23andMe without DNAGedcom, you will have to ask your matches to send you their segment match files.

For the Latest: Blog Posts

I will blog from time to time about DMT and how to make use of it. A list of my DMT-related blog posts that I try to keep up to date is at:

www.doublematchtriangulator.com/blog.php