MyHeritageDNA for Your Family Knot

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DNA tools can only help you if you use them appropriately. The family "knot" (instead of a tree) is a common problem confounding genetic genealogists who haven't realized what they are dealing with.

Part 1: Your Family Knot

Your "family knot" is an informal way of referring to a situation where the branches of your DNA tree are tangled up. For this lecture, it is used to mean situations where there is intermarriage between branches, cousin marriages, or any situation of inter-relatedness that is not as severe as endogamy.

Confusion in your shared matches is often the symptom that indicates this problem.

There is no easy to reference list of "knotted" populations. It can happen in large populations like southerners (people from the southeastern U.S.) but it can also happen in a small population that will only be identified by DNA users with those ancestors.

There are three major pitfalls to using shared matches as the primary tool if you have a knotted tree. If you do not have a knotted tree, focusing on the simple to use shared matches is a great place to start and keep focusing even as your project and skills progress.

Shared Match Pitfalls from Tangled Branches

You will be related to matches in more than one way. The number of shared ancestors in your family tree and your DNA tree most likely differs.

- You are more likely to incorrectly assume where the shared DNA comes from.
- You are more likely to have "false" shared matches.
- It is harder to determine which relationship the shared segment is for, making it harder to use that match to identify new ancestors.

You will also potentially (but not certainly) have shared amounts of DNA outside the standards for estimating relationships.

To review the material about identifying your family knot situation, see this blog post, http://bit.ly/your-family-knot-handout.

Part 2: MyHeritageDNA for Your Knot

MyHeritageDNA Process for "Knotted" Trees

This is my process specifically for MyHeritageDNA based on the tools they offer. My process is different at other sites because they have different tools.

Outline (from first steps to MyHeritage's unique tools):

1. Flesh out the test taker's tree as much as possible.
2. Review your closest DNA matches looking for known shared ancestors and clues.
3. Take notes, make sure you can find them again.
4. Build trees for your matches whenever necessary. Start with what they provide, check it, and take it farther.
5. Repeat steps 2–4 until you have enough information to start focusing on something more specific than just "my DNA results."

The above steps apply to any testing company.
The following steps are for MyHeritageDNA, specifically.

6. Choose a "close" or "extended" match with an identified shared ancestor (MRCA) you want to focus on.
7. Click "Review DNA Match"
8. Review any MRCAs already identified for the shared matches. Do they agree? Do they make sense?
9. Take notes.
10. Now review the triangulated matches.
11. Build trees for triangulated matches to attempt to find MRCAs for them.
12. Eventually…map the test taker's chromosomes to try and untangle the branches (versus mapping segments to an exact ancestor, that's a later step).
13. Bring in results for other testing companies and sites.

Remember, this process is for MyHeritageDNA based on their tools and also for people who have a "family knot" rather than distinct branches. The steps will work for anyone but distinct branches can rely on simpler to use tools without suffering from the multitude of pitfalls you find with a family knot.

MyHeritageDNA for Your Family Knot

General Tips

- Have tests for multiple test-takers to work from whenever possible. The general advice of having the oldest person (by generation) tested is important but having cousins (first and second) and half-siblings tested is especially helpful if your tree is knotted.
- If you can't identify any common ancestors with any matches, focus on that, first.
- You want to start with a "close" or "extended" match with an identified shared ancestor. Starting with a "distant" match can be too challenging for a knotted tree however you can use any clues from any match if you're still trying to identify a MRCA.
- You're starting with a match with an identified MRCA but we aren't assuming that's where the shared DNA comes from. With a "normal" tree that is often a safe assumption but that's the pitfall with a knotted tree.
- Keep a note of identified shared ancestors and notes about problems you see in the notes field at MyHeritageDNA.
- Use an online tree building tool, like MyHeritage's Family Tree Builder, for building "quick and dirty" trees for DNA matches. Keep all of these individual trees in one "tree" file so you can connect them together whenever you find a shared ancestor.
- MyHeritageDNA is a good "hub" for working with segments and triangulation data. AncestryDNA is a good "hub" for working with shared match clusters. Both might lead you to new ancestors but if your tree is really knotted, the AncestryDNA clusters might be more useful to identify the problems whereas the MyHeritageDNA triangulation groups can help you determine the shared ancestor for the actual DNA. (Put another way, AncestryDNA can help highlight pitfalls, MyHeritageDNA can help you untangle your knot. Use them together for best results).

REMINDER: Finding a shared ancestor who is NOT the source of the shared DNA is still helpful to your genealogy, it is just a red herring for your genetic genealogy. Don't get too focused on just the DNA.

Remember, you need to have lots of trees for your matches, which you will likely have to build, before other DNA tools begin to help. You can however use triangulated groups to help you decide whose tree to build first. Once you have trees to start from, you can continue to build on to them as clues start to appear. That means you need to be able to find a tree for a specific match again, and quickly!

Triangulation at MyHeritageDNA

The simplicity of identifying triangulated matches at MyHeritageDNA is a huge help if you come from a "knotted" population.

For clarity, there are three players in triangulation, the test-taker, the "match," and the "shared match" which I'll abbreviate "TSM" for triangulated shared match(es).

Using the easy to access TSM is a way to avoid the pitfall of "false" shared matches. When your tree is knotted, you have the common type of "false" shared matches (the shared ancestor between the match and shared match is not your ancestor) but also a case where you do share that ancestor but he/she is not the source of the shared DNA.

This is a double whammy. Tangled branches lead to more cases of the common false shared matches plus have this unusual type. Using TSMs can save a lot of frustration.

Details of using Triangulation at MyHeritageDNA

- Review "all" the triangulated shared matches. It isn't necessary to literally review all of these. Make the decision based on how many there are and how much free time you realistically have. Use these guidelines.
    - Review the closest triangulated shared matches to the test-taker. I try and make sure to look through 40cMs. I don't recommend going below 20cMs at this point.
    - Make sure you are reviewing some triangulated matches under 200cMs.
    - If you really have a lot of TSM, consider if you are dealing with an endogamous population (or a really large project where many close relatives were tested).
    - If there are only a handful of triangulated matches, review them all.
    - Use the shared cMs and the potential shared ancestor to further refine which TSMs to focus on if there are too many to review "right now."
    - Focus on the TSMs with larger trees.
- Review the closest TSM to the match, too, using the same guidelines.
- Make note of all identified MRCAs. Also make note of where there is a tree you can build out and any TSMs of particular interest that you want to try and contact.

The initial goal of this process is to identify any pitfalls as quickly as possible. A pitfall is where the shared DNA does not come from the identified MRCA.

Tips

- The primary goal is to identify where the shared DNA comes from. This can be from multiple ancestors if there are multiple segments. Make sure you are aware which triangulation group you are reviewing.
- Knotted trees often mean even a triangulation group shares more than one ancestor from different branches. Don't assume a shared ancestor based only on one (three-person) triangulation group.
    - Expand the group.
    - Look-out for "projects" (many close relatives were tested).
    - Use cMs/segment sizes to check the reasonableness of potential common ancestors. This is important before moving on to the mapping step as major inconsistencies may indicate a problem. Realize a knotted tree can throw off the estimates but often they will still be in the ballpark. Keep track of this type of information to help improve your estimates.
- Keep an eye out for patterns or themes. These may not appear until you start mapping segments but you want to notice that you consistently share more or less DNA with all or most of the matches with a certain branch. This does not require segment data so also take into consideration the information from other sites. Even AncestryDNA provides enough information for you to determine important patters of this type.

Segment Data + Chromosome mapping

MyHeritageDNA makes it easy to use chromosome mapping (I love DNAPainter).

The goal of starting to map your chromosomes earlier in the analysis process is to overcome the pitfalls of using shared matches. It also has another advantage.

It can help identify pile-up regions. These *can* be situations where it would be a waste of time to focus on finding your shared ancestor with a group of TSMs because that ancestor is unusually far back in the tree (prior to a point where genealogical research is reasonable).

- Import data (vs. individual mapping segments) to quickly look for pile-ups.

Inductive Mapping

Use inductive mapping to give yourself the best chance of success. You may want this map to be a separate file because the goal is NOT to map segments to the exact ancestor they came from but to untangle the knot in your DNA tree.

- You MUST be familiar with several (preferably 5+) generations of the test taker's tree to be sure this will help. The exception is when a branch is mostly unknown but is known to be a distinct population (i.e. there should be no identifiable genetic overlap into the known branches).
    - Wait to try mapping if there is a likely related but unknown branch.
- Do not map any immediate relatives that share both maternal and paternal (no siblings, no descendants, no nieces/nephews, etc.).
- Do map first cousins and half-siblings. If you have first cousins/half-siblings who share significant DNA on both maternal and paternal, it is up to you whether to use them. Their segments will not help unless you know which are maternal and which are paternal segments.
- Map all segments for closer matches with a known MRCA and no confusion between maternal and paternal.
- Map all large segments for matches who **only share one large segment** and have a known MRCA. It does not matter if there is confusion between maternal and paternal if they only share one segment. Do not mark them as maternal as paternal, if you are not sure, though.
- Use direct and inductive mapping to sort segments into maternal and paternal. This may not work for endogamous populations but can work wonders for knotted but non-endogamous test-takers' trees.
- Be careful when doing this and don't add matches to a group prematurely.

Tips

The purpose of doing this mapping at this early stage of analysis is to identify problems and get matches generally to the correct branch.

- Create additional groups when you want to tentatively mark a segment or match as belonging to a branch or if they belong to more than one branch. Being able to easily move matches between groups, which can have descriptive names, is one of the advantages of using DNAPainter.

- Use branches instead of ancestors so you can add meaningful information as quickly as possible. You want to be as specific as possible without causing the same problems that arise from using just shared matches.

The exact process, steps, and focus are determined by your results. I tend to work on "large" segments until a potential clue to a shared ancestor captures my attention and then I focus on that chromosome or segment. You may *want* to work differently or *have* to work differently.

- Add in matches from GEDmatch and FamilyTreeDNA (ADSA from DNA GEDCOM can help if you want to focus on a chromosome or segment).
- Don't forget to transfer findings and notes back to MyHeritage (to your tree, if appropriate, or to the notes field for quick reference, later).

WARNING, WARNING!

Auto-clustering can cause worse problems if you have a family knot, especially if you don't realize it.

- Auto-cluster tools use shared matches to create the clusters.
- Shared matches are the big "tool" that doesn't work the same if you have a knot instead of a tree.
- Once you know your situation, you can adjust your strategy to use auto-clustering or not.
- DNAPainter's new CAP tool can help you evaluate the usefulness of your MyHeritage auto-clusters. You will need lots of identified MRCAs before this will help, though.
- An auto-cluster can always be used as a way to focus on a select group of matches, it just won't always relate to a shared ancestor when your tree is knotted.

Reminder

Don't forget to **focus on a specific goal**. Just reviewing "all" the matches over and over again can only take you so far. Adapting to the exact "knotted" situation can only be done for a specific test taker and goal.