- A: The field has one value per alternate allele. The values must be in the same order as listed in the ALT column (described in section 1.6).
- R: The field has one value for each possible allele, including the reference. The order of the values must be the reference allele first, then the alternate alleles as listed in the ALT column.
- G: The field has one value for each possible genotype. The values must be in the same order as prescribed in section 1.6.2 (see GENOTYPE ORDERING).
- . (dot): The number of possible values varies, is unknown or unbounded.

The 'Flag' type indicates that the INFO field does not contain a Value entry, and hence the Number must be 0 in this case. The Description value must be surrounded by double-quotes. Double-quote character must be escaped with backslash \ and backslash as \\. Source and Version values likewise must be surrounded by double-quotes and specify the annotation source (case-insensitive, e.g. `"dbsnp"`) and exact version (e.g. `"138"`), respectively for computational use.

1.4.3 Filter field format

FILTER meta-information lines are structured lines with require fields of ID and Description that define the possible content of the FILTER column in the VCF records:

```
##FILTER=<ID=ID,Description="description">
```

1.4.4 Individual format field format

FORMAT meta-information lines are structured lines with require fields of ID, Number, Type, and Description that define the possible content of the per-sample/genotype columns in the VCF records:

```
##FORMAT=<ID=ID,Number=number,Type=type,Description="description">
```

Possible Types for FORMAT fields are: Integer, Float, Character, and String (this field is otherwise defined precisely as the INFO field). The Number field is defined as per the INFO Number field.

1.4.5 Alternative allele field format

ALT meta-information lines are structured lines with require fields of ID and Description that describe the possible symbolic alternate alleles in the ALT column of the VCF records:

```
##ALT=<ID=type,Description="description">
```

Structural Variants
In symbolic alternate alleles for structural variants, the ID field indicates the type of structural variant, and can be a colon-separated list of types and subtypes. ID values are case sensitive strings and must not contain whitespace, commas or angle brackets. The first level type must be one of the following:

- DEL Region of lowered copy number relative to the reference, or a deletion breakpoint
- INS Insertion of novel sequence relative to the reference
- DUP Region of elevated copy number relative to the reference, or a tandem duplication breakpoint
- INV Inversion of reference sequence
- CNV Copy number variable region (may be both deletion and duplication)

The CNV category should not be used when a more specific category can be applied.
Implementations are free to define their own subtypes. The presence of a subtype does not change either the copy number or breakpoint interpretation of a symbolic structural variant allele. The following subtypes are recommended:

- CNV:TR Tandem repeat. See 5.6 for further details.
- DUP:TANDEM Tandem duplication