My Family Tree™ GEDCOM 7 Extensions



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This document provides details of all GEDCOM extensions used in GEDCOM 7.0 files produced by My Family Tree.

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Extensions to existing Record Structures

Extensions to existing structures are shown in highlight mode.

```
HEADER:=
 n HEAD
                                                                 {0:1}
   +1 TITLE <Text>
RECORD:=
ſ
 n <<TASK_RECORD>>
                                                                 {1:1}
 n <<LABEL_RECORD>>
                                                                 {1:1}
]
FAMILY_RECORD:=
  n @<XREF:FAM>@ FAM
                                                                 {1:1}
   +1 _RELATIONSHIP_STATUS <Enum>
                                                                 {0:1}
```

The _RELATIONSHIP_STATUS payload is used to store the relationship status as this cannot always be accurately inferred from the included events.

INDIVIDUAL RECORD:= n @<XREF:INDI>@ INDI {1:1} +1 <<A_DNA_STRUCTURE>> $\{0:M\}$ +1 <<M DNA STRUCTURE>> {0:M} +1 <<Y_DNA_STRUCTURE>> $\{0:M\}$ +1 _LABEL @<XREF:LABEL>@ $\{0:M\}$ **MULTIMEDIA_RECORD:=** n @<XREF:OBJE>@ OBJE {1:1} +1 FILE <MULTIMEDIA FILE REFERENCE> {1:1} +2 _FILE_TAKEN_DATE <DateValue> {0:1} +3 PHRASE <Text> {0:1} +3 TIME <Time> {0:1} +3 _DATE_SERIAL <Special> {0:1} +2 FILE RATING <Integer> {0:1} +2 _FILE_LOCATION <Text> {0:1} **REPOSITORY_RECORD:=** n @<XREF:REPO>@ REPO {1:1} +1 _RESN <List:Enum> {0:1} **SOURCE RECORD:**= n @<XREF:SOUR>@ SOUR {1:1} +1 _RESN <List:Enum> {0:1} **SUBMITTER_RECORD:=** n @<XREF:SUBM>@ SUBM {1:1} +1 _RESN <List:Enum> {0:1}

Extension Record Structures

n @ <xref:task>@_TASK</xref:task>
+1 _TASK_DESCRIPTION <text> {0:1} +1 _TASK_COMMENTS <text> {0:1} +1 _TASK_RESULTS <text> {0:1} +1 _TASK_LOCATION <text> {0:1} +1 _TASK_START_DATE <datevalue> {0:1} +2 PHRASE <text> {0:1} +2 TIME <time> {0:1} +2 _DATE_SERIAL <special> {0:1} +1 _TASK_REVIEW_DATE <datevalue> {0:1}</datevalue></special></time></text></datevalue></text></text></text></text>
+1 _TASK_COMMENTS <text> {0:1} +1 _TASK_RESULTS <text> {0:1} +1 _TASK_LOCATION <text> {0:1} +1 _TASK_LOCATION <text> {0:1} +1 _TASK_START_DATE <datevalue> {0:1} +2 PHRASE <text> {0:1} +2 TIME <time> {0:1} +2 _DATE_SERIAL <special> {0:1} +1 _TASK_REVIEW_DATE <datevalue> {0:1}</datevalue></special></time></text></datevalue></text></text></text></text>
+1 _TASK_RESULTS <text> {0:1} +1 _TASK_LOCATION <text> {0:1} +1 _TASK_START_DATE <datevalue> {0:1} +2 PHRASE <text> {0:1} +2 TIME <time> {0:1} +1 _TASK_REVIEW_DATE <datevalue> {0:1}</datevalue></time></text></datevalue></text></text>
+1 _TASK_LOCATION <text> {0:1} +1 _TASK_START_DATE <datevalue> {0:1} +2 PHRASE <text> {0:1} +2 TIME <time> {0:1} +2 _DATE_SERIAL <special> {0:1} +1 _TASK_REVIEW_DATE <datevalue> {0:1}</datevalue></special></time></text></datevalue></text>
+1 _TASK_START_DATE <datevalue> {0:1}</datevalue>
+2 PHRASE <text> {0:1} +2 TIME <time> {0:1} +2 _DATE_SERIAL <special> {0:1} +1 _TASK_REVIEW_DATE <datevalue> {0:1}</datevalue></special></time></text>
+2 TIME <time> {0:1} +2 _DATE_SERIAL <special> {0:1} +1 _TASK_REVIEW_DATE <datevalue> {0:1}</datevalue></special></time>
+2 _DATE_SERIAL <special> {0:1} +1 _TASK_REVIEW_DATE <datevalue> {0:1}</datevalue></special>
+1 _TASK_REVIEW_DATE <datevalue> {0:1}</datevalue>
+2 PHRASE <text> {0:1}</text>
+2 TIME <time> {0:1}</time>
+2 _DATE_SERIAL <special> {0:1}</special>
+1_TASK_CLOSED_DATE <datevalue> {0:1}</datevalue>
+2 PHRASE <text> {0:1}</text>
+2 TIME <time> {0:1}</time>
+2 _DATE_SERIAL <special> {0:1}</special>
+1_TASK_STATUS <enum> {0:1}</enum>
+2 PHRASE <text> {0:1}</text>
+1_TASK_PRIORITY <enum> {0:1}</enum>
+2 PHRASE <text> {0:1}</text>
+1_TASK_TYPE <text> {0:1}</text>
+1_TASK_CATEGORY <text> {0:1}</text>
+1 SOUR @ <xref:sour>@ {0:1}</xref:sour>
+1 REPO @ <xref:repo>@ {0:1}</xref:repo>
+1 INDI @ <xref:indi>@ {0:M}</xref:indi>
+1 < <identifier_structure>> {0:M}</identifier_structure>
+ < <change_date>> {0:1}</change_date>
+ < <creation_date>> {0:1}</creation_date>
LABEL_RECORD:=
n @ <xref:label>@ _LABEL {1:1}</xref:label>
+1 NAME <text> {0:1}</text>
+1 < <identifier_structure>> {0:M}</identifier_structure>
+1 < <note_structure>> {0:M}</note_structure>

Extensions to existing Substructures

+1 NAME_PART_TYPE <Enum>

Extensions to existing structures are shown in highlight mode.

PERSONAL_NAME_STRUCTURE:=

n NAME <personal name=""></personal>	{1:1}
+1 _RESN <list:enum></list:enum>	{0:1}
PERSONAL_NAME_PIECES:=	
n GIVN <text></text>	{0:M}
+1 <mark>_NAME_PART_TYPE <enum></enum></mark>	{0:1}
n SURN <text></text>	{0:M}

The _NAME_PART_TYPE is used to provide additional context to the parent GIVN or SURN payload.

{0:1}

EVENT_DETAIL:=

n DATE <datevalue></datevalue>	{0:1}
+1 _DATE_SERIAL <special></special>	{0:1}

NOTE_STRUCTURE:=

n NOTE <text></text>	{1:1}
+1 _NOTE_USES <list:enum></list:enum>	{0:1}
+1 _RESN <list:enum></list:enum>	{0:1}

The _NOTE_USES payload provides additional context about the note. It is used to specify that the note be considered an individual's story, or a note that should be displayed in the family chart.

MULTIMEDIA_LINK:=

n OBJE @ <xref:obje>@</xref:obje>	{1:1}
+1 MULTIMEDIA USES <list:enum></list:enum>	{0:1}

The _MULTIMEDIA_USES payload provides additional context about the linked file. It is used to specify that the linked image be considered an individual's primary image, family crest, or both.

SOURCE CITATION:=

n SOUR @ <xref:sour>@</xref:sour>	{1:1}
+1 _CITE_REFERENCE <text></text>	{0:1}
+1 _CITE_URL <special></special>	{0:1}
+1 _RESN <list:enum></list:enum>	{0:1}

The _CITE_REFERENCE payload stores a user formatted text representation of this citation. The _CITE_URL payload specifies a URL where a copy of the cited part of the source may be accessed.

Extension Substructures

+1 _SNP_RSID <Special>

+1_SNP_CHROMOSOME <Special>

+1 _SNP_POSITION <Integer>

+1 _SNP_GENOTYPE <Special>

A_DNA_STRUCTURE:=	
n _A_DNA	{1:1}
+1 _DNA_DESCRIPTION <text></text>	{0:1}
+1 _DNA_NAME <text></text>	{0:1}
+1 < <dna_str_structure>></dna_str_structure>	{0:M}
+1 < <dna_snp_structure>></dna_snp_structure>	{0:M}
+1 < <note_structure>></note_structure>	{0:M}
The results of an autosomal DNA test.	
M_DNA_STRUCTURE:=	
n _M_DNA	{1:1}
+1 _DNA_DESCRIPTION <text></text>	{0:1}
+1 _DNA_NAME <text></text>	{0:1}
+1 _DNA_HAPLOGROUP <special></special>	{0:1}
+1 _DNA_REFERENCE_SAMPLE <special></special>	{0:1}
+1 _DNA_SEQUENCE <special></special>	{0:1}
+1 < <dna_snp_structure>></dna_snp_structure>	{0:M}
+1 < <note_structure>></note_structure>	{0:M}
The results of a mitochondrial DNA test.	
Y_DNA_STRUCTURE:=	
n _Y_DNA	{1:1}
+1 _DNA_DESCRIPTION <text></text>	{0:1}
+1 _DNA_NAME <text></text>	{0:1}
+1 _DNA_HAPLOGROUP <special></special>	{0:1}
+1 < <dna_snp_structure>></dna_snp_structure>	{0:M}
+1 < <dna_str_structure>></dna_str_structure>	{0:M}
+1 < <note_structure>></note_structure>	{0:M}
The results of a Y-chromosome DNA test.	
DNA_SNP_ STRUCTURE:=	
n _DNA_SNP	{1:1}
+1 _SNP_DIFFERENCE <special></special>	{0:1}
A CND DCID (Co. 1.1)	(0.4)

A single nucleotide polymorphism (SNP) DNA sequence variation occurring when a single nucleotide adenine (A), thymine (T), cytosine (C), or guanine (G) in the genome (or other shared sequence) differs between members of a species or paired chromosomes in a person. The cardinality of the elements of the DNA_SNP_STRUCTURE is constrained by the type of DNA test.

{0:1}

{0:1}

{0:1}

{0:1}

DNA_STR_ STRUCTURE:=

n _DNA_STR	{1:1}
+1 _STR_MARKER <special></special>	{1:1}
+1 _STR_REPEATS <integer></integer>	{1:1}

A short tandem repeat (STR) is a section of DNA which repeats several times in a row on a DNA strand. The STRs present and the number of times they repeat is used distinguish one DNA sample from another.

Extension Enumeration Values

GIVN. _NAME_PART_TYPE:=

Value	Meaning
_FIRST	First name(s).
_MIDDLE	Middle name(s).
_RUFNAME	Rufname.

SURN. _NAME_PART_TYPE:=

Value	Meaning
_MATRONYMIC	Matronymic surname.
_PATRONYMIC	Patronymic surname.

_TASK_STATUS:=

Value	Meaning
_NOT_STARTED	A not-started task
_IN_PROGRESS	An in-progress task.
_COMPLETED	A completed task.
_POSTPONED	A postponed task.
_CANCELED	A canceled task.
_PROBLEM	A task blocked by a problem.
_OTHER	A status not listed here; should have a PHRASE substructure.

_TASK_PRIORITY:=

Value	Meaning
_LOW	A low priority.
_NORMAL	A normal priority.
_MEDIUM	A medium priority.
_HIGH	A high priority.
_OTHER	A priority not listed here; should have a PHRASE substructure.

RELATIONSHIP_STATUS:=

Value	Meaning
_ENGAGED	Participants are engaged.
_CURRENT	The relationship is current.
_FORMER	The relationship is not current.
_DECEASED	One participant is deceased.
_DIVORCED	The relationship has been dissolved.
_DIVORCE_FILED	Participant(s) have filed for divorce.
_ANNULLED	The relationship is annulled.
_DISSOLVED	The relationship has been dissolved.
_SEPARATED	Participants have separated.

INDI.OBJE._MULTIMEDIA_USES:=

Value	Meaning
_PRIMARY_IMAGE	The associated image is the individual's primary image.
_FAMILY_CREST	The associated image is the individual's family crest.

INDI.NOTE. _NOTE_USES:=

Value	Meaning
_CHART	The associated note is displayed in the family chart.
_STORY	The associated note is the individual's story.

Extension tags

A DNA:=

The results of an autosomal DNA test.

_CITE_REFERENCE:=

The user formatted text representation of a citation.

_CITE_URL:=

The URL where a copy of the cited part of the source may be accessed.

_DATE_SERIAL:=

[V<Version>T<DateType>S<StartDate>E<EndDate>T<Text>]

A representation of date and time information. This is used, along with an associated standard DATE.PHRASE payload, when there is no standard way to represent the date in GEDCOM. If present, any associated DATE, DATE.PHRASE, and DATE.TIME payloads are ignored.

```
<Version>
              version [00 .. 99]
               a date descriptor [00 .. 99] where
<DateType>
               00 = default, 01 = about,
               02 = before, 03 = after,
               04 = estimated, 05 = calculated,
               06 = interpreted, 07 = to only,
               08 = \text{from only}, 09 = \text{span},
               10 = range, 11 = text only, 12 = either ... or ...
<StartDate>
               <Date>
<EndDate>
               <Date>
<Text>
               text representing the date, can be empty
<Date>
               <Calendar><Era><Day><Month><Year><LDay><LMonth><DualYear><Time>
               calendar type [00 .. 99] where
<Calendar>
               00 = Gregorian, 01 = Julian, 03 = French Republican, 04 = Swedish,
               05 = Icelandic, 06 = Hebrew, 07 = AstronomicalSolarHijri, 08 = LunarHijri,
               09 = UmmAlQura, 10 = ISO, 11 = Armenian, 12 = Bahá'í,
               13 = HinduSolar, 14 = HinduLunisolar, 15 = ThaiBuddhist, 16 = TibetanLunisolar,
               17 = Japanese, 18 = JapaneseLunisolar, 19 = Korean, 20 = KoreanLunisolar,
               21 = Taiwan, 22 = TaiwanLunisolar,
               23 = ChineseLunisolar, 24 = VietnameseLunisolar,
               25 = Coptic, 26 = Ethiopic, 27 = Egyptian, 28 = Quaker
               a zero padded era [00 .. 99], the first era in a calendar is denoted with a zero
<Era>
               a zero padded day [00 .. 99], the day is unspecified if the value is zero
<Day>
               a zero padded month [00 .. 99], the month is unspecified if the value is zero*
<Month>
               a zero padded year [0000 .. 9999], the year is unspecified if the value is zero
<Year>
<LDay>
               is leap day [0 .. 1], 1 if the day is a leap day in a lunisolar calendar, zero otherwise
<LMonth>
               is leap month [0..1], 1 if the day is a leap month in a lunisolar calendar, zero
               otherwise
              is dual year [0..1], 1 if the year is a dual year in the Gregorian or Julian calendar,
<DualYear>
               zero otherwise
<Time>
               [ HHmmssfff [Z|L] ], a time in HHmm format using the 24-hour clock
               HH = zero-padded hour [00 .. 23]
```

mm = zero-padded minute [00 .. 59]

ss = zero-padded second [00 .. 59] fff = zero-padded millisecond [000 .. 999] Z = UTC, L = local time

* the <Month> is interpreted as a week number in the ISO calendar.

_DNA_SEQUENCE:=

A DNA sequence, described as a sequence of characters representing single nucleotides of adenine (A), thymine (T), cytosine (C), or guanine (G).

_DNA_DESCRIPTION:=

The description of this DNA test.

_DNA_NAME:=

The name of the person for whom this DNA test relates to.

_DNA_HAPLOGROUP:=

A human DNA haplogroup. The name should correspond with those found in the phylogenetic tree of global human DNA variation.

_DNA_REFERENCE_SAMPLE:=

The reference sample used for determining human mitochondrial DNA SNPs and haplogroups. Current reference samples include:

RSRC = The Reconstructed Sapiens Reference Sequence

RCRS = The revised Cambridge Reference Sequence

CRS = The Cambridge Reference Sequence

FAMILY CREST:=

A link to a multimedia record which is to be used as a person's family crest.

FILE DATE:=

The date associated with a file. For a photograph, this might be the date taken. For a newspaper cutting this may be the publication date of the article.

FILE NAME:=

The friendly file name of a file.

FILE LOCATION:=

The place a depicted in an image.

_FILE_RATING:=

A number from [0 .. 5] which describes the star rating of a multimedia item.

LABEL:=

See _LABEL_RECORD.

M DNA:=

The results of a mitochondrial DNA test.

_NAME_PART_TYPE:=

A value that provides additional context to a name piece.

_NOTE_CHART:=

A flag indicating that the associated person note may be displayed in the family tree chart.

_RELATIONSHIP_STATUS:=

The status of a relationship between the HUSB and WIFE individuals in a FAM record.

_RESN:=

A non-standard use of the standard RESN tag.

_SNP_DIFFERENCE:=

A difference between the mitochondrial DNA reference sample and the test subject's mitochondrial DNA.

_SNP_CHROMOSOME:=

The identifier of a chromosome which, for humans, is a number [1 .. 22], X, or Y.

SNP GENOTYPE:=

The genotype present at a given position on a chromosome.

_SNP_POSITION:=

The position of a genotype on a chromosome.

_SNP_RSID:=

The Reference SNP cluster ID of the SNP.

_STR_MARKER:=

The identifying name of a single tandem repeat (STR) on a DNA strand.

STR REPEATS:=

The number of times a single tandem repeat (STR) marker repeats on a DNA strand.

TASK:=

See _TASK_RECORD.

TASK CATEGORY:=

The category of a task.

_TASK_COMMENTS:=

The comments about a task.

TASK CLOSED DATE:=

The closed date of a task.

TASK DESCRIPTION:=

A detailed description of a task.

_TASK_LOCATION:=

The location of a task.

_TASK_RESULTS:=

The results of a task.

_TASK_REVIEW_DATE:=

The review date of a task.

_TASK_START_DATE:=

The start date of a task.

_TASK_TITLE:=

The title of a task.

_TASK_TYPE:=

The type of a task.

_TITLE:=

The title of the family tree.

XREF:LABEL:=

A pointer to, or a cross-reference identifier of, a label record.

XREF:TASK:=

A pointer to, or a cross-reference identifier of, a task record.

_Y_DNA:=

The results of a Y-chromosome DNA test.