
Protocol Documentation

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vmc.proto

Allele

Allele represents a single contiguous change on a specific reference sequence

Table 1. Allele Fields

Field	Type	Label	Description
seqref	SequenceReference	optional	sequence reference (namespace and accession)
interval	Interval	optional	location of sequence change
replacement	string	optional	replacement sequence
id	string	optional	Allele identifier

Genotype

Genotype represents multiple changes at a single location

Table 2. Genotype Fields

Field	Type	Label	Description
allele_ids	string	optional	list of haplotypes by id
id	string	optional	Genotype identifier

Haplotype

Haplotype represents a collection of phased changes on a single reference.

Table 3. Haplotype Fields

Field	Type	Label	Description
allele_ids	string	optional	list of haplotypes by id

Field	Type	Label	Description
id	string	optional	Haplotype identifier

Interval

Represents the definite (i.e., not fuzzy) location of a sequence feature using an interval of interbase coordinates.

Interbase coordinates refer to the points *between* residues. For a sequence of length n , $0 \leq \text{start} \leq \text{end} \leq n$, where 0 refers to the point before the start of the sequence, n refers to the point at the end of the sequence. An interval in which $\text{start} == \text{end}$ is a zero width point between two nucleotides. See http://gmod.org/wiki/Introduction_to_Chado#Interbase_Coordinates for more information.

Table 4. Interval Fields

Field	Type	Label	Description
start	uint64	optional	start position
end	uint64	optional	end position

IntervalEdit

IntervalEdit represents a located sequence change.

Consider renaming fields to match message name. One possibility is `location` \Rightarrow `interval` and `replacement` \Rightarrow `edit`, thus matching the message name `IntervalEdit`.

Table 5. IntervalEdit Fields

Field	Type	Label	Description
location	Interval	optional	location of sequence change
replacement	string	optional	replacement sequence; empty for deletion

SequenceReference

SequenceReference represents a named reference to a sequence in a database. For the purposes of VMC, it is essential that the mapping from SequenceReference to sequence is many-to-one and immutable.

Table 6. SequenceReference Fields

Field	Type	Label	Description
namespace	string	optional	name of recognized sequence reference
accession	string	optional	replacement sequence; empty for deletion

Scalar Value Types

.proto Type	Notes	C++ Type	Java Type	Python Type
double		double	double	float

.proto Type	Notes	C++ Type	Java Type	Python Type
float		float	float	float
int32	Uses variable-length encoding. Inefficient for encoding negative numbers – if your field is likely to have negative values, use sint32 instead.	int32	int	int
int64	Uses variable-length encoding. Inefficient for encoding negative numbers – if your field is likely to have negative values, use sint64 instead.	int64	long	int/long
uint32	Uses variable-length encoding.	uint32	int	int/long
uint64	Uses variable-length encoding.	uint64	long	int/long
sint32	Uses variable-length encoding. Signed int value. These more efficiently encode negative numbers than regular int32s.	int32	int	int
sint64	Uses variable-length encoding. Signed int value. These more efficiently encode negative numbers than regular int64s.	int64	long	int/long
fixed32	Always four bytes. More efficient than uint32 if values are often greater than 2 ²⁸ .	uint32	int	int
fixed64	Always eight bytes. More efficient than uint64 if values are often greater than 2 ⁵⁶ .	uint64	long	int/long
sfixed32	Always four bytes.	int32	int	int
sfixed64	Always eight bytes.	int64	long	int/long
bool		bool	boolean	boolean
string	A string must always contain UTF-8 encoded or 7-bit ASCII text.	string	String	str/ unicode
bytes	May contain any arbitrary sequence of bytes.	string	ByteString	str