

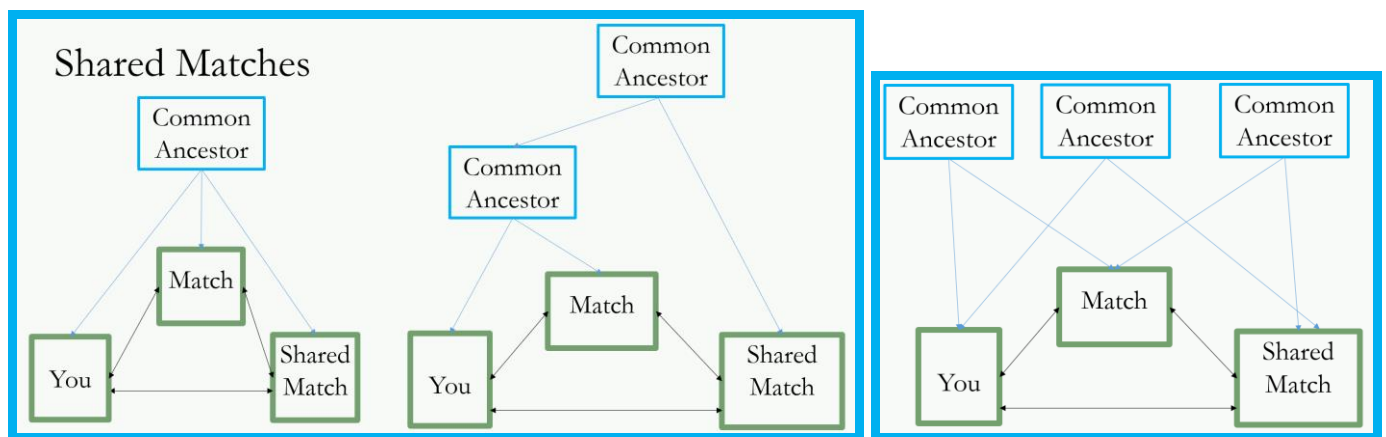
Using DNA to Support Family History Research – Handout

This handout supports the ‘Using DNA to Support Family History Research’ talk presented to the West Middlesex Family History Society online on 19 September 2024.

Key Concepts

Shared Matches

- DNA Match = someone you share DNA with
- Shared Match = someone who shares DNA with you and your DNA match
- You, your match and your shared match will usually share a common ancestor
- Small risk you do not have common ancestor if you have three separate connections (see third scenario below)



Finding Shared Matches

- AncestryDNA – see ‘Shared Matches’ tab on Match page. To appear on the list, the Shared Match must share greater than 20cM with you and share greater than 20cM with your match. If you have AncestryDNA Pro Tools then only your match must share greater than 20cM.
- MyHeritageDNA – scroll down to ‘Shared DNA Matches’ on Match page – click on ‘Show more DNA matches’ at bottom of list to show more
- FTDNA – click on the people symbol on right hand side of match list and choose ‘In Common With’
- 23andMe – scroll down to ‘Find Relatives in Common’ and click button to show shared matches

MyHeritageDNA and 23andMe also give amount of DNA the shared match shares with your match.

Grouping/Clustering Matches

Groups of matches that share DNA will be connected within the same family lines.

Use groups to find connections between matches to identify their family lines.

- Known groups (e.g. you know the family line)
- Unknown groups (use these to solve brickwalls/unknown parentage cases)

To carry out grouping/clustering;

- Identify starting match (usually second cousin or more distant) – the most recent common ancestor with the starting match indicates the family line for the group
- Identify their shared matches (and add them to group)
- Identify the shared matches of the shared matches (and add them to the group)
- Only include matches that are at the same or more distant relationship distance than the starting match
- Identify next match down the list not in a group and use as starting match for next group

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- Continue until all matches (down to a chosen level) are in groups
- Use 'No shared matches' identifier for matches without any shared matches

Methods for Grouping:

- Leeds Method – instructions at: <https://www.danaleeds.com/dna-color-clustering-the-leeds-method-for-easily-visualizing-matches/> - aims to group into your four grandparent lines. Do not include matches with less than 400cM if they are related via two of your grandparents (e.g. first cousin twice removed). Extend below 90cM to get enough matches (noting you may get more groups linked to great-grandparent or great-great grandparent lines).
- Ancestry Coloured Dots/Squares – <https://support.ancestry.com/s/article/Grouping-and-Filtering-AncestryDNA-Matches> - give chosen starting match a colour (named e.g. *Group 1* or *Group 9 – Bull Family*) then add all shared matches (excluding any closer than the starting match and (if you have Pro Tools) low matches (e.g. below about 15cM) and the shared matches' shared matches. Then go to next match without a group and start again. First check if any of their shared matches already belong to a group. If so, then add them to that group rather than starting a new group. Use the SideView technology (which splits your matches into Parent 1 and Parent 2 where possible) to help identify which side the group belongs to. Note Parent 1 can be either paternal or maternal; Parent 2 will be the opposite of Parent 1. More information at <https://support.ancestry.co.uk/s/article/DNA-Matches-Split-Up-By-Parent>
- MyHeritageDNA Labels - be wary of shared matches that are less than 15cM with either you or your match (do not include in grouping) - <https://blog.myheritage.com/2021/12/labels-for-dna-matches-now-improved/>
- Auto-clustering - MyHeritageDNA inbuilt tool or use Genetic Affairs (<https://www.geneticaffairs.com/>) for 23andMe and FamilyTreeDNA¹. Visual (.html) and tabular (.csv and .html) results are provided.

Use the groups formed to research the trees of the matches to find the common line. Further sub-cluster the group (by using a more distant match within the group) to find more distant family lines.

Overlapping groups – this could be due to:

- One match being more closely related than the starting match (remove them from grouping and start again)
- One match being related to a shared match by an unrelated line
- Multiple paths (endogamy (<https://isogg.org/wiki/Endogamy>), pedigree collapse (e.g. due to cousins marrying) or double cousins (e.g. two sisters marrying two brothers))
- Two groups are actually one and can be merged

Quick and Dirty Trees

- Used to quickly find a common ancestor with a match
- Do not need to follow normal good practice:
 - Use other people's trees (with caution)
 - Only one piece of evidence for a relationship
 - Use transcriptions rather than original documents
- Once a connection is found, confirm the 'quick and dirty' tree with more detailed research
- Check all lines for possible connection to ensure found correct path
- Remember a DNA match alone cannot prove a relationship

¹ The use of Genetic Affairs is more limited at the moment as the files required to be downloaded from the DNA companies have been affected since the security issues in 2023.

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- Build ‘Quick and Dirty’ trees on paper, computer files or on an electronic tree.
- Make Ancestry trees private and unsearchable (go to ‘Tree Settings’, ‘Privacy Settings’, then tick ‘Private Tree’ and the tick box to ‘prevent your tree from being found in the search index’)
- Identify your DNA matches – add *** before first name; add test company and shared DNA in Suffix (e.g. A-35cM) (note these both help if you export your GEDCOM to WATO) – or use Ancestry Tags.
- Add someone from another tree via ‘Tools’ dropdown on right-hand side and choosing ‘Save to Tree’.

Methods for Using DNA for Family History

Verifying known tree

Two approaches

- Identify how individual matches are connected
- Group matches then work out common ancestral line

Once identified known matches:

- Work out where shared matches to the known match fit on that line (e.g. back to the common ancestors)
- Identify lines without DNA matches. This may be because:
 - Inherited less DNA from that line
 - Line is too far back (e.g. further back than 2xgreat-grandparents are less likely to be seen in DNA results)
 - No-one tested on that line
 - Paper trail may be wrong – if this is the case do you have a group of matches that does not fit into known tree? This group may indicate the alternative line to the paper trail.
- Be prepared that not all matches/groups can be identified – await further information to solve these

Strategy for Solving Brickwalls with DNA

- 1) Clearly define the problem/brickwall
- 2) Identify your relationship to the brickwall person (e.g. great-great grandparent)
- 3) Ensure that DNA can help (e.g. within an appropriate time period/number of generations)
- 4) Identify unknown groups
- 5) Examine groups to see which are most likely to be related to your brickwall
- 6) Identify a common ancestor/line within the cluster(s)
- 7) Confirm if the common ancestor/line are in the same area/location as your brickwall or if they have a possible link
- 8) Use Shared cM project (<https://dnainter.com/tools/sharedcmv4>) to identify the possible relationships between each match and you
- 9) Work out the different possibilities (candidates) for where you could fit within their family tree
- 10) Research each possible scenario to see if the paper records put the candidate in the right place at the right time
- 11) Eliminate any that do not work
- 12) Given the remaining candidates, you can work out your hypotheses (e.g. the possible places you fit in their tree)
- 13) Test the hypotheses using What Are the Odds? (WATO - <https://dnainter.com/tools/probability> - see FAQ and videos on DNA Painter website)
- 14) Remove any hypotheses on WATO that are not possible statistically (e.g. ones that are red (probability 0) – all others are possible even it is only 1)
- 15) Accept that you may not get a definitive answer and further work or more information is required
- 16) Keep reviewing match lists
- 17) Upload to or test at other companies where possible

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- 18) Test other relations on the same family line
- 19) Consider if a Y-DNA or mtDNA test will help (noting mtDNA can normally only be used to eliminate possibilities)
- 20) Write up what you find to ensure you have thought through all possibilities
- 21) Continue reviewing your hypotheses to build up your confidence (or disprove a hypothesis) as more information and matches become available

Identifying Biological Parents

The key steps for identifying biological parents are:

- Identify any close relatives
- Group DNA matches
- If relatively close match, build tree up and back down again to identify candidates
- Identify common ancestor in each group
- Identify where the families of common ancestors overlap
- Identify possible candidates for parents
- Use identifying information (dates, places, names) to shortlist candidates

Note if you are helping an adoptee in the UK, there are specific rules for approaching their birth family on their behalf. You should advise them to contact their local council adoption services or find a private Ofsted approved intermediary to support making contact.

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