

# Introduction to Unix Shell Scripting

Day 2 - Project, part I

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# FASTA to TSV converter script project

# The Trouble with Fasta

Here are some operations that one might wish to perform on a FASTA file:

- ▶ Count the number of records.
- ▶ Count the number of species.
- ▶ Find the longest sequence.
- ▶ Reject sequences with ambiguous nucleotides (N, Y, etc.).
- ▶ Discard aligned sequences with too many gaps.
- ▶ Partition records by species.

With shell tools, the first two are trivial, but **the last four are next to impossible.**

# Why ?

- ▶ Unix shell tools (sed, awk, grep, etc.) are predominantly *line-oriented*.
- ▶ Some bioinformatics formats are line-oriented (*e.g.* **GFF**, **VCF**)... but Fasta is not (neither are GenBank, UniProt, ...).
- ▶ Converting FASTA to some line-oriented format (*e.g.* CSV) would solve the problem.<sup>1</sup>

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<sup>1</sup>The *format* problem, that is - the rest can be left to grep and the like.

# The project

To be able to perform more operations easily on FASTA file content, we are going to write a **FASTA → CSV converter script**.

# WARNING

## Didactical Script!

The script is meant to *illustrate* concepts, **not** to be efficient.  
⇒ We'll write it in pure style. A real-world script would be in delegation style and very different (but mostly useless for teaching).

# WARNING

## Didactical Script!

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⇒ We'll write it in pure style. A real-world script would be in delegation style and very different (but mostly useless for teaching).

Indeed, a FASTA → CSV converter could be written in one line of sed...

```
sed -n '1{h;b};${H;bo};/^>/!{H;b};:o;x;  
s/^>//;s/\n/\t/;s/\n//g;p'
```

# Practice

→ **Exercise 2.1** - FASTA to CSV converter: program logic.



Now that we can run scripts, it's time to read in our first line of data: let's have a look at some ways of getting data into our script.

# Input

There are many ways of getting data into our script, including:

- ▶ Reusing **standard input**.
- ▶ **Positional parameters**.
- ▶ The **read** and **mapfile** functions.
- ▶ Command substitution: **`$(...)`**.
- ▶ Environment variables.

# Standard Input (stdin)

Commands called by a script inherit its standard input:

```
#!/bin/bash
# reuse_stdin.sh
grep Spo0
# at this point, stdin is used up!
```

```
./reuse_stdin.sh < ../data/Spo0A.msa
```

Here `grep`'s `stdin` is the same as `reuse_stdin.sh`'s, namely `../data/Spo0A.msa`.

# Practice

→ **Exercise 2.2** - Reusing standard input.

# Arguments and Positional Parameters

A command's arguments are accessed through special parameters \$1, \$2, etc., which hold the first, second, etc. arguments, respectively.

These are called **positional parameters**.

```
./show_args.sh -f -y optarg arg1 arg{2..4}
```

- ▶ \$0 holds the name of the script (or function).
- ▶ \$@ holds all argument values passed to the script (or function).
- ▶ \$# hold the count of the number of argument values passed to the script (or function).

We can now change our script to:

```
#!/bin/bash  
# pos_arg.sh  
grep Spo0A "$1"
```

```
./pos_arg.sh ../data/Spo0A.msa
```

Sadly, the script now longer works with the < redirection, because then there is no \$1 (do set -u to check).<sup>2</sup>

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<sup>2</sup>But there is a way to make a script work in both ways.

## Arguments don't have to be filenames

- ▶ We have used \$1 to specify a data file (by its name).
- ▶ The effect is similar to redirecting stdin to that file.
- ▶ This is very frequent.
- ▶ But positional parameters can of course be used for countless other purposes.

Up to here we have been reading whole files. We can have finer control by reading only **one *line* at a time**.



# read

The `read` builtin<sup>3</sup> sets variables to values passed on `stdin`. It reads one line, word-splits it, and sets the corresponding identifiers:

```
read name  
echo "Hi, $name!"
```

The command fails (returns 1) if it can't read anything.

There can be more than one identifiers:

```
read x y z <<< '1 2 3'  
# x=1, y=2, y=3
```

---

<sup>3</sup>A builtin command works like a program but is part of the shell

If there are more words (after splitting) than there are identifiers, the last identifier gets the extra words:

```
read x y z <<< '1 2 3 4 5'  
# x: 1, y: 2, z: 3 4 5
```

If there is only one identifier, it captures the whole line:

```
read line
```

If there are fewer words than identifiers, the extra identifiers are set to an empty string.

# Practice

→ **Exercise 2.3** - Getting user input from arguments.

This works, but it only reads *one* line - we need to read *all* of them. For this, we need a way of repeating things: a **loop**. This brings us to *control structures*.

# Control Structures

Beyond a sequence of simple commands, the script's structure is given by *compound commands*:

- ▶ **Loops** (repetition) - shortly
- ▶ **Conditionals** (choice) - later
- ▶ **Groups** (sequential flow) - not covered

They start and stop with a specific *keyword* (`if...fi`, `{...}`, `while...done`, etc.)

# Loops

- ▶ Loops are *iterative* **control structures**: they *repeat* commands (called the *body*), typically with minor modifications.
- ▶ They operate either:
  - ▶ For a **fixed** number of iterations (`for ... in`).
  - ▶ Until some **condition** is met (`while, until, for ((...))`). This condition is expressed as a *test command* (details later). The test succeeds **iff** the command has 0 exit status.

## for loop - 1st form

```
for <name> in <words> ; do <commands> ; done
```

Expands <words>, and executes <commands>, binding name to each of the resulting values in turn.

The “;” can be (and often is) replaced with a newline.

# for loop - Example 1

for loops are frequently used with file globs.

The following copies a bunch of \*.fasta files to \*.fas:

```
for file in *.fasta ; do
    # body
    cp $file ${file/.fasta/.fas} # more on ${//} later.
done
```



## for loop - Example 2

Another typical case is with a sequence, often generated by a brace expansion (here `{1..10}` expands to the numbers from 1 to 10):

```
# Compute the squares of numbers from 1 to 10.  
for n in {1..10} ; do echo $((n**2)) ; done
```

(recall that `$((...))` is arithmetic expansion)

## for loop - 2nd form

Another way to write a for loop is using the **C syntax**<sup>4</sup>.

```
for ((<start-cmd>; <condition>; <iteration-cmd>)); do  
    <list>;  
done
```

1. Evaluate <start-cmd>.
2. Evaluate <condition>; if true execute <list>, if not exit loop.
3. Evaluate <iteration-cmd> and go back to 2.

The evaluations are done in shell arithmetic.

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<sup>4</sup>So named because it was copied from the C language

## Example: for loop, 2nd form

```
# Powers of 2 smaller than 10000.  
for ((p=1; p<10000; p=2*p)); do  
    echo $p  
done
```

### Notes:

- ▶ Geometric, not arithmetic progression (as in  $\{1..10\}$ ).
- ▶ Only numeric (no globs, etc.).

# while loop

In while loops, the body is executed **as long as** **<test-command> succeeds.**

```
while <test-command> ; do  
    <commands> # body  
done
```

while-example.sh - print suffixes of a string.

```
#!/bin/bash

# Get user input and assign it to a variable.
input=$1

# This succeeds as long as $input is not empty
while [[ $input ]] ; do
    echo $input
    input="${input:1}" # shorten by 1
done
```

# until loop

This works like the while loop, except that the body is executed as long as the test *fails*.

```
until <conditional> ; do  
  <statements>  
done
```

# The `continue` keyword

All loops (`for`, `while` and `until`) support the use of the `continue` keyword that makes execution of code **skip the remainder of the current loop**.

**Example:** print all multiples of 7 between 0 and 100.

```
for x in {0..100}; do
  ((x % 7 != 0)) && continue
  echo $x
  # Further operations when x is a multiple of 7
done
```

# Practice

→ **Exercise 2.4** - a simple for loop.



# Iterating over lines in a file

So, how do we iterate on lines of a file?

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Reading an entire file, one line at a time.

```
#!/usr/bin/env bash

while read line; do
    # print the line, just to check.
    echo "$line"
done
```

We've just reinvented cat! (except that ours is slower...)

Now we need to treat header lines differently from sequence lines. How do we tell them apart?

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Suggestions ?

→ We look at the first character of the line (> for headers, residue symbol for sequence lines). Time for a deeper look at *parameters*.

# Parameters

- ▶ A *parameter* (also called a *variable*) is just a name for a value.
- ▶ Values are essentially just strings, although
  - ▶ They can be interpreted numerically
  - ▶ They can be stored in indexed structures (arrays)
- ▶ Variables are the way a script stores values for later use (often a transformation or decision).
- ▶ There are multiple ways of setting them, and many more ways of retrieving their values (including handy operations).

# Setting

The simplest way is to use `=`, the *assignment* operator:

```
answer=42                # no need to declare
human='Homo sapiens'     # quotes!
date=$(date); shell_msg="I use $SHELL"
species=$human           # no word splitting
answer="nuts!"           # can reassign freely
```

- ▶ There is **no whitespace** around the equals sign!
- ▶ Identifiers contain letters, digits, or underscores; they cannot not start with a digit.
- ▶ Word splitting is disabled (except for arrays - see below).

# Getting

The basic form for getting the value of variable `var` is `${var}`. As we have seen, this occurs during the *parameter expansion* step.

```
place=London  # set value
echo ${place} # get value: ${...}
echo $place   # short form
```



Beware of the short form! Say we have filenames like `<spc>-18S.dna`: etc.

```
# Count nb lines in mammals
for spc in cat dog gnu hog rat; do
    wc -l $spc_18S.dna # WRONG!
    wc -l ${spc}_18S.dna
done
```

Can you guess what the rule is?

`set -u` guards against unset variables<sup>5</sup>.

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<sup>5</sup>See Appendix I (day 3 slides).

# Unset and Null

- ▶ A *null* variable has the empty string for a value.
- ▶ An *unset* variable does not exist at all (and it's usually a mistake to try to use its value<sup>6</sup>).
- ▶ A variable can be deleted with `unset`.

```
place=Seoul      # non-empty
place=''         # empty
place=           # same as place=''
unset place      # (NOT $place!) - deleted
```

---

<sup>6</sup>Think of `NULL`, `null`, `nil`, `None`, or `Nothing` in your favorite language.

# Defaults for Null and Unset

The “default” operator `: -` substitutes a value if a parameter is unset or null.

```
unset notset
echo $notset
echo ${notset:-default}
null=
echo $null
echo ${null:-default}
```

# Variants

- ▶  $:=$  also *sets* the variable.
- ▶ Both have forms  $(-, =)$  that only check for unset (not null).

## Notes:

- ▶ There must be **no whitespace** around `-`, `:-`, etc..
- ▶ The right-hand side is *expanded*:

```
unset var; msg="Unset var!"; echo ${var-$msg}
```

# Constants

You can prevent a parameter from changing values

```
declare -r PI=3.14159  
PI=4096  
# -> bash: PI: readonly variable
```

Readonly variables can't be unset.

# Type

By default, Bash's *simple* values are **strings**:<sup>7</sup> In certain contexts, Bash treats them as numbers:

```
a=20; b=30; echo $a+$b      # string
a=20; b=30; echo $(( $a+$b )) # arithmetic
declare -i n                # arithmetic
```

---

<sup>7</sup>I.e., it doesn't know about numbers (let alone different kinds of them!), dates, characters – IOW it's a (very) weakly typed language.

# String Operations I

```
genus=Harpagofututor
${#genus}           # length -> 14
${genus:7}          # substring from 7 (0-based)
${genus:0:7}        # substring of length 7 from 0
${genus: -5:4}      # SPACE is required (:-)
a=7; b=14
${genus:a:b}        # arithmetic evaluation
```



# String Operations II

```
prog=BLASTN
${prog/N/P}      # substitute 1st match
DNA=cgatgtattcag
RNA=${DNA//t/u}  # idem, all matches (t->u)
img=figure1.jpeg
${img%jp*g}svg   # delete pattern at end
ext=.png
${img/.jp?g/$ext} # expansion happens
```

Many more variants (man bash).

# Arrays

- ▶ *indexed* arrays (or just “arrays” for short) store lists of values referred to by a nonnegative integer. They work like the (1D) arrays of other languages, e.g. `weights[7]` could be the 7th element<sup>8</sup> in an array of weight values.
- ▶ *associative* arrays store key-value pairs, like Python’s dictionaries or Ruby/Perl’s hashes, e.g. `nb_reads['rec_A']`<sup>9</sup> for the number of reads mapping to the *recA* gene.

---

<sup>8</sup>Or the 8th, depending on the language

<sup>9</sup>Again, the syntax is language-dependent.

# Indexed Arrays

```
ary=(1 two 'Hey there') # create whole array
ary[3]=foo               # set individual element
ary+=(bar)               # append
unset ary[1]             # delete element
unset ary                # delete array
echo ${ary[0]}           # 0-based
declare -p ary            # inspect array
```

# Accessing All Array Elements

Using `*` or `@` as index refers to all array elements, but with subtle differences depending on quoting:<sup>10</sup>

```
names=('Bilbo Baggins' Beorn Gollum)
showa ${names[@]}    # (or *): 4 arguments!
showa "${names[@]}"  # 3 arguments
showa "${names[*]}"  # 1 argument
IFS=','; echo "${names[*]}"; unset IFS
```

The `#` operator yields the number of elements

```
echo ${#names[@]} # (or *)
```

---

<sup>10</sup>And also on whether or not word splitting occurs.

# Iterating over an Array

```
for e in "${array[@]}; do ... ; done
```

or

```
for ((i=0; i < ${#ary[*]}; i++)); do ... done
```

# Example of Array Usage

Cf. `../src/pascal.sh`

# Arrays and Word Splitting

Word splitting is *NOT disabled* when creating arrays:

```
elements='A B "C D" '  
array=($elements) # 4 elements!
```

Neither is file globbing:

```
pdf_glob='*.pdf'; echo "$pdf_glob"  
PDF_S=$pdf_glob ; echo "$PDF_S"  
PDF_A=($pdf_glob); declare -p PDF_A
```

# Array Caveats

- ▶ If no index is given, 0 is assumed:

```
names=(Frodo Lobelia Arwen)
echo $names # = ${names[0]} -> Frodo
```

- ▶ Arrays can't be assigned as values:

```
# Try to make a copy of `names`
lotr_names=names # WRONG - string assignment
lotr_names=$names # WRONG - see above
lotr_names=(${lotr_names[@]}) # OK
```



# Associative Arrays

Associative arrays *must* be declared as such:

```
declare -A aar
aar[key1]=val1
declare -A aar=(K1 V1 K2 V2)
echo ${aar[key1]}
```

The behaviour is otherwise very similar to that of indexed arrays.

**Note:** \* and @ work on the *values*, to expand the *keys* use a !:  
\${!aar[\*]}, etc.

# Associative Array Caveats

The order in which associative array elements are expanded is **unpredictable**. In particular, there is *no guarantee* that values (or keys) will be listed in the order they were added to the array.

# Practice

Back to our **FASTA to TSV converter script!**

After this long survey of parameters, we are now equipped to formulate an expression that will extract the first character of a line, to check whether it is a header line or not.

→ **Exercise 2.5** - FASTA to CSV converter: reading the input file line by line.

Now that we have the first character of each line, we need to **test** if it's '>' or something else.

This is going to be a long excursion into testing.

# Conditionals

Conditionals are *branching* **control structures**. They enable the script to **choose what to do** between two or more possibilities.

The main conditional constructs are:

- ▶ `if` - yes-or-no decisions (possibly nested), based on a *test command*
- ▶ `case` - multi-way decision, based on pattern matching

# if

The basic idea:

```
if <test-command> ; then
    <statements> # iff test-command returns 0
fi
```

See `check_user.sh` for an example.

Before we look in detail at test commands, we need to see the full version:

```
if <test-command> ; then
    <statements>
elif <other-test-commands> ; then
    <other-statements>
else
    <default-commands>;
fi
```

- ▶ There can be 0 or more elif clauses.
- ▶ There can be 0 or 1 else clause.

## A shortcut

Due to how lists work, an if clause can be<sup>11</sup> (and often is) shortened to one of the following forms:

```
<test-command> && <success-command>  
<test-command> || <failure-command>  
<test-command> && <success-command> || \  
    <failure-command>  
grep $USER /etc/passwd && echo found || \  
echo 'NOT found'
```

---

<sup>11</sup>Strictly speaking, the `<cmd> && ... || ...` is not equivalent to `if <cmd> then ... else ... fi`



Now we can look at **test commands**.

# Test Commands

Test commands are the main ingredient of `if...then` **conditionals** and `while/until` **loops**. They can be:

- ▶ a *list* - the test succeeds iff the list itself succeeds (returns 0);
- ▶ a *conditional expression* between `[]` and `]` - the test succeeds if the expression is true, the expression involves *strings* (including filenames);<sup>12</sup>
- ▶ an *arithmetic expression* between `((` and `)`) - the test succeeds iff the expression is **nonzero**.

---

<sup>12</sup>An older form for conditional expression used `[...]` or `test`.

# Why can 0 signal both success and failure?

## Historical aside

- ▶ Unix: (many) more ways to fail than to succeed  $\rightarrow$  0 for success,  $> 0$  for various kinds of errors.
- ▶ Early shells: crude Boolean and arithmetic expressions (if at all).
- ▶ C language: Boolean algebra with 0 for false and nonzero for true.

$\Rightarrow$  When (or “if”) arithmetic and Boolean expressions were added to shells, they were strongly influenced by C.<sup>a</sup>

---

<sup>a</sup>As was the for (( ; ; )) loop.

# Commands as Tests

Quite simply: check if the command succeeds. We have already seen this in `check_user.sh`.

# Conditional Expressions

The expression between `[[` and `]]` is a *conditional expression*. It may involve the following:

- ▶ file attributes (*e.g.* existence, permissions, ...)
- ▶ variable properties (*e.g.* set or unset, integer, ...)
- ▶ string properties (*e.g.* length)
- ▶ string comparison (equality, order, etc.)
- ▶ numeric comparison

Word splitting is **disabled** between `[[ ]]`, so `" "` have no effect.

# File Properties

They take the form `-c filename`, where the character `c` denotes a file property. For example, to check if a file exists, use `-e`:

```
if [[ -e file.txt ]]; then echo "exists!"; fi
# short form
[[ -e file.txt ]] && echo "exists!"
```

Many properties can be tested in this way (see next slide).

## A few file property test operators

operator	true if
-d	file is a directory
-f	file exists and is a regular file ( <i>e.g.</i> , not a dir)
-r	file is readable
-w	file is writable
-x	file is executable
-s	file exists and has a size greater than 0

There are also a few file *comparison* operators, such as `f1 -nt f2` which is true iff `f1` is newer than `f2`. Obviously, they expect *two* arguments.

# String Conditionals

The following operate on strings

Operator	True if
<code>s</code>	<code>s</code> is a non-empty string
<code>s1 == s2</code>	<code>s1</code> and <code>s2</code> are equal <b>strings</b>
<code>s1 = s2</code>	idem (note spaces!)
<code>s1 != s2</code>	<code>s1</code> and <code>s2</code> are different
<code>s1 &lt; s2</code>	<code>s1</code> comes before <code>s2</code> <b>alphabetically</b>
<code>s1 &gt; s2</code>	<code>s1</code> comes after <code>s2</code> <b>alphabetically</b>



**Note** that the above operators interpret their operands as *strings* (also, `>` and `<` have an entirely different meaning here from I/O redirection)

```
[[ 2+2 == 4 ]] # false!  
[[ 10 < 2 ]]   # true!
```

`[[...]]` *can* compare numbers<sup>13</sup> (we'll see this in a moment).

---

<sup>13</sup>Though perhaps it shouldn't be used for that.

# Pattern Matching

If unquoted, the right-hand argument of a `==` or `!=` is treated as a pattern (“glob”):

```
[[ abc == ?bc ]]      # true
[[ abc == "?bc" ]]    # false (quotes)
gene=lacZ; [[ $gene == lac? ]]
```

**Note** that the glob pattern isn't matched against files, but against the **left-hand argument**.

# Matching Regular Expressions

The `=~` operator matches against POSIX regular expressions<sup>14</sup>

```
[[ abc =~ .bc ]] # true
[[ abc =~ abc? ]] # true
[[ abc == abc? ]] # false (glob)
```

---

<sup>14</sup>à la `grep`, `Perl`, `sed`, and so many others... each with its own dialect, all different from globs :-)

# Practice

Back to our **FASTA to TSV converter script!**

→ **Exercise 2.6** - FASTA to CSV converter: testing for header lines.

# Numeric Conditionals

The following operators also operate on strings, but *treat their operands numerically*<sup>15</sup>:

Operator	Meaning (numerically)
s1 -eq s2	s1 = s2
s1 -ne s2	s1 $\neq$ s2
s1 -lt s2	s1 < s2
s1 -le s2	s1 $\leq$ s2
s1 -gt s2	s1 > s2
s1 -ge s2	s1 $\geq$ s2

<sup>15</sup>Using shell arithmetic, more on this shortly

This way things make more sense:

```
[[ 2+2 -eq 4 ]] # true  
[[ 10 -lt 2 ]] # false!
```

# Expansion Happens

I have given examples mostly with literals for simplicity's sake, but (most) expansions are entirely possible in test commands:

```
[[ -x "$HOME" ]] # better not be false
[[ "$SHELL" == /usr/bin/bash ]]
[[ /usr/bin/echo == $(which echo) ]]
a=1; b=1; [[ $a -eq $b ]]
```

# Logical Operations

The expressions can be connected with the logical operators `(...)`, `!`, `&&`, and `||` (decreasing order of precedence).

```
a=2; [[ a == a && ! (b == b) ]]
```

**Note** that the *logical* operators `&&`, `||` and `!` are **not the same** as the *control* operators `&&`, `||` and `!`.



- ▶ Comparing numbers with `[[...]]` is cumbersome (to say the least).
- ▶ Fortunately, there is a another way of doing numerical comparisons.

# Arithmetic Tests

In this test, the expression between `(( and ))` is evaluated using the rules of shell arithmetic (more on this shortly). The test succeeds if the numerical result is **not** zero (contrary to command exit status).

```
(( 2+2 == 4 )) # true  
(( 10 < 2 ))    # false!  
a=2; ((a+a == a*a))
```

# Shell Arithmetic

1. Parameters are expanded (\$ not needed) and treated as numbers<sup>16</sup>
  2. The resulting expression is evaluated numerically (operators on next slide)
- ▶ Shell arithmetic is used in arithmetic expansion, arithmetic conditionals, and a few other contexts.
  - ▶ Bash can only do *integer* arithmetic! (more on this later)

---

<sup>16</sup>As far as possible

Table 4: Main Arithmetic Operators, by decreasing precedence - () override.

operator	function
!	logical negation
**	exponentiation
*, /, %	multiplication, division, remainder
+, -	addition, subtraction
<, >, <=, >=	comparison
==, !=	logical equality and inequality
&&	logical AND
	logical OR
=, +=, *=, ...	assignment

# Shell Arithmetic - Examples

To illustrate shell arithmetic, we can simply use arithmetic expansion

```
a=2; b=5  
echo $((a**3)) # spaces matter less than in [[...]]  
echo $((a ** 3))  
echo $((a**3 % 3))  
echo $((a < b))
```

**Recall** that in this context 1 represents true and 0 represents false (contrary to command exit status).

# No floating-point?

```
echo $((5/2))      # wtf?  
echo $((5.0/2.0))  # fails!
```

→ use an external program<sup>17</sup>

```
echo "scale=1; $b/$a" | bc  
bc <<< "$scale=1; $b/$a"  
result=$(bc <<< "$scale=1; $b/$a") && echo $result
```

---

<sup>17</sup>In the same way you use sed, awk etc. when the shell's string functions are too limited

# Appendix I: Sample Formats

# General Feature Format (GFF)

```
##gff-version 3.1.26
##sequence-region ctg123 1 1497228
ctg123 . gene 1000 9000 . + . ID=gene00001;Name=EDEN
ctg123 . mRNA 1050 9000 . + . ID=mRNA00001;Parent=...
ctg123 . mRNA 1050 9000 . + . ID=mRNA00002;Parent=...
ctg123 . mRNA 1300 9000 . + . ID=mRNA00003;Parent=...
ctg123 . exon 1300 1500 . + . ID=exon00001;Parent=...
ctg123 . exon 1050 1500 . + . ID=exon00002;Parent=...
ctg123 . exon 3000 3902 . + . ID=exon00003;Parent=...
```



# Variant Call Format (VCF)

```
##fileformat=VCFv4.3
##source=myImputationProgramV3.1
...
#CHROM POS ID REF ALT QUAL FILTER INFO ...
20 14370 rs6054257 G A 29 PASS NS=3;...
20 17330 . T A 3 q10 NS=3;...
20 1110696 rs6040355 A G,T 67 PASS NS=2;...
20 1230237 . T . 47 PASS NS=3;...
20 1234567 microsat1 GTC G,GTCT 50 PASS NS=3;...
```