

Forensic Investigative Genetic Genealogy (FIGG):

Practical Guidance for Implementation & Workflow

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Presentation Outline

1. Current Policies/Laws/Guidance
2. FIGG Workflow
3. Best Practices Recommendations
4. The Future of FIGG
5. University of New Haven FIGG Program

1. Current Policies / Laws / Guidance

Policy & Guidance

2019



THE UNITED STATES
DEPARTMENT of JUSTICE

UNITED STATES DEPARTMENT OF JUSTICE
INTERIM POLICY
FORENSIC GENETIC GENEALOGICAL DNA ANALYSIS AND SEARCHING

I. Purpose and Scope¹

2020

Approved by the Scientific Working Group on DNA Analysis Methods --February 18, 2020



Overview of
Investigative Genetic Genealogy

- ✓ Violent Crimes; homicide and sexual assault, unidentified remains of homicide victims, and criminal acts that present a substantial and ongoing threat to public safety and national security
- ✓ Requires STR typing and CODIS upload first – no hits
- ✓ Requires Familial DNA Searching (if allowed within the jurisdiction)
- ✓ Only databases that provide explicit notice to users that LE use their sites
- ✓ No arrests on FIGG results alone
- ✓ Requires STR profile confirmation

Individual State Laws

Oct 2021

The Washington Post
Democracy Dies in Darkness

ons Voices Across America Post Opinión D.C., Md. & Va. Cartoons

LOCAL OPINIONS

Opinion | Maryland can be a model for regulating law enforcement use of genetic databases

By Sonia M. Suter, Erin E. Murphy and Natalie Ram

June 18, 2021 at 2:00 p.m. EDT



- ✓ Effective October 1, 2021
- ✓ Requires judicial authorization to initiate FIGG
- ✓ Violent crimes only (Homicide and Sexual Assault) and unidentified human remains of a homicide victim
- ✓ Only databases with strict policies around user consent
- ✓ Establishes procedures & authorizations for obtaining additional DNA (e.g., non-suspect third-party reference testers and suspect reference collection)
- ✓ Provides defense access to FIGG
- ✓ Requires reporting and review of all FIGG cases
- ✓ Requires sequencing labs and FIGG practitioners be “licensed”

Individual State Laws

March 2023

Radio Video Obituaries Weather 80° MARKETPLACE Classifieds Cars

Legislature passes 'Sherry Black bill' to regulate genealogy search by law enforcement

By Bridger Beal-Cvetko, KSL.com | Posted - March 1, 2023 at 5:03 p.m.

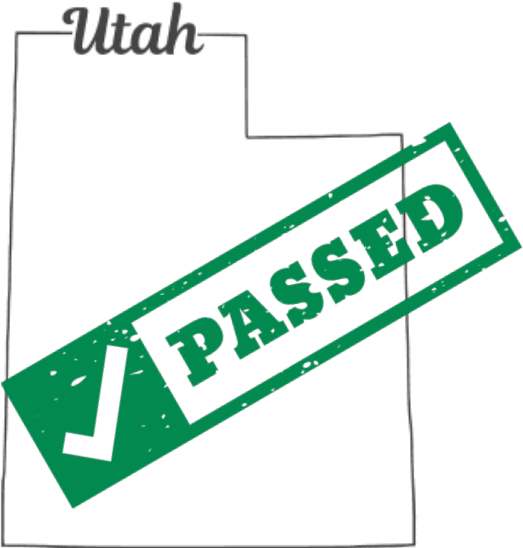


The sun shines through columns at the Utah Capitol in Salt Lake City on Jan. 31. The Utah Legislature passed a law that would allow genetic test users to optionally provide their information for law enforcement investigations of violent crimes. (Jeffrey D. Allred, Deseret News)

Staples Buy HP® C
Staples

hp instant Ink
Enrollment Kit
The hassle-free, money-saving Ink subscription service
\$9.99 MSRP
for 3 Months of Printing.*
Offer is for purchase of the enrollment kit. Cartridges provided as part of instant ink subscription service.

HP 910 Black & C
Ink Cartridges wi



National Technology Validation and Implementation Collaborative

Established in 2022

- 22 Federal, State, and large Local Crime Lab Directors
- Private Forensic Science Service Providers
- Forensic Academics and Researchers

**SCAN
ME!**



Forensic Investigative Genetic Genealogy (FIGG) Working Group



Subcommittees

#1

Public Entity
FIGG Policy and
Procedure

#2

Public Laboratory
FIGG Technical
Validation

#3

FIGG Education
& Training for
Public Entities

#4

FIGG Contracts
between Public
& Private Entities



ELSEVIER

Contents lists available at [ScienceDirect](https://www.sciencedirect.com)

Forensic Science International: Synergy

journal homepage: www.sciencedirect.com/journal/forensic-science-international-synergy



Establishment of the National Technology Validation and Implementation Collaborative (NTVIC) and Forensic Investigative Genetic Genealogy Technology Validation Working Group (FIGG-TVWG)



ELSEVIER

Contents lists available at [ScienceDirect](https://www.sciencedirect.com)

Forensic Science International: Synergy

journal homepage: www.sciencedirect.com/journal/forensic-science-international-synergy



National Technology Validation and Implementation Collaborative (NTVIC) policies and procedures for Forensic Investigative Genetic Genealogy (FIGG)



Guidance from Genetic Genealogy Databases:



Both require users/general members to **opt-in** or **opt out** for law enforcement matching



FIGG: 2018 – 2023

Building the plane while flying it



Forensic Science International: Genetics 58 (2022) 102679



Contents lists available at [ScienceDirect](#)

Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsigen



Research paper

Forensic genetic genealogy: A profile of cases solved

Tracey Leigh Dowdeswell

Douglas College, Criminology, Department of Humanities & Social Sciences, 700 Royal Avenue, New Westminster, BC V3M 5Z5 Canada



As of 31 Dec 2022:
545 cases

2. The FIGG Workflow

Case
Assessment

SNP
Sequencing

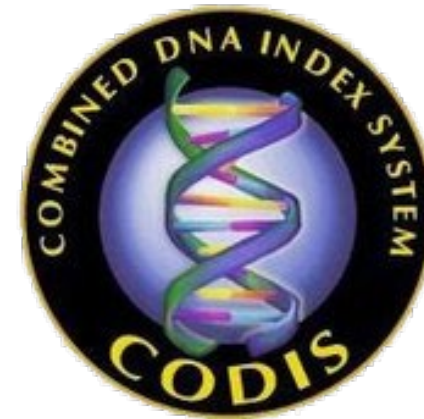
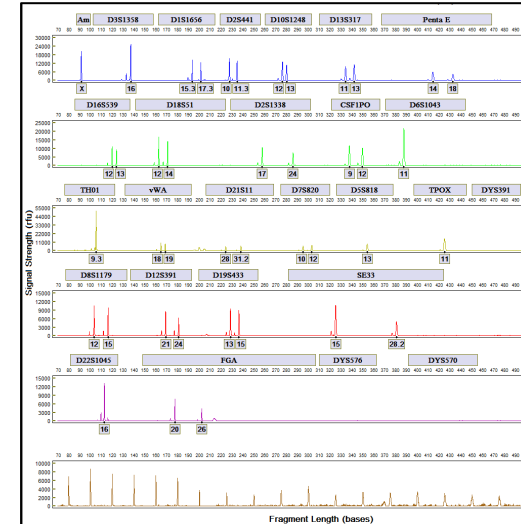
Genetic
Genealogy

Tree
Building

Review/
Report

Case Eligibility:

- ✓ Violent Crimes (Homicide/Sexual Assault)
- ✓ Unidentified Human Remains
- ✓ STR Profile Generated
- ✓ Uploaded to CODIS – No Hits
- ✓ Familial Search (if allowed)



Case
Assessment

SNP
Sequencing

Genetic
Genealogy

Tree
Building

Review/
Report

Sample Assessment:

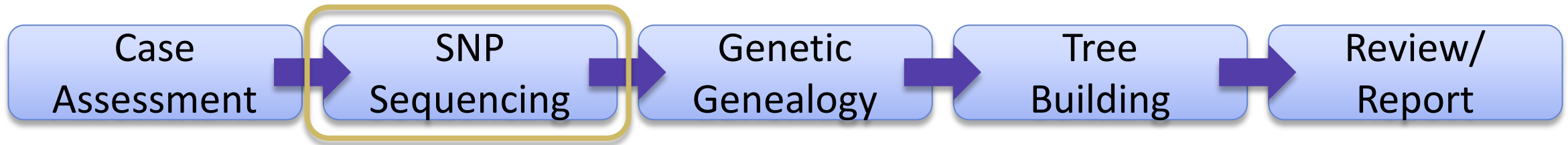
✓ Retained DNA Extract

Or

✓ Return to original evidence item to re-extract

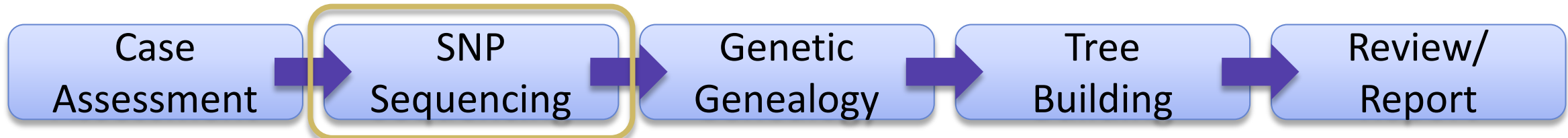
- ✓ What is the DNA quantity & quality?
- ✓ When was the extract last quantitated?
- ✓ Does the extract need to be rehydrated?
- ✓ What is the volume of extract remaining?
- ✓ Where is the DNA extract/evidence item?
- ✓ Authorizations for whole sample consumption





Choose SNP Technology:

- ✓ DNA Quality & Quantity will inform
- ✓ In-house versus outsourcing to vendor lab
- ✓ Funding & State Contracts



SNP Microarray

~600,000 SNPs

<200ng

Cheapest

Not good with Degraded DNA

Whole Genome Sequencing

>1 million SNPs

>50pg

Most Expensive

Recommended for Degraded DNA

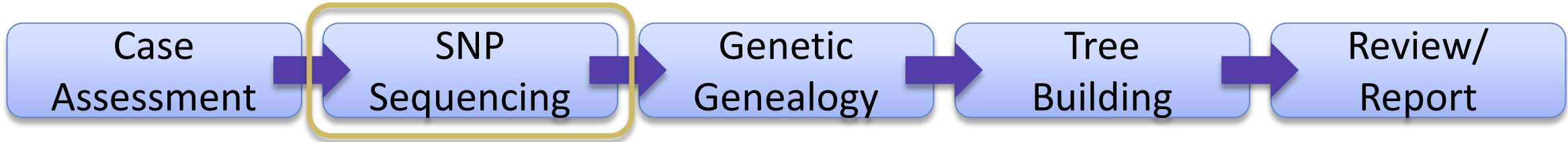
Targeted Kit: Kintelligence®

~10,230 SNPs

>50pg

Mid-Range

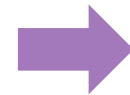
Future in-house (Crime Lab) Capability



raw DNA data

rsID	chromosome	position	allele 1	allele 2
rs4477212	1	72017	A	A
rs3094315	1	742429	G	A
rs3131972	1	742584	G	G
rs12124819	1	766409	G	G
rs12564807	1	734462	A	A

Upload to genetic genealogy databases allowed to be used for law enforcement investigations



Case
Assessment

SNP
Sequencing

Genetic
Genealogy

Tree
Building

Review/
Report

GENE
BY
GENE



INVESTIGATIVE GENETIC GENEALOGY SERVICES & RATES FOR THIRD PARTY AGENCIES

1445 N Loop W, Suite 760
Houston, TX 77008
www.genebygene.com/forensics

All pricing includes raw data SNP profile, FTDNA account creation, and upload to the FTDNA database for matching.

Service	Description	Rate
Forensic Array: single source	The forensic microarray is run using a customized version of the Illumina Global Screening Array (GSA) to generate a single nucleotide polymorphism (SNP) profile for use in Investigative Genetic Genealogy (IGG). Once a data file is generated, the contents are suitable for uploading into databases such as FamilyTreeDNA (FTDNA) and GEDmatch for IGG and familial matching. The forensic microarray can be used with DNA extracted from sample sources such as blood, saliva, semen and tissue (non-FFPE).	\$800 for third party agencies
Forensic Array: mixed source Two source mixtures only	It may be possible to run a forensic array on a mixed source DNA sample if a reference sample can be provided. Using both, it may be possible to reconstruct a SNP profile from the second DNA source. Mixed source samples are evaluated on a case by case basis to determine the chance of success, which depends on factors such as the % of each DNA in the mixture and the amount of DNA available.	Starts at \$1800 Depends on sample quality
Forensic Array File Reformat	Raw data files not generated by Gene By Gene or created by methods other than microarrays can be reviewed, reanalyzed, and reformatted so that they are compatible with the FamilyTreeDNA database. Includes raw data SNP profile, FTDNA account creation, and upload to the FTDNA database for matching.	\$700 for third party agencies
Whole Genome Sequencing	Samples that are not candidates for the forensic array due to low quantities or poor quality may be analyzed using whole genome sequencing. Gene By Gene will process the sample and provide a SNP profile that is compatible with results from all genetic genealogy companies.	\$2000
Y-111 DNA Testing	The Y-111 DNA tests for 111 STRs (Short Tandem Repeats) markers and looks for matching markers or "STRs" between two men. If they match, this indicates a genetic relationship. This allows for investigation into the male's paternal line by helping to identify potential surnames, Y-DNA relatives, and a Y-DNA haplogroup.	\$350
Reference Testing	Target testing is used to test potential family members of individuals identified using the Forensic Array to confirm relationships. Informed consent from tester is required.	\$169



Forensic Requisition Form for Sample Submission

Public Information Officer Contact Information (for Law enforcement only)

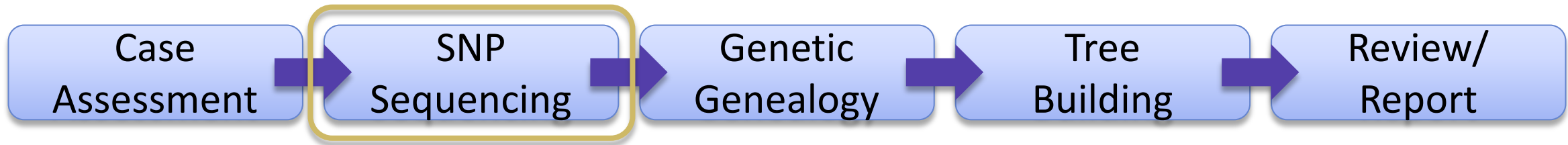
Title	
First Name	
Last Name	
Agency/Organization	
Email	
Phone Number	

Billing Information

Agency/Organization	
First Name	
Last Name	
Email	
Phone Number	
Address	
Address	
Additional Contacts?	
Notes	
Notes	

For Lab Use

File Received Date	
Jira Ticket	
GXG/FTDNA Kit#	
GXG/FTDNA GRC#	
Order/Invoice #	
Payment Date	



- ✓ Kit has been uploaded by LE/Forensic Lab.
- ✓ Kit has completed all processing.

ANNOUNCEMENT

Upload Credit Price Change

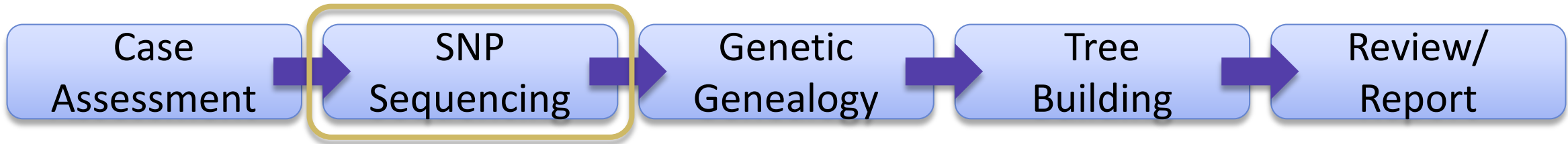
Please note that as of December 1, 2022, the price has increased for upload credits.

The new price is now \$700 per upload credit.

[Okay, got it!](#)

[View Legend](#) (Status indicators shown to the right of each kit below)

- ✓ Kit has completed all processing
- ⚠ Possible problem with kit - please contact customer support
- 📄 Duplicate - need to be deleted
- 🕒 Kit is processing
- 👤 Kit is pending owner transfer
- ❓ Unknown status



GEDmatch PRO™ | Genealogist | Hi Claire

PRO TOOLS ▾ | YOUR KITS | YOUR PROJECTS

Dashboard > Your Projects

GEDmatch PRO™ projects allow you to manage kit access and the users involved in each case. You can easily see with whom you have shared your kits and which users are participating in which cases.

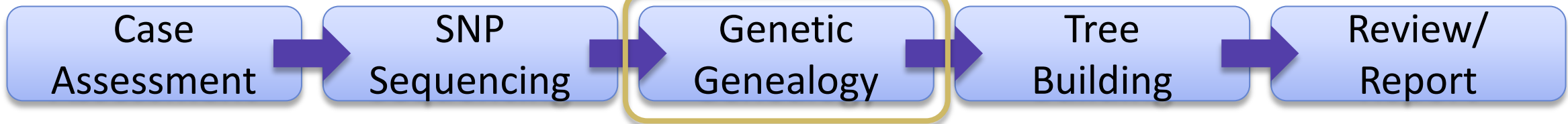
Your Projects

Search

Project title	Your status	Project Owner	Contributors
Case #1	✓ Active	LE/Forensic Person	4 people
Case #2	✓ Active	LE/Forensic Person	3 people
Case #3	✓ Active	LE/Forensic Person	5 people
Case #4	✓ Active	LE/Forensic Person	4 people
Case #5	✓ Active	LE/Forensic Person	5 people
Case #6	✓ Active	LE/Forensic Person	3 people

Only people added to the “Project” can access the kit.

Other GEDmatch users cannot access the LE Kit nor will the LE kit show up as a “match” to any user.

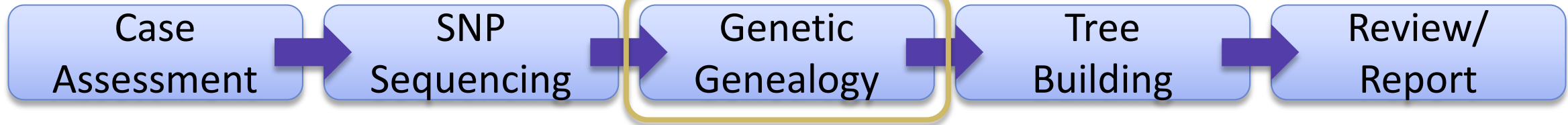


Free Tools ▾ GEDmatch Forums Tier 1 tools ▾ Family Trees ▾ Genealogy ▾

<ul style="list-style-type: none"> One-To-Many - Limited Version One-To-Many - Original Version Relationship Probability One-To-One Autosomal One-To-One X Admixture (heritage) Admixture / Oracle Match Both or 1 of 2 DNA File Diagnostics Are Your Parents Related? 3D Chromosome Browser Archaic DNA Matches Ancestor Projects 	<ul style="list-style-type: none"> One-To-Many - Full Version One-To-Many - Classic Version Q Matching One-To-One Segment Search Phasing Triangulation AutoSegment AutoKinship Multiple Kit Analysis (MKA) Lazarus My Evil Twin Combine multiple kits into 1 superkit AutoTree Clustering MRCA From DNA Matches Surname Matches From DNA Matches
---	---

All Pro Tools

- A**
 - Admixture (Eurogenes/K13)
 - Are Your Parents Related?
- K**
 - Kit Evaluation
- M**
 - Multiple Kit Analysis
- O**
 - One-to-Many Kinship
 - One-to-Many Segment-Based
 - One-to-One Autosomal DNA Comparison
 - One-to-One Kinship DNA Comparison
 - One-to-One Q Matching
- S**
 - Segment Search
- T**
 - Triangulation
- U**
 - User Lookup



Biogeographic Ancestry:

- Admixture Tool
- myOrigins

GEDmatch Home Upload DNA Free Tools GEDmatch Forums Tier 1 tools Family Trees Genealogy

Kit number: [blurred] Elapsed time: 10.51 seconds.

No Oracle Spreadsheet available for this calculator.

Population	Percentage
North_Atlantic	52.84 Pct
Baltic	23.52 Pct
West_Med	13.56 Pct
West_Asian	5.37 Pct
East_Med	2.33 Pct
Red_Sea	0.48 Pct
South_Asian	0.32 Pct
East_Asian	0.45 Pct
Siberian	0.98 Pct
Amerindian	0.15 Pct
Oceanian	-
Northeast_African	-
Sub-Saharan	-

Oracle
Oracle-4

myOrigins® Version 3

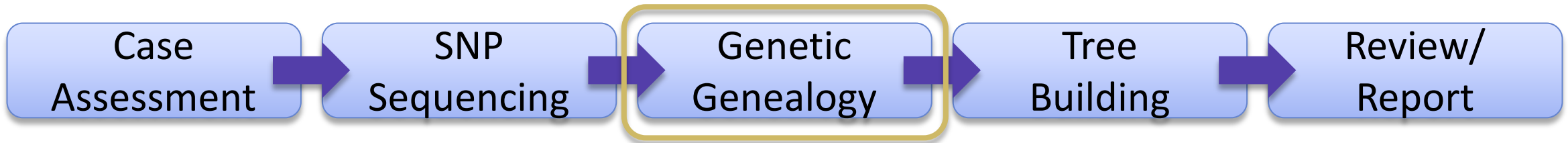
Uncover the unique genetic assemblage that has been passed down to you from your ancestors, and see to which of our 90 reference populations from ... [Read more](#)

myOrigins® Compare Origins

Claire Glynn

Europe	100%
Western Europe	
• Ireland	98%
Eastern Europe	
• East Slavic	<2%





GEDmatch - Are your parents related?

Software Version Nov *Kit #/Names redacted
Evaluating Kit [redacted] for related parents.

Minimum segment threshold size is set dynamically
Minimum threshold size to be included in total = 200 SNPs
Minimum segment cM to be included in total = 7.0 cM
[Here](#) is a link to a useful YouTube video on using the Are Your Parents Related tool.

Largest segment = 0 cM
Total of segments > 7 cM = 0 cM

No shared DNA segments found

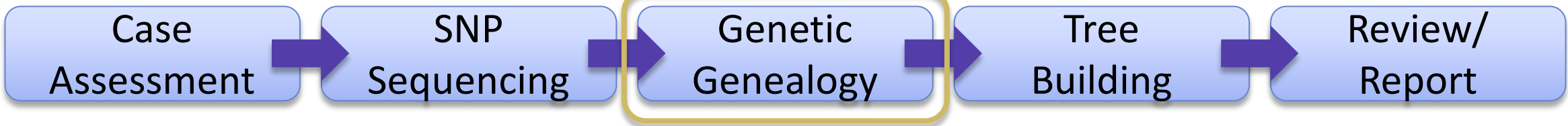
This analysis indicates that your parents are probably not related within recent generations.

Kitty Cooper has a blog article on this program: [When the DNA says your parents are related](#)

Comparison took 0.0126 seconds.

Assess Endogamy:

- Are Your Parents Related Tool



matches 1:500 for *unhGGaj, cglynn@newhaven.e

Assess DNA Matches:

VISUALIZATION OPTIONS

Select	Match No.	Kit	Name (* => alias)	Email	GED WikiTree	Age(days)	Type	Sex	Mt	Y	Total cM	Largest	Gen	Total cM	Largest	Source	Overlap
<input type="checkbox"/>	1					2118	?	M			226.5	28.8 Q	2.99	0	0	Migration - F2 - A	188777
<input type="checkbox"/>	2										188.7	26.6 Q	3.12	0	0	Ancestry	215186
<input type="checkbox"/>	3										151.7	30 Q	3.28	0	0	Ancestry	196920
<input type="checkbox"/>	4										129.5	33.5 Q	3.40	0	0	Ancestry	243685
<input type="checkbox"/>	5										112.6	40.4 Q	3.50	0	0	-	204449
<input type="checkbox"/>	6										112.4	40.4 Q	3.50	0	0	Ancestry	245500
<input type="checkbox"/>	7										99.4	39 Q	3.59	0	0	Migration - F2 - A	186680
<input type="checkbox"/>	8										62.8	26.1 Q	3.92	0	0	Migration - F2 - T	192441
<input type="checkbox"/>	9										52.1	29.6 Q	4.05	0	0	Migration - F2 - A	187712
<input type="checkbox"/>	10										52	29.2 Q	4.05	0	0	Migration - F2 - A	187038
<input type="checkbox"/>	11										51.7	29.2 Q	4.06	0	0	Migration - V4 - M	134550
<input type="checkbox"/>	12										51.7	29.2 Q	4.06	0	0	Migration - F2 - A	188217
<input type="checkbox"/>	13										49.7	17 Q	4.09	0	0	Ancestry	215524
<input type="checkbox"/>	14										48.9	26 Q	4.10	0	0	Migration - F2 - T	192258
<input type="checkbox"/>	15										48	14.2 Q	4.11	0	0	Ancestry	233937
<input type="checkbox"/>	16										46	25 Q	4.14	0	0	Migration - F2 - T	192819

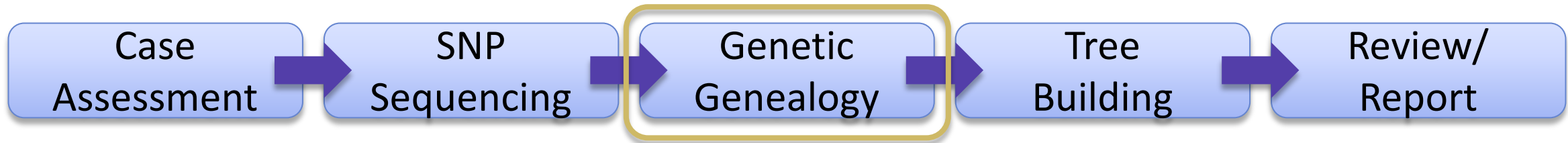
*Kit #/Names redacted

Relationship Probabilities for 227 total shared cM

Relationship Type	Probability	Group
2C Group		53.7%
2C, 1C2R, Half-1C1R	53.7%	
2C1R Group		35.0%
2C1R, Half-2C, Half-1C2R, 1C3R	35.0%	
3C Group		5.6%
3C, 2C2R, Half-2C1R, Half-1C3R	5.6%	
Half-1C Group		2.6%
Half-1C, Half-G-Aunt/Uncle/Niece/Nephew	2.6%	
1C1R Group		2.0%
1C1R	2.0%	
3C1R Group		1.0%
3C1R, Half-3C, Half-2C2R, 2C3R	1.0%	

Relationship prediction algorithm developed by Brit Nicholson. [Read the methodology here.](#)

CLOSE

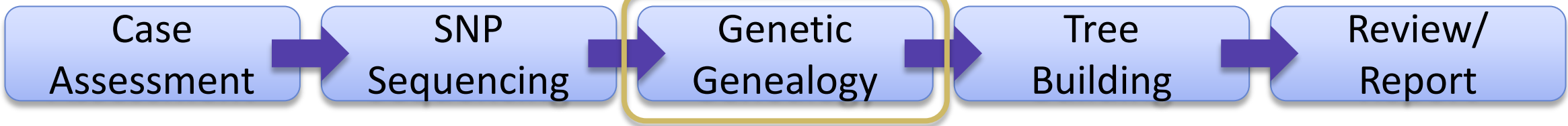


VISUALIZATION OPTIONS

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

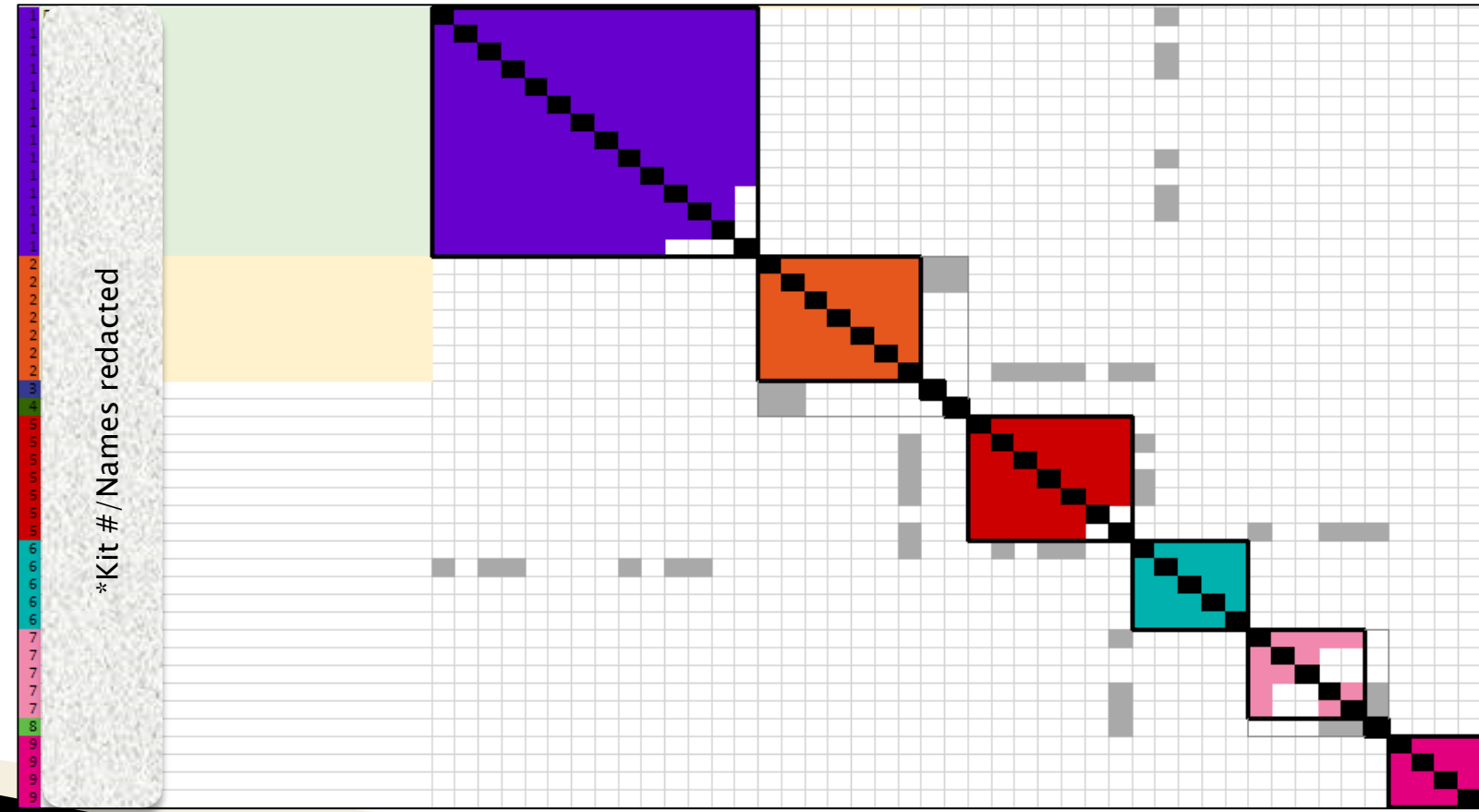
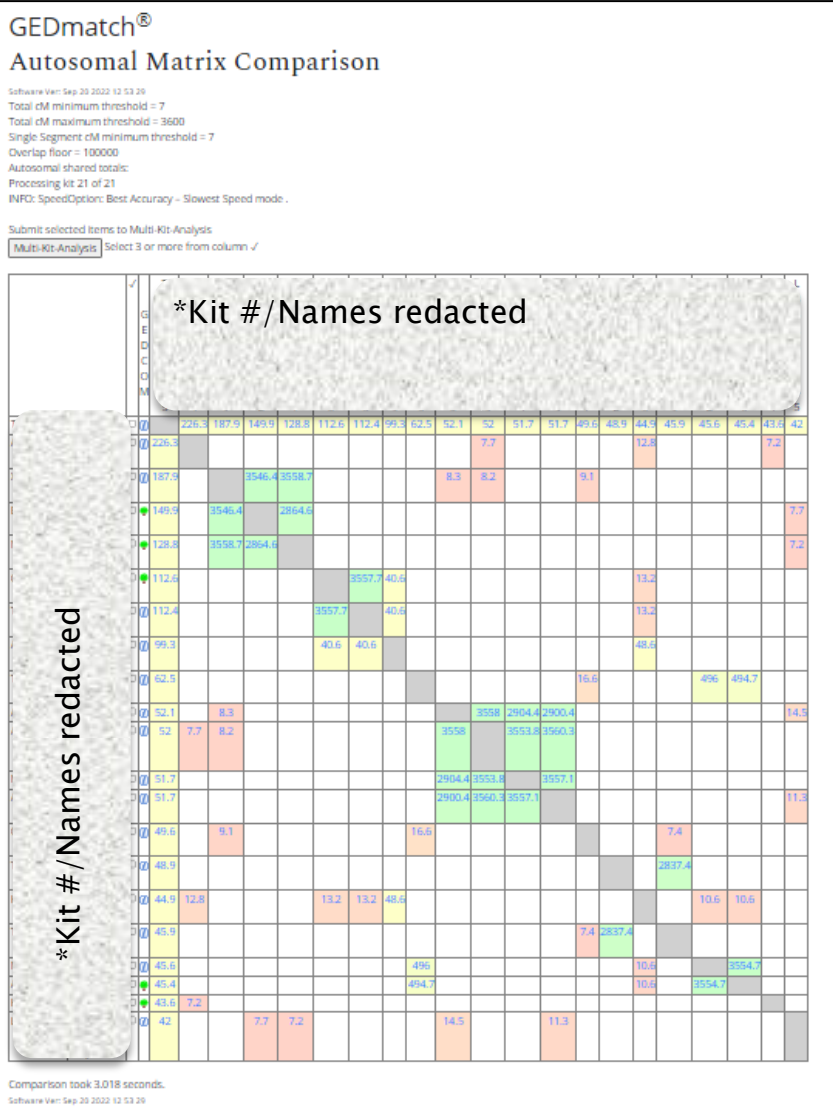
Chromosome Browsers & Matching Segment Analysis

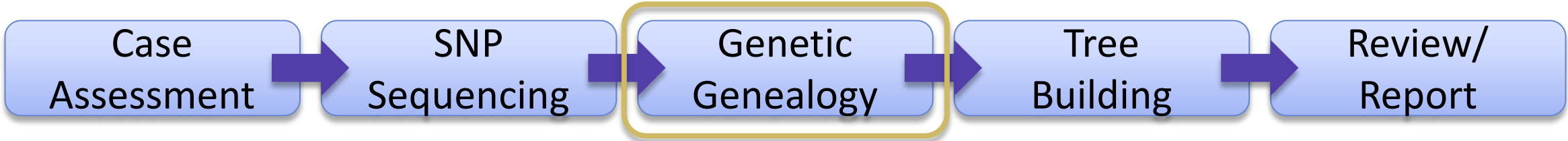
Display Type	Note	cM Value	Misc-Options	Action
Segment Search		7	<input type="checkbox"/> Prevent Hard Breaks	SEGMENT SEARCH
Triangulation		7 cm	<input type="checkbox"/> Cross Match	TRIANGULATION
2-D Chromosome Browser	Graphics may be limited to fewer kits	7		2D CHR-BROWSE
3-D Chromosome Browser	Graphics may be limited to fewer kits	7		3D CHR-BROWSE
Compact Segment Mapper	Graphics may be limited to fewer kits			COMPACT MAP



Assess how the DNA Matches match each other:

- Clusters
- Side Phasing





Assess if any DNA matches have inheritance from one common ancestor:

- Triangulation Tool

GEDmatch Home Upload DNA Free Tools GEDmatch Forums Tier 1 tools Family Trees Genealogy Comparisons / Searches

Triangulation with Kit *Kit #/Names redacted

All kits shown in columns Kit1 and Kit2 are taken from the closest 500 matches to [redacted] with a total segment sum that is greater than 30 cM and less than 3000 cM. Matches above 3000 cM (total) are not shown.

3-Way (Triangulated) segment matches are shown in green. This is an indication of common ancestry. Segments shown are larger than 30 cM and between 200 and 400 SNPs. Triangulated chromosome group 0 kits : 23 of 23

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

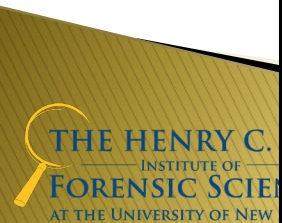
Choose How To View The Results

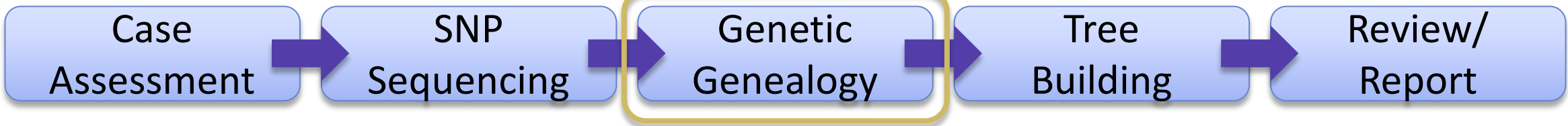
OPTION 1: By Chromosome:

OPTION 2: By Kit Number, Then Chromosome:

Triangulated results sorted by Chromosome, Start Position:

Chr	Kit 1	Kit 2	B37 Start	B37 End	cM	
3	*Kit #/Names redacted	[redacted]	123339834	150675887	30.6	
3	[redacted]	[redacted]	123395755	150675887	30.5	
3	[redacted]	[redacted]	123395755	159173074	36.4	





Assess DNA matches that share the same segments on the same chromosomes

GEDmatch®
Matching Segment Search - V1.0

Software Version Aug 31 2022 06:19:14
Kit: *Kit #/Names redacted

Minimum segment threshold size to be included in total = SNPs
Minimum segment cM to be included in total = 30 cM
To conserve system resources, matches closer than 2100 cM will not be shown.
Comparison Finished (1000 kits)

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
Chromosome 1										
	<input type="checkbox"/>	1	1926087	20064575	40.8	3468		M		
	<input type="checkbox"/>	1	188086156	218584419	34.4	4067		F		
	<input type="checkbox"/>	1	188086156	218584419	34.4	4067		F		
Chromosome 2										
	<input type="checkbox"/>	2	20850439	46995893	30	4608		F		
	<input type="checkbox"/>	2	21520172	66266799	44	6481		M		
	<input type="checkbox"/>	2	31454609	66005571	32.9	5762		M		
	<input type="checkbox"/>	2	31454609	66005571	32.9	3866		M		
	<input type="checkbox"/>	2	31454609	66005571	32.9	3879		M		
	<input type="checkbox"/>	2	55028892	106104856	38.6	5438		F		
	<input type="checkbox"/>	2	78756447	124531331	31.5	4715		F		
	<input type="checkbox"/>	2	86376474	133739616	35.7	4363		M		
	<input type="checkbox"/>	2	103756416	138868450	33.5	2955		M		
	<input type="checkbox"/>	2	105097129	138868450	33	4092		F		
	<input type="checkbox"/>	2	191896054	220714502	30.7	4771		F		
	<input type="checkbox"/>	2	192436267	221241860	31	3438		F		

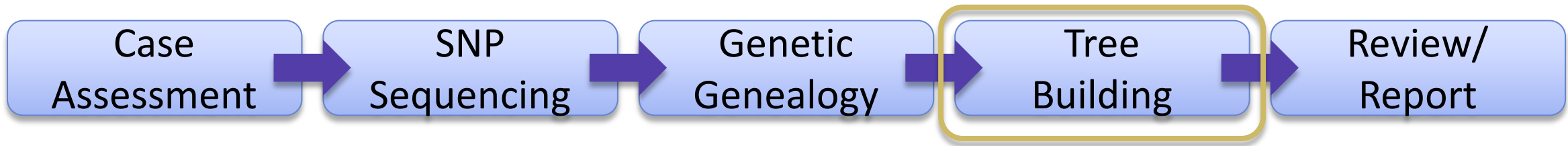
Home Upload DNA Free Tools GEDmatch Forums Tier 1 tools Family Trees

People who match both kits, or 1 of 2 kits

Useful YouTube video on using the Matching One or Two Kits tool. [WATCH VIDEO](#)

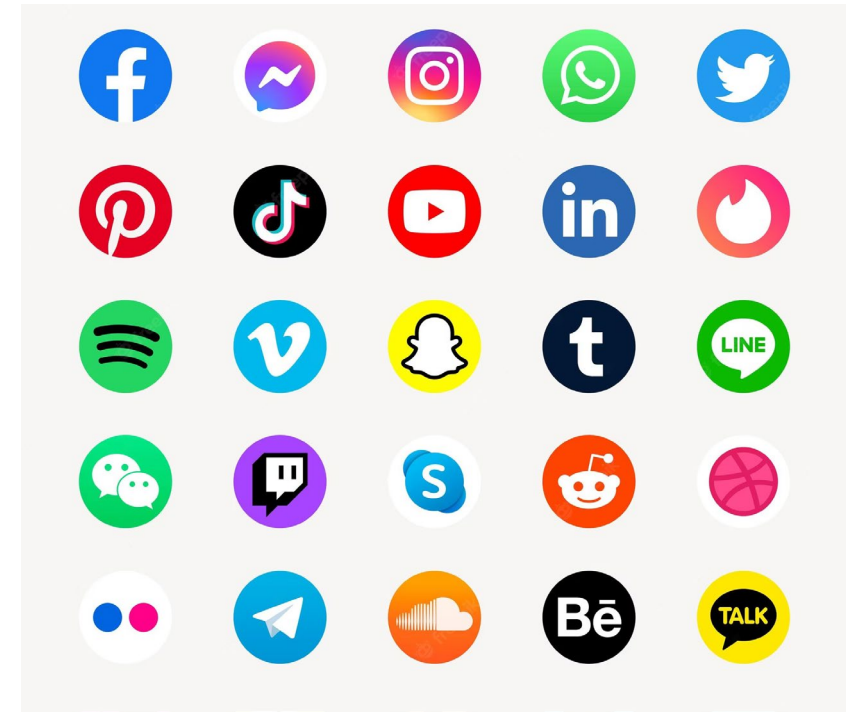
Kit Number 1

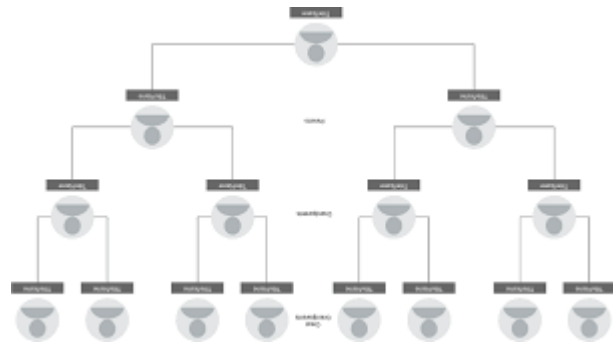
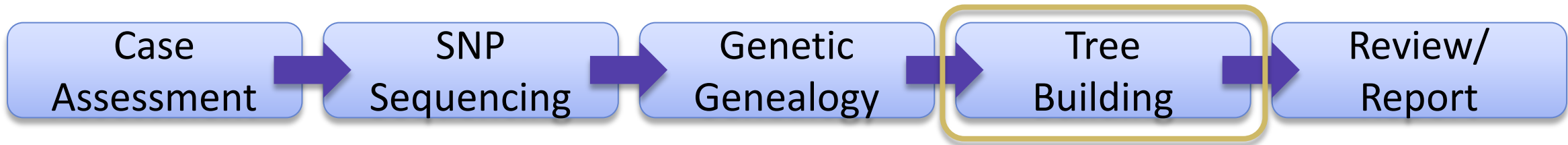
Kit Number 2



Verify identities of DNA matches:

- John Smith: johnsmith84@gmail.com
- Some use aliases

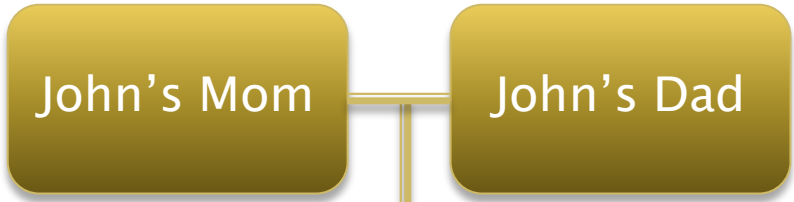
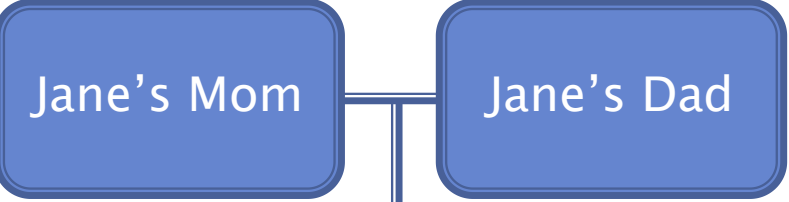
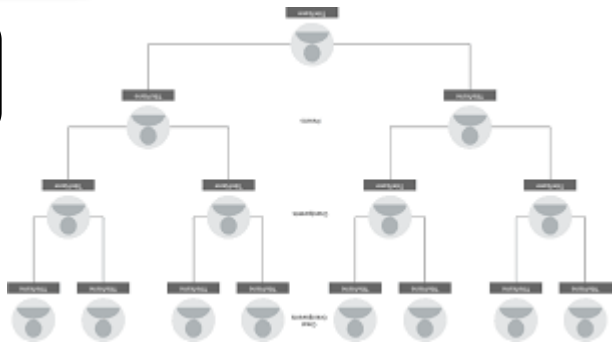


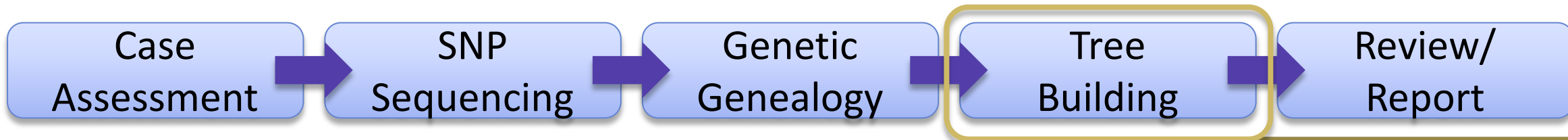


MRCA

Build back generations

MRCA





STR Profile Comparison

Proposed Candidate Name(s) provided to Law Enforcement Agency



Suspect:
Overt or Covert Collection

UHR:
Closest Living Relative Collection

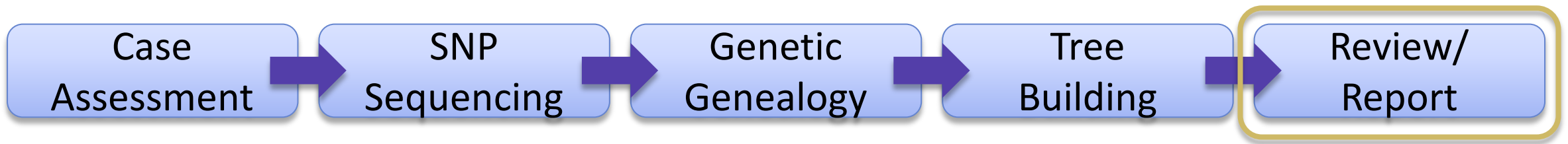
Locus	Forensic Unknown	Reference Known
D3	15, 16	15, 16
vWA	14, 16	14, 16
D16	9, 10	9, 10
D2S1	14, 15	14, 15
D8	12, 13	12, 13
D21	28, 31	28, 31
D18	12, 15	12, 15
D19	14, 15	14, 15

INCLUDED ✓

TGA	24, 20	24, 20
D1	13, 16	13, 16

EXCLUDED ✗

D12	18, 19	18, 19
D22	11, 16	11, 16
SE33	17, 25.2	17, 25.2
D7	7, 12	7, 12
CSF1PO	11, 12	11, 12
D13	11	11
TPOX	8	8
D5	11	11
Amelo	XY	XY
DYS391	11	11



- ✓ Every step of a FIGG investigation should be documented.
- ✓ Every genetic genealogy tool performed should be recorded.
- ✓ Every record sourced to build the family trees should be recorded.
- ✓ Final report detailing the investigation should be provided.
- ✓ Any other competent FIGG practitioner should be able to interpret your findings.

Report Contents

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3. Best Practices Recommendations

Case Management

Case Selection:

Violent Crimes
Unidentified Remains



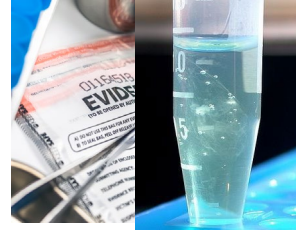
STR Profile:

CODIS Upload/No Hits
FDS (if allowed)



Bio Evidence Retained:

Original crime scene
sample/DNA extract



DNA Assessment:

Re-quant over 1yr



Recommendation:

Designated FIGG/Lab Official (DFO/DLO):

- ✓ Oversees the administration and security of all uses of FIGG
- ✓ Assesses case eligibility (legal policies and TOU of databases)
- ✓ Performs forensic sample quality checks

Technology & Data Management

Choose SNP Technology
Microarray/WGS/
Kintelligence

Choose Vender
Sequencing Lab

Receive & Store DNA Data
Generated

DNA Data Upload to
FTDNA & GEDmatch



VEROGEN
Webinars
The Forensic
Kintelligence



raw DNA data

rsID	chromosome	position	allele 1	allele 2
rs4477212	1	72017	A	A
rs3094315	1	742429	G	A
rs3131972	1	742584	G	G
rs12124819	1	766409	G	G
rs12564807	1	734462	A	A



NA

Recommendation:

Designated FIGG/Lab Official (DFO/DLO):

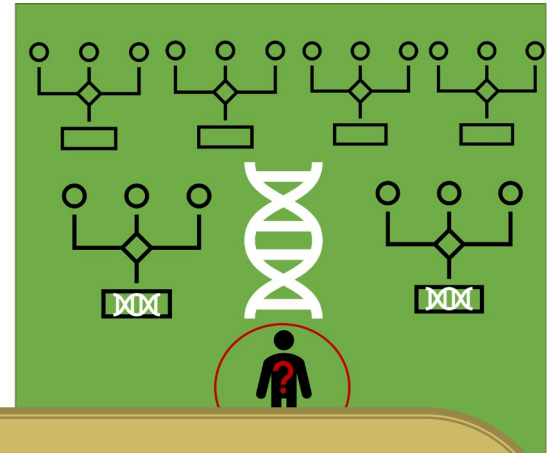
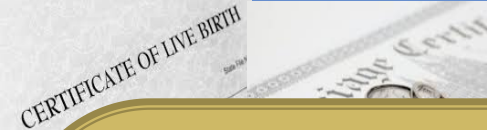
- ✓ Selects appropriate technology based on Quantity/Quality of DNA
- ✓ Coordinates outsourcing to vendor sequencing labs
- ✓ Receives and maintains custody of genetic data from vendor labs
- ✓ Responsible for data upload to/removal from databases

FIGG Analysis

Genetic Genealogy Analysis in
Databases & External Tools

Cousin D Chr 5 Triangulation Group - Shared cM									
Name	Cousin D	NV	EG	EDB	Me	Sib S	Sib H	Sib L	
Cousin D	-	49.1	16.3	32.9	41.4	51.1	46.6	40.9	
NV	49.1	-	7.7	14.5	17.7	17.9	17.7	18	
EG	16.3	7.7	-	10.6	17.8	16.3	21.8	16.7	
EDB	32.9	14.5	10.6	-	27.3	23.7	26.9	18.1	
Me	41.4	17.7	17.8	27.3	-	2497.4	2759.8	2486.8	

Documentary Evidence
& Tree Building



Recommendation:

All Analyses Documented:

- ✓ Each genetic genealogy tool performed.
- ✓ Records used to build trees.
- ✓ “Visual Citations” appropriate.
- ✓ All documentation submitted to DFO

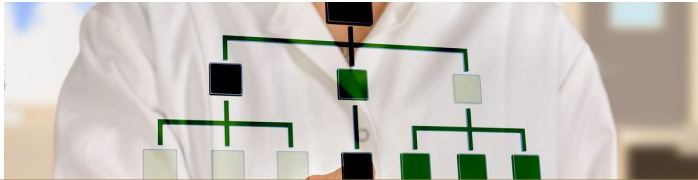
Recommendation:

Data Security:

- ✓ Secure platforms & servers approved for data storage, data sharing, tree building, etc.
- ✓ Public sites e.g., ancestry.com, are not secure for forensic work.

Candidate Analysis

Assess/Review Potential
Candidate Identitie(s)



Recommendation:

Review of Analyses:

- ✓ An administrative/technical review of the documentation and reports should be performed to assess conclusions reached.
- ✓ DFO provides candidate identity to LE.

Confirm with STR Profile:

- Suspect Reference DNA Sample
- Family Reference Sample

Unknown Candidate



Recommendation:

STR Confirmation:

- ✓ LE collects reference DNA sample.
- ✓ DFO compares Reference STR profile to original Forensic Unknown STR profile.
- ✓ Provides inclusion/exclusion to LE.

Outsourcing Recommendations

Vendor Sequencing Labs

- ✓ Provide documentation about their Quality Management Systems.
 - Evidence of performance checks
 - Run data for positive/negative/reagent blanks
 - Environmental controls, etc.
- ✓ Maintain a staff elimination database for contamination checks prior to any FIGG analyses are started.
- ✓ Have policies and procedures in place to maintain sample/data chain of custody, storage, retention, disposition, etc.

Outsourcing Recommendations

Private FIGG Practitioners

- ✓ Contractual agreements with external FIGG practitioners should include non-disclosure agreements and state the ownership of the data/kit is with the forensic lab/agency.
- ✓ External FIGG practitioners should be vetted for authorization and security (e.g., background checks).
- ✓ External FIGG practitioners should agree to turnover full documentation and reports of analyses performed to the DFO, and also be prepared for providing written or oral testimony.

5. The Future of FIGG

Active/Current Investigations

Idaho student killings suspect identified by DNA in public genealogy database

Bryan Christopher Kohberger was arrested in Pennsylvania on accusations that he murdered four students

Ramon Antonio Vargas
Tue 3 Jan 2023 09:46 EST



 Officers investigate the deaths of four University of Idaho students at an apartment complex south of campus. Photograph: Zach Wilkinson/AP

The suspect in the killings of four University of Idaho students that has

Wrongful Convictions – The Innocence Project

News 07.17.19

DNA Testing Identifies Actual Perpetrator in 1996 Idaho Falls Rape and Murder, Confirming Christopher Tapp's Innocence

By Innocence Staff



Christopher Tapp hugging his lawyer John K. Thomas - Post Conviction Relief Proceedings on Wednesday, July 17, 2019 in Idaho Falls, Idaho. (Image: Otto Kitsinger/AP Images for The Innocence Project)

NATION

California man spent 15 years in prison. DNA, genealogy websites were just used to free him.

Don Thompson The Associated Press

Published 7:42 a.m. ET Feb. 14, 2020 | Updated 8:57 a.m. ET Feb. 14, 2020



INNOCENCE PROJECT

Mass Graves



1921 Tulsa Identification Project

Our nonprofit DNA laboratory is honored to assist the City of Tulsa in identifying victims of the 1921 Tulsa Race Massacre. A number of massacre victims were buried in unmarked graves. As part of an important effort to identify victims, the City exhumed a number of bodies in the summer of 2021.

Before we can start the work of identification, we are asking for help from anyone with information regarding stories, records, and more. We are especially interested in those that had family members in Tulsa in 1921.


[Provide Information](#)


[See Here For More Information on the Genealogical Process We Are Using](#)

[Learn more about uploading your DNA information to GEDMatch](#)



Applied Research



WELCOME GUEST  SIG

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[Home](#) > [News](#) > Bode Technology Awarded NIJ Grant to Advance Genetic Genealogy

Bode Technology Awarded NIJ Grant to Advance Genetic Genealogy

January 06, 2023



Bode Technology announced it has been awarded a \$437K grant from the National Institute of Justice (NIJ) under the Research and Development in Forensic Science for Criminal Justice Purposes grant program to address pressing research in the field of investigative genetic genealogy (IGG).

The grant titled "[Comparative Evaluation of Genotyping Technologies for Investigative Genetic Genealogy in Sexual Assault Casework](#)" will evaluate the reliability and effectiveness of the various laboratory approaches utilized in IGG on the samples typically encountered by crime laboratories. Investigative genetic genealogy is increasingly being used to uncover new investigative leads on cold cases.


"Investigative genetic genealogy has proven to be one of the most powerful new forensic techniques of the past decade. However, more underlying research is needed to allow users of the technology to make informed decisions on the best approach for their forensic evidence which can often be limited in both quality and quantity," said Mike Cariola, President and CEO of Bode Technology.


Since no two IGG cases are alike, by evaluating the different technologies currently available, forensic genealogists will be able to better apply the correct technology to the case type to enhance successful outcomes.

[Press release by Bode Technology.](#)



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Comparative Evaluation of Genotyping Technologies for Investigative Genetic Genealogy in Sexual Assault Casework

Award Information

Awardee: [BODE CELLMARK FORENSICS, INC.](#)
Award #: 15PNIJ-21-GG-04143-MUMU
Funding Category: Competitive Discretionary
Location: [LORTON, VA](#)
Congressional District: [11](#)
Status: Open
Funding First Awarded: 2021
Total funding (to date): \$437,383
Original Solicitation: [Research and Development in Forensic Science for Criminal Justice Purposes, Fiscal Year 2021](#)


- Current Funding
- Forthcoming Funding
- Expired Funding
- Awards: Listing of Funded Projects
- Guidance for Applicants and Awardees
- Fellowship & Student Programs
- Travel Scholarships
- NIJ Challenge Program

Degraded DNA

**THE IMPACT OF MANUALLY DEGRADED SNP
MICROARRAY DATA ON GEDMATCH TOP GENETIC
MATCHES FOR FORENSIC INVESTIGATIVE GENETIC
GENEALOGY (FIGG) PURPOSES**

JUSTIN RIVERA
FACULTY ADVISOR: DR. CLAIRE GLYNN

INTERNAL COMMITTEE MEMBER: DR. SAN PIETRO
EXTERNAL COMMITTEE MEMBER: MELINDE BYRNE

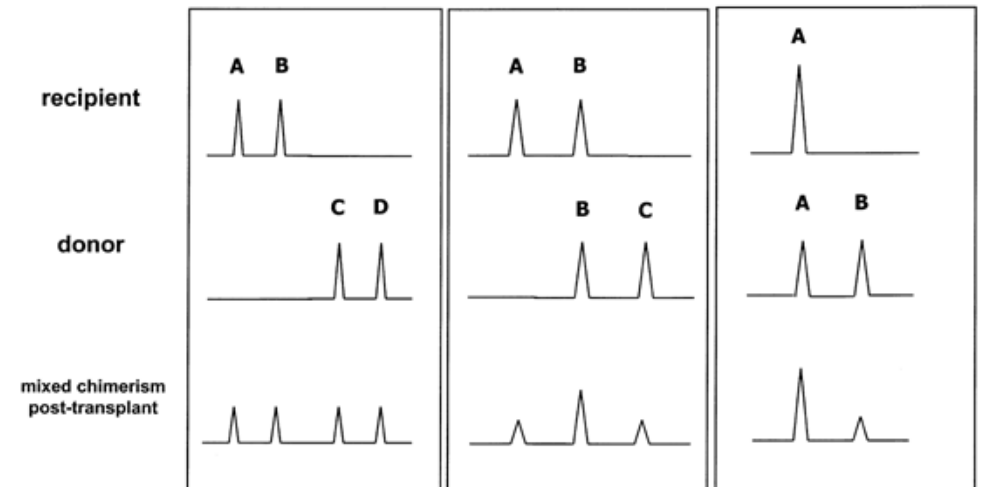
 University of New Haven
HENRY C. LEE COLLEGE OF
CRIMINAL JUSTICE AND FORENSIC SCIENCES
Department of Forensic Science

Full	-5%	-10%	-15%	-20%	-25%	-30%	-40%	-50%
TM_1	TM_1	TM_1	TM_1	TM_1	TM_1	TM_1	TM_1	TM_1
TM_2	TM_2	TM_2	TM_2	TM_2	TM_2	TM_2	TM_2	TM_2
TM_3	TM_3	TM_3	TM_3	TM_3	TM_3	TM_3	TM_3	TM_3
TM_4	TM_4	TM_4	TM_4	TM_4	TM_4	TM_4	TM_4	TM_9
TM_5	TM_5	TM_5	TM_9	TM_9	TM_9	TM_9	TM_9	TM_4
TM_6	TM_6	TM_6	TM_5	TM_5	TM_5	TM_5	TM_6	TM_?
TM_7	TM_7	TM_7	TM_6	TM_6	TM_6	TM_6	TM_7	TM_?
TM_8	TM_8	TM_8	TM_7	TM_7	TM_7	TM_7	TM_?	TM_?
TM_9	TM_9	TM_9	TM_8	TM_8	TM_8	TM_8	TM_8	TM_10
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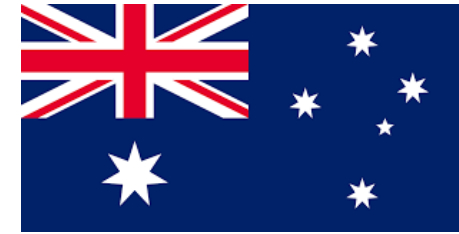
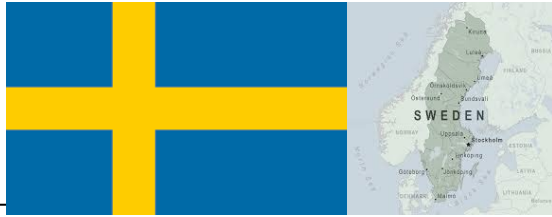
Mixtures & Chimeras

IMPACT OF BONE MARROW TRANSPLANTATION ON FORENSIC HUMAN IDENTIFICATION AND GENETIC GENEALOGY TESTING

Lisa Sikop
lsiko1@unh.newhaven.edu
University of New Haven
Tuesday, December 13, 2022



International Use



 Forensic Science International: Genetics
Volume 53, July 2021, 102525

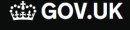
Research paper

Getting the conclusive lead with investigative genetic genealogy – A successful case study of a 16 year old double murder in Sweden

Andreas Tillmar^{a, b, c, d, e}, Siri Aili Fagerholm^c, Jan Staaf^d, Peter Sjölund^c, Ricky Ansell^{c, f, g, h}

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 GOV.UK

Home > Crime, justice and law > Use of genetic genealogy techniques to assist with solving crimes

Biometrics and Forensics
Ethics Group

Should we be making use of genetic genealogy to assist in solving crime? A report on the feasibility of such methods in the UK (accessible version)

Research and analysis

Published 9 September 2020

> Forensic Sci Int. 2020 Nov;316:110543. doi: 10.1016/j.forsciint.2020.110543. Epub 2020 Oct 11.

Operationalising forensic genetic genealogy in an Australian context

Nathan Scudder¹, Runa Daniel², Jennifer Raymond³, Alison Sears³

Affiliations + expand

PMID: 33152660 DOI: 10.1016/j.forsciint.2020.110543

 Independent.ie

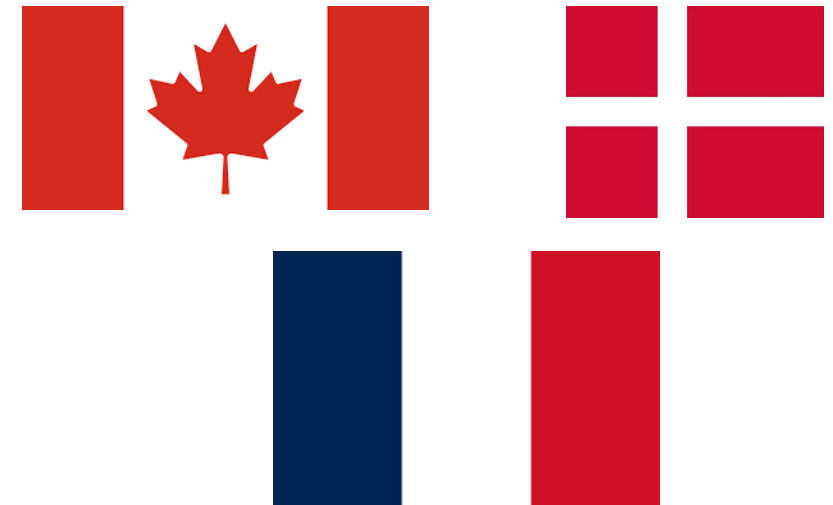
News Opinion Business Sport Life Style Entertainment Travel Sections

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Premium

How home DNA tests are helping to catch killers – and could be used to investigate Irish crimes

A leading 'DNA detective' who has helped solve US murders believes public ancestry sites could be used to investigate Irish crimes, including the Kerry babies case. But what are the privacy implications? Kim Bielenberg reports



6. The University of New Haven FIGG Program

ONLINE GRADUATE CERTIFICATE

FORENSIC GENETIC GENEALOGY

Spring I:
Fundamentals Forensic
Biological Evidence

Spring II:
Genetic Genealogy
Principles & Methods

Forensic Experts:
Test-Out or Forensic
DNA Phenotyping

Grad Cert in
FIGG

Summer:
Genealogy Principles &
Methods

Fall I:
FIGG Practicum

4 x 3 credit courses

12 credits total

Fully Online – Asynchronous

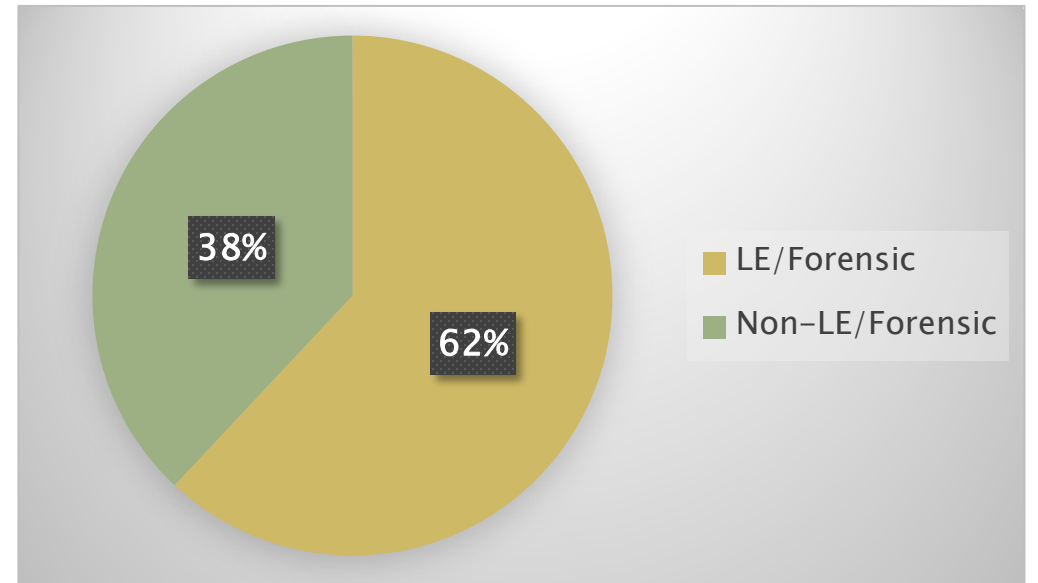
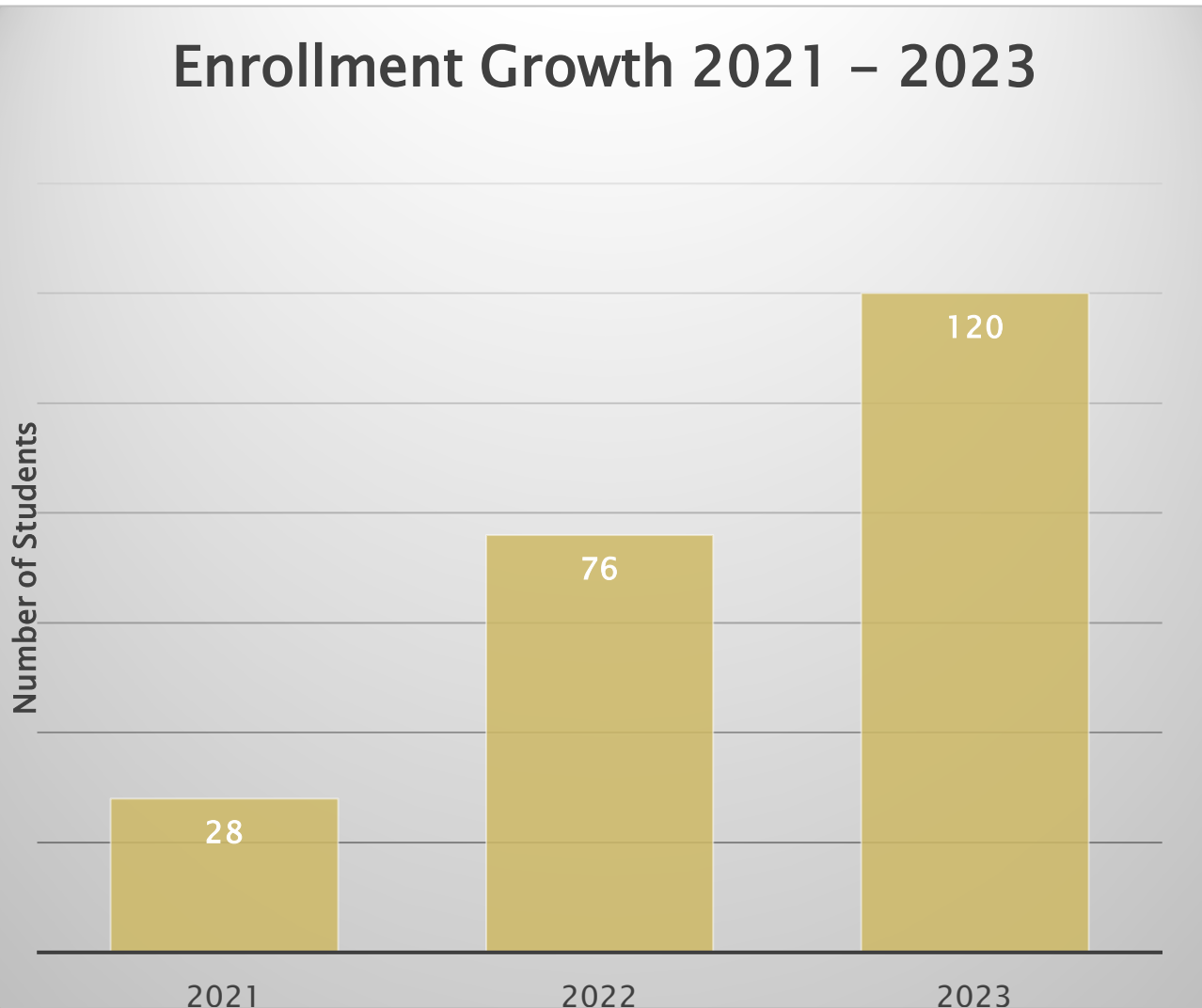
Accelerated Terms (January – October)

**30% Tuition Discount for Law Enforcement
& Forensic Professionals**



Student Demographics

Enrollment Growth 2021 – 2023



Students from >35 States,
Australia, France, Canada, Switzerland, Ireland

~91% Female
Average Age: 45.6 yrs
(min: 22; max:74)

~85% possess Masters Degrees
~35% possess Terminal Degrees (e.g., Ph.D., JD.)

Future – Training & Education

- ▶ Education/Training Requirements
- ▶ Proficiency Testing
 - Mock Cases
- ▶ Continuing education
 - Advances in technology
 - New Tools
 - Artificial Intelligence
- ▶ Training
 - Designed for Crime Lab Personnel
 - Designed for Law Enforcement/Investigators



**PROFICIENCY
TESTING**



As of 31 Dec 2022:
545 cases



Thank you to

**Green  ountain
DNA Conference**



University of New Haven

HENRY C. LEE COLLEGE OF
CRIMINAL JUSTICE AND FORENSIC SCIENCES

Department of Forensic Science

Claire Glynn
cglynn@newhaven.edu

