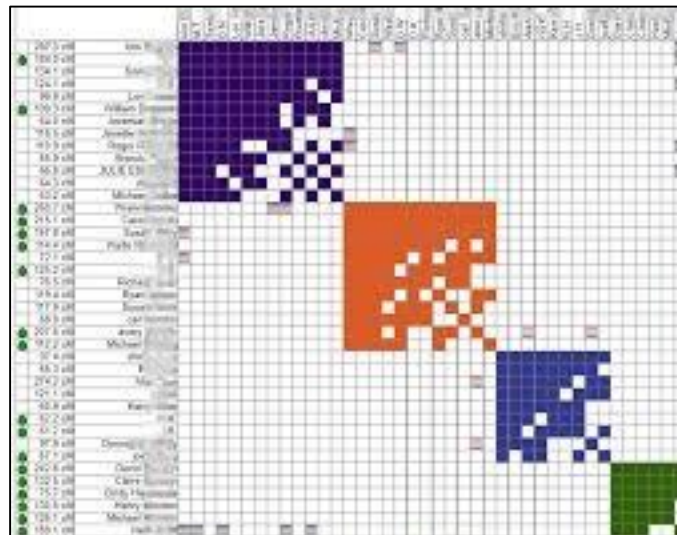


Genetic Genealogy

“Clustering Tools”
Baltimore County Genealogical Society
November 22, 2020
Andrew Hochreiter

Clustering Tools

- Analysis Tools for Autosomal DNA
- Clustering Tools were created to produce **Visualization** of Matches with shared DNA
- Makes it easier to see Genetic Networks, Shared Segments, Ancestral Groups, identify Data Patterns

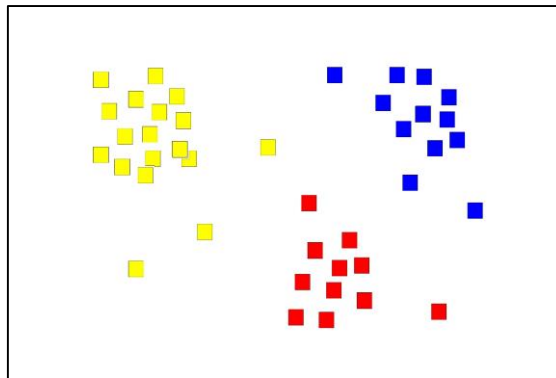


Clustering Tools

- A Clustering tool analyzes your In Common With (ICW) company matches
- Clustering tools can automate grouping your matches
 - Visualize matches sharing a set of common ancestors
 - Shared matches create Genetic Networks
 - Each cluster potentially shares a common ancestor
- Listed down & across to show who matches whom
- Clusters are presented as colored groupings on graph with data tables that provide more detail
- Diagonal line is where each match matches themselves

BC Era (Before Clustering)

- Cluster analysis is the task of grouping a set of objects in such a way that objects in the same group (called a cluster) are more similar (in some sense) to each other than to those in other groups (clusters).
- People developed their own means
- Spreadsheets were the norm



Primary Component Analysis

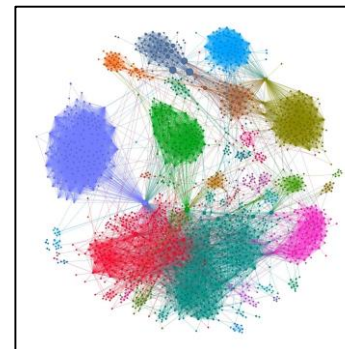
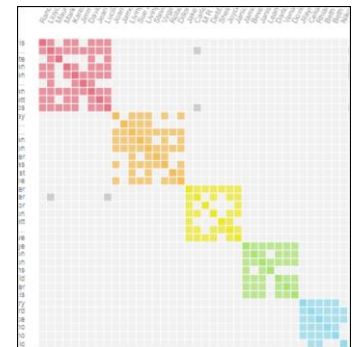
name	cM	groupName	icw	group	largestCm
Cluster 1					
Alan Scott	31.2	3rd - 5th cousin	1	1	10.4
Alex Jacobs	39.7	3rd - 5th cousin	4	1	20.2
Diane Richardson	30.9	3rd cousin - distant cousin	7	1	24.4
Gerene Vickery	26.7	3rd - 5th cousin	6	1	26.7
Hillary Potts	32.7	3rd - 5th cousin	6	1	26.3
Micki Two	30.3	3rd - 5th cousin	3	1	23.3
Scott Schaeffer	35.6	3rd - 5th cousin	5	1	23.2
Cluster 2					
Alexandra Marier	29.4	3rd - 5th cousin	5	2	29.4
Brandon O'Malley	27.2	3rd cousin - distant cousin	3	2	14.1
Dave Beauregard	27.6	3rd cousin - distant cousin	2	2	19.5
katherine allen	29.9	3rd - 5th cousin	3	2	13.8
Melanie Peabody	32.3	3rd - 5th cousin	2	2	17
Ron Ransom	27.2	3rd cousin - distant cousin	3	2	21.1
Cluster 3					
Bert Jensen	26	3rd cousin - distant cousin	5	3	14.7
Bert Ted Jensen	26	3rd cousin - distant cousin	6	3	14.7
Emma Daigle	32.6	3rd - 5th cousin	4	3	19.5
Lacey Carpenter	29.2	3rd cousin - distant cousin	2	3	9.9
Sue Gibbs	28.4	3rd - 5th cousin	3	3	14.5
Terry Walton	29.5	3rd - 5th cousin	5	3	14.4
Cluster 4					
Carolyn Rogers	29.3	3rd cousin - distant cousin	2	4	19.5
Curtis Hathcock	28.1	3rd - 5th cousin	2	4	10.9
David Heaver	27.4	3rd - 5th cousin	5	4	14.1
Delilah Clark	29.6	3rd cousin - distant cousin	2	4	9.4
Patrick Hannes-Karg	29.2	3rd cousin - distant cousin	4	4	9.1

Spreadsheets

Available Clustering Tools

- **Manual**
 - Leeds Method
- **Automated**
 - Genetic Affairs
 - DNAdgedcom (Collins' Leeds Method 3D)
 - MyHeritage
 - GEDmatch Genesis Tier 1
 - Shared Clustering
- **Network Graphs**
 - RootsFinder
 - Connected DNA

	A	B	C	D	E
1	Ralph				
2	Herbert				
3	Robert				
4	Stacy				
5	Julie				
6	Kristen				
7	Robert				
8	Suzette				
9	Stephanie				
10	Winnifred				
11	Kristi				
12	Victor				
13	Chuck				
14	Carol				
15	David				



Clustering Tools

- **Leeds Method (Dana Leeds)**
 - Began as a color coding method of grouping close Matches at AncestryDNA into four columns, one for each grandparent. It has been expanded.
- **MyHeritage**
 - An automatic tool that organizes your DNA Matches into clusters that likely descended from common ancestors.
- **Genetic Affairs (Evert-Jon Blom)**
 - automates the retrieval of new genetic Matches from 23andMe, FTDNA and AncestryDNA to a periodic email; and the **AutoCluster** tool will cluster close/large Matches

Clustering Tools

- **DNAGedcom (Rob Warthen)**
 - Log onto your DNA company, and download Match and ICW files
 - Use Collins” Leeds Method 3D to run cluster report
- **GEDmatch (Curtis Rogers & John Olson)**
 - New to Genesis Tier 1
- **Shared Clustering (Jonathan Brecher)**
 - Installs program on your computer
 - Currently need to download Match and ICW files at DNAGedcom Client

Dana Leeds Method

- Began as a color coding method of grouping close Matches at AncestryDNA into four columns, one for each grandparent. It has been expanded.
- Simple Color-Clustering
- 2nd to 4th cousin matches
- Color Tag by shared matches
- Color Groups represent a Grandparent
- Perfect for adoptees
- Free

	A	B	C	D	E
1	Ralph				
2	Herbert				
3	Robert				
4	Stacy				
5	Julie				
6	Kristen				
7	Robert				
8	Suzette				
9	Stephanie				
10	Winnifred				
11	Kristi				
12	Victor				
13	Chuck				
14	Carol				
15	David				

Leeds Method Steps

1. Open DNA Match List
2. Extract 2C to 3C/4C
3. Put in Excel Spreadsheet
4. Choose Color for first Match
5. Open Shared Match List
6. Color other Matches same color
7. Go to next uncolored name & choose new color
8. Open Shared Match List and color other Matches
9. Repeat until list is done
10. Identify Columns by Grandparent

	1	2	3	4
Robert				
Jenna				
Andre				
John				
Paul				
Anne				
Barbara				
Richard				
Jonas				
Sam				
Melissa				
Laura				
Thomas				
Florence				
Charlie				
1 = PGF				
2 = MGM				
3 = MGF				
4 = PGM				

DNAgedcom

- DNAgedcom by Rob Warthen (\$5/mo fee; \$50/yr Silver, \$100/yr Gold incl Client)
- Tool is on Client application (DGC)
- Log onto your DNA company, and download Match and ICW files
- Use Collins Leeds Method to run cluster report

<https://www.dnagedcom.com/>



DNAgedcom

Collins Leeds Method

Kit Filter:

DNA Kit:

cM Range: to

Inclusion Threshold:

Sort:

Cluster Sort:

Surname List:

Include Unclustered Matches ☒ Open HTML When Done ☒

Paint Midline ☒ Include Chromo Data ☒

Include Ancestors ☒

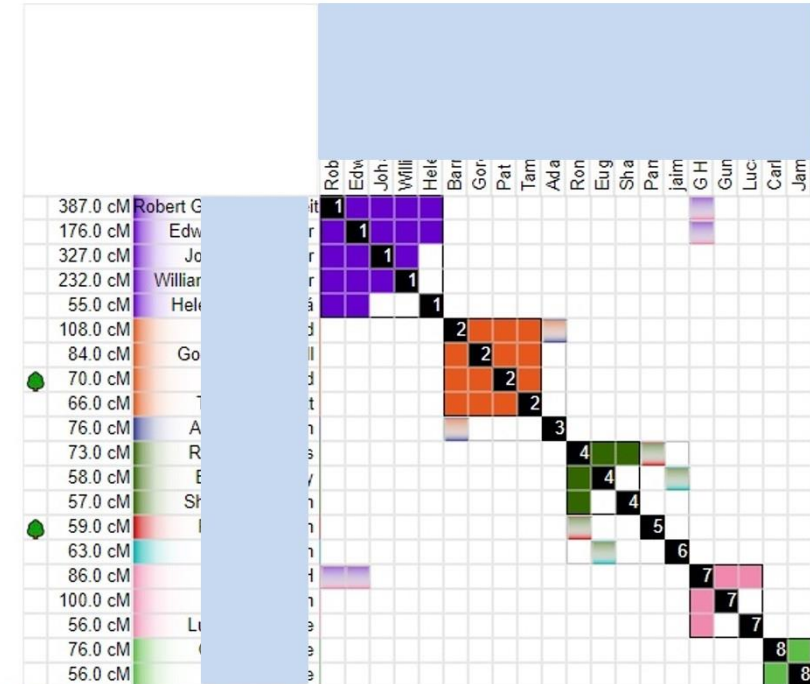
Run Grouping

Choose your DNA Kit and parameters and hit Run grouping

View Help

The Collins Leeds Method for Andrew Hochreiter(FTDNA)

cM: 55 - 400. 1/2 Inclusion. Clusters ordered by inclusion, sorted by size with Superclusters.
Unclustered Matches Included.



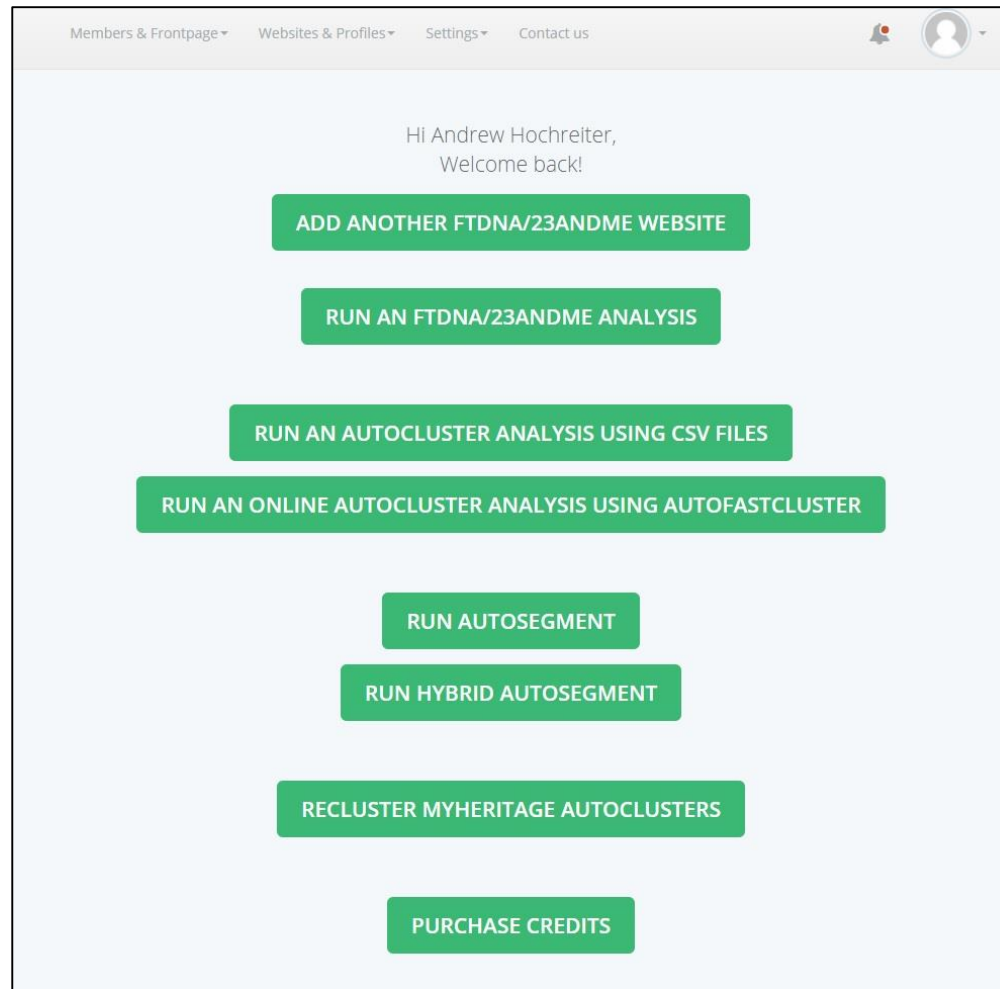
<https://www.dnagedcom.com/>

Genetic Affairs

- Developed by Evert-Jon Blom
- Retrieval of new genetic Matches from 23andMe and FTDNA
- The AutoCluster tool will cluster close/large Matches
- First 200 credits are free
 - Monthly Subscription rates (includes 10% bonus)
 - Additional credits ~1 cent/credit
 - Credits charged from 25 to 100 for product

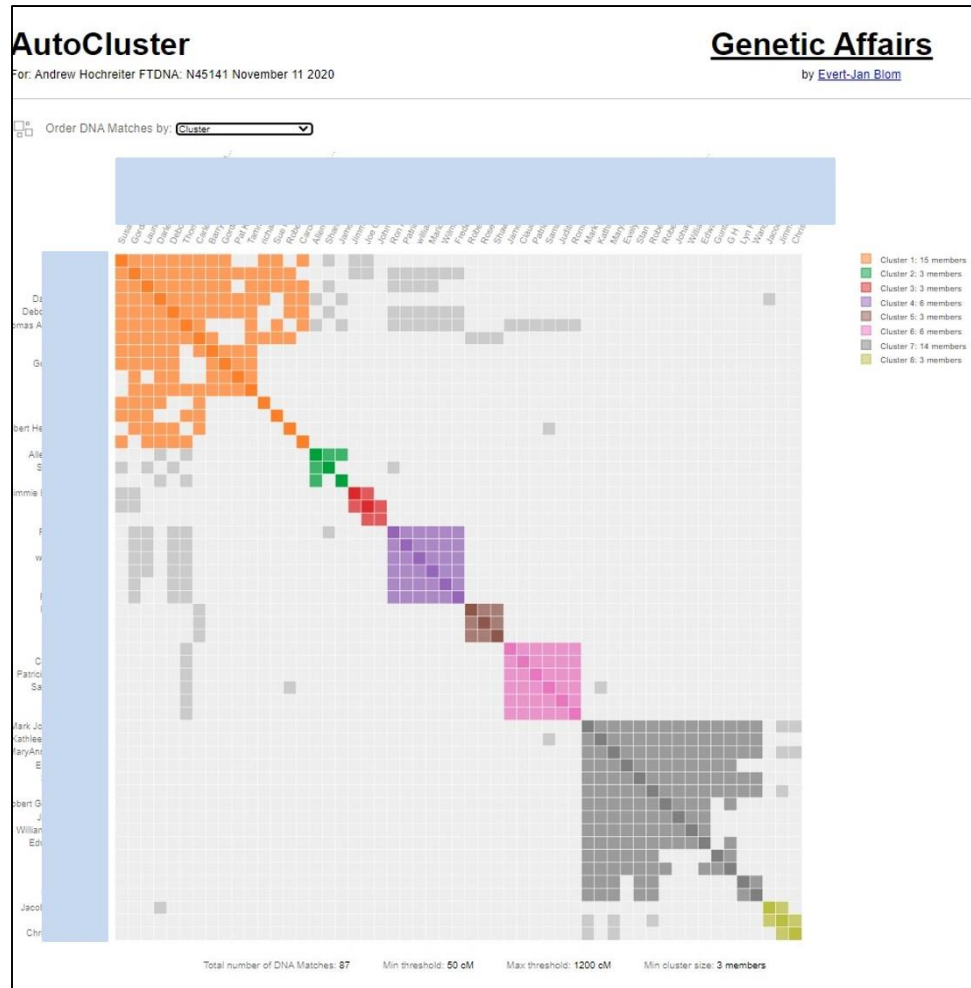
<http://www.geneticaffairs.com/>

Genetic Affairs Tools



<http://www.geneticaffairs.com/>

Genetic Affairs

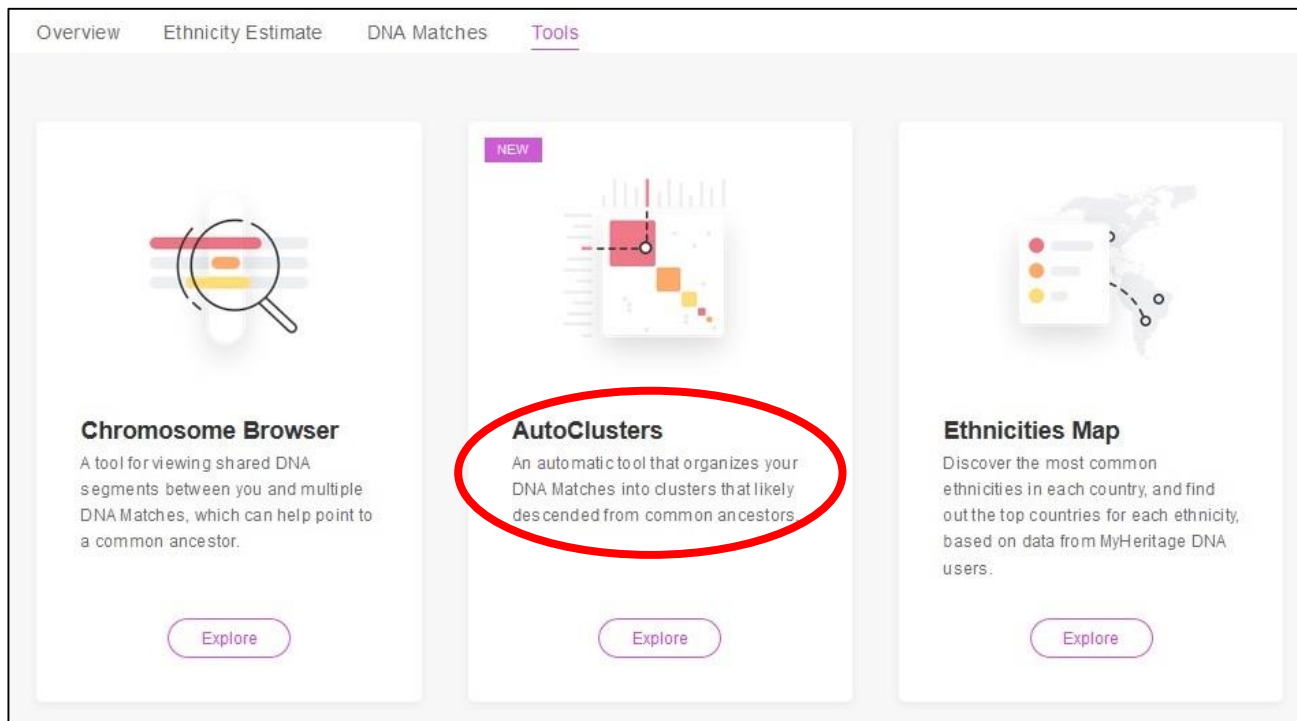


Threshold
50-1200 cMs

87 matches

MyHeritage AutoClusters

- Offers AutoClusters feature in DNA Tools
- Transfer DNA & unlock tools (\$29) or Subscription



<https://www.myheritage.com/>

MyHeritage AutoClusters

- Genetic Affairs cluster with MyHeritage matches

MyHeritage

Home

Family tree

Discoveries

DNA

Health NEW

Research

AutoClusters

An automatic tool that organizes your DNA Matches into clusters that likely descended from common ancestors.

AutoClustering organizes your MyHeritage DNA Matches into shared match clusters that likely descended from common ancestors. Each of the colored cells represents an intersection between two of your matches, meaning that both individuals match you and each other. These cells are grouped together physically and by color to create a powerful visual chart of your shared match clusters. Each color represents one shared match cluster. Members of a cluster match you and most or all of the other cluster members.

Generate clusters for: Kit: **Andrew Hochreiter** **23-27Z6C8**

Generate

The AutoClustering feature on MyHeritage was developed in collaboration with Evert-Jan Blom.

AutoClusters

For: Andrew Hochreiter · Kit: 23-27Z6C8 · March 13 2019

☐ ☐ Order DNA Matches by: **Cluster**

Cluster 1: 7 members

Cluster 2: 6 members

Cluster 3: 6 members

Cluster 4: 5 members

Cluster 5: 4 members

Cluster 6: 4 members

Cluster 7: 4 members

Cluster 8: 4 members

Cluster 9: 4 members

Cluster 10: 4 members

Cluster 11: 4 members

Cluster 12: 3 members

Cluster 13: 3 members

Cluster 14: 3 members

Cluster 15: 3 members

Cluster 16: 3 members

Cluster 17: 3 members

Cluster 18: 3 members

Cluster 19: 3 members

Total number of DNA Matches: 79

Min threshold: 25 cM

Max threshold: 300 cM

Shared DNA Matches min threshold: 10 cM

AutoClusters Information

Name	cM	Largest Cm	Segments	ICW	Cluster
Cluster 1 (7 people)					
Hillary	32.7	26.3	2	6	1
Tree Notes					
https://www.myheritage.com/pedigree-tree-488802151-1500001/potts?familyTreeID=1					
11.2	10.4	4	1	1	
tree-tree-294004301-1500003/scott?familyTreeID=1					
99.7	20.2	2	4	1	
tree-tree-521723461-1500001/jacobs?familyTreeID=1					
26.7	26.7	1	6	1	
tree-tree-348540801-1500003/vickery?familyTreeID=1					
30.9	24.4	2	7	1	
tree-tree-243456751-1500003/richardson?familyTreeID=1					

<https://www.myheritage.com/>

16

GEDmatch Auto-Clustering

- Offers a Clustering under Tier 1 (\$10/mo fee)
- Any Min/Max choice

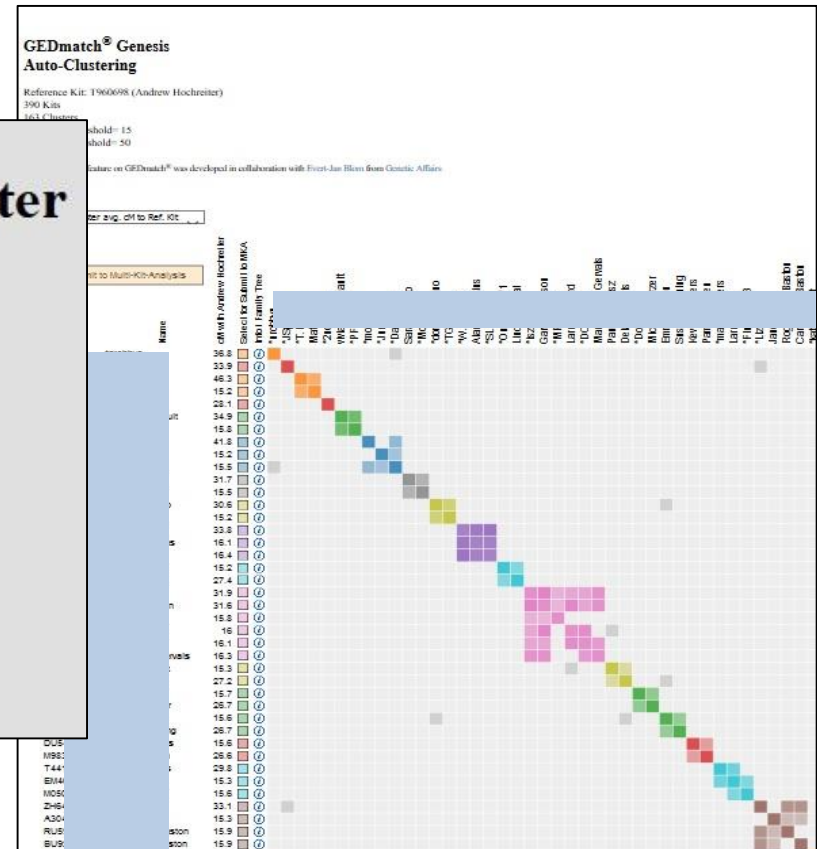
GEDmatch[®] Genesis Basic Cluster

GEDmatch Genesis Kit Number:

Up to 500 matches will be used between these thresholds:

Lower cM Threshold:

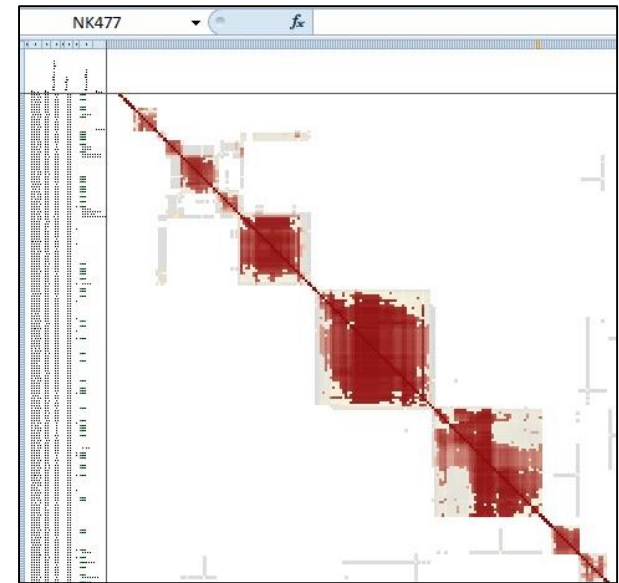
Upper cM Threshold:



<https://www.gedmatch.com/login1.php/>

Shared Clustering

- Created by Jonathan Brecher
- Installs program on your computer
- Download Match and ICW files at DNAGedcom Client
- “Heat Map” not colors
- Open Source Tool
- Free

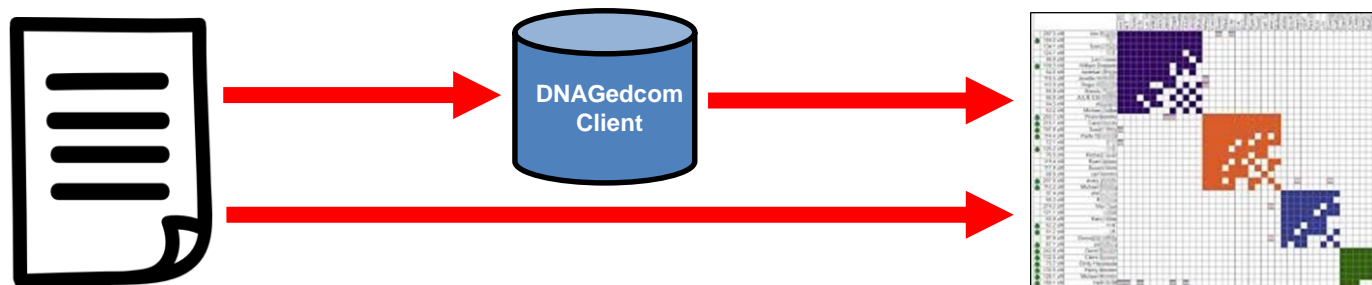


<https://github.com/jonathanbrecher/sharedclustering/wiki/Quick-start>

Clustering Step 1

Gather your Match List

- Match Lists exist at Test Companies & GEDmatch
 - DNAGedcom facilitates download
 - Some Cluster tools request Direct Access
- Upload List info as instructed
- Ancestry prohibition
 - Issued “Cease and Desist” order preventing use
 - Cluster tools no longer download matches from Ancestry



Clustering Step 2

Set Parameters and Run Tool

- **Cluster tools have various Defaults**
 - Genetic Affairs: 50 - 250 cM
 - GEDmatch: 15 - 50 cM
 - DNAGedcom: 50 – 400 cM
 - Shared Clustering: 20 – Max from List
 - MyHeritage: Selected by MH
- **Some Sites allow adjustments**
 - Minimum & Maximum Thresholds
 - Minimum Size of Largest segment
 - Minimum Cluster Size

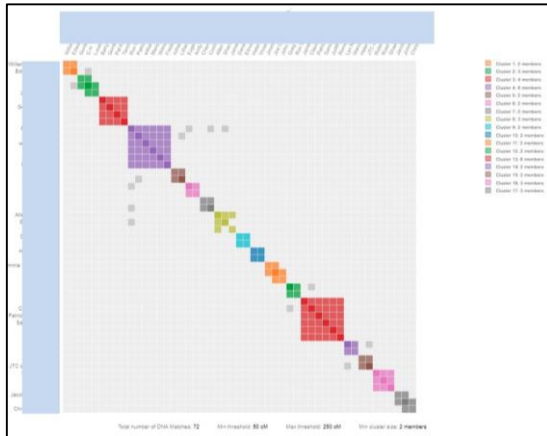
Adjustable Settings

- Experiment with Settings
 - Dana Leeds suggests start at 400 and 90 cM
 - Jim Bartlett suggests start at 200 to 80 cM
- Reducing the lower threshold increases # of matches and probably produces more clusters
- Reducing the range between min & max threshold will reduce # of clusters
- Higher threshold will include close relatives

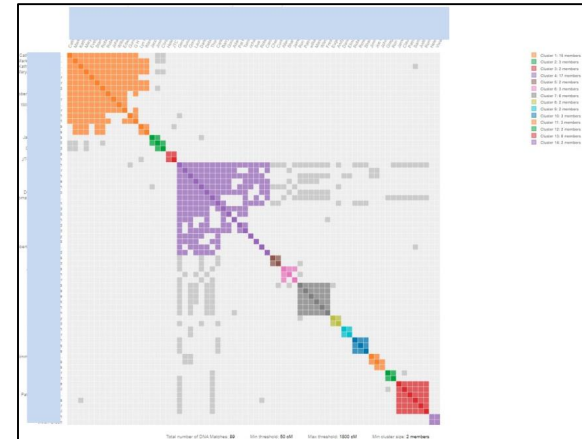
Clustering Tips

- Jim Bartlett's recommendations include:
 - Use a large threshold (80cM to 200cM) first to get the hang of it. This will only include your closest cousins.
 - If offered, use an upper threshold of 1000cM or so, to cull out parents, siblings, children, aunt/uncle – they only appear in one Cluster anyway, and don't really add any value in most cases.
 - Reducing the threshold will increase the number of Clusters, and those Clusters will tend to form on more distant Ancestors.

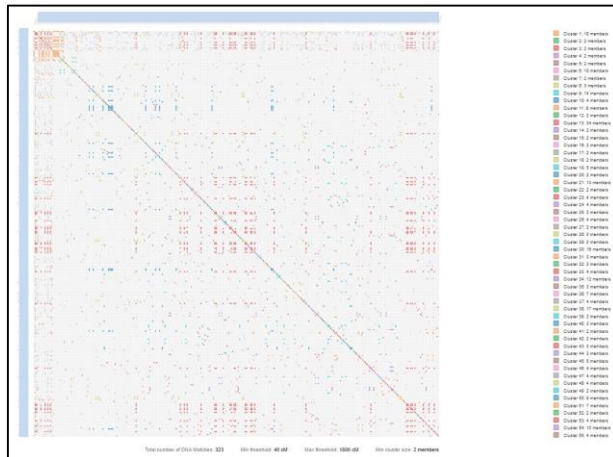
Effects of Settings



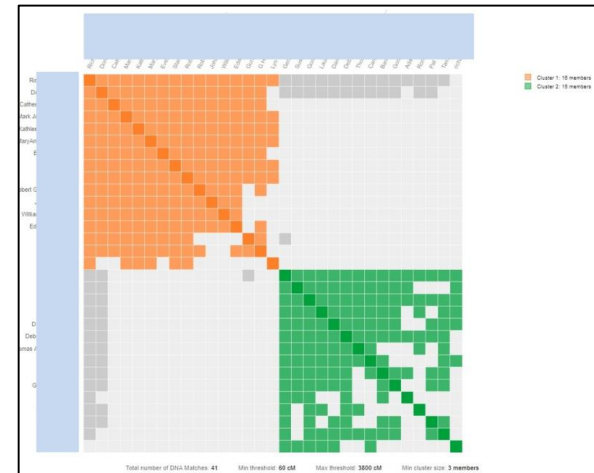
Default 250 max - 50 min
41 Matches, 17 Clusters



1800 max - 50 min
87 Matches, 14 Clusters



1800 max - 40 min
323 Matches, 55 Clusters

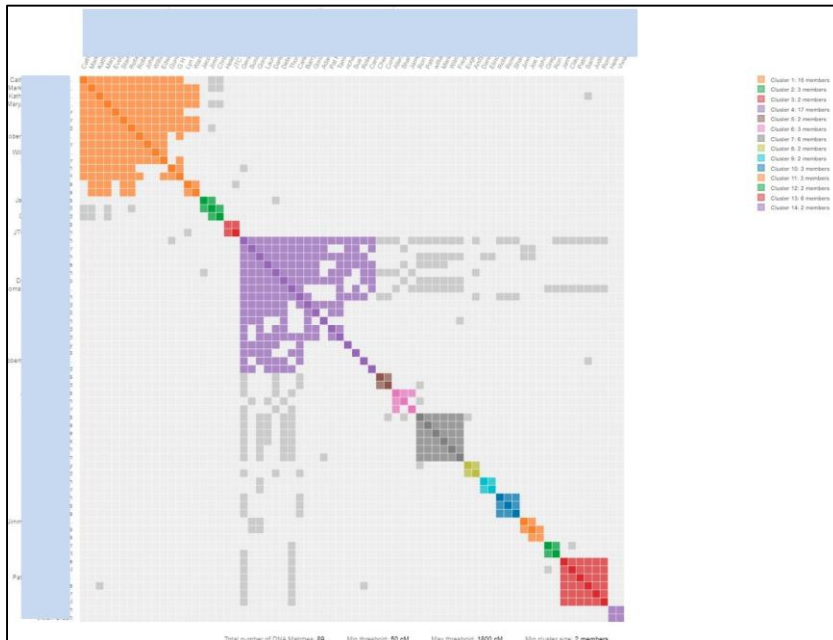


3800 max - 60 min
41 Matches, 2 Clusters

Clustering Step 3

Review Clusters

- Look for Patterns, Names, Known Matches
- Use supplemental material like Spreadsheet
- Rerun if too many or too few



Supplemental Materials

Spreadsheet
Autocluster Cluster Information
Chromosome Segments
Chromosome segment statistics

Supplemental Info

Chromosome segment statistics per AutoCluster cluster

Cluster	single_segments	multiple_segments	x_segments	Paternal	Maternal
	<input type="text" value="filter column..."/>	<input type="text" value="filter column..."/>	<input type="text" value="filter column..."/>	<input type="text" value="filter column..."/>	<input type="text" value="filter column..."/>
▼ (3 items)					
Segments for cluster 1	0	90	0	0	0
Segments for cluster 2	0	74	0	0	0
Segments for cluster combined	0	97	0	0	0

AutoCluster Cluster Information

<input type="button" value="Download spreadsheet with clusters"/>											
Name	c...	l...	ICW	Cluster	Tree	X	Predicted	m...	Y	Not...	Notes
<input type="text" value="Search"/>	<input type="text" value="M"/>	<input type="text" value="Li"/>	<input type="text" value="Max"/>	<input type="text" value="Search"/>		<input type="text" value="M"/>	<input type="text" value="Search"/>	<input type="text" value="Si"/>	<input type="text" value="Search"/>	<input type="text" value="Search"/>	<input type="text" value="Search"/>
► Cluster 1 (18 items)											
▼ Cluster 10 (4 items)											
+		45	13	11	10	tree	0	4th Cousin			
+		45	13	9	10	tree	0	4th Cousin			
+		42	12	6	10	tree	0	-	R-M269		
+		41	13	5	10	tree	0	4th Cousin			
▼ Cluster 11 (8 items)											
+		72	10	9	11	-	0	-			

Spreadsheet Data

- Look at data for surnames, DNA segment data (start, stop, length), family trees, e-mail

1	Full Name	Match Date	Relationship Range	Suggested Relationship	Shared	Longest Known	E-mail	AncestryDNA	YDNA	FamilyTreeDNA	Results	Notes
20	Jc	2014-09-11	1st Cousin - 3rd Cousin	2nd Cousin	327.0	35.0	11	a			3003895	
21	W	2011-02-16	2nd Cousin - 3rd Cousin	2nd Cousin	232.0	50.0	12	b		E-BY5856	97507	
22	E	2016-01-17	2nd Cousin - 3rd Cousin	2nd Cousin	176.0	58.0	12	s	@	E-M35	97506	
23	B	2014-07-11	2nd Cousin - 4th Cousin	3rd Cousin	108.0	28.0	13	a			3008999	
24	G	2017-09-16	2nd Cousin - 4th Cousin	3rd Cousin	100.0	50.0	13	a		R-M269	3261115	
25	G	2016-08-25	2nd Cousin - 4th Cousin	3rd Cousin	86.0	19.0	13	a		R-M269	3023863	H
26	G	2018-08-07	3rd Cousin - 5th Cousin	4th Cousin	84.0	15.0	14	g		G-M201	4550351	
27	A	2016-11-29	2nd Cousin - 4th Cousin	3rd Cousin	76.0	24.0	13	a			3559799	
28	H	2020-09-24	4th Cousin - Remote Cousin	-	76.0	12.0	15	h			5663871	
29	C	2019-08-15	5th Cousin - Remote Cousin	-	76.0	9.0	16	c			4860970	
30	R	2019-03-17	3rd Cousin - 5th Cousin	4th Cousin	73.0	15.0	14	r	@Henderso	R-M269	4752470	

all_your_dna_matches AutoClusters-1--1 clustering_dna_matches

1	Identifier	Name	total share	matche	cluster	notes	tree	Rol	Rol	Joh	Wil	Ed	Gu	G	H	Lyr	Wa	He	JTC	Jac	Jim	Chi	Dai	Elir	He	Viv	Jim	Joe
11	3065588	H	53	none	3																							
12	4761074	J	51	none	3																							
13	4771684	J	72	none	4																							
14	5657267	J	62	none	4		tree																					
15	4748519	C	52	none	4																							
16	3558197	D	51	none	5																							
17	2993336	E	50	none	5		tree																					
18	3242120	H	53	none	6																							
19	5344752	V	50	none	6																							
20	3226729	J	63	none	7		tree																					
21	823653	J	51	none	7		tree																					

all_your_dna_matches AutoClusters-1--1 clustering_dna_matches

Clustering Step 4

- Find the Cluster Common Ancestor
 - Apply Traditional Research
 - Correlate Family Trees of Cluster Members

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	
1	DNA Matc	Name	Age	Country	Contact D	DNA man	Contact D	Status	Estimated	Total cM	s	Percent D	Number o	Largest se	Review DI	Has family tre	Number o	Tree man	View tree	Contact tr	Number o	Shared an	All ancest	Notes
2	D-2726C8	Catherine Hochreiter				You			grandmot	1,838.20		25.9	44	158.7	https://w	Yes		14	You	https://www.myheritage.com/site-famil hochreiter				
3	D-2726C8	Gerald R V 80's				You			half broth	1,690.30		23.8	42	156.3	https://w	Yes		14	You	https://www.myheritage.com/site-famil turner,wilson,brice,p				
4	D-2726C8					You			great-niec	847.2		12	30	87.6	https://w	Yes		14	You					
5	D-2726C8			USA	https://w	Michelle C	https://www.myher	1st cousin	413.6		5.8	20	39.5	https://w	No									
6	D-2726C8			Canada	https://w	Mildred R	https://www.myher	1st cousin	274.3		3.9	10	69.3	https://w	Yes			10	Mildred R					
7	D-2726C8			USA	https://w	alissa sorr	https://www.myher	1st cousin	98.2		1.4	4	64.1	https://w	Yes			62	alissa sorr					
8	D-2726C8					Dave Perr	https://www.myher	3rd - 5th c	77.6		1.1	6	32	https://w	Yes			2	Dave Perr					
9	D-2726C8			USA	https://w	Kenneth S	https://www.myher	3rd - 5th c	51.5		0.7	3	36	https://w	No									
10	D-2726C8					Katharina	https://www.myher	3rd - 5th c	50.2		0.7	3	25.8	https://w	Yes			13	Katharina					
Ancestry FTDNA Maternal FTDNA Paternal 23andMe MyHeritage																								

- “Walking the Clusters Back”
 - Identify each grandparent cluster
 - Proceed to earlier ancestors
 - <https://segmentology.org/2019/12/01/walking-the-clusters-back/>

Clustering Step 5

- **Identify the DNA Segment**
 - Use Spreadsheet to examine segment data
 - Utilize other tools
 - Autosegment at Genetic Affairs
 - Multi-Kit Analysis at GEDmatch
 - Surname & Ancestor Search at DNAGedcom
 - Chromosome Browser/Triangulation at MyHeritage

Identify Segment (a)

GEDmatch Visualization Options

Kits included --- T960698 T005406 T830889

Chromosomes & Segments Matrices GEDCom Lazarus List/CSV Tag Groups Edit Kit List Clustering

Chromosome Browsers & Matching Segment Analysis

Display Type	Note	cM Value	Misc-Options	Action
Segment Search		7	<input type="checkbox"/> Prevent Hard Breaks	Seg-Srch
Triangulation		7 cM	<input type="checkbox"/> Cross Match	Triangulation
2-D Chromosome Browser		7		2D Chr-Browse
3-D Chromosome Browser		7		3D Chr-Browse
Compact Segment Mapper				Compact Map

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GEDmatch® Auto-Clustering

[Here](#) is a link to a useful YouTube video on using the Tier 1 Clustering tool.

Reference Kit: T960698 (Andrew Hochreiter)
13 Kits
3 Clusters
Lower cM threshold= 25
Upper cM threshold= 1200

The AutoCluster feature on GEDmatch® was developed in collaboration with [Eugen & Blom](#) from [Genetic Affairs](#)

2020-11-19

Order: [by Cluster avg. cM to Ref. Kit](#)

[Submit to Multi-Kit Analysis](#)

Kit Number	Name	cM with Andrew Hochreiter	Select for Submit to MK/A	Info / Family Tree
T911971	*G	1027.6	<input type="checkbox"/>	Info
T204666	*D	876.9	<input type="checkbox"/>	Info
M345905	Ga	31.6	<input type="checkbox"/>	Info
T429829	*B	26.4	<input type="checkbox"/>	Info
T005406	*RobGH	423.6	<input checked="" type="checkbox"/>	Info
T830889	*WTH	229.5	<input checked="" type="checkbox"/>	Info
UG6572070	Su	25	<input type="checkbox"/>	Info
A714449	Su	25.1	<input type="checkbox"/>	Info
T266589	Ed	25.3	<input type="checkbox"/>	Info
XR6539919	Ka	25.8	<input type="checkbox"/>	Info
MX1574503	*D	26.2	<input type="checkbox"/>	Info
NZ2339086	Hi	28.6	<input type="checkbox"/>	Info
TW2115597	Ke	28.8	<input type="checkbox"/>	Info

Select for MK/A	Cluster Number	Size of Cluster	cM to Ref. Kit
<input type="checkbox"/> All Clusters			
<input type="checkbox"/> 1	4	503.13	
<input checked="" type="checkbox"/> 2	2	322.05	
<input type="checkbox"/> 3	7	26.4	

- In GEDmatch, select a cluster to analyze (checks in box)
- Select the “Submit for Multi-Kit Analysis” box
- Analyze with Segment Search or Triangulation

Identify Segment (b)

GEDmatch®
Matching Segment Search - V1.0

Software Version Oct 28 2020 22:57:37
 Kit: T960698 (Andrew Hochreiter) [Migration - F2 - F]

Segment threshold size will be adjusted dynamically between 200 and 400 SNPs
 Minimum segment cM to be included in total = 7.0 cM

Submit selected items to Multi-Kit-Analysis
 [Multi-Kit-Analysis] Select 2 or more from column ✓

Click [HERE](#) to download segment match csv data to a comma-separated CSV file.

Kit	✓	Chr	B37 Start Posn	B37 End Posn	cM	SNPs	Name	Sex	Email	Segments
T005406	<input type="checkbox"/>	1	1087683	13176463	28.3	3303	*RobGH	M	ajhochreiter@comcast.net	
T005406	<input type="checkbox"/>	1	13775122	20281949	15.1	2085	*RobGH	M	ajhochreiter@comcast.net	
T005406	<input type="checkbox"/>	1	80446510	89847444	9.3	2388	*RobGH	M	ajhochreiter@comcast.net	
Chromosome 2										
T830889	<input type="checkbox"/>	2	78845631	89125131	8.8	2032	*WTH	M	ajhochreiter@comcast.net	
T830889	<input type="checkbox"/>	2	95439005	112669950	11.5	3075	*WTH	M	ajhochreiter@comcast.net	
T005406	<input type="checkbox"/>	2	102546801	140071800	35.7	7666	*RobGH	M	ajhochreiter@comcast.net	
Chromosome 3										
T830889	<input type="checkbox"/>	3	7011661	26806383	29.3	5665	*WTH	M	ajhochreiter@comcast.net	
Chromosome 4										
T005406	<input type="checkbox"/>	4	27125382	37285195	9.3	1877	*RobGH	M	ajhochreiter@comcast.net	
Chromosome 5										
T005406	<input type="checkbox"/>	5	9218895	46399093	42.4	7544	*RobGH	M	ajhochreiter@comcast.net	
T005406	<input type="checkbox"/>	5	49462228	68828296	14.6	4090	*RobGH	M	ajhochreiter@comcast.net	
Chromosome 10										
T830889	<input type="checkbox"/>	10	109525838	135434303	49.0	8111	*WTH	M	ajhochreiter@comcast.net	
Chromosome 11										
T830889	<input type="checkbox"/>	11	30567671	41057977	12.3	2503	*WTH	M	ajhochreiter@comcast.net	
T005406	<input type="checkbox"/>	11	59487281	70671860	11.5	2436	*RobGH	M	ajhochreiter@comcast.net	
T005406	<input type="checkbox"/>	11	111116479	119518006	12.2	2359	*RobGH	M	ajhochreiter@comcast.net	
Chromosome 12										
T830889	<input type="checkbox"/>	12	52807280	61945917	8.5	1912	*WTH	M	ajhochreiter@comcast.net	
Chromosome 13										
T005406	<input type="checkbox"/>	13	27552701	115090193	114.5	22988	*RobGH	M	ajhochreiter@comcast.net	
T830889	<input type="checkbox"/>	13	29610405	63542512	36.4	8388	*WTH	M	ajhochreiter@comcast.net	
T830889	<input type="checkbox"/>	13	65366134	98755398	33.5	8090	*WTH	M	ajhochreiter@comcast.net	
Chromosome 15										
T005406	<input type="checkbox"/>	15	57620958	78370775	26.8	4769	*RobGH	M	ajhochreiter@comcast.net	
T005406	<input type="checkbox"/>	15	95578439							
Chromosome 19										
T830889	<input type="checkbox"/>	19	3299482							
T005406	<input type="checkbox"/>	19	3315718							
T005406	<input type="checkbox"/>	19	13278822							
T005406	<input type="checkbox"/>	19	48866214							
Chromosome 22										
T005406	<input type="checkbox"/>	22	22697014							

Total 25 segments

Var: Oct 28 2020 22:57:37
 Search took 0.40268 seconds.
 CPU time used: 0.07918 cpu seconds.

- Segment Search will reveal shared DNA of Cluster members
- Look for longest segment to identify chromosome, start/stop points and length

Chromosome 13										
T005406	<input type="checkbox"/>	13	27552701	115090193	114.5	22988	*RobGH	M	ajhochreiter@comcast.net	
T830889	<input type="checkbox"/>	13	29610405	63542512	36.4	8388	*WTH	M	ajhochreiter@comcast.net	
T830889	<input type="checkbox"/>	13	65366134	98755398	33.5	8090	*WTH	M	ajhochreiter@comcast.net	

Identify Segment (c)

GEDmatch Triangulation of Selected Kits-- V0.3)

Triangulation with Kit T960698 - Andrew Hochreiter.

All kits shown in columns Kit1 and Kit2 are taken from the selected kit matches to T960698.
3-Way (Triangulated) segment matches are shown in **green**. This is an indication of common ancestry.
Segments shown are larger than 7.0 cM and between 200 and 400 SNPs.

Triangulated results sorted by Chromosome, Start Position

Chr		Kit1		Kit2		B37 Start	B37 End	cM	
2		T005406	*RobGH	ajhochreiter@comcast.net	T830889	*WTH	ajhochreiter@comcast.net	102,546,801	111,807,027 7.3
13		T005406	*RobGH	ajhochreiter@comcast.net	T830889	*WTH	ajhochreiter@comcast.net	29,610,405	63,237,821 36.2
13		T005406	*RobGH	ajhochreiter@comcast.net	T830889	*WTH	ajhochreiter@comcast.net	66,201,817	98,527,439 32.4
19		T005406	*RobGH	ajhochreiter@comcast.net	T830889	*WTH	ajhochreiter@comcast.net	3,315,718	6,100,473 8.4

Triangulated results sorted by Kit Number, Chromosome, Start Position:

Submit Select 2 or more kits, and click this button for additional display and processing options.

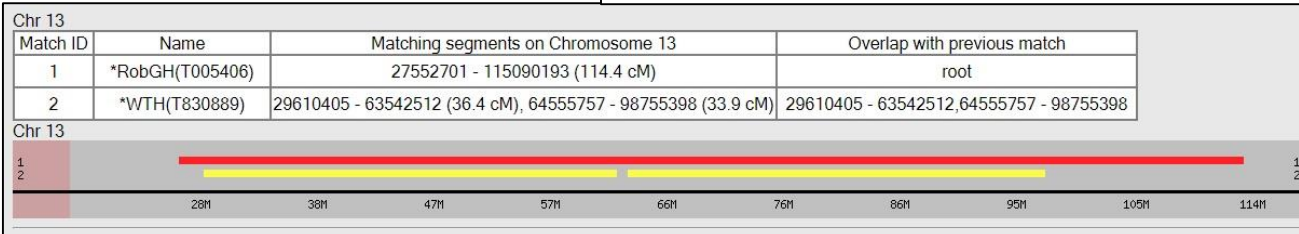
Chr		Kit1		Kit2		B37 Start	B37 End	cM			
2	<input type="checkbox"/>	T005406	*RobGH	ajhochreiter@comcast.net	<input type="checkbox"/>	T830889	*WTH	ajhochreiter@comcast.net	102,546,801	111,807,027	7.3
13	<input type="checkbox"/>	T005406	*RobGH	ajhochreiter@comcast.net	<input type="checkbox"/>	T830889	*WTH	ajhochreiter@comcast.net	29,610,405	63,237,821	36.2
13	<input type="checkbox"/>	T005406	*RobGH	ajhochreiter@comcast.net	<input type="checkbox"/>	T830889	*WTH	ajhochreiter@comcast.net	66,201,817	98,527,439	32.4
19	<input type="checkbox"/>	T005406	*RobGH	ajhochreiter@comcast.net	<input type="checkbox"/>	T830889	*WTH	ajhochreiter@comcast.net	3,315,718	6,100,473	8.4
2	<input type="checkbox"/>	T830889	*WTH	ajhochreiter@comcast.net	<input type="checkbox"/>	T005406	*RobGH	ajhochreiter@comcast.net	102,546,801	111,807,027	7.3
13	<input type="checkbox"/>	T830889	*WTH	ajhochreiter@comcast.net	<input type="checkbox"/>	T005406	*RobGH	ajhochreiter@comcast.net	29,610,405	63,237,821	36.2
13	<input type="checkbox"/>	T830889	*WTH	ajhochreiter@comcast.net	<input type="checkbox"/>	T005406	*RobGH	ajhochreiter@comcast.net	66,201,817	98,527,439	32.4
19	<input type="checkbox"/>	T830889	*WTH	ajhochreiter@comcast.net	<input type="checkbox"/>	T005406	*RobGH	ajhochreiter@comcast.net	3,315,718	6,100,473	8.4

Click [HERE](#) to download triangulated segment data to a tab-separated TSV file.

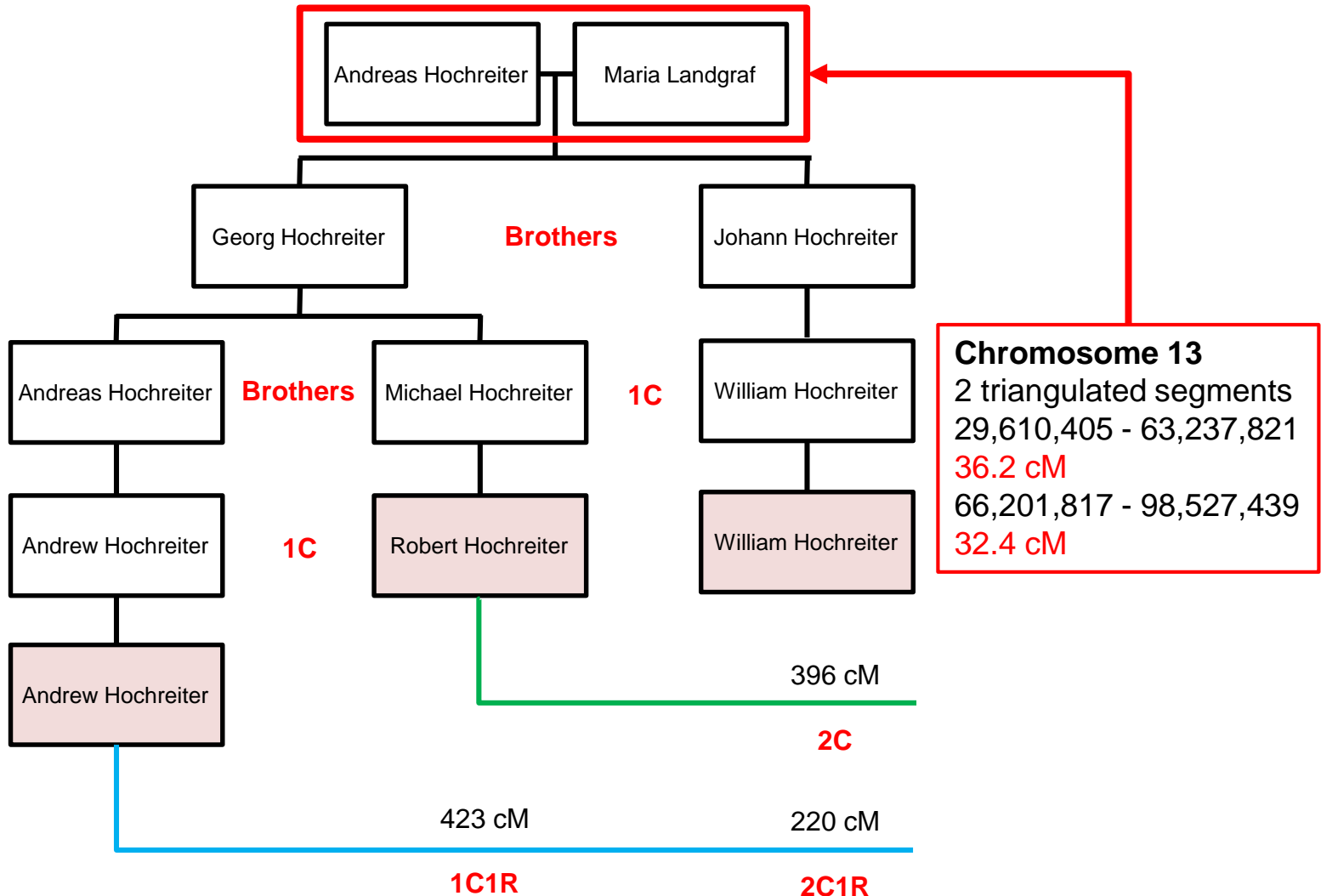
Software Ver: Oct 1 2020 12:26:38
Triangulation took 0.03 seconds.
CPU time used: 0.03 cpu seconds.
Triangulated Segments Displayed: 4

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- Select Triangulation tool to identify and visualize triangulated segments of cluster members
- Also use Chromosome Browser for another perspective of shared DNA

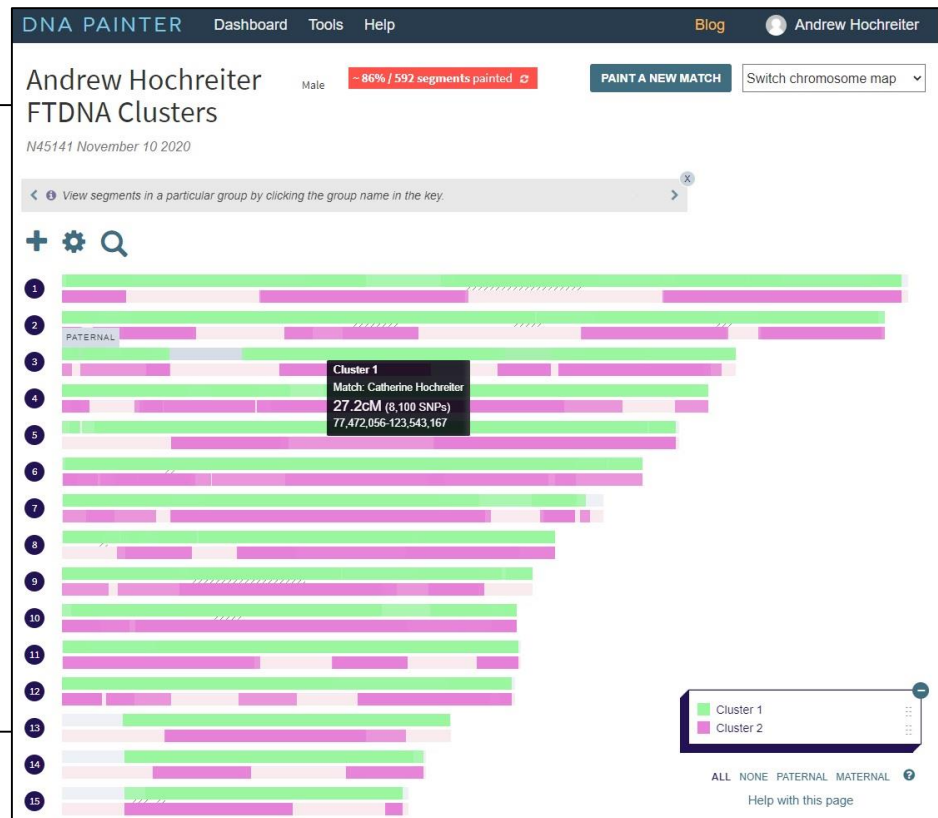
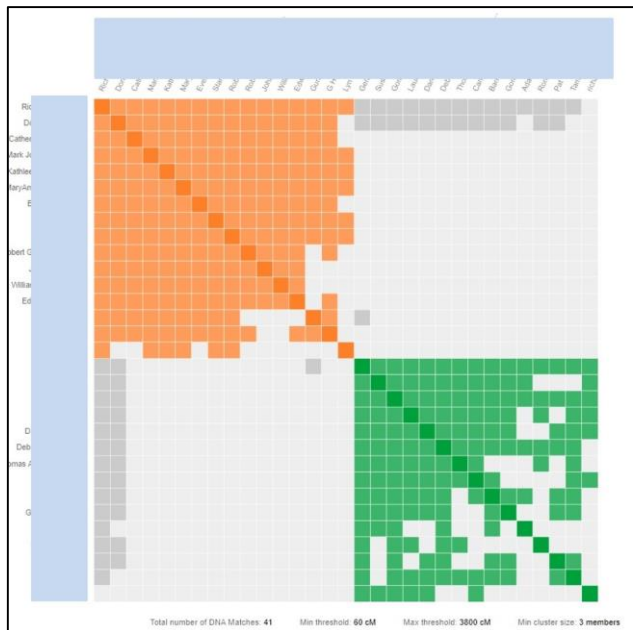


Segment to Ancestor



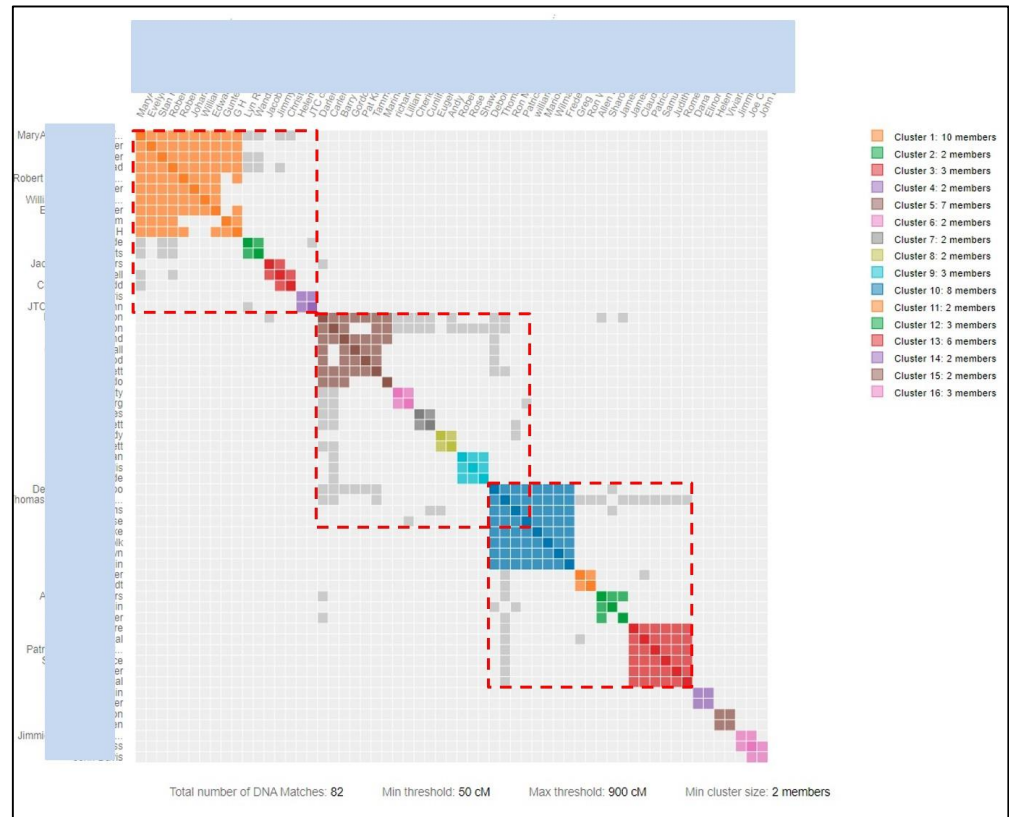
DNA Painter

- Cluster Auto Painter
 - Generate chromosome map from Clusters
 - Identify Clusters as Maternal or Paternal



Superclusters

- Superclusters are clusters related to each other
- Indicated by the gray boxes (matches who fit into other clusters)
- Coined by DNAGedcom developers



Caveats & Variables

- Clusters are NOT Perfect
- Matches do not always match each other
- Common Ancestor may vary by generation
- No guarantee shared segment is IBD
- Cluster tool & Match Lists
 - Parameter Settings
 - Algorithms
 - Match Lists Differ
 - Dissimilar Databases
 - Company Threshold

Points to Remember

- The Gray Ungrouped Boxes represent how people match others outside the cluster
- Experiment with additional Parameter settings besides the Default settings
- Identify Grandparent groups and move on to earlier generations: “Walk the Clusters Back”
- Clusters are represented by colors. Each cluster can “possibly” show relationship represented by a Common Ancestor
- The Two Goals are to create Genetic Networks and Identify the Common Ancestor and Segment

References

- Help at Cluster Tool
 - Genetic Affairs:
[https://www.geneticaffairs.com/images/Manual Genetic Affairs.pdf](https://www.geneticaffairs.com/images/Manual%20Genetic%20Affairs.pdf)
 - Shared Clustering:
<https://github.com/jonathanbrecher/sharedclustering/wiki>
- Dana Leeds: www.danaleeds.com/the-leeds-method/
- Jim Bartlett: <https://segmentology.org/>
- Family Locket: <https://familylocket.com/10-ways-to-group-your-dna-matches-into-genetic-networks>
- Kitty Cooper's Blog: <https://blog.kittycooper.com/2019/05/more-clustering-tools/>
- DNAeXplained (Roberta Estes): <https://dna-explained.com/>