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# THE SKETCH THAT SAT UNUSED FOR TEN MONTHS

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*How an overlooked composite and an ancestry test broke open a serial killer investigation, and what the case reveals about genetic genealogy, facial comparison, and Germany's DNA law.*

**F**or roughly 10 months, a large manhunt across south Louisiana chased the wrong man. Not the wrong individual, but the wrong category of human being altogether.

In 2002, the FBI, the Baton Rouge police, and a task force assembled for the purpose were hunting a serial killer who had murdered women inside their own homes, with no signs of forced entry. The profile circulating at the time described a white man between 25 and 35, physically strong. Witness accounts put a white man in a white pickup near one of the scenes, and from those accounts the task force produced a composite of a white person of interest (Genome News Network, 2003). Keep that sketch apart from the other one in this story, because the whole case turns on the difference between them. So the investigators did what their assumption made obvious, they hunted a white man, and in the course of that theory they collected cheek swabs from more than 1,000 white men (CBS News, 2003; Wired, 2007).

And now the part that turns this case from a blunder into a lesson. The investigation was not hunting the wrong man because no witness existed, it was hunting him although a woman had seen the perpetrator, survived him, and described him. On July 9, 2002, Diane Alexander survived an attack in her own home in Breaux Bridge, about 45 minutes west of Baton Rouge, because her son arrived and the attacker fled. On July 15, 2002, she gave a parish detective a detailed description of a Black assailant, and a composite sketch was drawn from it. That sketch bore, in the words of the Louisiana Supreme Court in the judgment affirming Lee's conviction, a striking resemblance to the defendant (State v. Lee, 2008). The sentence that follows immediately after is the real scandal, and it stands in a criminal judgment rather than a newspaper article: despite the existence of this sketch, the investigative leads at that time remained focused on an unknown white male driving a white pickup truck (State v. Lee, 2008).

Two incompatible sketches existed in separate investigative files, one depicting the white person of interest the task force was pursuing, the other depicting Alexander's Black attacker. What failed here was not Alexander's observation or the sketch drawn from it, but an investigative structure that kept both outside the serial killer inquiry while the white suspect theory dominated it. The court puts it without euphemism: the drawing remained underutilized for nearly a year because the focus of attention was not on an African American male (State v. Lee, 2008). Whether an earlier pursuit of that sketch would have prevented the later crimes cannot be proven, and I therefore do not claim it. What is documented is the chronology alone, and it is enough: after July 15, 2002, the day Alexander gave her description, further women of this series died, the last in March 2003 (State v. Lee, 2008). What I make of that is an assessment and not a finding, and it runs as follows: in this field, confirmation bias is no academic footnote, it is a quantity whose price is written into case files.

They found nothing while they swabbed the cheeks of more than 1,000 innocent men, and in that same window the killer struck again.

In March 2003, the task force did something most American police agencies of that era would not have touched with a 10-foot pole. They sent the crime-scene DNA to a molecular biologist named Tony Frudakis, who claimed at a small company in Florida that he could read a suspect's ancestry out of the sample (Wired, 2007). The investigators did not believe him, so they tested him. They sent him 20 blind DNA samples from people of known background and asked him to sort them. He got all 20 right. Then he told them what the DNA of their killer revealed: the man they wanted was, with very high probability, of predominantly sub-Saharan African ancestry with a smaller Native American component, and the result strongly contradicted the task force's white-donor hypothesis (ABC News, 2006). Contemporary accounts of the exact split differ, which is itself worth noting in a text about false precision, and the criminal judgment records only the substance, that a Florida laboratory found several rare markers suggesting the suspect was African American (State v. Lee, 2008). By the account of those on the conference call, the line went very quiet at that point.

One of the prosecutors who later tried the case put the lesson with a sharpness I have never bettered. Without that test, he conceded, they would still be chasing the white man in the white pickup, and in the same breath he said that if he could press a button and make the technology disappear, he would (Wired, 2007). His objection was not to the result in this case but to the larger meaning he believed the technology might acquire. Tony Clayton, a Black prosecutor who tried one of these cases, said he distrusted anything implying that people do not all bleed the same blood, and behind that lies the fear that treating genetic differences as investigatively significant will be mistaken for treating people as inherently unequal (Wired, 2007). The tool that helped rescue the case was the same one he wished could disappear, and a clear head holds both thoughts at once.

The investigators then widened their search to include African Americans, and only now could the piece of evidence work that had been available for 10 months. What reopened the file was not one thing but two, a Florida laboratory reporting rare markers that suggested an African American suspect, and witness reports of a Black man near the last victim's house, and only then did the task force widen its focus (State v. Lee, 2008). On May 22, 2003, an FBI behavioral analyst interviewed the survivor again. On May 23, 2003, the task force released the composite drawn from her description, together with her son's description of the vehicle, to the public through television and print. Within hours, citizens called in and gave a name, and one caller said the vehicle in question was sitting in that man's mother's front yard (State v. Lee, 2008).

The name was Derrick Todd Lee, and here the timeline deserves care, because it is where the story is usually told wrong. A buccal swab had been taken from him on May 5, 2003 by two agencies working an older, unrelated case, and it reached the crime laboratory the next day. The analyst began testing it on May 20, completed the analysis on May 23, and her finding reached the task force on May 25 (State v. Lee, 2008). The sketch went public on May 23, the tips naming Lee came in over the following two days, and the laboratory result arrived independently of them. Neither the sketch nor the calls set the analysis in motion, the two lines simply converged within 48 hours. On May 25, 2003, Alexander picked him out of a

photographic lineup, on May 26 his name was released publicly, and on May 27, 2003 he was arrested in Atlanta (State v. Lee, 2008). The man arrested was 34 years old, born in 1968. He was linked to at least seven killings and convicted in two separate trials (Smith, 2020).

And notice the decisive point: no database hit named this man. His name came from the public tips, and the laboratory comparison independently established that his profile matched the crime-scene DNA. In this case the DNA did not generate the suspect, it cleared the ground and then confirmed him. It destroyed the false picture of the perpetrator and thereby opened the way for a piece of evidence that had been lying there the whole time and that nobody took seriously as long as everyone expected a white man.

One closing note I cannot suppress as an expert witness. The May swabs that produced the first match had, in the assessment of the Louisiana Supreme Court, been obtained through an unconstitutional procedure, and they survived the motion to suppress only under the inevitable discovery doctrine, because the tips generated by Alexander's sketch would have led to him regardless (State v. Lee, 2008). A later blood sample, taken after his arrest under a court order, independently confirmed the DNA match, and the prosecution rested on a good deal more besides. Alexander's evidence became a crucial part of the independent investigative path on which that ruling depended, alongside earlier tips naming Lee and the task force's own procedures for closing leads (State v. Lee, 2008).

And here is the sentence that carries this whole text, right at the top, so you do not have to go looking for it. The ancestry question that broke Baton Rouge open is precisely the one German law forbids DNA to answer. The rest of this text explains what that question can do, what it cannot do, why an American prosecutor feared it while he needed it, and why my own country, of all places, keeps tripping over itself when it comes time to answer it.

A word on standing, before anyone asks why they should listen to me. I am not a molecular geneticist, and where this text explains genetics it leans on the literature, not on me. The second half of this text, by contrast, is my own field. I spent decades identifying people and vehicles from image material, across hundreds of evaluated traffic-camera images and expert reports in proceedings up to and including homicide. Both halves are bound by the same logic I have always worked by: a lead that narrows the circle is not a proof that names a name, and whoever confuses the two ends up convicting the wrong person.

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## **WHEN THE PROFILE IS WRONG, THE MOLECULE IS UNMOVED**

What Frudakis read out of that sample has a precise name, and the name matters, because it is often described inaccurately. The DNA did not reveal the killer's race. It revealed his biogeographic ancestry, and the two are not the same animal.

Biogeographic ancestry is simply the geographic region, or regions, from which a person's biological ancestors came. It says nothing about culture, language, religion, citizenship, or the social category we call race, because all of these are shaped by factors that have nothing to do with the sequence in your cells (Schneider et al., 2019). Across the long history of

humanity, mutation, migration, isolation, and local selection have made certain DNA markers common in one part of the world and rare in another, and reading enough of these ancestry-informative markers places a person's deep root at the level of broad continental regions (Schneider et al., 2019). You name a region of origin, not a guilt, and certainly not a character.

How the cells carry this information explains both the power and the limit. Autosomal markers, reshuffled every generation, map the recent admixed ancestry of the last few generations, while the Y chromosome reports only the paternal line and the mitochondrial markers only the maternal one, both of them nearly unchanged across long stretches of time (Fleckhaus et al., 2025). Combine the channels and a mixed background can be sketched, coarsely, usually at the level of continents. Push for the subcontinental answer, this valley rather than that province, and the signal thins out fast, because people have spent the entirety of history moving and mixing (Schneider et al., 2019). The honest result is a region, broad and probabilistic, not a passport.

How you compute an ancestry out of such markers is no sorcery, it is population genetics that has been standard for years. Model-based methods compare the unknown profile against selected reference populations and estimate its affinities to them, or the proportions in which it appears admixed, and dedicated forensic tools rest on large public reference datasets (Fleckhaus et al., 2025). Read that sentence carefully, because the wording carries the whole limitation. The output is a relation to the reference data chosen, not a statement that a person biologically belongs to a cluster, and how well any given result can be bounded depends on those data. It is not an oracle, it is statistics that knows its own sources of error.

This sits inside a larger toolbox that forensic geneticists call forensic DNA phenotyping. From a crime-scene sample it can predict three kinds of things, namely externally visible traits such as eye, hair, and skin color, biogeographic ancestry, and by way of methylation patterns an approximate age (Schneider et al., 2019). The pigment predictions are good for the easy categories and mediocre for the hard ones. The widely used HIrisPlex-S system runs on 41 markers and turns the observed genotypes into probabilities per trait (Fleckhaus et al., 2025). Blue and brown eyes it predicts well, while intermediate colors such as gray, green, and hazel remain substantially harder to predict. Black and red hair are easy, blond and brown a mess, partly because so many blond children become brown-haired adults that the model cannot tell them apart from the DNA alone (Schneider et al., 2019). Whoever sells DNA phenotyping as a photograph of the suspect is selling a horoscope with footnotes.

Reading age out of DNA follows a different chemistry and carries its own uncertainty. The method rests on DNA methylation, small chemical tags on the genome whose pattern shifts with age, and illness, lifestyle, and the use of certain substances can shift that pattern, so that two people of the same age can look differently aged by the DNA (Fleckhaus et al., 2025). A good examiner gives no single year but a window, and whoever turns that window into a point estimate has quietly cut off the rest of the distribution. A properly reported age interval can narrow an investigation, but its width and its uncertainty depend on the assay, the tissue, and the model used.

The notion that a tiny trace can be built into a genetic mugshot, a wanted poster out of letter strings, is popular and it is the one claim in this field that does not hold. Phenotyping can produce probabilistic trait predictions, but it cannot currently generate a reliable, individualized facial portrait of an unknown donor (Verfassungsblog, 2025). What the machine delivers is not a face but a sheet of probabilities, blue eyes with this certainty, medium skin with that, an age inside a window of a decade. Whoever paints a likeness out of that paints it in with their own prejudices, and that is the danger. The printout says less than the viewer wants to hear, and what the viewer fills in comes rarely from the sequence and often from the gut.

One essential distinction belongs here, and I would rather make it cleanly than bury it, because the distinction is essential to understanding what the test actually established. The Louisiana sample announced no race. It announced a continental ancestry that strongly contradicted the task force's white-donor hypothesis. The investigative value was enormous precisely because the predicted ancestry was rare among those actually being hunted. A prediction that only confirms what everyone already assumes moves nothing. A prediction that blows up the central assumption of the whole investigation moves everything.

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## WHAT THE MOLECULE CANNOT DO, AND NEVER COULD

Now the part the television crime shows leave out, because it is undramatic and therefore inconvenient.

DNA helps only when DNA is there. That sounds obvious, until you stand in a real case. The sample has to exist, it has to be tied unambiguously to the crime and not to the delivery driver who touched the doorframe last Tuesday, and there has to be enough of it. Modern contact traces, the few cells a hand leaves on a surface, often hold so little material that the whole sample is used up just building a standard profile, and nothing is left for phenotyping (Schneider et al., 2019). Mixed traces from two or more people frequently cannot be untangled into a clean phenotype at all.

The deeper limit is the one investigators forget in their excitement. Classical profiling identifies a person only by direct comparison, against a named suspect's sample or a profile already in a database, and no hit means no name (Schneider et al., 2019). That is why the task force could swab 1,000 men and learn nothing. Phenotyping does not overcome that limitation, because it is an investigative tool and not a method for evidential identification of an individual (Schneider et al., 2019). Even a hit names a probable donor rather than a proven perpetrator, because transfer, contamination, and a perfectly legitimate presence at the scene still have to be excluded.

Here the model offers something an eyewitness cannot, an explicit output that can be tested, calibrated, and audited. A prediction of 95 percent for brown eyes is a model output and not an error rate, and reading it as a guaranteed 5 percent chance of being wrong is a mistake I want no reader to take from this text. It is a stated quantity attached to a documented model,

and it can be argued about in court. A frightened witness at three in the morning offers no such quantity at all, and history is not kind here. In the United States, the Innocence Project found that of 350 wrongful convictions later overturned by DNA, eyewitness misidentification had contributed to roughly 70 percent of that historical cohort (Schneider et al., 2019). The human eye, unlike the marker, has no error figure printed on the side.

A postscript to the Louisiana story says a lot about how this field actually moves. The company that read that sample was a tiny outfit in Florida that never really turned a profit. A single baseline test cost more than 1,000 US dollars, and most police agencies kept their distance from the whole uncomfortable subject (Wired, 2007). The company dissolved in 2009, and the technology did not die with it, because continental ancestry inference is today an established forensic method with its own validated marker sets, reference data, and software (Schneider et al., 2019). It is worth being precise about what that does not mean. It is no routine component of an ordinary STR profile, it runs on additional markers and needs its own reference data, validation, and interpretation, and a laboratory has to decide to do it. That is how a method climbs from scandal to standard, not by winning the argument but by outliving it.

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## THE GERMAN FIGHT, AND WHY IT FLARED AGAIN

Here my own country does something that would be comic if it were not quietly costing investigations their best lead. Since late 2019, after a fight that ran for years, German law permits so-called extended DNA analysis. The mechanism of that provision matters more than its reputation, so it is worth setting out exactly. Paragraph 1 of § 81e of the Code of Criminal Procedure lists what may be determined from the material: the DNA identification pattern, descent, and sex, and sentence 2 of that same paragraph bolts the door, because other determinations may not be made and examinations directed at them are inadmissible (Strafprozessordnung, § 81e). Paragraph 2 extends the list for the case that it is unknown which person a trace came from, and then additionally permits determinations of eye, hair, and skin color as well as age (Strafprozessordnung, § 81e). The word descent in paragraph 1 means kinship descent and not the geographic origin of the ancestors. So German investigators may compute several of the traits a phenotyping panel offers, but not the one that broke Baton Rouge open. Frudakis was not asked about eye color, he was asked where the man's ancestors came from, and that is precisely the question the list omits. The one thing the German legislature deliberately left out, against the express recommendation of forensic physicians and the police themselves, is biogeographic ancestry (Schneider et al., 2019). It appears in neither list, and precisely for that reason it falls under the prohibition of paragraph 1, which bars not only the finding but already the examination aimed at it.

Read that sentence again, slowly. A German investigator may ask the cells what color the suspect's eyes were. He may not ask those same cells where that suspect's ancestors came from. Eye color, yes; ancestry, no. The very question that cracked Baton Rouge open is the one question German law forbids the molecule to answer.

The reason is not stupidity, and the worry behind it is real. Germany of all countries has cause to be nervous when a state laboratory sorts people by origin and files the result in an investigative record, and the debate here began in 2016 amid a political mood that tied migration and crime tightly together (Gen-ethisches Netzwerk, 2025). The fear is concrete: that a printout reading “sub-Saharan African,” stapled to an open murder case, becomes a license to pressure a minority rather than to find one man. That fear is warranted, and so is the lead. The tool cuts both ways, and in a Dutch case from 1999 an ancestry-based prediction was exactly what lifted an unfounded suspicion off a local minority (Schneider et al., 2019). What can point at a group can also clear one, and that is the half of the story the alarmed side never tells.

What makes the German compromise scientifically incoherent rather than merely cautious is a detail the debate usually skips, and it has grown larger with fresh numbers from the country itself. In early 2025, a group of German forensic physicians around Jan Fleckhaus, Katja Anslinger, Sabine Lutz-Bonengel, Marielle Vennemann, and Marta Diepenbroek laid out a scientific plea (Fleckhaus et al., 2025). The pigment models the law permits were largely built and calibrated on European reference data, because for eye color 97 percent of the reference samples come from Europeans, and for hair color it is 85 percent (Fleckhaus et al., 2025). The accuracy of a prediction depends on how well the ancestry of the tested person is represented in that reference set. Strike ancestry, and you do not protect the suspect of non-European origin, you worsen the very predictions the law does permit, and precisely for the people the models already handle worst.

How strong the effect can be is shown by numbers from the same work, and they have to be read correctly. In a particular, heavily admixed Brazilian sample, 87.7 percent of the predictions for blue eyes were correct, but only 74.8 percent for brown. For skin color the correct rate was 95 percent for light skin, but only 10 percent for medium and 13.3 percent for dark. When eye, hair, and skin were scored together, only 19.16 percent of the predictions were fully correct (Fleckhaus et al., 2025). Those are the values of a single sample and no universal performance figure, and they do not say the permitted predictions are worthless without ancestry. They say something narrower, that ancestry as a co-factor sharpens them and reduces misclassification, especially where the population is admixed. The empirical part of the authors' conclusion I hold to be sound, while the legal and political judgment stays a separate matter: a categorical ban strikes exactly the factor that makes the permitted predictions more reliable (Fleckhaus et al., 2025).

There is something almost circular about the ban, because several appearance traits are strongly correlated with biogeographic ancestry. Brown eyes with black hair and a medium skin tone appear among the original populations of Europe, Asia, and the Americas alike, and appearance predictions alone cannot reliably separate those broad affinities, while the ancestry analysis German law refuses to read adds discriminating information that pigmentation does not (Schneider et al., 2019). So the law lets the investigator infer traits that smuggle ancestry back in through the side door, while forbidding him to name it at the front.

And the line on the map is absurd once you step back. The same ancestry inference that is forbidden in Germany is permitted in Austria, the Netherlands, and Switzerland, and is used there successfully in investigations (Fleckhaus et al., 2025). The molecule does not know which side of the border it happens to be lying on.

Bavaria delivers the irony free of charge, and it is legally documented. In a Munich homicide case, the investigators had a deepened DNA analysis run in Innsbruck, which yielded among other things a probability of 68.9 percent for brown hair and pointed, through Y-chromosomal markers, to paternal ancestry associated with northeastern Europe (Legal Tribune Online, 2020). The twist sits in the legal basis. Because the Code of Criminal Procedure forbids an analysis aimed at ancestry, the Bavarian police based the examination not on criminal procedure law but reclassified the measure as preventive policing and invoked the Bavarian Police Tasks Act (Legal Tribune Online, 2020). So the ban was circumvented by simply declaring the very same measure to be danger prevention, and exactly this cherry-picking was heavily disputed among lawyers. In the same state, the legislature then struck biogeographic ancestry back out of its own police tasks act in 2021 (Verfassungsblog, 2025). Anyone who finds that absurd has read it correctly.

One has to picture the price concretely so that it does not stay abstract. Take a homicide with a clean foreign trace that matches no profile in the database, no witness, no usable image, only the cell. The permitted procedure gives the investigator eye, hair, and skin color and an age, all with the known fuzziness, and stays silent on the one datum that calibrates the permitted rest. The investigation then proceeds with a profile that is worse calibrated for one part of the population than for another, and nobody in the room knows for which part, because that is exactly the question that may not be asked.

The exclusion is not as settled as it is often assumed to be, because it has been in motion again since late 2024. The Conference of Interior Ministers came out on December 6, 2024 in favor of extending the legal basis to include biogeographic ancestry analysis (Fleckhaus et al., 2025). Bavaria and Baden-Württemberg then brought a corresponding motion into the Conference of Justice Ministers. The initiative stalled on June 6, 2025, when the motion failed to secure a majority among the sixteen state delegations and ended in a tie, and the federal justice minister was also skeptical and said she wanted to await an evaluation of the method (taz, 2025; Verfassungsblog, 2025). Under current German criminal procedure law the provision stays unchanged, and the exclusion stands.

Against the ancestry analysis stand the German Bar Association, the Republican Lawyers Association, the Gen-ethical Network, and the Central Council of German Sinti and Roma, who warn of racial profiling, misdirected investigations, and intrusions into data protection (Legal Tribune Online, 2025; Gen-ethisches Netzwerk, 2025). Their strongest argument is no gut feeling, it is an asymmetry that has to be taken seriously. An ancestry finding is most operationally salient when it names a trait that is rare in the region at hand, an African line for instance, whereas European ancestry is comparatively common in German investigations and therefore often provides less discriminatory information (taz, 2025). Put differently, the investigative value of the method arises exactly where it steers suspicion onto a minority,

and that is at the same time the point where it becomes most dangerous. That tension does not dissolve by arguing it away.

I still make no secret of where the science points on this question, and I do not pretend to stand neutrally in the middle. Striking ancestry from the analysis makes the permitted predictions less accurate, not the minority safer, and a ban that claims to protect while it lowers precision exactly where precision is already weakest is a poor instrument. That does not mean the other side is wrong, and exactly for that reason the honest answer is uncomfortable. The defensible answer likely lies neither in a blanket ban nor in unrestricted authorization, but in a narrow, controlled authorization with clear limits, of the kind several neighboring countries have long had for ancestry analysis. Whoever shies from this difficult middle and would rather freeze the debate in a tie has protected nothing, they have merely failed to decide.

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## THE METHOD THAT DOES NAME A NAME AFTER ALL

There is a development that was not yet established as a criminal investigation method in 2018, and it shakes the pretty, clean rule that “DNA names no name.” It is called forensic genetic genealogy, and it has become one of the most consequential developments in modern forensic investigation.

The rule still holds for the classical database search. It no longer holds for the detour through the relatives. The police in California arrested Joseph James DeAngelo on April 24, 2018, a former police officer whom they had identified as the Golden State Killer, responsible for a series of murders and rapes in the 1970s and 1980s (NPR, 2018). The crime-scene DNA had lain in the evidence locker for decades and matched no profile in any police database, exactly the dead end that had paralyzed Baton Rouge too. Then the investigators did something new. They uploaded the crime-scene profile to GEDmatch, an open genealogy database that two hobby researchers had founded in 2010 so that people could find distant relatives through shared stretches of DNA, and the profile matched third and fourth cousins of the killer there (NPR, 2018). Out of those matches, a genetic genealogist and the investigators built a family tree of roughly 1,000 people and narrowed it, branch by branch, to a single man.

Hold on to what happened here. The DNA named relatives who had uploaded their own samples for a hobby, and out of that web a name fell out. Formally the old rule holds, in practice the detour through strangers' cells reached where the standard search never did, and the last step was still the direct comparison against the suspect's discarded sample.

The Golden State Killer was, of all things, a former police officer (NPR, 2018). Whatever the reason his profile was absent from the databases, and I will not speculate about it, the outcome is the instructive part: his profile produced no match in the conventional law-enforcement databases, but DNA uploaded by distant relatives made genealogical identification possible, and exactly that made the case a blueprint. After his arrest, agencies and specialized providers took up the method for hundreds of shelved cases, faster than laws

and ethical guidelines could keep up (National Academies of Sciences, Engineering, and Medicine, 2024). A tool that solves decades-old murders sells itself, and the uncomfortable questions always come afterward.

The method came fast and stayed controversial, and both for the same reason. It works because millions of people have laid their DNA into consumer databases out of pure curiosity, and whoever does that unwittingly also hands their relatives into the light of investigators. The US Department of Justice drew a line in 2019 and issued an interim policy that took effect on November 1 of that year (US Department of Justice, 2019). It restricts genetic genealogy to unsolved violent crime and to identifying human remains, forbids such a search from becoming the sole basis of an arrest, requires ordinary investigative work on top, and prohibits slipping a crime-scene sample into a database under a false name (US Department of Justice, 2019). The catch is that this is departmental policy rather than statute, binding the federal agencies and the bodies they fund while investigators at state level work in a patchwork of their own rules (US Department of Justice, 2019; National Academies of Sciences, Engineering, and Medicine, 2024).

Then the thing happened that happens to every data collection once people grasp who else is reading along. After GEDmatch forced its users in May 2019 to opt in actively to police use, the searchable pool collapsed from roughly 1.4 million profiles to well under 200,000, with the figure shifting as users opted back in (Kaiser, 2019). A database is only as useful as the consent behind it. The same method has a second side that usually drowns in the privacy dispute, because it also returns names to the recovered dead whom nobody reported missing, and a retrospective study published in 2025 examined 477 successfully identified North American remains cases submitted to one provider, Othram, whose staff also wrote the paper (Lasyone et al., 2025). The legal framework grew more slowly than the technique, with Maryland passing the first dedicated state law in 2021 (National Academies of Sciences, Engineering, and Medicine, 2024).

What makes the method powerful is also what makes it uncanny: you need not sit in any database yourself. It is enough that a third cousin you have never met ordered a saliva test and uploaded the result. The net no longer holds only the convicted and the suspect but anyone with a genetically curious relative, which is nearly everyone, and a system that reaches the guilty through the cells of the unwitting deserves sober thought before it becomes routine.

How close this reaches to the present is shown by the Idaho case. On the night of November 13, 2022, four students were stabbed to death in their house in Moscow (Associated Press, 2025). A single-source male DNA profile recovered from the snap button of a leather knife sheath left at the scene produced no match in CODIS, and investigative genetic genealogy subsequently generated a lead pointing to Bryan Kohberger, then a doctoral student of criminology (PBS News, 2025). How the chain ran after that matters more here than the sentence does. From the trash at his parents' house in Pennsylvania investigators secured a sample whose profile was, by the prosecution's account, not his but his biological father's, establishing kinship to the trace and nothing more (Cable News Network, 2025). The direct

comparison came only after the arrest, from a cheek swab that matched the sheath (Cable News Network, 2025). The distinction worth holding is not naming against not naming, it is generating a suspect against confirming one. The prosecution itself described the genealogy in that register, as something that pointed investigators toward the defendant without supplying substantive evidence of guilt, and the court recorded that nothing from the genealogy was used to obtain either the arrest warrant or the warrant for his DNA (State v. Kohberger, 2023). He pleaded guilty on July 2, 2025 and was sentenced on July 23, 2025 to four life terms without parole (PBS News, 2025).

The case also carries the conflict this text criticizes in American practice. Searching for relatives, the FBI used databases whose terms of use expressly excluded law enforcement, among them MyHeritage, and the defense motion to keep those findings out of the proceeding was denied (Cable News Network, 2025). That is the gray zone of consent: whoever uploads DNA for a hobby and expressly refuses the police can still become a lead through a relative, and whether that is admissible is decided by a judge and not by a terms-of-use page.

The defense fought hard for the sealed genealogy records, because it wanted to know how investigators had reached Kohberger at all (PBS News, 2025). The prosecution relied on other evidence, the direct DNA comparison, the cellphone records, and the surveillance images, which is exactly why the American policy forbids a genealogical lead from carrying an arrest by itself (US Department of Justice, 2019). The procedure has grown more powerful, the limit has not moved.

One more sentence that knots the German thread to the American. Forensic genetic genealogy, which over there pulls serial killers out of anonymity after decades, is not currently available as a routine criminal investigative method in Germany, and the reason is not cultural but legal. The procedure lives on access to commercial genealogy databases, and for such access by law enforcement there is no legal basis here. The search for relatives is also tightly limited, because § 81h StPO permits, within a mass screening, only to check whether the trace came from a participant, from a direct-line relative, or from a collateral relative through the third degree, and not from the networks of distant cousins the American method lives on (beck-aktuell, 2025). So Germany stands twice before the same door and twice does not go through, it forbids its own cell the question of ancestry, and it has no legal path for the detour through the relatives.

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## WHEN THERE IS NO DNA, SOMETIMES THERE IS A CAMERA

Everything so far presupposes a usable biological trace. A great many crimes leave none. The robber wears his gloves precisely because he knows the chain that runs from the cell to the name. The mugging happens out on the open street. The hit-and-run driver never touches a surface you could swab. What these crimes increasingly leave behind is a recording, and that is the gap where my own field, the forensic analysis of images, earns its keep.

The image can come from a fixed traffic camera, the kind that trips on speed, tailgating, or a red light. It can come from the silent surveillance eyes above bank counters, gas station registers, jewelry cases, and turnstiles, or from a dashcam, the small witness on the windshield that now and then records a crime its owner never expected to catch. Each of these sources produces still frames, and a still frame can be worked on.

It is worth pausing before we celebrate that. The same density of lenses that convicts a hit-and-run driver also traces the path of every innocent person through the city, and the line between solving a crime and logging a life is a question of the access rules, not of the technology. The camera is, like the molecule, a tool without a morality of its own, and what counts is the discipline of the hand that guides it.

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## WHAT AN IMAGE GIVES YOU, AND WHERE IT QUIETLY LIES

From here on I am no longer talking about the literature, but about my own workbench, because identifying people and vehicles from image material was my main field for years. And since I spent the first half of this text hammering on the limits of the molecule, let me start here with the opposite direction. Yes, a person can be identified from images. Not always, not out of every video, but whenever the material supports it, and how often it does support it is something most people badly underestimate.

The soberest example is the duller picture in the country, the traffic-camera photo. I have evaluated hundreds of them, and that work succeeds for reasons that have nothing to do with genius and everything to do with imaging geometry. A traffic enforcement installation is a comparatively constrained imaging environment, where distance, angle, and optics are often known or recoverable, the illumination is usually frontal, and the driver sits in a broadly predictable position. The confounders that wreck a comparison from some arbitrary surveillance camera are largely switched off. What makes the task solvable at all is that the accused is already established from the preceding investigation, so I am not searching the general population. That is why the question of whether the registered owner was driving can often be assessed through a controlled one-to-one comparison, and the answer is by no means always the incriminating one.

How far this work can carry is shown by an assignment in a Bavarian homicide case, which I describe here only as far as it goes without allowing conclusions about anyone involved. The responsible criminal investigation unit made video material and photographs available to me of a vehicle connected to the crime. On the phone, before the first file reached me, I set a condition. I did not want to know the license plate, and they were to obscure it on every image they sent. The officers respected that without any fuss and followed the reasoning at once, which I note expressly, because it is the opposite of the swipe at officialdom a reader might expect here. The reasoning is uncomfortably simple. The moment I know even parts of that plate I am burned on the witness stand, because the defense will rightly hold against me that I found what I knew I was looking for. Whoever knows the solution will find it again in any noise.

Then came the work that never appears on television, because it consists of sitting still for days. Over days I reviewed a very large number of surveillance videos that had been collected from all around, from company premises, from entrances and exits, from private home installations, a patchwork of angles, timestamps, and image qualities. Out of that patchwork the route of the vehicle could be reconstructed, camera by camera, until the drive lay there as a continuous line. At one single spot the image quality was high enough for the decisive step. There the license plate could be reconstructed, as far as the material would possibly allow, and I gave the officer the result without having known the answer beforehand. He then confirmed the match to me.

Combined with the reconstructed route and the verification that followed, that finding supported the conclusion that the vehicle associated with the registration had been present at the scene. In the later trial, the defendant received a life sentence followed by preventive detention. There were further assignments for me in that proceeding which I am not disclosing here. The reconstructed string pointed to a particular registration, and it still required verification against the associated vehicle, the route, and the possibility of cloning, transfer, or misreading. Who sat behind the wheel was a separate question, answered by other evidence and ultimately by the court.

This is also the point where it becomes clear why image forensics can, in one respect, be sharper than the facial comparison I am about to discuss. A license plate is not a resemblance, it is a discrete string that has to be read rather than judged against another face. That difference is real, but it stops well short of DNA-like uniqueness, and I want no reader to overshoot it. Plates are cloned, swapped, mounted on the wrong vehicle, and misread from bad frames, so what a reconstruction delivers is a registration lead that has to be verified against everything else in the file. That is why the craft there lies not in comparison but in reconstruction out of a signal that is really too poor for it, and why the honest report always states which characters are secured and which are merely probable.

So much for what the work can do, and I described it first on purpose, because a field that recites nothing but its own limits in a courtroom is of no use to anyone standing in it. Now the other side of the same discipline, because that same image analysis also gets sold in court with a certainty the underlying science has not always earned, and here I go as hard on my own field as I went on the molecule.

The version of the work most readily accepted in court is the comparison. You have a questioned image from the scene and a known image of a suspect, and you ask whether both can be the same person. The recommended method is morphological analysis, in which a trained examiner compares the face feature by feature and reaches a reasoned conclusion about similarity (ENFSI, 2018). Two reservations belong beside it. Recommended does not mean abstractly validated for every application, since each laboratory must validate its own procedure, and unlike forensic DNA profiling, facial comparison currently lacks the population frequency data and the validated evaluative models needed to calculate robust likelihood ratios for many observed feature combinations. The result is a reasoned expert

judgment, and where it carries a number, that number is a convention rather than a calculated quantity. Exactly there sits the system I worked with until the end.

Anyone reading an anthropological identity report in Germany runs into a scale that goes back to Friedrich Schwarzfischer, introduced in 1992 in a chapter of the German reference work *Kriminalistik Handbuch für Praxis und Wissenschaft*. What follows is how I have used and understood that scale across my own casework, set out at greater length in a separate piece of mine on that scale, and I flag that provenance rather than dress it up as settled literature (Rauscher, 2024). It consists of nine verbal predicates running from practically proven identity through an undecidable middle to practically proven non-identity. Each predicate carries an assigned probability range. Practically proven identity begins above 99.72 percent, highly probable identity lies between 99.00 and 99.72 percent, very probable between 95.00 and 99.00 percent, and at the lower end the scale mirrors itself symmetrically until, below 0.28 percent, practically proven non-identity stands (Rauscher, 2024). Between 30.00 and 70.00 percent the report says nothing more than that the question cannot be decided from the image material, and awarding that predicate is not a weakness, it is craft.

I applied this scale until the end of my work and still never spoke the bare number in a courtroom, only the predicate. When an expert says 99.72 percent in front of a criminal court, the room hears a measurement, and that impression cannot be called back afterward.

And now comes the part where I am dissatisfied with the foundation of my own field. This scale comes from a time when surveillance imagery was coarse, washed out, and small, and its top tier was set during an era dominated by that poorer material. Today, in newer cases, cameras with 4K resolution sit on the walls, and there is considerably more to be extracted from that material. When I see on such a recording a mole at a particular spot, a scar with an individual course, together with exclusively matching morphological features and not one single incompatible divergence, then the problem is not that the top category needs a higher percentage. It is that a single conventional label compresses findings of very different descriptive richness into the same category.

And here I have to rein myself in before somebody else does it for me. Higher resolution does not produce higher probability, it makes more features visible and allows a denser, better reasoned finding. It supplies none of the missing frequency data, and without those no mathematical certainty comes out of a 4K image either, which is why the expert body states expressly that reports should carry no statements of absolute certainty (ENFSI, 2018). My criticism is thus no demand for a higher number, and a verbal scale does not become a calculated probability merely because more features are visible. Anything worth calling quantitative would need validated models, an analysis of how far features depend on one another, relevant population data, likelihood ratios rather than bare percentages, systematic testing against image quality, and validation on cases whose true answer is known. That is a research program and not a software update, and I would rather name it than promise it.

It becomes clearer with full-body video, where the assessment leaves the face. Gait is a feature complex in its own right, made of stride length, cadence, arm swing, and posture.

Add a conspicuous detail, a limp favoring the right leg, or an axial deviation of the legs, the genu valgum the layman knows as knock-knee or the genu varum he knows as bowleg, and the combination carries considerably more information than a face alone. I deliberately do not call it rare, having just explained that the frequency data justifying that word do not exist, and I am not borrowing them back the moment they suit me. What can be said is that each additional independent feature complex constrains the set of people compatible with the recording. Such a multimodal finding lies outside the original scope of a facial comparison scale, and it would need its own validated evaluation framework rather than a further tier bolted onto an old one. That is a professional position of mine and not a consensus of my field.

That is why I have been working for some time on rewriting this classification and fitting it to what modern recording technology actually delivers (Rauscher, 2024). A second undertaking belongs to it, and here I have to make my own complaint accurate, because feature lists do exist. The Facial Identification Scientific Working Group has built a detailed list for morphological analysis that breaks the face into 19 components, each with sub-components, and the European manual expressly recommends working from such a checklist with standardized terminology (ENFSI, 2018). So the list is not what is missing. What is missing is a uniformly used catalog backed by robust frequency data. That gap has narrowed since, and honesty requires saying so in a text dated 2026. The working group's methodology guidelines now stand at version 2.1 of February 2026 (FISWG, 2026), and the feature list itself has long been carried into a published consensus standard for morphological analysis (ASTM International, 2026). Standardized terminology is therefore no longer the open question it was in 2018. What remains missing is not frequency data alone, but sufficiently robust population data, validated evaluative models, and evidence about dependencies between features, and without those the number at the top of the scale stays a convention. That is the gap I work on, and whether a book comes out of it in the end I leave open here.

Three things ruin this work, and all of them are the rule rather than the exception. The first is image quality, because the smeared, low-resolution frame from a real gas station camera at two in the morning drives the error rate up. The second sits in the examiner's own head. Confirmation bias is documented for exactly this task: tell an examiner the police already favor a suspect, and the comparison drifts obligingly toward a match (Heyer and Semmler, 2013). The eye sees what the file instructs it to see, which is no slander of examiners but a fact about brains, mine included. The principal safeguards are controlled contextual information, blinding where practicable, fixed procedures, full documentation, and independent review. That is exactly why I did not want to know the license plate in that Bavarian case. Had I carried the sought-after character string in my head, I would have found it in the pixels, of that I am convinced, and no one could ever have proven that I read it into them rather than out of them.

From this follows a procedural safeguard I have always advocated: the examiner should not receive irrelevant case information before completing the image analysis. Whoever reads, before the examination, what the accused has been convicted of before, what the witnesses

say, what the investigators suspect, and where the cellphone was logged in, is burned as an independent examiner. He then already carries the answer in his head, and his eye dutifully hands it back to him out of the image noise. Such a contamination cannot be subtracted afterward, because no one can prove what he would have seen without that prior knowledge. When I received the file anyway, and that did happen, I let it lie. The image material first, feature by feature, findings written down, and only afterward the file, in order to check whether my finding fits the case or cuts across it. That order costs nothing and is one of the simplest and most effective safeguards available.

The third sits before the analysis begins, in the provenance of the image itself. A still frame from a surveillance system is not a photograph, it is the end of a long chain of sensor, compression, transmission, and export, and every link of that chain can invent a feature or swallow one. Heavy compression lays blocks over a face that turn a mole into a shadow and a shadow into a mole. Whoever has never seen the raw recording, but only the fourth screenshot of a file passed along, ends up comparing not a face with a face, but an artifact with a suspicion. That is why I ask first for the original and for the metadata, for camera, timestamp, and export path, long before I look at the first feature. An image whose origin and authenticity no one can prove may still hold investigative value, but it is no reliable basis for a robust comparison.

I want to be open about how thin the safeguard is even under the accepted method. Morphological analysis is at bottom a structured version of what your own brain does when it decides that two snapshots show the same cousin, and on the degraded images real crimes produce, accuracy sinks while disagreement between examiners rises (ENFSI, 2018). Admissibility is not the same statement as fingerprint or DNA certainty, and any expert who lets a court hear it that way has crossed the edge of what the evidence supports. Nor does automatic facial recognition take that uncertainty off the human. An open database search yields a candidate list, a ranking of computed similarities, and the European body treats reviewing such a list not as an evidential comparison but as the starting point of an examination (ENFSI, 2018).

With an enforcement photo the case is fundamentally different, and here what stood at the start of this section about controlled imaging geometry pays off. The difference does not lie in the camera, though, it lies in the question. Because the accused is already established, as the registered owner for instance or as a relative of the owner, the expert receives the enforcement photo and comparison images of exactly that person. What gets examined is therefore no open one-to-many search but a targeted one-to-one comparison, and the question is solely whether both show the same person. That is exactly how the European manual defines the forensic facial image comparison as well, as a rigorous one-to-one analysis followed by an evaluation (ENFSI, 2018).

This is precisely where I am starting with a software development of my own. Into the system go the questioned enforcement photo and suitable comparison images of the already identified person. A reproducible algorithm first checks image quality, camera angle, occlusion, and basic comparability. A facial recognition component then computes the

similarity of the submitted faces. A language model is not meant to decide about identity, but solely to convert the structured individual findings into a uniform and checkable documentation, to flag possible omissions and contradictions, and to standardize the documentation for expert review.

The system does not identify the accused and does not compare them against the population. It examines exclusively the comparison person specified by the authority or the court. A high similarity score is thus no statement that no one else could carry the same features, and certainly no mathematical probability of identity. It describes only the agreement within the comparison actually submitted.

Every finding derived from it holds, in addition, under the express reservation that among the realistically possible drivers there are no close blood relatives who, through family resemblance, could equally be compatible with the enforcement photo. If a brother, a parent, an adult child, or above all an identical twin comes into question as the driver, that person has to enter the examination as a concrete alternative hypothesis with suitable comparison material. That is no quirk of mine, it applies what the manual demands anyway, a competing proposition framed neither too broadly nor too narrowly (ENFSI, 2018). Without such a comparison, the report must not be worded as though identity had been delimited against that relative.

Neutrality does not arise here either from the fact that a machine is computing. It arises through fixed and validated examination steps, the restriction to genuinely comparable features, the separation of investigation and assessment, the documentation of divergent findings, and the express naming of what was not examined. The technical building blocks for this have long existed, what has been missing is their controlled and forensically robust connection, and that is exactly what I am working on.

What this looks like in the report is unspectacular and still among the most important things in it. "No comparison with the general population was conducted. The accused had already been identified through the preceding investigation and was not identified by the expert from the enforcement image. This examination was limited to comparing the depicted driver with the submitted reference images of the accused. The conclusion assumes that no close biological relative is a realistic alternative driver. It does not distinguish the accused from any relative who was not included in the examination." Whoever takes these five sentences for bureaucracy has never watched a court take a finding for something it never was.

Now the harder claim, and it is one I want to make with more care than it usually gets. Can you read a stranger's ancestry out of a surveillance still, the way Frudakis read it out of the DNA? Not with anything like the same certainty, and never as proof. What an image offers are apparent traits, a build, a hairline, a set of proportions, and they have to be held loosely. Whoever treats an apparent ancestry from a washed-out image as an identification is trusting the eye over the evidence, and you already know how that ends.

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## NO RIVALS, BUT TOOLS OF THE SAME INVESTIGATIVE LOGIC

The old frame I want to bury here is that DNA analysis and forensic image work compete with each other, that the one is the real science and the other the poor relation. In truth they do not compete. They cover different holes in the investigation. The DNA speaks when there is a biological trace, and stays silent when there is none. The image speaks when there is a recording, and stays silent when there is none. The cases in which both exist are the rare, rich ones, and there the two methods reinforce each other rather than quarrel.

There is a third tool of the same logic, older than both. When neither a usable cell nor a usable image remains, but only a bone, classical forensic anthropology begins, and from a skeleton a biological sex, an age range, and an approximate stature can be estimated. That is again the same motion, a narrowing of the circle rather than the naming of a person. Whether population affinity can be read from the shape of a skull is contested in that discipline on both scientific and ethical grounds, and I am not going to settle it in a paragraph. What carries over is only the rule this whole text runs on: the form narrows, it does not judge.

The traffic runs mostly one way. The softer method usually underpins an early suspicion and builds a first profile, and that profile can justify the targeted mass test § 81h permits, in which people meeting the defined investigative criteria are asked for comparison samples (Schneider et al., 2019). At this seam the German ban costs more than a single prediction, because a more precise and properly validated profile may reduce the number of uninvolved people invited to provide samples. The converse risk is real too, since a poorly communicated ancestry result may concentrate suspicion unfairly on a minority, and both effects have to be weighed rather than one of them assumed.

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## WHAT SHRINKS THE HAYSTACK DOES NOT NAME THE STRAW

A witness in Baton Rouge reported a white man in a white pickup. The decisive error was not necessarily the report itself, but the decision to elevate it into a fixed offender profile despite conflicting evidence. The ancestry result dismantled that false profile, and members of the public then named Lee after recognizing Alexander's composite, which had been lying there for nearly a year. DNA comparison subsequently confirmed that his profile matched the crime-scene evidence. Every honest tool in this story did the same modest work, it shrank the circle, and none of them convicted a person on its own. I owe that sentence one qualification out of my own field, because sometimes a tool does name the straw after all. The reconstructed license plate in that Bavarian proceeding was no resemblance and no probability. The reconstructed character string pointed to a particular registration. It did not by itself establish which physical vehicle carried the plate, still less who was driving it. Between that registration lead and the person behind the wheel lay the entire remaining body of proof.

That gap is exactly where investigations go wrong when they are in a hurry, and exactly there everything is decided. Hold the line bright, between the haystack you have narrowed and the person you have not yet named, and DNA analysis and forensic image work are among the most valuable tools an investigation can possess. Blur it, in whichever direction, out of the molecule or out of the lens, and you have built something worse than an old-fashioned erring eyewitness. You have built a machine that does the eyewitness's oldest job, to convict the wrong man, and it does it faster, with a lab coat on.

## DISCLAIMER

This article is provided for general information and commentary only. It does not constitute legal advice, and it is not a substitute for advice from a qualified lawyer based on the facts of a particular case. It likewise does not constitute a forensic opinion in any individual matter. The legal situation described relates to Germany and, where expressly indicated, to the United States, and it is subject to change. Statements on scientific methods reflect the state of the cited literature as of the editorial date, and the described procedures of DNA phenotyping, biogeographic ancestry analysis, forensic genetic genealogy and forensic image comparison are investigative tools whose limits are set out in the text. Statements expressly identified as the author's personal assessment reflect opinion rather than established scientific or legal doctrine. Information on criminal proceedings reflects the information available as of the editorial date, and the presumption of innocence applies to all defendants. Anyone with a specific legal or forensic concern should obtain qualified professional advice. Liability for decisions readers make on the basis of this text is excluded to the extent permitted by law.

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# IMPRINT

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