The Zeroth law of bioinformatics[1]

> The software programmer and his wife relocate to a new house in the city. Counting the cardboard boxes the movers dropped off, they discover one box is missing.
>
> “How can this be?” the wife wonders. “I'm sure I've packed forty boxes. Are you sure you've counted them right?”.
>
> "Yes, thirty nine it is", says the husband. “Don't believe me? let's count them together: zero, one, two, three,..."

The Problem

Here's the start of chromosome 1 (hg18):

```
>chr1
taaccctaaccctaaccctaaccctaaccctaaccctaaccctaaccctaacccta
accctaaccctaaccctaaccctaaccctaaccctaaccctaaccctaac
```

What should be the genomic position for the first nucleotide (the yellow 't') ?
Answering 1 (one) would make you a AWK programmer.
Answering 0 (zero) would make you a C programmer.

Let's consider genomic location of the first ten nucleotides in chromosome 1: `taaccctaac`

With zero-based notation, we would use the following genomic location:

```
     chr1 0    9
```

With one-based notation, we would use the following genomic location:

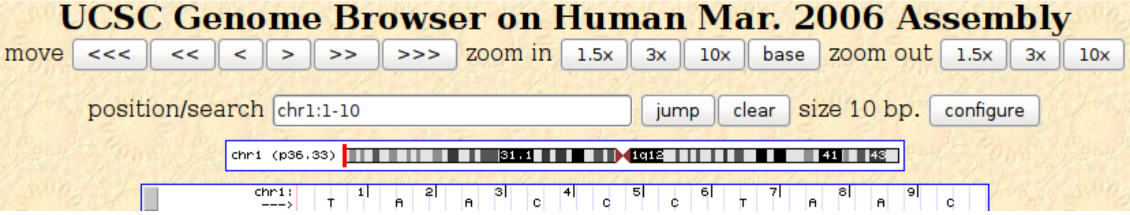
```
     chr1 1    10
```

The question is:
Which program / database / browser / other public resouce uses what notation ?

[1] Compare with Fowler's Zeroth law of Thermodynamics (http://en.wikipedia.org/wiki/Zeroth_law_of_thermodynamics) and Asimov's Zeroth law of robotics (http://en.wikipedia.org/wiki/Laws_of_Robotics#Zeroth_Law_added)

UCSC Browser

When ***displaying*** genomic positions, the UCSC browser uses one-based notation:



UCSC Genome Browser on Human Mar. 2006 Assembly

position/search chr1:1-10

size 10 bp.

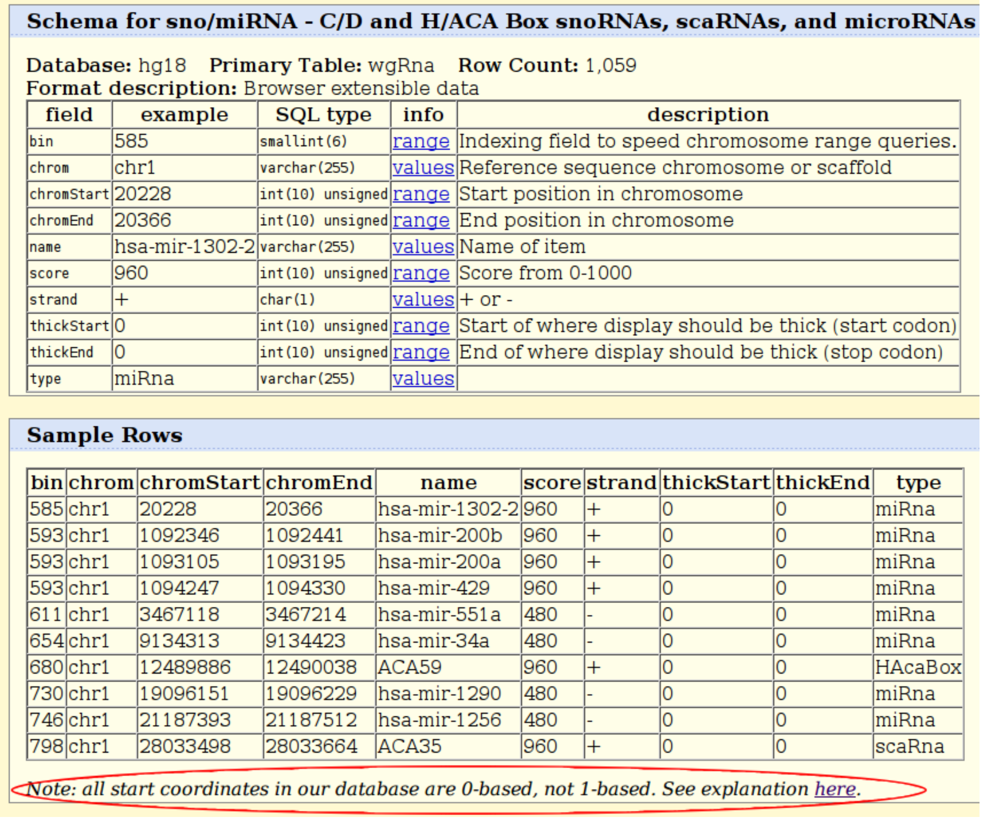
Note that for the genomic location `chr:1-10` we get the the first ten nucleotides `taaccctaac.`

In the UCSC browser, there is no position 'zero'. Requesting the genomic location `chr:0-9,` the UCSC browser will display genomic location `chr:1-9` (ignoring our zero value).

UCSC Browser's tables

Unlike the UCSC's web interface, all the tables and data files in the UCSC browser use zero-based notation for the *start* coordinate, but a one-based notation for the *end* coordinate.

When downloading raw data (using UCSC's table-browser), the following warning is displayed (when you click on the describe table schema button):



Schema for sno/miRNA - C/D and H/ACA Box snoRNAs, scaRNAs, and microRNAs

Database: hg18 **Primary Table:** wgRna **Row Count:** 1,059
Format description: Browser extensible data

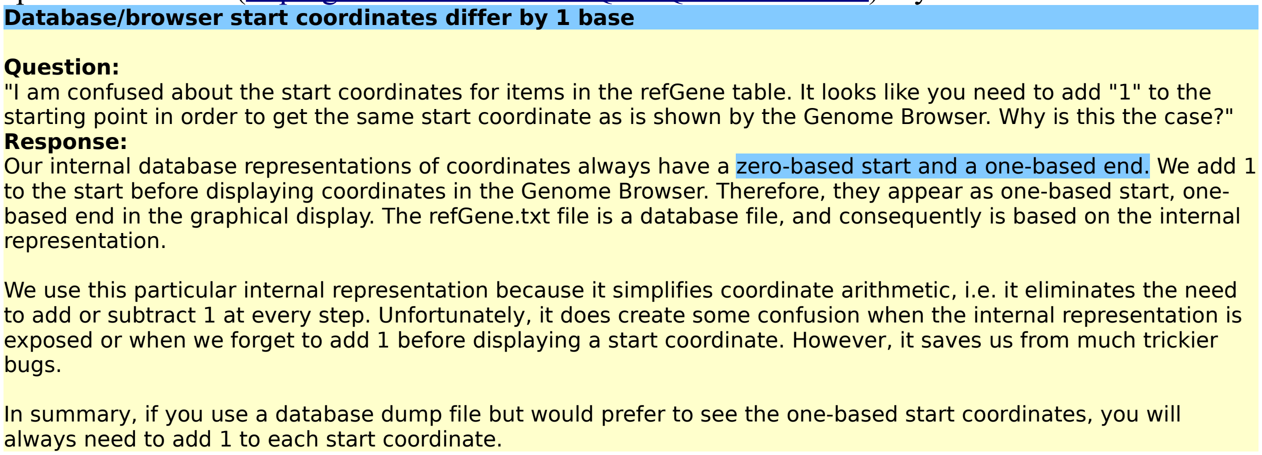
field	example	SQL type	info	description
bin	585	smallint(6)	range	Indexing field to speed chromosome range queries.
chrom	chr1	varchar(255)	values	Reference sequence chromosome or scaffold
chromStart	20228	int(10) unsigned	range	Start position in chromosome
chromEnd	20366	int(10) unsigned	range	End position in chromosome
name	hsa-mir-1302-2	varchar(255)	values	Name of item
score	960	int(10) unsigned	range	Score from 0-1000
strand	+	char(1)	values	+ or -
thickStart	0	int(10) unsigned	range	Start of where display should be thick (start codon)
thickEnd	0	int(10) unsigned	range	End of where display should be thick (stop codon)
type	miRna	varchar(255)	values	

Sample Rows

bin	chrom	chromStart	chromEnd	name	score	strand	thickStart	thickEnd	type
585	chr1	20228	20366	hsa-mir-1302-2	960	+	0	0	miRna
593	chr1	1092346	1092441	hsa-mir-200b	960	+	0	0	miRna
593	chr1	1093105	1093195	hsa-mir-200a	960	+	0	0	miRna
593	chr1	1094247	1094330	hsa-mir-429	960	+	0	0	miRna
611	chr1	3467118	3467214	hsa-mir-551a	480	-	0	0	miRna
654	chr1	9134313	9134423	hsa-mir-34a	480	-	0	0	miRna
680	chr1	12489886	12490038	ACA59	960	+	0	0	HAcaBox
730	chr1	19096151	19096229	hsa-mir-1290	480	-	0	0	miRna
746	chr1	21187393	21187512	hsa-mir-1256	480	-	0	0	miRna
798	chr1	28033498	28033664	ACA35	960	+	0	0	scaRna

Note: all start coordinates in our database are 0-based, not 1-based. See explanation here.

The explanation "here" (http://genome.ucsc.edu/FAQ/FAQtracks#tracks1) says:



Database/browser start coordinates differ by 1 base

Question:
"I am confused about the start coordinates for items in the refGene table. It looks like you need to add "1" to the starting point in order to get the same start coordinate as is shown by the Genome Browser. Why is this the case?"
Response:
Our internal database representations of coordinates always have a zero-based start and a one-based end. We add 1 to the start before displaying coordinates in the Genome Browser. Therefore, they appear as one-based start, one-based end in the graphical display. The refGene.txt file is a database file, and consequently is based on the internal representation.

We use this particular internal representation because it simplifies coordinate arithmetic, i.e. it eliminates the need to add or subtract 1 at every step. Unfortunately, it does create some confusion when the internal representation is exposed or when we forget to add 1 before displaying a start coordinate. However, it saves us from much trickier bugs.

In summary, if you use a database dump file but would prefer to see the one-based start coordinates, you will always need to add 1 to each start coordinate.

Uploading Custom Tracks (BED files) to UCSC Browser

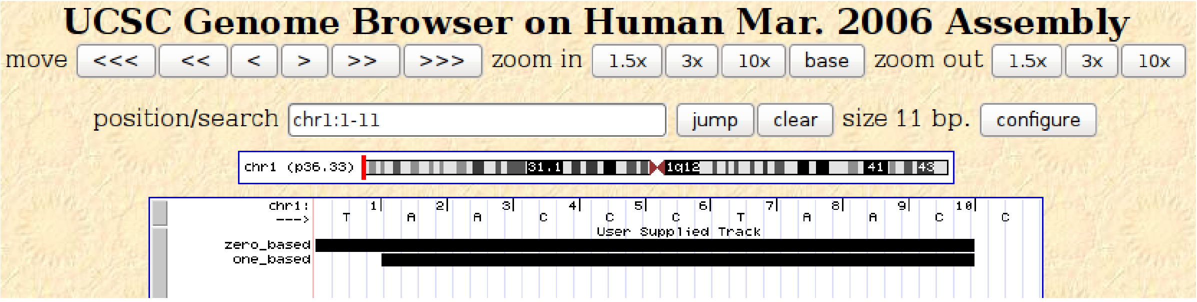
BED files (http://genome.ucsc.edu/FAQ/FAQformat#format1) are textual files containing genomic locations. As such, UCSC Genome Browser treats BED files as database files, and assumes they have a zero-based starting coordinate. When displaying the custom track, the browser will add 1 to all start coordinates (but not to the end coordinates).

Example:

Consider the following BED file:

```
chr1    0    10    zero_based
chr1    1    10    one_based
```

Uploading and displaying it in the UCSC genome browser:



UCSC Genome Browser on Human Mar. 2006 Assembly

position/search chr1:1-11 size 11 bp.

Notes:

- The start coordinate for both sequences was incremented by 1:
  `zero_based` starts on position 1,
  `one_based` starts on position 2.
- The end coordinate for both sequences was not altered.
- The first sequence (`zero_based`) is 10 nucleotides long.
- The second sequence (`one_based`) is 9 nucleotides long.

Sanger's miRBase

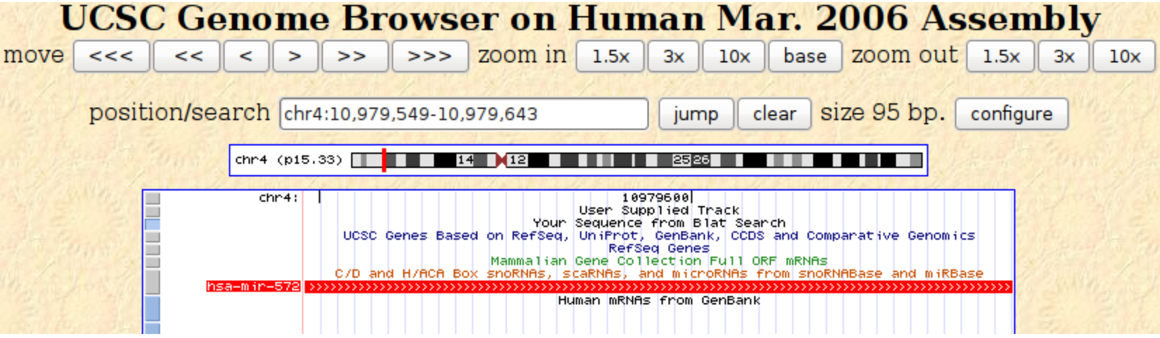
On sanger's miRBase website (http://microrna.sanger.ac.uk/sequences/ftp.shtml), the GFF files with the genomic locations use one-based notation for both start and end coordinates.

An Example with hsa-mir-572

Relevant line from `hsa.gff` (downloaded from miRBase):

```
4 . miRNA 10979549 10979643 .  +  .   ACC="MI0003579"; ID="hsa-mir-572";
```

hsa-mir-572 in UCSC Genome browser:



UCSC Genome Browser on Human Mar. 2006 Assembly

position/search chr4:10,979,549-10,979,643 size 95 bp.

move
<<<
<<
<
>
>>
>>>
zoom in
1.5x
3x
10x
base
zoom out
1.5x
3x
10x
jump
clear
configure
chr4 (p15.33)
14
12
25
26
chr4:
10979600
User Supplied Track
Your Sequence from Blat Search
UCSC Genes Based on RefSeq, UniProt, GenBank, CCDS and Comparative Genomics
RefSeq Genes
Mammalian Gene Collection Full ORF mRNAs
C/D and H/ACA Box snoRNAs, scaRNAs, and microRNAs from snoRNABase and miRBase
hsa-mir-572
Human mRNAs from GenBank

Relevant line from UCSC sno/miRNA track (using the table browser):

```
668    chr4     10979548     10979643   hsa-mir-572   960   +     0   0    miRna
```

Notes:

- miRBase uses one-based notation for both start, end coordinates
- UCSC displays data using one-based notation for both start, end coordinates
- UCSC stores data using zero-based notation for the start coordinate (10979548 in UCSC vs. 10979549 in miRBase).