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Information technology — Biometric data interchange formats —

Part 14: DNA data

Technologies de l'information — Formats d'échange de données biométriques —

Partie 14: Données ADN

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Foreword

ISO (the International Organization for Standardization) and IEC (the International Electrotechnical Commission) form the specialized system for worldwide standardization. National bodies that are members of ISO or IEC participate in the development of International Standards through technical committees established by the respective organization to deal with particular fields of technical activity. ISO and IEC technical committees collaborate in fields of mutual interest. Other international organizations, governmental and non-governmental, in liaison with ISO and IEC, also take part in the work. In the field of information technology, ISO and IEC have established a joint technical committee, ISO/IEC JTC 1.

International Standards are drafted in accordance with the rules given in the ISO/IEC Directives, Part 2.

The main task of the joint technical committee is to prepare International Standards. Draft International Standards adopted by the joint technical committee are circulated to national bodies for voting. Publication as an International Standard requires approval by at least 75 % of the national bodies casting a vote.

Attention is drawn to the possibility that some of the elements of this document may be the subject of patent rights. ISO and IEC shall not be held responsible for identifying any or all such patent rights.

ISO/IEC 19794-14 was prepared by Joint Technical Committee ISO/IEC JTC 1, *Information Technology*, Subcommittee SC 37, *Biometrics*.

ISO/IEC 19794 consists of the following parts, under the general title *Information technology — Biometric data interchange formats*:

— *Part 1: Framework*

— *Part 2: Finger minutiae data*

— *Part 3: Finger pattern spectral data*

— *Part 4: Finger image data*

— *Part 5: Face image data*

— *Part 6: Iris image data*

— *Part 7: Signature/sign time series data*

— *Part 8: Finger pattern skeletal data*

— *Part 9: Vascular image data*

— *Part 10: Hand geometry silhouette data*

— *Part 11: Signature/Sign processed dynamic data*

— *Part 13: Voice data*

— *Part 14: DNA data*

Introduction

In the last 20 years, forensic molecular genetics has evolved from a rapidly developing field with changing technologies into a highly recognized and generally accepted forensic science.

Forensic genetics using deoxyribonucleic acid (DNA) profiling comprises a number of important applications. Examples are the investigation of biological stains to obtain evidence for the presence of an alleged perpetrator at a crime scene by comparing the genetic profiles from crime scene samples of human origin, to those available at DNA databases administrated by legal enforcement agencies. These also include the identification of unknown corpses in the context of both natural death and of crime, immigration, paternity testing, and disaster victim identification.

The purpose of this document is to define a standard for the exchange of human DNA identification data. The standard defines DNA attributes and a data record format for the exchange of DNA data. It includes a sample record and conformance criteria.

This data interchange format standard is based on DNA data from forensic DNA typing techniques that are standardized and most commonly used, namely STR profiling and other DNA typing techniques that are standardized by scientific bodies for the purpose of discriminating between individuals.

Note that the purpose of this data interchange format is to enable the exchange of DNA data from different systems, not to impose any constraints on the specific DNA typing system/technique to be used.

Where existing DNA data exchange formats have been referenced in the preparation of this document these formats are listed as references.

Standard profiling systems exploit the non-coding regions of DNA that are referred to “junk DNA”. The coding regions are deliberately avoided in order to maintain the privacy and civil rights of the donor. However, national data protection and privacy legislation may impose special security safeguards, such as – but not limited to – encryption of data transfers and/or storage.

Information technology — Biometric data interchange formats —

Part 14: DNA data

1 Scope

This part of ISO/IEC 19794 specifies a data interchange format for the exchange of DNA data for person identification or verification technologies that utilize human DNA.

It will provide the ability for DNA profile data to be exchanged and used for comparison (subject to privacy regulations) with DNA profile data produced by any other system that is based on a compatible DNA profiling technique and where the data format conforms to this part of ISO/IEC 19794.

This part of ISO/IEC 19794 is intended to cover current forensic DNA profiling or typing techniques that are based on short tandem repeats (STRs), including STRs on the Y chromosome (Y-STRs), as well as mitochondrial DNA.

A single DNA data record for a subject may require data resulting from more than one of these different DNA techniques. This part of ISO/IEC 19794 enables data for multiple DNA techniques to be presented in a single record for a given subject.

This data format has been prepared in light of ongoing efforts to reduce human involvement in the processing (enrolment and comparison) of DNA. In anticipation of the data format requirements for automated DNA techniques this part of ISO/IEC 19794 will describe a format for both processed and raw (electrophoretic) DNA data. Extensible Mark-up Language (XML) encoding of the data is used to specify DNA data interchange. A normative XML Schema Definition (XSD) specification is provided in Annex B.

This part of ISO/IEC 19794 is not intended for any other purposes than exchange of DNA for biometric verification and identification of individuals, in particular does not exchange medical and other health-related information.

2 Conformance

Applications claiming conformance with this part of ISO/IEC 19794 shall be capable of presenting DNA biometric data as defined by this standard. Minimum conformance shall require the ability to transmit (exchange) and extract interoperable DNA biometric information.

3 Normative references

The following referenced documents are indispensable for the application of this document. For dated references, only the edition cited applies. For undated references, the latest edition of the referenced document (including any amendments) applies.

ISO/IEC 19794-1:2011, *Information technology — Biometric data interchange formats — Part 1: Framework*

ISO/IEC 19794-1:2011/Amd.2, *Framework for XML encoding*

4 Terms and definitions

4.1
allele
one member of a series of possible alternative forms of a DNA sequence found at a particular genetic location

4.2
chromosome
structure within the cell that bears the genetic material as a linear strand of DNA

NOTE Human cells consist of 23 pairs of chromosomes.

4.3
deoxyribo nucleic acid
DNA
complex molecule found in virtually every cell in the body that carries the genetic information from one generation to another

4.4
DNA profiling or typing
technique used by scientists to discriminate between individuals by examining variations in their DNA

4.5
locus
unique physical location on the DNA molecule and the plural of locus is loci

4.6
mitochondrial DNA
mtDNA
small circular DNA molecules located in structures used to provide energy to the cell (mitochondria)

NOTE Their small size and abundant nature make them particularly useful when examining small or much damaged biological material. It can be used to trace maternal lineages as it is only inherited from one's mother.

4.7
power of discrimination
potential power of a genetic marker or set of markers to differentiate between any two people chosen at random

4.8
short tandem repeat
STR
short sequences of DNA that are repeated numerous times in direct succession

NOTE The number of repeated units may vary widely between individuals and this high level of variation makes STRs particularly useful for discriminating between people.

4.9
Y chromosome
organized structure of the DNA molecule containing male-specific DNA only

4.10
Y-STR
STR regions found in male specific DNA on the Y chromosome only

NOTE It can be used to trace paternal lineages as it is male specific and only inherited from one's father.

4.11
electrophoretic data
raw profile data output from a profiling system that is used to measure the number of allele repeats at a specific loci

4.12
mobile processing unit
fully functional DNA laboratory which is mobile

4.13
rapid DNA unit
self-contained device which automates all DNA analysis processes and produces a DNA profile quickly (e.g. ~1 hour)

5 Abbreviated terms

DNA	DeoxyriboNucleic Acid
mtDNA	Mitochondrial DNA
STR	Short Tandem Repeat
Y-STR	Y chromosome STR

6 DNA format specification

6.1 Overview

The DNA record format specified in this document is a structural definition used to exchange DNA data. This formatted data shall contain the DNA identification data. In conformance to the regulations described in the ISO/IEC 19794-1, a DNA record should be specified upon the definition of the BDIR or may be embedded in the biometric data block (BDB) of a CBEFF compliant structure (BIR).

When referring to the objects of a record, they are grouped into three data structures (field, block and record). A field denotes the elementary one to store data. There are two kinds of fields: simple and combined field. A simple field contains only one simple data object and a combined field contains one or more fields which may be a simple or a combined one. One or more data fields can be grouped together into a data block. The part consisting of several uniquely named components (data fields and blocks) forms a data record.

A whole DNA record according to the BDIR structure is depicted in the Figure 1.

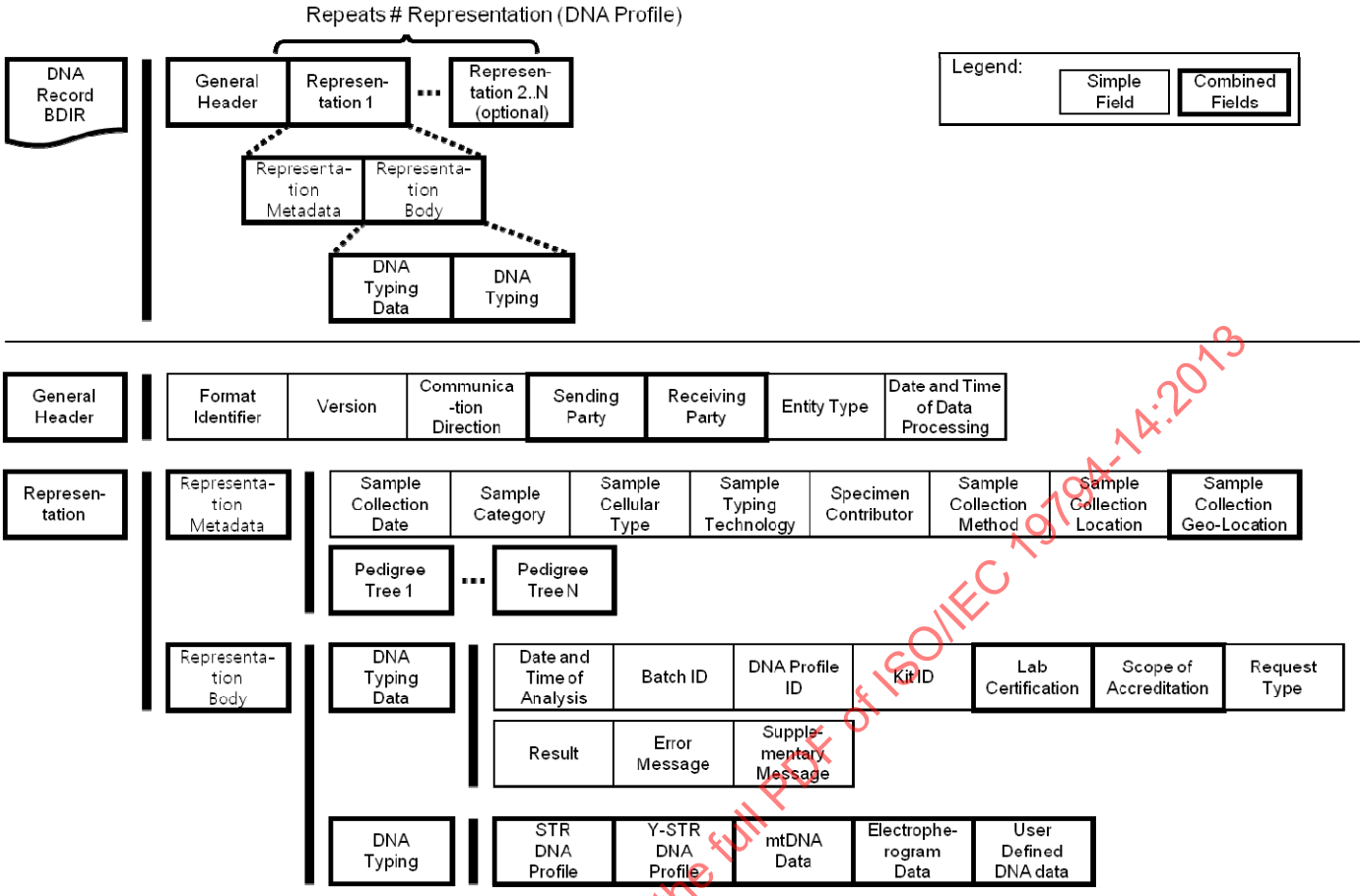

Figure 1 — The DNA Record Format

6.2 Data Conventions

6.2.1 Unknown field value

A field value labeled by the identifier “Unknown” shall be used to denote the information encoded in this field is not yet determined.

6.2.2 XML Encoding

The framework for XML encoding is dealt with in the document ISO/IEC 19794-1:2011/Amd.2. The XML encoding schema for DNA data enclosed in the Annex B of this document is in compliance with the specification in the parts-overlapping XML framework (ISO/IEC 19794-1:2011/Amd.2).

6.3 The CBEFF Header

The structure of a BDIR consisting of one mandatory General Header and one or more representation parts should be used to describe a DNA record.

The biometric data record represented using the DNA record format may be embedded in the biometric data block (BDB) of the CBEFF patron format in compliance with ISO/IEC 19785-1:2004. If a CBEFF header is used, the following specifications apply:

The CBEFF patron format requests to specify both CBEFF_BDB_format_owner and CBEFF_BDB_format_type as mandatory items in the CBEFF Header.

The CBEFF_BDB_format_owner shall be specified by the CBEFF biometric organization identifier issued by the CBEFF registration authority to ISO/IEC JTC1/SC37. This value is the sixteen bit value 0x0101.

The CBEFF_BDB_format_type shall be specified by the CBEFF BDB format type identifier assigned by ISO/IEC JTC1/SC37 to this DNA record format. This value is the sixteen bit value 0x0008.

Complete CBEFF header information required for coding is given in ISO/IEC 19794-1.

6.4 Content of a DNA schema

6.4.1 Structure of a DNA Record General Header

The DNA Record General Header block consists of 7 fields as shown in Table 1. The data fields listed in the first column in Table 1 are described in more detail in sections 6.4.1.1 – 6.4.1.7.

Table 1 — The DNA Record General Header

Field	Item Type	Valid values	Mandatory / Optional
Format Identifier	string	"DNA"	Mandatory
Version	VersionType	Major = 3, Minor = 0	Mandatory
Communication Direction	string	"Request", "Answer"	Mandatory
Sending Party	PartyType		Mandatory
Receiving Party	PartyType	-	Mandatory
Entity Type	string	"G", "GM", "GR", "I", "IM", "IR", "O", "OM", "OR", "U", "UM", "UR"	Mandatory
Date and Time of Data Processing	dateTime	-	Mandatory

6.4.1.1 Format Identifier

The format identifier for DNA data shall be the string "DNA".

6.4.1.2 Version

This version number shall consist of major version number and minor revision number. The format given in ISO/IEC 19794-1:2011/Amd.2. The version number of this part of ISO/IEC 19794 shall be major version 3 and minor revision 0.

6.4.1.3 Communication Direction

The communication direction field shall indicate whether this message contains a request or an answer to a request. This field shall be a string

Table 2 — Communication Direction

Description	Value
Request	"Request“
Answer	"Answer"

6.4.1.4 Sending Party

Data to describe the sending party shall be used PartyType and it consists of Nationality code, Name of the Entity, Name of the Person in charge (Sender).

Table 3 — Party Type

Field	Item Type	Description
Nationality Code	string	ISO 3166-2 code of the party
Name of the Entity	string	The name of the Entity
Name of the Person	string	The name of the Sender/Receiver

6.4.1.5 Receiving Party

Data to describe the receiving party shall be used PartyType (Table 3) and it consists of Nationality code, Name of the Entity, Name of the Person in charge (Receiver).

6.4.1.6 Entity Type

The entity type is either a "Government lab" (G), "Industry lab" (I), "Other lab" (O) or "Unknown lab" (U). Also, there are "Rapid DNA unit" (R) and "Mobile processing unit" (M) per each entity. This field shall be a string with values of either "G", "GM", "GR", "I", "IM", "IR", "O", "OM", "OR", "U", "UM", "UR".

6.4.1.7 Date and Time of Data Processing

The date and time of data exchange. This field shall be stated in Coordinated Universal Time (UTC). The format given in ISO/IEC 19794-1:2011/Amd.2 shall be used for any absolute time values. This field encodes date and time of data processing not data capture. This field shall be the XML built-in type "dateTime".

6.4.2 Representation Metadata

For each profile there is a "Representation" and this block is split into the "Representation Metadata" and "Representation Body". The representation metadata provides metadata regarding the data exchanged.

Table 4 — Representation Metadata

Field	Item Type	Valid values	Mandatory / Optional
Sample Collection Date	dateTime	-	Optional
Sample Category	string	See Table 5	Mandatory
Sample Cellular Type	string	See Table 6	Mandatory
Sample Typing Technology	string	See Table 7	Mandatory
Specimen Contributor	string	"Known" or "Unknown"	Mandatory
Sample Collection Method	string	-	Optional
Sample Collection Location	string	-	Optional
Sample Collection Geo-Location	GeoLocationType	-	Optional
Pedigree Tree	PedigreeTreeType	-	Optional

6.4.2.1 Sample Collection Date

The date the sample was collected. This field shall be stated in Coordinated Universal Time (UTC). The format given in ISO/IEC 19794-1:2011/Amd.2 shall be used for any absolute time values. This field shall be the XML built-in type "dateTime".

6.4.2.2 Sample Category

The Sample Category field shall represent the category which the DNA sample belongs. This shall be a string value.

Table 5 — Sample Category

Value
Arrestee
Claimed Biological Child
Claimed Biological Father
Claimed Biological Mother
Claimed Biological Sibling
Claimed Biological Spouse
Actual Biological Child
Actual Biological Father
Actual Biological Mother
Actual Biological Sibling
Actual Biological Spouse
Adoptive Biological Child
Adoptive Biological Father
Adoptive Biological Mother
Adoptive Biological Sibling
Adoptive Biological Spouse
Convicted Offender
Forensic, Unknown
Insurgent
Known Suspected Terrorist
Maternal Relative
Missing Person
Paternal Relative
Suspect, Known
Unidentified Living
Unidentified Dead
Victim, Known
Detainee
Other
Unspecified

NOTE Some of the entries in this table(e.g. detainee, arrestee, convicted offender) may have different meaning in different jurisdictions.

6.4.2.3 Sample Cellular Type

The Sample Cellular type field shall represent the origination cell type from where the sample was extracted. This shall be a string value.

Table 6 — Sample Cellular Type

Value
Blood
Bone
Buccal Cell
Commingled Biological Material
Hair
Saliva
Semen
Skin
Sweat/Fingerprint
Tissue
Tooth (including Pulp)
Other
Unknown
Unspecified

6.4.2.4 Sample Typing Technology

The Sample Typing technology field shall represent the technology utilized to type the DNA sample. This shall be a string value.

Table 7 — Sample Typing Technology

Value
STR
Y-STR
mtDNA
Electropherogram
User Defined Typing

6.4.2.5 Specimen Contributor

An indicator whether the identity of the specimen contributor is known or not. This shall be a string value.

Table 8 — Sample Source Indicator

Description	Value
Specimen contributor is known	"Known“
Specimen contributor is unknown	"Unknown“

NOTE For example, this may be useful in the case of an unidentified living, the sample is collected from the individual. In the case of a missing person, the sample may not come from the person claimed missing.

6.4.2.6 Sample Collection Method

The description of the method used to collect the sample. This field shall be a string.

NOTE For example, in case of the sample "hair", it is gathered from suspect directly, or it is picked up from the crime scene.

6.4.2.7 Sample Collection Location

The location where the sample was collected. This is a string denoting, e.g. houses, buildings and/or postal addresses, etc.

6.4.2.8 Sample Collection Geo-Location

The GPS coordinates of the location the sample was collected. This supports processing of large scale disasters. This consists of two float values. The former is lattitude, and the latter is longitude in WGS (World Geodetic System) 84 respectively.

Table 9 — Sample Collection Geo-Location (GeoLocationType)

Field	Item Type	Notes
Lattitude	float	+ for north, - for south
Longitude	float	+ for East, - for West

6.4.2.9 Pedigree Tree

This field might be repeated to enable the development of a full pedigree tree. A pedigree tree must have at least one member. Genetic data should be consistent with the information provided. Pedigree trees greatly support the identification of a missing person or the identification of victims of mass disasters. Each Pedigree Tree may have one or more unidentified nodes representing the unknown.

Table 10 — Pedigree Tree

Field	Item Type	Valid values	Note
Pedigree Tree 1 … Pedigree Tree n	PdgrTreeType	-	repeats number of pedigree tree

Table 11 — Pedigree (PdgrTreeType)

Field	Item Type	Valid values	Note
Pedigree ID	string	-	A unique identifier for the pedigree
Pedigree Member 1 … Pedigree Member N	PdgrMbrType	-	repeats number of pedigree member

Table 12 — Pedigree Member (PdgrMbrType)

Field	Item Type	Valid values	Note
Pedigree Member ID	integer	-	A unique integer within the pedigree
Specimen ID	string	Length <= 24	If a specimen is associated to the pedigree node, then the specimen ID should be specified and be included in the specimen section of the pedigree import file. Pedigree nodes that have specimens associated are considered “typed”. If no specimen is associated to the pedigree node, then the node is considered “untyped”.
Mother ID	integer	-	If MotherID is present, then the FatherID must also be present
Father ID	integer	-	If FatherID is present, then the MotherID must also be present.
Pedigree Member Status	string	"Known" or "Unknown"	Known or Unknown
Gender	string	"Male" or "Female"	Male or Female

6.4.3 Representation Body

6.4.3.1 DNA Typing Data

Table 13 — DNA Typing Data

Field	Item Type	Valid Value	Mandatory / Optional
Date and Time of Analysis	dateTime	-	Optional
Batch ID	string	-	Mandatory
DNA Profile ID	string	-	Mandatory
Kit ID	string	-	Mandatory
Lab Certification	LabCertType	-	Mandatory
Scope of Accreditation	SOAType	-	Mandatory
Request Type	string	-	Mandatory when communication direction equals to "R", otherwise Optional
Result	string	-	Mandatory when communication direction equals to "R", otherwise Optional
Error Message	string	-	Optional
Supplementary Message	string	-	Optional

6.4.3.1.1 Date and Time of Analysis

The date and time of data Analysis. This field shall be stated in Coordinated Universal Time (UTC). The format given in ISO/IEC 19794-1:2011/Amd.2 shall be used for any absolute time values. This field shall be a dateTime type (xs:dateTime).

6.4.3.1.2 Batch ID An identifier for the batch within which the DNA type was analysed. The Batch ID shall be a string.

NOTE If the Batch ID is unknown, the string should be "Unknown".

6.4.3.1.3 DNA Profile ID

The sending party's unique identifier for the DNA profile being exchanged. DNA Profile ID shall be a string.

6.4.3.1.4 Kit ID

An identifier for the Kit used. The Kit ID shall be a string. Some examples of the DNA analysis Kits are listed in the Annex C. Kit ID.

NOTE If the Kit ID is unknown, the string should be "Unknown".

6.4.3.1.5 Lab Certification

The Lab Certification field means quality status of the lab. The lab may have multiple validations (Certifications). The Lab Certification field means quality status of the lab. The lab may have multiple validations (Certifications).

Table 14 — Lab Certification (LabCertType)

Field	Item Type	Valid values	Notes
LabCertification	string	See Table 15	Repeats # certification

Table 15 — Lab Certification Value

Values
No validation
ISO/IEC 17025 certification
GLP validation
AABB certification
ISO/ILAC Guild 19 accreditation
Unknown
Unspecified

6.4.3.1.6 Scope of Accreditation

Scope of Accreditation describes the certification scope of the laboratory that processed the DNA. More than one scope of certification is permitted.

Table 16 — Scope of Accreditation (SOAType)

Field	Item Type	Valid values	Notes
ScopeOfAccreditation	string	See Table 17	Repeats # accreditation

Table 17 — Scope of Accreditation Value

Value
Nuclear
Mitochondrial
Database
Other
Unspecified

The field shall allow more than one value to allow the full certification status of the laboratory to be represented.

6.4.3.1.7 Request

This field has been reserved for specifying legal constraints and regulations. This field shall be defined as a string with the following values:

Table 18 — Request Type

Field	Item Type	Valid values	Notes
RequestValue	RequestValue		See Table 19
UserDefined	UserDefinedType		See Table 44

Table 19 — Request Value

Value
DataSubmission
DataSubmissionAndSearch
Search
UserDefined

6.4.3.1.8 Result

A comparison result denotes that an unidentified or a reference DNA type is transmitted to other parties' databases for matching and/or comparison. If matches in a search with this unidentified or reference DNA type are found with the corresponding reference or unidentified DNA type in other parties' databases, these matches are called a matching/comparison result. A result is only valid when the Communication Direction is "A" (answer). This field shall be a string with following values:

Table 20 — Result Type

Field	Item Type	Valid values	Notes
ResultValue	ResultValue		See Table 21
HitUserDefined	UserDefinedType		See Table 44
UserDefined	UserDefinedType		See Table 44

Table 21 — Result Value

Value
UnableToProcess
NoHit
HitUserDefined
UserDefined

6.4.3.1.9 Error Message

An error message indicating an inconsistent DNA type, a matching and/or communication failure is to be included in the field. This shall be a string.

6.4.3.1.10 Supplementary Message

This field contains a string of additional information or comments.

6.4.3.2 DNA Typing

Table 22 — DNA Typing

Field	Item Type	Valid values	Mandatory / Optional
STR DNA Profile	LocusType	-	Mandatory when sample typing technology field equals to "STR", otherwise Optional
Y-STR DNA Profile	LocusType	-	Mandatory when sample typing technology field equals to "Y-STR", otherwise Optional
mtDNA Data	mtDNAType	-	Mandatory when sample typing technology field equals to "mtDNA", otherwise Optional
Electropherogram Data	EPGType	-	Mandatory when sample typing technology field equals to "Electropherogram", otherwise Optional
User Defined	VendorSpecificDataType	-	Optional

6.4.3.2.1 STR DNA Profile

STR DNA type shall be represented by LocusType. LocusType consists of Locus information.

Table 23 — LocusType

Field	Item Type	Valid values	Notes
Locus information	LocusInfoType	-	Repeats # Loci See Table 24

Locus information shall be represented by LocusInfoType and it is consists of Locus header and Allele call.

Table 24 — Locus Information (LocusInfoType)

Field	Item Type	Valid values	Notes
Locus header	LocusHeaderType	-	See Table 25
Allele call	AlleleCallType	-	Repeats # Allele call See Table 26

Locus header shall be represented by LocusHeaderType and it consists of Name of locus marker, Number of allele call, and Status.

Table 25 — Locus Header (LocusHeaderType)

Field	Item Type	Valid values	Notes
Name of Locus marker	string	-	See Annex D. DNA loci
Status	string	"Normal", "SilentAllele", "NotDetermined", "NotAnalysed"	see description below the table

The status “Normal” indicates there is no problem.

The status “Silent Allele” indicates no allele is found.

The status “Not determined” indicates the precise call is not definitive.

Finally the status “Not Analysed” indicates the locus is not analyzed.

Allele call header shall be represented by AlleleCallType and it consists of Operator and Allele call numbers.

Table 26 — Allele Call (AlleleCallType)

Field	Item Type	Valid values	Notes
Operator	string	"Equal", "LowerLimit", "UpperLimit", "Range"	
Allele call number #1	float		always
Allele call number #2	float		Only for the operator "Range“

The name of locus marker can be referenced at Annex D. DNA Loci

6.4.3.2.2 Y-STR DNA Profile

Each Y-STR locus call shall be represented in LocusType. The name of marker of STR loci are listed in Annex D. DNA Loci.

6.4.3.2.3 Mitochondrial DNA data

Despite the maturity of mtDNA sequencing as an analysis tool, there remain differences in interpretation. To accommodate the differences in how mtDNA types are derived (differences from reference), the interpretation issue is avoided by dividing the control region into 2 regions (even though HV3 exists) to ensure any insertions/deletions/C-stretches are included. This method enables any receiver of the data to use it in the

way they are accustomed (either use the full sequence or interpret the full sequence by their method). The resultant data use would be then fully consistent with the receiver's database and enable processing.

— Mito Control Region 1: Defined as inclusive of HV1, starting at 16024 and ending at 16569. The string length shall be 546 characters.

— Mito Control Region 2: Defined as inclusive of HV2 and HV3, starting at 1 and ending at 576. The string length shall be 576 characters.

Table 27 — Mitocondrial DNA data (mtDNAType)

Field	Item Type	Notes
Mito control region 1	string	See Table 28
Mito control region 2	string	See Table 28
Mito DNA Quality 1	string	
Mito DNA Quality 2	string	

The table below shows the character values established by the International Union of Pure and Applied Chemistry for DNA base type measurements. The valid sequence alphabet is "A", "T", "C", "G" and the IUPAC ambiguity codes. Although not in the table below, the character "U" is often used to represent the chemical degradation of "C". Any location that does not have a value shall be set to zero (0).

Table 28 — Character Values established by IUPAC

IUPAC Value	Definition
G	Guanine
A	Adenine
T	Thymine
C	Cytosine
R	G, A
Y	T, C
M	A, C
K	G, T
S	G, C
W	A, T
H	A, C, T
B	G, T, C
V	G, C, A
D	G, A, T
N	G, A, T, C
-	Deletion

6.4.3.2.4 Electropherogram data

An electropherogram is a plot of results from an analysis done by electrophoresis automatic sequencing. Electropherograms may be used for deriving results from: genealogical DNA testing, paternity testing, DNA sequencing, Genetic fingerprinting.

Table 29 — Electropherogram data (ElectropherogramType)

Field	Item Type	Valid values	Note
Electropherogram Data	EPGType	-	See Table 30
Reference Electropherogram Data	EPGRefType	-	See Table 41
Electropherogram Data for Mitochondrial sequence	EPGmitoType		See Table 42

For the electropherogram, these four data shall be included as raw data

— Time and Fluorescence Strength Data

— Time and Base Pair Correspondence Data

— Panel Data

— Bin Data

Table 30 — Electropherogram Data (EPGType)

Field	Item Type	Valid values	Note
Time and Fluorescence Strength Data	TFSDType	-	See Table 31
Time and Base Pair Correspondence Data	TBPCType	-	See Table 34
Panel Data	PanelType	-	See Table 36
Bin Data	BinType		See Table 38

Locus Wave Information consists two data, "Time and Fluorescence Strength Data" and "Time and Base Pair Correspondence Data".

"Time and Fluorescence Strength Data" expresses the pair of Fluorescence detection peak height and time.

Table 31 — Time and Fluorescence Strength Data (TFSDType)

Field	Item Type	Valid values	Note
Run Name	string	-	
Sample File Name	string	-	
Electropherogram Dye Data	ElectropherogramDyeDataType	-	See Table 32
Electropherogram Time Data 1 …. Electropherogram Time Data n	ElectropherogramTimeDataType		Repeats number of time data See Table 33

Table 32 — Electropherogram Dye Data (ElectropherogramDyeDataType)

Field	Item Type	Valid values	Note
Dye name 1 … Dye name n	string	-	name of dye color repeats number of dyes

Table 33 — Electropherogram Time Data (ElectropherogramTimeDataType)

Field	Item Type	Valid values	Note
Time in the run	integer	-	
fluorescence strength for dye 1 … fluorescence strength for dye n	float	-	repeats number of dyes

"Time and Base Pair Correspondence Data" is usually produced in the electrophoresis analysis. Since the electrophoresis can only detect time and peak strength, size markers are utilized. From the electropherogram of the size markers (which can be regarded as "the reference sample"), the correspondence between time and Base Pair is calculated. "Time and Base Pair Correspondence Data" is the result of this calculation, which contains the time and base pair correspondence.

Table 34 — Time and Base Pair Correspondence Data Type (TBPCType)

Field	Item Type	Valid values	Note
Run Name	string	-	
Sample File Name	string	-	
Correspondence Data 1 … Correspondence Data n	CorrespondenceDataType		repeats number of correspondence See Table 35

Table 35 — Correspondence Data (CorrespondenceDataType)

Field	Item Type	Valid values	Note
Time in the run	integer	-	
Base Pair Size	float	-	

Loci Call Information consists two data, "Panel Data" and "Bin Data".

Both Panel Data and Bin Data are used to determine allele call from the electropherogram. "Panel Data" expresses a set of bin definitions for one or more loci. This includes the dye colour and correct amplicon size range. It also includes the electrophoresis peak height ratio, which range must be accepted as a call. "Bin Data" expresses the amplicon size range. Each locus call (repeat number) is defined.

Table 36 — Panel Data (PanelType)

Field	Item Type	Valid values	Note
Primer Set Name	string		
Panel Allele Data 1 … Panel Allele Data n	PanelAlleleDataType		repeats number of alleles See Table 37

Table 37 — Panel Allele Data (PanelAlleleDataType)

Field	Item Type	Valid values	Note
Locus Name	string	-	locus name such as D8S1179
Dye name	string	-	Dye used to analyze this locus
Minimum Allele Size	float	-	
Maximum Allele Size	float	-	
Noise Ratio	float	0.0-1.0	indicates which strength is analyzed as valid call

"Bin Data" expresses the amplicon size range. Each locus call (repeats numbers) is defined..

Table 38 — Bin Data (BinType)

Field	Item Type	Valid values	Note
Primer Set Name	string		
Bin Locus Data 1 … Bin Locus Data n	BinLocusDataType		Repeats number of Bin Locus Data See Table 39

Table 39 — Bin Locus Data (BinLocusDataType)

Field	Item Type	Valid values	Note
Locus Name	string	-	Locus name such as D8S1179
Bin Call Data 1 … Bin Call Data n	BinCallDataType		Repeats number of Bin Call Data See Table 40

Table 40 — Bin Call Data (BinCallDataType)

Field	Item Type	Valid values	Note
Allele Call	AlleleCallType	-	See Table 26
Average Base Pair Size	float	-	Average Base Pair Size for this call
Minus Deviation Base Pair Size	float	-	Maximum minus deviation from the average base pair size
Plus Deviation Base Pair Size	float	-	Maximum plus deviation from the average base pair size

For the reference electropherogram data,the ' Time and Fluorescence Strength Data' shall be included as raw data

— Time and Fluorescence Strength Data

Table 41 — Reference Electropherogram Data (EPGRefType)

Field	Item Type	Valid values	Note
Time and Fluorescence Strength Data	TFSDType	-	See Table 31

For the purpose to express electrophoresis data for mitochondrial sequence data, "Time (in the run) and Fluorescence Strength Data" and "Dye assignment for base data" is required. "Dye assignment for base" shall represents correspondence Dye name and Base type. Thus it should have two fields, "Dye name" and "Base type".

Table 42 — Electropherogram Data Mitocondrial Sequence Data (EPGmitoType)

Field	Item Type	Valid values	Note
Time and Fluorescence Strength Data	TFSDType	-	See Table 31
Dye assignment for Base 1 ... Dye assignment for Base n	DyeBaseAssignType		Repeats # IUPAC value See Table 43

Table 43 — Dye Assignment for Base (DyeBaseAssignType)

Field	Item Type	Valid values	Note
Dye name	string	-	
Base type	string	IUPAC value	See Table 27

6.4.3.2.5 User Defined DNA Data

This item shall be defined upon the Table 44.

Table 44 — User Defined DNA Type Data

Field	Item Type	Valid values	Note
TypeCode	string	-	
Data	base64Binary	-	Base 64 Encoding

Annex A
(normative)

Conformance Testing Methodology

A.1 Overview

This part of ISO/IEC 19794 specifies a biometric data interchange format for storing, recording, and transmitting one or more DNA representations. Each representation is accompanied by modality-specific metadata contained in a header record. This annex establishes tests for checking the correctness of the record.

The objective of this part of ISO/IEC 19794 cannot be completely achieved until biometric products can be tested to determine whether they conform to those specifications. Conforming implementations are a necessary prerequisite for achieving interoperability among implementations; therefore there is a need for a standardized conformance testing methodology, test assertions, and test procedures as applicable to specific modalities addressed by each part of ISO/IEC 19794. The test assertions will cover as much as practical of the ISO/IEC 19794 requirements (covering the most critical features), so that the conformity results produced by the test suites will reflect the real degree of conformity of the implementations to ISO/IEC 19794 data interchange format records. This is the motivation for the development of this conformance testing methodology.

This normative annex is intended to specify elements of conformance testing methodology, test assertions, and test procedures as applicable to this part of ISO/IEC 19794. For this edition of this part of ISO/IEC 19794, the content of this annex will be available as a separate document (Amendment), to supplement this part of ISO/IEC 19794.

Annex B
(normative)

DNA XML Schema

This annex including the example of a DNA XML Schema shall be customized and synchronized in conformity with the rules and definitions set by ISO/IEC 19794-1:2011/Amd.2 (XML Encoding Framework)

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targetNamespace="http://standards.iso.org/iso-iec/19794/-14/ed-1" elementFormDefault="qualified" attributeFormDefault="unqualified">
    <xs:annotation>
        <xs:documentation>Permission is hereby granted, free of charge in perpetuity, to any person obtaining a copy of the Schema, to use, copy, modify, merge and distribute free of charge, copies of the Schema for the purposes of developing, implementing, installing and using software based on the Schema, and to permit persons to whom the Schema is furnished to do so, subject to the following conditions: THE SCHEMA IS PROVIDED "AS IS", WITHOUT WARRANTY OF ANY KIND, EXPRESS OR IMPLIED, INCLUDING BUT NOT LIMITED TO THE WARRANTIES OF MERCHANTABILITY, FITNESS FOR A PARTICULAR PURPOSE AND NONINFRINGEMENT. IN NO EVENT SHALL THE AUTHORS OR COPYRIGHT HOLDERS BE LIABLE FOR ANY CLAIM, DAMAGES OR OTHER LIABILITY, WHETHER IN AN ACTION OF CONTRACT, TORT OR OTHERWISE, ARISING FROM, OUT OF OR IN CONNECTION WITH THE SCHEMA OR THE USE OR OTHER DEALINGS IN THE SCHEMA.</xs:documentation>
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    <xs:annotation>
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        <xs:documentation>Status: DIS v1.0</xs:documentation>
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<xs:simpleType name="EntityType">
    <xs:restriction base="xs:string">
        <xs:enumeration value="G"/>
        <xs:enumeration value="GM"/>
        <xs:enumeration value="GR"/>
        <xs:enumeration value="I"/>
        <xs:enumeration value="IM"/>
        <xs:enumeration value="IR"/>
        <xs:enumeration value="O"/>
        <xs:enumeration value="OM"/>
        <xs:enumeration value="OR"/>
        <xs:enumeration value="U"/>
        <xs:enumeration value="UM"/>
        <xs:enumeration value="UR"/>
    </xs:restriction>
</xs:simpleType>
<xs:complexType name="PartyType">
    <xs:sequence>
        <xs:element name="NationalityCode" type="xs:string"/>
        <xs:element name="EntityName" type="xs:string"/>
        <xs:element name="PersonName" type="xs:string"/>
    </xs:sequence>
</xs:complexType>
<xs:complexType name="GeneralHeaderType">
    <xs:sequence>
```

```
            <xs:element name="FormatIdentifier" type="FormatIdentifierType"/>
            <xs:element name="Version" type="cmn:VersionType"/>
            <xs:element name="CommunicationDirection" type="CommunicationDirectionType"/>
            <xs:element name="SendingParty" type="PartyType"/>
            <xs:element name="ReceivingParty" type="PartyType"/>
            <xs:element name="EntityType" type="EntityType"/>
            <xs:element name="DateAndTimeOfDataProcessing" type="xs:dateTime"/>
        </xs:sequence>
    </xs:complexType>
    <xs:element name="Dna">
        <xs:complexType>
            <xs:sequence>
                <xs:element name="GeneralHeader" type="GeneralHeaderType"/>
                <xs:element name="Representations" minOccurs="0">
                    <xs:complexType>
                        <xs:sequence>
                            <xs:element name="Representation" type="DnaRepresentationType" maxOccurs="unbounded"/>
                        </xs:sequence>
                    </xs:complexType>
                </xs:element>
            </xs:sequence>
        </xs:complexType>
    </xs:element>
</xs:schema>
```