



Help! Part 1.26

I Got My DNA Results and I'm Confused -- handout

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Goal of This Seminar

Help you prioritize "tree-friendly" unknown matches to create a manageable contact list of relatives likely to help grow your family tree.

Key Concepts

- You are doing **data analysis**. Follow the **evidence**, not what you *hope* is true.
 - **DNA doesn't lie**, but it can be misinterpreted.
 - You may discover family **secrets** — be emotionally prepared.
 - Let's reduce the confusion by:
 - Organizing your match list
 - Prioritizing the best leads
 - Managing expectations
-

Important Caveats

- Works best in the **3rd Cousin Range +/-** (2C2R to 4C1R)
- These are **guidelines**, not rules. **RULE 1 – EXPECT EXCEPTIONS**
- Test **siblings and cousins!** They may share DNA with matches that you don't.

What DNA Can Tell You (in cM)

Relationship	DNA Shared (Range)	Chance of Zero DNA
3rd Cousins	Wide range	~10% may share 0 cM
4th Cousins	Often less than expected	45-50% may share 0 cM

 More info: [Lara Diamond DNA Chart](#)

AScM (Average Segment Size Method)

Helps filter your **endogamous** matches into **priority buckets** so you don't waste time chasing down unhelpful leads.

Look for matches with a higher **Average Segment size** (Total cM / # Segments).

Focus on matches with an **AScM ≥ 12.0** in the 2C2R to 4C1R range. Keep notes. Prioritize. Expect exceptions!

How to Use This on DNA Testing Sites

AncestryDNA – Slide 12

- Go to your **DNA Matches** list.
 - Click the **predicted relationship** for segment info.
 - Use the **Notes section** to track progress.
 - Take **screenshots** or copy/paste into spreadsheets.
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Family Tree DNA (FTDNA) – Slide 12

- Use the **Chromosome Browser** tab (not just match list).
- Check boxes to select matches.
- Chart or log the AScM results.

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- Repeat the process with **siblings' matches**.
 - Take **screenshots** or copy/paste into spreadsheets.
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MyHeritage – Slide 12

- Go to **DNA Tools > Chromosome Browser**.
 - See **20 matches per page** (great for screenshots).
 - Enter data in a spreadsheet or use our **template**.
 - Few high-value matches, but they're gold!
 - Take **screenshots** or copy/paste into spreadsheets.
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23andMe – Slide 13

- Go to **Family & Friends > View DNA Relatives**.
 - Sort by **% Shared DNA**.
 - Focus on matches sharing **≥ 1.2% DNA**.
 - Convert % to cM with the table provided.
 - Highlight AScM **≥ 12.0**. Ignore the rest (for now).
 - Take **screenshots** or copy/paste into spreadsheets.
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Rinse and Repeat

1. Prioritize and contact matches using the AScM method.
2. Repeat for your **siblings** and **cousins**.
3. Compare notes. Each tester gets different matches.

SEE IMAGES THAT FOLLOW



Want Gil Bardige to Speak at Your Society?

Topics available for 2026 (Zoom or in-person):

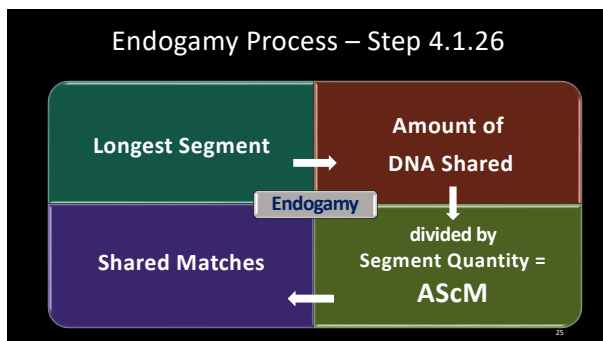
1. **Part 1.26 – Help! I Got My Autosomal DNA Results and I’m Confused!**
Average Segment Method (AScM) – 75 min + Q&A
2. **Part 2.26 – Next Steps...**
Segment Triangulation, Pile-Up areas, Case Studies, AScM-LS, MyHeritage & Ancestry Pro Tools
3. **Part 3.26 – Understanding y-DNA and mtDNA**
Using them alongside autosomal matches
4. **Part 4.26 – A New Perspective of Family History by using AI for Storytelling**
How the AI Prompt Process Allowed Me to Look at My Data from a New Perspective to see the Obvious Right In Front of My Face, using ChatGPT, Gemini, Claude & Perplexity.
5. **Part 5.26 – I Got My DNA Results – Case Studies – Success?**
Genealogy & DNA Analysis – the processes that I have used that you can too
6. **Part 6.26 – Help! I Got My DNA Cluster Results – Now What?** *You have heard about clusters at Ancestry and MyHeritage. Confused? I will show you what they are and how easy they are to use. They are a different perspective on your shared matches. This can be done as a workshop as well.*

Generations Back	~% of DNA	Most Recent Common Ancestor MRCA	Max # Possible Ancestors	Matches*
1	50	Parent	2	Sibling
2	25	Grandparent	4	1st Cousin 1C
3	12.5	Great Grandparent GGP	8	2C
4	6.25	2nd Great Grandparent 2XGGP	16	3C
5	3.12	3rd Great Grandparent 3XGGP	32	4C
6	1.56	4th Great Grandparent 4XGGP	64	5C
7	0.78	5th Great Grandparent 5XGGP	128	6C

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Relationship	Min total shared cM	Max total shared cM	Jewish Average total shared cM	Average Shared cM Project v4.0
Parent/Child	3461	3730	3505	3485
Siblings	2206	3037	2662	2613
Half Siblings	1699	2167	1958	1759
Grandparent/Grandchild	1426	2215	1825	1754
Uncle or Aunt / Niece or Nephew	671	2303	1792	1741
Great-Aunt/Uncle / Great-Niece/Nephew	42	2035	823	850
First cousins	54	1610	927	866
First cousins once removed	24	1878	496	433
Second cousins	42	698	280	229
Second cousins once removed	0	446	171	122
Third cousins	0	315	122	73
Third cousins once removed	0	205	80	48
Fourth cousins	0	664	61	35
Fourth cousins once removed	0	148	44	28
Fifth cousins	0	116	46	25
Sixth cousins	0	110	44	18

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Smarter Jewish Genealogy: The AScM Method for Prioritizing DNA Matches

A simple, step-by-step process to cut through the noise and find true relatives, especially with endogamy.

STEP 1: Check the Longest Segment

20cM

Start by filtering your match list to only include people with a longest shared DNA segment of 20cM or more.

STEP 2: Review Total Shared DNA

90cM

From that smaller list, only focus on matches who share a total of 90cM or more of DNA with you.

STEP 3: Calculate the AScM Score

$\text{AScM} = \frac{\text{Total Shared cM} \times \text{Number of Segments}}{\text{Total cM}}$

For your remaining matches, calculate the Average Segment Size in cM (AScM) using this formula.

STEP 4: Prioritize High AScM Matches

AScM \geq 12cM

Your highest priority matches are those with an AScM score of 12cM or higher. These are your most likely relatives.

Real-World Example: Drastic Reduction in Matches

Total Matches (Unfiltered)	→	After Step 1 & 2 (Longest Segment \geq 20cM + Total \geq 90cM)	→	After Step 4 (AScM \geq 12cM)
196,537		9		4

This table shows a real-world example of how the AScM filtering process dramatically reduces an overwhelming match list to a manageable number of high-priority contacts.

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AScM \geq 12 cM Test

<div style="border: 1px solid black; padding: 5px; margin-bottom: 5px; background-color: #e0f0e0;">135cM</div> <div style="border: 1px solid black; padding: 5px; margin-bottom: 5px; background-color: #e0f0e0;">15 segments</div> <div style="border: 1px solid black; padding: 5px; background-color: #e0f0e0;">25cM Longest</div>	<div style="border: 1px solid black; padding: 5px; margin-bottom: 5px; background-color: #e0f0e0;">135cM</div> <div style="border: 1px solid black; padding: 5px; margin-bottom: 5px; background-color: #e0f0e0;">8 segments</div> <div style="border: 1px solid black; padding: 5px; background-color: #e0f0e0;">25cM Longest</div>
Match 1	Match 2

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Prioritize Unknown Matches 1.25

Ancestry – MyHeritage -- FTDNA

Ignore "Cousins" estimates - use AScM 2C2R → 4C

Shared DNA

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Segment Quantity

=

AScM \geq 12 cM

+

Longest Segment/Block \geq 20 cM

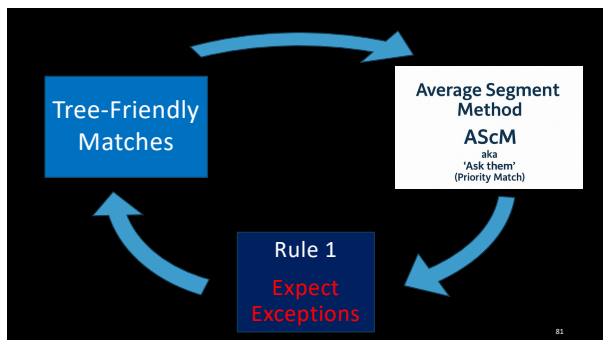
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Interpreting the Score: Signal vs. Noise

Low AScM (< 10 cM) Endogamy Warning. The DNA is comprised of many tiny, distant segments piling up. This is likely "noise".	10-12 cM: The Grey Zone (Proceed with Caution)	High AScM (≥ 12 cM) Priority Match ("Ask Them!") This indicates a likely recent relationship (2nd-4th cousin).
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Rule of Thumb: Even if the total cM is high, a low AScM suggests the connection is ancient, not recent.

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Average Segment Method = AScM for 23andme

DNA % up to	DNA cM Shared	Max # Segments	AScM >= 12cM
Example	135	11	12.3
3.2	238	19	12.5
3.1	231	19	12.2
3.0	224	18	12.4
2.9	216	17	12.7
2.8	209	17	12.3
2.7	201	16	12.6
2.6	194	16	12.1
2.5	186	15	12.4
2.4	179	14	12.8
2.3	171	14	12.2
2.2	164	13	12.6
2.1	156	13	12.0
2.0	149	12	12.4
1.9	142	11	12.9
1.8	134	11	12.2
1.7	127	10	12.7
1.6	119	9	13.2
1.5	112	9	12.4
1.4	104	8	13.0
1.3	97	8	12.1
1.2	89	7	12.8
1.1	82	6	13.7
1.0	75	6	12.4
0.9	67	5	13.4
0.8	60	4	14.9
0.7	52	4	13.0
0.6	45	3	14.9
0.5	37	3	12.4
Use with: 23andme			
AScM = DNA cM Shared / Qty of Segments			
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