

[www.leedsomics.org](http://www.leedsomics.org)  
@leedsomics  
[omics@leeds.ac.uk](mailto:omics@leeds.ac.uk)

## Good Practices in Writing Code: variable types

**Club Moderators:** Elton Vasconcelos, Euan McDonell, Chew Cheng, and Dapeng Wang

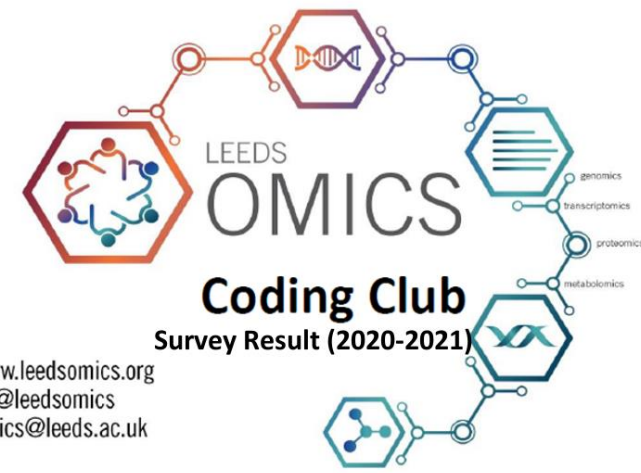
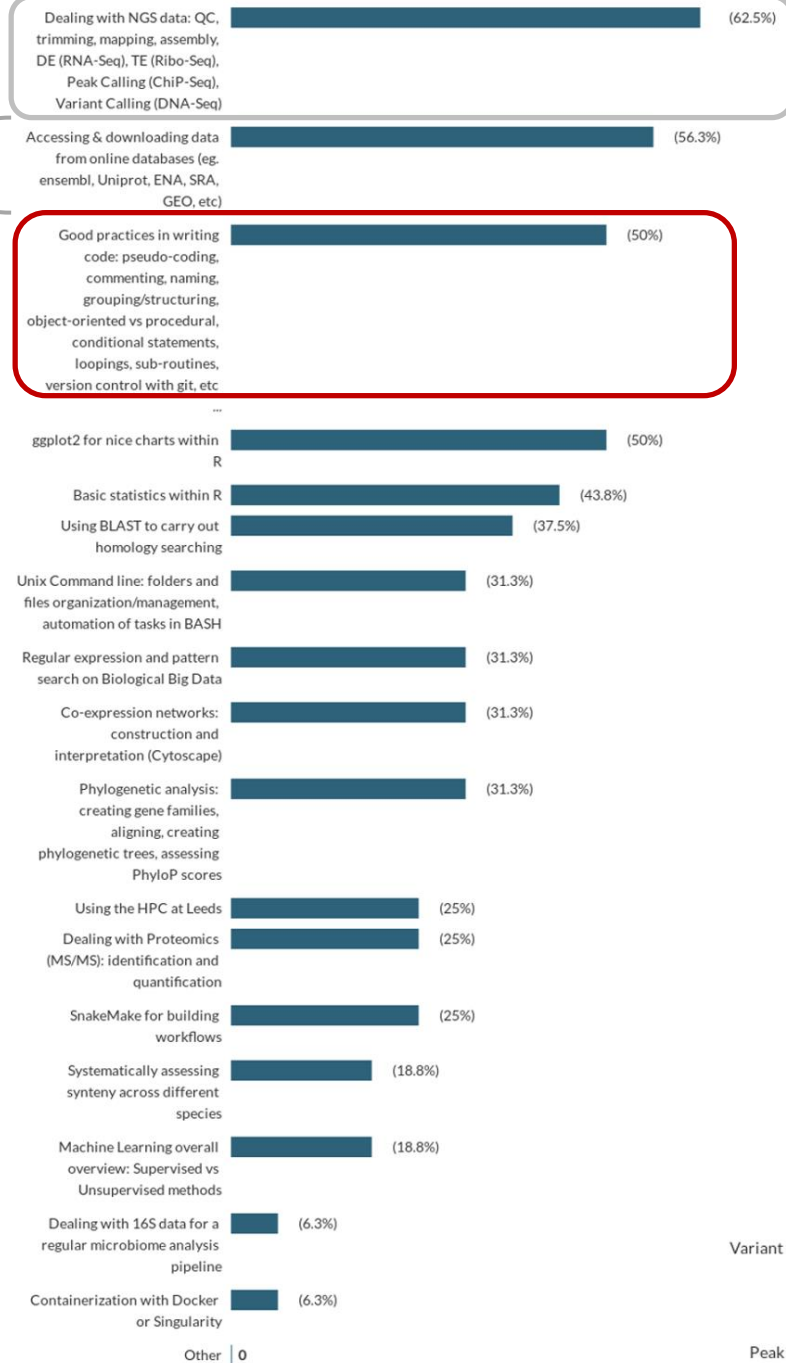
# Topics to be addressed on the 2020-21 season - Survey Result

1st, 4th, 6th, 8th, ... sessions

2nd session

3rd, 5th, 7th, 9th, ... sessions

## 1 Which of the following topics would you like to attend in our Coding Club sessions?



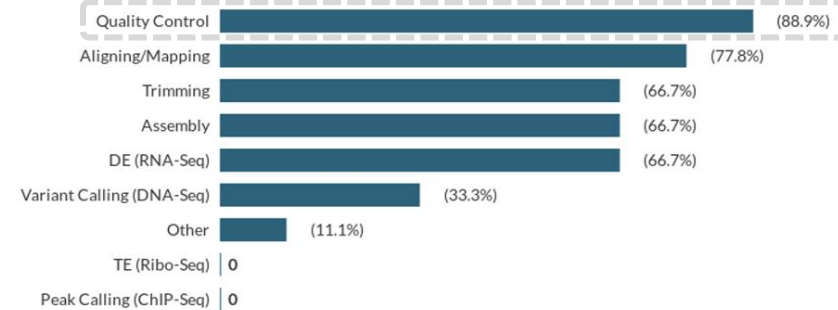
## 1.b Do you think we should address "Good practices in writing code" topic in more sessions?



## 1.c Do you think we should address "Dealing with NGS data" topic in more sessions?



## 1.c.i Which sub-topics would be of most interest to you?



1st session (15/06/20)

- **Variable in programming** → programmer-predefined entity that will store information in the code

## Different types of variables/data in the three main languages used in Bioinformatics



PERL

- Scalars (\$)

- Arrays (@)

- Hashes (%)



Python

- Numbers

- String

- List

- Tuple

- Dictionary



- Numeric

- Character

- Vectors

- Factors

- Data Frames

[https://www.tutorialspoint.com/perl/perl\\_variables.htm](https://www.tutorialspoint.com/perl/perl_variables.htm)

[https://www.tutorialspoint.com/python3/python\\_variable\\_types.htm](https://www.tutorialspoint.com/python3/python_variable_types.htm)

[https://www.tutorialspoint.com/r/r\\_data\\_types.htm](https://www.tutorialspoint.com/r/r_data_types.htm)

NOTE: List and Array terminologies in R have different and more complex concepts than in PERL and Python.

# Examples in PERL

## ■ Scalars

```
#!/usr/bin/perl

$age = 25;           # An integer assignment
$name = "John Paul"; # A string
$salary = 1445.50;  # A floating point

print "Age = $age\n";
print "Name = $name\n";
print "Salary = $salary\n";
```

Live Demo

This will produce the following result –

```
Age = 25
Name = John Paul
Salary = 1445.5
```

# Examples in PERL

## ■ Arrays

```
#!/usr/bin/perl

@ages = (25, 30, 40);
@names = ("John Paul", "Lisa", "Kumar");

print "\$ages[0] = $ages[0]\n";
print "\$ages[1] = $ages[1]\n";
print "\$ages[2] = $ages[2]\n";
print "\$names[0] = $names[0]\n";
print "\$names[1] = $names[1]\n";
print "\$names[2] = $names[2]\n";
```

Live Demo

Here we used escape sign (\) before the \$ sign just to print it. Other Perl will understand it as a variable and will print its value. When executed, this will produce the following result –

```
$ages[0] = 25
$ages[1] = 30
$ages[2] = 40
$names[0] = John Paul
$names[1] = Lisa
$names[2] = Kumar
```

# Examples in PERL

- Hash table

Live Demo

```
#!/usr/bin/perl

%data = ('John Paul', 45, 'Lisa', 30, 'Kumar', 40);

print "\$data{'John Paul'} = $data{'John Paul'}\n";
print "\$data{'Lisa'} = $data{'Lisa'}\n";
print "\$data{'Kumar'} = $data{'Kumar'}\n";
```

This will produce the following result –

```
$data{'John Paul'} = 45
$data{'Lisa'} = 30
$data{'Kumar'} = 40
```

→ Useful short code that employs all three PERL variable types in order to combine information from two files

```
#!/usr/bin/perl
```

```
open(FILE1, "x.tsv");
```

```
open(FILE2, "y.tsv");
```

```
while(<FILE2>) {
```

```
    chomp($_);
```

```
    @array2 = split(/\t/, $_);
```

```
    $hash{$array2[0]} = $array2[2];
```

```
}
```

```
while(<FILE1>) {
```

```
    chomp($_);
```

```
    @array1 = split(/\t/, $_);
```

```
    if($hash{$array1[0]} ne "") {
```

```
        print("$_\t$hash{$array1[0]}\n");
```

```
    }
```

```
    else {
```

```
        print("$_\tNA\n");
```

```
    }
```

```
}
```

FILE1 x.tsv → a typical DE analysis output table with 3125 rows

Long_geneID	LogFC.2h	LogFC.17h	logCPM_LR	PValue	FDR					
NC_018726.3	mrna_XM_023252992.1_17213	-0.0115539525378653	12.3552392903438	2.86329600280231	153.177804483085	5.46842652825283e-34	3.97729598252885e-29			
NC_018737.3	mrna_XM_023245341.1_62253	-2.41190133112974e-08	10.7952771226017	1.31660408910246	123.483120559081	1.53455008109868e-27	5.10785193903218e-23			
NC_018729.3	mrna_XM_023256742.1_28810	0.000496516357557754	10.763096713483	1.28333375331224	122.849205260556	2.10685197947211e-27	5.10785193903218e-23			
NC_018736.3	mrna_XM_019818127.2_58617	-9.33346500212488	-10.032294222076	0.293441063845244	111.291091024287	6.81469842628745e-25	1.23911661485185e-20			
NC_018736.3	mrna_XM_019818041.1_58415	-8.34999208356182	-9.51603983117479	0.890988635810215	108.822101347149	2.34196789867635e-24	3.40672018413056e-20			
NC_018731.3	mrna_XM_019839937.2_40571	-9.53613707062572	-9.53619935953011	-0.197449535373358	105.301303647077	1.36179722364347e-23	1.65077059450061e-19			
NC_018735.3	mrna_XM_023242979.1_55286	1.31546722469771	9.94937447648528	0.58790776418027	100.232406950434	1.71715451761346e-22	1.78417260535803e-18			
NC_018741.3	mrna_XM_023249335.1_70881	0.450036882025638	9.6533406059691	0.228666387292216	99.2434452989686	2.81552683373531e-22	2.55973622089046e-18			
NC_018724.3	mrna_XM_019822718.2_7002	3.71124136142327e-08	9.38866457539553	-0.0287171084086663	97.1391471277462	8.06310309653979e-22	6.51606238241702e-18			

FILE2 y.tsv → gene product descriptions with 72,732 lines

NC_018723.3	ncrna_XR_002147070.2_1	XR_002147070.2	uncharacterized LOC102899061, transcript variant X3
NC_018723.3	ncrna_XR_002147044.2_2	XR_002147044.2	uncharacterized LOC102899061, transcript variant X2
NC_018723.3	ncrna_XR_002147038.2_3	XR_002147038.2	uncharacterized LOC102899061, transcript variant X1
NC_018723.3	mrna_XM_023247174.1_4	XM_023247174.1	peptidoglycan recognition protein 4
NC_018723.3	trna_5	5	tRNA-Glu
NC_018723.3	mrna_XM_011289120.3_6	XM_011289120.3	coiled-coil domain containing 115, transcript variant X1
NC_018723.3	mrna_XM_003980242.5_7	XM_003980242.5	coiled-coil domain containing 115, transcript variant X2
NC_018723.3	mrna_XM_003980243.4_8	XM_003980243.4	IMP4, U3 small nucleolar ribonucleoprotein
NC_018723.3	mrna_XM_023250065.1_9	XM_023250065.1	protein tyrosine phosphatase, non-receptor type 18
NC_018723.3	mrna_XM_023250181.1_10	XM_023250181.1	neurogenic locus notch homolog protein 3-like

Script's output file → FILE1 with the gene product description on the last column

Long_geneID	LogFC.2h	LogFC.17h	logCPM_LR	PValue	FDR	Description				
NC_018726.3	mrna_XM_023252992.1_17213	-0.0115539525378653	12.3552392903438	2.86329600280231	153.177804483085	5.46842652825283e-34	3.97729598252885e-29			heterogeneous nuclear ribonucleoprotein D, transcript variant X6
NC_018737.3	mrna_XM_023245341.1_62253	-2.41190133112974e-08	10.7952771226017	1.31660408910246	123.483120559081	1.53455008109868e-27	5.10785193903218e-23			CCCTC-binding factor, transcript variant X1
NC_018729.3	mrna_XM_023256742.1_28810	0.000496516357557754	10.763096713483	1.28333375331224	122.849205260556	2.10685197947211e-27	5.10785193903218e-23			peroxisomal biogenesis factor 5, transcript variant X1
NC_018736.3	mrna_XM_019818127.2_58617	-9.33346500212488	-10.032294222076	0.293441063845244	111.291091024287	6.81469842628745e-25	1.23911661485185e-20			phosphatidylinositol transfer protein, cytoplasmic 1, transcript variant X2
NC_018736.3	mrna_XM_019818041.1_58415	-8.34999208356182	-9.51603983117479	0.890988635810215	108.822101347149	2.34196789867635e-24	3.40672018413056e-20			integrin subunit beta 3, transcript variant X1
NC_018731.3	mrna_XM_019839937.2_40571	-9.53613707062572	-9.53619935953011	-0.197449535373358	105.301303647077	1.36179722364347e-23	1.65077059450061e-19			ring finger protein 168, transcript variant X2
NC_018735.3	mrna_XM_023242979.1_55286	1.31546722469771	9.94937447648528	0.58790776418027	100.232406950434	1.71715451761346e-22	1.78417260535803e-18			vav guanine nucleotide exchange factor 2, transcript variant X7
NC_018741.3	mrna_XM_023249335.1_70881	0.450036882025638	9.6533406059691	0.228666387292216	99.2434452989686	2.81552683373531e-22	2.55973622089046e-18			lysine demethylase 5C, transcript variant X1
NC_018724.3	mrna_XM_019822718.2_7002	3.71124136142327e-08	9.38866457539553	-0.0287171084086663	97.1391471277462	8.06310309653979e-22	6.51606238241702e-18			polybromo 1, transcript variant X23

→ The following is the same code from previous slide written in a single command line to be executed straight from the terminal prompt:

```
$ perl -e 'open(FILE1, "x.tsv"); open(FILE2, "y.tsv"); while(<FILE2>) {chomp($_); @array2 = split(/\t/, $_); $hash{$array2[0]} = $array2[1];} while(<FILE1>) {chomp($_); @array1 = split(/\t/, $_); if($hash{$array1[0]} ne "") {print("$_\t$hash{$array1[0]}\n");} else {print("$_\tNA\n");}}' >z.tsv
```



Bring your issues on!