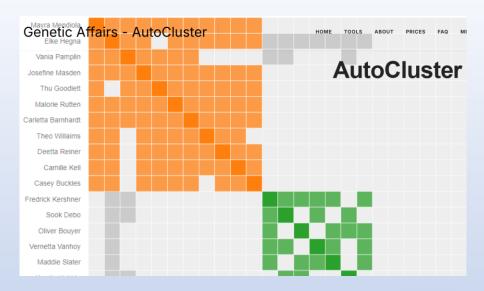


# Clustering



Aug 7, 2025

Phoenix East Valley DNA Special Interest Group



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### All slides and handouts can be found at:

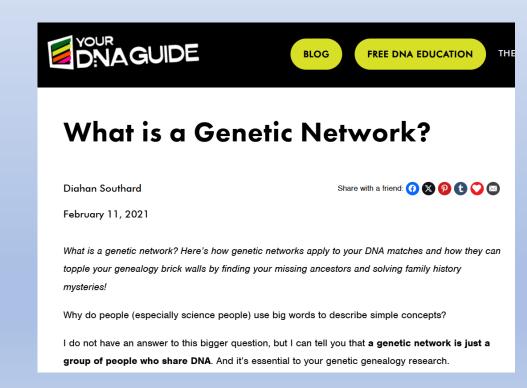
http://www.familytreeaz.com/Presentations/



QR Code: take photo to open to presentations

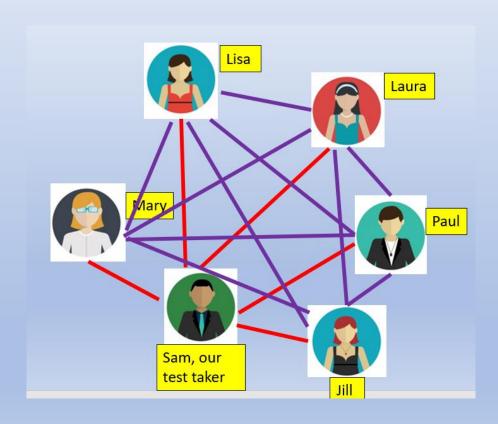
# Starting Off: What is Clustering?

- Clustering (or AutoClustering) is a semi-automated process to attempt to group your DNA matches by ancestral lines
- Your DNA matches often can be sorted into Genetic Networks, groups that share a common ancestor(s)
  - For example, descendants of a common 2<sup>nd</sup> great-grandparent couple



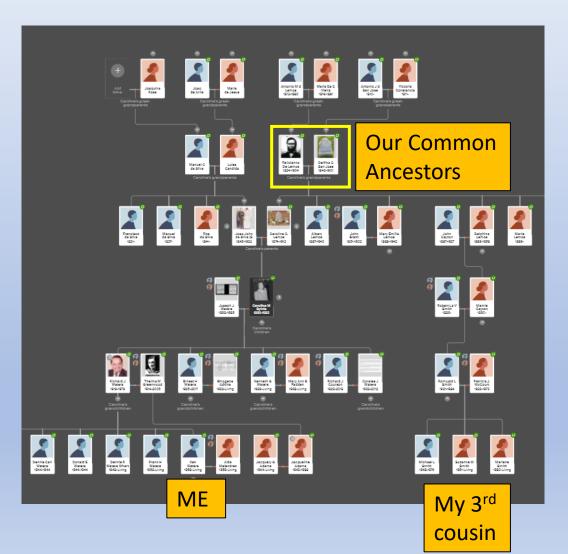
# Why would we want to try AutoClustering?

- By grouping a number of your DNA matches together you can possibly identify how you are related to each of the different matches
- Sorting matches into Genetic Networks can allow you to focus on one particular network of interest, sometimes by "sorting out" networks that are not your primary focus
- Each of the members in a Genetic Network share DNA with others in the group and provide clues to a common ancestor



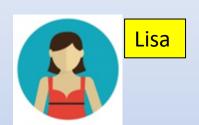
# Goal: Find the Most Recent Common Ancestor (MRCA)

- Finding common ancestors allows determination of exact relationship
- Once this is found then we can compare to other matches to help see how they are related as well



## Our Genetic Network

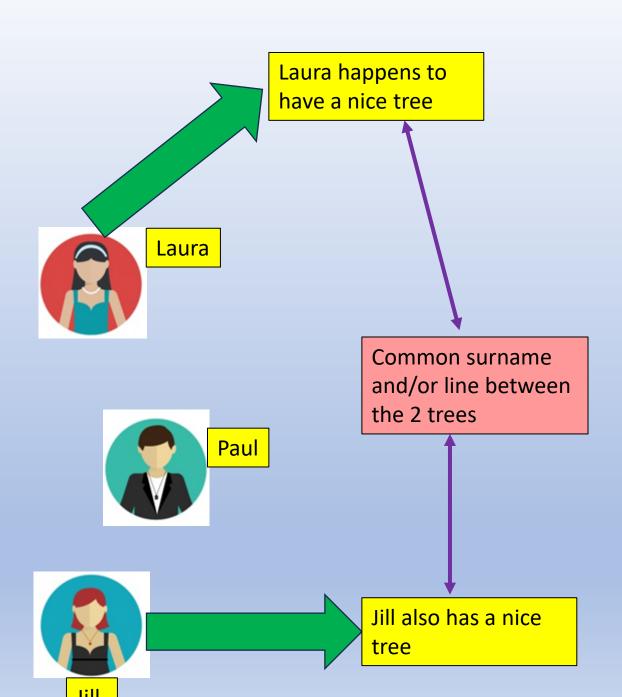
If one member of the Genetic Network has a tree then it can facilitate finding the common ancestor(s)





Mary





# Non-automated ways to cluster matches



https://www.danaleeds.com/the-leeds-method/

elative in common		You	Michael	DNA Overlap G
мн	man	1st Cousin, Once Removed (5.94)	Distant Cousin (0.08)	No
CR =		2nd Cousin (3.37)	Sister (49.67)	Request sent
HOUSE TOUR	100	2nd Cousin (2.41)	3rd Cousin (1.55)	Yes
cw	iikeiike	2nd Cousin, Once Removed (2.25)	3rd Cousin (1.14)	Request sent
<b></b>	(inminy)	2nd Cousin, Once Removed (2.19)	Daughter (50.00)	Yes
BV House And	natio:	3rd Cousin (1.01)	3rd Cousin (9.85)	Yes
DH HIMM		3rd Cousin (0.90)	5th Cousin (9.11)	Yes
JM HINNE HIN	negy	3rd Cousin (9.78)	3rd Cousin (0.62)	Yes
LV Harle Annu	ner.	3rd Cousin (0.67)	4th Cousin (0.45)	Yes
LA HAME WARE		3rd Cousin (0.66)	4th Cousin (0.41)	Yes

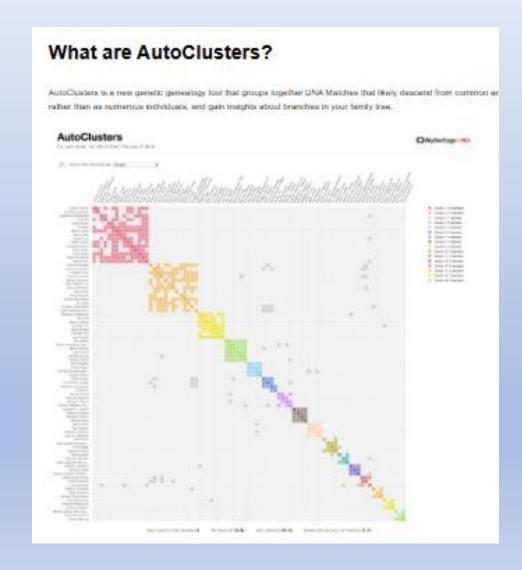
Testing Company Identified Matches in a group

Create a new group	Groupa
25/64 groups created	🔛 🙀 Starred matches (33)
2010 T groupe created	0 0 - Distant Saved Matches (16)
Group name	
	1 1 - Waters/Unknown (48)
	2 2 - Berkley/Wheeler 41
	3 3 - Sylvia/Correia (95)
Assign a color	4 - Lemos/San Jose (163)
	5 - Craddock/Spivey (201)
	6 6 - Wood/Thurman (272)
	7 - Unknown/Unknown MYSTERY 9
	8 8 - Spencer/Cummings 225
	B Berkley/Berkeley line from DC 49
	D Dad's non-Portuguese side (Waters or Berkley or Wheeler)
	D DI Mom's side (15)
	F Ferry/Elder on Spencer/Cummings 3 line (maybe Tyler/Robbins)
	G GM Father Mystery Network #6 (20)
	Inner Family 17
	L Low matches (6-8)
	Mystery Network #7 Mom's side; Grandma

Manually Assigning Matches to a Group using colored dots

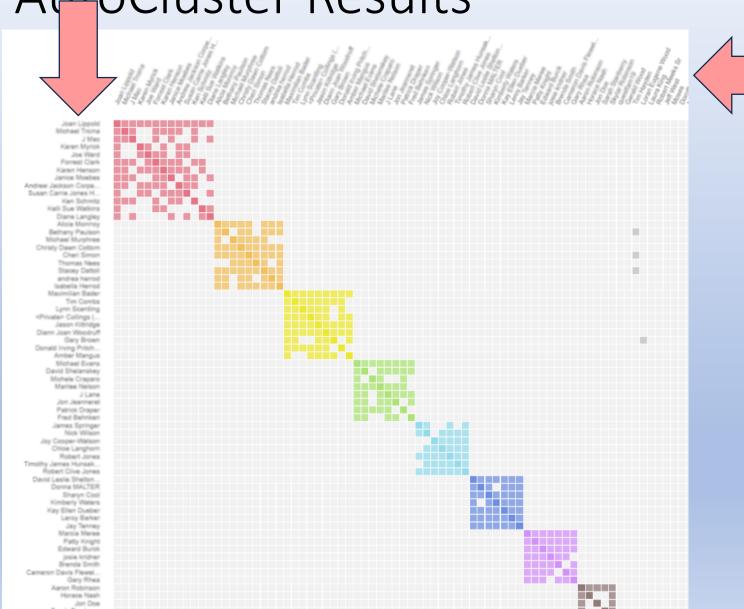
# Automated Methods – On to AutoClustering

- A method to automatically take matches and sort into groups
- Result is most often a grid showing Genetic Networks



Interpreting AutoCluster Results

- Matches grouped into common groups, each a different color
- Match names across top row and left of chart
- Hovering over the different boxes provide more info
- Often there is an additional listing of the group members



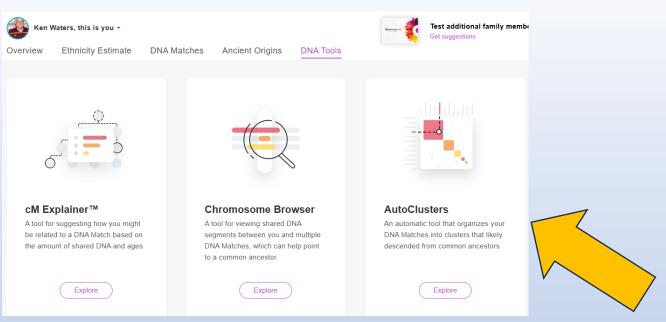
# At Least 4 Ways to do AutoClustering

- MyHeritage/Genetic Affairs
- GEDMatch
- DNAGedcom
- Ancestry

NOTE: all of these methods do typically require additional fees

# 1 - MyHeritage

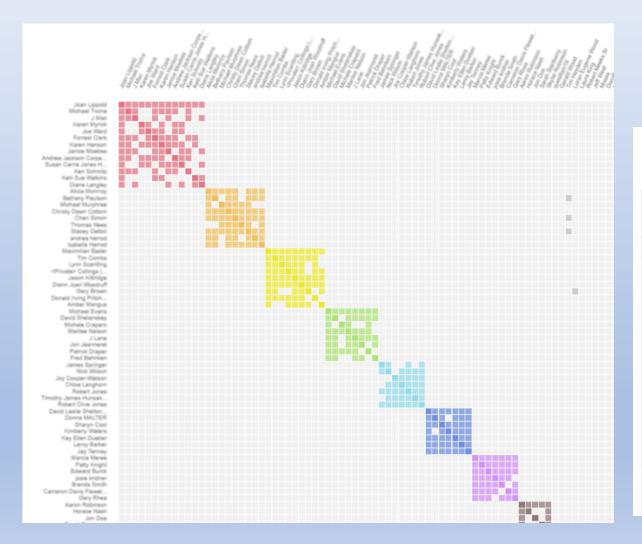
- Requires one-time upgrade fee (\$19?)
- Has set centiMorgan ranges (35-400 cMs, can not be adjusted)
- Not interactive, sends email when the cluster chart is available
- 3 files in Zip file:
  - Readme
  - HTML
  - Spreadsheet



<b>○</b> MyHeritage ►NA	
Dear Ken,	
A zip file with Joan Waters (born Craddock)'s report of AutoClusters is attached. In it, you will find three files — an HTML file which contains a visual representation of the AutoCluster analysis, a CSV file which contains a spreadsheet version of the AutoCluster analysis, and a ReadMe PDF file.	
Some files may be displayed incorrectly when opened directly from this email. For best results, view the files on a desktop device. To do this, save the zip file to your hard drive, extract the contents, and then open the files.	
Please note that this file is intended for your personal use only. The attached file is no longer protected by MyHeritage security and privacy mechanisms, so please take additional measures to secure your data and avoid sharing it.	

Name	Date modified	Туре	Size
Joan Waters (born Craddoc	8/7/2025 11:44 AM	Microsoft Excel Co	38 KB
Joan Waters (born Craddoc	8/7/2025 11:44 AM	Chrome HTML Do	369 KB
ReadMe	8/7/2025 11:44 AM	Chrome PDF Docu	38 KB

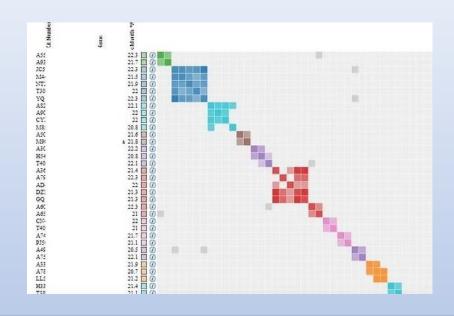
# 1 - MyHeritage



#### **AutoClusters Information** Largest cM **ICW** Name сМ Segments Cluster Tree Min cM Min Largest cM Min Segmer Min# Search fo Search ▼ Cluster 1 (13 people) 58.2 2 14 44.1 45.8 45.8 9 2 42.2 36.1 9 1 <u>89</u> 38.3 32.3 2 5 <u>13</u> 2 7 42.1 34.7 <u>49</u> 41.7 35.6 2 9 1 46.6 39.5 2 10 <u>123</u> 40.4 40.4 1 9 7 36.4 36.4 1 8 <u>651</u> 2 38 29.4 7 <u>178</u>

## 2 - GEDMatch

- Adjustable centiMorgan range
- Requires Tier 1
   subscription (\$15 onetime or \$10 monthly
  recurring)
- One BIG negative: Small database size (only ~1 million estimated)



https://www.familyhistoryfanatics.com/gedmatch-clustering

https://dna-explained.com/2022/02/21/autokinship-atgedmatch-by-genetic-affairs/

## 3 - DNAGedcom

- Most flexible
- Requires download of client and paid registration
- Requires download of match data (can take hours or even days)
- Once downloaded you have very flexible options, not just centiMorgan ranges
- Works best with Ancestry but can be affected by Ancestry's periodic backend changes; can work with other testing services but these may or may not work at any given time
- Has the CLM (C-Leeds Method) AutoClustering tool
- Cost is \$5/mo or \$50/yr

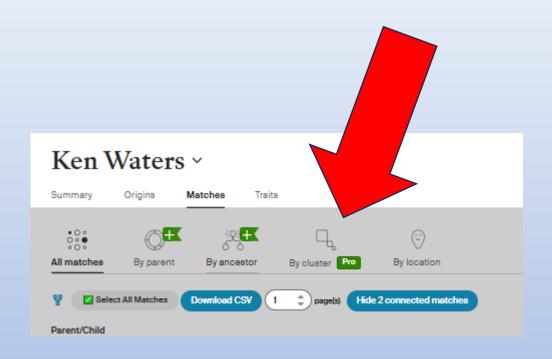


#### **Most Flexible**

Allows filtering by cM range as well as grouping (your colored dots) --- that's a BIG deal as it allows working on just a single ancestral group of interest

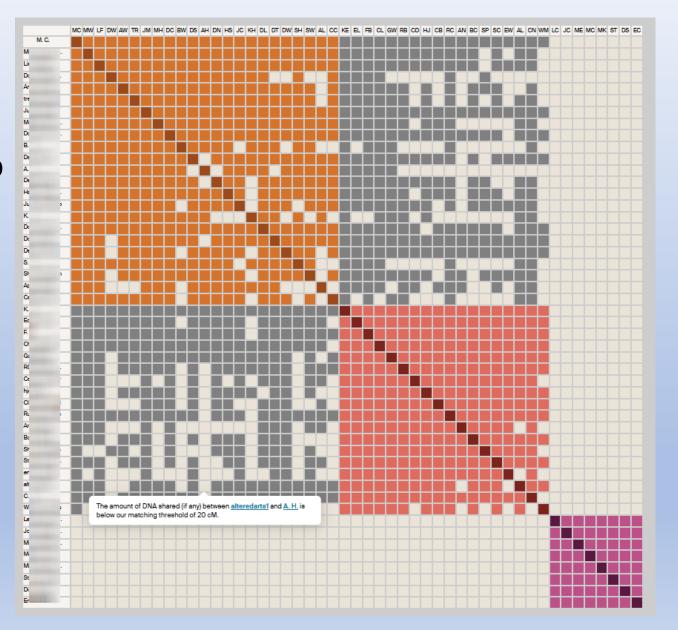
## 4 - Ancestry

- Just released in 2025
- Takes advantage of the largest database of DNA kits
- Currently the centiMorgan range is fixed at 65 to 1300 cMs but the ability to modify the ranges has been announced to come out soon
- Does require ProTools subscription (~\$45/quarter)



# 4 - Ancestry

- My kit only produced three clusters, two of them relatedto each other (see the grey boxes); the large one is paternal and the small one is maternal
  - Not very useful without ability to adjust cM ranges

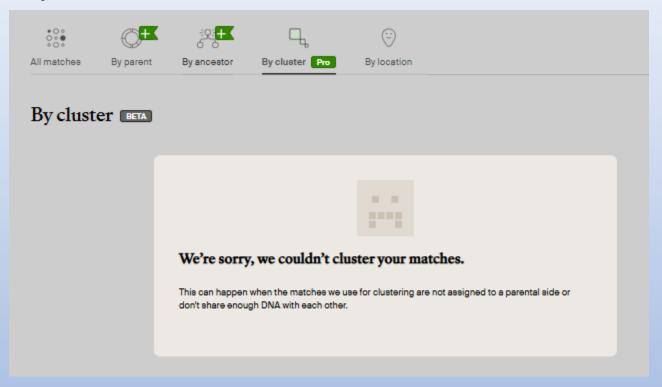


# Why is it useful to be able to adjust ranges?

- Allows fine tuning of the clusters to get the desired grouping
- Focus on a particular cluster of interest that may not be shown with set ranges currently on MyHeritage and Ancestry (supposedly soon to change)
- At this time, only 2 services allow setting custom ranges:
  - GEDMatch
  - DNAGedcom/CLM

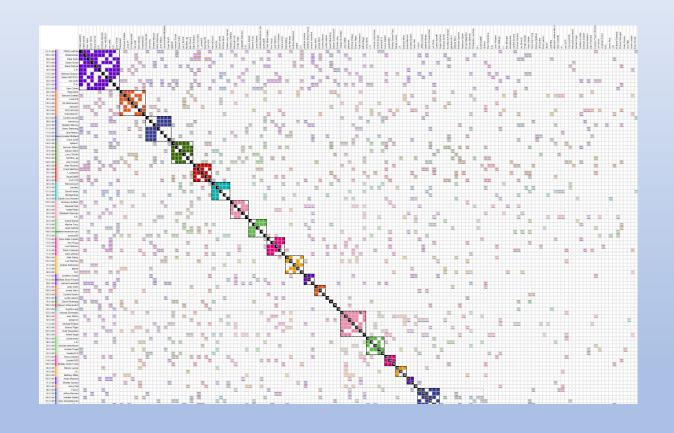
# One Note on Endogamy

- AutoClustering of endogamous kits can be particularly problematic due to too many interrelated kits
- Ancestry won't even try to build a cluster (this is for an identified 100% Ashkenazi Jewish kit)



# One Note on Endogamy

- AutoClustering of endogamous kits can be particularly problematic due to too many interrelated kits
- This is what the DNAGedcom CLM (AutoCluster) tool shows for a 100% Ashkenazi kit
  - Notice all the grey boxes and the small cluster sizes
  - Multiple relationships---makes interpreting very difficult



# My Recommendation...?

- For now, best option is DNAGedcom (most flexible and powerful) but does require lengthy download
- Second preference goes to Ancestry due to the large database; maybe after they implement the ability to adjust cM ranges it might be my top pick but for now it's limited due to fixed ranges

- Are these useful...?
  - My opinion: can be helpful to visualize grouping of matches --- but: mostly require additional analysis/grouping using spreadsheets or other methods



#### Presentations:

http://familytreeaz.com/Presentations



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