DNA Misconceptions

Kelli Bergheimer
kbergheimer@gmail.com

Sometimes our misconceptions can lead us astray! To make accurate conclusions about the genetic relationships to our matches, we need to make sure we set aside confirmation bias and our assumptions.

Common misconceptions and links for more information:

Siblings share the same DNA.
Brothers and sisters each inherit 50 percent of mom's DNA and 50 percent of dad's, but not the same 50 percent unless the siblings are identical multiples.
https://www.genealogyexplained.com/dna-testing/do-siblings-have-same-dna/

Siblings have the same ethnicity estimates.
Ethnicity estimates are based on the DNA you have inherited. Your siblings can have slightly different or very different ethnicity estimates based on what they inherited and you did not.
https://blogs.ancestry.com/cm/whos-more-irish-you-or-your-sibling/

Your ethnicity estimates will match your known genealogy.
Remember, some of your known genealogy hasn't been verified by DNA testing, so it's possible your known genealogy is not correct. In general, ethnicity is more representative at the continental level rather than the country level.
https://www.legacytree.com/blog/introduction-to-genetic-admixture

All your ancestors' ethnicities will be in your ethnicity report.
Many of the ancestors in your family will not be represented in your ethnicity report based on what you inherited and a genealogical timeframe.
https://www.yourdnaguide.com/ydgblog/dna-ethnicity-estimation-reference-panels

There is no way to guess how closely two men are related in Y-DNA testing.
FamilyTreeDNA has a chart to show Expected Relationships with Y-DNA STR Matches.
https://www.familytreedna.com/

Small segments are genealogically relevant for determining MRCA (most recent common ancestor.)
It's quite possible that a small segment can lead you to a MRCA; however, proving it is another issue. The trouble with small segments is the relationship is far back in time and most people do not have a complete-enough tree to be able to rule out multiple relationships.
https://thegeneticgenealogist.com/2022/08/07/an-in-depth-analysis-of-the-use-of-small-segments-as-genealogical-evidence/

Sorting matches is the same as filtering matches.
Sorting is the process of dividing up shared matches into genetic groups. Filtering is choosing one DNA match to a particular line and using that DNA match to remove other matches from consideration to answer a research question. Most of the testing companies offer filtering options to use on our match lists.
https://customercare.23andme.com/hc/en-us/articles/212170718-Sorting-and-Filtering-DNA-Matches-in-23andMe-DNA-Relatives

Broad v. narrow definition of triangulation.
Triangulation is three or more people sharing a segment that possibly leads back to an ancestral couple. But technically, it's not triangulation is all three people inherited this DNA segment from the same close ancestor.
https://thegeneticgenealogist.com/2016/06/19/a-triangulation-intervention/

23andMe haplogroups are as accurate as FamilyTreeDNA.
Comparing haplogroups from 23andMe and FamilyTreeDNA can definitely show two men are not related to each other on the patrilineal line. To determine if two men are related on the patrilineal line, check whether one haplogroup is upstream or downstream from another.
https://www.genetichomeland.com

23andMe Ancestry Compositions visually shows maternal as one whole copy and paternal as another whole copy of the chromosome.
It may be that's true, but the top copy could be maternal in Chromosome 1 and the bottom copy could be paternal in Chromosome 1, but they can flip in other chromosomes. If you have a parent in the database, the tool will phase your DNA.
https://customercare.23andme.com/hc/en-us/articles/212860507-Chromosome-Painting-23andMe-Ancestry-Results

The surname trap: Two people are DNA matches, and one has Reeds and the other has Reeds, so we are related through the Reed.
Maybe that is the case if the matches are close, for example, 1C, 1C1R, or H1C, but if matches are more remote, use other evidence to build your case. You could be related on more than one ancestral line.
https://dna-explained.com/2018/12/18/when-dna-leads-you-astray/

The relationship category provided by the testing company is the actual relationship between two testers.
The relationship categories are default categories of relationship, but many other relationships are possible. Use the Shared cM Project at DNAPainter to see what relationships need to be ruled in or ruled out.
https://dnapainter.com/tools/sharedcmv4
https://www.legacytree.com/blog/genetically-equivalent-relationships
https://thednageek.com/the-limits-of-predicting-relationships-using-dna/

Assuming a full relationship to a match in your match list.
Sometimes we assume we know how someone is related to us, but we don't check that the amount of shared cMs reported matches a full or half relationship.
https://support.ancestry.com/s/article/Assigning-Relationships-to-AncestryDNA-Matches

Everyone adopted knows they are adopted.
Sometimes adoptees discover they have different biological parentage by taking a DNA test. Be gentle in your messages and helpful in your responses. The Board for Certification of Genealogists has a code of ethics to help with some of these situation.
https://bcgcertification.org/ethics-standards/code/

My family tree is correct, the others are wrong.
It's important that we set aside what we think we know and follow the DNA where it leads. Confirmation bias is something of which to be keenly aware.
https://www.yourdnaguide.com/ydgblog/confidence-intervals