Graphs for Genealogists
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Graphs for Genealogists

The future is faster than you think!

An invitation …

How to Get Involved

An invitation to help build the future of genealogy graph analytics.

Testers

GFG needs testers to shake down new features and provide feedback. You'll get an inside track to the latest features and help influence improvements and new features. To volunteer send us an email.
info@wai.md

Advocates

GFG encourages thought leaders to learn about its capabilities and write reviews for their constituency. To request a demonstration or interview send us an email.
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Developers

GFG is an open source project with modular components. Plug-Ins are coded in Java. If you'd like help design, build or manage new capabilities send us an email.
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Innovators

Have an idea? GFG can help you explore its feasibility and develop a plan. There are many opportunities for entrepreneurs using graphs in genealogy. We'd like to help expand the innovation community.
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Collaborators

Would you like to incorporate graph capabilities into your products? GFG can help. DNA analytics, forensic genealogy, document and image management have significant opportunities.
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Meeting Planners

GFG can provider speakers or workshop leaders who bring graph thinking and methods to your meeting.
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Volunteer: https://wai.md/gfg

Collaborators

- **Wesley Johnston**
  - DNA Coverage
  - User's Guide
- **Weidong Yang**
  - GraphXR: 3D visualizations
- **Peter Cunningham**
  - In common with report
  - GDS Bug - Change in neo4j.conf files
- **Michelle Wilson**
  - Endogamy analytics and reporting
- **Ian Logan**
  - mt-haplotree
- **Tim Janzen**
  - Mennonite Project endogamy reporting
- **Philip Gasaatura**
  - Rwanda oral history project

Acknowledgements

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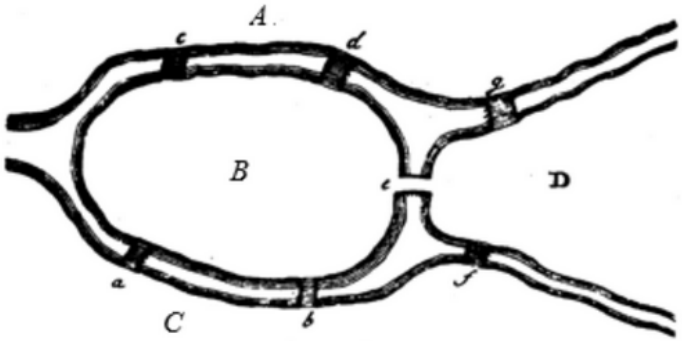
Thinking in Graphs

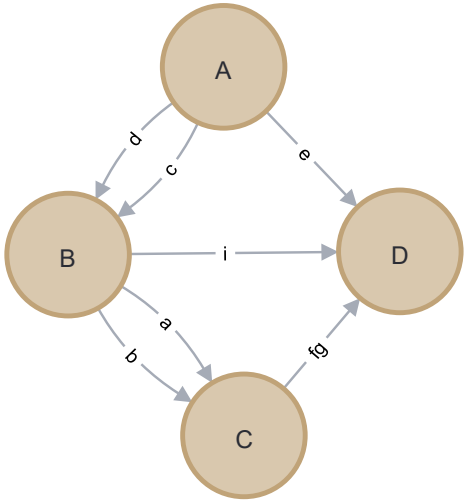
Leonhard Euler (1707-1783)

Euler is the “father of graph theory” who originally found the bridges of in Königsberg problem too trivial for his attention.

The question was: can you cross each of the seven bridges only once?

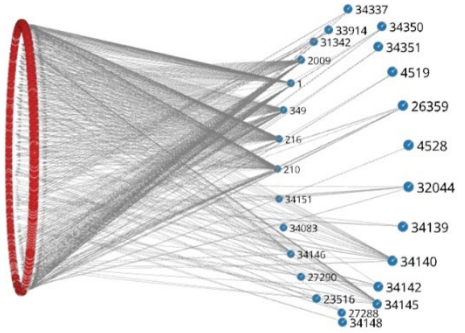
Replaced a brute force solution with a graph.





What we'll cover

- The GFG Strategy
- "Thinking in Graphs" Get ready to be amazed
- Why graph methods? Bigger, better, faster
- If graphs, how? The strategy
- Making it feasible
  - Enabling software
  - Professor's Rounds
- What does it do? Seeing is believing.

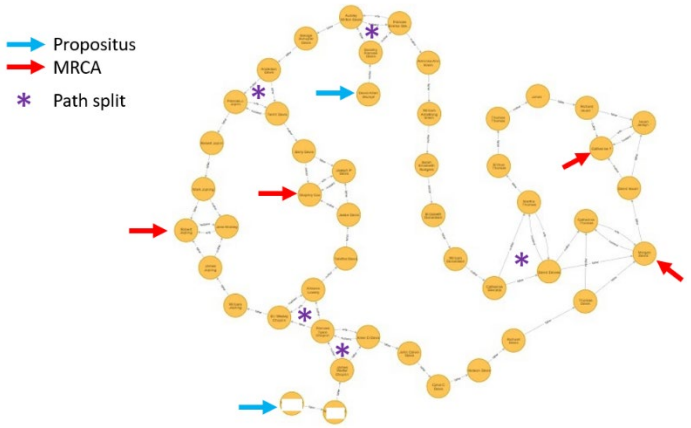


The GFG Strategy

- Align with interests and skills of genealogists
- Use available data
- Tools to do the heavy lifting
- Enhance extant analytic reporting
- Expand the analytic repertoire
- Make it open source; encourage collaboration
- Modular design for numerous graphs
- Support interoperability with 3rd party tools
- Develop standards for genealogy graphs

Feasibility

- Graph database technology is mature
- Genealogy graph resources are available
- Thought leaders are aware
- >100 downloads of GFG software
- First server-based deployments in progress
- Mentoring program in place



GFG: Making the Complex Simple

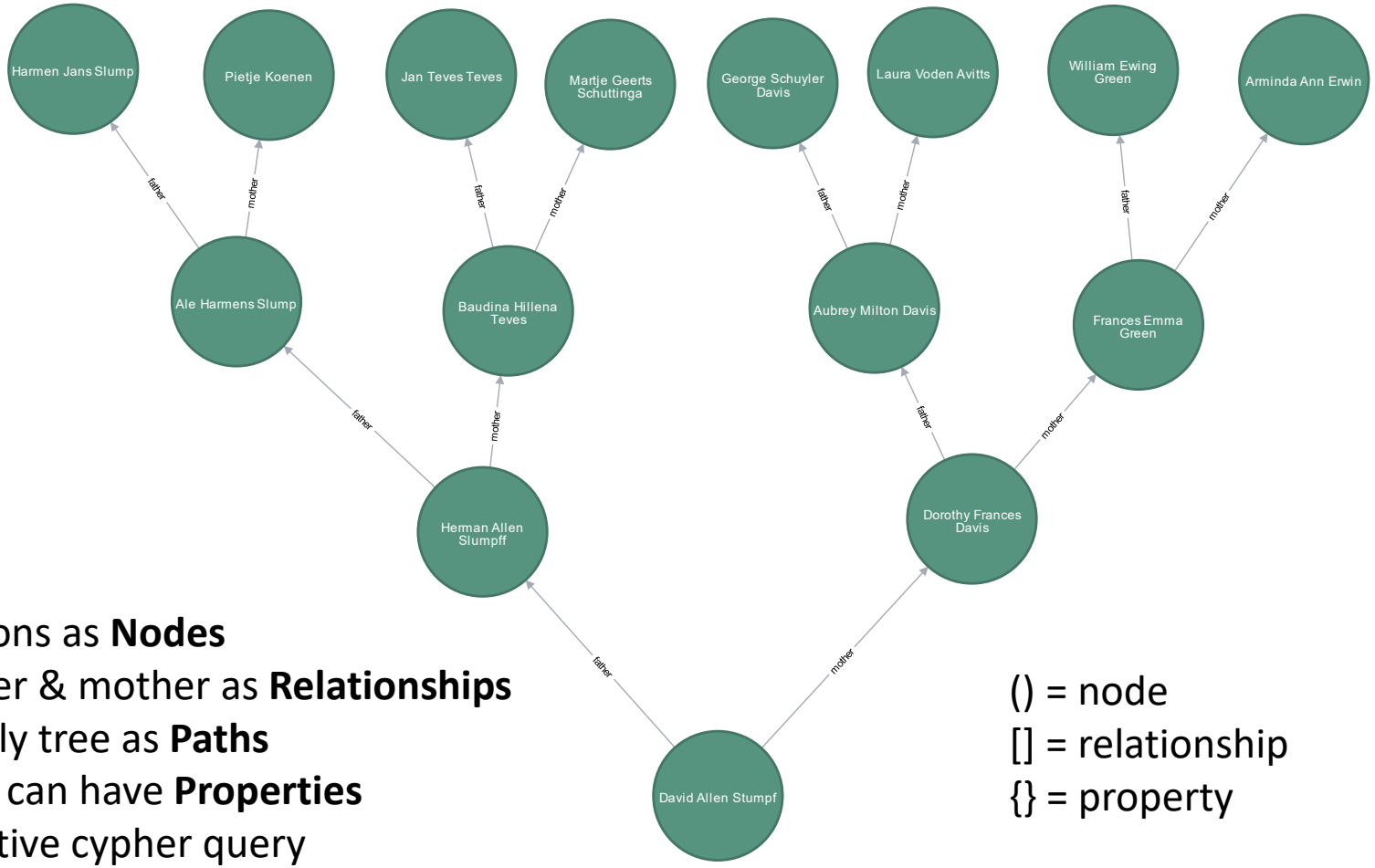
```
match (s1:Segment)
with s1 order by s1.chr,s1.strt_pos,s1.end_pos
with collect(distinct s1) as segs1
match (m1:DNA_Match)-[r1:match_segment]-(s2:Segment) where s2 in segs1 and r1.cm>=7 and r1.snp_ct>=500 and
r1.p_anc_rn is not null and r1.m_anc_rn is not null
with r1.p_anc_rn as anc_rn,
case when m1.RN>0 then '*' + m1.fullname + ' [' + m1.RN + ']' else m1.fullname end as m2,
case when m1.RN>0 then m1.RN else null end as rns1,
case when r1.m_rn>0 then r1.m_rn else null end as rns2,
case when r1.m_rn>0 then '*' + r1.m + ' [' + r1.m_rn + ']' else r1.m end as m3,
max(r1.cm) as max_cm,min(r1.cm) as min_cm,
s2,count(r1) as edgect, sum(case when r1.p=m1.fullname then 1 else 0 end) as unidir_ct_p,
sum(case when r1.m=m1.fullname then 1 else 0 end) as unidir_ct_m
with anc_rn,s2,min_cm,max_cm,
apoc.coll.union(collect (distinct m2), collect(distinct m3)) as matches,
apoc.coll.union(collect(distinct rns1),collect(distinct(rns2))) as rns,
sum(edgect) as edgect,sum(unidir_ct_m) as unidir_ct_m,sum(unidir_ct_p) as unidir_ct_p order by s2.chr,s2.strt_pos,s2.end_pos
with anc_rn,s2,min_cm,max_cm,
apoc.coll.sort(apoc.coll.flatten(matches)) as matches,
apoc.coll.sort(apoc.coll.flatten(rns)) as rns,
edgect,unidir_ct_m,unidir_ct_p
return s2.chr as chr,s2.strt_pos as start_pos,s2.end_pos as end_pos,apoc.math.round(min_cm,1) as cm,edgect,unidir_ct_p,unidir_ct_m,size(rns) as kits,size(matches) as match_ct,anc_rn,rns,matches


matches_by_segments_anc_desc()
```

Why Graph Methods?

- Queries are intuitive
- Big data is manageable
- Little change in performance as data added
- Graph traversals outperform iterations

- Enhancements create knowledge
- Knowledge graphs enable discovery

Thinking in Graphs



Persons as **Nodes**
Father & mother as **Relationships**
Family tree as **Paths**
Each can have **Properties**
Intuitive cypher query

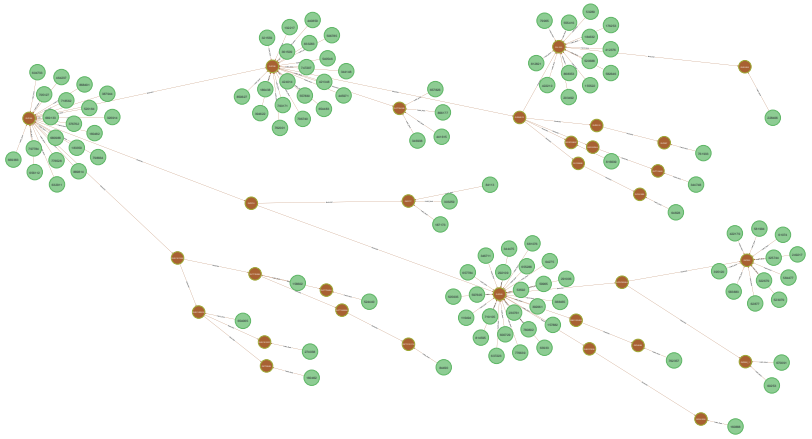
() = node
[] = relationship
{} = property

```
match path=(p:Person{RN:1})-[r:father|mother*0..3]->(a:Person) return path
```

Family Tree Functions

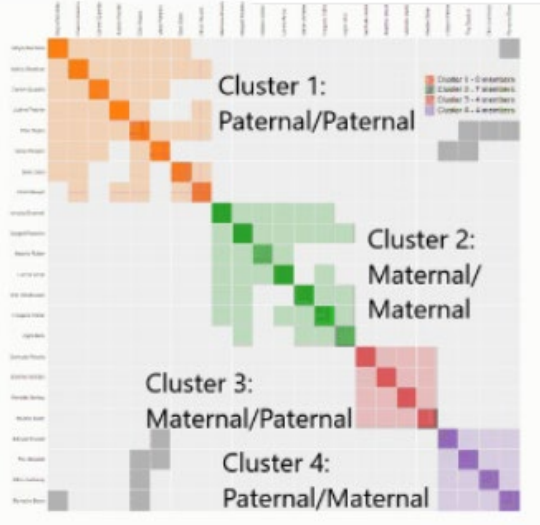
- Patrilineal trees
- Matrilineal trees
- X-inheritance trees
- Double cousins
- Relationships of all in the project
- X-genetic distance for all
- Pedigree completeness
- Correlation of relationship

Haplotrees

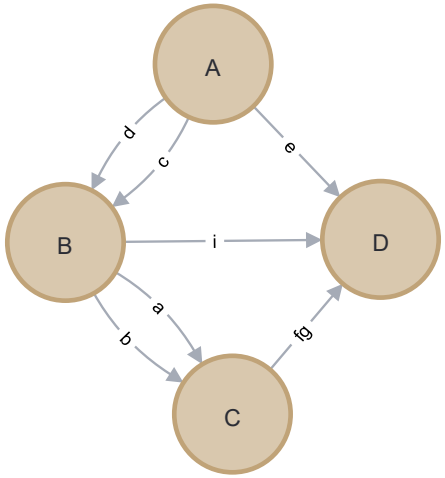


- FTDNA
  - Y-haplotree
  - Mt-haplotree
- Analytics
  - Inferred haplogroup => knowledge
  - Clade-mates
  - Dual matches: at- and either Y- or mt-matches
- Display
  - ORDPATH

Graphs as Adjacency Matrices
… when big data is overwhelming



The N^2 problem

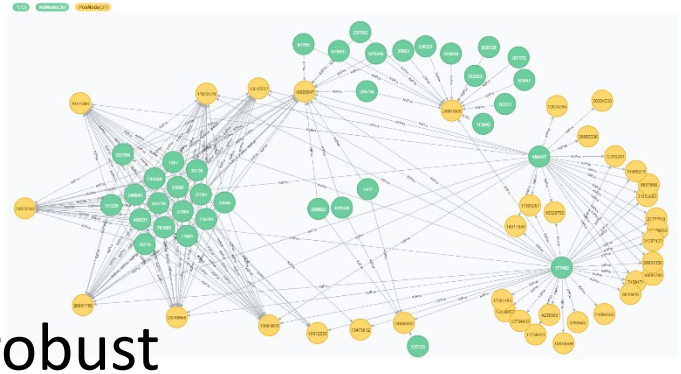


DNA Matches = sparse matrix
Great for limited set of close matches
Quickly become non-computable
Graph methods handle 250,000 matches
  Avoids a 62 trillion cell matrix!
  Performs well

$$\begin{Bmatrix} 0 & 2 & 0 & 1 \\ 2 & 0 & 2 & 1 \\ 0 & 2 & 0 & 1 \\ 1 & 1 & 1 & 0 \end{Bmatrix}$$

Thinking in Graphs
Avoid a common trap

- If you've worked with relational databases
  - Nodes ≅ tables
  - Relationships ≅ joins
  - Properties ≅ table fields
- Don't do this!
  - It's a simplification that is not robust
  - It diverts you from thinking differently
- Graphs have new first-class citizens
  - Relationships are more robust than joins
  - Path and List data types are not in relational systems
- Graphs are a unique ecosystem



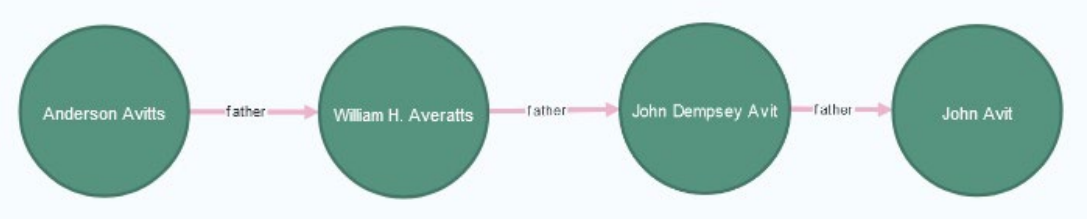
NoSQL databases are NOT native graph databases

New Ways of Thinking

- Can I relate these two graphs?
- What properties should the relationship have?
- How do I speed up traversal queries?
- Can I create a new perspective? Union tree?
- What can I do with traversal collected data?
- How do I manage provenance of data?
- How do I leverage graph specific capabilities?
- How can I enhance the knowledge graph?

Think in Path Traversals

- Query uses an index to find start node(s)
- Traverses from start through relationships
- Several methods for collecting data as **Lists**



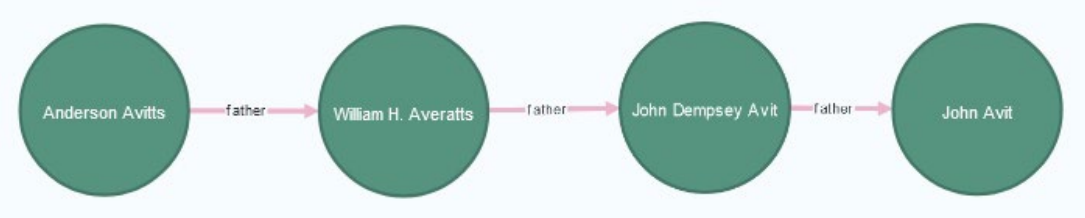
- Graphs have data types
  - Node
  - Relationship
  - Path
  - List

Each can have properties which can be indexed

Ahnentafel from traversal data

Collecting 1's and 0's

```
match path=(n:Person{RN:27})-[r:father|mother*0..2]->(x)
with x.fullname as Name,'1' + reduce(srt ='', q IN nodes(path)|srt + case when
 q.sex='M' then '0' else '1' end ) AS Anh
with Name, '1' + right(Anh,size(Anh)-2) as Ahnen
return Name,Ahnen as Ahen_base_2 , gen.rel.ahnentafel(Ahnen) as Ahnentafe
l order by Ahnentafel
```



Name	Ahen_bas	Ahnentafe
Anderson	1	1
William H	10	2
Tabitha Br	11	3
John Dem	100	4
Nancy Mc	101	5
Joshua H.	110	6
Rebecca L	111	7

Triple magic
Adding record numbers and sex

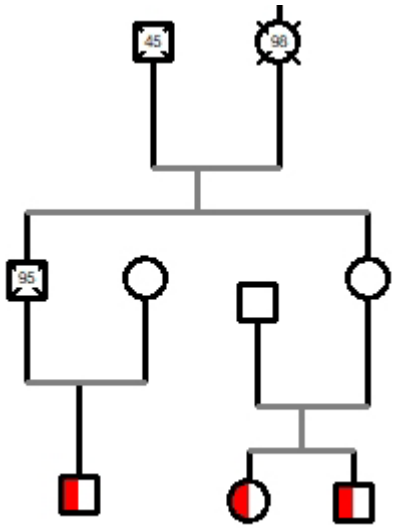
Name	gen	sex_path	Ahnentafel	Dewey	ORDPATH
Martha Elizabeth Stinnett [32] (1843-1928)	0	F	1	[32]	1018
Samuel Lewis Stinnett [63] (1822-1864)	1	FM	2	[32,63]	101810127
Alpha Loggins [64] (1823-1906)	1	FF	3	[32,64]	101810128
Mary Elizabeth Nichols [101] (1785-1855)	2	FMF	5	[32,63,101]	1018101271100d
Samuel Loggins [102] (1776-1826)	2	FFM	6	[32,64,102]	1018101281100e
Martha Scott [103] (1795-1880)	2	FFF	7	[32,64,103]	1018101281100f
William Nichols [130] (1754-1850)	3	FMFM	10	[32,63,101,130]	1018101271100d11002a
Nancy Blankenship [131] (1765-1850)	3	FMFF	11	[32,63,101,131]	1018101271100d11002b

- X-chromosome ancestors of Martha Elizabeth Stinnett
- Sex path excludes male to male inheritance
- Dewey is an aggregation of record numbers of persons in he path
- ORDPATH a hexadecimal number created from the Dewey by a UDF
- Notice that sorting on the Dewey will not order the list properly
- Sorting on ORDPATH provides a proper sort
- SQL Server hierarchyId datatype is an ORDPATH string

O'Neil, P. *et al.* ORDPATHs: insert-friendly XML node labels. in *Proceedings of the 2004 ACM SIGMOD international conference on Management of data* 903–908 (Association for Computing Machinery, 2004). https://www.cs.umb.edu/~poneil/ordpath.pdf

Common ancestors
… bread and butter graph task

```
match (p1:Person{RN:1})-
[r1:father|mother*0..15]->(mrca:Person)<-[r2:father|mother*0..15]-
(p2:Person{RN:600})
return collect(mrca.fullname) as mrca
```



- Pictured pedigree: Query returns grandparents
- Two paths converge on MRCA(s)
- Three variables define a relationship
  - Path length 1
  - Path length 2
  - MRCA count
- Represent as concatenated string
  - Pictured 2:2:2 = 1C
  - 2:2:1 = H1C
  - 4:5:1 = H3C1R
- fam_rel node set also includes Shared Centimorgan Project data

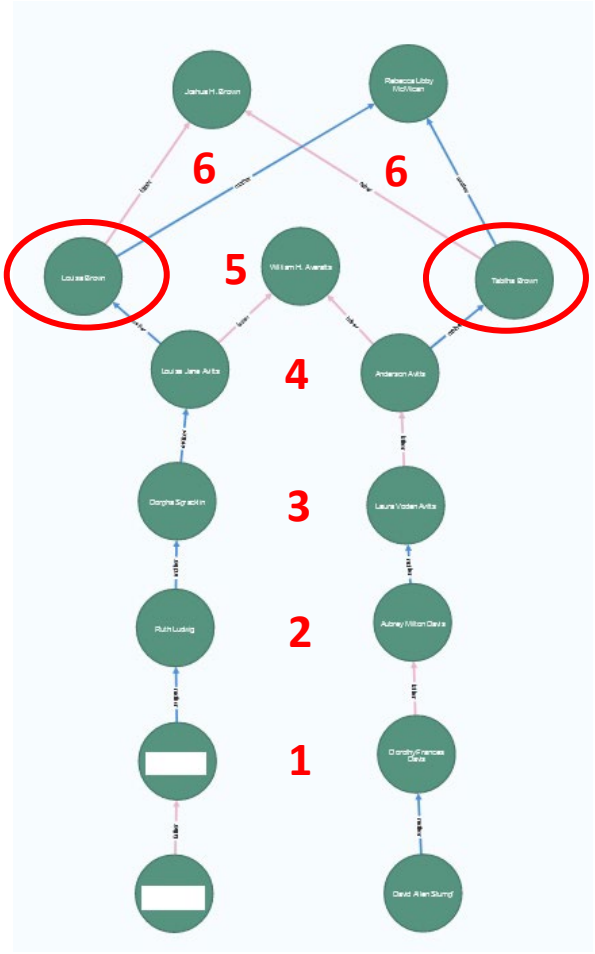
Node Properties

fam_rel

<id>	52093
HighSharedCM	1225
Indx	2:2:2
LowSharedCM	553
MeanSharedCM	874
nmrca	2
path1	2
path2	2
relationship	1C

There are many GFG functions for common ancestors

Easier to see in a graph



My 3G grandfather married sisters

His descendant is both my 5C and H4C, sharing 3 MRCAs in two different generations.

5:5:1 = H4C
6:6:2 = 5C

The sisters' children are ¾ siblings

Correlation of Relationship
… a number with added value

- Single value
- Detailed view
  - Count hops on each path and do the math
  - Estimate or look up the expected shared cM

propositi	relationship	ancestors	path1	path2	genetic_distance	COR
David Allen Stumpf 1 (1945-) ; anonymized 26429 (-)	H5C	Rebecca Libby McMican 4607 (1790-1863)	6	6	12	.0002441
David Allen Stumpf 1 (1945-) ; anonymized 26429 (-)	H5C	Joshua H. Brown 4441 (1780-1840)	6	6	12	.0002441
David Allen Stumpf 1 (1945-) ; anonymized 26429 (-)	H4C	William H. Averatts 53 (1813-2022)	5	5	10	.0009766

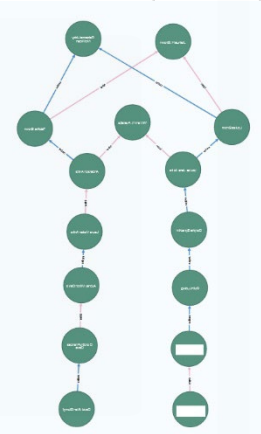
The total COR is 0.00146484375
From the shared centimorgan project the expected value and range is unknown cm.
The observed shared DNA is 82.9.
The predicted DNA is 0.00146484375 x 6000 = 8.7890625 cm

5c
25
0 – 117

UDF:
return gen.rel.shared_DNA(1,26429)

The coefficient of relationship (COR) is a measure of pedigree collapse resulting from ancstors appearing more that one in the family tree.
The paths are the generations to the common ancestor for each person in the analysis.

references:
https://www.yourdnaguide.com/ydgblog/2019/7/26/pedigree-collapse-and-genetic-relationships
http://www.genetic-genealogy.co.uk/Toc115570135.html
https://isogg.org/wiki/Coefficient_of_relationship
database: avitts



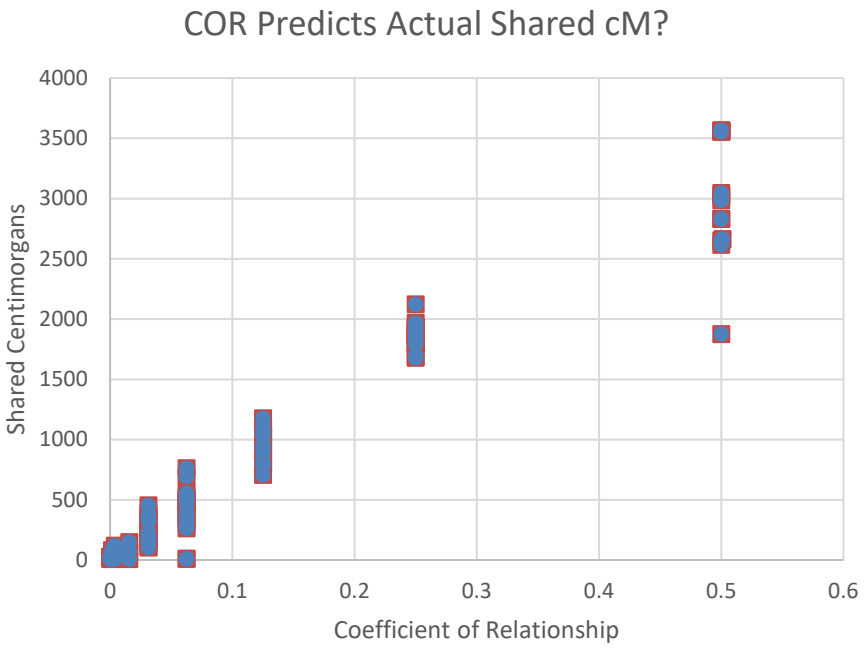
COR, if available, can be a better filter than relationship or centimorgans.

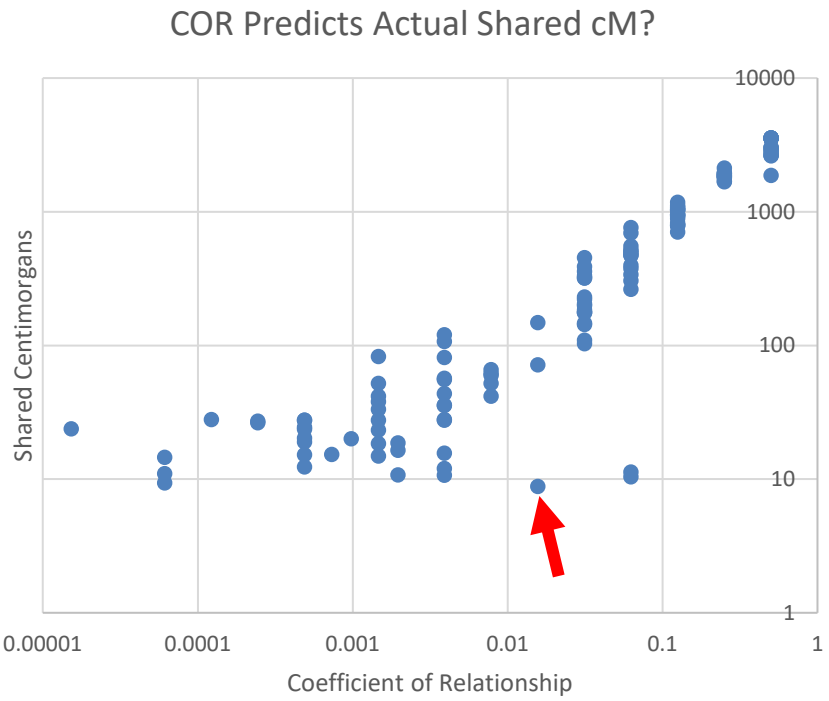
What's going on?

The illusion of linearity is exposed in a log-log plot

Is segregation really random? Are there outliers?

Sticky segments? Selection bias? Something else?

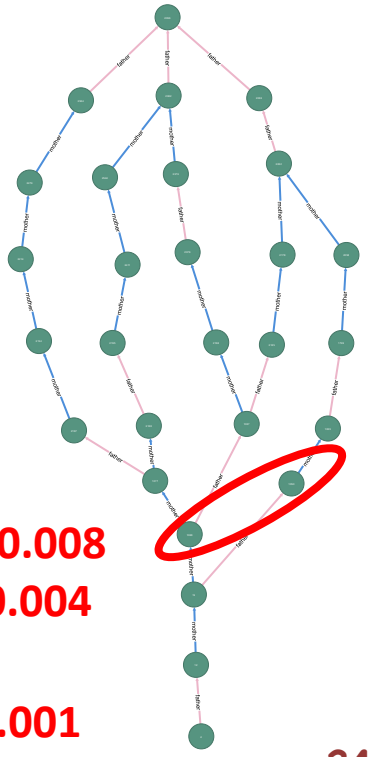




Mother Nature and "Thinking in Graphs" offer some possible explanations.

Pedigree Collapse

- Duplicate ancestors
- Multiple positions in a standard pedigree chart
- Multiple paths
- Coefficient of inbreeding
  - Most recent endogamous ancestor
  - COR of MREA halved for each descendant generation

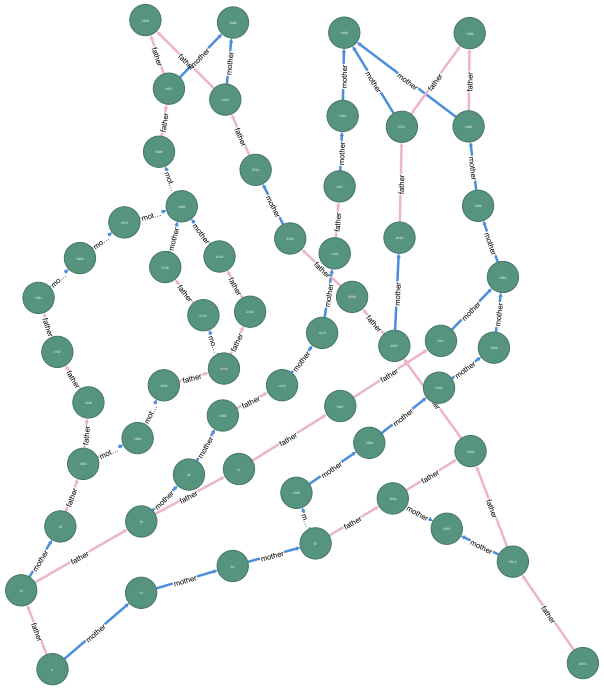


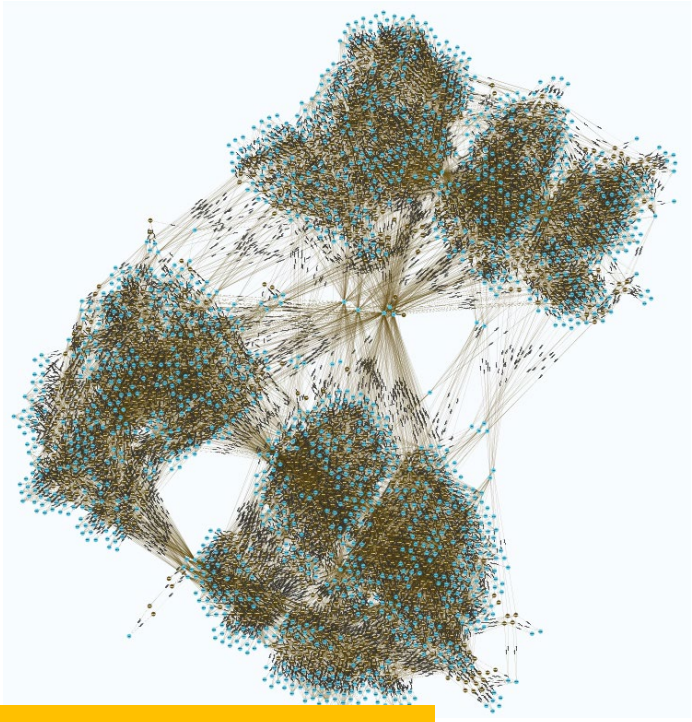
COR = 0.008
COI = 0.004

COI= 0.001

Graph Topology
Paths in Endogamy

- Paths are first-class citizens in a graph database
- GFG creates path nodes and relationship to them
- Path have intersections
- GFG creates intersect nodes and path-intersect relationships

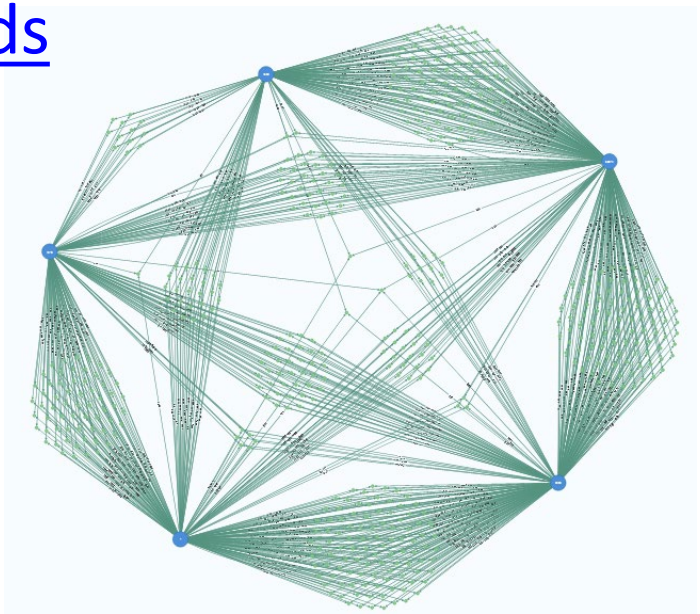




https://www.wai.md/blog/categories/endogamy

Getting Started

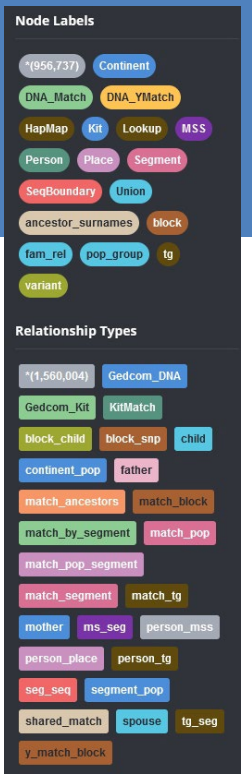
- Explore the GFG Blog
- Join the FB GFG Forum
- Wes Johnston's Guide to Getting Started with GFG
- Download GFG Software
- Install Neo4j Software
- Mentoring at Professor's Rounds



Neo4j

- “Native” Graph Database
- Industry leader
- Open Source
- Free versions
- PlugIn functions and procedures
  - From Neo4j:
    - APOC: awesome procedures on cypher
    - GDS: graph and machine learning algorithms
  - GFG capitalizes on these, adding ~200 functions

The GFG Neo4j PlugIn
~200 functions



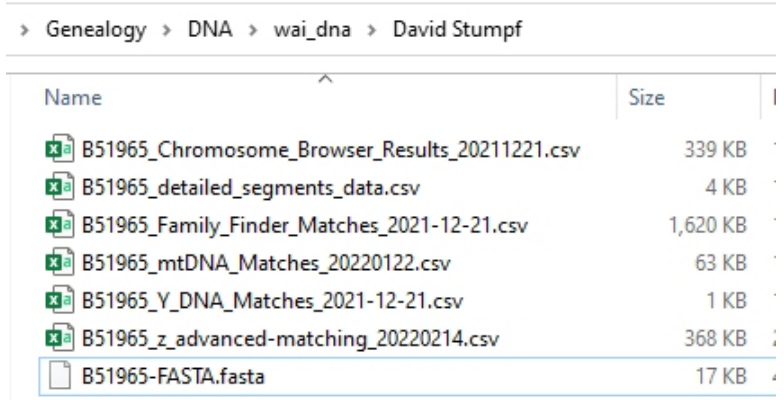
- Loads GEDCOM and FTDNA data files
- Uses curated files to link graphs
- Loads reference data
- Generates reports
- Uses Neo4j PlugIns
- Memorializes analytics => knowledge graph
- Optimized schema => perhaps a standard?
- Incremental learning for users

Curation by the Genealogist

Linking the family tree to the DNA

```
0 @I1@ INDI
1 NAME David Allen/Stumpf/
1 REFN 1
1 SEX M
1 BIRT
2 DATE 8 May 1945
2 PLAC Los Angeles, California
1 DEAT
2 DATE
1 FAMC @F308@
1 FAMS @F306@
1 FAMS @F307@
0 @I2@ INDI
1 NAME Herman Allen/
1 REFN 2
1 SEX M
1 BIRT
2 DATE 7 Dec 1916
2 PLAC Detroit, Mich
1 DEAT
2 DATE 27 Nov 1990
2 PLAC South Laguna,
1 FAMC @F309@
1 FAMS @F308@
```

```
340657 0 @F42@ FAM
340658 1 WIFE @I17145@
340659 0 @F43@ FAM
340660 1 WIFE @I17147@
340661 0 @F44@ FAM
340662 1 WIFE @I17148@
340663 0 @F45@ FAM
340664 1 WIFE @I17154@
340665 0 @F46@ FAM
340666 1 WIFE @I17304@
340667 1 CHIL @I17306@
340668 1 CHIL @I17307@
340669 0 @F47@ FAM
340670 1 WIFE @I17311@
340671 1 CHIL @I17313@
340672 1 CHIL @I21426@
```

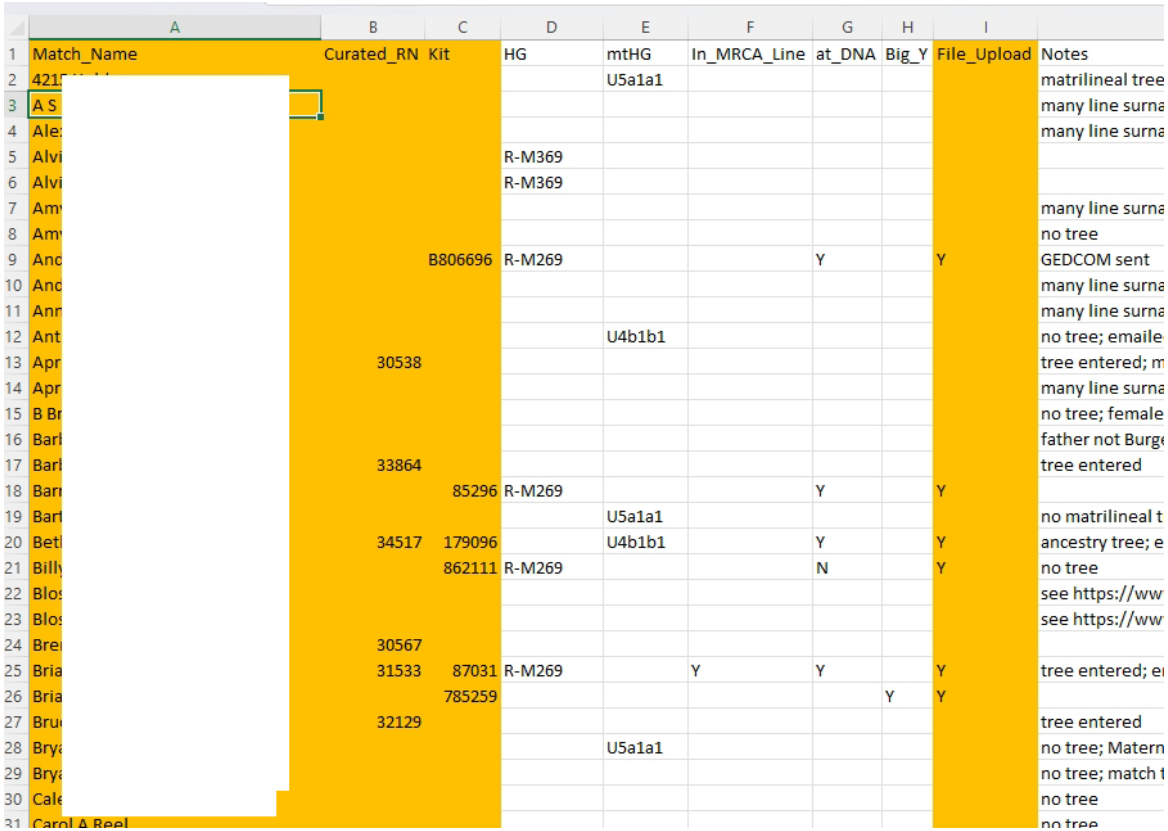


Curation File

GEDCOM-DNA curation file

linkages plus research nodes

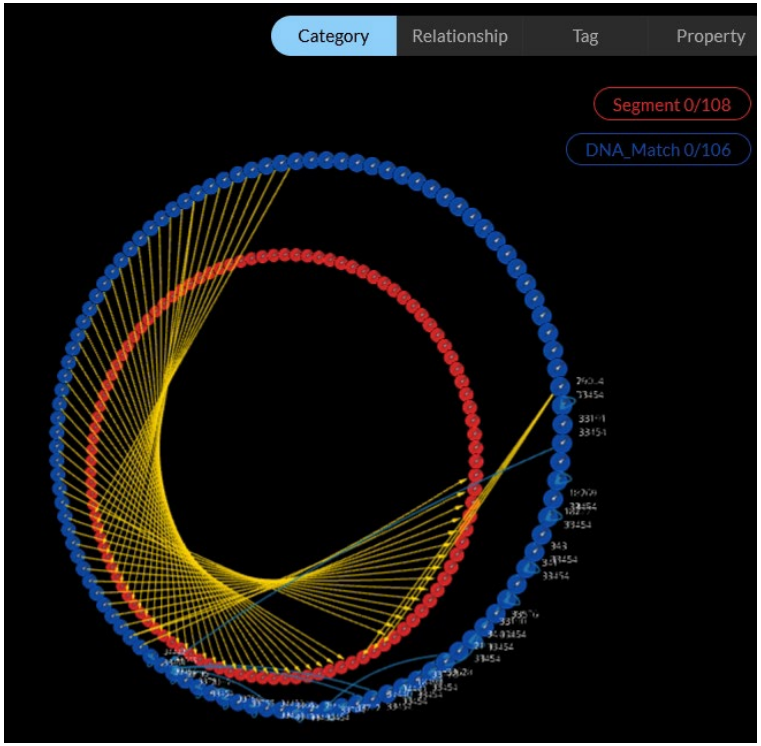
- Links your GEDCOM to the FTDNA kit
- Match name is from the file in which the person is a match
- Curated_RN is the GEDCOM number: 0 @I**5678**@ INDI



	A	B	C	D	E	F	G	H	I	
1	Match_Name	Curated_RN	Kit	HG	mtHG	In_MRCA_Line	at_DNA	Big_Y	File_Upload	Notes
2	421				U5a1a1					matrilineal tree
3	A S									many line surna
4	Ale									many line surna
5	Alvi			R-M369						
6	Alvi			R-M369						
7	Am									many line surna
8	Am									no tree
9	And		B806696	R-M269			Y		Y	GEDCOM sent
10	And									many line surna
11	Ann									many line surna
12	Ant				U4b1b1					no tree; emaile
13	Apr	30538								tree entered; m
14	Apr									many line surna
15	B Br									no tree; female
16	Barl									father not Burg
17	Barl	33864								tree entered
18	Barr		85296	R-M269			Y		Y	
19	Bart				U5a1a1					no matrilineal t
20	Bet	34517	179096		U4b1b1		Y		Y	ancestry tree; e
21	Billy		862111	R-M269			N		Y	no tree
22	Blos									see https://ww
23	Blos									see https://ww
24	Bre	30567								
25	Bria	31533	87031	R-M269		Y	Y		Y	tree entered; e
26	Bria		785259					Y	Y	
27	Bru	32129								tree entered
28	Brya				U5a1a1					no tree; Matern
29	Brya									no tree; match t
30	Cale									no tree
31	Carol A Beel									no tree

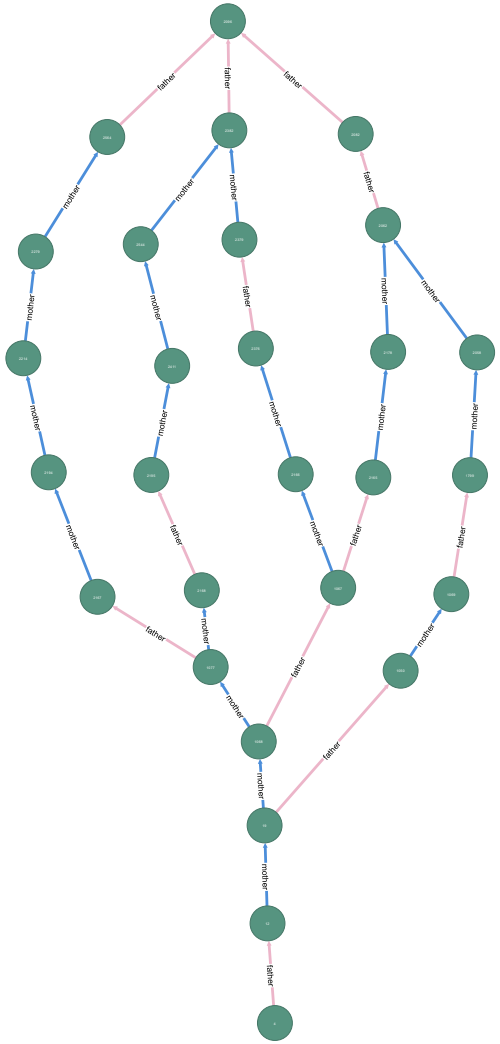
Example Project
My Avitts/Brown line

- Persons: 34,601
- Unions: 12,527
- Kits: 54
- DNA_Matches: 251,553
- Segments: 434,025
- Avatars: 41
- Family paths: 406



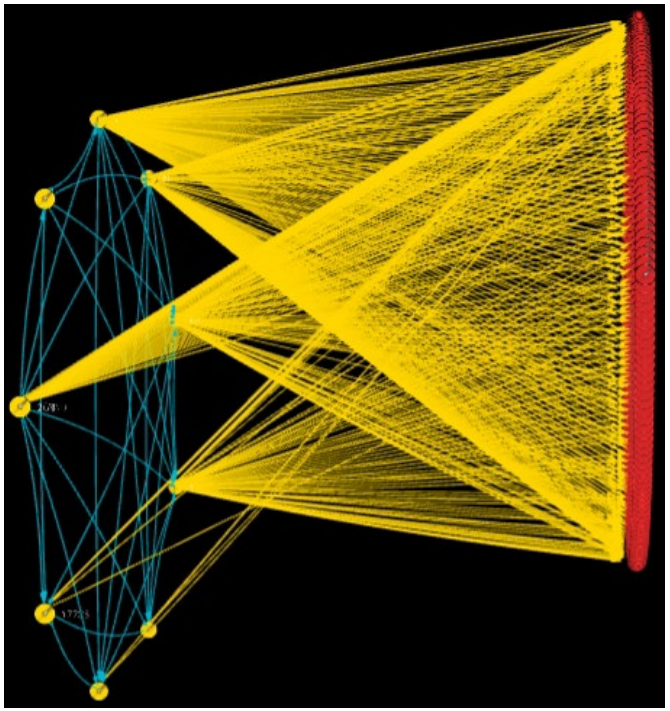
French-Canadian Project
… with Michelle Bray Wilson

- Persons: 2,822
- Unions: 1,369
- Kits: 12
- DNA Matches: 27,476
- Segments: 47.776
- Avatars: 0
- Family paths: 1,797
  with 2,337 intersections



Mennonite Project

- Persons: 1,503,531
- Unions: 482,742
- Kits: 1 (test sample)
- DNA Matches: 921
- Segments: 3403
- Family paths: 21,764,710

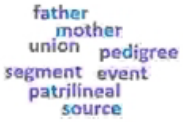


Workflow

Data Lakes

Family Tree

DNA



Ontology

Ingest

GFG ETL

APOC

Curated files

Reference Data

Knowledge Graph Components

GFG Plug-In

GraphXR

GDS Plug-In

Use Cases

Family Trees

Pedigree analytics

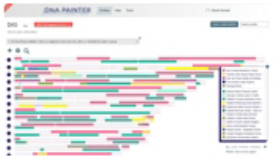
DNA Match Communities

Triangulations

FAN Groups

Actionable Insights

Visualizations



DNA Painter

GraphXR

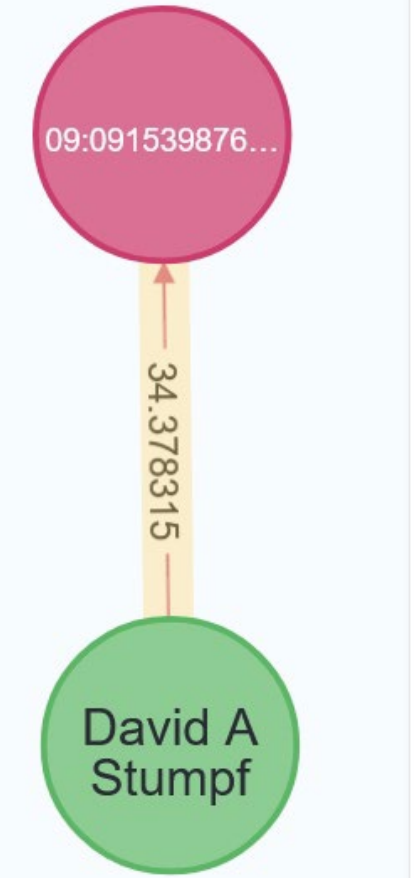
Knowledge Graph

- Turning facts into actionable insights
- Analytic results memorialized in the graph
- Iterative process: knowledge builds more
- One-time effort => any time benefit
- “Cost” is more storage space
- Benefit is faster, better queries

Advanced analytics require an optimized knowledge graph!

Key Knowledge

Provenance of data
Match-Pair names & RN
Their relationship
Their COR
Genetic distance
Parental side for both MRCAs
cM
SNP count



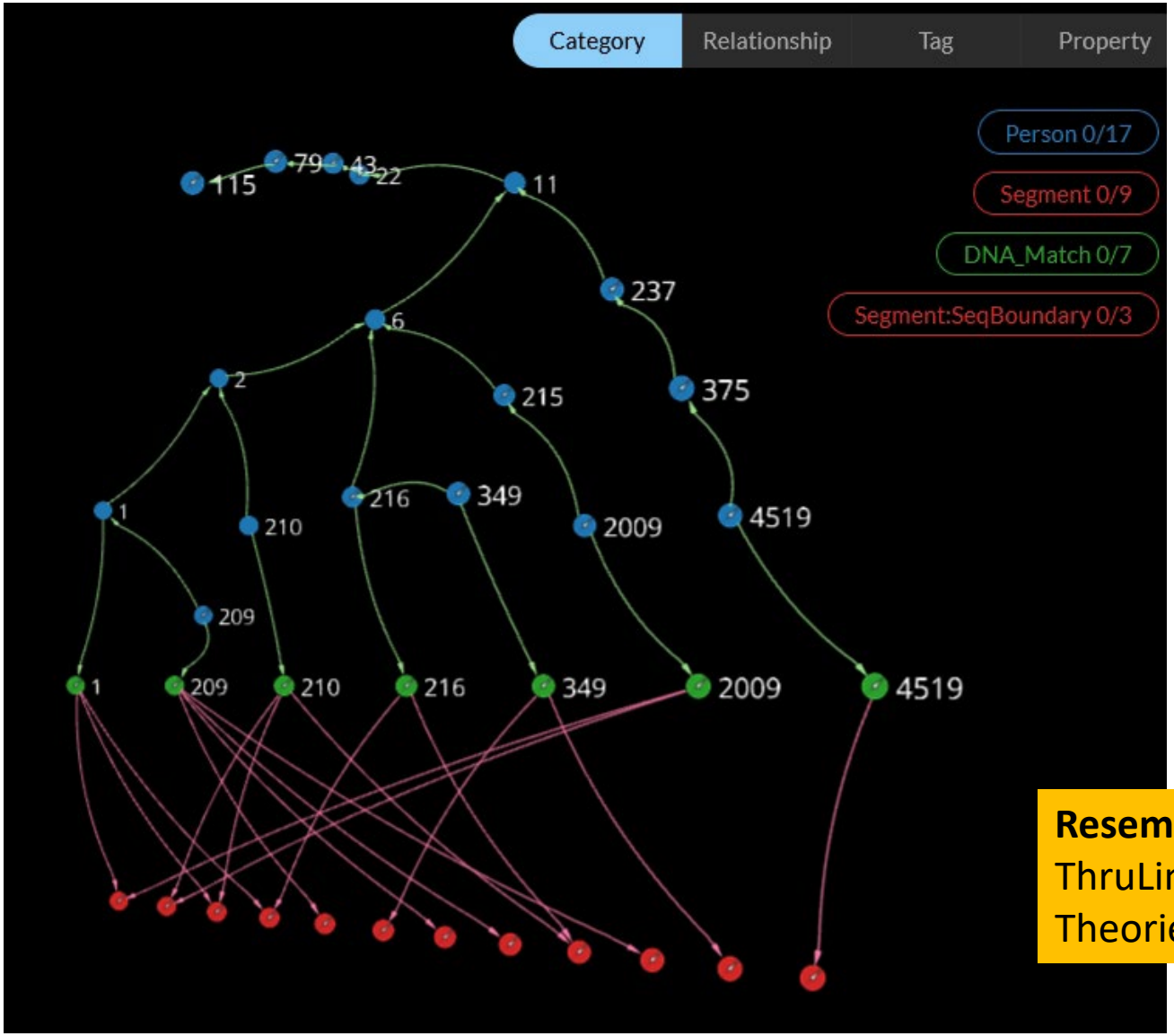
Relationship properties

match_segment

<id>	1162099
cb_version	new
cm	34.378315
cor	0.125
gen_dist	4
m	David A Stumpf
m_anc_rn	4441
m_rn	1
m_side	maternal
mrca_rn	7, 8
p	P D
p_anc_rn	4441
p_rn	343
p_side	paternal
pair_mrca	Aubrey Milton Davis [7] (1892-1976), Frances Emma Green [8] (1893-1972)
rel	1C
snp_ct	7465

at-haplotree

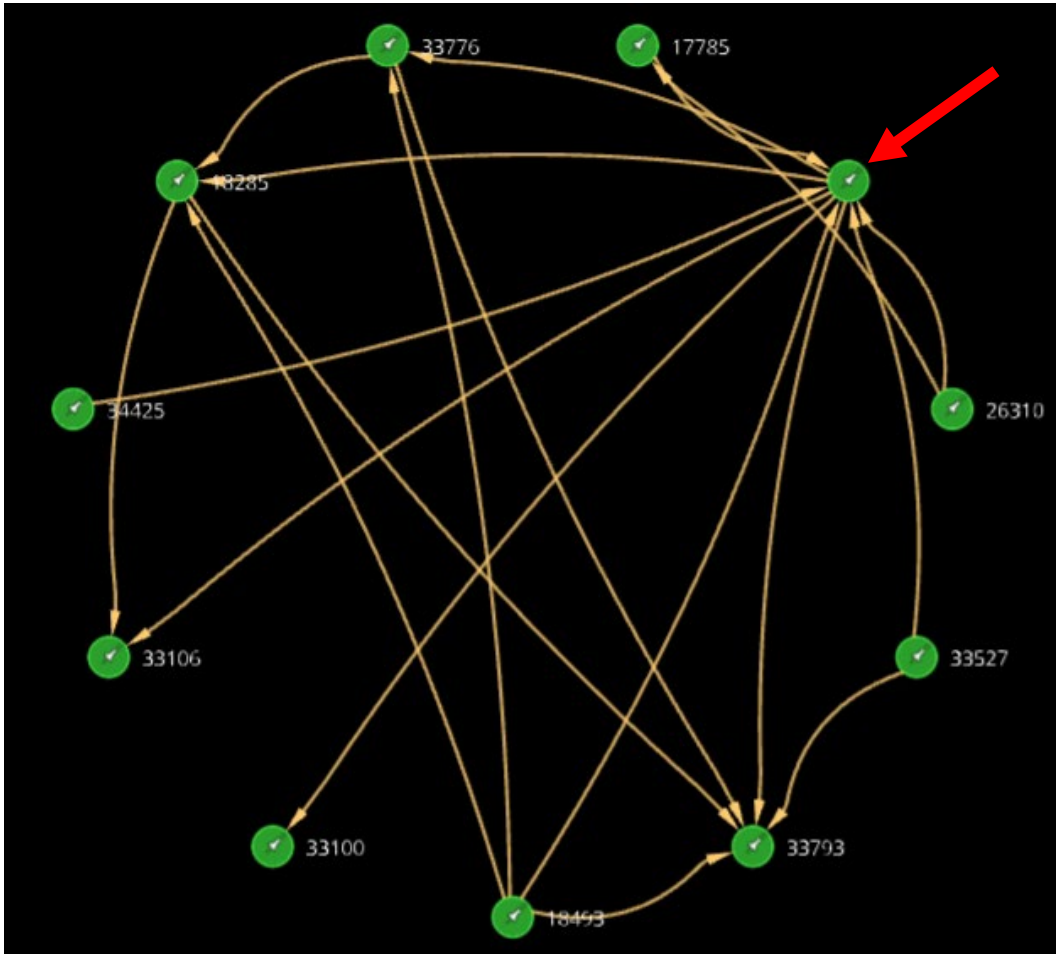
…family tree → matches → segments



Resembling
ThruLines®
Theories of Relationship®

Cluster match circle

… DNA_Match nodes linked by match_by_segment



All but one match has a record number.

The unknown match (red arrow) has many relationships, providing a motive for additional research.

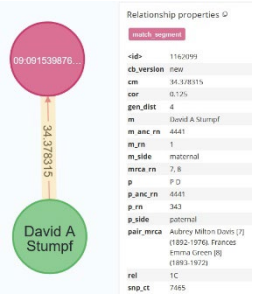
Field of Dreams: Avatars

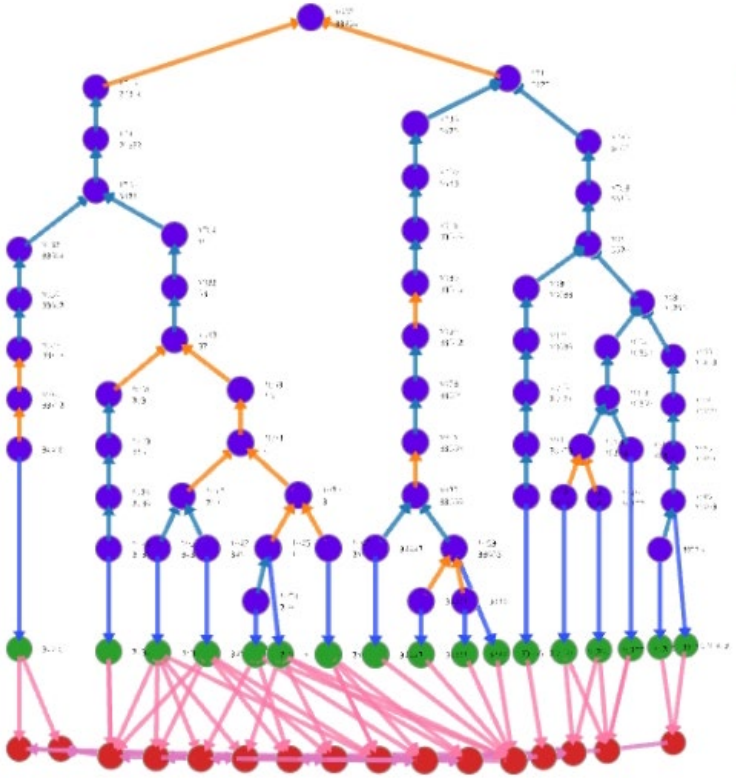
… *in silico* reconstruction of ancestors

- Your ancestor emerges from the corn field
- DNA available for your research
- Quick and easy in a graph database

https://www.wai.md/post/the-field-of-dreams-ancestor-avatars

Knowledge Graph
… enables amazing advanced analytics



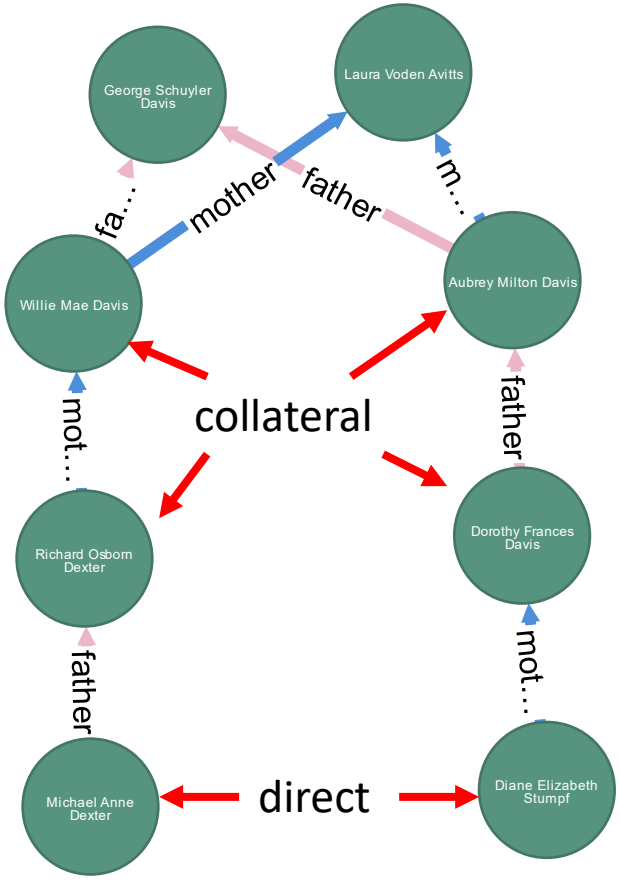


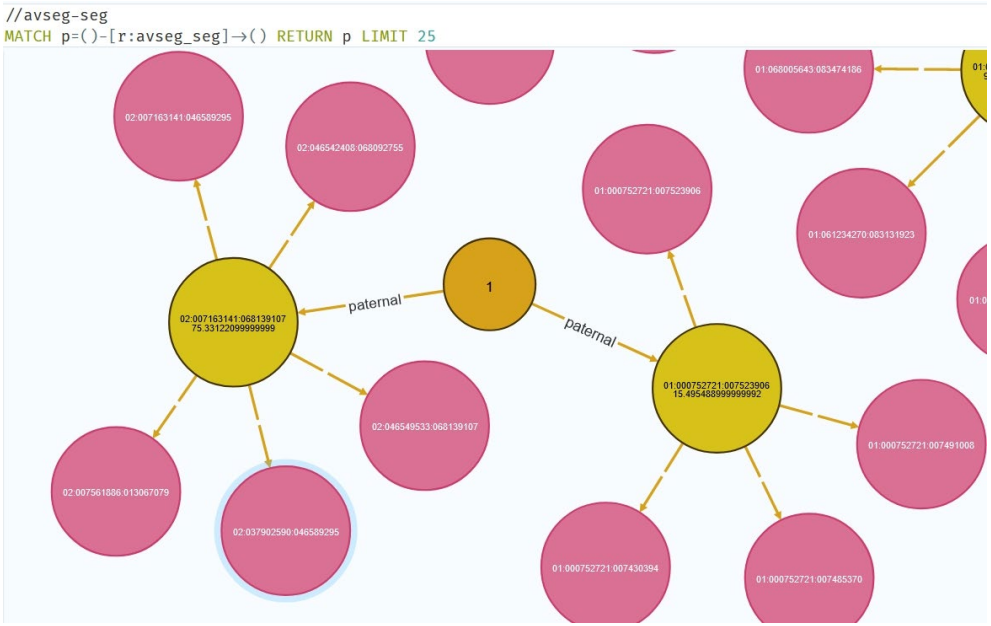
- match_segment relationships
  - GFG adds knowledge
    - parental origin of segment
    - Relationship between match-pair
    - MRCAs

Avatar creation is enabled by the knowledge.

Assigning segments with parental side

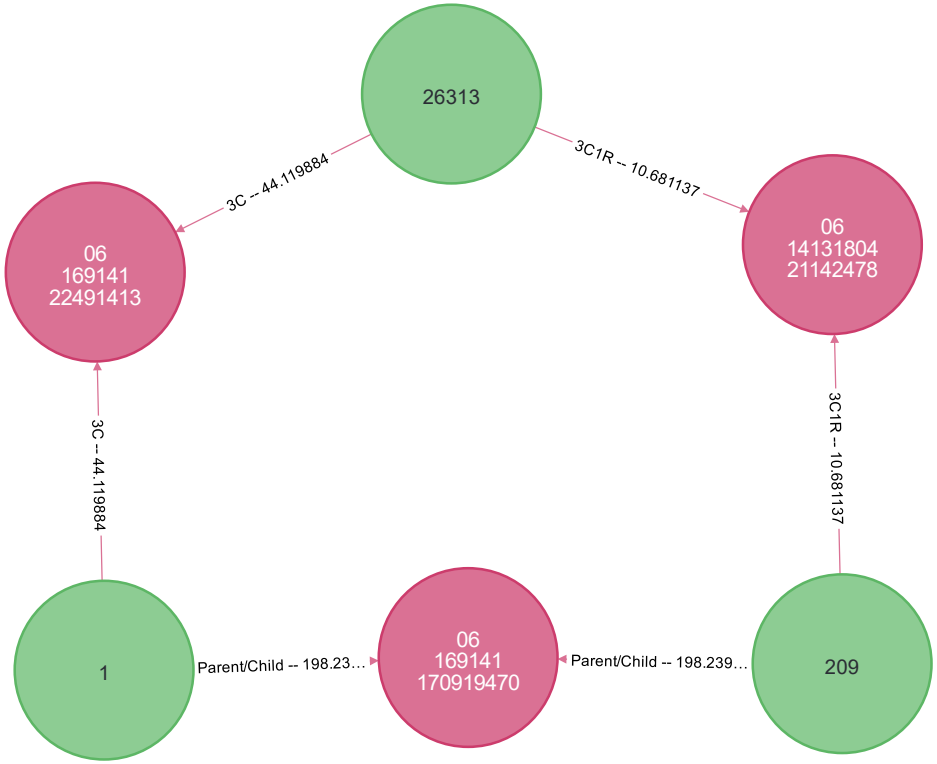
- match path=(p1:Person{RN:210})-[r1:father|mother*0..6]->(mrca:Person)<-[r2:father|mother*0..6]-(p2:Person{RN:582}) return path





Inferred Segments
Assigning a grandparent's segment

- Inferred segments when segments overlap



One query does it all!

Find base and close relation using cor ⩾0.25

Find compare relative who matches base and close cor ⩾ >0.00125

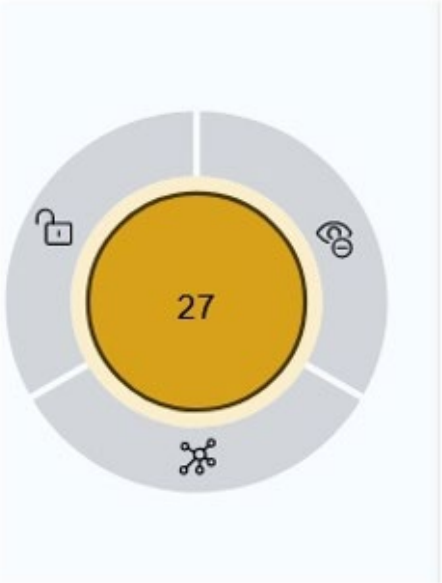
Identify segments shared with compare relative and compute flanking regions that are not shared.

Assign the flanking regions to the grandparent who is NOT in the shared family line.

https://familytreewebinars.com/webinar/inferred-mapping-explained/

Anderson Avitts (1843-1877)

- Details at blog post
  https://www.wai.md/post/the-field-of-dreams-ancestor-avatars



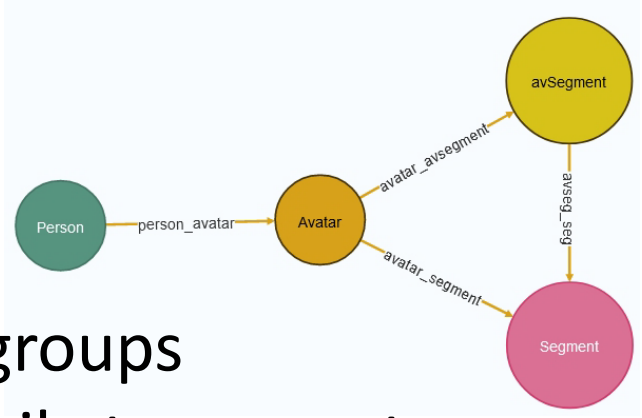
Node Properties

Avatar

<id>	1159404
RN	27
dna_coverage	0.0553478301388889
fullname	Anderson Avitts
maternal_cm	21.322249999999993
paternal_cm	377.18212700000004
total_cm	398.5043770000001

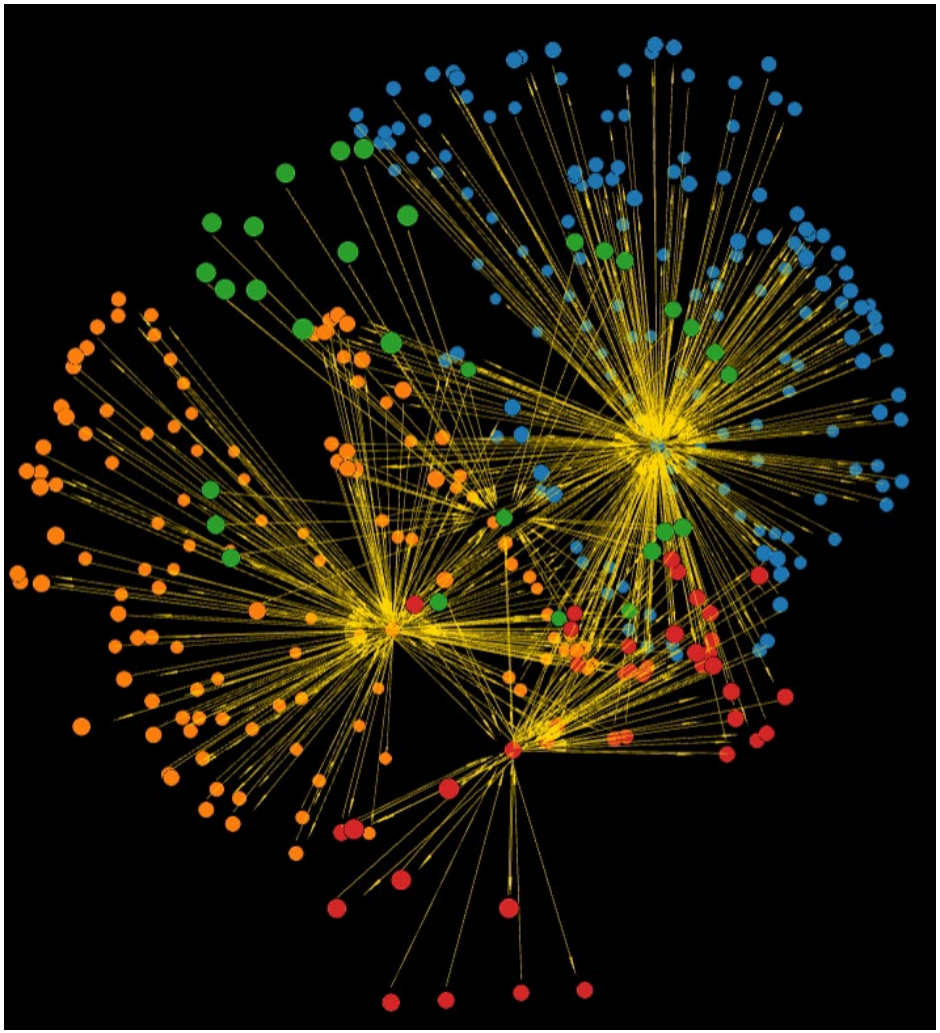
A. Avitts

The Field of Dreams
What your ancestor and relative avatars tll you



- Avatars have family trees
- Avatar match their descendants
- Avatars define crisp triangulation groups
- Avatars match a few not in the family tree … yet
- Avatars illuminate autosomal haplotrees
  - Avatar segments are linked to their source
  - Descendants know the ancestral origin of segments
  - Segment “checkerboard” enhances analytic specificity
- Relative avatars segments: help place new matches?
- Inferred segments help with tangential line research

Graph Algorithms



GFG uses Neo4j Graph Data Science Plug-In and its community detection algorithms

Louvain
Modularity optimization
Page Propagation

Community members align with family tree branches.

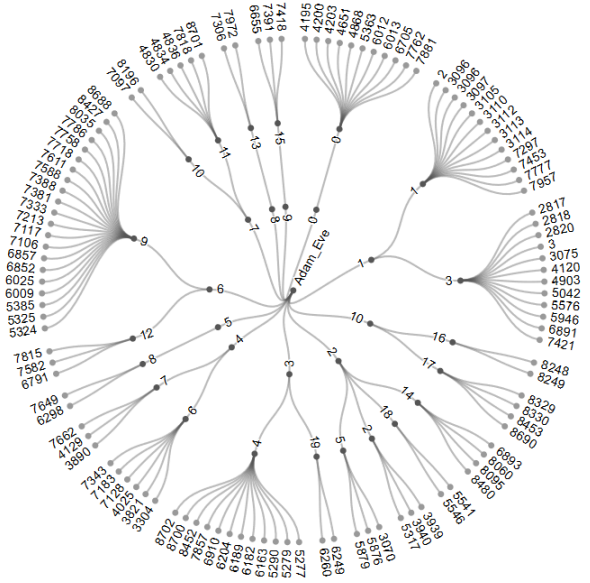
Community segments identified.

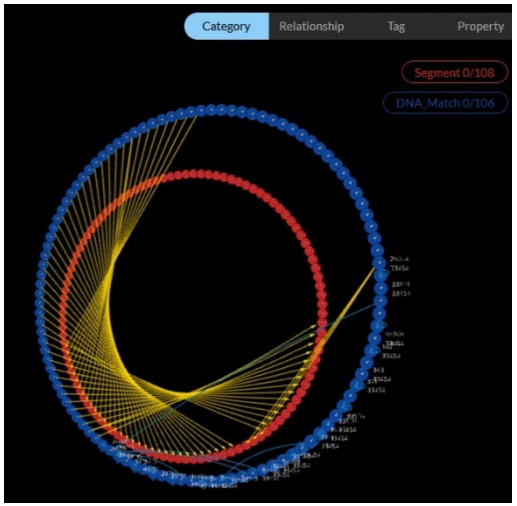
GFG queues up query for …
DNA Painter
GraphXR (3D renderings)

What's Next

Many Opportunities

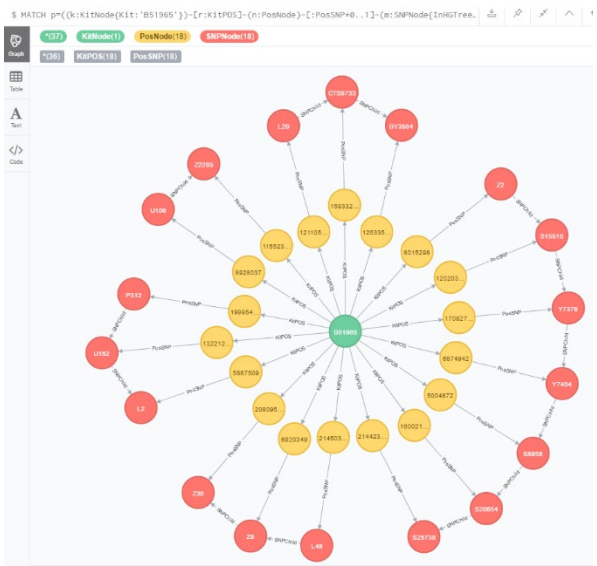
- Machine Learning
- Y-DNA analytics
- mt-DNA analytics
- FAN groups
- Spatial analytics
- Automated 3rd party interfaces
- 3-D renderings
- Virtual reality
- Forensic graphs
- Evidence graphs





Knowledge Graph Enhancements
… driven by user engagement

- Avatars on many family lines
- mt-haplotree enhancements
- Improved surname linkages
- FAN Groups capabilities
- Other vendor DNA results
-
-
-

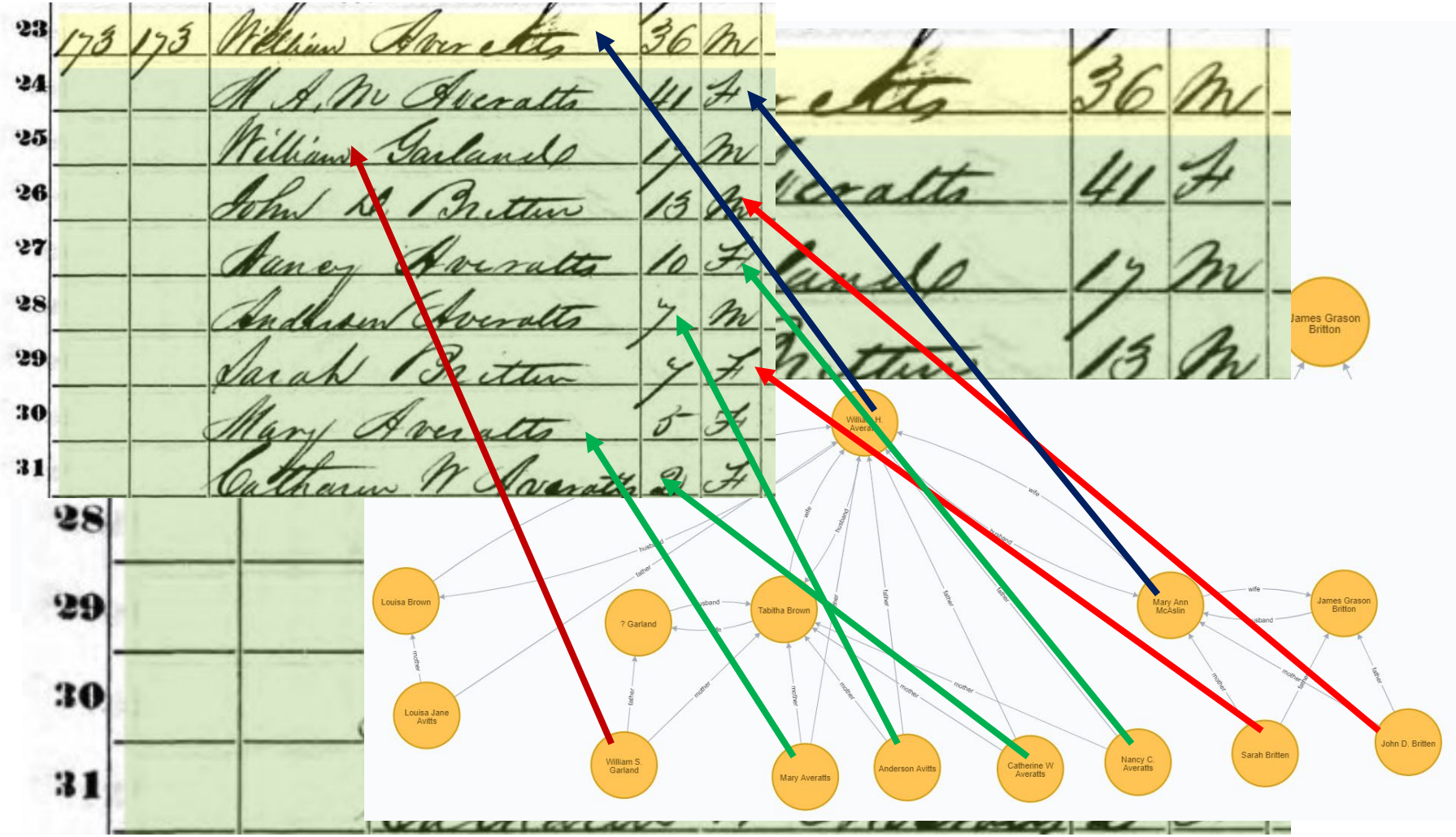


Ancestral surname reports
… 3 worksheets

- Matches with the surnames
  - Match
  - Source kit
  - Shared cm and segment count
- In-common-with matches
  - Match
  - Cluster of icw matches
  - MRCAs of the cluster of matches, if identifiable
- Shared segments
  - Matches at segments (usually a short list)

CALVERT,KENT
CALVERT,KENT,STINNETT
CALVERT,KENT,STINNETT
CALVERT,KENT
KENT,STINNETT

FAN Groups from 1850 Census

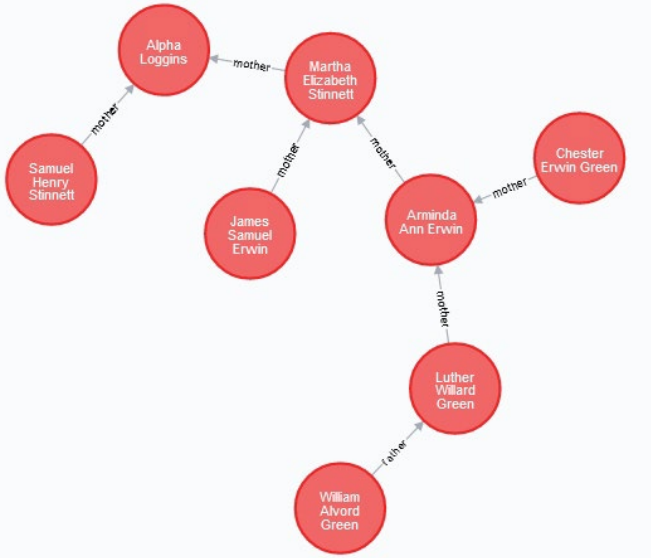


“Four generations of uncles”

Sabanno, Eastland Co., Texas about 1917

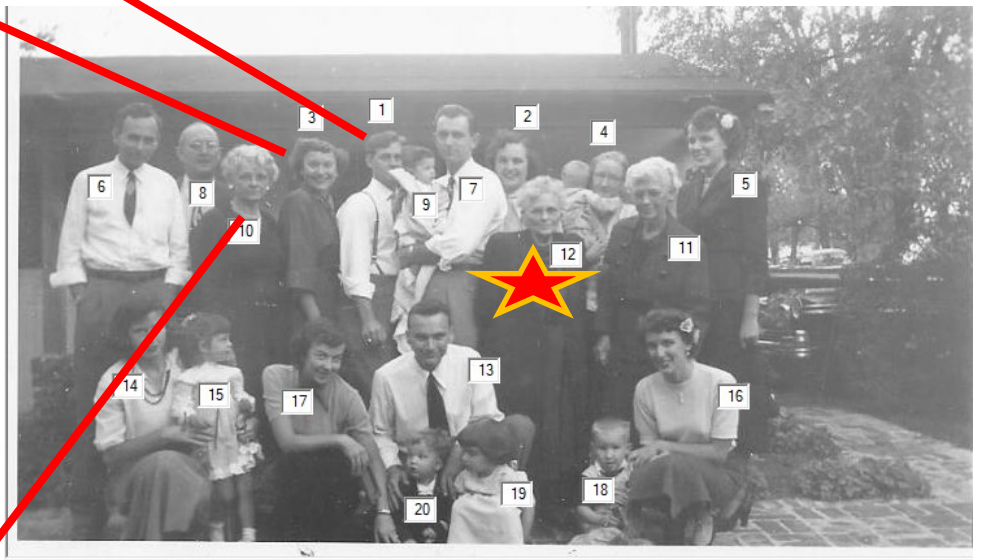
1. Stinnett, Samuel Henry [679] (1854-1928) M
2. Erwin, James Samuel [283] (1861-1949) M
3. Green, Chester Erwin [243] (1889-1949) M
4. Green, William Alvord [422] (1916-2008) M

Also, 1917 Stevens touring car?



FAN Group from Multiple Sources

- Smith, Joseph [26427] (1919-) M :Img -
  - father: Smith, William Franklin [22779] (1890-1956) M
  - wife: Davis, Willie Mae [240] (1889-1967) F
  - mother: Avitts, Laura Voden [14] (1868-1966) F
- Sorenson, Marie [26428] (1924-) F :Img -
  - husband: Smith, Joseph [26427] (1919-) M
  - father: Smith, William Franklin [22779] (1890-1956) M
  - wife: Davis, Willie Mae [240] (1889-1967) F
  - mother: Avitts, Laura Voden [14] (1868-1966) F
- Avitts, Anderson [27] (1843-1877) M :Cen - father
- Burklow, Carolyn Rebecca [28] (1844-1873) F :Cen - mother
- Avitts, William Henry [270] (1866-1944) M :Cen - brother
  - father: Avitts, Anderson [27] (1843-1877) M
  - daughter: Avitts, Laura Voden [14] (1868-1966) F
- Cain, Margaret Penecia [200] (1840-1907) F :Cen - 36
  - husband: Avitts, Anderson [27] (1843-1877) M
  - daughter: Avitts, Laura Voden [14] (1868-1966) F
- Avitts, Luther Smith [272] (1870-1888) M :Cen - brother
  - father: Avitts, Anderson [27] (1843-1877) M
  - daughter: Avitts, Laura Voden [14] (1868-1966) F
- Avitts, Arthur Anderson [432] (1875-1943) M :Cen - half brother
  - father: Avitts, Anderson [27] (1843-1877) M
  - daughter: Avitts, Laura Voden [14] (1868-1966) F
- Davis, Aubrey Milton [7] (1892-1976) M :Cen - son
- Davis, George Schuyler [13] (1869-1910) M :Cen - husband
- Davis, Willie Mae [240] (1889-1967) F :Cen - daughter
- Davis, Lessie Wenonah [242] (1890-1988) F :Cen - daughter
- Davis, Rosalie [244] (1896-1972) F :Cen - daughter
- Davis, Patsy Ola [245] (1899-1963) F :Cen - daughter
- Nybye, Julius Oscar [191] (1861-1942) M :Cen - husband

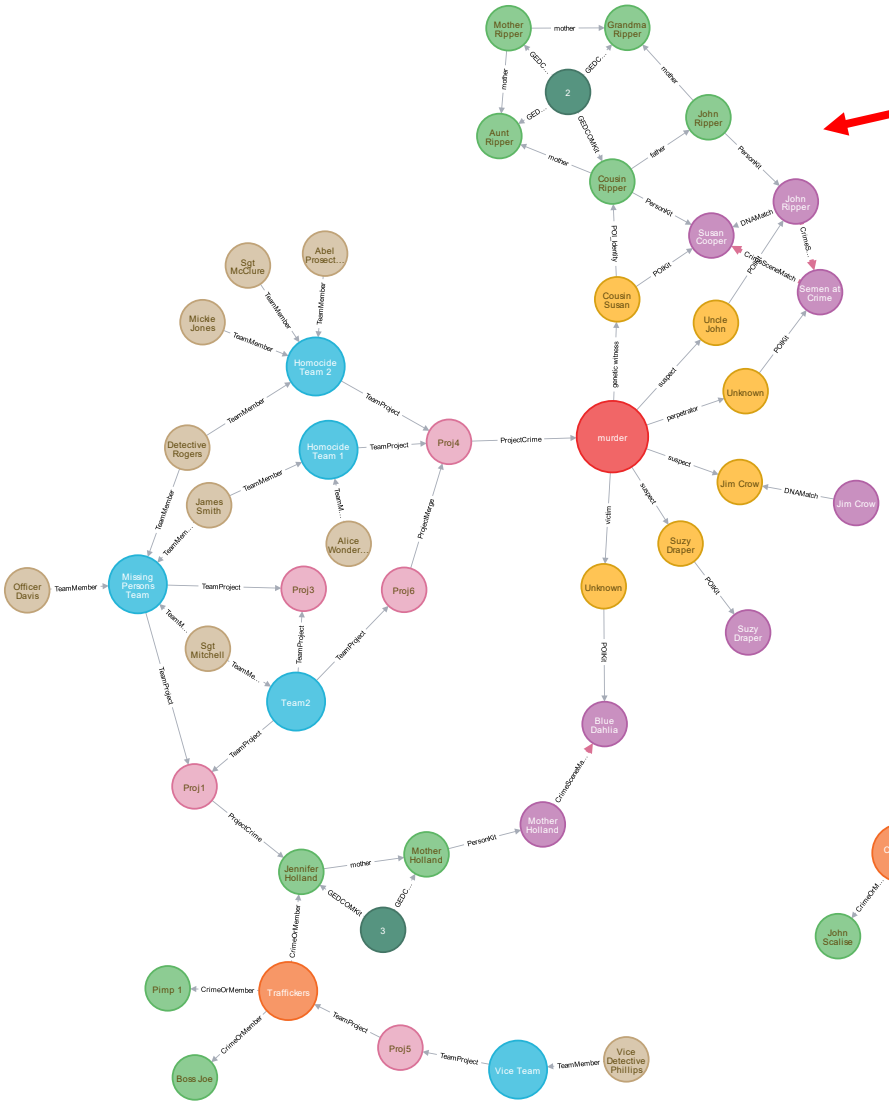


Capture and preserve the knowledge

Painted segments
… UDFs generate query for DNA Painter

Forensic Genealogy

… violent crimes, missing persons, abandoned bodies, etc.



Current GFG schema

Forensic enhancements

LE social networks

LE Cases

Crime site evidence

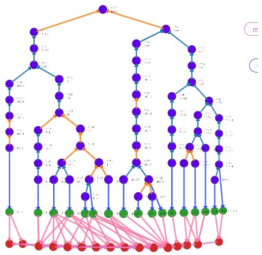
Suspects

Forensic repositories

An opportunity for forensic genetic genealogists!

Let's discuss: https://wai.md/gfg

A Good Place to End

David A Stumpf, MD, PhD
dave@wai.md
https://wai.md/gfg
https://facebook.com/groups/gfgforum

GRAPHS FOR GENEALOGISTS