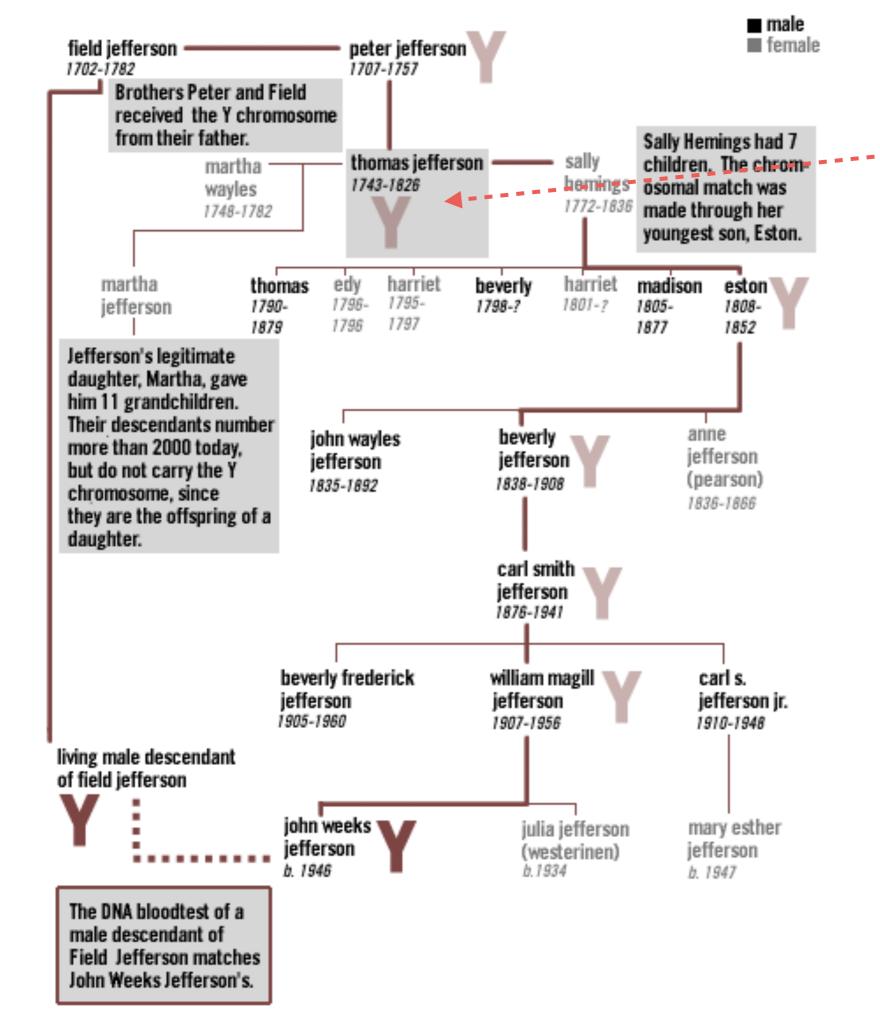
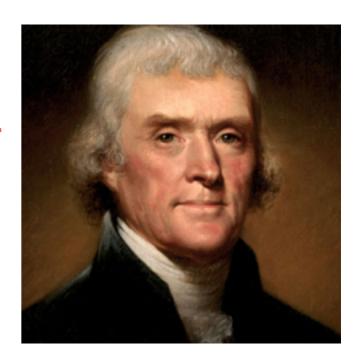
Forensic DNA analysis of historical samples

Two case studies

Thomas Jefferson and Sally Hemings

http://www.pbs.org/wgbh/pages/frontline/shows/jefferson/true/

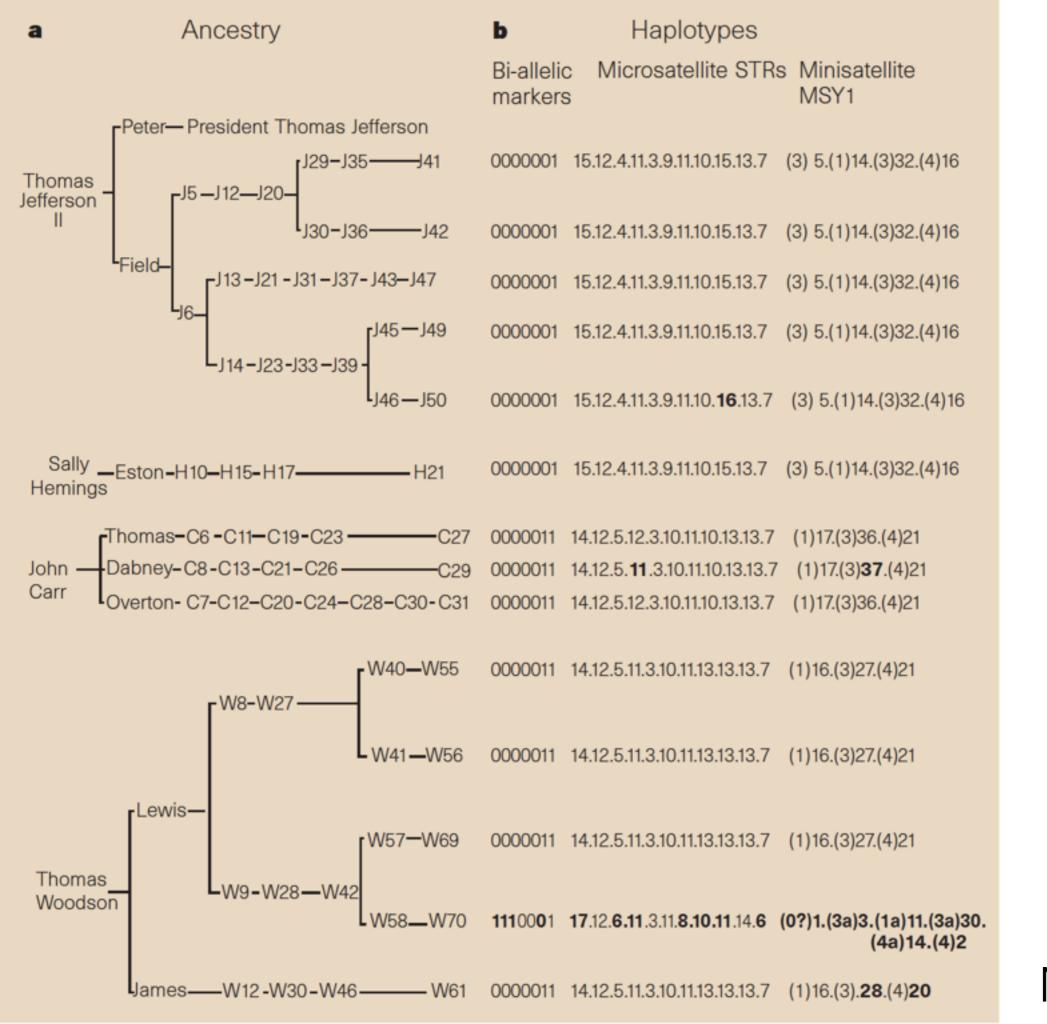




b	Haplotypes	
Bi-alleli marker	c Microsatellite STRs Minisatellite s MSY1	
0000001	15.12.4.11.3.9.11.10.15.13.7 (3) 5.(1)14.(3)32.(4)16	
0000001	15.12.4.11.3.9.11.10.15.13.7 (3) 5.(1)14.(3)32.(4)16	
0000001	15.12.4.11.3.9.11.10.15.13.7 (3) 5.(1)14.(3)32.(4)16	
0000001	15.12.4.11.3.9.11.10.15.13.7 (3) 5.(1)14.(3)32.(4)16	
0000001	15.12.4.11.3.9.11.10. 16 .13.7 (3) 5.(1)14.(3)32.(4)16	
0000001	15.12.4.11.3.9.11.10.15.13.7 (3) 5.(1)14.(3)32.(4)16	
0000011	14.12.5.12.3.10.11.10.13.13.7 (1)17.(3)36.(4)21 14.12.5. 11 .3.10.11.10.13.13.7 (1)17.(3) 37 .(4)21	
0000011	14.12.5.12.3.10.11.10.13.13.7 (1)17.(3)36.(4)21	
0000011	14.12.5.11.3.10.11.13.13.13.7 (1)16.(3)27.(4)21	
0000011	14.12.5.11.3.10.11.13.13.13.7 (1)16.(3)27.(4)21	
0000011	14.12.5.11.3.10.11.13.13.13.7 (1)16.(3)27.(4)21	
111 00 0 1	17.12.6.11.3.11.8.10.11.14.6 (0?)1.(3a)3.(1a)11.(3a)30. (4a)14.(4)2	
0000011	14.12.5.11.3.10.11.13.13.13.7 (1)16.(3).28.(4)20	

Ancestry

Foster et al Nature, 1998



Foster et al Nature, 1998

- "TJF and most historians believe that, years after his wife's death, Thomas Jefferson was the father of the six children of Sally Hemings mentioned in Jefferson's records, including Beverly, Harriet, Madison, and Eston Hemings.' — Thomas Jefferson Foundation (TJF), https://www.monticello.org/site/plantation-and-salvery/thomas-jefferson-and-sally-hemings-brief-account
- But the Thomas Jefferson Heritage Society disputes this conclusion
- http://uvamagazine.org/articles/ anatomy_of_a_mystery/

The Romanovs

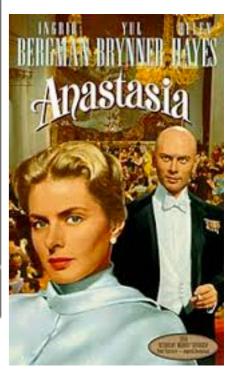














Published study in 1994 showed remains belonged to Romanov family

Table 1 STR genotypes for the nine skeletons

Skeleton	HUMVWA/31	HUMTH01	HUMF13A1	HUMFES/FPS	HUMACTBP2
1	14,20	9,10	6,16	10,11	ND
2	17,17	6,10	5,7	10,11	11,30
3	15,16	8,10	5,7	12,13	11,32
4	15,16	7,10	7,7	12,12	11,32
5	15,16	7,8	5,7	12,13	11,36
6	15,16	8,10	3,7	12,13	32,36
7	15,16	8,8	3,5	12,13	32,36
8	15,17	6,9	5,7	8,10	ND
9	16,17	6,6	6,7	11,12	ND

Gill et al, Nature Genetics 1994 http://www.nature.com/ng/journal/v6/n2/abs/ng0294-130.html

Table 1 STR genotypes for the nine skeletons

HUMVWA/31	HUMTH01	HUMF13A1	HUMFES/FPS	HUMACTBP2
		6,16	10,11	ND
•	•	•	10,11	11,30
•	*		12,13	11,32
•	,	7,7	12,12	11,32
*	•	5,7	12,13	11,36
•		3,7	12,13	32,36
	•	3,5	12,13	32,36
* .			8,10	ND
16,17	6,6	6,7	11,12	ND
	HUMVWA/31 14,20 17,17 15,16 15,16 15,16 15,16 15,17 16,17	14,20 9,10 17,17 6,10 15,16 8,10 15,16 7,8 15,16 8,10 15,16 8,8 15,17 6,9	14,20 9,10 6,16 17,17 6,10 5,7 15,16 8,10 5,7 15,16 7,8 5,7 15,16 8,10 3,7 15,16 8,8 3,5 15,17 6,9 5,7	14,20 9,10 6,16 10,11 17,17 6,10 5,7 10,11 15,16 8,10 5,7 12,13 15,16 7,8 5,7 12,13 15,16 8,10 3,7 12,13 15,16 8,8 3,5 12,13 15,17 6,9 5,7 8,10

Gill et al, Nature Genetics 1994 http://www.nature.com/ng/journal/v6/n2/abs/ng0294-130.html

Table 2 Summary	of mtDNA differences compared to the Anderson ²¹ reference sequence
-----------------	--

Origin of sample	DNA source	Length sequenced (bp)				Pos	sitio		of		toc			ble r	egior A	ıs (l		R) VR	2		
							O 16264								V 73		т 195	× 263		* 309.2	, 315.1
	Femur skeleton 1 Femur skeleton 8 Femur skeleton 9 Femur skeleton 2	760 742 650 736	:	:	:	÷	†	Ť	G	:	:	:	C	:	<u>.</u>	:	Ċ	G G		:	0000
	Femur skeleton 3 Femur skeleton 5 Femur skeleton 6 Femur skeleton 7 Blood sample	755 634 760 744 760	T T	:	:	:		:	:	:	:	:	:	CCC	:	:	:	G G		:	00000
	Femur skeleton 4 Blood sample	782 781					:							:	G G	:	:	G		:	C
	Blood sample	782		С	Т					Т	т				G			G			С

^{.,} Sequence unchanged from reference sequence; -, No nucleotide assignment; *, Nucleotide absent from reference sequence; Y, C/T heteroplasmy.

Gill et al, Nature Genetics 1994 http://www.nature.com/ng/journal/v6/n2/abs/ng0294-130.html

Table 2 Summary of mtD	NA differences compared to the	Anderson ²¹ reference sequence
------------------------	--------------------------------	---

DNA source	Length sequenced (bp)				Pos	sitio		of	mi	toc				_	s (H			2		
							16278	16293	16294	16296									* 309.2	, 315.1
Femur skeleton 1 Femur skeleton 8 Femur skeleton 9 Femur skeleton 2	760 742 650 736	:	:	:	Ė	:	Ė	G	:	:	:	C	:	<u>.</u>	:	ċ	G G	:	:	C
Femur skeleton 3 Femur skeleton 5 Femur skeleton 6 Femur skeleton 7 Blood sample	755 634 760 744 760	T T T	:	:	:	:	:	:	:	:	:	:	CCC	:	:	:	G G	:	:	CCC
Femur skeleton 4 Blood sample Blood sample	782 781 782		С	T					Ŧ	Ť				G			G		•	С
	Femur skeleton 1 Femur skeleton 8 Femur skeleton 9 Femur skeleton 2 Femur skeleton 3 Femur skeleton 5 Femur skeleton 6 Femur skeleton 7 Blood sample Femur skeleton 4 Blood sample	Femur skeleton 1 760 Femur skeleton 8 742 Femur skeleton 9 650 Femur skeleton 2 736 Femur skeleton 3 755 Femur skeleton 5 634 Femur skeleton 5 634 Femur skeleton 6 760 Femur skeleton 7 744 Blood sample 760 Femur skeleton 4 782 Blood sample 781	Femur skeleton 1 760 . Femur skeleton 8 742 . Femur skeleton 9 650 . Femur skeleton 2 736 . Femur skeleton 3 755 T Femur skeleton 5 634 T Femur skeleton 6 760 T Femur skeleton 7 744 T Blood sample 760 T Femur skeleton 4 782 . Blood sample 781 .	Sequenced (bp) Femur skeleton 1 760	Sequenced (bp) Femur skeleton 1 760 1 1 1 1 1 1 1 1 1	Sequenced (bp) Femur skeleton 1 760 742 736 755 7 756 756 756 757	Sequenced (bp) Femur skeleton 1 760	Sequenced (bp) Sequenced (bp) Sequenced (bp) Femur skeleton 1 760 C T C C C C C Femur skeleton 8 742 C T C C C C Femur skeleton 9 650 C T C T C T C C C C Femur skeleton 2 736 C T C C C C C Femur skeleton 5 634 T C C C C C C C Femur skeleton 6 760 T C C C C C C C C C C C C C C C C C C	Sequenced (bp) Sequ	Sequenced (bp) Of min HVR 1	Sequenced (bp) Of mitoc HVR 1	Sequenced (bp) Of mitochon HVR 1	Sequenced (bp) Of mitochondria	Sequenced (bp) Of mitochondrial DNA HVR 1	Sequenced (bp) Of mitochondrial DNA HVR 1 PR PR PR PR PR PR PR	Sequenced (bp) Of mitochondrial DNA HVR 1	Sequenced (bp) Of mitochondrial DNA HVR 1 HVR 1	Sequenced (bp) Of mitochondrial DNA	Sequenced (bp) Of mitochondrial DNA	Sequenced (bp) Of mitochondrial DNA HVR 2

^{.,} Sequence unchanged from reference sequence; -, No nucleotide assignment; *, Nucleotide absent from reference sequence; Y, C/T heteroplasmy.

Gill et al, Nature Genetics 1994

http://www.nature.com/ng/journal/v6/n2/abs/ng0294-130.html

What about the other two children?

	VWA	TH01	F13A1	FES/FPS	ACTBP2	AMELOGENIN
Tsar (Skeleton 4) ^a	15,16	7,9,3 ^b	7,7	12,12	11,32	X,Y
Tsarina (Skeleton 7) ^a Anna Anderson	15,16	8,8	3.2°,5	12,13	32,36	X,X
(intestine sample)	14,16	7,9.3	3.2,7	11,12	15,18	X,X

Origin of sample	DNA source	Length sequenced (bp)	Position within the non-coding region (ref. 11)								
			16111	16126	16266	16294	16304	16357			
Reference sequence	-		C	T	C	C	T	Т			
Duke of Edinburgh											
(Great nephew of Tsarina)	Blood sample	403	T					C			
Anna Anderson	Intestine sample	403		C	T	T	C				
Anna Anderson	Hair sample	344-362 (3 hairs)		С	Т	Т	С				
C. Maucher (Great nephew											
of Schanzkowska	Blood sample	380		C	T	T	C				



Stoneking et al, Nature Genetics 1995

Remains of two other bodies discovered 2007

Table 3. Autosomal STR Genotypes for the Romanov Family.

Marker	Sample 4.3	Sample 7.4	Sample 3.46	Sample 5.21	Sample 6.14	Sample 147	Sample 146.1
	Tsar Nicholas II	Tsarina Alexandra	Olga	Tatiana	Maria or Anastasia	Anastasia or Maria	Alexei
Amelog	X, Y	X, X	X, X	X, X	X, X	X, X	X, Y
D3S1358	14, 17	16, 18	17, 18	17, 18	16, 17	17, 18	14, 18
TH01	7, 9.3	8, 8	8, 9.3	7, 8	8, 9.3	7, 8	8, 9.3
D21S11	32.2, 33.2	30, 32.2	30, 33.2	32.2, 33.2	30, 33.2	30, 33.2	32.2, 33.2
D18S51	12, 17	12, 13	12, 12	12, 12	13, 17	12, 17	12, 17
D5S818	12, 12	12, 12	12, 12	12, 12	12, 12	12, 12	12, 12
D13S317	11, 12	11, 11	11, 11	11, 11	11, 11	11, 11	11, 12
D7S820	12, 12	10, 12	12, 12	10, 12	12, 12	10, 12	12, 12
D16S539	11, 14	9, 11	11, 11	11, 11	11, 14	9, 11	11, 14
CSF1PO	10, 12	11, 12	11, 12	11, 12	10, 11	10, 12	10, 12
D2S1338	17, 25	19, 23	17, 19	23, 25	17, 19	17, 23	23, 25
vWA	15, 16	15, 16	15, 16	15, 16	15, 16	15, 16	15, 16
D8S1179	13, 15	16, 16	13, 16	15, 16	13, 16	15, 16	15, 16
TPOX	8, 8	8, 8	8, 8	8, 8	8, 8	8, 8	8, 8
FGA	20, 22	20, 20	20, 22	20, 20	20, 22	20, 22	20, 22
D19S433	13, 13.2	13, 16.2	13.2, 16.2	13.2, 16.2	13, 16.2	13, 13	13, 13.2

doi:10.1371/journal.pone.0004838.t003

Topics	Data type	Information wanted	Main tool
HIV	nucleotide sequences (DNA)	evolutionary relationship	distances, visualizations
Personal Genomics	single nucleotide polymorhisms (SNPs)	trait association	hypothesis tests
Forensics	short tandem repeats (STRs)	identity	probability

Take-away messages

- 1. getting data ready for analysis can be timeconsuming for non-routine data types
- 2. making (reasonable) assumptions is difficult
- 3. programming automates the calculations, making this step easy
- 4. interpreting results properly is difficult