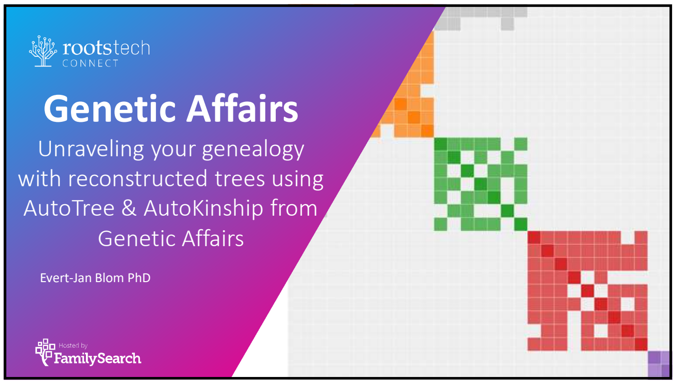


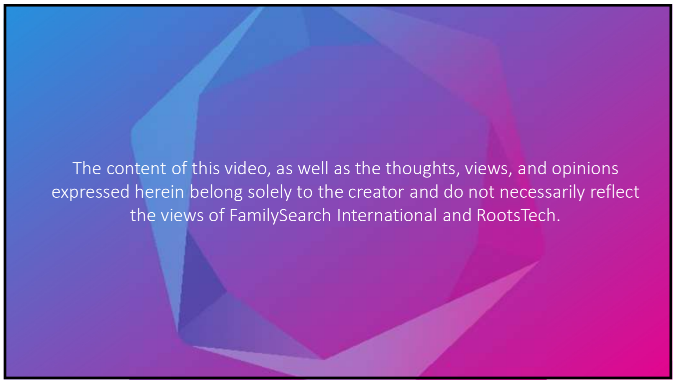
rootstech CONNECT

Genetic Affairs

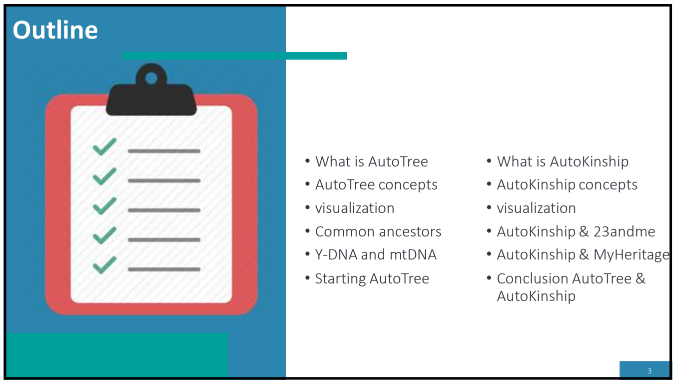
Unraveling your genealogy with reconstructed trees using AutoTree & AutoKinship from Genetic Affairs

Evert-Jan Blom PhD

Hosted by FamilySearch



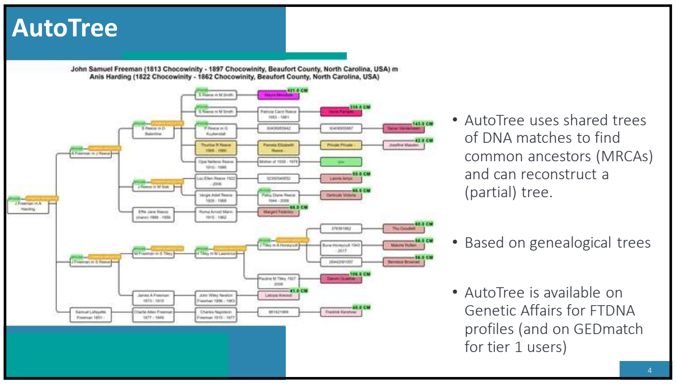
The content of this video, as well as the thoughts, views, and opinions expressed herein belong solely to the creator and do not necessarily reflect the views of FamilySearch International and RootsTech.



Outline

- What is AutoTree
- AutoTree concepts
- visualization
- Common ancestors
- Y-DNA and mtDNA
- Starting AutoTree

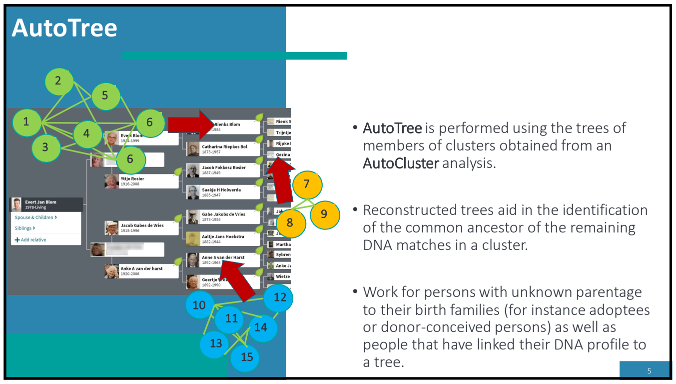
- What is AutoKinship
- AutoKinship concepts
- visualization
- AutoKinship & 23andme
- AutoKinship & MyHeritage
- Conclusion AutoTree & AutoKinship



AutoTree

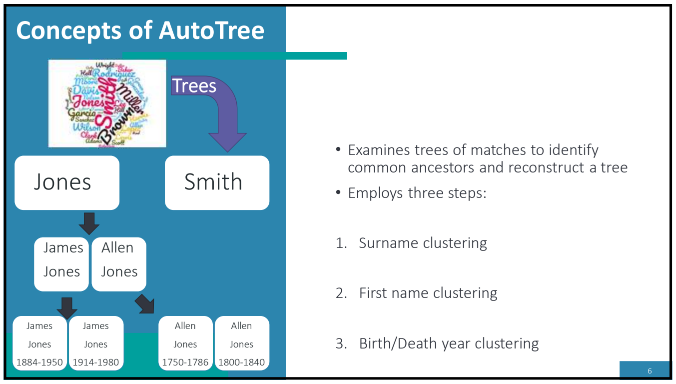
John Samuel Freeman (1813 Chocowinity - 1897 Chocowinity, Beaufort County, North Carolina, USA) m Anis Harding (1822 Chocowinity - 1862 Chocowinity, Beaufort County, North Carolina, USA)

- AutoTree uses shared trees of DNA matches to find common ancestors (MRCAs) and can reconstruct a (partial) tree.
- Based on genealogical trees
- AutoTree is available on Genetic Affairs for FTDNA profiles (and on GEDmatch for tier 1 users)



AutoTree

- **AutoTree** is performed using the trees of members of clusters obtained from an **AutoCluster** analysis.
- Reconstructed trees aid in the identification of the common ancestor of the remaining DNA matches in a cluster.
- Work for persons with unknown parentage to their birth families (for instance adoptees or donor-conceived persons) as well as people that have linked their DNA profile to a tree.



Concepts of AutoTree

Trees

Jones

Smith

James Jones

Allen Jones

James Jones 1884-1950

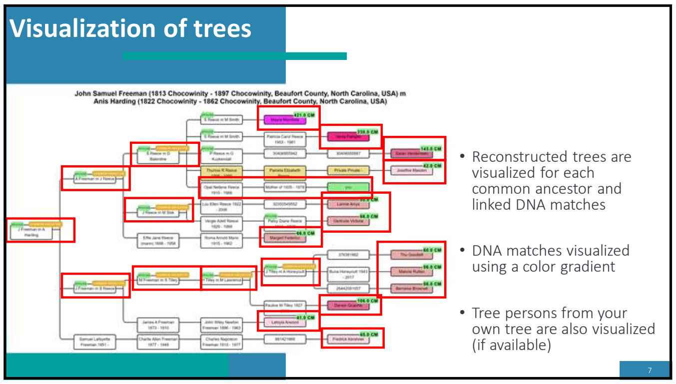
James Jones 1914-1980

Allen Jones 1750-1786

Allen Jones 1800-1840

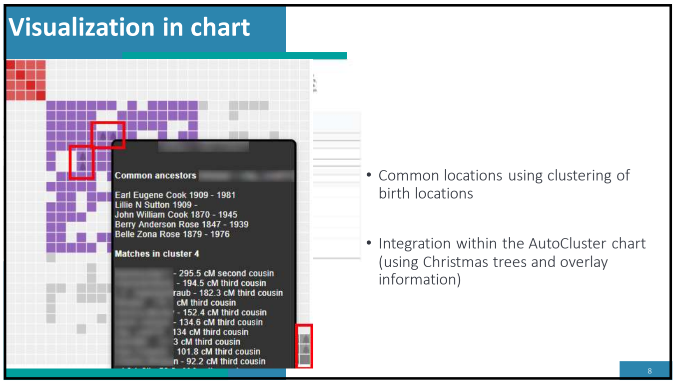
- Examines trees of matches to identify common ancestors and reconstruct a tree
- Employs three steps:

1. Surname clustering
2. First name clustering
3. Birth/Death year clustering



Visualization of trees

- Reconstructed trees are visualized for each common ancestor and linked DNA matches
- DNA matches visualized using a color gradient
- Tree persons from your own tree are also visualized (if available)



Visualization in chart

[redacted]

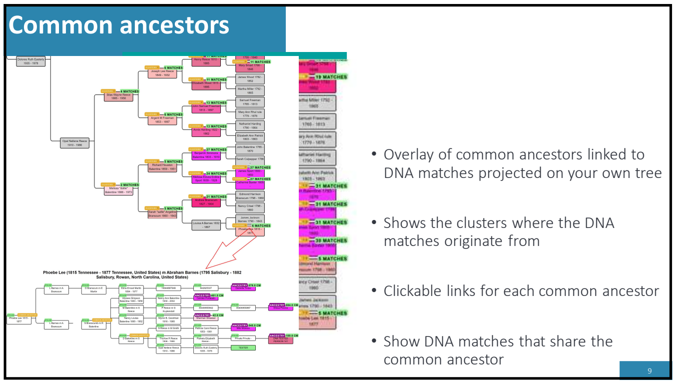
Common ancestors [redacted]

Earl Eugene Cook 1909 - 1981
Lillie N Sutton 1909 -
John William Cook 1870 - 1945
Berry Anderson Rose 1847 - 1939
Belle Zona Rose 1879 - 1976

Matches in cluster 4

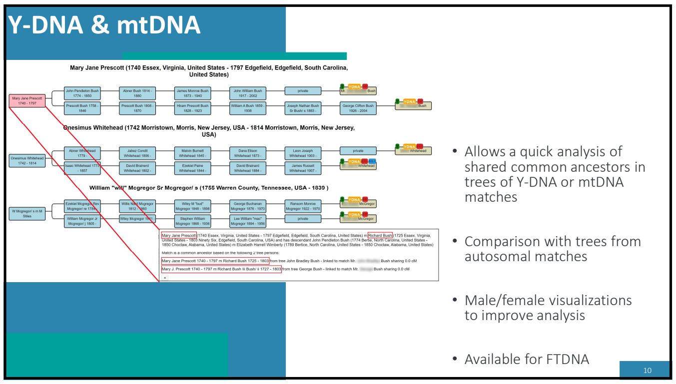
[redacted] - 295.5 cM second cousin
- 194.5 cM third cousin
raub - 182.3 cM third cousin
cM third cousin
- 152.4 cM third cousin
- 134.6 cM third cousin
134 cM third cousin
3 cM third cousin
101.8 cM third cousin
n - 92.2 cM third cousin

- Common locations using clustering of birth locations
- Integration within the AutoCluster chart (using Christmas trees and overlay information)



Common ancestors

- Overlay of common ancestors linked to DNA matches projected on your own tree
- Shows the clusters where the DNA matches originate from
- Clickable links for each common ancestor
- Show DNA matches that share the common ancestor



Y-DNA & mtDNA

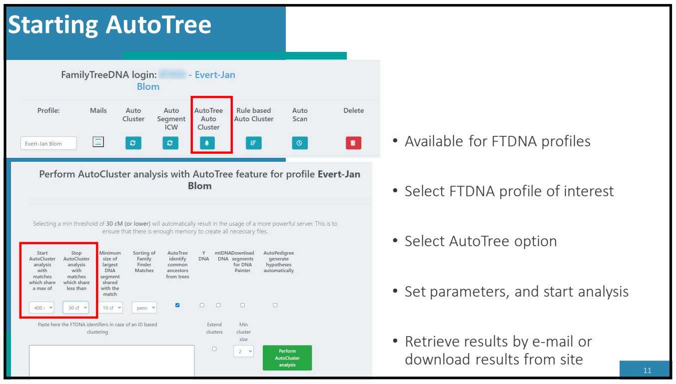
Mary Jane Prescott (1740 Essex, Virginia, United States - 1797 Edgefield, Edgefield, South Carolina, United States) m Richard Bush (1725 Essex, Virginia, United States - 1803 Ninety Six, Edgefield, South Carolina, USA) and has descendant John Pendleton Bush (1774 Bertie, North Carolina, United States - 1850 Choctaw, Alabama, United States) m Elizabeth Harrell Wimberly (1789 Bertice, North Carolina, United States - 1850 Choctaw, Alabama, United States)

Match is a common ancestor based on the following 2 tree persons:

Mary Jane Prescott 1740 - 1797 m Richard Bush 1725 - 1803 from tree John Bradley Bush - linked to match Mr. [redacted] Bush sharing 0.0 cM

Mary J. Prescott 1740 - 1797 m Richard Bush Iii Bush/ ii 1727 - 1803 from tree George Bush - linked to match Mr. [redacted] Bush sharing 0.0 cM

- Allows a quick analysis of shared common ancestors in trees of Y-DNA or mtDNA matches
- Comparison with trees from autosomal matches
- Male/female visualizations to improve analysis
- Available for FTDNA



Starting AutoTree

FamilyTreeDNA login: [redacted] - Evert-Jan Blom

Profile: Evert-Jan Blom

Perform AutoCluster analysis with AutoTree feature for profile **Evert-Jan Blom**

Selecting a min threshold of 30 cM (or lower) will automatically result in the usage of a more powerful server. This is to ensure that there is enough memory to create all necessary files.

Start AutoCluster analysis with matches which share a max of: 400

Stop AutoCluster analysis with matches which share less than: 30 cM

Minimum size of largest DNA segment shared with the match: 10 cM

Sorting of Family Finder Matches: perc

AutoTree identify common ancestors from trees: ☑

Y DNA: ☐

mtDNA DNA: ☐

Download segments for DNA Painter: ☐

AutoPedigree generate hypotheses automatically: ☐

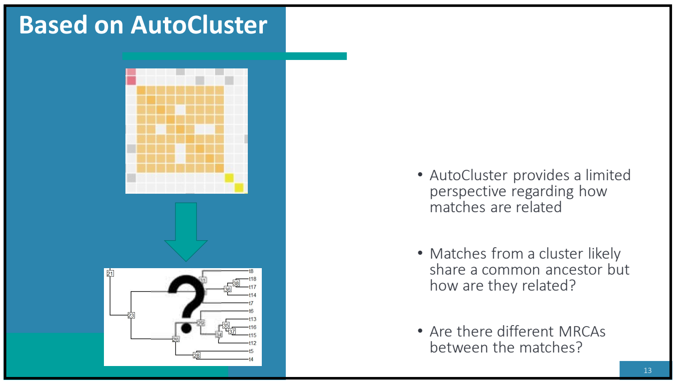
Paste here the FTDNA identifiers in case of an ID based clustering

Extend clusters: ☐

Min cluster size: 2

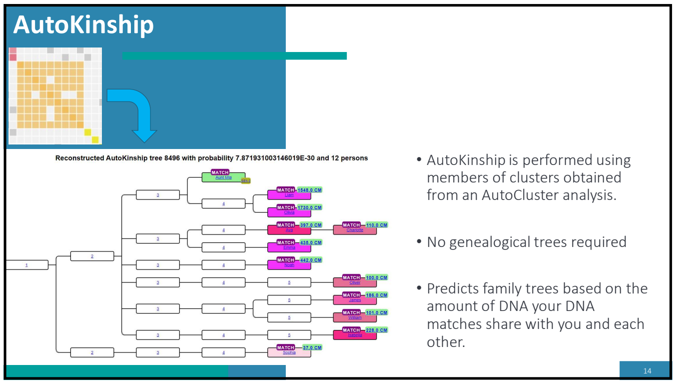
- Available for FTDNA profiles
- Select FTDNA profile of interest
- Select AutoTree option
- Set parameters, and start analysis
- Retrieve results by e-mail or download results from site

AutoKinship



Based on AutoCluster

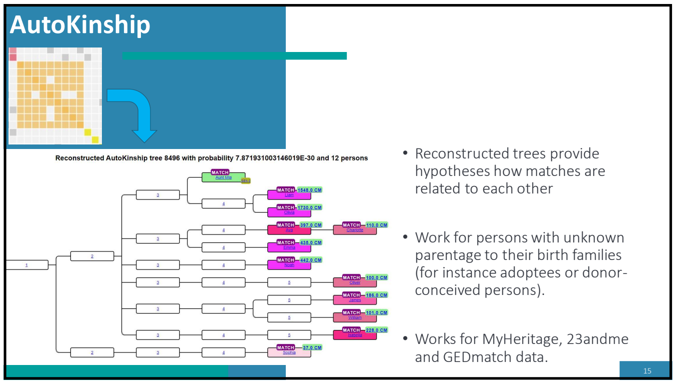
- AutoCluster provides a limited perspective regarding how matches are related
- Matches from a cluster likely share a common ancestor but how are they related?
- Are there different MRCAs between the matches?



AutoKinship

Reconstructed AutoKinship tree 8496 with probability 7.871931003146019E-30 and 12 persons

- AutoKinship is performed using members of clusters obtained from an AutoCluster analysis.
- No genealogical trees required
- Predicts family trees based on the amount of DNA your DNA matches share with you and each other.

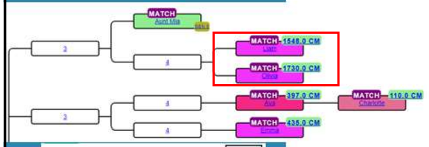


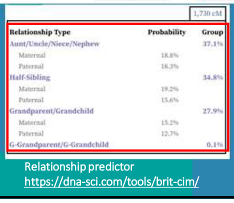
AutoKinship

Reconstructed AutoKinship tree 8496 with probability 7.871931003146019E-30 and 12 persons

- Reconstructed trees provide hypotheses how matches are related to each other
- Work for persons with unknown parentage to their birth families (for instance adoptees or donor-conceived persons).
- Works for MyHeritage, 23andme and GEDmatch data.

AutoKinship example





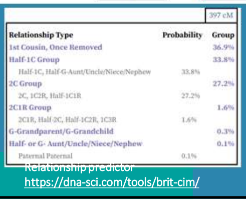
1,730 cM

Relationship Type	Probability	Group
Aunt/Uncle/Niece/Nephew		37.1%
Maternal	18.8%	
Paternal	18.3%	
Half-Sibling		34.8%
Maternal	19.2%	
Paternal	15.6%	
Grandparent/Grandchild		27.9%
Maternal	15.2%	
Paternal	12.7%	
G-Grandparent/G-Grandchild		0.1%

Relationship predictor
https://dna-sci.com/tools/brit-cim/

- Aunt Mia is the tested person
- Liam and Olivia shared 2905 cM and are predicted siblings
- They share 1548/1730 cM with Aunt Mia

AutoKinship example



397 cM

Relationship Type	Probability	Group
1st Cousin, Once Removed		36.9%
Half-1C Group		33.8%
Half-1C, Half-G-Aunt/Uncle/Niece/Nephew	33.8%	
2C Group		27.2%
2C, 1C2R, Half-1C1R	27.2%	
2C1R Group		1.6%
2C1R, Half-2C, Half-1C2R, 1C3R	1.6%	
G-Grandparent/G-Grandchild		0.3%
Half- or G- Aunt/Uncle/Niece/Nephew		0.1%
Paternal Paternal	0.1%	

Relationship predictor
https://dna-sci.com/tools/brit-cim/

- Ava and Charlotte share 3452 cM, parent child relationship. Who is the child?
- Aunt Mia shares 397 cM with Ava, and 110 cM with Charlotte
- Ava is the parent, most likely a 1C1R

AutoKinship example

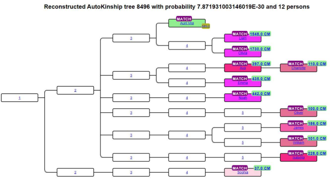
435 cM

Relationship Type	Probability	Group
1st Cousin, Once Removed		43.0%
Half-1C Group		38.9%
Half-1C, Half-G-Aunt/Uncle/Niece/Nephew	38.9%	
2C Group		16.4%
2C, 1C2R, Half-1C1R	16.4%	
G-Grandparent/G-Grandchild		0.7%
2C1R Group		0.5%
2C1R, Half-2C, Half-1C2R, 1C3R	0.5%	
Half- or G- Aunt/Uncle/Niece/Nephew		0.3%
Pat. Mat. or Mat. Pat. (x2)	0.1%	
Paternal Paternal	0.1%	

Relationship predictor
https://dna-sci.com/tools/brit-cim/

- Aunt Mia and Emma share 435 cM, potential 1C1R?
- Emma and Ava share 1084 cM, so most likely a 1C
- The 1C prediction of Emma and Ava fits nicely with the 1C1R prediction of Emma with Aunt Mia.

AutoKinship concepts



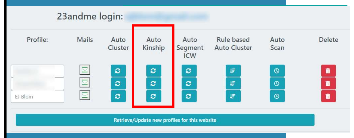

Brit ciM | DNA Science

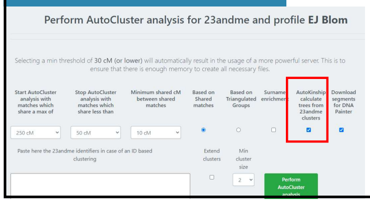
Discover the most probable relationship types for your DNA matches

Enter your shared cM or % in the applicable box below

- Examines many possible relationships, similar to WATO but from the perspective of all matches
- Generated trees are sorted based on the combined probabilities
- Employs probabilities from https://dna-sci.com, created by Brit Nicholson

AutoKinship & 23andme


23andme login:


Perform AutoCluster analysis for 23andme and profile **EJ Blom**

Selecting a min threshold of 30 cM (or lower) will automatically result in the usage of a more powerful server. This is to ensure that there is enough memory to create all necessary files.

Start AutoCluster analysis with matches which share a max of: 250 cM

Stop AutoCluster analysis with matches which share less than: 50 cM

Minimum shared cM between shared matches: 10 cM

● Based on Shared matches

○ Based on Triangulated Groups

☐ Surname enrichment

☑ AutoKinship calculate trees from 23andme clusters

☑ Download segments for DNA Painter

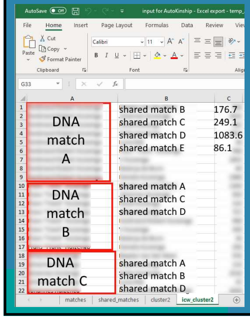
Paste here the 23andme identifiers in case of an ID based clustering

☐ Extend clusters

Min cluster size: 2

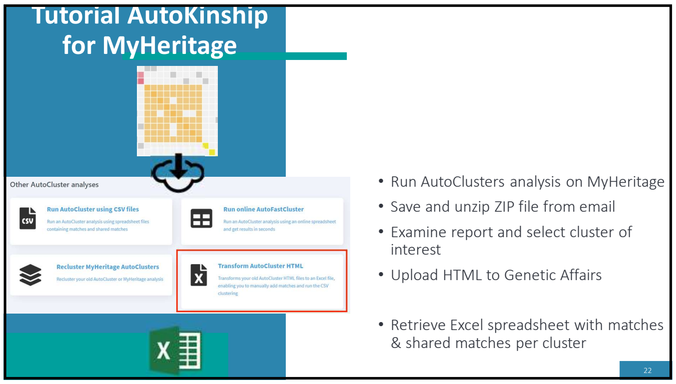
- Available for 23andme profiles
- Select 23andme profile of interest
- Select AutoKinship option
- Set parameters, and start analysis
- Retrieve results by e-mail or download results from site

Running AutoKinship for MyHeritage



	A	B	C
1–9	DNA match A	shared match B	176.7
		shared match C	249.1
		shared match D	1083.6
		shared match E	86.1
10–17	DNA match B	shared match A	
		shared match C	
		shared match D	
18–22	DNA match C	shared match A	
		shared match B	
		shared match D	

- (semi) manual data retrieval using 2 CSV files
- Requires matches file, 2 or 3 columns
  - 1st column: match name
  - 2nd column: amount of shared cM
  - 3rd column: generation (optional)
- Requires shared matches file, 3 columns
  - 1st column: match name
  - 2nd column: shared match name
  - 3rd column: amount of shared DNA between shared matches



Tutorial AutoKinship for MyHeritage

- Run AutoClusters analysis on MyHeritage
- Save and unzip ZIP file from email
- Examine report and select cluster of interest
- Upload HTML to Genetic Affairs

- Retrieve Excel spreadsheet with matches & shared matches per cluster

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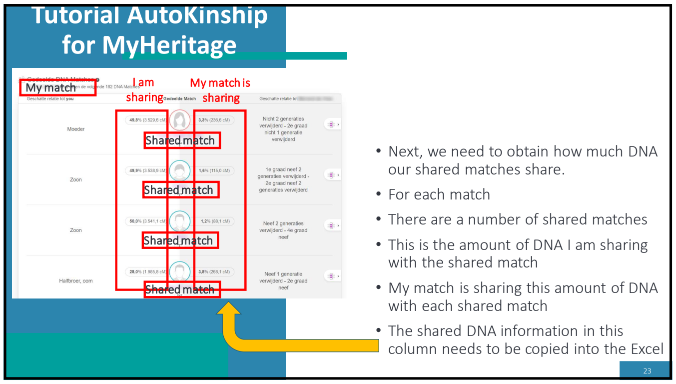

Tutorial AutoKinship for MyHeritage

Geschatte relatie tot **you**		**Gedeelde Match**		Geschatte relatie tot [redacted]
Moeder	**49,8%** (3.529,6 cM)		**3,3%** (236,6 cM)	Nicht 2 generaties verwijderd - 2e graad nicht 1 generatie verwijderd
Zoon	**49,9%** (3.538,9 cM)		**1,6%** (115,0 cM)	1e graad neef 2 generaties verwijderd - 2e graad neef 2 generaties verwijderd
Zoon	**50,0%** (3.541,1 cM)		**1,2%** (88,1 cM)	Neef 2 generaties verwijderd - 4e graad neef
Halfbroer, oom	**28,0%** (1.985,8 cM)		**3,8%** (268,1 cM)	Neef 1 generatie verwijderd - 2e graad neef

- Next, we need to obtain how much DNA our shared matches share.
- For each match
- There are a number of shared matches
- This is the amount of DNA I am sharing with the shared match
- My match is sharing this amount of DNA with each shared match
- The shared DNA information in this column needs to be copied into the Excel

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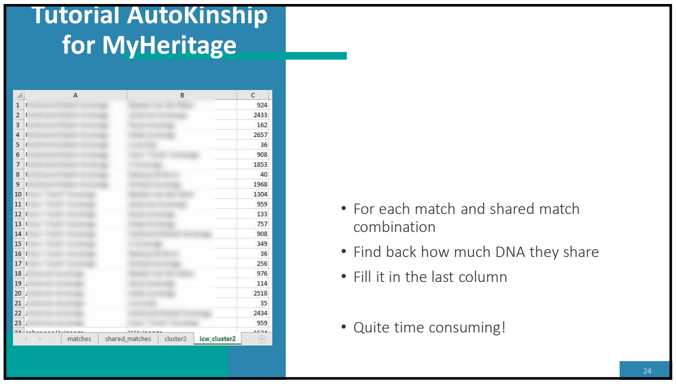

Tutorial AutoKinship for MyHeritage

	A	B	C
1	[redacted]	[redacted]	924
2	[redacted]	[redacted]	2433
3	[redacted]	[redacted]	162
4	[redacted]	[redacted]	2657
5	[redacted]	[redacted]	36
6	[redacted]	[redacted]	908
7	[redacted]	[redacted]	1853
8	[redacted]	[redacted]	40
9	[redacted]	[redacted]	1968
10	[redacted]	[redacted]	1304
11	[redacted]	[redacted]	959
12	[redacted]	[redacted]	133
13	[redacted]	[redacted]	757
14	[redacted]	[redacted]	908
15	[redacted]	[redacted]	349
16	[redacted]	[redacted]	36
17	[redacted]	[redacted]	256
18	[redacted]	[redacted]	976
19	[redacted]	[redacted]	114
20	[redacted]	[redacted]	2518
21	[redacted]	[redacted]	35
22	[redacted]	[redacted]	2434
23	[redacted]	[redacted]	959

- For each match and shared match combination
- Find back how much DNA they share
- Fill it in the last column

- Quite time consuming!

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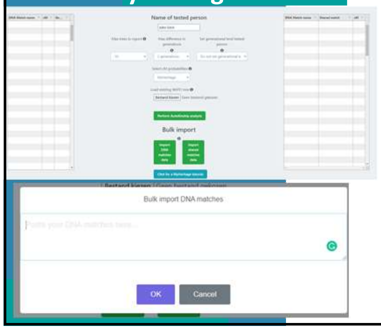
Tutorial AutoKinship for MyHeritage



- Visit Genetic Affairs: https://members.geneticaffairs.com/autokinship
- Use bulk import to paste matches & shared matches
- (optional) set generational level of tested person
- Provide name, select cM probabilities and start analysis

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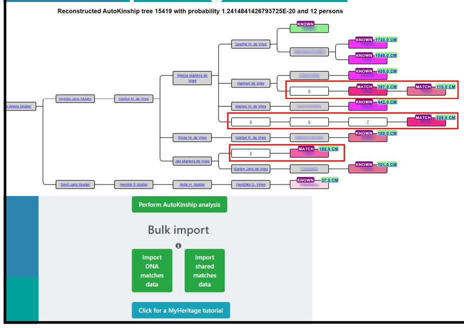
Tutorial AutoKinship for MyHeritage


Reconstructed AutoKinship tree 15419 with probability 1.2414841426793725E-20 and 12 persons

- Parts of the predicted tree can be known
- Make a tree in WATO (https://dnapainter.com/tools/probability) and load it into AutoKinship

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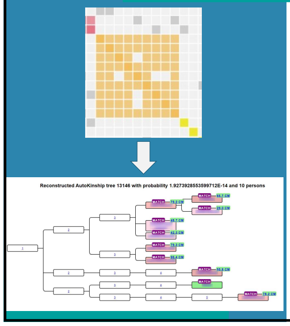
Conclusion


Reconstructed AutoKinship tree 13146 with probability 1.9273928553599712E-14 and 10 persons

- **AutoTree** reconstructs genealogical trees based on trees shared by (FTDNA) DNA matches
  - Available on GEDmatch (tier 1)
- **AutoKinship** reconstructs trees based on shared DNA between shared matches
  - Automatically for 23andme matches
  - Semi automatically for MyHeritage
  - Available on GEDmatch (tier 1)

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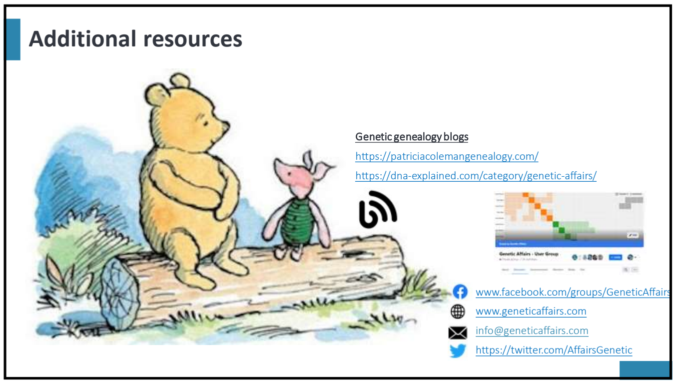

Additional resources

Genetic genealogy blogs

https://patriciacolemangenealogy.com/

https://dna-explained.com/category/genetic-affairs/

www.facebook.com/groups/GeneticAffairs

www.geneticaffairs.com

info@geneticaffairs.com

https://twitter.com/AffairsGenetic

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