Contents

1 Introduction and scope 6
   1.1 DNA and forensic science 7

2 Science 9
   2.1 DNA analysis in forensic science – short tandem repeats 10
   2.2 DNA analysis in forensic science – Y Chromosome DNA 11
   2.3 DNA analysis in forensic science – Mitochondrial DNA 12
   2.4 Comparison of DNA profiles 13

3 The future 15

4 Summary 16

Appendix 1: Defining DNA and its use in forensic science 18
   A 1.1 DNA used in forensic science 18
   A 1.2 Current DNA profiling methods 21
   A 1.3 Y STR 22
   A 1.4 Mitochondrial DNA 23

Appendix 2: DNA analysis in forensic science 24
   A 2.1 Samples generally analysed for DNA profiling 24
   A 2.2 How should DNA samples be collected and preserved for analysis? 25
   A 2.3 How is a DNA profile generated? 26
   A 2.4 Interpreting DNA profiles 29
   A 2.5 What is DNA contamination and how can it be controlled? 32
   A 2.6 What is the National DNA Database and what types of samples does it contain? 33
Appendix 3: Comparison of DNA profiles in forensic casework  
A 3.1  How DNA profiles are compared and the calculation of the likelihood ratio and match probability  
A 3.2  Low-template, degraded and compromised DNA profiles  
A 3.3  Assessing the weight of evidence of DNA profiles  
A 3.4  Factors to consider in the evaluation of DNA  
A 3.5  The current understanding of error rates in DNA

Appendix 4: Some case examples

Appendix 5: Glossary
Science and the law primers

Foreword

The judicial primers project is a unique collaboration between members of the judiciary, the Royal Society and the Royal Society of Edinburgh. The primers have been created under the direction of a Steering Group chaired by Lord Hughes of Ombersley and are designed to assist the judiciary when handling scientific evidence in the courtroom. They have been written by leading scientists and members of the judiciary, peer reviewed by practitioners, and approved by the Councils of the Royal Society and the Royal Society of Edinburgh.

Each primer presents an easily understood, accurate position on the scientific topic in question, as well as considering the limitations of the science, and the challenges associated with its application. The way scientific evidence is used can vary between jurisdictions, but the underpinning science and methodologies remain consistent. For this reason we trust these primers will prove helpful in many jurisdictions throughout the world and assist the judiciary in their understanding of scientific topics.

The production of this primer on forensic DNA analysis has been led by Lady Justice Rafferty DBE and Professor Niamh Nic Daéid FRSE. We are most grateful to them, to the Executive Director of the Royal Society, Dr Julie Maxton CBE, the former Chief Executive of the Royal Society of Edinburgh, Dr William Duncan, and the members of the Primers Steering Group, the Editorial Board and the Writing Group. Please see the back page for a full list of acknowledgments.

Sir Venki Ramakrishnan
President of the Royal Society

Professor Dame Jocelyn Bell Burnell
President of the Royal Society of Edinburgh
1. Introduction and scope

The aim of this primer is to present:
1. a scientific understanding of current practice for DNA analysis used in human identification within a forensic science context
2. guidance to the Judiciary in relation to the limitations of current interpretation and evaluations that can be made, so that they can be informed when making decisions relating to DNA evidence.
3. The primer has been laid out in sections providing the basic information relating to DNA analysis used in forensic science.

Section 1 provides an introduction to DNA and its use as a forensic science tool as well as the nature of the questions that can be addressed with the most commonly used DNA analysis methods.

Section 2 addresses the following specific questions as they relate to forensic science:
1. What is DNA?
2. How is DNA inherited?
3. What parts of DNA are analysed and how are DNA profiles generated?
4. How are DNA profiles compared and interpreted?
5. How are mixed DNA profiles assessed?
6. What are the limitations to DNA profiling of complex samples?

Some of these areas and questions are expanded upon in the Appendices 1–3. Examples are provided in Appendix 4 and a glossary in Appendix 5.

Section 3 provides a short insight into future areas of development in relation to DNA profiling and Section 4 presents a summary of the current state of the art, including current limitations.
1.1 DNA and forensic science

DNA profiling was first proposed by Sir Alec Jeffreys in 1984 when he found that individuals could be differentiated on the basis of readily detectable differences in their DNA. DNA profiling was first used in a criminal case in the UK in the investigation of the 1983 and 1986 rapes and murders of Lynda Mann and Dawn Ashworth. In this case, Richard Buckland was exonerated through DNA analysis in 1987 and Colin Pitchfork was subsequently convicted. Since 1987, considerable scientific study and resource has been devoted to the development and refinement of DNA analysis technologies. In 1995 the UK National DNA Database was established to maximise the investigative use of DNA profiles and to identify repeat offenders. On a global scale, most countries now use forensic DNA analysis in one form or another. The main questions that a forensic DNA scientist is asked to address are:

1. Whose DNA is it?
2. From what body fluid has it originated?
3. How did it get there?
4. Have the results been reported in a fair and balanced way?

Provided there is sufficient DNA, the interpretation of a DNA profile from a single individual’s sample is straightforward and can provide powerful scientific evidence either to exclude or to include any one individual as a possible source of that DNA. That is done by calculating and presenting the match probability; that is, by calculating statistically how rare any matching DNA profile is in a population.

Technological improvements in DNA analysis resulting in the ability to analyse ever smaller quantities of DNA have led to the main developments in this area. This capability has raised important questions relating to:

1. understanding and controlling contamination
2. the interpretation of complex DNA samples.
A variety of computer software programs have been developed for complex sample interpretation, using a range of statistical methods. In the UK, the Forensic Science Regulator’s Codes of Practice and Conduct set out the requirements for the validation of software programs used for complex mixed DNA sample interpretation. This necessitates:

1. defining the type of DNA profiles the software program is being used to analyse
2. demonstrating that the model used by the software is acceptable for these DNA profiles
3. scientifically validating the software program to address specifically the type of casework samples it is being used to interpret
4. issuing a statement of validation completion. This statement must clearly identify the uses for which the method is validated and any weaknesses, strengths and limitations.

There is a developing scientific research base on the evaluation of how DNA transfers onto an item, and DNA scientists rely on the published scientific literature as well as on their experience and knowledge of the underlying circumstances of each case.
2. Science

DNA is composed of four chemical constituents (labelled A, T, C and G), known as bases, attached to a sugar backbone which can form a strand millions of bases long. There are two such strands in DNA, which run in opposite directions. The bases pair up to form a twisted ladder. Each base pairs exclusively with one other base on the opposite strand: A to T and G to C. This means that when the strands separate, each one can act as a template to reproduce the other precisely. The linear sequence of bases can act as a code, providing the instructions for many biological functions. Figure 1 shows how the bases in DNA are held in paired strands which naturally twist into a double helix structure. Each cell in the human body contains 6,500,000,000 pairs of bases. The full complement, 3 metres in length, is termed the genome. It is packaged into 23 different pairs of chromosomes. During the formation of sperm or eggs, the chromosome pairs are separated with one member of each pair randomly allocated to each sperm or egg. When an egg and sperm fuse during fertilisation, the full set of 23 pairs is re-established. This means that half of a child’s DNA comes from the mother and half from the father, and full siblings will on average share half of their DNA.

**FIGURE 1**

Basic representation of DNA (image adapted from Creative Commons).
Changes in the sequence of bases on the DNA strands (mutations) can arise as a result of errors in DNA replication or repair. As a result an individual might acquire 30–100 mutations relative to their two parents’ genomes. This constant influx of new mutations has allowed differences to build up over generations so that the chances of two human genomes being the same are infinitesimally small. An exception is identical twins, who will have identical DNA, except for new mutations.

Forensic DNA analysis focuses on examining specific sections of DNA that are known to be particularly variable between individuals in order to create a DNA profile. The part of the DNA that is examined is called a locus (plural loci), which is a unique site along the DNA of a chromosome characterised by a specific sequence of bases. Currently, an individual’s entire genome is not analysed to create his or her DNA profile. This means that part or all of the same DNA profile could be shared by more than one person. The statistical analysis of forensic DNA data therefore focuses on establishing the weight of evidence that should be attached to the similarity between the DNA profile of a person of interest and DNA taken from a crime scene.

Appendix 1 provides a more in-depth focus on DNA inheritance and the use of DNA in forensic science.

2.1 DNA analysis in forensic science – short tandem repeats

Only small sections of an individual’s DNA are analysed routinely for forensic evidence. The parts analysed are called short tandem repeats (STRs). Mutations that affect the number of repeats are relatively common so within a population there are usually several different versions of the DNA at an STR locus with different repeat lengths. The different versions are called alleles (Figure 2).

The frequency of occurrence of a specific allele (ie a specific number of repeating units) at the tested locus in a specific population provides a measure of how common that allele is in that population. This information is essential for calculating match probabilities. If only one STR were analysed, there would be many people with the same allele, purely by chance. It is therefore necessary to analyse a number of different STR loci to ensure that the chance of two unrelated people having matching DNA profiles is very small. Over time, the number of different STR loci analysed has increased as technology has developed. Since 2014 in the UK, 16 loci are examined. In some Scottish cases, 23 loci are examined.
2.2 DNA analysis in forensic science – Y chromosome DNA

A second form of DNA analysis involves study of loci found only on the male specific Y chromosome. Y chromosome DNA is inherited by sons from their father with little change between the generations. As a consequence, the profiles generated from Y chromosome DNA are very similar between males with a shared direct male ancestor, with only very rare mutations leading to differences between males who share their Y chromosome. Analysing Y chromosome STRs can be helpful where there is a mixture of DNA from male and female contributors, for example, in a sexual assault case.
2.3 DNA analysis in forensic science – mitochondrial DNA

It is also sometimes helpful to analyse mitochondrial DNA (mtDNA) which is contained in small structures (called mitochondria) within cells. They are found in the cell body, rather than in the nucleus. The mitochondrial genome consists of only 16,500 bases, arranged in a circle (Figure 3). In contrast to the presence of only two parental copies of the nuclear DNA, there are thousands of copies of mitochondrial DNA in the same cell. Both males and females have mitochondrial DNA but it is exclusively inherited from the mother. All of a mother’s children have the same mitochondrial DNA, which is the same as that of all their relatives in the same maternal line. Because of the many copies of mitochondrial DNA present in a cell, this analysis is useful when there is a minute amount of DNA present or when the DNA sample is very old and has broken down. STR profiling and mtDNA / Y chromosome analysis are distinctly different and there are many more individuals who would have matching mtDNA profiles by chance than with STR profiling.

Appendix 2 provides more in-depth information on how DNA is analysed and how a DNA profile is obtained.

FIGURE 3

Mitochondrial and nuclear DNA (image adapted from Creative Commons).
2.4 Comparison of DNA profiles

2.4.1 Collection of DNA samples – avoiding contamination

Biological evidence from a crime scene needs to be collected carefully, transported and stored properly prior to examination. Most biological evidence is best preserved when stored dry and/or frozen. Contamination in the context of DNA analysis can be defined as the introduction of extraneous DNA (or biological material containing DNA) to a sample. The DNA profiling process is extremely sensitive and constant vigilance is required to ensure that contamination does not affect the results. Because of this sensitivity, contaminating DNA may still be observed even with careful precautions, and will routinely be monitored in laboratories. The forensic scientist must use all the information available to them to assess whether a contamination event, if it occurs, has had an impact on the results in a specific case.

2.4.2 Evaluating the statistical weight of matching a single DNA profile

If there is a match between the STR profiles of two DNA samples, then there are three possible explanations:

1. The suspect is the source of the material.
2. The material came from a second person who has an identical DNA profile to that of the suspect.
3. The match is a false positive due to contamination or some other kind of error.

The match probability is an estimate of the likelihood (or chance) of observing the DNA profile obtained if someone other than, and unrelated to, the suspect, was the source of the DNA. An expanded explanation is presented in Appendix 3.

2.4.2.1 Complex DNA profiles

In some instances, the amount of DNA in a sample might be lower than optimal, or it might be of poor quality (degraded) or consist of many contributors (a mixture). In such a situation, particular care must be taken in interpreting the DNA profile. There will always come a point below which no interpretation can deal effectively with the level of variability in a poor DNA profile. There is no simple way of defining the lowest-level profile that should be interpreted. A scientist should always stay within the validated range for his or her interpretation methods using the relevant laboratory equipment and tests and should not attempt to interpret profiles that fall outside this range.
2.4.2.2 Factors to be considered in the evaluation and weight of evidence of DNA profiles

In evaluating matching DNA profiles, it is important to consider how the DNA came to be present in a particular place. Understanding from which material the DNA came can assist in this evaluative process. Current tests for body fluids are not definitive and forensic scientists may not be able to give an opinion as to the body fluid from which a DNA profile originated. Other samples (hair, skin etc) can also provide DNA profiles.

DNA can in some instances be transferred from person A to person B and then onto object 1 (‘secondary transfer’) or from person A to object 1 to person B and then onto object 2 (‘tertiary transfer’). In both cases, traces of person A’s DNA might be found on an object even when they have never been in direct contact with that object. It is also perfectly possible that the DNA of person B will not be present on an object with which they have had direct contact. In some cases (but not always) it will be possible to make a comparative assessment between alternative explanations for the presence of the DNA.

Appendix 3 provides more information relating to the evaluation of DNA profiles and the weight which can be put on such evidence, in the light of factors such as transfer and persistence of DNA.
3. The future

Scientists are exploring new DNA methods, which may, for example, enable prediction of an individual’s skin, hair or eye colour. These methods, at their current stage of scientific development, would be primarily of use in an investigation for intelligence purposes rather than as evidence presented in court. Methods to examine an individual’s entire genome have also been developed and are becoming faster and less costly. The use of different parts of the genome for human identification purposes within the Criminal Justice system has not yet been fully explored.

More accurate chemical testing methods for determining the type of body fluid from which a sample originated are also being developed. Although not yet widely in use, these would enable scientists to be more certain about the type of material (blood, semen, saliva or other cellular material) from which a DNA sample might have originated.
4. Summary

Forensic DNA analysis has been established as a core scientific technique since the mid-1980s and has been used widely in the UK courts and many courts around the globe. Its underpinning science is reliable, repeatable and accurate, and based on validated technology and techniques for both the generation of a DNA profile and the interpretation of that profile. When forensic DNA analysis is adduced as evidence in court, the following matters should be borne in mind when assessing both admissibility and weight of evidence:

- DNA profiles are generated using scientifically accepted techniques and following validated scientific methods.
- When a DNA profile is obtained from one person, the interpretation of that DNA profile is normally straightforward and provides powerful scientific evidence to either exclude or include an individual as a possible source of the DNA.
- DNA profiles can provide exclusionary evidence as well as evidence of association.
- Contamination and errors can occur in the DNA analysis process. Scientists can address case-specific issues through the processes, checks and control samples associated with that case.
- The analysis and interpretation of complex DNA profiles should be undertaken only within guidelines validated by the organisation performing the work. These guidelines should be made available.
- The weight of evidence from complex/mixed DNA profiles is largely estimated using computer software. There are a range of software programs available, which use different assumptions and statistical methods to analyse the complex/mixed DNA profiles and to produce ‘unmixed’ profiles. This means that:
  1. the same data derived from complex/mixed DNA profiles analysed repetitively by the same software can exhibit small differences in the resulting ‘unmixed’ DNA profiles.
  2. the same data derived from complex/mixed DNA profiles analysed by different software programs can exhibit more marked differences in the resulting ‘unmixed’ DNA profiles.
• The choice of software program and why it was used for the specific complex/mixed DNA samples being analysed should be explored with the scientist.

• Any estimate of weight of evidence is calculated with probability estimates: a match probability is a probability estimate, while a likelihood ratio is the ratio of two probability estimates. In the UK, match probabilities smaller than one in one billion are capped at one in one billion. Likelihood ratios greater than one billion are also capped at one billion.

• Tests to determine which body fluid(s) may have produced a DNA profile generally give only an indication of the body fluid and not a definite identification.

• There are some published studies addressing the transfer and persistence of DNA but specific circumstances relating to individual criminal cases are not likely to have been studied.
Appendix 1: Defining DNA and its use in forensic science

A 1.1 DNA used in forensic science
DNA is composed of four chemical constituents (labelled A, T, C and G), known as bases, attached to a sugar backbone, which can form a strand millions of bases long. Forensic DNA analysis typically assesses specific stretches of DNA (loci) where there are repeating blocks of four bases known as short tandem repeats or STRs. Mutations resulting in the gain or loss of a four-base block are relatively common and as a result the number of four-base blocks present at an STR locus shows considerable variation within a population. Each version of the locus, called an allele, has a specific number of repeats of the four-base blocks. Forensic DNA analysis is concerned with measuring the length of DNA at these sites, which correlates with the number of repeats of the four-base blocks (Figure 4).

In order to determine the length of DNA at any one locus, a technique known as a polymerase chain reaction (PCR) is used to generate many copies of the relevant stretch of DNA from material recovered at the crime scene. These DNA fragments can be separated according to their size using a technique known as electrophoresis.
A single strand of DNA illustrating a short tandem repeat (STR) composed of repeats of the four-base pair block GATA. It is the number of repeats of this block that varies between individuals. In Figure 4(a), the DNA ‘type’ or ‘allele’ is 13 as there are 13 repeats. In Figure 4(b), the allele is 12 as there are 12 repeats, and in Figure 4(c) the allele is 10 as there are 10 repeats. The locus is the region of the DNA where the STR is located. Each individual will have two copies of each locus – one from each parent, which could be the same or different alleles.

Resulting DNA profiles are represented as a numerical code (corresponding to the number of repeats of units of four bases on each allele at each STR locus), and the length of each STR is visualised on a chart known as an ‘electropherogram’. On this chart, the horizontal axis shows the length of the DNA fragments and the vertical axis shows their relative abundance. Figure 5 is a schematic of part of an electropherogram showing two loci A and B. At locus A, there are two STR alleles of length 13 (one allele of length 13 from each parent) and at locus B there are two alleles of length 10 and 12 (again one allele from each parent, this time of different lengths). Because the two ‘13’ alleles at locus A are the same length, they occur at exactly the same position on
the DNA profile chart. When there are two copies, there is twice as much of the ‘13’ DNA present, and so the height of the peak, which represents the amount of DNA present, is about twice as tall as if there were one ‘13’ allele present. Examining different loci and determining the alleles (a process known as ‘genotyping’) generates a person’s DNA profile. The allele frequency is how often that number of repeating units at a particular STR locus occurs in a given population. For example, if allele 13 at locus A occurs ten times in 100 individuals, then its frequency would be ten in 200 alleles (100 people with two alleles each – one from their father and one from their mother). The statistical analysis of forensic DNA data focuses on establishing the weight of evidence that should be attached to the similarity between the DNA profile from a person of interest and material recovered from a crime scene or from a complainant/complainer.

**FIGURE 5**

Diagram of the alleles representing the STRs from each of the two copies of DNA present (one contributed by each parent) at two loci A and B.
A 1.2 Current DNA profiling methods

The principal method of forensic DNA analysis is to consider the profile of the STRs. If only one STR section of DNA were analysed, many people would share the same DNA profile. Therefore, it is necessary to analyse a number of different STRs to ensure that the chance of two unrelated people’s STR profiles matching is acceptably small. Over time, the number of STRs analysed in human DNA profiling has been increased to the point that the chance of two unrelated people sharing the same DNA profile has become infinitesimally small. Table 1 illustrates the evolution of the numbers of STRs analysed. There are various commercial analytical kits containing the chemicals required for the analysis of groups of STRs at the same time. These kits are called multiplexes. In addition to the STRs, each of the systems also includes a test to determine whether the sample comes from a male or a female.

### Table 1

The STR DNA profiling systems used in the UK.

<table>
<thead>
<tr>
<th>Years used</th>
<th>Number of STRs analysed</th>
<th>The commercial kits (multiplexes) used for the analysis of groups of STRs present at different loci</th>
</tr>
</thead>
<tbody>
<tr>
<td>1995 – 1999</td>
<td>6</td>
<td>SGM (Second Generation Multiplex): Few of the DNA profiles held on the National DNA Database are SGM profiles – where possible, a sample matching an SGM profile would be upgraded to SGM Plus® or a later system.</td>
</tr>
<tr>
<td>1999 – 2014</td>
<td>10</td>
<td>AmpFISTR® SGM Plus® (Second Generation Multiplex Plus): Many of the DNA profiles held on the National DNA Database are SGM Plus® profiles. SGM Plus® profiles contain all the STRs in the SGM grouping plus four more. This amplification kit has not been in routine use since 2014.</td>
</tr>
<tr>
<td>2014 – present</td>
<td>16</td>
<td>The names of the multiplexes used in the UK are: PowerPlex® ESI 17, AmpFISTR® NGM (Next Generation Multiplex) SElect™, Investigator ESS (European Standard Set) Plex SE. All are collectively referred to as DNA 17 multiplexes and contain the same 16 STRs, which include the 10 SGM Plus® STRs plus six more, and a gender identifier.</td>
</tr>
<tr>
<td>2014 – present (in Scotland)</td>
<td>23</td>
<td>AmpFISTR® GlobalFiler®: GlobalFiler contains the 16 STRs in ESI 17, NGM SElect and ESS Plex SE, plus an additional five STRs and two Y chromosome markers, plus a gender identifier.</td>
</tr>
</tbody>
</table>
A second form of DNA analysis involves the analysis of DNA found in one particular chromosome found only in males, called the Y chromosome. Analysing Y chromosome STRs can be helpful where there is a mixture of DNA from male and female contributors. For example, if a sample contains a large amount of female DNA and there is only a small amount of male DNA present, then examining the Y chromosome gives just the male contributor’s DNA profile rather than a mixture (Figure 6).

**FIGURE 6**

Diagram of Y STR links between males. Squares represent males, circles represent females.
A 1.4 Mitochondrial DNA

A third technique is the analysis of mitochondrial DNA (mtDNA). Both males and females have mitochondrial DNA which is always inherited from the mother. All of a mother’s children have the same mitochondrial DNA, which is the same as that of all their relatives in the same maternal line (Figure 7).

Many copies of mitochondrial DNA are present in each cell, so mitochondrial DNA analysis is useful when there are very small amounts of DNA present (such as in hair shafts without roots), or when a DNA sample is very old and has broken down. In mitochondrial DNA analysis, scientists assess part of the DNA sequence rather than the length of a region of repeated blocks. As with Y chromosome analysis, and in contrast to nuclear DNA profiling, there are always more individuals who would have the same mitochondrial DNA profile. This is because relatives in the same female line over many generations share the same mitochondrial DNA. An example of mitochondrial DNA from two people who are unrelated maternally (with the differences underlined) might be:

Person 1: ACGGTTGCAAG
Person 2: AGCGGTACCAAG

Diagram of mtDNA links between mother and children. Squares represent males, circles represent females.

Mitochondrial DNA
(passed on complete from mothers to sons and daughters)
Appendix 2: DNA analysis in forensic science

A 2.1 Samples generally analysed for DNA profiling

Forensic DNA analysis relies upon comparing DNA profiles. A DNA profile is produced from body fluids and/or other cellular material deposited during the course of the commission of a crime (for example, hair, blood, saliva from a discarded cigarette or drinks can, semen from an intimate swab from an alleged rape complainant/complainer). Such samples are called ‘questioned samples’. The DNA profile from the questioned sample is compared to the DNA profile of one or more known samples from:

- suspect(s)
- complainant(s)/complainer(s)
- other people with regular access to the location from which the crime-scene samples were collected
- other relevant people such as family members (in missing person’s investigations, paternity testing and mass disaster events).

Generally, for known samples, mouth (buccal) cells are collected rather than drawing blood. Buccal cell collection involves wiping a swab against the inside cheek of an individual’s mouth to collect skin cells. The swab is generally frozen for storage. Known samples are collected from people already known to the investigation or from people found following a DNA database search.
A 2.2 How should DNA samples be collected and preserved for analysis?

A 2.2.1 Sample collection

The biological material present at crime scenes first needs to be detected. Body fluids may be identified visually, by chemical analysis/test/reaction or with the use of different types of light source. Sometimes the approach to targeting for testing is more intuitive and relies on the scientist’s expectations of where a person may have handled an object depending on the circumstances of each case. One of the most common methods for collecting biological material from hard surfaces (such as a broken window or a knife) is using a swab. The swab is moistened with sterile DNA-free water, and then rubbed over the surface to be sampled. This might be followed by a second swab to ensure any remaining material is collected. Biological material might be collected from fabrics by cutting out a stain or by using sticky tape to collect surface material (such as from the collar of a shirt).

In choosing sampling sites for material not visible to the eye, such as cells left by handling an object, the forensic examiner will use their knowledge of the circumstances to determine where to collect the material. For example, if an assailant has grabbed a bag, the area of the bag which was grabbed will be sampled, or if an assailant has tied a ligature around a complainant’s/complainer’s neck, the areas where the ligature will have been handled most in tying the knot will be sampled. In allegations of rape or sexual assault, a complainant/complainer will be medically examined, and will have intimate samples, such as from the vagina or anus, and swabs of any skin areas alleged to have been touched or licked by the perpetrator, taken by a medical practitioner.

A 2.2.2 Sample preservation

Most biological evidence is best preserved when stored dry and/or frozen. These conditions reduce the rate at which DNA will break down, and prevent mould and bacteria from growing. Samples are packaged carefully, often using ‘tamper-evident’ bags that show a visible warning if someone has attempted to open them. They are then transported to the forensic laboratory, where they are inspected and signed for on arrival. Inside the laboratory, the samples are generally frozen, although very heavily stained, wet items might be dried in a controlled environment. Drying will assist with preservation but would generally only be used for large, heavily stained, wet items. The DNA is then chemically extracted and purified from the biological material and stored in sealed tubes either in a refrigerator at 4°C or a freezer at -20°C.
A 2.3 How is a DNA profile generated?

A DNA profile is generated from the analysis of a submitted sample or from a sample taken from a known individual. Once an item of evidence from a crime scene has been presented to the forensic scientist for DNA analysis, the following general steps are undertaken (steps 4 to 9 are also undertaken to generate a DNA profile from a sample taken from a known individual):

1. laboratory examination of the submitted item to locate any body fluid(s) present
2. recovery/sampling of body fluid
3. evaluation of the collected sample
4. DNA extraction
5. establishing how much DNA is present within the extracted sample (quantification)
6. copying (known as amplifying) of the STR regions many times using a chemical process called PCR (polymerase chain reaction)
7. separation of PCR products by size
8. detection of PCR products
9. data interpretation.

The DNA profile looks like a chart with different coloured peaks rising from a baseline (Figure 8).
STR DNA single person profiles from (a) good-quality DNA and from (b) poor-quality DNA. Going from left to right along the horizontal axis, the size of the DNA fragments gets larger. The vertical height of each peak shows how much DNA of that size is present. The numbers in the good-quality profile refer to the 16 STR loci and the gender marker, (labelled 17). Different colours are used for loci where the expected DNA fragments are of similar size, allowing alleles at one locus to be readily distinguished from alleles of similar length at a different locus. The larger DNA targets are missing from the poor-quality sample because the DNA sample was broken down and could not be profiled. The PCR process relies on fully intact DNA across the locus of interest, so detection of longer fragments is more sensitive to degradation of the sample DNA.

Figure courtesy of Margaret Kline, National Institute of Standards and Technology (NIST). From J M Butler (2012) Methodology book, Figure 10.3
The scientist can use this chart (called an electropherogram) to determine whether the sample is from a male or female, and whether it is from a single individual or from multiple individuals. In a male, the gender marker (known as amelogenin) shows two different sized peaks. In a female, only one of these peaks is seen.

At each STR locus, the number of peaks observed on the graph will give an indication of the number of individuals whose DNA has contributed to the profile. One individual will have either one or two peaks (alleles) at each STR locus.

The vertical scale of the graph represents the amount of DNA detected at each STR locus and the scientist will use the height of the peaks as an approximation for the amount of DNA of that particular type.

If the DNA profile has arisen from a mixture of DNA from two people, then three or four peaks would be expected to be observed at a number of the STR loci. As the number of contributors to the mixture increases, the number of peaks seen at each STR locus will tend to rise. However, as the number of contributors to a mixture increases, the chances are that those contributors will share some of the same peaks and so the scientist may not be able to determine with certainty how many people’s DNA is present.

When mixed samples are obtained then the number of peaks at each STR locus can become difficult to determine. In some instances, there may be sufficient difference between the amount of DNA contributed by one person in a mixture and that of others, so that the entire DNA profile of the person contributing the most DNA to the mixture (the major profile) can be unequivocally determined. If all of the individuals have contributed about the same amount of DNA to the mixture, then there will be no discernible difference in height between the peaks originating from one individual versus another.

The scientist will also check whether or not the DNA profile is of the quality and clarity they would expect, given that they have already determined approximately how much DNA was present in the sample. If the DNA profile is not as good as expected, given the amount of DNA that was analysed, the scientist may choose to repeat the analysis. However, if a minute amount of DNA was available for the analysis yet a very strong and clear DNA profile was obtained, the scientist will want to double check that contamination has not occurred.
A 2.4 Interpreting DNA profiles

When viewing DNA profiles, scientists first judge whether the overall quality of the data is appropriate for reliable interpretation. In a fresh, good-quality DNA sample, the scientist will observe large peaks, which are a similar height to each other. They may be able to confidently evaluate how many people have contributed to a mixed DNA profile from good-quality DNA profiles.

A complex DNA profile is one in which one or more of the following conditions occur:

1. Less than the optimal amount of DNA present (low template).
2. A mixed DNA profile where the number of contributors is unclear.
3. The DNA has degraded, which means it has broken down into small pieces insufficient for a full profile to be produced.
4. There are chemical components stopping the DNA profiling process from working efficiently (inhibition).

In a complex DNA profile, the scientist will often observe small peaks that are close to the baseline of the graph. This will mean that there will be ambiguity regarding what constitutes a true allele rather than an artefact of the analysis. There will also be uncertainty in defining the number of possible contributors to a mixture. If the DNA is old, or has been in a warm, humid environment, it will have started to degrade into smaller pieces, and larger STRs (longer alleles) might give disproportionately low peaks or even be missing (Figure 8(b)) giving a characteristic ‘ski slope’ appearance. All of these effects are increased if there is less than an optimal amount of DNA present in the sample to start with. As the quantity and quality of DNA decreases, some STRs show only one instead of an expected two peaks and some will give no results at all. These are known as partial DNA profiles. Figure 9 shows portions of DNA profiles with ‘noise’ artefacts marked. These artefacts will generally be excluded from the comparison between a crime-scene sample and a known sample.
Scientists must judge whether all of the parts of the DNA profile can be confidently assigned to one person or, in the case of a mixture of DNA from multiple people, how many different people’s DNA might be present. Depending on the quantity and quality of DNA present, the interpretation process might be straightforward with no ambiguity, or it might leave room for a range of opinions. In a fresh known sample such as a mouth swab taken from a person of interest, scientists can distinguish which of the peaks are known and understood technical artefacts with certainty, as they will be at a very low level compared to the alleles in the DNA profile.

**FIGURE 9**

Sections of STR DNA profiles showing a range of technical artefacts.

**Stutters:**
these are low peaks (highlighted by yellow arrows), generally one repeat unit smaller than the true peak; they are caused by slippage during the process of making copies of the DNA.

**A peaks:**
the copying process usually adds one single ‘A’ base at the end of every DNA fragment, but when this has not happened completely, the result is a ‘shoulder’ to the left of the main peak, which is one base smaller than the main peak.

**Pull-up:**
during the detection part of the process, a strong signal in one colour can cause small peaks of the same size to appear in the adjacent colour.
As the amount of good-quality DNA decreases and/or the number of people’s DNA present in the sample increases, the level of certainty in distinguishing sample DNA from noise decreases. Take for example, a DNA profile originating from two people, where person A has contributed most of the DNA and therefore has high peaks, but person B is only present at a very low level, with low peaks. It would not be possible to determine whether a small peak near to the baseline is a stutter from person A’s strong profile or might be part of person B’s very weak profile.

In general, scientists are aided in their interpretation of DNA profiles by computer software and by data produced during extensive testing (validation) of the analytical processes. The results from validation testing, which would include the maximum level at which each artefact (illustrated in Figure 9) is observed, are used to generate ‘standard operating procedures’. Standard operating procedures are written guidelines to ensure that the scientists within an organisation make consistent interpretation decisions, supported by analytical data. While different organisations will have different procedures, each will have scientifically validated their methods. The way in which methods should be validated is prescribed in the Forensic Science Regulator’s Codes of Practice and Conduct and associated guidance. These Codes also set out the required quality standards; for DNA analysis, accreditation to an international standard (ISO 17025) is required. The accreditation process includes independent external scrutiny of each organisation’s methods and competence, to ensure they meet the required standards. This external scrutiny is provided by the United Kingdom Accreditation Service (UKAS). Appendix 3 provides a detailed analysis of how DNA profiles are compared.

2. Available at: www.gov.uk/government/publications/forensic-science-providers-validation
A 2.5 What is DNA contamination and how can it be controlled?

Contamination can be defined as the introduction of DNA, or biological material containing DNA, to a sample after a (trained) responsible official has control of the crime scene.

Because the DNA profiling process is extremely sensitive, constant vigilance against contamination is required. A police officer or crime-scene examiner collecting evidence can contaminate samples if proper care is not taken. Examples of ways in which contamination could occur at a crime scene include a crime-scene examiner not changing gloves between handling different exhibits, or talking without a properly fitted face mask. Likewise, the scientist analysing the DNA can inadvertently add his or her own DNA to the sample. For this reason, detailed guidance has been published by the UK Forensic Science Regulator on avoiding DNA contamination at crime scenes, in laboratories, and in sexual assault referral centres and police custody.

It is important that all disposable items (for example swabs) and all chemicals and kits used in the analytical process are free from DNA before use. An international standard for DNA-free items has been published and all purchasing of items by police and laboratories should take account of its requirements. It is critical that police ensure that, during the arrest of suspects and their processing in custody suites, cross-contamination between suspects or from a suspect to a police officer and hence potentially to a complainant/complainer or crime scene is avoided. For example, a suspect in relation to a sexual assault should not be transported in the same vehicle as was previously used to transport the complainant/complainer. Similarly, if multiple suspects are arrested, they should be processed, detained and forensic samples taken separately. If intimate samples are to be taken, they should be taken by different medical practitioners in different facilities.

Laboratories recognise that contamination can occur between people, consumables and other items in the forensic process. The working practices of labs are geared to prevent contamination and to detect it, should it happen. The use of appropriate controls and testing provides assurances that the general risks of contamination are minimised.

3. ISO 18385:2016 Minimizing the risk of human DNA contamination in products used to collect, store and analyze biological material for forensic purposes – Requirements. Available at www.iso.org/standard/62341.html
Even with all these precautions, the sensitivity of DNA profiling methods means that sometimes contaminating DNA will still be seen. This may either be as a complete or nearly complete profile, or merely one or two peaks (alleles). In the latter case, this type of very minimal contamination is known as ‘drop-in.’ A suggestion that contamination has adversely affected any particular case is dealt with by assessing the information available relating to the continuity of the specific evidence and evaluating particular scenarios.

A 2.6 What is the National DNA Database and what types of samples does it contain?
The UK National DNA Database (NDNAD) was established in April 1995 and is managed and operated by the Home Office on behalf of UK police forces. DNA databases can generate investigative leads in cases without suspects, and can also enable linking of serial crimes involving biological evidence. Two data sets exist, which are searched against each other:

(1) DNA profiles from offenders who have been convicted or in some cases arrested for a recordable offence.

(2) DNA profiles from evidence recovered from crime-related samples.

In addition, the DNA profiles of crime-scene staff, many police officers, all forensic science laboratory staff, many staff involved in manufacture of the reagents and consumables used in laboratory processes and some external experts are retained on elimination databases and are checked to ensure that these individuals did not inadvertently contaminate the results. These DNA elimination databases are separate from the National DNA Database. DNA samples from volunteers and missing persons are also held, but again, separately from the National DNA Database.

Over time, the number of STRs used to generate the profiles stored on the NDNAD has increased as the technology has developed. Neither Y chromosome STR data nor mitochondrial DNA sequences are held or searched against the National DNA Database.
Appendix 3: Comparison of DNA profiles in forensic casework

A 3.1 How DNA profiles are compared and the calculation of the likelihood ratio and match probability

A 3.1.1 Comparison process
The best approach to DNA interpretation, which should be followed, is for the scientist to interpret the crime sample first, and to document their findings. Exceptions should be rational and documented. Only after the crime sample has been interpreted should the scientist interpret any known samples, before making a comparison between the two. This is to reduce the risk of confirmation bias. When the crime sample DNA and the known sample DNA have been interpreted in isolation, they can be compared, to see if they may be from the same or a different source. This comparison refers to the origin of the DNA only. How and when the DNA was deposited is a matter for further evaluation.

A 3.1.2 Match probability
If there is a perfect match between the STR profiles of two DNA samples, then there are three possible explanations:

1. the suspect is the source of the material at the crime scene
2. the material came from a second person who has an identical DNA profile
3. the match is a false positive due to a sample switch or some other kind of error.

The match probability is an estimate of the likelihood of observing that profile if someone other than, and unrelated to, the suspect was the source of the DNA.

In order to calculate the weight of evidence if a match is observed, a frequency estimate for the profile is generated from representative data sets and appropriate statistical correction factors are applied so that the figure presented in court is fair and reasonable and does not overstate the strength of the evidence. About 1 in 1,000 individuals within a population has an identical twin. If there is no information as to whether a suspect has a twin, an upper limit of 1 in 1,000 should be assumed, although typically such information is available. In the UK, the lowest match probability that is reported is one in a billion, even though the actual calculation might result in an even smaller chance of a match, such as one in a trillion or even less. The reasons for this ‘cap’ on match probability are that:
1. it becomes difficult to test the assumptions required in the calculation to the point where even smaller match probabilities can be assured to be accurate

2. The real meaning of numbers in the trillions or beyond is difficult to comprehend.

Assuming that the match probability has been calculated accurately and in accordance with the laboratory’s standard operating procedures, its interpretation still requires care.

Suppose the match probability is 1 in 3 million. This is the probability that a randomly chosen individual has the particular DNA profile revealed by analysis of the crime-related samples. However, this means a little over 20 people in the UK would be expected to have the same profile. The ‘defence lawyer’s fallacy’ is to argue that there is therefore a 1 in 20 chance of the suspect being the source of the material. However, this is only true if all members of the population (including the suspect) had an equal probability of committing the crime and leaving biological material at the scene or the suspect was only identified by searching a national database of DNA profiles of randomly chosen individuals. Typically, other sources of evidence have been used to lead prosecutors to a suspect.

In contrast, the ‘prosecutor’s fallacy’ argues that the match probability implies a 1 in 3 million chance that the suspect is innocent. Again, the statement is false. The probability of guilt or innocence given the DNA profile match is dependent on a wide variety of non-DNA factors that are unique to each case. The highest level of confidence in a match occurs when the match probability is so low that there is unlikely to be any other individual within the population with the same DNA profile.

There can, however, be other credible reasons to find a particular person’s DNA at a crime scene and these should be explored. Such reasons may include whether there was evidence of any other explanation for the presence of the suspect’s DNA, whether the article on which the DNA was found was associated with the offence, how readily removable the article in question was, whether there was some geographical association between the offence and the suspect and whether the DNA in question was more likely to be there by primary or by secondary transfer. As a consequence, a DNA ‘match’ alone should never be used to imply a suspect’s involvement in a crime.
A 3.1.3 The likelihood ratio
The likelihood ratio (LR) divides the probability of obtaining the observed genetic similarity under a hypothesis associated with the prosecution view (which is generally that the suspect has contributed the DNA) by the probability of obtaining the observed match under an hypothesis relating to the defence view (for example that the suspect and actual donor of the DNA are unrelated). In simple cases, the likelihood ratio is one over the match probability for well-amplified profiles coming from one person. In more complex cases, the evidence may be evaluated under a range of hypotheses.

Likelihood ratios are generally accepted as being the most appropriate method for evaluating the evidential strength of DNA profiles. The calculation allows for different explanations for the observed evidence. For example, in a mixed DNA sample containing DNA from three people, the prosecution hypothesis might be that the DNA originated from the suspect, the complainant and an unknown, unrelated individual. The defence, however, might claim that the DNA originated from the complainant, the suspect's brother and an unknown, unrelated individual. Or indeed it might be that the DNA originated from three completely different people. The calculations for these different defences will be different and will give different results.

Scientists should communicate clearly the propositions they have considered, including the number of contributing individuals, any assumptions they have made regarding known or assumed contributors and any assumptions concerning the relationship between individuals eg that they are unrelated, as these will all affect the calculation of evidential strength. The likelihood ratio also enables scientists to account for artefacts, low-level contamination and other complexities such as low-template DNA effects, which are discussed in the following section.

As for match probabilities, there is a ‘cap’ placed on the likelihood ratio in the UK and the largest likelihood ratio that would be reported is one billion.
A 3.2 Low-template, degraded and compromised DNA profiles

In the past, ‘low-template DNA analysis’, sometimes referred to as Low Copy Number or LCN DNA analysis, was used to refer to methods where the sensitivity of the analysis was specifically boosted by altering the analysis method, to enable results to be gained from lower quantities of DNA. However, due to the very high analytical sensitivity of all current methods used for DNA analysis, specific technical boosts to sensitivity are now rarely employed.

DNA profiles can now be obtained routinely from just a few cells. The optimal amount of DNA is the amount of DNA that will yield a full DNA profile without the potential for interference from artefacts or other technical issues in the interpretation process. Sometimes, the amount of DNA from each contributor in a sample is lower than optimal because the DNA is a mixture from more than one individual – the total amount of DNA (by weight) added to the chemical reaction might contain enough of the major contributor of the mixture to generate a good-quality profile, but there might be insufficient DNA from a minor contributor to enable a high-quality profile to be generated from this (minor) contributor.

Alternatively, there might have been a sufficient quantity of DNA, but it is of poor quality, with many short segments and little of the required length for analysis. This is termed degraded DNA. DNA degrades (or breaks down) gradually as it ages, but the process is quicker if the biological material stays warm and wet. For these reasons, the amount of DNA measured and added to the chemical reaction cannot be used as a standalone guide to whether a DNA profile should be regarded as ‘low template’. When the quantity of good-quality DNA is lower than optimal, particular care must be taken in interpreting the DNA profile. The optimal level of DNA is determined through the validation processes of the laboratory based on the multiplexes used to generate the profiles.

Section A 3.1 laid out the general approach to interpretation, and Figure 8(b) shows the loss of part or all of the information at one or more STRs that can occur. These effects all happen to some extent, and in a less predictable manner, when the input level of DNA is lower than optimal. In addition, the impact of DNA contamination can be greater when the amount of DNA in the evidence sample is very small – if there is very little DNA to begin with, then even a minute amount of contaminating DNA could ‘take over’, with the result that only the contaminant DNA and not the source DNA is seen.
One useful way to determine whether the profile is from a low level of input DNA is to analyse it two or three times, and to look at the level of reproducibility between the replicates. If the pattern of peaks remains similar between replicates (such as in Figure 10(a)), then there is sufficient DNA present to interpret reliably using standard methods. If, however, each replicate gives a very different pattern of taller and smaller peaks and some peaks are missing (such as in Figure 10(b)), then the scientist must either reject the profile as being insufficiently reproducible for reliable interpretation, or must employ special interpretation methods that have been thoroughly tested (validated) to deal with such low levels, accounting for the high degree of variability seen.

**FIGURE 10**

A portion of a DNA profile involving replicate tests from low-template DNA (a) where reproducible peak heights were observed in the replicate samples and (b) where drop-out occurred, shown by arrows.
There will always come a point below which no software or method of interpretation can deal effectively with the level of variability in extremely low-level DNA profiles and such profiles should not be interpreted. There is no simple way of defining the lowest-level profile that should be interpreted. A scientist should always stay within the validated range for his or her interpretation methods using the relevant laboratory equipment and tests and should not attempt to interpret profiles that fall outside this range.

(Source: www.cstl.nist.gov/strbase/LTDNA.htm (Identifiler 31 cycles, sample 1) 100 pg (left) and 10 pg (right))
A 3.3 Assessing the weight of evidence of DNA profiles

There are a range of software programs available to assist scientists in calculating the weight of evidence resulting from genetic similarity between a known sample and a crime sample. However, the interpretation method does not solely consist of the software, but also the standard operating procedures of the laboratory, which are based on validation data (including the demonstration of repeatability, reproducibility and accuracy) and the judgment of the scientist, for example in:

1. assessing whether a DNA profile is suitable for statistical evaluation, including interpretation of the various quality controls employed
2. assessing the optimal software to use for the profile(s) in question
3. ensuring that at least two suitable alternative propositions are clearly stated (occasionally there can be more than two alternatives)
4. evaluating the output from the software used
5. evaluating the combined meaning of the various biological stains, amounts of input DNA, profiles from crime samples, known samples and controls in the context of the case.

Software used for calculating the weight of evidence from DNA profiles can be divided into three types, as shown in Table 2. Whichever software is used, the interpretation method, including the software, must be validated (including the demonstration of repeatability, reproducibility and accuracy) for the types of DNA profiles that are being interpreted. The Forensic Science Regulator’s Codes of Practice and Conduct publication has set out the required approach to validation. It starts with clearly defining what the method is to be used for and ends with a ‘statement of validation completion’, which sets out the strengths and weaknesses of the method, what it can be used for and any limitations. A scientist presenting evidence using software to aid their interpretation should therefore be able to state clearly the types of DNA samples for which their method (including the software) is validated.
There has been rapid development in methods for calculating the weight of DNA evidence in recent years, which has increased the range of complex profiles that can be evaluated. Each weight of evidence method:

1. makes different assumptions
2. uses a different subset of the raw or processed data comprising a DNA profile
3. employs different statistical models.

This means that when the weight of evidence from a complex DNA profile is estimated using the different software approaches, even if the hypotheses being tested are identical, different values for the likelihood ratio will be obtained, as each is an estimate of probability. Weight of evidence software using binary or discrete methods (Table 2) does not take account of the height of the peaks in the DNA profile, so would not use peak height to distinguish between the DNA contributors. Continuous methods (Table 2) incorporate more information from the profile, such as peak heights and artefacts. Frequently, but not always, this approach will provide stronger likelihood ratios for true contributors.

New refinements and developments in computer software are ongoing. Given that the current software programs essentially use very different statistical methods, when the same DNA data are analysed by different software systems, different results can be obtained. However, for many DNA profiles, no difference will be seen, as any software would calculate the likelihood ratio to be over a billion, and all results are capped at this level. It will only be where DNA profiles are incomplete or at low levels that differences might be seen.
**TABLE 2**

Types of DNA mixture interpretation software.

<table>
<thead>
<tr>
<th>Software type</th>
<th>Typical uses</th>
<th>How does it work?</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Binary</strong></td>
<td>Simple DNA mixtures (two or three persons’ DNA present). There is sufficient DNA present so that low-template DNA issues do not need to be considered.</td>
<td>The scientist evaluates which of the DNA peaks are from the source DNA. The software does not use information about the height of the various DNA peaks (although the scientist will already have considered peak height information), nor does it consider the possibility of unpredictable effects as described for low-template DNA. Therefore, this type of software is not suitable for evaluation of evidential strength where one or more of the profiles shows low-template effects. The software makes a straightforward calculation of the estimated match probability or likelihood ratio.</td>
</tr>
<tr>
<td>Discrete variables</td>
<td>Continuous variables</td>
<td></td>
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<tr>
<td>-----------------------------------------------------------------------------------</td>
<td>---------------------------------------------------------------------------------------</td>
<td></td>
</tr>
<tr>
<td>DNA mixtures (up to four persons’ DNA present) or DNA mixtures where there might be low-template DNA issues to interpret.</td>
<td>Complex mixtures with low-template DNA issues to interpret. Can be used to interpret DNA mixtures from at least three different people. Some software might be capable of interpreting mixed profiles with DNA from more than three contributors.</td>
<td></td>
</tr>
<tr>
<td>The scientist evaluates which of the DNA peaks are from the source DNA.</td>
<td>The scientist rules out a small number of technical artefacts (see Figure 5), but does not need to evaluate which of the DNA peaks are from the source DNA and which are due to other technical artefacts (such as stutter). The software is programmed to know how these artefacts and low-template DNA effects vary in different samples, and in estimating the likelihood ratio, takes account of all the possibilities for each peak: whether it is really part of the source DNA or an artefact, whether it might be part of person A or person B’s profile, whether the DNA might be broken down into smaller lengths (degraded) and so on.</td>
<td></td>
</tr>
<tr>
<td>The software does not take account of the various peak heights, but it does make allowances for low-template DNA effects.</td>
<td>Some software of this type requires data from the laboratory using it, to ensure it reflects correctly how the effects vary between samples in that laboratory’s processes. So before the laboratory uses the software for casework, it will analyse samples with known DNA profiles at various dilutions and feed the data from this analysis into the software. This enables the software to model the characteristics of the laboratory’s process, for example stutter heights.</td>
<td></td>
</tr>
<tr>
<td>Software type</td>
<td>Reproducibility</td>
<td></td>
</tr>
<tr>
<td>--------------</td>
<td>--------------------------------------------------------------------------------</td>
<td></td>
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</tbody>
</table>
| Binary       | If the same DNA profiles were evaluated on different occasions, the same result would be expected.  
If different software of this type were used by different scientists, it would be expected that there would be a close agreement (less than one order of magnitude difference) between the results. |

| Examples of interpretation software available | Many forensic science laboratories will have developed their own spreadsheets to perform calculations of this type. |
If the same DNA profiles were evaluated on different occasions, the same result would be expected.

If different software of this type were used by different scientists to analyse the same data, it would be expected that there would be a close agreement between the results (generally within one order of magnitude). Any differences would be due to variations in how the software is set up to deal with low-template DNA results. If the same data were analysed by different software packages these might produce results that are more markedly different, and so the reasons why the scientist believes their method is scientifically validated and appropriate for the samples being analysed in the case should be explored.

This type of software often uses simulations (thousands of different estimations of the result) to give a final overall evaluation that is the best ‘fit’ for the DNA profile data. If the software was used to analyse the same set of DNA profiles on several different occasions, it would produce slightly different results each time. These variations are normal, and because they are very small in comparison to the overall result, they do not have a significant impact.

If the same data were analysed by different software packages these might produce results that are more markedly different, and so the reasons why the scientist believes their method is scientifically validated and appropriate for the samples being analysed in the case should be explored.

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**Discrete variables**

<table>
<thead>
<tr>
<th>Software type</th>
<th>Continuous variables</th>
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</thead>
<tbody>
<tr>
<td>Binary</td>
<td>Reproducibility</td>
</tr>
<tr>
<td>Discrete variables</td>
<td>Continuous variables</td>
</tr>
<tr>
<td>If the same DNA profiles were evaluated on different occasions, the same result would be expected.</td>
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<td>If different software of this type were used by different scientists to analyse the same data, it would be expected that there would be a close agreement between the results (generally within one order of magnitude). Any differences would be due to variations in how the software is set up to deal with low-template DNA results. If the same data were analysed by different software packages these might produce results that are more markedly different, and so the reasons why the scientist believes their method is scientifically validated and appropriate for the samples being analysed in the case should be explored.</td>
<td>If the same data were analysed by different software packages these might produce results that are more markedly different, and so the reasons why the scientist believes their method is scientifically validated and appropriate for the samples being analysed in the case should be explored.</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Software examples</th>
<th>Additional software examples</th>
</tr>
</thead>
<tbody>
<tr>
<td>LRmix Studio; Resolve; LikeLTD 4+; LabRetriever; LiRa.</td>
<td>STRmix; TrueAllele; LiRA-HT; DNA View Mixture Solution; LikeLTD 6.+; European Forensic Mixtures.</td>
</tr>
</tbody>
</table>

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A 3.4 Factors to consider in the evaluation of DNA

The assessment of weight of evidence as described in Section A 3.3 addresses the source of the DNA but does not consider how or when the DNA was deposited. We all transfer DNA to objects that we touch, objects onto which we sneeze, cough or bleed, and onto each other through social or sexual contact. Transfer events require three things to be in place in order to be considered – source, opportunity and mechanism. Each of these parameters is considered by scientists in the context of each case and the information supplied.

The first consideration by the scientist will concern whether or not it is possible to attribute the DNA profile to a particular body fluid. Depending on the type of sample, it might be possible to say that the DNA came from blood, semen or saliva. Scientists use chemical tests or special lighting to gain an indication of what body fluids might be present. However, the tests for these body fluids vary in their sensitivity and specificity, and there might be more than one body fluid present. If, for example, there is a very tiny, weak blood stain, but a very strong DNA profile is obtained, it is also possible that the DNA might not have originated from the blood stain, but might have been from someone who subsequently touched the blood stain. Therefore, there are occasions when a forensic scientist will not be able to give an opinion on the body fluid of origin. If the forensic scientist has sufficient information to infer that the DNA came from an identifiable body fluid, this information might assist with assessing by what activity the DNA came to be present in a sample.

Often DNA is transferred by touch rather than from a specific body fluid; this is known as ‘touch DNA’. DNA can persist for many months on an item, and determining when it was deposited is not possible. Not all touches will result in a DNA transfer and the amount of DNA we transfer in each situation will depend on a variety of factors, including:

1. person to person variability
2. how long it has been and what we have done since washing our hands/body
3. the intensity of contact (for example, a brief touch or a robust handshake)
4. whether surfaces are wet or dry, rough or smooth, absorbent or non-absorbent.
In certain circumstances, DNA can be transferred from person A to person B and then to an object, leaving traces of person A’s DNA on the object when they might have never been in direct contact with that object. This is known as secondary transfer. Tertiary transfer (person A to object 1 to person B to object 2) has also been demonstrated. Possible secondary and tertiary transfers are illustrated in Figure 11.

In Figure 11(a), person A touches the gun with primary transfer of A’s DNA to the gun. In Figure 11(b), person A touches person B, who then touches the gun. It would be possible to see person B’s profile, a mix of person A and person B, or just person A’s profile on the gun. This secondary transfer is more likely if the contact from A to B and from B to the gun happens soon after each other. In Figure 11(c), person A touches the mobile phone, which is then touched by person B, who touches the gun. If person A’s DNA profile were observed on the gun, this would have occurred by tertiary transfer. Although there is a low expectation of observing tertiary transfer, it is more likely if the contacts from A to the phone, from the phone to B and from B to the gun happen very soon after each other.
Questions as to how long after a transfer of material occurs can DNA related to that transfer still be recovered, or how much DNA will be transferred given a specific type of contact, are currently largely unknown. Each transfer possibility is dependent on the specific circumstances of the alleged activity and, as such, in looking at transfer scenarios, the scientist would rank possibilities rather than saying activity A is true and activity B is false. Because each case is different, there is not always directly applicable research or data related to each specific set of circumstances. The published research addresses different questions, and the experiments have been carried out in different ways, so it is not always possible to compare them directly. However, the published scientific research includes the following general principles regarding the transfer and persistence of touch DNA:

1. It is not possible to determine when the DNA was deposited.
2. DNA could persist for many months depending on a range of variables.
3. Secondary (or tertiary) transfer can occur such that a person’s DNA might be on an object they have never touched.
4. Secondary or tertiary transfer without also leaving the transferring person’s DNA has been demonstrated but only when the transfers occur immediately after each other. Transfer of DNA remains the subject of continuing research.
5. With each transfer we would normally expect a loss of available DNA, but the quality of the DNA profile cannot rule out a particular type of transfer since the end result will always depend on the available starting material.

In some instances, the scientific findings cannot provide any assistance in assessing how or when DNA came to be present, but in other cases, considering specific case circumstances, a comparative assessment can be made between alternative explanations. The scientist, in carrying out such an evaluation, should state their assumptions clearly. Having knowledge of the specific circumstances of the case after the interpretation and comparison process has been concluded, is considered important and will facilitate the scientist in effectively evaluating these transfer scenarios, and such evaluations should be contextualised in the latest relevant research.
A 3.5 The current understanding of error rates in DNA

If a match is observed between a suspect and crime-scene evidence, then three possibilities exist: (1) the suspect deposited the sample, (2) the suspect did not provide the sample but has the profile by chance, and (3) the suspect did not provide the sample and the matching result is a false positive due to a sample switch or some other kind of error or transfer. Genotyping errors (such as can occur from analysing very small traces of biological material) can also lead to imperfect matches.

### Table 3

Table 3: Error rates in submission of samples to the National DNA Database. A year’s data have been considered in compiling these figures.

<table>
<thead>
<tr>
<th>Source of error</th>
<th>General frequency of occurrence (as a proportion of samples processed)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Police force handling of suspect sample or suspect sample records</td>
<td>Less than 1 in 2,000</td>
</tr>
<tr>
<td>Police force handling of crime sample or crime sample records</td>
<td>Less than 1 in 50,000</td>
</tr>
<tr>
<td>Forensic laboratory handling of suspect sample or suspect sample records</td>
<td>Less than 1 in 10,000</td>
</tr>
<tr>
<td>Forensic laboratory handling of crime sample or crime sample records</td>
<td>Less than 1 in 5,000</td>
</tr>
<tr>
<td>Forensic laboratory error in known sample DNA profile interpretation*</td>
<td>Less than 1 in 10,000</td>
</tr>
<tr>
<td>Forensic laboratory error in the interpretation of mixed profile crime samples DNA*</td>
<td>Less than 1 in 500</td>
</tr>
</tbody>
</table>

* Each error in the laboratory interpretation error rates quoted refers to a single part of the DNA profile only. A full DNA profile in England, Wales and N. Ireland consists of 32 numbers and ‘XX’ for a female or ‘XY’ for a male. Each of these errors would relate to only one of the 34 alphanumeric values, with the remaining 33 being correct.
Many quality assurance measures are in place to prevent or reduce the possibility of error in performing DNA testing. All laboratories analysing DNA for evidential purposes must comply with stringent quality standards. Each is externally assessed at least annually to ensure they comply with the international standard set by the Forensic Science Regulator and must declare if they are not compliant. However, errors can still occur, as in any process where there is an element of human intervention. There are quarterly checks of the quality of DNA profiling laboratories submitting to the National DNA Database. This enables an estimate of general error rates to be made (Table 3). These are errors that have been detected through the systems and processes designed for that purpose. For example, a ‘near miss’ check is run regularly on the National DNA Database, to ensure that any profiles that are extremely similar but differ in a single designation are identified. It is important to note that the error rates in Table 3 are for submission of samples to the National DNA Database; in a case coming to court, additional quality checks are made during and after the comparison between the suspect’s sample and the crime sample, both by the scientist reporting the results to the court and by a second scientist. The error rates in Table 3 are therefore higher than would be expected for cases coming to court. In any particular case, the important question is whether an error was made in that case – a realistic suspicion of error in a case can be explored in more detail by examination of the records and quality controls in that case.
Appendix 4: Some case examples

Body fluid attribution

Example 1: The complainant/complainer has been stabbed and a DNA profile has been obtained from a large area of heavy staining that has the appearance of blood, on a suspect’s clothing. The forensic scientist carried out a test to check if the stain on the clothing was consistent with being from blood. Although this test is not perfect (there is a possibility of false positives from other substances), it gave a very strong indication that the stain was in fact blood. A mixed DNA profile was obtained from the stained area, of which the major contribution matched the complainant/complainer and the minor contribution matched the suspect. In this example, it is reasonable to assume that the major component of the DNA profile was from the heavy blood staining and that the minor component might have been from the habitual wearer of the clothing.

Example 2: An allegation of rape has been made by a complainant/complainer. The suspect claims not to have had intercourse with the complainant/complainer, but only to have touched her external genital region. He says he masturbated two hours previous to the alleged incident. A swab taken from high within the vagina of the rape complainant/complainer has been examined for semen, and a significant number of sperm heads were visually observed. A process whereby sperm are separated from all other cells has been carried out, and the DNA extracted from the sperm fraction matches the suspect. The DNA from the other cells is a mixture, with the major part matching the complainant/complainer. Because the sperm were chemically separated from the other cells and because a significant number of sperm heads were observed, it is possible to say with confidence that the DNA extracted from this fraction was from sperm. Because the swab was from high within the vagina, the scientific findings would be highly unlikely if the defendant merely touched the complainant/complainer after having masturbated earlier. The scientific findings are much more probable if sexual intercourse with ejaculation into the vagina occurred than if the external genital area was touched by hand after masturbation.
DNA transfer

Example 3: A knife has been recovered, which might have been used in a stabbing. The blade has been cleaned and there is no visible bloodstaining. The forensic scientist carried out a test for blood, but found none. The surface of the blade was swabbed to sample for DNA, and the handle of the knife was swabbed separately. The swab from the blade produced a weak DNA profile matching the complainant/complainer, and the swab from the handle produced a weak mixed DNA profile, of which the major component matched the suspect. In this example, it cannot automatically be assumed that the complainant’s/complainer’s profile from the blade originated from blood. Questions such as ‘where was the knife found?’ become highly relevant: if it was a kitchen knife from the complainant’s/complainer’s house, then his DNA could have been there because he had handled the knife recently, and not because it was used to stab him. If the suspect had previously had access to the complainant’s/complainer’s kitchen (eg if the defendant also lived there or was a regular visitor), then the finding of his DNA on the handle could be explained by contact with the knife at some time in the past. If it was a kitchen knife from the suspect’s house, then the finding of his DNA on the handle is to be expected, but the finding of the complainant’s/complainer’s DNA might or might not have relevance, depending on whether the suspect and complainant/complainer had had previous contact and whether the complainant/complainer had been at the defendant’s house.

Example 4: An illegal firearm is found wrapped in a plastic bag at a lock-up rented by the suspect. The prosecution alleges it is the suspect’s gun, but he claims to have no knowledge of it. The trigger of the gun is swabbed; this is chosen for swabbing because it is to some extent protected from accidental contact by the trigger guard, and because it would be expected to be an area of the gun that would be touched by a person using the gun. This yields a low-template DNA profile matching the defendant, with no other contributing DNA from any other person. The handle and barrel of the gun were also swabbed but no profiles were obtained. The suspect claims that the plastic bag was his and that the DNA must have been transferred from him to the bag and from the bag to the gun. In assessing the scientific findings, the scientist will consider the current level of knowledge regarding transfer and persistence of DNA, and the physical transfers that would need to take place under each scenario. The steps and considerations are summarised in Table 4.
In this example, the simplest transfer would be direct transfer to the gun. The suspect’s scenario is also possible, but there are additional requirements for it to occur (the right part of the bag managing to get between the trigger guard and the trigger etc). The scientist would therefore be likely to give an opinion that the findings are more likely if the prosecution scenario is true than if the defence scenario is true.

**TABLE 4**

Transfer stages for DNA to be detected on gun trigger.

<table>
<thead>
<tr>
<th>Transfers</th>
<th>Suspect’s scenario</th>
<th>Prosecution scenario</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>1</strong></td>
<td>DNA is transferred from the defendant to the bag (this will not be all over the bag, but at the points of contact). To assess this scenario fully, multiple areas of the bag were swabbed and profiled but the suspect’s DNA was not detected other than on the handles.</td>
<td>DNA is directly transferred from the defendant to the trigger of the gun</td>
</tr>
<tr>
<td><strong>2</strong></td>
<td>The DNA on the bag must line up with the trigger of the gun, and get between the trigger guard and the trigger. The DNA must then transfer from the bag to the trigger. This would happen more easily if the DNA were in a moist state, such as just after it was deposited.</td>
<td></td>
</tr>
</tbody>
</table>

In this example, the simplest transfer would be direct transfer to the gun. The suspect’s scenario is also possible, but there are additional requirements for it to occur (the right part of the bag managing to get between the trigger guard and the trigger etc). The scientist would therefore be likely to give an opinion that the findings are more likely if the prosecution scenario is true than if the defence scenario is true.
Appendix 5: Glossary

**Accuracy:** the degree of agreement or conformity of a measured value with its actual true) value.

**Allele:** one of two or more versions of a genetic sequence at a particular location (locus) in the genome.

**Allele drop-in:** allelic peak(s) in an electropherogram that are not reproducible across multiple independent analyses; also one hypothesis used to explain the observation of one or more allelic peaks in an electropherogram that are inconsistent with the assumed/known contributor(s) to a sample.

**Allele drop-out:** failure of an otherwise detectable allele to produce a signal above the analytical threshold because the allele was not present or was not present in sufficient quantity in the DNA sample.

**Allele frequency:** the number of times that an allele appears in a data set; the proportion of a particular allele in a population.

**Allelic ladder:** in STR testing, a measurement calibration tool, consisting of the most commonly observed alleles, used for assigning an allele designation to a peak in an electropherogram at a particular genetic locus.

**Amelogenin gene:** located on the X and Y chromosome used in the determination of sex from a DNA sample.

**Base:** a chemical unit within DNA that forms part of its structure. There are four bases that are linked together to make up the long strands of the DNA helix: adenine, thymine, cytosine and guanine, known as A, T, C, G respectively.

**Base pair:** two complementary bases on opposite strands of the DNA double helix joined by chemical bonds called hydrogen bonds; base pairing occurs between A and T and between G and C.

**Billion:** one thousand million.

**Buccal swab:** a relatively non-invasive technique of scraping the inside of a mouth with a cotton swab or similar collection device to collect cells from the inner cheek lining; a common method for collecting and preserving samples for DNA testing from known individuals.

**Cell:** the basic building block of an organism; humans have approximately 100 trillion cells in their body, most containing DNA.

**Chromatid:** thread-like strand into which a chromosome divides longitudinally prior to cell division. Each contains a double helix of DNA.
Chromosome: long continuous strand of DNA found in the nucleus of cells.

Complainant/complainer: Terminology used to describe the person who instigates a criminal investigation within the legal framework. The latter is used in Scotland, while the former is used in the rest of the UK.

Deoxyribonucleic acid (DNA): a genetic material of organisms, usually double-stranded; composed of large chemical molecules called nucleic acids composed of smaller chemical molecules called nucleotides identified by the presence of deoxyribose, a sugar, and four chemical bases; DNA is a fairly stable molecule, and variations in DNA sequence between individuals permits DNA profiling to distinguish individuals from one another.

Detection limit: the smallest amount of some component of interest that can be measured by a single measurement with a stated level of confidence.

DNA database: a computer repository of DNA profiles.

DNA degradation: the fragmentation, or breakdown, of DNA by chemical, physical, or biological means; a common occurrence when biological samples containing DNA encounter warm moist environments or excessive UV light.

DNA profile: a string of values (numbers or letters) compiled from the results of DNA testing at one or more genetic loci; a count of the STR lengths contributed from the maternal and paternal copies of DNA at each locus tested; can be from a single source or a mixture from multiple contributors.

Double helix: the native form of DNA, which looks like a twisted ladder; two linear strands of DNA assume this shape when held together by complementary base pairing, analogous to the rungs on the twisted ladder.

Electropherogram: a graphical representation of a DNA profile, where the horizontal axis represents the size of the DNA fragments analysed and the vertical axis represents the relative abundance of the DNA fragments analysed.

Gene: the basic unit of heredity; a sequence of DNA nucleotides on a chromosome passed from parents to offspring that influences various traits.

Genetics: branch of biology that deals with the heredity.

Genome: the entire DNA sequence found in a cell; the human genome consists of approximately 6,500,000,000 pairs of bases.
**Genotype:** the genetic make-up of an organism as characterised by its DNA sequence. With STR DNA testing, a locus genotype generally consists of two alleles, inherited from an individual’s mother and father.

**Haplotype:** a group of genes or DNA sequences inherited together from one parent.

**Likelihood ratio:** the probability of the evidence under one proposition divided by the probability of the evidence under an alternative, mutually exclusive proposition; the magnitude of its value expresses the weight of the evidence. A larger likelihood ratio occurs if the ‘top’ scenario is the more likely to have occurred.

**Loci:** plural of locus.

**Locus:** a unique physical location of a gene (or a specific sequence of DNA) on a chromosome; in Scotland the ‘locus’ is the name given to a crime scene.

**Low Copy Number (LCN) DNA testing:** the analysis of a small quantity of DNA often conducted by increasing the number of PCR amplification cycles.

**Low-level or low-template DNA:** usually defined as less than approximately 100 picograms (pg) or about the amount in 15 human cells.

**Major profile:** The profile derived from the predominant DNA source in a mixed sample.

**Match probability:** a conditional probability used to address the question ‘given that a particular DNA profile has been generated from evidence related to a case and an identical DNA profile has been generated from a sample taken from the person of interest, what is the chance of the same DNA profile also being generated from another person at random?’

**Matching profile:** genetic profiles that show the same alleles at all loci tested and with unexplainable differences.

**Mitochondrial DNA (mtDNA):** a small, circular DNA molecule located in the mitochondria of a cell that consists of approximately 16,500 base pairs; the presence of hundreds of copies of mtDNA in each cell make it useful for analysing samples originating from limited or damaged biological material.

**Multiplex PCR:** co-amplification of multiple regions of a genome enabling information from the different target sequences to be collected simultaneously.

**Mutation:** any change in DNA sequence.

**Partial profile:** a DNA profile for which complete results are not obtained at all tested loci.
Polymerase chain reaction (PCR): an *in vitro* process that yields millions of copies of the desired DNA through repeated cycling of a reaction involving the DNA polymerase enzyme.

**Precision**: a measure of the closeness of results when experiments are repeated.

**Probabilistic genotyping**: use of statistical modelling informed by biological data, statistical theory, computer algorithms and/or probability distributions to infer genotypes and/or calculate likelihood ratios.

**Pull-up**: an artefact that may occur during analysis of fluorescently labelled DNA fragments when signal from one dye colour channel produces artificial peaks in another, usually adjacent colour, at a similar position on the horizontal axis in an electropherogram; sometimes referred to as bleed-through or spectral calibration failure.

**Short tandem repeats (STR)**: multiple copies of an identical (or similar) DNA sequence arranged in direct succession where the repeat sequence unit is between two base pairs and six base pairs in length. The number of repeat units can vary between individuals.

**Stutter product**: a minor peak primarily appearing one repeat unit smaller than the primary STR allele; this results from strand slippage during the amplification process; usually <15% of the height of the true allele peak.

**Touch DNA**: DNA that is transferred to or from surfaces via contact.

**Validation**: The process of providing objective evidence that a method, process or device is fit for the specific purpose intended.

**Weight of evidence**: refers to either match probability, likelihood ratio or exclusionary evidence.

**X chromosome**: one of the sex chromosomes; normal females possess two copies and males one copy.

**Y chromosome**: one of the sex chromosomes; normal males possess one copy and females none.
The members of the groups involved in producing this primer are listed below. The members acted in an individual and not organisational capacity and declared any conflicts of interest. They contributed on the basis of their own expertise and good judgement. The Royal Society and the Royal Society of Edinburgh gratefully acknowledges their contribution.

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(a) In General.—Upon a written motion by an individual sentenced to imprisonment or death pursuant to a conviction for a Federal offense (referred to in this section as the “applicant”), the court that entered the judgment of conviction shall order DNA testing of specific evidence if the court finds that all of the following apply:

(1) The applicant asserts, under penalty of perjury, that the applicant is actually innocent of—
   (A) the Federal offense for which the applicant is sentenced to imprisonment or death; or
   (B) another Federal or State offense, if—
      (i) evidence of such offense was admitted during a Federal sentencing hearing and exoneration of such offense would entitle the applicant to a reduced sentence or new sentencing hearing; and
      (ii) in the case of a State offense—
         (I) the applicant demonstrates that there is no adequate remedy under State law to permit DNA testing of the specified evidence relating to the State offense; and
         (II) to the extent available, the applicant has exhausted all remedies available under State law for requesting DNA testing of specified evidence relating to the State offense.

(2) The specific evidence to be tested was secured in relation to the investigation or prosecution of the Federal or State offense referenced in the applicant’s assertion under paragraph (1).

(3) The specific evidence to be tested—
   (A) was not previously subjected to DNA testing and the applicant did not knowingly fail to request DNA testing of that evidence in a prior motion for postconviction DNA testing; or
   (B) was previously subjected to DNA testing and the applicant is requesting DNA testing using a new method or technology that is substantially more probative than the prior DNA testing.

(4) The specific evidence to be tested is in the possession of the Government and has been subject to a chain of custody and retained under conditions sufficient to ensure that such evidence has not been substituted, contaminated, tampered with, replaced, or altered in any respect material to the proposed DNA testing.
The proposed DNA testing is reasonable in scope, uses scientifically sound methods, and is consistent with accepted forensic practices.

(6) The applicant identifies a theory of defense that—
(A) is not inconsistent with an affirmative defense presented at trial; and
(B) would establish the actual innocence of the applicant of the Federal or State offense referenced in the applicant’s assertion under paragraph (1).
(7) If the applicant was convicted following a trial, the identity of the perpetrator was at issue in the trial.
(8) The proposed DNA testing of the specific evidence may produce new material evidence that would—
(A) support the theory of defense referenced in paragraph (6); and
(B) raise a reasonable probability that the applicant did not commit the offense.
(9) The applicant certifies that the applicant will provide a DNA sample for purposes of comparison.
(10) The motion is made in a timely fashion, subject to the following conditions:
(A) There shall be a rebuttable presumption of timeliness if the motion is made within 60 months of enactment of the Justice For All Act of 2004 or within 36 months of conviction, whichever comes later. Such presumption may be rebutted upon a showing—
(i) that the applicant’s motion for a DNA test is based solely upon information used in a previously denied motion; or
(ii) of clear and convincing evidence that the applicant’s filing is done solely to cause delay or harass.
(B) There shall be a rebuttable presumption against timeliness for any motion not satisfying subparagraph (A) above. Such presumption may be rebutted upon the court’s finding—
(i) that the applicant was or is incompetent and such incompetence substantially contributed to the delay in the applicant’s motion for a DNA test;
(ii) the evidence to be tested is newly discovered DNA evidence;
(iii) that the applicant’s motion is not based solely upon the applicant’s own assertion of innocence and, after considering all relevant facts and circumstances surrounding the motion, a denial would result in a manifest injustice; or

(iv) upon good cause shown.

(C) For purposes of this paragraph—

(ii) the term “manifest” means that which is unmistakable, clear, plain, or indisputable and requires that the opposite conclusion be clearly evident.

(b) Notice to the Government; Preservation Order; Appointment of Counsel.—

(1) Notice.—Upon the receipt of a motion filed under subsection (a), the court shall—

(A) notify the Government;

(B) allow the Government a reasonable time period to respond to the motion; and

(C) order the Government to—

(i) prepare an inventory of the evidence related to the case; and

(ii) issue a copy of the inventory to the court, the applicant, and the Government.

(2) Preservation order.—

To the extent necessary to carry out proceedings under this section, the court shall direct the Government to preserve the specific evidence relating to a motion under subsection (a).

(3) Appointment of counsel.—

The court may appoint counsel for an indigent applicant under this section in the same manner as in a proceeding under section 3006A(a)(2)(B).

(c) Testing Procedures.—

(1) In general.—

The court shall direct that any DNA testing ordered under this section be carried out by the Federal Bureau of Investigation.

(2) Exception.—

Notwithstanding paragraph (1), the court may order DNA testing by another qualified laboratory if the court makes all necessary orders to ensure the integrity of the specific evidence and the reliability of the testing process and test results.

(3) Costs.—The costs of any DNA testing ordered under this section shall be paid—

(A)
by the applicant; or

(B)
in the case of an applicant who is indigent, by the Government.

(d) Time Limitation in Capital Cases.—In any case in which the applicant is sentenced to death —

(1) any DNA testing ordered under this section shall be completed not later than 60 days after the date on which the Government responds to the motion filed under subsection (a); and

(2) not later than 120 days after the date on which the DNA testing ordered under this section is completed, the court shall order any post-testing procedures under subsection (f) or (g), as appropriate.

(e) Reporting of Test Results.—

(1) Results.—

(A) In general.—
The results of any DNA testing ordered under this section shall be simultaneously disclosed to the court, the applicant, and the Government.

(B) Results exclude applicant.—

(i) In general.—
If a DNA profile is obtained through testing that excludes the applicant as the source and the DNA complies with the Federal Bureau of Investigation’s requirements for the uploading of crime scene profiles to the National DNA Index System (referred to in this subsection as “NDIS”), the court shall order that the law enforcement entity with direct or conveyed statutory jurisdiction that has access to the NDIS submit the DNA profile obtained from probative biological material from crime scene evidence to determine whether the DNA profile matches a profile of a known individual or a profile from an unsolved crime.

(ii) NDIS search.—
The results of a search under clause (i) shall be simultaneously disclosed to the court, the applicant, and the Government.

(2) NDIS.—
The Government shall submit any test results relating to the DNA of the applicant to NDIS.

(3) Retention of dna sample.—

(A) Entry into ndis.—
If the DNA test results obtained under this section are inconclusive or show that the applicant was the source of the DNA evidence, the DNA sample of the applicant may be retained in NDIS.

(B) Match with other offense.—
If the DNA test results obtained under this section exclude the applicant as the source of the
DNA evidence, and a comparison of the DNA sample of the applicant results in a match between the DNA sample of the applicant and another offense, the Attorney General shall notify the appropriate agency and preserve the DNA sample of the applicant.

(C) No match.—
If the DNA test results obtained under this section exclude the applicant as the source of the DNA evidence, and a comparison of the DNA sample of the applicant does not result in a match between the DNA sample of the applicant and another offense, the Attorney General shall destroy the DNA sample of the applicant and ensure that such information is not retained in NDIS if there is no other legal authority to retain the DNA sample of the applicant in NDIS.

(f) Post-Testing Procedures; Inconclusive and Inculpatory Results.—

(1) Inconclusive results.—
If DNA test results obtained under this section are inconclusive, the court may order further testing, if appropriate, or may deny the applicant relief.

(2) Inculpatory results.—If DNA test results obtained under this section show that the applicant was the source of the DNA evidence, the court shall—

(A) deny the applicant relief; and

(B) on motion of the Government—

(i) make a determination whether the applicant’s assertion of actual innocence was false, and, if the court makes such a finding, the court may hold the applicant in contempt;

(ii) assess against the applicant the cost of any DNA testing carried out under this section;

(iii) forward the finding to the Director of the Bureau of Prisons, who, upon receipt of such a finding, may deny, wholly or in part, the good conduct credit authorized under section 3632 on the basis of that finding;

(iv) if the applicant is subject to the jurisdiction of the United States Parole Commission, forward the finding to the Commission so that the Commission may deny parole on the basis of that finding; and

(v) if the DNA test results relate to a State offense, forward the finding to any appropriate State official.

(3) Sentence.—
In any prosecution of an applicant under chapter 79 for false assertions or other conduct in proceedings under this section, the court, upon conviction of the applicant, shall sentence the applicant to a term of imprisonment of not less than 3 years, which shall run consecutively to any other term of imprisonment the applicant is serving.

(g) Post-Testing Procedures; Motion for New Trial or Resentencing.—
(1) In general.—
Notwithstanding any law that would bar a motion under this paragraph as untimely, if DNA test results obtained under this section exclude the applicant as the source of the DNA evidence, the applicant may file a motion for a new trial or resentencing, as appropriate. The court shall establish a reasonable schedule for the applicant to file such a motion and for the Government to respond to the motion.

(2) Standard for granting motion for new trial or resentencing.—The court shall grant the motion of the applicant for a new trial or resentencing, as appropriate, if the DNA test results, when considered with all other evidence in the case (regardless of whether such evidence was introduced at trial), establish by compelling evidence that a new trial would result in an acquittal of—

(A) in the case of a motion for a new trial, the Federal offense for which the applicant is sentenced to imprisonment or death; and

(B) in the case of a motion for resentencing, another Federal or State offense, if evidence of such offense was admitted during a Federal sentencing hearing and exoneration of such offense would entitle the applicant to a reduced sentence or a new sentencing proceeding.

(h) Other Laws Unaffected.—
(1) Post-conviction relief.—
Nothing in this section shall affect the circumstances under which a person may obtain DNA testing or post-conviction relief under any other law.

(2) Habeas corpus.—
Nothing in this section shall provide a basis for relief in any Federal habeas corpus proceeding.

(3) Not a motion under section 2255.—
A motion under this section shall not be considered to be a motion under section 2255 for purposes of determining whether the motion or any other motion is a second or successive motion under section 2255.
133 S.Ct. 1958, 186 L.Ed.2d 1, 81 USLW 4343, 13 Cal. Daily Op. Serv. 5551...

KeyCite Yellow Flag - Negative Treatment
Not Followed on State Law Grounds State v. Medina, Vt., July 11, 2014
133 S.Ct. 1958
Supreme Court of the United States
MARYLAND, Petitioner
v.
Alonzo Jay KING, Jr.
No. 12–207.
Decided June 3, 2013.

Synopsis
Background: Following denial of his motion to suppress DNA evidence, defendant was convicted in the Maryland Circuit Court, Wicomico County, Kathleen L. Beckstead, J., of first-degree rape. Defendant appealed. The Court of Appeals of Maryland, Harrell, J., 425 Md. 550, 42 A.3d 549, reversed and remanded. State filed application for stay of judgment pending disposition of its petition for writ of certiorari. The Supreme Court, Chief Justice Roberts, as Circuit Justice, ––– U.S.––––, 133 S.Ct. 1, 183 L.Ed.2d 667, granted the stay. Certiorari was subsequently granted.

Holdings: The Supreme Court, Justice Kennedy, held that:

[1] search using buccal swab to obtain defendant’s DNA sample after arrest for serious offense was reasonable under Fourth Amendment, abrogating People v. Buza, 129 Cal.Rptr.3d 753, Mario W. v. Kaipio, 228 Ariz. 207, 265 P.3d 389; and

[2] the analysis of defendant’s DNA did not render the DNA identification impermissible under the Fourth Amendment.

Reversed.

Justice Scalia, filed a dissenting opinion, in which Justice Ginsburg, Justice Sotomayor, and Justice Kagan joined.

West Codenotes

Negative Treatment Reconsidered
**1962 Syllabus**

*435 After his 2009 arrest on first- and second-degree assault charges, respondent King was processed through a Wicomico County, Maryland, facility, where booking personnel used a cheek swab to take a DNA sample pursuant to the Maryland DNA Collection Act (Act). The swab was matched to an unsolved 2003 rape, and King was charged with that crime. He moved to suppress the DNA match, arguing that the Act violated the Fourth Amendment, but the Circuit Court Judge found the law constitutional. King was convicted of rape. The Maryland Court of Appeals set aside the conviction, finding unconstitutional the portions of the Act authorizing DNA collection from felony arrestees.

Held: When officers make an arrest supported by probable cause to hold for a serious offense and bring the suspect to the station to be detained in custody, taking and analyzing a cheek swab of the arrestee’s DNA is, like fingerprinting and photographing, a legitimate police booking procedure that is reasonable under the Fourth Amendment. Pp. 1966 – 1980.

(a) DNA testing may “significantly improve both the criminal justice system and police investigative practices,” District Attorney’s Office for Third Judicial Dist. v. Osborne, 557 U.S. 52, 55, 129 S.Ct. 2308, 174 L.Ed.2d 38, by making it “possible to determine whether a biological tissue matches a suspect with near certainty,” id., at 62, 129 S.Ct. 2308. Maryland’s Act authorizes law enforcement authorities to collect DNA samples from, as relevant here, persons charged with violent crimes, including first-degree assault. A sample may not be added to a database before an individual is arraigned, and it must be destroyed if, e.g., he is not convicted. Only identity information may be added to the database. Here, the officer collected a DNA sample using the common “buccal swab” procedure, which is quick and painless, **1963 requires no “surgical intrusio[n] beneath the skin,” Winston v. Lee, 470 U.S. 753, 760, 105 S.Ct. 1611, 84 L.Ed.2d 662, and poses no threat to the arrestee’s “health or safety,” id., at 763, 105 S.Ct. 1611. Respondent’s identification as the rapist resulted in part through the operation of the Combined DNA Index System (CODIS), which connects DNA laboratories at the local, state, and national level, and which standardizes the points of comparison, i.e., loci, used in DNA analysis. Pp. 1966 – 1969.

(b) The framework for deciding the issue presented is
well established. Using a buccal swab inside a person’s cheek to obtain a DNA sample is a search under the Fourth Amendment. And the fact that *436 the intrusion is negligible is of central relevance to determining whether the search is reasonable, “the ultimate measure of the constitutionality of a governmental search,” Vernonia School Dist. 47J v. Acton, 515 U.S. 646, 652, 115 S.Ct. 2386, 132 L.Ed.2d 564. Because the need for a warrant is greatly diminished here, where the arrestee was already in valid police custody for a serious offense supported by probable cause, the search is analyzed by reference to “reasonableness, not individualized suspicion,” Samson v. California, 547 U.S. 843, 855, n. 4, 126 S.Ct. 2193, 165 L.Ed.2d 250, and reasonableness is determined by weighing “the promotion of legitimate governmental interests” against “the degree to which [the search] intrudes upon an individual’s privacy,” Wyoming v. Houghton, 526 U.S. 295, 300, 119 S.Ct. 1297, 143 L.Ed.2d 408. P. 1970.

(c) In this balance of reasonableness, great weight is given to both the significant government interest at stake in the identification of arrestees and DNA identification’s unmatched potential to serve that interest. Pp. 1970 – 1977.

(1) The Act serves a well-established, legitimate government interest: the need of law enforcement officers in a safe and accurate way to process and identify persons and possessions taken into custody. “[P]robable cause provides legal justification for arresting a [suspect], and for a brief period of detention to take the administrative steps incident to arrest,” Gerstein v. Pugh, 420 U.S. 103, 113–114, 95 S.Ct. 854, 43 L.Ed.2d 54; and the “validity of the search of a person incident to a lawful arrest” is settled, United States v. Robinson, 414 U.S. 218, 224, 94 S.Ct. 467, 38 L.Ed.2d 427. Individual suspicion is not necessary. The “routine administrative procedure[s] at a police station house incident to booking and jailing the suspect” have different origins and different constitutional justifications than, say, the search of a place not incident to arrest, Illinois v. Lafayette, 462 U.S. 640, 643, 103 S.Ct. 2605, 24 L.Ed.2d 65, which depends on the “fair probability that contraband or evidence of a crime will be found in a particular place,” Illinois v. Gates, 462 U.S. 213, 238, 103 S.Ct. 2317, 76 L.Ed.2d 527. And when probable cause exists to remove an individual from the normal channels of society and hold him in legal custody, DNA identification plays a critical role in serving those interests. First, the government has an interest in properly identifying “who has been arrested and who is being tried.” Hibbel v. Sixth Judicial Dist. Court of Nev., Humboldt Cty., 542 U.S. 177, 191, 124 S.Ct. 2451, 159 L.Ed.2d 292. Criminal history is critical to officers who are processing a suspect for detention. They already seek identity information through routine and accepted means: comparing booking photographs to sketch artists’ depictions, showing mugshots to potential witnesses, and comparing fingerprints against electronic databases of known criminals and unsolved crimes. The only difference between DNA analysis and fingerprint **1964 databases is the unparalleled accuracy DNA provides. DNA is another metric of identification used to connect the arrestee with his or her public persona, as reflected in records of his *437 or her actions that are available to the police. Second, officers must ensure that the custody of an arrestee does not create inordinate “risks for facility staff, for the existing detainee population, and for a new detainee.” Florence v. Board of Chosen Freeholders of County of Burlington, 566 U.S. ——, ——, 132 S.Ct. 1510, 182 L.Ed.2d 566. DNA allows officers to know the type of person being detained. Third, “the Government has a substantial interest in ensuring that persons accused of crimes are available for trials.” Bell v. Wolfish, 441 U.S. 520, 534, 99 S.Ct. 1861, 60 L.Ed.2d 447. An arrestee may be more inclined to flee if he thinks that continued contact with the criminal justice system may expose another serious offense. Fourth, an arrestee’s past conduct is essential to assessing the danger he poses to the public, which will inform a court’s bail determination. Knowing that the defendant is wanted for a previous violent crime based on DNA identification may be especially probative in this regard. Finally, in the interests of justice, identifying an arrestee as the perpetrator of some heinous crime may have the salutary effect of freeing a person wrongfully imprisoned. Pp. 1970 – 1975.

(2) DNA identification is an important advance in the techniques long used by law enforcement to serve legitimate police concerns. Police routinely have used scientific advancements as standard procedures for identifying arrestees. Fingerprinting, perhaps the most direct historical analogue to DNA technology, has, from its advent, been viewed as a natural part of “the administrative steps incident to arrest.” County of Riverside v. McLaughlin, 500 U.S. 44, 58, 111 S.Ct. 1661, 114 L.Ed.2d 49. However, DNA identification is far superior. The additional intrusion upon the arrestee’s privacy beyond that associated with fingerprinting is not significant, and DNA identification is markedly more accurate. It may not be as fast as fingerprinting, but rapid fingerprint analysis is itself of recent vintage, and the question of how long it takes to process identifying information goes to the efficacy of the search for its purpose of prompt identification, not the constitutionality of the search. Rapid technical advances are also reducing DNA processing times. Pp. 1974 – 1977.

(1) By comparison to the substantial government interest and the unique effectiveness of DNA identification, the intrusion of a cheek swab to obtain a DNA sample is minimal. Reasonableness must be considered in the context of an individual’s legitimate privacy expectations, which necessarily diminish when he is taken into police custody. Bell, supra, at 557, 99 S.Ct. 1861. Such searches thus differ from the so-called special needs searches of, e.g., otherwise law-abiding motorists at checkpoints. See Indianapolis v. Edmond, 531 U.S. 32, 121 S.Ct. 447, 148 L.Ed.2d 333. The reasonableness inquiry considers two other circumstances in which particularized suspicion is *438 not categorically required: “diminished expectations of privacy [and a] minimal intrusion.” Illinois v. McArthur, 531 U.S. 326, 330, 121 S.Ct. 946, 148 L.Ed.2d 838. An invasive surgery may raise privacy concerns weighty enough for the search to require a warrant, notwithstanding the arrestee’s diminished privacy expectations, but a buccal swab, which involves a brief and minimal intrusion with “virtually no risk, trauma, or pain,” Schmerber v. California, 384 U.S. 757, 771, 86 S.Ct. 1826, 16 L.Ed.2d 908, does not increase the indignity already attendant to **1965 normal incidents of arrest. Pp. 1977 – 1979.

(2) The processing of respondent’s DNA sample’s CODIS loci also did not intrude on his privacy in a way that would make his DNA identification unconstitutional. Those loci came from noncoding DNA parts that do not reveal an arrestee’s genetic traits and are unlikely to reveal any private medical information. Even if they could provide such information, they are not in fact tested for that end. Finally, the Act provides statutory protections to guard against such invasions of privacy. Pp. 1979 – 1980.

425 Md. 550, 42 A.3d 549, reversed.

KENNEDY, J., delivered the opinion of the Court, in which ROBERTS, C.J., and THOMAS, BREYER, and ALITO, JJ., joined. SCALIA, J., filed a dissenting opinion, in which GINSBURG, SOTOMAYOR, and KAGAN, JJ., joined.

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Opinion

Justice KENNEDY delivered the opinion of the Court.

*439 In 2003 a man concealing his face and armed with a gun broke into a woman’s home in Salisbury, Maryland. He *440 raped her. The police were unable to identify or apprehend the assailant based on any detailed description or other evidence they then had, but they did obtain from the victim a sample of the perpetrator’s DNA.

In 2009 Alonzo King was arrested in Wicomico County, Maryland, and charged with first- and second-degree assault for menacing a group of people with a shotgun. As part of a routine booking procedure for serious offenses, his DNA sample was taken by applying a cotton swab or filter paper—known as a buccal swab—to the inside of his cheeks. The DNA was found to match the DNA taken from the Salisbury rape victim. King was tried and convicted for the rape. Additional DNA samples were taken from him and used in the rape trial, but there seems to be no doubt that it was the DNA from the cheek sample taken at the time he was booked in 2009 that led to his first having been linked to the rape and charged with its commission.

The Court of Appeals of Maryland, on review of King’s rape conviction, ruled that the DNA taken when King was booked for the 2009 charge was an unlawful seizure because obtaining and using the cheek swab was an unreasonable search of the person. It set the rape conviction aside. This *441 Court granted certiorari and now reverses **1966 the judgment of the Maryland court.
When King was arrested on April 10, 2009, for menacing a group of people with a shotgun and charged in state court with both first- and second-degree assault, he was processed for detention in custody at the Wicomico County Central Booking facility. Booking personnel used a cheek swab to take the DNA sample from him pursuant to provisions of the Maryland DNA Collection Act (or Act).

On July 13, 2009, King’s DNA record was uploaded to the Maryland DNA database, and three weeks later, on August 4, 2009, his DNA profile was matched to the DNA sample collected in the unsolved 2003 rape case. Once the DNA was matched to King, detectives presented the forensic evidence to a grand jury, which indicted him for the rape. Detectives obtained a search warrant and took a second sample of DNA from King, which again matched the evidence from the rape. He moved to suppress the DNA match on the grounds that Maryland’s DNA collection law violated the Fourth Amendment. The Circuit Court Judge upheld the statute as constitutional.

In a divided opinion, the Maryland Court of Appeals struck down the portions of the Act authorizing collection of DNA from felony arrestees as unconstitutional. The majority concluded that a DNA swab was an unreasonable search in violation of the Fourth Amendment because King’s “expectation of privacy is greater than the State’s purported interest in using King’s DNA to identify him.” 425 Md. 550, 561, 42 A.3d 549, 556 (2012). In reaching that conclusion the Maryland Court relied on the decisions of various other courts that have concluded that DNA identification of arrestees is impermissible. See, e.g., *442 People v. Buza, 129 Cal.Rptr.3d 753 (App.2011) (officially depublished); Mario W. v. Kaipio, 228 Ariz. 207, 265 P.3d 389 (App.2011).

Both federal and state courts have reached differing conclusions as to whether the Fourth Amendment prohibits the collection and analysis of a DNA sample from persons arrested, but not yet convicted, on felony charges. This Court granted certiorari, 568 U.S. ———, 133 S.Ct. 594, 184 L.Ed.2d 390 (2012), to address the question. King is the respondent here.

The advent of DNA technology is one of the most significant scientific advancements of our era. The full potential for use of genetic markers in medicine and science is still being explored, but the utility of DNA identification in the criminal justice system is already undisputed. Since the first use of forensic DNA analysis to catch a rapist and murderer in England in 1986, see J. Butler, Fundamentals of Forensic DNA Typing 5 (2009) (hereinafter Butler), law enforcement, the defense bar, and the courts have acknowledged DNA testing’s “unparalleled ability both to exonerate the wrongly convicted and to identify the guilty. It has the potential to significantly improve both the criminal justice system and police investigative practices.” District Attorney’s Office for Third Judicial Dist. v. Osborne, 557 U.S. 52, 55, 129 S.Ct. 2308, 174 L.Ed.2d 38 (2009).

A

The current standard for forensic DNA testing relies on an analysis of the chromosomes located within the nucleus of all human cells. “The DNA material in chromosomes is composed of ‘coding’ and ‘noncoding’ **1967 regions. The coding regions are known as genes and contain the information necessary for a cell to make proteins.... Non-protein-coding regions ... are not related directly to making proteins, [and] have been referred to as ‘junk’ DNA.” Butler 25. The adjective “junk” may mislead the layperson, for in fact this is the DNA region used with near certainty to identify a person. *443 The term apparently is intended to indicate that this particular noncoding region, while useful and even dispositive for purposes like identity, does not show more far-reaching and complex characteristics like genetic traits.

Many of the patterns found in DNA are shared among all people, so forensic analysis focuses on “repeated DNA sequences scattered throughout the human genome,” known as “short tandem repeats” (STRs). *Id., at 147–148. The alternative possibilities for the size and frequency of these STRs at any given point along a strand of DNA are known as “alleles,” *id., at 25; and multiple alleles are analyzed in order to ensure that a DNA profile matches only one individual. Future refinements may improve present technology, but even now STR analysis makes it “possible to determine whether a biological tissue matches a suspect with near certainty.” Osborne, supra, at 62, 129 S.Ct. 2308.

The Act authorizes Maryland law enforcement authorities to collect DNA samples from “an individual who is charged with ... a crime of violence or an attempt to
commit a crime of violence; or ... burglary or an attempt to commit burglary.” Md. Pub. Saf. Code Ann. § 2–504(a)(3)(i) (Lexis 2011). Maryland law defines a crime of violence to include murder, rape, first-degree assault, kidnapping, arson, sexual assault, and a variety of other serious crimes. Md. Crim. Law Code Ann. § 14–101 (Lexis 2012). Once taken, a DNA sample may not be processed or placed in a database before the individual is arraigned (unless the individual consents). Md. Pub. Saf. Code Ann. § 2–504(d)(1) (Lexis 2011). It is at this point that a judicial officer ensures that there is probable cause to detain the arrestee on a qualifying serious offense. If “all qualifying criminal charges are determined to be unsupported by probable cause ... the DNA sample shall be immediately destroyed.” § 2–504(d)(2)(i). DNA samples are also destroyed if “a criminal action begun against the individual ... does not result in a conviction,” “the conviction is finally reversed or vacated and no new trial is permitted,” *444 or “the individual is granted an unconditional pardon.” § 2–511(a)(1).

The Act also limits the information added to a DNA database and how it may be used. Specifically, “[o]nly DNA records that directly relate to the identification of individuals shall be collected and stored.” § 2–505(b)(1). No purpose other than identification is permissible: “A person may not willfully test a DNA sample for information that does not relate to the identification of individuals as specified in this subtitle.” § 2–512(c). Tests for familial matches are also prohibited. See § 2–506(d) (“A person may not perform a search of the statewide DNA data base for the purpose of identification of an offender in connection with a crime for which the offender may be a biological relative of the individual from whom the DNA sample was acquired”). The officers involved in taking and analyzing respondent’s DNA sample complied with the Act in all respects.

Respondent’s DNA was collected in this case using a common procedure known as a “buccal swab.” “Buccal cell collection involves wiping a small piece of filter paper or a cotton swab similar to a Q-tip against the inside cheek of an individual’s **1968 mouth to collect some skin cells.” Butler 86. The procedure is quick and painless. The swab touches inside an arrestee’s mouth, but it requires no “surgical intrusio[n] beneath the skin,” Winston v. Lee, 470 U.S. 753, 760, 105 S.Ct. 1611, 84 L.Ed.2d 662 (1985), and it poses no “threat[t] to the health or safety” of arrestees, id., at 763, 105 S.Ct. 1611. All 50 States require the collection of DNA from felony convicts, and respondent does not dispute the validity of that practice. See Brief for Respondent 48. Twenty-eight States and the Federal Government have adopted laws similar to the Maryland Act authorizing the collection of DNA from some or all arrestees. See Brief for State of California et al. as Amici Curiae 4, n. 1 (States Brief) (collecting state statutes). Although those statutes vary in their particulars, such as what charges require a DNA sample, their similarity means that this case implicates more than the specific Maryland *446 law. At issue is a standard, expanding technology already in widespread use throughout the Nation.

One of the most significant aspects of CODIS is the standardization of the points of comparison in DNA analysis. The CODIS database is based on 13 loci at which the STR alleles are noted and compared. These loci make possible extreme accuracy in matching individual samples, with a “random match probability of approximately 1 in 100 trillion (assuming unrelated individuals).” Ibid. The CODIS loci are from the non-protein coding junk regions of DNA, and “are not known to have any association with a genetic disease or any other genetic predisposition. Thus, the information in the database is only useful for human identity testing.” Id., at 279. STR information is recorded only as a “string of numbers”; and the DNA identification is accompanied only by information denoting the laboratory and the analyst responsible for the submission. Id., at 270. In short, CODIS sets uniform national standards for DNA matching and then facilitates connections between local law enforcement agencies who can share more specific information about matched STR profiles.

CODIS collects DNA profiles provided by local laboratories taken from arrestees, convicted offenders, and forensic evidence found at crime scenes. To participate in CODIS, a local laboratory must sign a memorandum of understanding agreeing to adhere to quality standards and submit to audits to evaluate compliance with the federal standards for scientifically rigorous DNA testing. Butler 270.
defines that term. [1] [2] Although the DNA swab procedure used here presents a question the Court has not yet addressed, the framework for deciding the issue is well established. The Fourth Amendment, binding on the States by the Fourteenth Amendment, provides that “[t]he right of the people to be secure in their persons, houses, papers, and effects, against unreasonable searches and seizures, shall not be violated.” It can be agreed that using a **1969 buccal swab on the inner tissues of a person’s cheek in order to obtain DNA samples is a search. Virtually any “intrusio[n] into the human body,” Schmerber v. California, 384 U.S. 757, 770, 86 S.Ct. 1826, 16 L.Ed.2d 908 (1966), will work an invasion of “cherished personal security” that is subject to constitutional scrutiny,” Cupp v. Murphy, 412 U.S. 291, 295, 93 S.Ct. 2000, 36 L.Ed.2d 900 (1973) (quoting Terry v. Ohio, 392 U.S. 1, 24–25, 88 S.Ct. 1868, 20 L.Ed.2d 889 (1968)). The Court has applied the Fourth Amendment to police efforts to draw blood, see Schmerber, supra ; Missouri v. McNeely, 569 U.S. —, 133 S.Ct. 1552, 185 L.Ed.2d 696 (2013), scraping an arrestee’s fingernails to obtain trace evidence, see Cupp, supra, and even to “a breathalyzer test, which generally requires the production of alveolar or ‘deep lung’ breath for chemical analysis,” Skinner v. Railway Labor Executives’ Assn., 489 U.S. 602, 616, 109 S.Ct. 1402, 103 L.Ed.2d 639 (1989).

[3] A buccal swab is a far more gentle process than a venipuncture to draw blood. It involves but a light touch on the inside of the cheek; and although it can be deemed a search within the body of the arrestee, it requires no “surgical intrusions beneath the skin.” Winston, 470 U.S., at 760, 105 S.Ct. 1611. The fact than an intrusion is negligible is of central relevance to determining reasonableness, although it is still a search as the law defines that term.

B

[4] [5] [6] To say that the Fourth Amendment applies here is the beginning point, not the end of the analysis. “[T]he Fourth Amendment’s proper function is to constrain, not against all intrusions as such, but against intrusions which are not justified in the circumstances, or which are made in an improper manner.” Schmerber, supra, at 768, 86 S.Ct. 1826. “As the text of the Fourth Amendment indicates, the ultimate measure of the constitutionality of a governmental search is ‘reasonableness.’ ” Vernonia School Dist. 47J v. Acton, 515 U.S. 646, 652, 115 S.Ct. 2386, 132 L.Ed.2d 564 (1995). In giving content to the inquiry whether an intrusion is reasonable, the Court has preferred “some quantum of individualized suspicion ... as a prerequisite to a constitutional search or seizure. But the Fourth Amendment imposes no irreducible requirement of such suspicion.” United States v. Martinez–Fuerte, 428 U.S. 543, 560–561, 96 S.Ct. 3074, 49 L.Ed.2d 1116 (1976) (citation and footnote omitted).

[7] [8] In some circumstances, such as “[w]hen faced with special law enforcement needs, diminished expectations of privacy, minimal intrusions, or the like, the Court has found that certain general, or individual, circumstances may render a warrantless search or seizure reasonable.” Illinois v. McArthur, 531 U.S. 326, 330, 121 S.Ct. 946, 148 L.Ed.2d 838 (2001). Those circumstances diminish the need for a warrant, either because “the public interest is such that neither a warrant nor probable cause is required,” Maryland v. Buie, 494 U.S. 325, 331, 110 S.Ct. 1093, 108 L.Ed.2d 276 (1990), or because an individual is already on notice, for instance because of his employment, see Skinner, supra, or the conditions of his release from government custody, see Samson v. California, 547 U.S. 843, 126 S.Ct. 2193, 165 L.Ed.2d 250 (2006), that some reasonable police intrusion on his privacy is to be expected. The need for a warrant is perhaps least when the search involves no discretion that could properly be limited by the “interposition of a neutral magistrate between the citizen and the law enforcement officer.” **1970 Treasury Employees v. Von Raab, 489 U.S. 656, 667, 109 S.Ct. 1384, 103 L.Ed.2d 685 (1989).

[9] The instant case can be addressed with this background. The Maryland DNA Collection Act provides that, in order to obtain a DNA sample, all arrestees charged with serious crimes must furnish the sample on a buccal swab applied, as *448 noted, to the inside of the cheeks. The arrestee is already in valid police custody for a serious offense supported by probable cause. The DNA collection is not subject to the judgment of officers whose perspective might be “colored by their primary involvement in ‘the often competitive enterprise of ferreting out crime.’ ” Terry, supra, at 12, 88 S.Ct. 1868 (quoting Johnson v. United States, 333 U.S. 10, 14, 68 S.Ct. 367, 92 L.Ed. 436 (1948)). As noted by this Court in a different but still instructive context involving blood testing, “[b]oth the circumstances justifying toxicological testing and the permissible limits of such intrusions are defined narrowly and specifically in the regulations that authorize them.... Indeed, in light of the standardized
nature of the tests and the minimal discretion vested in those charged with administering the program, there are virtually no facts for a neutral magistrate to evaluate.”

“arrestee may be carrying a false ID or lie about his identity,” and “criminal history records ... can be inaccurate or incomplete.”

**1971** The “routine administrative procedure[s] at a police station house incident to booking and jailing the suspect” derive from different origins and have different constitutional justifications than, say, the search of a place, **Illinois v. Lafayette**, 462 U.S. 640, 643, 103 S.Ct. 2605, 77 L.Ed.2d 65 (1983); for the search of a place not incident to an arrest depends on the “fair probability that contraband or evidence of a crime will be found in a particular place,” **Illinois v. Gates**, 462 U.S. 213, 238, 103 S.Ct. 2317, 76 L.Ed.2d 527 (1983). The interests are further different when an individual is formally processed into police custody. Then “the law is in the act of subjecting the body of the accused to its physical dominion.” **People v. Chigles**, 237 N.Y. 193, 197, 142 N.E. 583, 584 (1923) (Cardozo, J.). When probable cause exists to remove an individual from the normal channels of society and hold him in legal custody, DNA identification plays a critical role in serving those interests.

First, “[i]n every criminal case, it is known and must be known who has been arrested and who is being tried.” **Hiibel v. Sixth Judicial Dist. Court of Nev., Humboldt Cty.**, 542 U.S. 177, 191, 124 S.Ct. 2451, 159 L.Ed.2d 292 (2004). An individual’s identity is more than just his name or Social Security number, and the government’s interest in identification goes beyond ensuring that the proper name is typed on the indictment. Identity has never been considered limited to the name on the arrestee’s birth certificate. In fact, a name is of little value compared to the real interest in identification at stake when an individual is brought into custody. “It is a well recognized aspect of criminal conduct that the perpetrator will take unusual steps to conceal not only his conduct, but also his identity. Disguises used while committing a crime may be supplemented or replaced by changed names, and even changed physical features.” **Jones v. Murray**, 962 F.2d 302, 307 (C.A.4 1992). An arrestee may be carrying a false ID or lie about his identity,” and “criminal history records ... can be inaccurate or incomplete.”

**449** IV

A

The legitimate government interest served by the Maryland DNA Collection Act is one that is well established: the need for law enforcement officers in a safe and accurate way to process and identify the persons and possessions they must take into custody. It is beyond dispute that “probable cause provides legal justification for arresting a person suspected of crime, and for a brief period of detention to take the administrative steps incident to arrest.” **Gerstein v. Pugh**, 420 U.S. 103, 113–114, 95 S.Ct. 854, 43 L.Ed.2d 54 (1975). Also uncontested is the “right on the part of the Government, always recognized under English and American law, to search the person of the accused when legally arrested.” **Weeks v. United States**, 232 U.S. 383, 392, 34 S.Ct. 341, 58 L.Ed. 652 (1914), overruled on other grounds, **Mapp v. Ohio**, 367 U.S. 643, 81 S.Ct. 1684, 6 L.Ed.2d 1081 (1961). “The validity of the search of a person incident to a lawful arrest has been regarded as settled from its first enunciation, and has remained virtually unchallenged.” **United States v. Robinson**, 414 U.S. 218, 224, 94 S.Ct. 467, 38 L.Ed.2d 427 (1973). Even in that context, the Court has been clear that individual suspicion is not necessary, because “[t]he constitutionality of a search incident to an arrest does not depend on whether there is any indication that the person arrested possesses weapons or evidence. The fact of a lawful arrest, standing alone, authorizes a search.” **Michigan v. DeFillippo**, 443 U.S. 31, 35, 99 S.Ct. 2627, 61 L.Ed.2d 343 (1979).

[20] A suspect’s criminal history is a critical part of his identity that officers should know when processing him for detention. It is a common occurrence that “[p]eople detained for minor offenses can turn out to be the most devious and dangerous criminals. Hours after the Oklahoma City bombing, Timothy McVeigh was stopped by a state trooper who noticed he was driving without a license plate. Police stopped serial killer Joel Rifkin for the same reason. One of the terrorists involved in the September 11 attacks was stopped and ticketed for speeding just two days before hijacking Flight 93.” Id., at ———, 132 S.Ct., at 1520 (citations omitted). Police already seek this crucial identifying information. They use routine and accepted means as varied as comparing the suspect’s booking photograph to sketch artists’ depictions of persons of interest, showing his mugshot to potential witnesses, and of course making a computerized comparison of the arrestee’s fingerprints against electronic databases of known criminals and unsolved crimes. In this respect the only difference between DNA analysis and the accepted use of fingerprint databases is the unparalleled accuracy DNA provides.

[21] The task of identification necessarily entails searching public and police records based on the identifying information provided by the arrestee to see what is already known about him. The DNA collected from arrestees is an irrefutable identification of the person from whom it was taken. Like a fingerprint, the 13 CODIS loci are not themselves evidence of any particular crime, in the way that a drug test can by itself be evidence of illegal narcotics use. A DNA profile is useful to the police because it gives them a form of identification to search the records already in their valid possession. In this respect the use of DNA for identification is no different than matching an arrestee’s face to a wanted poster of a previously unidentified suspect; or matching tattoos to known gang symbols to reveal a criminal affiliation; or matching the arrestee’s fingerprints to those recovered from a crime scene. See Tr. of Oral Arg. 19. DNA is another metric of identification used to connect the arrestee with his or her public persona, as reflected in records of his or her actions that are available to the police. Those records may be linked to the arrestee by a variety of relevant forms of identification, including name, alias, date and time of previous convictions and the name then used, photograph, Social Security number, or CODIS profile. These data, found in official records, are checked as a routine matter to produce a more comprehensive record of the suspect’s complete identity. Finding occurrences of the arrestee’s CODIS profile in outstanding cases is consistent with this common practice. It uses a different form of identification than a name or fingerprint, but its function is the same.

[23] Second, law enforcement officers bear a responsibility for ensuring that the custody of an arrestee does not create inordinate “risks for facility staff, for the existing detainee population, and for a new detainee.” Florence, supra, at ———, 132 S.Ct., at 1518. DNA identification can provide untainted information to those charged with detaining suspects and detaining the property of any felon. For these purposes officers must know the type of person whom they are detaining, and DNA allows them to make critical choices about how to proceed.

“Knowledge of identity may inform an officer that a suspect is wanted for another offense, or has a record of violence or mental disorder. On the other hand, knowing identity may help clear a suspect and allow the police to concentrate their efforts elsewhere. Identity may prove particularly important in [certain cases, such as] where the police are investigating what appears to be a domestic assault. Officers called to investigate domestic disputes need to know whom they are dealing with in order to assess the situation, the threat to their own safety, and possible danger to the potential victim.” Hiibel, supra, at 186, 124 S.Ct. 2451.

Recognizing that a name alone cannot address this interest in identity, the Court has approved, for example, “a visual inspection for certain tattoos and other signs of gang affiliation as part of the intake process,” because “[t]he identification and isolation of gang members before they are admitted protects everyone.” Florence, supra, at ———, 132 S.Ct., at 1519.

Third, looking forward to future stages of criminal prosecution, “the Government has a substantial interest in ensuring that **1973 persons accused of crimes are available for trials.” Bell v. Wolfish, 441 U.S. 520, 534, 99 S.Ct. 1861, 60 L.Ed.2d 447 (1979). A person who is arrested for one offense but knows that he has yet to answer for some past crime may be more inclined to flee the instant charges, lest continued contact with the criminal justice system expose one or more other serious offenses. For example, a defendant who had committed a prior sexual assault might be inclined to flee on a burglary charge, knowing that in every State a DNA sample would be taken from him after his conviction on the burglary charge that would tie him to the more serious charge of rape. In addition to subverting the administration of justice with respect to the crime of arrest, this ties back to the interest in safety; for a detainee who absconds from custody presents a risk to law enforcement officers, other detainees, victims of previous crimes, witnesses, and society at large.
Fourth, an arrestee’s past conduct is essential to an assessment of the danger he poses to the public, and this will inform a court’s determination whether the individual should be released on bail. “The government’s interest in preventing crime by arrestees is both legitimate and compelling.” United States v. Salerno, 481 U.S. 739, 749, 107 S.Ct. 2095, 95 L.Ed.2d 697 (1987). DNA identification of a suspect in a violent crime provides critical information to the police and judicial officials in making a determination of the arrestee’s future dangerousness. This inquiry always has entailed some scrutiny beyond the name on the defendant’s driver’s license. For example, Maryland law requires a judge to take into account not only “the nature and circumstances of the offense charged” but also “the defendant’s family ties, employment status and history, financial resources, reputation, character and mental condition, length of residence in the community.” 1 Md. Rules 4–216(f)(1)(A), (C) (2013). Knowing that the defendant is wanted for a previous violent crime based on DNA identification is especially probative of the court’s consideration of “the danger of the defendant to the alleged victim, another person, or the community.” Rule 4–216(f)(1)(G); *454 *see also 18 U.S.C. § 3142 (2006 ed. and Supp. V) (similar requirements).

This interest is not speculative. In considering laws to require collecting DNA from arrestees, government agencies around the Nation found evidence of numerous cases in which felony arrestees would have been identified as violent through DNA identification matching them to previous crimes but who later committed additional crimes because such identification was not used to detain them. See Denver’s Study on Preventable Crimes (2009) (three examples), online at http://www.denverda.org/DNA_Documents/Denver%27s%20Preventable%20Crimes%20Study.pdf (all Internet materials as visited May 31, 2013, and available in Clerk of Court’s case file); Chicago’s Study on Preventable Crimes (2005) (five examples), online at http://www.denverda.org/DNA_Documents/Arrestee_Database/Chicago%20Preventable%20CrimesFinal.pdf; Maryland Study on Preventable Crimes (2008) (three examples), online at http://www.denverda.org/DNA_Documents/MarylandDNAarresteestudy.pdf.

Present capabilities make it possible to complete a DNA identification that provides information essential to determining whether a detained suspect can be released pending trial. See, e.g., States Brief 18, n. 10 (“DNA identification database samples have been processed in as few as two days in California, although around 30 days has been average”). Regardless of when the initial bail decision is made, release is not appropriate until a further determination is made as to the person’s identity in the sense not only of what his birth certificate states but also what other records and data disclose to give that identity more meaning in the whole context of who the person really is. And even when release is permitted, the background identity of the suspect is necessary for determining what conditions must be met before release is allowed. If release is authorized, it may take time for the conditions to be met, and so the time before actual *455 release can be substantial. For example, in the federal system, defendants released conditionally are detained on average for 112 days; those released on unsecured bond for 37 days; on personal recognizance for 36 days; and on other financial conditions for 27 days. See Dept. of Justice, Bureau of Justice Statistics, Compendium of Federal Justice Statistics 45 (NCJ–213476, Dec. 2006) online at http://bjs.gov/content/pub/pdf/cfjs04.pdf. During this entire period, additional and supplemental data establishing more about the person’s identity and background can provide critical information relevant to the conditions of release and whether to revisit an initial release determination. The facts of this case are illustrative. Though the record is not clear, if some thought were being given to releasing the respondent on bail on the gun charge, a release that would take weeks or months in any event, when the DNA report linked him to the prior rape, it would be relevant to the conditions of his release. The same would be true with a supplemental fingerprint report.

Even if an arrestee is released on bail, development of DNA identification revealing the defendant’s unknown violent past can and should lead to the revocation of his conditional release. See 18 U.S.C. § 3145(a) (providing for revocation of release); see also States Brief 11–12 (discussing examples where bail and diversion determinations were reversed after DNA identified the arrestee’s violent history). Pretrial release of a person charged with a dangerous crime is a most serious responsibility. It is reasonable in all respects for the State to use an accepted database to determine if an arrestee is the object of suspicion in other serious crimes, suspicion that may provide a strong incentive for the arrestee to escape and flee.

Finally, in the interests of justice, the identification of an arrestee as the perpetrator of some heinous crime may have the salutary effect of freeing a person wrongfully imprisoned for the same offense. “[P]rompt [DNA] testing ... would *456 speed up apprehension of criminals before they commit additional crimes, and prevent the
grotesque detention of ... innocent people.” J. Dwyer, P. Neufeld, & B. Scheck, Actual Innocence 245 (2000).

[24] [27] Because proper processing of arrestees is so important and has consequences for every stage of the criminal process, the Court has recognized that the “governmental interests underlying a station-house search of the arrestee’s person and possessions may in some circumstances be even greater than those supporting a search immediately following arrest.” Lafayette, 462 U.S., at 645, 103 S.Ct. 2605. Thus, the Court has been reluctant to circumscribe the authority of the police to conduct reasonable booking searches. For example, “[t]he standards traditionally governing a search incident to lawful arrest are not ... commuted to the stricter Terry standards.” Robinson, 414 U.S., at 234, 94 S.Ct. 467. Nor are these interests in identification served only by a search of the arrestee himself. “[I]nspection of an arrestee’s personal property may assist the police in ascertaining or verifying his identity.” **1975 Lafayette, supra, at 646, 103 S.Ct. 2605. And though the Fifth Amendment’s protection against self-incrimination is not, as a general rule, governed by a reasonableness standard, the Court has held that “questions ... reasonably related to the police’s administrative concerns ... fall outside the protections of Miranda [v. Arizona, 384 U.S. 436, 86 S.Ct. 1602, 16 L.Ed.2d 694 (1966)] and the answers thereto need not be suppressed.” Pennsylvania v. Muniz, 496 U.S. 582, 601–602, 110 S.Ct. 2638, 110 L.Ed.2d 528 (1990).

B

DNA identification represents an important advance in the techniques used by law enforcement to serve legitimate police concerns for as long as there have been arrests, concerns the courts have acknowledged and approved for more than a century. Law enforcement agencies routinely have used scientific advancements in their standard procedures for the identification of arrestees. “Police had been using photography *457 to capture the faces of criminals almost since its invention.” S. Cole, Suspect Identities 20 (2001). Courts did not dispute that practice, concluding that a “sheriff in making an arrest for a felony on a warrant has the right to exercise a discretion ..., [if] he should deem it necessary to the safe-keeping of a prisoner, and to prevent his escape, or to enable him the more readily to retake the prisoner if he should escape, to take his photograph.” State ex rel. Bruns v. Clausmier, 154 Ind. 599, 601, 603, 57 N.E. 541, 542 (1900). By the time that it had become “the daily practice of the police officers and detectives of crime to use photographic pictures for the discovery and identification of criminals,” the courts likewise had come to the conclusion that “it would be [a] matter of regret to have its use unduly restricted upon any fanciful theory or constitutional privilege.” Shaffer v. United States, 24 App.D.C. 417, 426 (1904).

Beginning in 1887, some police adopted more exacting means to identify arrestees, using the system of precise physical measurements pioneered by the French anthropologist Alphonse Bertillon. Bertillon identification consisted of 10 measurements of the arrestee’s body, along with a “scientific analysis of the features of the face and an exact anatomical localization of the various scars, marks, &c., of the body.” Defense of the Bertillon System, N.Y. Times, Jan. 20, 1896, p. 3. “[W]hen a prisoner was brought in, his photograph was taken according to the Bertillon system, and his body measurements were then made. The measurements were made ... and noted down on the back of a card or a blotter, and the photograph of the prisoner was expected to be placed on the card. This card, therefore, furnished both the likeness and description of the prisoner, and was placed in the rogues’ gallery, and copies were sent to various cities where similar records were kept.” People ex rel. Jones v. Diehl, 53 A.D. 645, 646, 65 N.Y.S. 801, 802 (1900). As in the present case, the point of taking this information about each arrestee was not limited to verifying that the proper name *458 was on the indictment. These procedures were used to “facilitate the recapture of escaped prisoners,” to aid “the investigation of their past records and personal history,” and “to preserve the means of identification for ... future supervision after discharge.” Hodgeman v. Olsen, 86 Wash. 615, 619, 150 P. 1122, 1124 (1915); see also McGovern v. Van Riper, 137 N.J. Eq. 24, 33–34, 43 A.2d 514, 519 (Ch.1945) (“[C]riminal identification is said to have two main purposes: (1) The identification of the accused as the person who committed the crime for which he is being held; and, (2) the identification of the accused as the same person who has been previously charged with, or **1976 convicted of, other offenses against the criminal law”).

Perhaps the most direct historical analogue to the DNA technology used to identify respondent is the familiar practice of fingerprinting arrestees. From the advent of this technique, courts had no trouble determining that fingerprinting was a natural part of “the administrative steps incident to arrest.” County of Riverside v. McLaughlin, 500 U.S. 44, 58, 111 S.Ct. 1661, 114 L.Ed.2d 49 (1991). In the seminal case of United States v. Kelly, 55 F.2d 67 (C.A.2 1932), Judge Augustus Hand wrote that routine fingerprinting did not violate the Fourth
Amendment precisely because it fit within the accepted means of processing an arrestee into custody:

“Fingerprinting seems to be no more than an extension of methods of identification long used in dealing with persons under arrest for real or supposed violations of the criminal laws. It is known to be a very certain means devised by modern science to reach the desired end, and has become especially important in a time when increased population and vast aggregations of people in urban centers have rendered the notoriety of the individual in the community no longer a ready means of identification.

......

“We find no ground in reason or authority for interfering with a method of identifying persons charged with *459 crime which has now become widely known and frequently practiced.” Id., at 69–70.

By the middle of the 20th century, it was considered “elementary that a person in lawful custody may be required to submit to photographing and fingerprinting as part of routine identification processes.” Smith v. United States, 324 F.2d 879, 882 (C.A.D.C.1963) (Burger, J.) (citations omitted).

DNA identification is an advanced technique superior to fingerprinting in many ways, so much so that to insist on fingerprints as the norm would make little sense to either the forensic expert or a layperson. The additional intrusion upon the arrestee’s privacy beyond that associated with fingerprinting is not significant, see Part V, infra, and DNA is a markedly more accurate form of identifying arrestees. A suspect who has changed his facial features to evade photographic identification or even one who has undertaken the more arduous task of altering his fingerprints cannot escape the revealing power of his DNA.

[28] The respondent’s primary objection to this analogy is that DNA identification is not as fast as fingerprinting, and so it should not be considered to be the 21st-century equivalent. See Tr. of Oral Arg. 53. But rapid analysis of fingerprints is itself of recent vintage. The FBI’s vaunted Integrated Automated Fingerprint Identification System (IAFIS) was only “launched on July 28, 1999. Prior to this time, the processing of ... fingerprint submissions was largely a manual, labor-intensive process, taking weeks or months to process a single submission.” Federal Bureau of Investigation, Integrated Automated Fingerprint Identification System, online at http://www.fbi.gov/about-us/cjis/fingerprints_biometrics/iafis/iafis. It was not the advent of this technology that rendered fingerprint analysis constitutional in a single moment. The question of how long it takes to process identifying information obtained from a valid search goes only to the efficacy of the search for its purpose of prompt identification, not the constitutionality of the search. Cf. *460 Ontario v. Quon, 560 U.S. ——, ——, 130 S.Ct. 2619, 2632, 177 L.Ed.2d 216 (2010). Given the importance of DNA in the identification of police records pertaining to arrestees **1977 and the need to refine and confirm that identity for its important bearing on the decision to continue release on bail or to impose of new conditions, DNA serves an essential purpose despite the existence of delays such as the one that occurred in this case. Even so, the delay in processing DNA from arrestees is being reduced to a substantial degree by rapid technical advances. See, e.g., Attorney General DeWine Announces Significant Drop in DNA Turnaround Time (Jan. 4, 2013) (DNA processing time reduced from 125 days in 2010 to 20 days in 2012), online at http://ohioattorneygeneral.gov/Media/News-Releases/January–2013/Attorney–General–DeWine–Announces–Significant–Drop; Gov. Jindal Announces Elimination of DNA Backlog, DNA Unit Now Operating in Real Time (Nov. 17, 2011) (average DNA report time reduced from a year or more in 2009 to 20 days in 2011), online at http://www.gov.state.la.us/index.cfm?md=newsroom&tmp=detail&articleID=3102. And the FBI has already begun testing devices that will enable police to process the DNA of arrestees within 90 minutes. See Brief for National District Attorneys Association as Amicus Curiae 2619, 2632, 177 L.Ed.2d 216 (2010). Given the

[29] In sum, there can be little reason to question “the legitimate interest of the government in knowing for an absolute certainty the identity of the person arrested, in knowing whether he is wanted elsewhere, and in ensuring his identification in the event he flees prosecution.” 3 W. LaFave, Search and Seizure § 5.3(e), p. 216 (5th ed. 2012). To that end, courts have confirmed that the Fourth
Amendment allows police to take certain routine “administrative steps incident to arrest—i.e., ... book[ing], photograph[ing], and fingerprint[ing].” McLaughlin, 500 U.S., at 58, 111 S.Ct. 1661. DNA identification of arrestees, of the type approved by the Maryland statute here at issue, is “no more than an extension of methods of identification long used in dealing with persons under arrest.” Kelly, 55 F.3d, at 69. In the balance of reasonableness required by the Fourth Amendment, therefore, the Court must give great weight both to the significant government interest at stake in the identification of arrestees and to the unmatched potential of DNA identification to serve that interest.

V

A

By comparison to this substantial government interest and the unique effectiveness of DNA identification, the intrusion of a cheek swab to obtain a DNA sample is a minimal one. True, a significant government interest does not alone suffice to justify a search. The government interest must outweigh the degree to which the search invades an individual’s legitimate expectations of privacy. In considering **1978 those expectations in this case, however, the necessary predicate of a valid arrest for a serious offense is fundamental. “Although the underlying command of the Fourth Amendment is always that searches and seizures be reasonable, what is reasonable *462 depends on the context within which a search takes place.” New Jersey v. T.L.O., 469 U.S. 325, 337, 105 S.Ct. 733, 83 L.Ed.2d 720 (1985). “[T]he legitimacy of certain privacy expectations vis-à-vis the State may depend upon the individual’s legal relationship with the State.” Vernonia School Dist. 47J, 515 U.S., at 654, 115 S.Ct. 2386.

**1979 The reasonableness inquiry here considers two other circumstances in which the Court has held that particularized suspicion is not categorically required: “diminished expectations of privacy [and] minimal intrusions.” McArthur, 531 U.S., at 330, 121 S.Ct. 946. This is not to suggest that any search is acceptable solely
because a person is in custody. Some searches, such as invasive surgery, see Winston, 470 U.S. 753, 105 S.Ct. 1611; or a search of the arrestee’s home, see Chimel v. California, 395 U.S. 752, 89 S.Ct. 2034, 23 L.Ed.2d 685 (1969), involve either greater intrusions or higher expectations of privacy than are present in this case. In those situations, when the Court must “balance the privacy-related and law enforcement-related concerns to determine if the intrusion was reasonable,” McArthur, supra, at 331, 121 S.Ct. 946, the privacy-related concerns are weighty enough that the search may require a warrant, notwithstanding the diminished expectations of privacy of the arrestee.

Here, by contrast to the approved standard procedures incident to any arrest detailed above, a buccal swab involves an even more brief and still minimal intrusion. A gentle rub along the inside of the cheek does not break the skin, *464 and it “involves virtually no risk, trauma, or pain.” Schmerber, 384 U.S., at 771, 86 S.Ct. 1826. “A crucial factor in analyzing the magnitude of the intrusion ... is the extent to which the procedure may threaten the safety or health of the individual,” Winston, supra, at 761, 105 S.Ct. 1611, and nothing suggests that a buccal swab poses any physical danger whatsoever. A brief intrusion of an arrestee’s person is subject to the Fourth Amendment, but a swab of this nature does not increase the indignity already attendant to normal incidents of arrest.

First, as already noted, the CODIS loci come from noncoding parts of the DNA that do not reveal the genetic traits of the arrestee. While science can always progress further, and those progressions may have Fourth Amendment consequences, alleles at the CODIS loci “are not at present revealing information beyond identification.” Katsanis & Wagner, Characterization of the Standard and Recommended CODIS Markers, 58 J. Forensic Sci. S169, S171 (2013). The argument that the testing at issue in this case reveals any private medical information at all is open to dispute.

And even if non-coding alleles could provide some information, they are not in fact tested for that end. It is undisputed that law enforcement officers analyze DNA for the sole purpose of generating a unique identifying number against which future samples may be matched. This parallels a similar safeguard based on actual practice in the school drug-testing context, where the Court deemed it “significant that the tests at issue here look only for drugs, and not for whether the student is, for example, epileptic, pregnant, or diabetic.” Vernonia School Dist. 47J, 515 U.S., at 658, 115 S.Ct. 2386. If in the future police analyze samples to determine, for instance, an arrestee’s predisposition for a particular disease *465 or other hereditary factors not relevant to identity, that case would present additional privacy concerns not present here.

Finally, the Act provides statutory protections that guard against further invasion of privacy. As noted above, the Act requires that “[o]nly DNA records that **1980 directly relate to the identification of individuals shall be collected and stored.” Md. Pub. Saf. Code Ann. § 2–505(b)(1). No purpose other than identification is permissible: “A person may not willfully test a DNA sample for information that does not relate to the identification of individuals as specified in this subtitle.” § 2–512(c). This Court has noted often that “a ‘statutory or regulatory duty to avoid unwarranted disclosures’ generally allays ... privacy concerns.” NASA v. Nelson, 562 U.S. —–, —–, 131 S.Ct. 746, 750, 178 L.Ed.2d 667 (2011) (quoting Whalen v. Roe, 429 U.S. 589, 605, 97 S.Ct. 869, 51 L.Ed.2d 64 (1977)). The Court need not speculate about the risks posed “by a system that did not contain comparable security provisions.” Id., at 606, 97 S.Ct. 869. In light of the scientific and statutory safeguards, once respondent’s DNA was lawfully collected the STR analysis of respondent’s DNA pursuant to CODIS procedures did not amount to a significant invasion of privacy that would render the DNA identification impermissible under the Fourth Amendment.

[38] In addition the processing of respondent’s DNA sample’s 13 CODIS loci did not intrude on respondent’s privacy in a way that would make his DNA identification unconstitutional.

[39] [40] In light of the context of a valid arrest supported by probable cause respondent’s expectations of privacy were not offended by the minor intrusion of a brief swab of his cheeks. By contrast, that same context of arrest gives rise to significant state interests in identifying respondent not only so that the proper name can be attached to his charges but also so that the criminal justice system can make informed decisions concerning pretrial custody. Upon these considerations the Court concludes that DNA identification of arrestees is a reasonable search that can be considered part of a routine booking procedure. When officers make an arrest supported by probable cause to hold for a serious offense and they bring the suspect to the
station to be detained in custody, taking and analyzing a cheek swab of the arrestee’s DNA is, like fingerprinting and photographing, a legitimate police booking procedure that is reasonable under the Fourth Amendment.

The judgment of the Court of Appeals of Maryland is reversed.

It is so ordered.

Justice SCALIA, with whom Justice GINSBURG, Justice SOTOMAYOR, and Justice KAGAN join, dissenting.

The Fourth Amendment forbids searching a person for evidence of a crime when there is no basis for believing the person is guilty of the crime or is in possession of incriminating evidence. That prohibition is categorical and without exception; it lies at the very heart of the Fourth Amendment. Whenever this Court has allowed a suspicionless search, it has insisted upon a justifying motive apart from the investigation of crime.

It is obvious that no such noninvestigative motive exists in this case. The Court’s assertion that DNA is being taken, not to solve crimes, but to identify those in the State’s custody, taxes the credulity of the credulous. And the Court’s comparison of Maryland’s DNA searches to other techniques, such as fingerprinting, can seem apt only to those who know no more than today’s opinion has chosen to tell them about how those DNA searches actually work.

I

At the time of the Founding, Americans despised the British use of so-called “general warrants”—warrants not grounded upon a sworn oath of a specific infraction by a particular individual, and thus not limited in scope and application. The first **1981 Virginia Constitution declared that “general warrants, whereby any officer or messenger may be commanded to search suspected places without evidence of a fact committed,” or to search a person “whose offence is not particularly described and supported by evidence,” “are *467 grievous and oppressive, and ought not be granted.” Va. Declaration of Rights § 10 (1776), in 1 B. Schwartz, The Bill of Rights: A Documentary History 234, 235 (1971). The Maryland Declaration of Rights similarly provided that general warrants were “illegal.” Md. Declaration of Rights § XXIII (1776), in *id.*, at 280, 282. In the ratification debates, Antifederalists sarcastically predicted that the general, suspicionless warrant would be among the Constitution’s “blessings.” Blessings of the New Government, Independent Gazetteer, Oct. 6, 1787, in 13 Documentary History of the Ratification of the Constitution 345 (J. Kaminski & G. Saladino eds. 1981). “Brutus” of New York asked why the Federal Constitution contained no provision like Maryland’s, Brutus II, N.Y. Journal, Nov. 1, 1787, in *id.*, at 524, and Patrick Henry warned that the new Federal Constitution would expose the citizenry to searches and seizures “in the most arbitrary manner, without any evidence or reason.” 3 Debates on the Federal Constitution 588 (J. Elliot 2d ed. 1854).

Madison’s draft of what became the Fourth Amendment answered these charges by providing that the “rights of the people to be secured in their persons ... from all unreasonable searches and seizures, shall not be violated by warrants issued without probable cause ... or not particularly describing the places to be searched.” 1 Annals of Cong. 434–435 (1789). As ratified, the Fourth Amendment’s Warrant Clause forbids a warrant to “issue” except “upon probable cause,” and requires that it be “particula[r]” (which is to say, individualized ) to “the place to be searched, and the persons or things to be seized.” And we have held that, even when a warrant is not constitutionally necessary, the Fourth Amendment’s general prohibition of “unreasonable” searches imports the same requirement of individualized suspicion. See Chandler v. Miller, 520 U.S. 305, 308, 117 S.Ct. 1295, 137 L.Ed.2d 513 (1997).

Although there is a “closely guarded category of constitutionally permissible suspicionless searches,” *id.*, at 309, 117 S.Ct. 1295, that *468 has never included searches designed to serve “the normal need for law enforcement,” Skinner v. Railway Labor Executives’ Assn., 489 U.S. 602, 619, 109 S.Ct. 1402, 103 L.Ed.2d 639 (1989) (internal quotation marks omitted). Even the common name for suspicionless searches—“special needs” searches—itself reflects that they must be justified, always, by concerns “other than crime detection.” Chandler, supra, at 313–314, 117 S.Ct. 1295. We have approved random drug tests of railroad employees, yes—but only because the Government’s need to “regulat[e] the conduct of railroad employees to

So while the Court is correct to note (ante, at 1969 – 1970) that there are instances in which we have permitted searches without individualized suspicion, “[i]n none of these cases … did we indicate approval of a [search] whose primary purpose was to detect evidence of ordinary criminal wrongdoing.” Indianapolis v. Edmond, 531 U.S. 32, 38, 121 S.Ct. 447, 148 L.Ed.2d 333 (2000). That limitation is crucial. It is only when a governmental purpose aside from crime-solving is at stake that we engage in the free-form “reasonableness” inquiry that the Court indulges at length today. To put it another way, both the legitimacy of the Court’s method and the correctness of its outcome hinge entirely on the truth of a single proposition: that the primary purpose of these DNA searches is something other than simply discovering evidence of criminal wrongdoing. As I detail below, that proposition is wrong.

**B**

The Court alludes at several points (see ante, at 1970 – 1971, 1978 – 1979) to the fact that King was an arrestee, and arrestees may be validly searched incident to their arrest. But the Court does not really rest on this principle, and for good reason: *469 The objects of a search incident to arrest must be either (1) weapons or evidence that might easily be destroyed, or (2) evidence relevant to the crime of arrest. See Arizona v. Gant, 556 U.S. 332, 343–344, 129 S.Ct. 1710, 173 L.Ed.2d 485 (2009); Thornton v. United States, 541 U.S. 615, 632, 124 S.Ct. 2127, 158 L.Ed.2d 905 (2004) (SCALIA, J., concurring in judgment). Neither is the object of the search at issue here.

The Court hastens to clarify that it does not mean to approve invasive surgery on arrestees or warrantless searches of their homes. Ante, at 1978 – 1979. That the Court feels the need to disclaim these consequences is as damming a criticism of its suspicionless-search regime as any I can muster. And the Court’s attempt to distinguish those hypothetical searches from this real one is unconvincing. We are told that the “privacy-related concerns” in the search of a home “are weighty enough that the search may require a warrant, notwithstanding the diminished expectations of privacy of the arrestee.” Ante, at 1979. But why are the “privacy-related concerns” not also “weighty” when an intrusion into the body is at stake? (The Fourth Amendment lists “persons” first among the entities protected against unreasonable searches and seizures.) And could the police engage, without any suspicion of wrongdoing, in a “brief and … minimal” intrusion into the home of an arrestee—perhaps just peeking around the curtilage a bit? See ante, at 1979. Obviously not.

At any rate, all this discussion is beside the point. No matter the degree of invasiveness, suspicionless searches are never allowed if their principal end is ordinary crime-solving. A search incident to arrest either serves other ends (such as officer safety, in a search for weapons) or is not suspicionless (as when there is reason to believe the arrestee possesses evidence relevant to the crime of arrest).

Sensing (correctly) that it needs more, the Court elaborates at length the ways that the search here served the special purpose of “identifying” King. But that *1983 seems to *470 me quite wrong—unless what one means by “identifying” someone is “searching for evidence that he has committed crimes unrelated to the crime of his arrest.” At points the Court does appear to use “identifying” in that peculiar sense—claiming, for example, that knowing “an arrestee’s past conduct is essential to an assessment of the danger he poses.” Ante, at 1973. If identifying someone means finding out what unsolved crimes he has committed, then identification is indistinguishable from the ordinary law-enforcement aims that have never been thought to justify a suspicionless search. Searching every lawfully stopped car, for example, might turn up information about unsolved crimes the driver had committed, but no one would say that such a search was aimed at “identifying” him, and no court would hold such a search lawful. I will therefore assume that the Court means that the DNA search at issue here was useful to “identify” King in the normal sense of that word—in the sense that would identify the author of Introduction to the Principles of Morals and Legislation as Jeremy Bentham.

1

The portion of the Court’s opinion that explains the identification rationale is strangely silent on the actual workings of the DNA search at issue here. To know those facts is to be instantly disabused of the notion that what
happened had anything to do with identifying King.

King was arrested on April 10, 2009, on charges unrelated to the case before us. That same day, April 10, the police *471 searched him and seized the DNA evidence at issue here. What happened next? Reading the Court’s opinion, particularly its insistence that the search was necessary to know “who [had] been arrested,” ante, at 1971, one might guess that King’s DNA was swiftly processed and his identity thereby confirmed—perhaps against some master database of known DNA profiles, as is done for fingerprints. After all, was not the suspicionless search database of known DNA profiles, as is done for "existing detainee population," here crucial to avoid "inordinate risks for facility staff " or to the case before us. That same day, April 10, the police know "who [had] been arrested," here. What happened next? Reading the Court’s opinion, *133 S.Ct. 1958, 186 L.Ed.2d 1, 81 USLW 4343, 13 Cal. Daily Op. Serv. 5551...

Nothing could be further from the truth. Maryland officials did not even begin the process of testing King’s DNA that day. Or, actually, the next day. Or the day after that. And that was for a simple reason: Maryland law forbids them to do so. A “DNA sample collected from an individual charged with a crime ... may not be tested or placed in the statewide DNA data base system prior to the first scheduled arraignment date.” Md. Pub. Saf. Code Ann. § 2–504(d)(1) (Lexis 2011) (emphasis added). And King’s first appearance in court was not until three days after his arrest. (I suspect, though, that they did not wait three days to ask his name or take his fingerprints.)

This places in a rather different light the Court’s solemn declaration that the search here was necessary so that King could be identified at “every stage of the criminal process.” Ante, at 1974. I hope that the Maryland officials who read the Court’s opinion do not take it seriously. Acting on the Court’s misperception of Maryland law could lead to jail time. See Md. Pub. Saf. Code Ann. § 2–512(c)–(e) (punishing by up to five years’ imprisonment anyone who obtains or tests DNA information except as provided by statute). Does the Court really believe that Maryland did not know whom it was arraigning? The Court’s response is to imagine that King’s DNA sample was not received by the Maryland State Police’s Forensic Sciences Division until April 23, 2009—two weeks after his arrest. It sat in that office, ripening in a storage area, until the custodians got around to mailing it to a lab for testing on June 25, 2009—two months after it was received, and nearly three since King’s arrest. After it was mailed, the data from the lab tests were not available for several more weeks, until July 13, 2009, which is when the test results were entered into Maryland’s DNA database, together with information identifying the person from whom the sample was taken. Meanwhile, bail had been set, King had engaged in discovery, and he had requested a speedy trial—presumably not a trial of John Doe. It was not until August 4, 2009—four months after King’s arrest—that the forwarded sample transmitted (without identifying information) from the Maryland DNA database to the Federal Bureau of Investigation’s national database was matched with a sample taken from the scene of an unrelated crime years earlier.

A more specific description of exactly what happened at this point illustrates why, by definition, King could not have been identified by this match. The FBI’s DNA database (known as CODIS) consists of two distinct collections. FBI, CODIS and NDIS Fact Sheet, http://www.fbi.gov/about-us/lab/codis/codis-and-ndis-fact-sheet (all Internet materials as visited May 31, 2013, and available in Clerk of Court’s case *473 file). One of them, the one to which King’s DNA was submitted, consists of DNA samples taken from known convicts or arrestees. I will refer to this as the “Convict and Arrestee Collection.” The other collection consists of samples taken from crime scenes; I will refer to this as the “Unsolved Crimes Collection.” The Convict and Arrestee Collection stores “no names or other personal identifiers of the offenders, arrestees, or detainees.” Ibid. Rather, it contains only the DNA profile itself, the name of the agency that submitted it, the laboratory personnel who analyzed it, and an identification number for the specimen. Ibid. This is because the submitting state laboratories are expected already to know the identities of the convicts and arrestees from whom samples are taken. (And, of course, they do.)

Moreover, the CODIS system works by checking to see whether any of the samples in the Unsolved Crimes Collection match any of the samples in the Convict and Arrestee Collection. Ibid. That is sensible, if what one wants to do is solve those cold cases, but note what it requires: that the identity of the people whose DNA has
been entered into the Convict and Arrestee Collection already be known. If one wanted to identify someone in custody using **1985 his DNA, the logical thing to do would be to compare that DNA against the Convict and Arrestee Collection: to search, in other words, the collection that could be used (by checking back with the submitting state agency) to identify people, rather than the collection of evidence from unsolved crimes, whose perpetrators are by definition unknown. But that is not what was done. And that is because this search had nothing to do with identification.

In fact, if anything was “identified” at the moment that the DNA database returned a match, it was not King—his *474 identity was already known. (The docket for the original criminal charges lists his full name, his race, his sex, his height, his weight, his date of birth, and his address.) Rather, what the August 4 match “identified” was the previously-taken sample from the earlier crime. That sample was genuinely mysterious to Maryland; the State knew that it had probably been left by the victim’s attacker, but nothing else. King was not identified by his association with the sample; rather, the sample was identified by its association with King. The Court effectively destroys its own “identification” theory when it acknowledges that the object of this search was “to see what [was] already known about [King].” King was who he was, and volumes of his biography could not make him any more or any less King. No minimally competent speaker of English would say, upon noticing a known arrestee’s similarity “to a wanted poster of a previously unidentified suspect,” ante, at 1972, that the arrestee had thereby been identified. It was the previously unidentified suspect who had been identified—just as, here, it was the previously unidentified rapist.

Instead, the law provides that DNA samples are collected and tested, as a matter of Maryland law, “as part of an official investigation into a crime.” § 2–505(a)(2). (Or, as *475 our suspicionless-search cases would put it: for ordinary law-enforcement purposes.) That is certainly how everyone has always understood the Maryland Act until today. The Governor of Maryland, in commenting on our decision to hear this case, said that he was glad, because “[a]llowing law enforcement to collect DNA samples ... is absolutely critical to our efforts to continue driving down crime,” and “bolsters our efforts to resolve open investigations and bring them to a resolution.” Marbella, Supreme Court Will Review Md. DNA Law, Baltimore Sun, Nov. 10, 2012, pp. 1, 14. The attorney general of Maryland remarked that he “look[ed] forward to the opportunity to defend this important crime-fighting tool,” and praised the DNA database for helping to “bring to justice violent perpetrators.” Ibid. Even this Court’s order staying the decision below states that the statute “provides a valuable tool for investigating unsolved crimes and thereby helping to remove violent offenders from the general population”—with, unsurprisingly, no mention of identity. **1986 567 U.S. ———, ———, 133 S.Ct. 1, 3, 183 L.Ed.2d 667 (2012) (ROBERTS, C.J., in chambers).

More devastating still for the Court’s “identification” theory, the statute does enumerate two instances in which a DNA sample may be tested for the purpose of identification: “to help identify human remains,” § 2–505(a)(3) (emphasis added), and “to help identify missing individuals,” § 2–505(a)(4) (emphasis added). No mention of identifying arrestees. Inclusio unius est exclusio alterius. And note again that Maryland forbids using DNA records “for any purposes other than those specified”—it is actually a crime to do so. § 2–505(b)(2).

The Maryland regulations implementing the Act confirm what is now monotonously obvious: These DNA searches have nothing to do with identification. For example, if someone is arrested and law enforcement determines that “a convicted offender Statewide DNA Data Base sample already exists” for that arrestee, “the agency is not required to obtain a new sample.” *476 Code of Md. Regs., tit. 29, § 05.01.04(B)(4) (2011). But how could the State know if an arrestee has already had his DNA sample collected, if the point of the sample is to identify who he is? Of course, if the DNA sample is instead taken in order to investigate crimes, this restriction makes perfect sense: Having previously placed an identified someone’s DNA on file to check against available crime-scene evidence, there is no sense in going to the expense of taking a new sample. Maryland’s regulations further require that the “individual collecting a sample ... verify the identity of
the individual from whom a sample is taken by name and, if applicable, State identification (SID) number.” § 05.01.04(K). (But how?) And after the sample is taken, it continues to be identified by the individual’s name, fingerprints, etc., see § 05.01.07(B)—rather than (as the Court believes) being used to identify individuals. See § 05.01.07(B)(2) (“Records and specimen information shall be identified by ... [the] name of the donor” (emphasis added)).

So, to review: DNA testing does not even begin until after arraignment and bail decisions are already made. The samples sit in storage for months, and take weeks to test. When they are tested, they are checked against the Unsolved Crimes Collection—rather than the Convict and Arrestee Collection, which could be used to identify them. The Act forbids the Court’s purpose (identification), but prescribes as its purpose what our suspicionless-search cases forbid (“official investigation into a crime”). Against all of that, it is safe to say that if the Court’s identification theory is not wrong, there is no such thing as error.

II

The Court also attempts to bolster its identification theory with a series of inapposite analogies. See ante, at 1974 – 1977.

Is not taking DNA samples the same, asks the Court, as taking a person’s photograph? No—because that is not a Fourth Amendment search at all. It does not involve a *477 physical intrusion onto the person, see Florida v. Jardines, 569 U.S. 1, ——, 133 S.Ct. 1409, 1413–1414, 185 L.Ed.2d 495 (2013), and we have never held that merely taking a person’s photograph invades any recognized “expectation of privacy,” see Katz v. United States, 389 U.S. 347, 88 S.Ct. 507, 19 L.Ed.2d 576 (1967). Thus, it is unsurprising that the cases the Court cites as authorizing photo-taking do not even mention the Fourth Amendment. See State ex rel. Bruns v. Clausmier, 154 Ind. 599, 57 N.E. 541 (1900) (libel), **1987 Shaffer v. United States, 24 App.D.C. 417 (1904) (Fifth Amendment privilege against self-incrimination).

But is not the practice of DNA searches, the Court asks, the same as taking “Bertillon” measurements—noting an arrestee’s height, shoe size, and so on, on the back of a photograph? No, because that system was not, in the ordinary case, used to solve unsolved crimes. It is possible, I suppose, to imagine situations in which such measurements might be useful to generate leads. (If witnesses described a very tall burglar, all the “tall man” cards could then be pulled.) But the obvious primary purpose of such measurements, as the Court’s description of them makes clear, was to verify that, for example, the person arrested today is the same person that was arrested a year ago. Which is to say, Bertillon measurements were actually used as a system of identification, and drew their primary usefulness from that task.3

It is on the fingerprinting of arrestees, however, that the Court relies most heavily. Ante, at 1975 – 1977. The Court does not actually say whether it believes that taking a person’s fingerprints is a Fourth Amendment search, and our cases provide no ready answer to that question. Even assuming so, however, law enforcement’s post-arrest use of fingerprints *478 could not be more different from its post-arrest use of DNA. Fingerprints of arrestees are taken primarily to identify them (though that process sometimes solves crimes); the DNA of arrestees is taken to solve crimes (and nothing else). Contrast CODIS, the FBI’s nationwide DNA database, with IAFIS, the FBI’s Integrated Automated Fingerprint Identification System. See FBI, Integrated Automated Fingerprint Identification System, http://www.fbi.gov/about-us/cjis/fingerprints_biometrics/iafis/iafis (hereinafter IAFIS).

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<th>Fingerprints</th>
<th>DNA Samples</th>
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<td>The “average response time for an electronic criminal fingerprint submission is about 27 minutes.” IAFIS.</td>
<td>DNA analysis can take months—far too long to be useful for identifying someone.</td>
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IAFIS includes detailed identification information, including "criminal histories; mug shots; scars and tattoo photos; physical characteristics like height, weight, and hair and eye color."

CODIS contains “[n]o names or other personal identifiers of the offenders, arrestees, or detainees.” See CODIS and NDIS Fact Sheet.

“Latent prints” recovered from crime scenes are not systematically compared against the database of known fingerprints, since that requires further forensic work.\(^4\)

The entire point of the DNA database is to check crime scene evidence against the profiles of arrestees and convicts as they come in.

\(^{**1988\text{ *479}}\) The Court asserts that the taking of fingerprints was “constitutional for generations prior to the introduction” of the FBI’s rapid computer-matching system. \textit{Ante}, at 1977. This bold statement is bereft of citation to authority because there is none for it. The “great expansion in fingerprinting came before the modern era of Fourth Amendment jurisprudence,” and so we were never asked to decide the legitimacy of the practice. \textit{United States v. Kincade}, 379 F.3d 813, 874 (C.A.9 2004) (Kozinski, J., dissenting). As fingerprint databases expanded from convicted criminals, to arrestees, to civil servants, to immigrants, to everyone with a driver’s license, Americans simply “became accustomed to having our fingerprints on file in some government database.” \textit{Ibid}. But it is wrong to suggest that this was uncontroversial at the time, or that this Court blessed universal fingerprinting for “generations” before it was possible to use it effectively for identification.

The Court also assures us that “the delay in processing DNA from arrestees is being reduced to a substantial degree by rapid technical advances.” \textit{Ante}, at 1977. The idea, presumably, is that the snail’s pace in this case is atypical, so that DNA is now readily usable for identification. The Court’s proof, however, is nothing but a pair of press releases—each of which turns out to undercut this argument. We learn in them that reductions in backlog have enabled Ohio and Louisiana crime labs to analyze a submitted DNA sample in twenty days.\(^5\) But that is still longer than the eighteen days that Maryland needed to analyze King’s sample, \textit{*480}\ since it worked its way through the State’s labyrinthine bureaucracy. What this illustrates is that these times do not take into account the many other sources of delay. So if the Court means to suggest that Maryland is unusual, that may be right—it may qualify in this context as a paragon of efficiency. (Indeed, the Governor of Maryland was railing the elimination of that State’s backlog more than five years ago. See Wheeler, O’Malley Wants to Expand DNA Testing, Baltimore Sun, Jan. 11, 2008, p. 5B.) Meanwhile, the Court’s holding will result in the dumping of a large number of arrestee samples—many from minor offenders—onto an already overburdened system: Nearly one-third of Americans will be arrested for some offense by age 23. See Brame, Turner, Paternoster, & Bushway, Cumulative Prevalence of Arrest From Ages 8 to 23 in a National Sample, 129 Pediatrics 21 (2011).

The Court also accepts uncritically the Government’s representation at oral argument that it is developing devices that will be able to test DNA in mere minutes. At most, this demonstrates that it may one day be possible to design a program that uses DNA for a purpose other than crime-solving—not that Maryland has in fact designed such a program today. And that is the main point, which the Court’s discussion of the brave new world of instant DNA analysis should not obscure. The issue before us is not whether DNA can \textit{some day} be used for identification; nor even whether it can \textit{today} be used for identification; but whether it \textit{was} used for identification here.
Today, it can fairly be said that fingerprints really are used to identify people—so well, in fact, that there would be no need for the expense of a separate, wholly redundant DNA confirmation of the same information. What DNA adds—what makes it a valuable weapon in the law-enforcement arsenal—is the ability to solve unsolved crimes, by matching old crime-scene evidence against the profiles of people whose identities are already known. That is what was going on when King’s DNA was taken, and we should not disguise the fact. Solving unsolved crimes is a noble objective, but it occupies a lower place in the American pantheon of noble objectives than the protection of our people from suspicionless law-enforcement searches. The Fourth Amendment must prevail.

* * *

The Court disguises the vast (and scary) scope of its holding by promising a limitation it cannot deliver. The Court repeatedly says that DNA testing, and entry into a national DNA registry, will not befall thee and me, dear reader, but only those arrested for “serious offense[s].” Ante, at 1979 – 1980; see also ante, at 1965, 1969 – 1970, 1972 – 1973, 1974, 1976 – 1977, 1977, 1977 – 1978 (repeatedly limiting the analysis to “serious offenses”). I cannot imagine what principle could possibly justify this limitation, and the Court does not attempt to suggest any. If one believes that DNA will “identify” someone arrested for assault, he must believe that it will “identify” someone arrested for a traffic offense. This Court does not base its judgments on senseless distinctions. At the end of the day, logic will out. When there comes before us the taking of DNA from an arrestee for a traffic violation, the Court will predictably (and quite rightly) say, “We can find no significant difference between this case and King.” Make no mistake about it: As an entirely predictable consequence of today’s decision, your DNA can be taken and entered into a national DNA database if you are ever arrested, rightly or wrongly, and for whatever reason.

The most regrettable aspect of the suspicionless search that occurred here is that it proved to be quite unnecessary. All parties concede that it would have been entirely permissible, as far as the Fourth Amendment is concerned, for Maryland to take a sample of King’s DNA as a consequence of his conviction for second-degree assault. So the ironic result of the Court’s error is this: The only arrestees to whom the outcome here will ever make a difference are those who have been acquitted of the crime of arrest (so that their DNA could not have been taken upon conviction). In other words, this Act manages to burden uniquely the sole group for whom the Fourth Amendment’s protections ought to be most jealously guarded: people who are innocent of the State’s accusations.

Today’s judgment will, to be sure, have the beneficial effect of solving more crimes; then again, so would the taking of DNA samples from anyone who flies on an airplane (surely the Transportation Security Administration needs to know the “identity” of the flying public), applies for a driver’s license, or attends a public school. Perhaps the construction of such a genetic panopticon is wise. But I doubt that the proud men who wrote the charter of our liberties would have been so eager to open their mouths for royal inspection.

I therefore dissent, and hope that today’s incursion upon the Fourth Amendment, like an earlier one, will some day be repudiated.

All Citations

Footnotes

1 The Court’s insistence (ante, at 1978) that our special-needs cases “do not have a direct bearing on the issues presented in this case” is perplexing. Why spill so much ink on the special need of identification if a special need is not required? Why not just come out and say that any suspicionless search of an arrestee is allowed if it will be useful to solve crimes? The Court does not say that because most Members of the Court do not believe it. So whatever the Court’s major premise—the opinion does not really contain what you would call a rule of decision—the minor premise is “this search was used to identify King.” The incorrectness of that minor premise will therefore suffice to demonstrate the error in the Court’s result.
By the way, this procedure has nothing to do with exonerating the wrongfully convicted, as the Court soothingly promises. See ante, at 1974. The FBI CODIS database includes DNA from unsolved crimes. I know of no indication (and the Court cites none) that it also includes DNA from all—or even any—crimes whose perpetrators have already been convicted.

Puzzlingly, the Court’s discussion of photography and Bertillon measurements repeatedly cites state cases (such as Clausmier) that were decided before the Fourth Amendment was held to be applicable to the States. See Wolf v. Colorado, 338 U.S. 25, 69 S.Ct. 1359, 93 L.Ed. 1782 (1949); Mapp v. Ohio, 367 U.S. 643, 81 S.Ct. 1684, 6 L.Ed.2d 1081 (1961). Why the Court believes them relevant to the meaning of that Amendment is therefore something of a mystery.

