

## On Richard III's Y-DNA and Time-Asymmetric Mutation Rates (1.9.9)

**John Smith**

A skeleton excavated in 2012 is almost certainly that of the English king, Richard III (1452 -1485), and mtDNA (which is passed from mother to child) extracted from the skeleton matches mtDNA taken from descendants of Richard's sister Anne of York. However Y-DNA (which is passed from father to son) extracted from the skeleton apparently doesn't match Y-DNA taken from descendants of Henry Somerset the 5th Duke of Beaufort, who according to history descended from Richard's 2nd great grand father Edward III (1312 - 1377). The implication according to geneticists, and the media, is that there is a "false paternity event" somewhere between Edward and the Somersets. In this note, a formula for calculating the time of the most recent common ancestor is introduced, and some of its consequences outlined. This formula is attached to a mathematical framework within which it is possible that the traditional genealogy is correct. If this framework is the right framework for understanding of genetic inheritance, then it has been wrongly assumed that Y-DNA mutation rates are like-line, constant and smooth - in reality they are wave-like and decrease erratically in the direction of the future, and the contrary impression is an illusion created by an over-focus on the relatively constant and smooth nature of genetic change in the present and the near-present.

### PART I: RICHARD III AND THE CONFLICT BETWEEN GENEALOGY AND GENETICS

#### Thomas Jefferson and Richard III

An early example of the conflict between genealogy and genetics -when genealogy says one thing and genetics another- is the case of Thomas Jefferson. TJ was long rumoured to have fathered children by one of his slaves Sally Hemmings, and this rumor was substantiated in 1998 when DNA tests performed on one of his great nephews, and a descendant of Sally Hemming's youngest son, revealed a match. These tests also revealed that Jefferson's paternal DNA belongs to a rare Near-Eastern haplogroup (once known as K2 now T), despite the fact that the Jeffersons are a British family. This raised the further question of why TJ had Near Eastern Y-DNA, and lead to headlines such as *Could Thomas Jeffersons Trail Reveal Middle-Eastern Origins?*, *Study into Ancestry of Thomas Jefferson Reveals Rare Class of DNA*, and *Possibility of Jewish Tie for Jefferson*.

The Jefferson anomaly might seem easy to dispose of, but we turn now to a more challenging example. This concerns a skeleton excavated at the presumed site of the Grey Friars friary in Leicester in 2012 which DNA and historical analysis has proved beyond reasonable doubt to be that of English king, Richard III (1452-1485):



However, Y-DNA extracted from the skeleton apparently doesn't match Y-DNA taken from descendants of Henry Somerset the 5th Duke of Beaufort, who according to history descended from Richard's 2nd great grand father Edward

III (1312-1377). The implication according to geneticists, and the media, is that there is a 'false paternity event somewhere between Edward and the Somersets:

We find a perfect mitochondrial DNA match between the sequence obtained from the remains and one living relative, and a single-base substitution when compared with a second relative. Y-chromosome haplotypes from male-line relatives and the remains do not match, which could be attributed to a false-paternity event occurring in any of the intervening generations

The authors of the study maintain that this is “unremarkable”, but the false paternity events don’t end there, for only 4 of these 5 Somerset descendants actually match each other:

The Y-chromosome results also indicate one further false-paternity event between Henry Somerset and his five contemporary, presumed patrilinear descendants.

Markers	Somerset 1	Somerset 2	Somerset 4	Somerset 5	Somerset 3	Presumed skeleton of Richard III
DYS19	14	14	14	14	15	15
DYS385	11	11	11	11	12	13
DYS385 11	14	14	14	14	15	14
DYS3891	13	13	13	13	14	13
DYS389 11	29	29	29	29	30	30
DYS390	23	23	23	23	23	22
DYS391	11	11	11	11	10	10
DYS392	13	13	13	13	11	11
DYS393	13	13	13	13	13	14
DYS437	14	14	14	14	14	16
DYS438	12	12	12	12	10	10
DYS439	12	12	12	12	11	12
DYS447	20	20	20	20	18	22
DYS456	15	15	15	15	14	15
DYS458	18	18	18	18	20	18
DYS635	23	23	23	23	21	21
YGATA H4	12	12	12	12	10	11
DYS481	22	22	22	22	26	21
DYS533	12	12	12	12	13	10
DYS549	13	13	13	13	12	13
DYS570	19	19	18	18	17	16
DYS576	19	18	19	19	17	15
DYS643	10	10	10	10	12	12
HapLogroup	R1b	R1b	R1b	R1b	I2	G2a

And it turns out that there is more, for although the patrilinear line of a Frenchman named Patrice de Warren traces back to Richard III through the illegitimate son of Edward III's 4th great grandfather, Geoffrey Plantagenet, Count of Anjou (1113 - 1151), de Warren's Y-DNA doesn't match that of Richard III or any of the Somersets:

In December 2014, the University of Leicester’s DNA research in the King Richard III case showed that there was a break in the Y chromosome line.

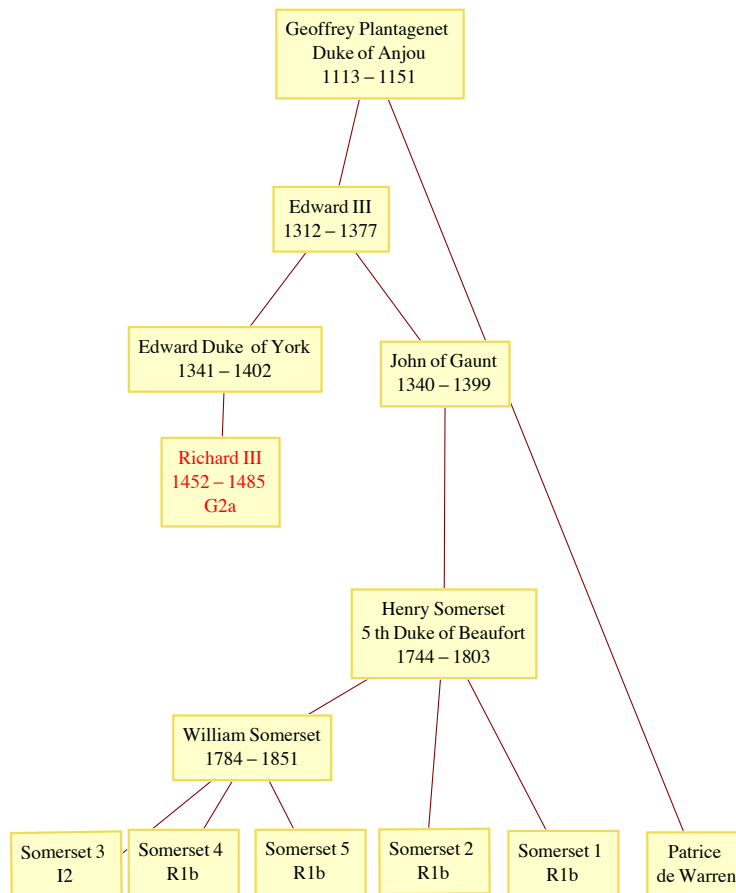
This indicated that a false paternity or paternities (where the father is not the recorded father) had taken place in the 19 generations separating Richard III from Henry Somerset, 5th Duke of Beaufort, the common ancestor of the living male-line relatives tested.

We didn’t know where this break occurred but it was interesting as a break in certain points in the tree would have implications for the historical monarchy: the Lancastrian and Yorkist Plantagenet kings and, indirectly, the Tudors.

Professor Kevin Schürer and I were approached by Patrice de Warren who could trace his male line to Richard through Geoffrey, the Count of Anjou. This was very exciting and as a result of the research we are revealing new information at the Science Museum into the ancestry of Richard III.

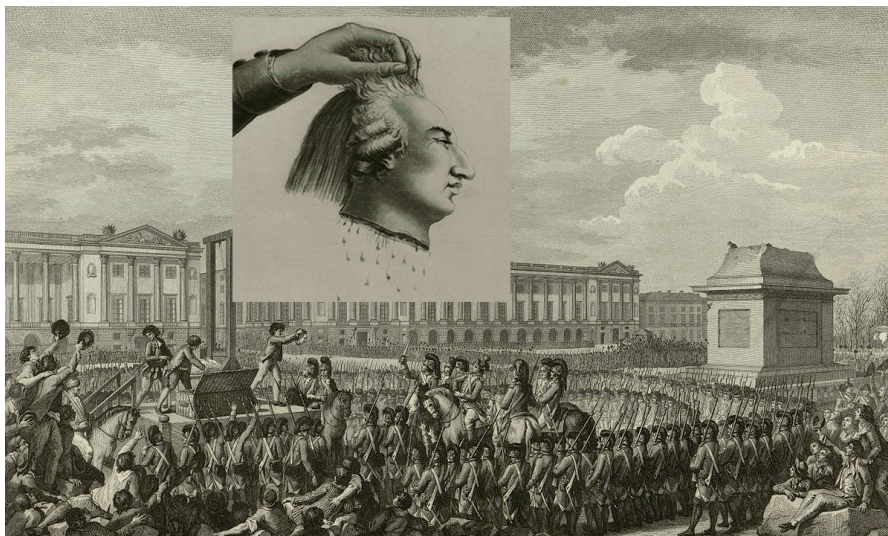
If Patrice de Warren’s Y chromosome matched that of Richard III, then this would mean that the break in the Y chromosome line occurred somewhere between Edward III and Henry Somerset. If it matched the Somerset line, then it would mean the break occurred between Edward III and Richard III. In short, it would help narrow down where the break in the line took place.

As it happens, it's revealed that another false paternity seems to have occurred in the tree as his Y chromosome type doesn't match either of them! The hunt continues, and another mystery has arisen!



### Louis XVI , Henry IV, and Marie-Antoinette

A similar and more anomalous case involving ancient DNA concerns the presumed Y - DNA of Louis XVI (1754-1793) and that of living members of the House of Bourbon. Y - DNA was successfully extracted from a cloth supposedly bloodied at the time of Louis's beheading, and belongs - like that of Richard III - to haplogroup G2a.



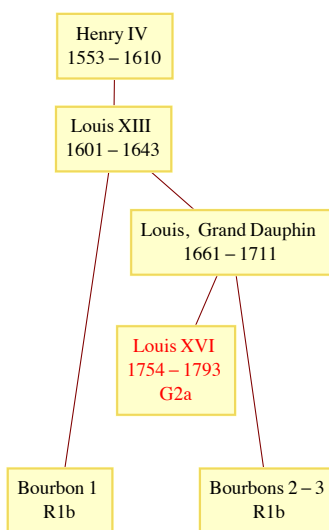
But the Y-DNA of 3 *living* members of the House of Bourbon belongs -like 4 of the 5 living Plantagenets- to R1b. Both Y-DNA and mtDNA were extracted from a mummified head presumed to be that of Louis's 5th great grandfather Henry IV (1553-1610). 5 Y-DNA markers were recovered -an insufficient number to determine a haplogroup- but

Charlier et al. concluded in 2013 that the blood and the head probably belonged to the people they were supposed to belong to:

Taking into consideration that the partial Y-chromosome profile is extremely rare in modern human databases, we concluded that both males could be paternally related. The likelihood ratio of the two samples belonging to males separated by seven generations (as opposed to unrelated males) was estimated as 246.3, with a 95% confidence interval between 44.2 and 9729. Historically speaking, this forensic DNA data would confirm the identity of the previous Louis XVI sample, and give another positive argument for the authenticity of the head of Henri IV.

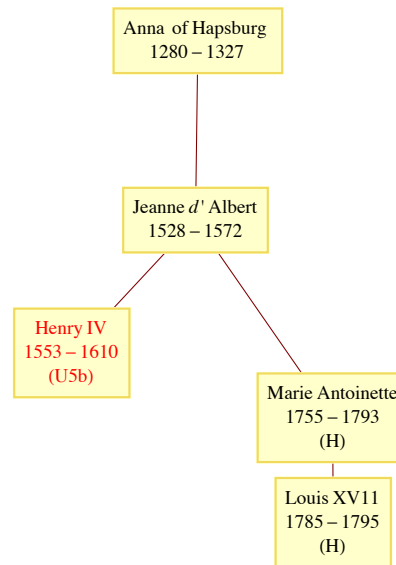
Markers	Bourbon 1	Bourbon 2	Bourbon 3	Presumed blood of Louis XVI	Presumed head of Henry IV
DYS393	13	13	13	14	14
DYS390	23	23	23	22	□
DYS19	14	14	14	15	□
DYS391	10	10	10	10	10
DYS385	11 - 14	11 - 14	11 - 14	13 - 18	? - 18
DYS426	12	12	12	□	□
DYS388	12	12	12	□	□
DYS439	12	12	12	12	□
DYS3891	13	13	13	12	13
DYS392	13	13	13	11	□
DYS389 b	16	16	16	18	□
DYS458	18	18	18	21	□
DYS459	9 - 10	9 - 10	9 - 10	□	□
DYS455	11	11	11	□	□
DYS454	11	11	11	□	□
DYS447	25	25	25	□	□
DYS437	15	15	15	15	15
DYS448	19	19	19	21	21
DYS449	28	28	28	□	□
DYS464	15 - 15 - 16 - 16	15 - 15 - 16 - 16	15 - 15 - 16 - 16	□	□
DYS460	12	12	12	□	□
YGATA H4	12	12	12	12	□
YCA 11	19 - 23	19 - 23	19 - 23	□	□
DYS456	17	17	17	15	□
DYS607	19	19	19	□	□
DYS576	16	16	16	□	□
DYS570	16	17	17	□	□
DYS724	35 - 38	35 - 39	35 - 40	□	□
DYS442	18	18	18	□	□
DYS438	12	12	12	10	□
DYS635	23	23	23	21	□
Haplogroup	R1b	R1b	R1b	G2a	G ?

In the light of the results of testing several living members of the House of Bourbon, this seems to imply that there are at least 2 false paternity events - Henry IV cannot have been the biological father of Louis XIII, and there is a false paternity event between Louis, Grand Dauphin, and Louis XVI:



The difficulty becomes even more pronounced when mtDNA extracted from the head is considered. This belongs to haplogroup U, but Henry IV was maternally related to Louis XVII, through his mother Jeanne d'Albret over Anna of Habsburg to Marie-Antoinette, and tests performed on a lock of her hair, and on her son's heart, show that Marie-

Antoinette's mtDNA belongs to haplogroup H.



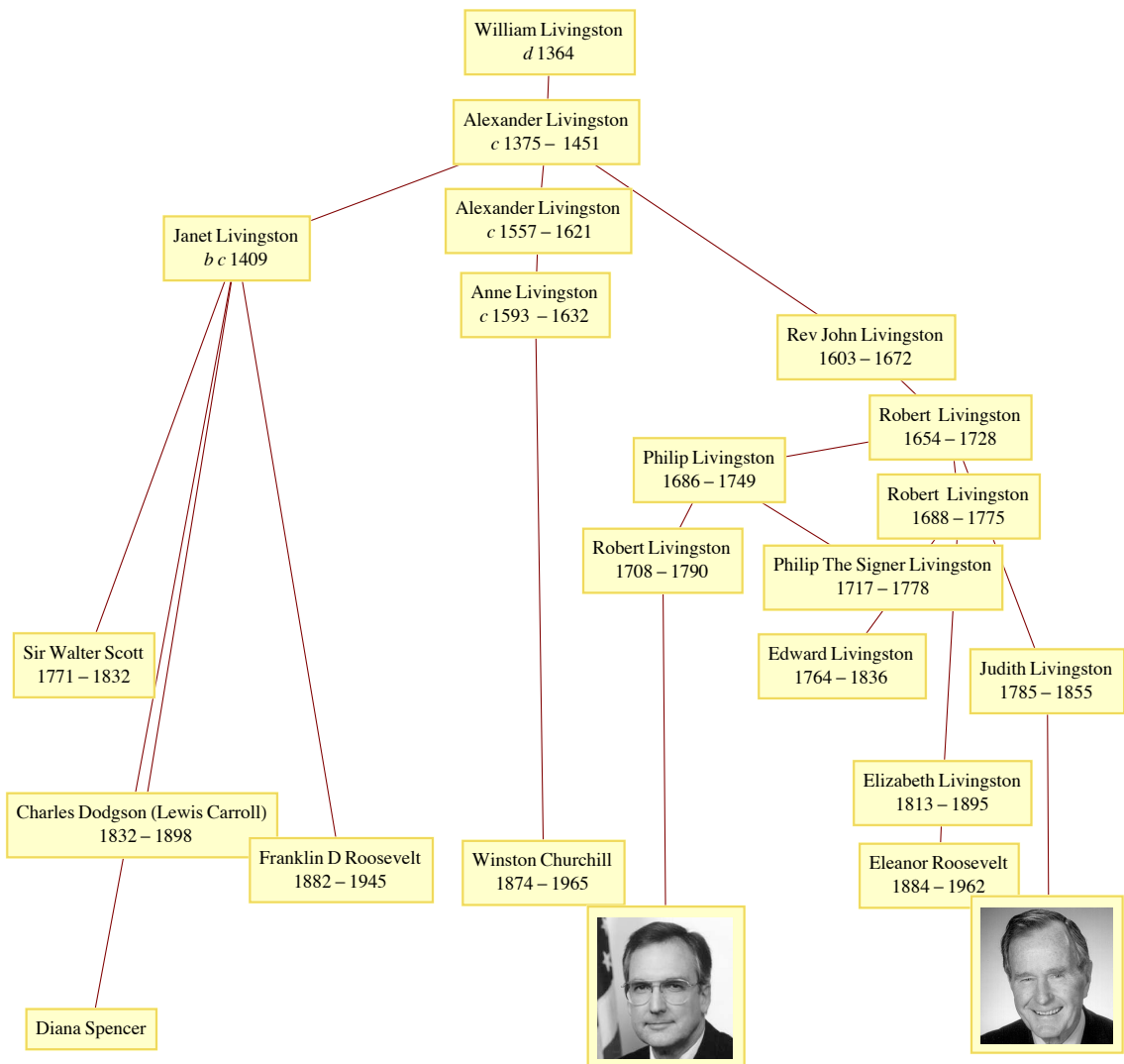
From an orthodox point of view, this means that the MRCA of the head donor and Louis XVII lived 10s of 1000s of years ago. If the mummified head belonged to Henry IV, then this view implies the existence of an exceptional *false-maternity* event somewhere between Henry IV and Marie-Antoinette.



Based on the work of King et al, and their presumed identification of the remains of Richard III, it is accepted that there are 3 false paternity events between Geoffrey Plantagenet and the Somersets and Patrice de Warren. Based on the work of Charlier et al, and the work of Larmuseau et al (2014) detailed in *Genetic genealogy reveals true Y haplogroup of House of Bourbon contradicting recent identification of the presumed remains of two French Kings*, there are 2 false paternity events between Henry IV and the Bourbons, *plus* a false *maternity* event between Henry IV and Marie-Antoinette, which prompted Larmuseau to deny that the identification of the remains of Louis XVI and Henry IV was correctly made. What we have here are a group of incompatible premises: (1) presumed identification of ancient remains; (2) presumed Y-DNA mutation rates; and (3) presumed relatives of the deceased. In the one case (3) is abandoned for the sake of consistency, and in the other it is (1) that is abandoned. But no one is considering that the source of the inconsistency might be the presumption contained in (2) rather than that contained in (3) or (1). Presumption, to modify the classic saying, is the mother of all mistakes.

**The Livingstons of Callendar**

An as yet unknown but *rich* example of the conflict between genealogy and genetics concerns the presumed descendants of a man named 'Leving' (or Levingus), who settled in an area to the southwest of Edinburgh ('Leving's Town' and finally 'Livingston') sometime during the reign of King Edgar (1097 - 1107). Leving's grandson, William was designated in a charter as William the Lion 'of Livingston', and David 11 granted his descendant Sir William Livingston the lands of Callendar in 1346. His great grand son, Sir Alexander Livingston of Callendar (d 1441), was described by Sir Hector L Duff as “a man of transcendent ability and far-reaching ambition”. He was the guardian of young James II of Scotland -during which time he was the effective ruler of the county- and was involved in the famous “Black Dinner” incident of 1440, in which the Lords Douglas were invited to a special dinner organised by Livingston and Lord Crichton, and summarily beheaded. Descendants of the Callendar line include Sir Walter Scott, Rev Charles Dodgson (Lewis Carroll), Winston Churchill, Franklin D Roosevelt, and more recently Princes William and Harry through their mother Lady Diana. But after enjoying 600 years of considerable power and wealth, the Livingston dynasty experienced a catastrophic fall from grace, when following their participation in the unsuccessful Jacobite Rising of 1715, their lands were confiscated and their titles nullified. In 1663, Rev John Livingston, a great grandson of Alexander Livingston, and a preacher of the Reformed Church in Scotland, was exiled to the Netherlands for refusing to swear allegiance to Charles II. He was joined there by his wife, and younger son Robert, and after his father’s death Robert migrated to New York where he established another Livingston dynasty from scratch, and the Livingstons of Callendar became the Livingstons of Livingston Manor. Descendants of the *Manor* line include Philip ‘the Signer’ Livingston, who signed the declaration of Independence, Edward Livingston (1764 - 1836), Mayor of New York, and US Secretary of State, who for his work on the *Louisiana Civil Code* of 1825 Edward was called by Sir Henry Maine "the first legal genius of modern times", and Eleanor Roosevelt. In more recent times, the Bushes, and ex-Senator Bob Livingston (depicted) descend from the Manor Livingston family.



The conflict concerns data collected by the *FTDNA Livingston/MacLea/Boggs Surname DNA Project* reveals the existence of no less than 5 Livingston haplotypes, some of whose owners have excellent genealogical reasons to believe that they derive from an unbroken line of Livingston men leading back to Andrew de Livingston (1240 - 1297), but none of whom match according to Y-DNA mutation rates observed in the present (there are two other Livingston haplogroups that have some claim to descend from the Callendar Livingston line that are also unmatching and unmatched).

Markers	Livingston 1	Livingston 2	Livingston 3	Livingston 4	Livingston 5
DYS393	14	13	13	13	13
DYS390	22	25	24	24	24
DYS19	15	15	14	14	15
DYS391	10	11	10	10	11
DYS385	14 - 16	11 - 14	11 - 14	11 - 14	11 - 14
DYS426	11	12	14	15	14
DYS388	14	12	12	12	12
DYS342	11	10	12	12	12
DYS391 1	12	14	13	13	13
DYS392	11	11	14	14	14
DYS 389 11	29	31	29	29	29
DYS458	16	15	16	16	17
DYS459	9 - 9	9 - 10	9 - 9	9 - 10	9 - 10
DYS455	11	10	11	11	11
DYS454	11	11	11	11	11
DYS447	22	23	22	25	24
DYS437	16	14	15	15	15
DYS448	21	20	19	19	19
DYS449	30	31	27	29	31
DYS464	12 - 13 - 13 - 14	12 - 15 - 15 - 16	15 - 15 - 17 - 17	15 - 15 - 17 - 17	15 - 15 - 16 - 17
DYS460	11	11	11	11	11
YGATA H4	11	11	11	11	11
YCA 11	20 - 20	19 - 23	20 - 23	19 - 23	19 - 23
DYS456	15	16	17	16	15
DYS607	13	18	15	15	15
DYS576	15	18	20	17	19
DYS570	17	18	17	18	18
CDY	37 - 37	34 - 38	36 - 38	36 - 39	35 - 38
DYS442	11	12	12	12	12
DYS438	10	11	12	12	12
Haplogroup	G2a	R1a	R1b	R1b	R1b

Of immediate interest is the Livingston haplotype belonging to the same haplogroup as Richard III and Louis XVI - G1a- and described by the administrators at the *Livingston/MacLea/Boggs DNA Project* as having the "best paper trail claim" to be a direct descendant of the Livingstons of Callendar:

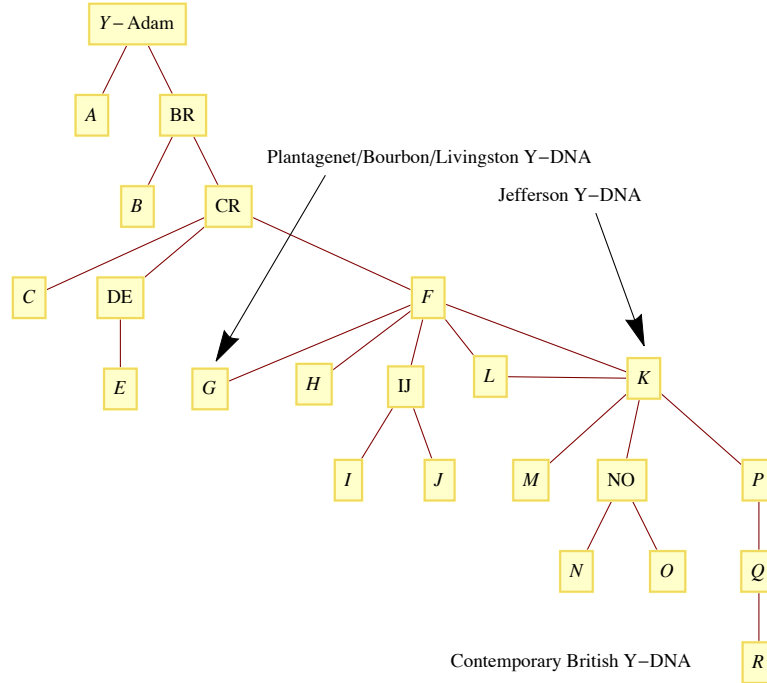
Our first G type Livingston is American, and has the best "paper trail" claim to be a direct descendent of the Livingstons of Clermont in New York and therefore from the Livingstons of Callendar. If the Callendar family really descended from the Dark Ages Living of Living's Town, then all sorts of theories exist about where he might have come from. This G haplotype is extremely unusual at *DYS388* and was in fact not recognized as such by Family Tree DNA's software.

...put simply, if aristocratic families often have unusual Y DNA, either because they come from a very old line, or because they come from a very geographically distant line, then this is such a DNA signature.

## PART II: PAST-FUTURE ASYMMETRIC -CURVED-Y-DNA MUTATION RATES

### Telescoping the Genetic Time-Line

One noticeable characteristic of the Jefferson, Plantagenet, Bourbon, and Livingston Y-DNA is its chronological seniority but its genetic youth (the genetically younger haplogroup is the group with the fewer SNPs):



It is mathematically possible then that British Y-DNA groups are mutated forms of rare haplogroups prevalent in Britain in earlier centuries, i.e. that rare haplogroups in Britain are traces of British haplogroups most of which have since mutated. But on our present assumptions about Y-DNA mutation rates *there is no such physical possibility* - SNP mutations on which haplogroups are based are supposed to be glacially slow and, as the graphic below indicates, the MRCA of the ancient and modern Jeffersons/ Plantagenets/Livingstons supposedly lived, not 1000s of years ago, but *10s of 1000s-* of years ago. But how much confidence should we have in these mutation rates, and in the assumption that they were always thus? After all, they are based on observations made in the tiny window of the near-present, and extrapolated more or less on faith to the unobserved and vast window of the distant-past. Imagine a cycle that turns at a seemingly constant rate within the context of the present, but in fact turns ever more slowly in the direction of the past, and let this cycle represent a clock for which times passes more rapidly in the direction of the future, and thus follows an inwardly spiraling motion. In terms of mathematical physics, we are imagining that there is an asymmetrical relationship between the past and the future, so that time is not reversible, and experiments performed in the present will not necessarily yield the same results as these same experiments performed at an earlier time. We are very weary of casting doubt on the uniformity of nature in other parts of the universe because, whilst it is quite possible that nature is dis-uniform from place to place and time to time, we depend on assumptions of uniformity to make predictions about these distant areas. But -as Einstein's Theory of Relativity in particular teaches us- dis uniformity is fine so long as there is a mathematical way to correct for the dis-uniformity between two points of view and translate either one into the other, and if genealogy rather than genetics is right when it comes to the genealogical-genetic conflicts described above, one way to account for the discrepancy is with the idea of past-future asymmetry and a notion time slowing and mutation rates speeding up on the direction of the past. In this case, the cycles of our clocks are surreptitiously spiralling inwards, and the assumption that they turn in the present as they did in the past results in an overestimation -a potentiality *gross* overestimation- of the total number of hours that have elapsed on these clocks (again, this is fine if we know the growth rate of the difference that exists between a uniform and dis uniform clock and can therefore calculate the amount of dis-uniformity). The significance of Richard III's DNA for this question, and for genetic genealogy generally, is that (at the time of writing) his is the only ancient genome belonging to someone with identifiable living relatives to be sequenced. We are provided then with an opportunity to make a Y-DNA comparison between family members separated in time by 5 centuries, and but for the example of Richard III, we are -from an empirical point of view- speculating as to what such a comparison might reveal.

Lets be more specific... A rate of change may be constant or it may be variable (follow a straight line or a curve). Also



it may be constant + variable (follow a straight but rough line) or variable + variable (follow a rough curve). With our anomalous findings in mind, we can consider the possibility that mutations rates are best represented by jagged curves that possess a decreasing slope, and so that DNA mutations occur more frequently at first and ever less frequently thereafter.

Let

$n$  = number of STR mutations

$m$  = sum of mutation rates

$g$  = the length of a generation

TMRCAs = years before present to the time the most recent common ancestor

and we have the simple formula whose mutation rates follows straight lines and which broadly reflects the way in which the TMRCAs is usually computed:

$$(f1) \text{ Present year} - \frac{gn}{2m} = \text{TMRCAs}$$

Applying (f1) to the 3 Livingstons that at least share the same haplogroup, we arrive -on the assumption of a mutation rate of 0.002- at TMRCAs of 189, 415 BC, and 215 BC:

$$2017 - \frac{30 \times 9}{2 \times 0.074} = 192.676$$

$$2017 - \frac{30 \times 12}{2 \times 0.074} = -415.432$$

$$2017 - \frac{30 \times 11}{2 \times 0.074} = -212.73$$

□	Livingston 3	Livingston 4	Livingston 5
Livingston 3	□	192	-415
Livingston 4	192	□	-212
Livingston 5	-415	-212	□

It is thus impossible that any more than 1 of these men is a *bona fide* Callendar Livingston because -as indicated- the eponymous founder of the Callendar Livingstons lived during the reign of Edgar (1097 - 1107). The time-scales naturally blow out *much further* if we consider the Callendar Livingstons that *don't* share the same haplogroup. An also simple formula that reflects the possibility that mutation rates follow *rough curves* rather than straight lines is

$$(f2) \text{ Present year} - \pi\left(\frac{gn}{2m}\right) = \text{TMRCAs}$$

The symbol  $\pi$  stand for a function that gives the number of prime numbers not greater than some integer. For example there are 25 primes not greater than 100, 168 not greater than 1000 and so on.

### Livingston 3

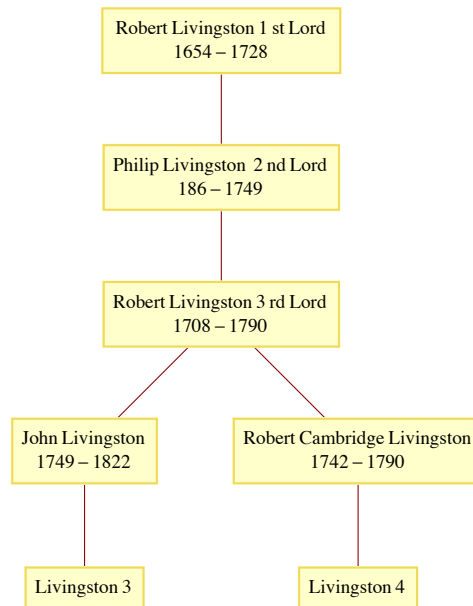
...has a family tree connecting him to the well-known Livingstons of Clermont in New York, via John Livingston, the son of Robert Livingston the "third lord" of Clermont, who was in turn grandson of Robert Livingston the "first lord".

### Livingston 4

...is said to descend from the Livingstons of Clermont via two sons of "Robert of Clermont", 3rd lord of the manor, Robert "Cambridge" Livingston (line carrying the Livingston paternal DNA), and John "of Oak Hill" Livingston (through two of his grand-daughters).

The great-grandfather of the participant was Col. Charles Edward Livingston of Red Hook, New York, who served with the Union N.Y. 76th Infantry Volunteers during the American Civil War. He was the son of Robert Francis Livingston, a Surveyor and Civil Engineer, who, in turn, was the son of Robert Swift Livingston. Robert Swift Livingston was the son of Robert "Cambridge" Livingston and Alice Swift.

The MRCA of Callendar's 3 and 4 is according to this information Robert Livingston 3rd Lord of Clermont Manor 1708 - 1790



and (f2) and a 37 marker comparison gives us a TMRCA of 1736 using the same assumptions that produced the times above.

$$2017 - \pi\left(\frac{30 \times 9}{2 \times 0.074}\right) = 1736$$

Note that while changing *g* or *m*, and modifying other assumptions, changes the predicted times dramatically, (f2) *always* predicts a common ancestor who lived much more recently than the time predicted by (f1). The difference made by the addition of the symbol  $\pi$  can be demonstrated by applying it to the estimated time of the origin of the Plantagenet/Livingston/Bourbon Y-DNA - between 10000 and 23000 ago.

$$1950 - \pi(23\,000) = -614$$

If the estimation is the right one based on mutation rates observed in the present, then (f2) says -if we take the larger date- that first person with the Plantagenet/Livingston/Bourbon Y-DNA may have lived, not in the impossible-to-imagine 21,050 BC, but around 614 BC, in the time of the 26th - 27th Dynasty of Egypt. Applying (f2) to the possible times of origin of Y-DNA based on mutation rates observed in the present to Y-DNA haplogroups, we arrive at the following -necessarily speculative- but telling chronology:

Haplogroup	Possible Time of Origin (ybp)	Possible Time of Origin Accordi to f2 (ybp)	BCE
A (Y - ADAM)	60 000 - 90 000	8713 - 6057	6763 - 4107
E	48 000	4946	3409
J	47 000	4581	2996
K	47 000	4851	2901
K2 (T)	39 800 - 45 500	4907 - 4707	2767 - 2233
E1b1b	42 000	4454	2504
I	31 - 35 000	3732 - 3340	1782 - 1390
R	27 000	2961	1011
R1a	22 - 25 000	2762 - 2454	812 - 514
G	10 - 23 000	2564 - 1299	614 BC - 721 AD
J2	15 - 22 000	2464 - 1754	514 BC - 196 AD

### The Riemann Hypothesis and the Arrow of Time

This flies in the face of everything we think we know about chronology, and there are ancient remains that seem to imply that this chronology is wrong, but like (f1), all of the calculations used to produce these chronologies make certain dubious assumptions about the nature of energy and time. Let me briefly explain... Richard Feynman invites us to imagine that atoms are divided into blue-coloured and white-coloured varieties, and separated into compartments. If the separation is removed, then just as blue dye turns water a luke-blue colour, the atoms form a luke-blue mixture. He observes that individual collisions provide no clue as to the irreversibility of the mixing process, but that studying a film of the mixing played in reverse reveals that

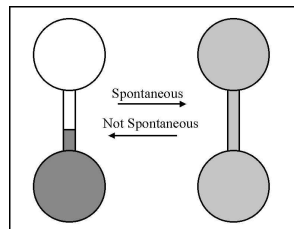
...every one of the collisions is absolutely reversible, and yet the whole moving picture shows something absurd, which is that in the reverse picture the molecules start in the mixed condition... and as time goes on, through all the collisions, the blue separates from the white...

He goes on to say that

...it is not natural that the accidents of life should be such that the blues will separate themselves from the whites...

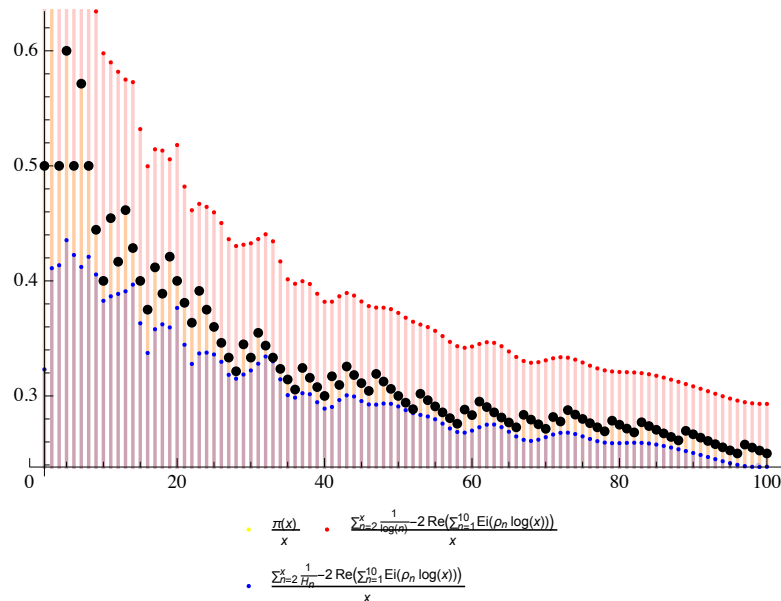
Yes, but why isn't it natural? The one-way nature of this process is familiar to us from the experiment in which a gas is confined to one of two compartments.

The one-way nature of this process is familiar to us from the experiment in which a gas is confined to one of two compartments.



If the separation between the compartments is removed, then the gas spontaneously distributes itself in a uniform manner throughout the two compartments, but it does not spontaneously revert to the separated state. More familiar still, is the breaking of an egg. We never see a broken egg spontaneously reassemble, and there is no way to reassemble an egg after it has been broken (“All the kings horses and all the kings men couldn't put Humpty together again.”). But although both these processes involve a one-way direction when viewed from a sufficiently global perspective, they can go either way when viewed from a sufficiently local perspective: the individual atoms comprising the gas molecules might just as well go from compartment *B* to compartment *A* as from compartment *A* to compartment *B*, and if we study the individual atoms comprising Humpty Dumpty we get no clue as to the fact that Humpty cannot be reassembled. It is only by considering a sufficiently large *group* of atoms that the loss of energy-density known as ‘entropy’ is found to involve a necessarily one-way direction (there is a well known distinction between those large-scale phenomena that are governed by classical mechanics, and those small-scale phenomena that are governed by quantum mechanics, and in the similar way that a galaxy is seen to take on a one-way spiral shape only from a sufficient distance, it is at the distance of the classical perspective that the one way-direction of entropy makes itself known). A film of a broken egg reassembling seems absurd, but in what does this impression of absurdity consist? Is it merely unfamiliarity with the reverse direction? If we play a film depicting the increase of prime numbers in the number line, we see something that to the mathematician's eyes is absurd. And the mathematician knows that this impression of absurdity *isn't* merely a matter of his unfamiliarity with the reverse direction; he knows from ‘the asymptotic law of distribution of prime numbers’ (which tells that the primes thin out and was proved independently by Hadamard and de la Vallée Poussin in 1896) that this is what *must* happen, that it is mathematically necessary that the repetition of a unit be accompanied by a global decrease in prime-density. This suggests the possibility that reproduction in mathematics and in life is subject to entropy - the possibility of past-future asymmetry. If this idea is *true*, and nature's clock is a clock that slows in the direction of the past, we will find *all* of the usual methods for estimating the age of ancient things to be prone to exaggerate this age. Take for example the method of radiocarbon dating. If the rates at which atomic nuclei emit energy follow the primes rather than the integers, then the assumption that the ratio of Carbon 12 to Carbon 14 decreases at a uniform rate will tend to lead to an exaggerated idea of the period of time that has elapsed between the death of a plant or animal and the measurement of this ratio in the present. If nature's clock slows in the direction of the past, then the accuracy of *any* estimate of an object's age based on the assumption of a past-future time symmetry will tend to be inversely proportional to the age of that object. Straight mutation rates are a special case of curved mutations for the present -the present is a locally flat section of a globally curved manifold- and a younger object in the context of such a manifold will be well accounted for by the assumption of past-future symmetry. But the older the object, the more likely it is that any estimate of its age based on the assumption of past-future symmetry will be inflated.

As indicated, the asymptotic law of distribution of prime numbers tells us that the primes thin out, and the Riemann Hypothesis is an extension of the asymptotic law of distribution of prime numbers. The latter says, not merely that the primes thin out, but that changes in prime-density are random, and that they cannot exceed upper and lower bounds marked in red and blue in the graphs below:



The graph above depicts several interlocking ideas:

- Globally speaking, prime-density decreases as a function of arithmetic increase (prime-density follows curves whose steepness decreases)
- Local fluctuations in density -which involve either a random increase or a decrease in prime-density- decrease as a function of arithmetic increase (these curves are *rough curves* whose roughness decreases)
- There are limits on both the global rate of decrease and on the frequency and size of the local fluctuations (the curves can't be arbitrarily steep or rough)

These ideas cast light on the question of why the symmetric direction of things governed by quantum mechanics gives way to the asymmetric direction of things governed by classical mechanics, and they also give us the following refinement of (f2):

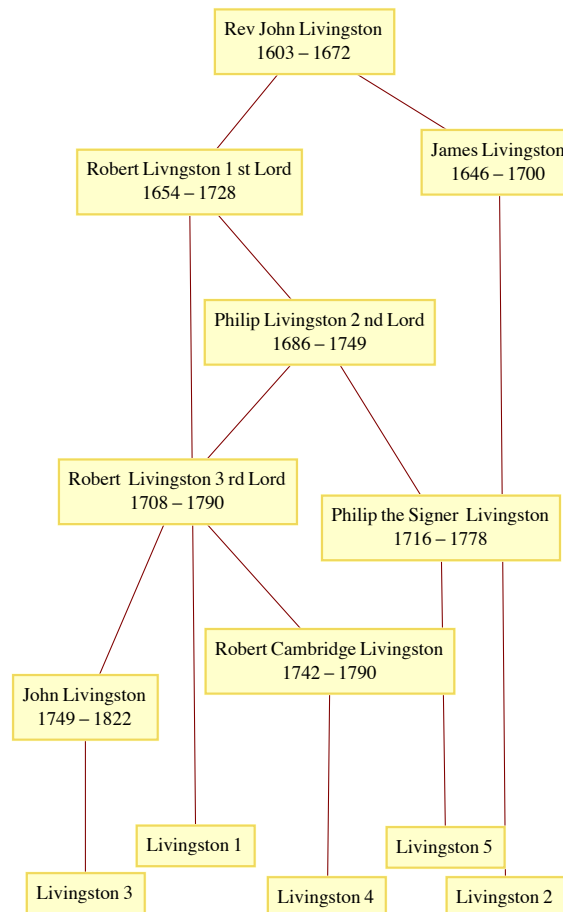
$$(f3) \text{ Present year} - \sum_{n=2}^{\frac{gn}{2m}} \frac{1}{\log(n)} \leq \text{TMRCA} \leq \text{Present year} - \sum_{n=2}^{\frac{gn}{2m}} \frac{1}{H_n}$$

$\pi(x)$  is what is called a 'step function', and it has been set up so that the jump from one step to another takes place only when a prime number appears in the number line. As we travel down the line, we find that these jumps become rarer, for the primes thin out. Despite this global decrease in prime-density, there are local irregularities. The red and blue colored staircase-curves keep the slope of the central staircase from being either impossibly steep (steeper than the red staircase) or impossibly gentle (less steep blue than the blue staircase). This means that they serve as criteria by reference to which it can be judged whether a change to the steepness of the central staircase represents a local decrease or rather a local *increase* in prime-density. If we identify prime-density with genetic simplicity, it follows that while the global direction of the Y-DNA tree is toward the upper bound and further genetic complexity, any local direction may with equal probability be toward either bound. If we accept the proposal that the mutation rates of SNPs correspond to the primes in the manner indicated by (f2) and by (f3), we must reject the assumption that genetic mutations occur at a constant rate (genetic mutations are curved rather than straight) *and* we must reject the assumption that they always follow the one-way simple-to-complex direction of the ISOGGY-DNA tree (genetic mutations are roughly curved not smooth).

Their numbers are all over the place, but we find that in the *light* of (*f3*) it is mathematically possible with the use of (*f2*) and (*f3*) that all 5 Livingstons are -regardless of their haplogroups- from the Livingston family traceable to Andrew de Livingston (1240 - 1297):

	Livingston 1	Livingston 2	Livingston 3	Livingston 4	Livingston 5
Livingston 1		1251 - 1309	1322 - 1375	1369 - 1420	1466 - 1510
Livingston 2	1251 - 1309		1298 - 1353	1204 - 1265	1204 - 1265
Livingston 3	1298 - 1353	1322 - 1375		1729 - 1756	1643 - 1675
Livingston 4	1204 - 1265	1369 - 1420	1722 - 1749		1669 - 1699
Livingston 5	1204 - 1265	1466 - 1510	1643 - 1675	1669 - 1699	□

But whilst the TMRCAs offered by (*f3*) fit the genealogical data better -far better- than those offered by (*f1*), they nonetheless fail to fit it in a way that fully agrees with genealogy. Livingston 1 (G2a), who has the “best paper trail”, descends from Robert Livingston the 1st Lord of the Manor (1654 - 1728), who was a descendant of the Callendar Livingstons via his father Rev. John Livingston. William Cutter in the *Genealogical and Family History of Central New York* writes that the ancestor of Livingston 2 (R1a) is said “by good authorities, to have been a lineal descendant of Rev. John Livingston through the latter’s son James (1662 - 1700.” As indicated, Livingston’s 3 and 4 (R1b) both have strong claims descend from Robert Livingston the 3rd Lord of the Manor (1705 - 1790), and Livingston 5 (R1b) is thought to be related to Philip ‘The Signer’ Livingston (1716 - 1778), a son of the 2nd Lord. The MRCA of all 5 Livingstons then is Rev. John Livingston (1603 - 1672), but it is mathematically *impossible* using (*f3*) to arrive at a MRCA who lived at this time.



Working with the data for Richard III and Somersets 1, 2, 4, and 5, we see that while our method yields an accurate TMRCAs with innocuous assumptions as to generation length and mutation rate

Edward III (1312 – 1377)

$$2017 - \pi \left( \frac{27 \times 18}{2 \times 0.046} \right) = 1316$$

$$2017 - \sum_{n=2}^{\frac{27 \times 18}{2 \times 0.046}} \frac{1}{\log(n)} = 1299.9$$

$$2017 - \sum_{n=2}^{\frac{27 \times 18}{2 \times 0.046}} \frac{1}{H_n} = 1354.96$$

it is nonetheless impossible to get everyone's TMRCA's come out right. Richard III and Somerset 1:

$$2017 - \pi\left(\frac{27 \times 15}{2 \times 0.046}\right) = 1418$$

The mismatch between Somersets 1, 2, 4, 5 is at most 2 markers and so

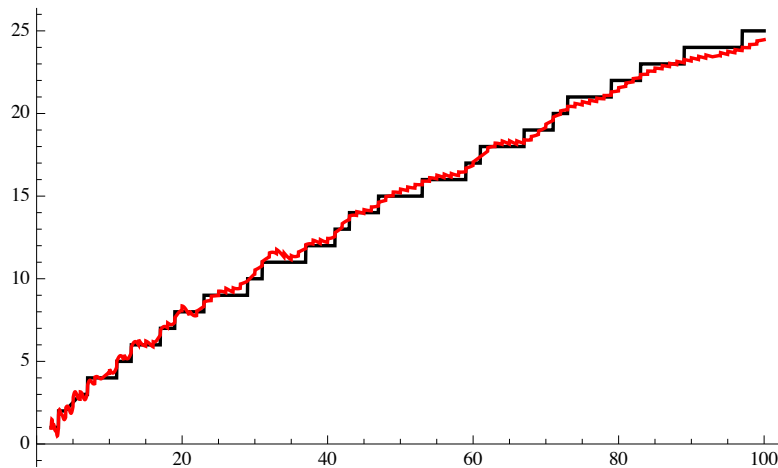
$$2017 - \pi\left(\frac{27 \times 1}{2 \times 0.046}\right) = 1955$$

and the MRCA of these men is Henry Somerset (1744 - 1803). The MRCA of Somerset 1 and Somersets 2 - 5 is the same man, and they are mismatched by 20 markers:

$$2017 - \pi\left(\frac{27 \times 20}{2 \times 0.046}\right) = 1244$$

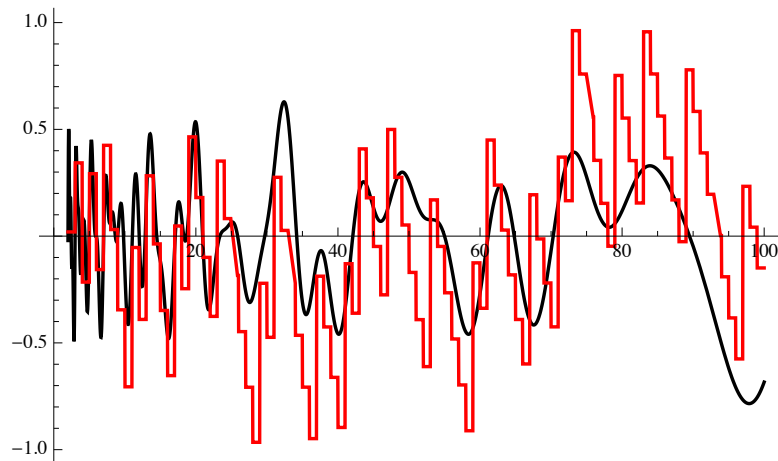
For a solution to these problems, consider that we can simulate  $\pi(x)$  by summing waves of various kinds using the function

$$f(x) := \frac{\sum_{n=2}^x \frac{a_{1-x+1}}{H_n} + \sum_{n=2}^x \frac{a_{2-x+1}}{\log(n)} + \dots}{n}$$



From another perspective on the same process, we see that we are combining the black waves arising from the differences between  $\pi(x)$  and  $\sum_{n=2}^x \frac{a_{1-x+1}}{\log(n)}$  and  $\sum_{n=2}^x \frac{a_{2-x+1}}{H_n}$  so that they increasingly take on the shape of the yellow waves corresponding to the superposition

$$2 \operatorname{Re}\left(\sum_{n=1}^{\infty} \operatorname{Ei}(\rho_{-n} \log(x))\right)$$



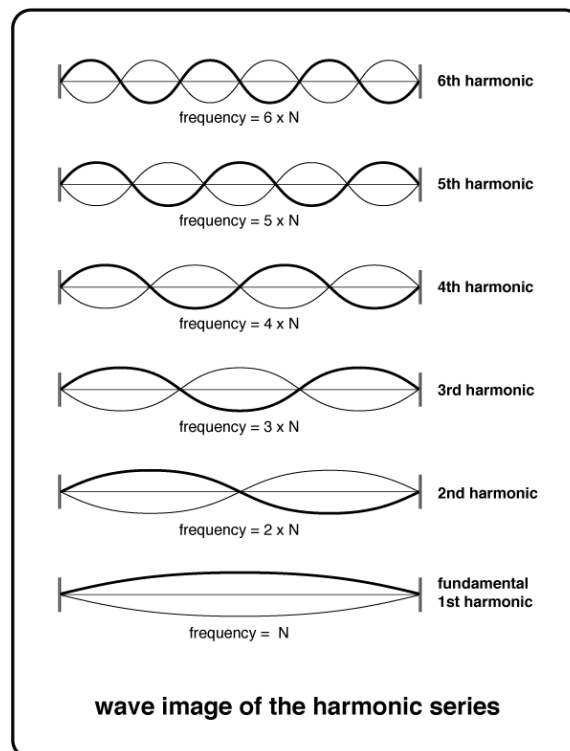
Littlewood showed in 1914 that the difference between  $\sum_{n=2}^x \frac{1}{\log(n)}$  and  $\pi(x)$  oscillates infinitely about the  $x$ -axis. But he *failed* to consider whether the same is true of the difference between  $\sum_{n=2}^x \frac{1}{\log[n]} - 2 \operatorname{Re}(\sum_{n=1}^x \operatorname{Ei}(\rho_n \log(x)))$ . Long wave lengths make it difficult to survey the oscillatory properties of the differences corresponding to

$$-2 \operatorname{Re} \left( \sum_{n=1}^x \operatorname{Ei}(\rho_n \log(x)) \right) + \sum_{n=2}^x \frac{a_{n-1}}{\log(n)} - \pi(x)$$

and

$$-2 \operatorname{Re} \left( \sum_{n=1}^x \operatorname{Ei}(\rho_n \log(x)) \right) + \sum_{n=2}^x \frac{a_{n-1}}{H_n} - \pi(x)$$

but the Riemann Hypothesis -which clearly says that the real part of  $\rho_n$  in the superposition  $2 \operatorname{Re}(\sum_{n=1}^x \operatorname{Ei}(\rho_n \log(x)))$  is equal  $1/2$ - is equivalent to saying also that, if and only if  $a_n = 1$ , then these wave have fundamental frequency, i.e. there can be *no* intersection of the  $x$ -axis:

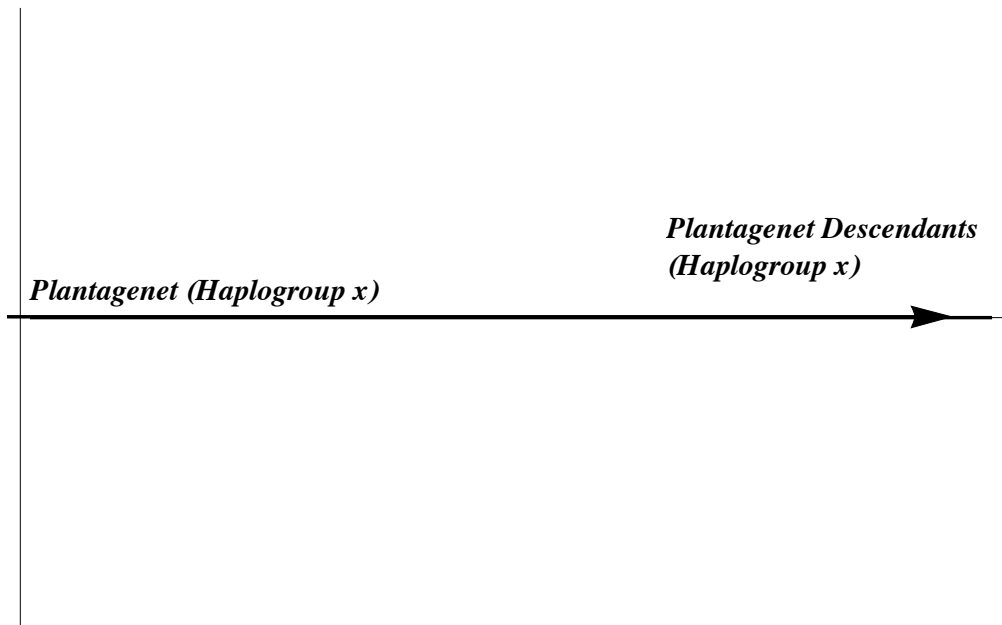


If by contrast  $a_n \neq 1$ , then certain differences oscillate infinitely. From here comes a foundation of idea that patrilineal lines -and lines generally- are more correctly regarded as waves - more particularly as *superpositions* of waves. From the notion of wave-like Y-DNA lines comes the idea of an updated formula for the TMRCA:

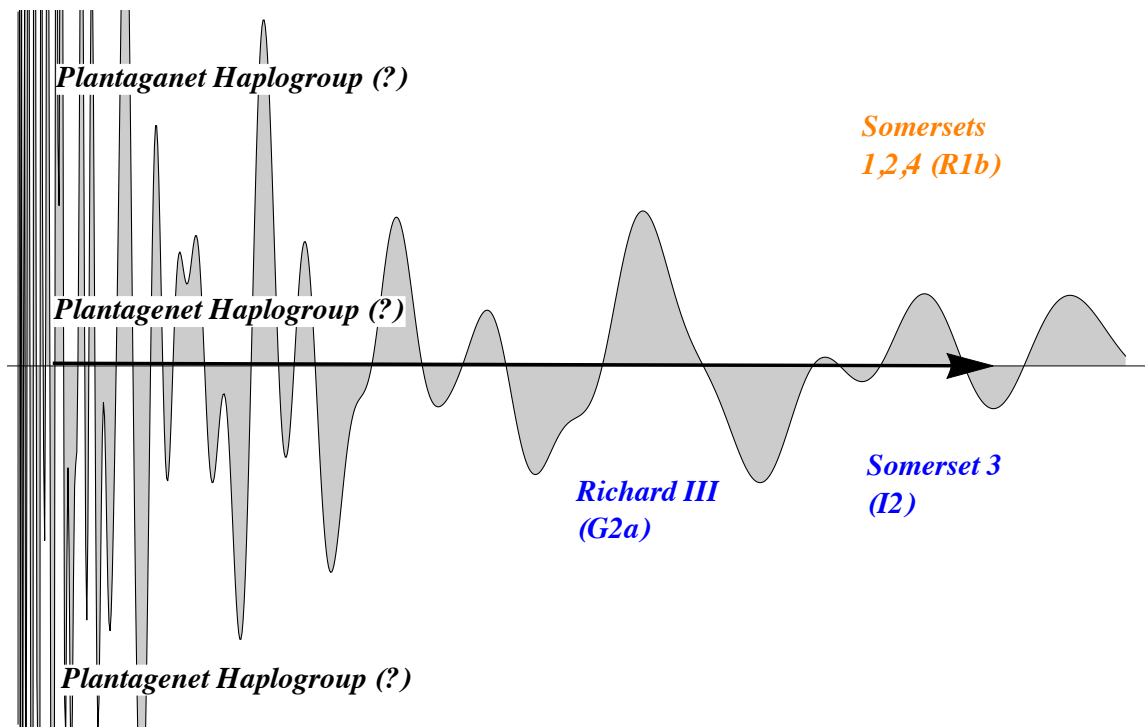
$$(f4) \text{ Present year} - \sum_{n=2}^{\frac{x}{a_1}} \frac{a_1}{\log(n)} \leq \text{TMRCA} \leq \text{Present year} - \sum_{n=2}^{\frac{x}{a_2}} \frac{a_2}{H_n}$$

From *here*, we simply input the right TMRCA and let  $a_1$  and  $a_2$  vary accordingly. Every well-trained geneticist will scoff at the proposal that it is possible to get from -say- G to R in any amount of time, since R isn't even an off-shoot of the G-branch of the Y-DNA tree. But there are a number of possibilities here: in the case of the Plantagenets, one is that the Y-DNA of the MRCA of Richard III and the Somersets -Edward III- belonged to F, another is that he belonged to G and a back mutation to F took place between Edward III and the Somersets. In the case of the Bourbons we know that the MRCA of the contemporary Bourbons Louis XVI belonged to G, and so it might be deemed inevitable that a back mutation to F is required to get to R. In the The Livingstons case, perhaps the MRCA of the contemporary Livingstons -John Livingston- belonged to F, which produces G and R, or perhaps he belonged to G or something else, and there were back mutations permitting the transition to R.

Curved, rough, mutation rates make such transitions mathematically and physically possible. Traditional view of genetic inheritance:



My view of genetic inheritance:



A knee-jerk objection to this approach to genetics might be “so what, this tell us nothing, because we could use this technique to produce more or less *any* TMRCA we like”, but the objection is baseless. We have seen that by adding functions of the form  $\sum_{n=2}^x \frac{a_1}{\log(n)}$  and  $\sum_{n=2}^x \frac{a_2}{H_n}$  we are able to simulate  $\pi(x)$ , from which it follows that the rigid  $\pi(\frac{x}{2^m})$  can be regarded as a sum of these more fluid sums, and therefore as imposing a strict constraint on the fluidity of these sums. And we can and must go further:  $\pi(\frac{x}{2^m})$  is associated with the canonical arithmetic progression 1, 2, 3... but an infinite number of prime-staircases can be generated by use of the formulation  $qn + a$ , and a result known as 'Dirichlet's Theorem' tells us that if  $a$  and  $q$  share no common factor other than 1 -if they are “co-prime”- then the progression  $a, a + q, a + 2q, a + 3q...$  contains infinitely many primes.



Each of these progressions is associated with a function -a so called "L-function"- of the form

$$f(x_{\cdot}) := \sum_{n=1}^{\infty} \frac{\chi_{m,k}(n)}{n^s}$$

and only in the most prime-dense canonical progression 1, 2, 3... is  $\chi_{m,k}(n)$  equal to 1. So in addition to the prime staircase associated with the progression  $a = 0$  and  $q = 1$ , there are an infinite number of prime staircases associated with co-prime values of  $a$  and  $q$ , each of which is constrained by a pair of staircases, and each of which possesses a different slope, and climbs in a different way. Each of these progressions possesses a certain maximum and minimum prime-density in the same way that the canonical progression does. And each such progression is associated with a pair of waves whose frequency is fundamental. If we associate sub-Y-DNA trees with these less prime-dense progressions, then the unifying principle of these sub-trees is the maximum prime-density of the tree in question, a maximum that determines -in a comparable way that in which the wattage of a light bulb determines the intensity of the light that the bulb can output- the genetic flexibility of the sub-tree in question. With a knowledge of  $\chi_{m,k}(n)$ , and this maximum, it is possible to determine which mutations are possible for a sub-tree, and which are not. The fluidity of the sums associated with ( $f4$ ) is thus constrained by the maximum prime-density of the canonical tree, but also by the maximum prime-density of the relevant sub-tree. Reviewing Livingstons 3 and 4 with this idea in mind:

MRCA = Robert Livingston (1708 – 1790)

$$n = 9$$

$$m = 0.002$$

$$\frac{30 \times 9}{2 \times 0.074} = 1824.32$$

$$2017 - \sum_{n=2}^{1824.32} \frac{1.06062}{\log(n)} = 1708$$

$$2017 - \sum_{n=2}^{1824.32} \frac{0.858003}{H_n} = 1790$$

Livingstons 3 (R1a) and 1 (G):

MRCA = Rev. John Livingstone 1603 – 1672

$$n = 24$$

$$m = 0.002$$

$$\frac{30 \times 24}{2 \times 0.075} = 4800$$

$$2017 - \sum_{n=2}^{4800} \frac{0.626742}{\log(n)} = 1603$$

$$2017 - \sum_{n=2}^{4800} \frac{0.566426}{H_n} = 1672$$

Reviewing Richard III and the Somersets with this new approach:

MRCA = Edward III (1312 – 1370)

$$n = 18$$

$$m = 0.002$$

$$\frac{27 \times 18}{2 \times 0.046} = 5282.61$$

$$2017 - \sum_{n=2}^{5282.61} \frac{0.983129}{\log(n)} = 1312$$

$$2017 - \sum_{n=2}^{5282.61} \frac{0.9926}{H_n} = 1370$$

$$n = 15$$

Somerset 3:

$$n = 15$$

$$m = 0.002$$

$$\frac{30 \times 15}{2 \times 0.046} = 4891.3$$

$$2017 - \sum_{n=2}^{4891.3} \frac{1.05023}{\log(n)} = 1312$$

$$2017 - \sum_{n=2}^{4891.3} \frac{1.03372}{H_n} = 1377$$

Somerset 3 doesn't match Somersets 1, 2, 4, and 5 in the traditional sense of the term 'match', prompting geneticists to appeal again to the catch-all 'false paternity event'. Somersets 1, 2, 4, and 5 match closely - there are at most 2 mismatched markers out of 23 between them. In the case of the 1 marker mismatch, we can hone in on their supposed MRCA Henry Somerset (1744 - 1803) in this way:

Henry Somerset 1744 - 1803

$$n = 1$$

$$m = 0.002$$

$$\frac{30 \times 1}{2 \times 0.046} = 326.087$$

$$2017 - \sum_{n=2}^{326.087} \frac{3.75507}{\log(n)} = 1744$$

$$2017 - \sum_{n=2}^{326.087} \frac{3.39641}{H_n} = 1803$$

Somersets 1, 2, 4 and 5 differ from Somerset 3 by 20 out of 23 markers:

Henry Somerset 1744 - 1803

$$n = 20$$

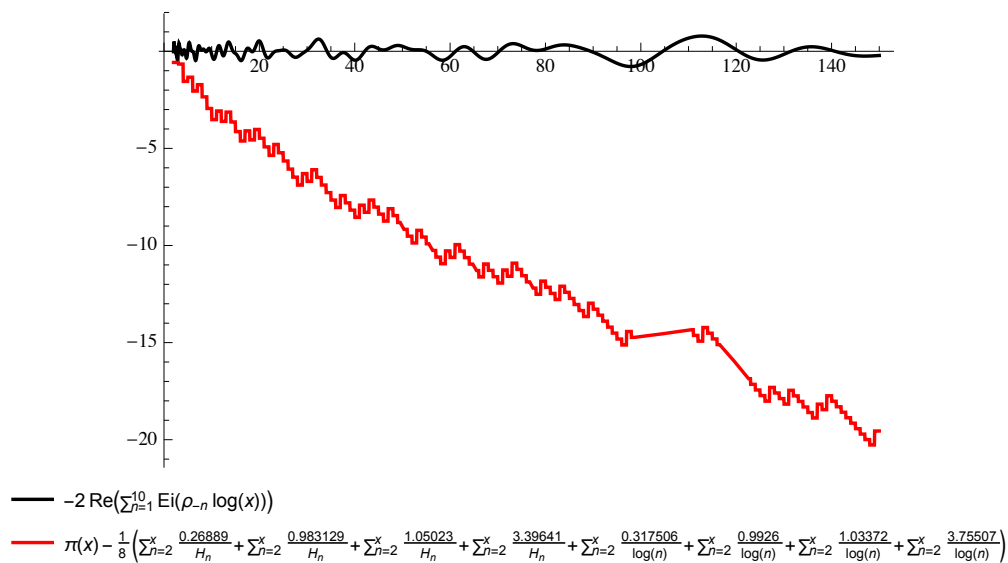
$$m = 0.002$$

$$\frac{30 \times 20}{2 \times 0.046} = 6521.74$$

$$2017 - \sum_{n=2}^{6521.74} \frac{0.317506}{\log(n)} = 1744$$

$$2017 - \sum_{n=2}^{6521.74} \frac{0.26889}{H_n} = 1803$$

The Plantagenet data then gives us the red wave below:



It appears to be out of bounds, but it is based on incomplete data - it will change as more markers and more haplotypes are added in. The question by which the veracity of a TMRCAs yielded by ( $f4$ ) stands or falls of is that of whether such a superposition of TMRCAs increasingly tends to be within bounds laid down by the Generalized Riemann Hypothesis as the number of waves tends to infinity, and by itself this wave gives *no* indication that implies the existence of any breaks in the official Plantagenet paternal 'line'. The same can be said for all of the putatively broken patrilineal lines we have examined so far.

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