

LEEDS METHOD CLUSTERING CHECKLIST

The complete step-by-step for sorting matches into four grandparent groups

Before you begin — quick glossary:

Cluster — a group of matches who all share DNA with each other, usually because they descend from the same ancestor or ancestral couple.

Shared-match / ICW list — the list of people who match both you and one specific other match — the raw material every cluster is built from.

Pedigree collapse — when the same ancestor appears more than once in your tree (common in small or isolated communities), which can merge clusters that should be separate.

Dana Leeds' clustering technique sorts your matches into up to four groups, each corresponding to one grandparent. Best used on matches in the 40–400 cM range. Budget 1–3 hours of focused time.

Step 1 — Prepare your match list

- ☐ Export or list matches between 40 and 400 shared cM — ★ *this range is not arbitrary — above 400 cM matches are usually too close and will appear in every cluster; below 40 cM the data gets noisy and harder to trust*
- ☐ Exclude very close matches (parents, siblings, children, and anyone above ~1,300 cM) — *they will match everyone and won't cluster cleanly — set them aside and handle them separately*
- ☐ Set up a spreadsheet with matches as rows — *one column per eventual cluster colour, plus name, total cM, and notes columns*
- ☐ Aim for at least 20–30 matches in your working list before starting — *fewer than this and clusters may not form clearly; if you have fewer, lower your cM floor slightly (e.g. to 30 cM) rather than starting with too little data*

Step 2 — Build the grid, one colour at a time

- ☐ Take your strongest (highest cM) unclustered match and assign it Colour 1
- ☐ Pull that match's shared-match list — *on Ancestry: "Shared Matches" tab; on MyHeritage: "Shared DNA Matches"; on FTDNA: "In Common With" filter in the match list*
- ☐ Colour every match on that shared list with Colour 1 — *in the spreadsheet, mark an X or shade the cell in that match's row under the Colour 1 column*
- ☐ Move to the next uncoloured match in your list and repeat with Colour 2 — *continue with Colour 3, Colour 4, and so on*
- ☐ Continue until every match is coloured, or is a clear outlier — *an outlier is a match that doesn't cleanly join any group after several attempts — set these aside rather than forcing them into a cluster*
- ☐ Expect the process to take 1–3 hours for a list of 30–50 matches — *this is normal — work through it over a few sessions rather than rushing*

Step 3 — Interpret the resulting clusters

- ☐ Confirm you have up to four distinct colour groups — *four is the expected maximum, corresponding to your four grandparents — fewer than four is common and fine*
- ☐ Assign each colour to a suspected grandparent line — *use any match whose relationship you already know for certain as an anchor — whichever colour that match falls into identifies that whole cluster*
- ☐ Flag matches that fall into two colours — *these "bridge" matches often connect to a shared ancestor further back than the grandparent level — set them aside as a special case rather than forcing a single colour*
- ☐ Note any grandparent line with unexpectedly few matches — *this can indicate that line tested less, immigrated recently, or — if it's a complete blank — may be the line worth investigating for an unknown-parentage situation*

Step 4 — Turn clusters into genealogy

- ☐ For each cluster, identify the earliest common surname among its members

- ☐ Build or extend the tree for that ancestral line using standard records — *census, church, and civil registration records for the relevant country/region*
- ☐ Cross-check cluster findings against paper-trail research — *a cluster tells you WHO is related, not automatically HOW — confirm the specific relationship with documents*
- ☐ Document which matches confirmed which ancestor — *record this directly in your master DNA match spreadsheet's "suspected ancestor" column*

Pro tip: Endogamy or pedigree collapse (common in some regions, including many Nordic populations) can blur clusters together. If your four colours won't separate cleanly, try re-running the grid using only matches above 90 cM before concluding the method has failed.

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