

Hashes

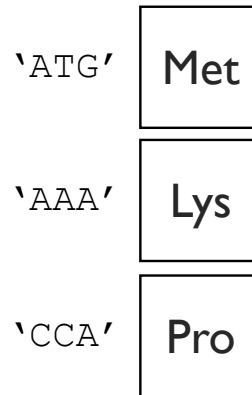
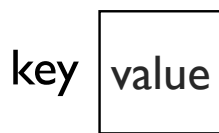
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Hashes

- Perl hashes are denoted with a '%' symbol like this
%data
- Each key and each value contains a scalar value for example this could be
 - a number
 - a letter
 - a word
 - a sentence
 - a scalar variable like \$scalar_variable
 - a gene ID
 - a sequence

What is a hash?

- A hash is an associative array made up of key/value pairs.
- Like a dictionary
- And unlike an array a hash is unordered.

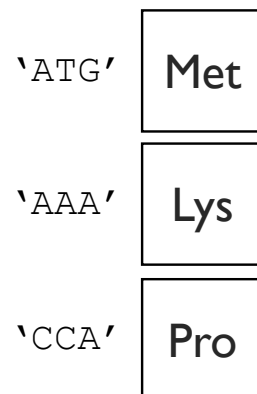


A key is like a descriptive array index.

An array



A hash



The array index [0] is similar to the key 'ATG'.

The key 'ATG' is used to access the value 'Met', just as [0] is used to access 'red'

But the key/value pairs are not stored in order

Creating a hash

The hash `%genetic_code` is built with key/value pairs

```
my %genetic_code = (  
  "ATG" => "Met",  
  "AAA" => "Lys",  
  "CCA" => "Pro",  
);
```

key	value
'ATG'	Met

Accessing a hash value using a key

```
my %genetic_code = (  
  "ATG" => "Met",  
  "AAA" => "Lys",  
  "CCA" => "Pro",  
);  
  
my $aa = $genetic_code{"ATG"};  
print "ATG translates to $aa\n";  
ATG translates to Met
```

Each value of the hash is a scalar therefore we use the '\$' when we refer to an individual value.

Hash keys are surrounded by squiggly brackets {}

keys() returns an unordered list of the keys of a hash

```
@array_of_keys = keys (%hash);

my %genetic_code = (
    "ATG" => "Met",
    "AAA" => "Lys",
    "CCA" => "Pro",
);

my @codons = keys (%genetic_code);
print join("--", @codons), "\n";
CCA--AAA--ATG
```

Iterating through a hash by looping through an list of hash keys.

```
my %genetic_code = (
    "ATG" => "Met",
    "AAA" => "Lys",
    "CCA" => "Pro",
);

Remember: the key is used to access
the value
$value = $hash{$key}

foreach my $codon (keys %genetic_code) {
    my $aa = $genetic_code{$codon};
    print "$codon translates to $aa\n";
}
CCA translates to Pro
AAA translates to Lys
ATG translates to Met
```

Sorting and iterating through the keys of a hash

```
my %genetic_code = (  
  "ATG" => "Met",  
  "AAA" => "Lys",  
  "CCA" => "Pro",  
);
```

Remember: hash keys are unordered so we use `sort` to be sure that the order is always the same.

```
foreach my $codon (sort keys %genetic_code) {  
  my $aa = $genetic_code{$codon};  
  print "$codon translates to $aa\n";  
}
```

```
AAA translates to Lys  
ATG translates to Met  
CCA translates to Pro
```

Iterating through a hash and sorting by the values

```
my %genetic_code = (  
  "ATG" => "Met",  
  "AAA" => "Lys",  
  "CCA" => "Pro",  
);
```

```
foreach my $codon (sort {$genetic_code{$a} cmp $genetic_code{$b}}  
keys %genetic_code) {  
  my $aa = $genetic_code{$codon};  
  print "$codon translates to $aa\n";  
}
```

```
AAA translates to Lys  
ATG translates to Met  
CCA translates to Pro
```

Remember: the key is used to access the value

`$value = $hash{$key}`



we can create a custom sort function using `{ $a cmp $b }`

values() returns an unordered list of values

```
@array_of_values = values(%hash);
```

```
my %genetic_code = (  
    "ATG" => "Met",  
    "AAA" => "Lys",  
    "CCA" => "Pro",  
);
```

You can use `sort values` to be sure that the order of the values is always the same.

```
my @amino_acids = values(%genetic_code);  
print join("--",@amino_acids), "\n";  
Pro--Lys--Met
```

Adding additional key/value pairs

```
my %genetic_code = (  
    "ATG" => "Met",  
    "AAA" => "Lys",  
    "CCA" => "Pro",  
);
```

```
$genetic_code{"TGT"} = "Cys";
```

```
foreach my $codon (keys %genetic_code){  
    print "$codon -- $genetic_code{$codon}\n";  
}  
CCA -- Pro  
AAA -- Lys  
ATG -- Met  
TGT -- Cys
```

Deleting key/value pairs

```
my %genetic_code = (  
  "ATG" => "Met",  
  "AAA" => "Lys",  
  "CCA" => "Pro",  
);  
  
delete $genetic_code{"AAA"};  
  
foreach my $codon (keys %genetic_code){  
  print "$codon -- $genetic_code{$codon}\n";  
}  
  
CCA -- Pro  
ATG -- Met
```

Use exists() to test if a key exists.

```
my %genetic_code = (  
  "ATG" => "Met",  
  "AAA" => "Lys",  
  "CCA" => "Pro",  
);
```

key exists?	return value
yes	1
no	' ' empty string is false

```
my $codon = "ATG";  
if (exists $genetic_code{$codon}){  
  print "$codon -- $genetic_code{$codon}\n";  
}else{  
  print "key: $codon does not exist\n";  
}  
  
ATG -- Met  
##when $codon= "TTT", code prints "key: TTT does not exist"
```

Auto increment hash values

Auto increment scalars:

```
my $num = 1;
print $num , "\n"; #prints 1
$num++;           #same as $num=$num +1;
print $num , "\n"; #prints 2
```

Auto increment hash values:

```
my %hash;
$hash{books} = 0;
print $hash{books}, "\n"; #prints 0
$hash{books}++; #same as $hash{books} = $hash{books} + 1
print $hash{books} , "\n"; #prints 1
```

nothing + 1 equals 1

```
my %hash;
```

```
$hash{books} = 0;
print $hash{books}, "\n";
```

```
$hash{books}++;
print $hash{books} , "\n"; # prints 1
```

**When we first start, the key 'books' doesn't exist.
We try to add 1 to nothing, so the total is 1.**

Using hashes for keeping count

```
my $seq = "ATGGGCGTATGCAATT";
my @nucs = split "", $seq;
print "@nucs\n";
#A T G G G C G T A T G C A A T T

my %nt_count;
foreach my $nt (@nucs){
    $nt_count{$nt}++;
}

foreach my $nt (keys %nt_count){
    my $count = $nt_count{$nt};
    print "$nt\t$count\n";
}

A      4
T      5
C      2
G      5
```

Creating a hash from variable input like data from a file

```
my $file = shift;
open (my $in_file, '<', $file)
    or die "can't open file $file $!\n";
my %hash;
while (my $line = <$in_file>){
    chomp $line;
    my ($key, $value) = split /\t/, $line;
    $hash{$key} = $value;
}
foreach my $key (sort keys %hash){
    my $value = $hash{$key};
    print "key:$key value:$value\n";
}
```