Perl for Biologists

Session 5

April 1, 2015

Hashes

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Review of Session 4

- Array explicit declaration

```
@array = (1, 5, "a", 77, "abcd", 99);
```

- Array range declaration

```
@array = 1..9;
```

- Array quoted word declaration

```
@array = qw(jon zhang perl 2013);
@array = qw*jon zhang perl 2013*;
```

Review of Session 4

- Array access

```
@array = (1, 5, "a", 77, "abcd", 99);
print $array[0]; # prints "1"
print $array[4]; # prints "abcd"
print $array[5]; # prints "99"

$i = 3;
print $array[$i]; # prints "77"
```

Review of Session 4

```
@array = (1, 5, "a", 77, "abcd", 99);
```

- push (@array, $value): Appends $value to the end of @array

```
$value = 88;
push (@array, $value);
print $array[6]; # prints "88"
```

- $value = pop (@array): Removes last element of @array, sets $value to the removed element

```
$value = pop (@array);
print $value; # prints "88"
```

Review of Session 4

```
@array = (1, 5, "a", 77, "abcd", 99);
```

- $value = shift (@array): Removes first element of @array, sets $value to the removed element

```
$value = shift (@array);
print $value; # prints "1"
print $array[0]; # prints "5"
```

- unshift (@array, $value): Adds $value to the front of @array, all other elements shifted back one index

```
$value = 1;
unshift (@array, $value);
print $array[0]; # prints "1"
```

Review of Session 4

```
@array = (1, 5, "a", 77, "abcd", 99);
```

- @reverse_array = reverse @array: Sets @reverse_array as a reverse order @array

```
@reverse_array = reverse (@array);
print $reverse_array[0]; # prints "99"
```

- @sorted_array = sort @array: Sets @sorted_array as an ACSII sorted @array

```
@sorted_array = sort @array;
print $sorted_array[5]; # prints "abcd"
```

Review of Session 4

```
@array = (5, 7, 23, 8, 1, 4);
```

- @sorted_array = sort {$a <=> $b} @array: Sets @sorted_array as a numeric sorted @array

```
@sorted_array = sort {$a <=> $b} @array;
print $sorted_array[0]; # prints "1";
print $sorted_array[5]; # prints "23";
```

Review of Session 4

```
@array = (1, 5, "a", 77, "abcd", 99);
```

- @spliced_array = splice (@array, $start_index): Removes everything @array starting at $start_index, and returns it to @spliced_array

```
$start_index = 3;
@spliced_array = splice (@array, $start_index);
print $spliced_array[0]; # prints "abcd";
```

Review of Session 4

- @spliced_array = splice (@array, $start_index, $length): Removes $length elements from @array starting at $start_index, and returns it to @spliced_array

- @spliced_array = splice (@array, $start_index, $length, @replacement): Removes $length elements @array starting at $start_index, and returns it to @spliced_array. Replaces removed with @replacement

Review of Session 4

- @string_array = split /pattern/, $string

```
$string = "1-800-123-4567";
@number_parts = split /-/, $string;
print "$number_parts[0]"; # prints "1“
print "$number_parts[3]"; # prints "4567"
```

Review of Session 4

- The Foreach loop

```
foreach $element (@number_parts)
{
       print "$element\n";
}
```

Exercise Review

A. Modify the program from session 3 exercise 3 (random DNA sequence) to produce a random DNA sequence of 5 Mb (originally 4.1kb), store the sequence string in a variable and discard the rest of the program (the part printing it to STDERR).

```
for($i=1; $i<=5_000_000; $i++)
```

B. Take the random DNA string obtained in step 1 and apply *in silico* restriction enzyme by cutting the DNA at each occurrence of the pattern of "ATGCAT" . The easiest way to do it is to use `split` function with ATGCAT as the splitting pattern, store the DNA fragments in an array.

```
@fragments = split /ATGCAT/, $seq;
```

Exercise Review

C. Create a new array containing lengths of the strings from the array obtained in step 2 (`length($str)` function returns the length of a string `$str`). Unlike the real restriction enzyme, `split` function removes ATGCAT pattern, to correct for this you need to add 6 to each middle fragment, 1 to first and 5 to the last (simulating cutting A{cut}TGCAT).

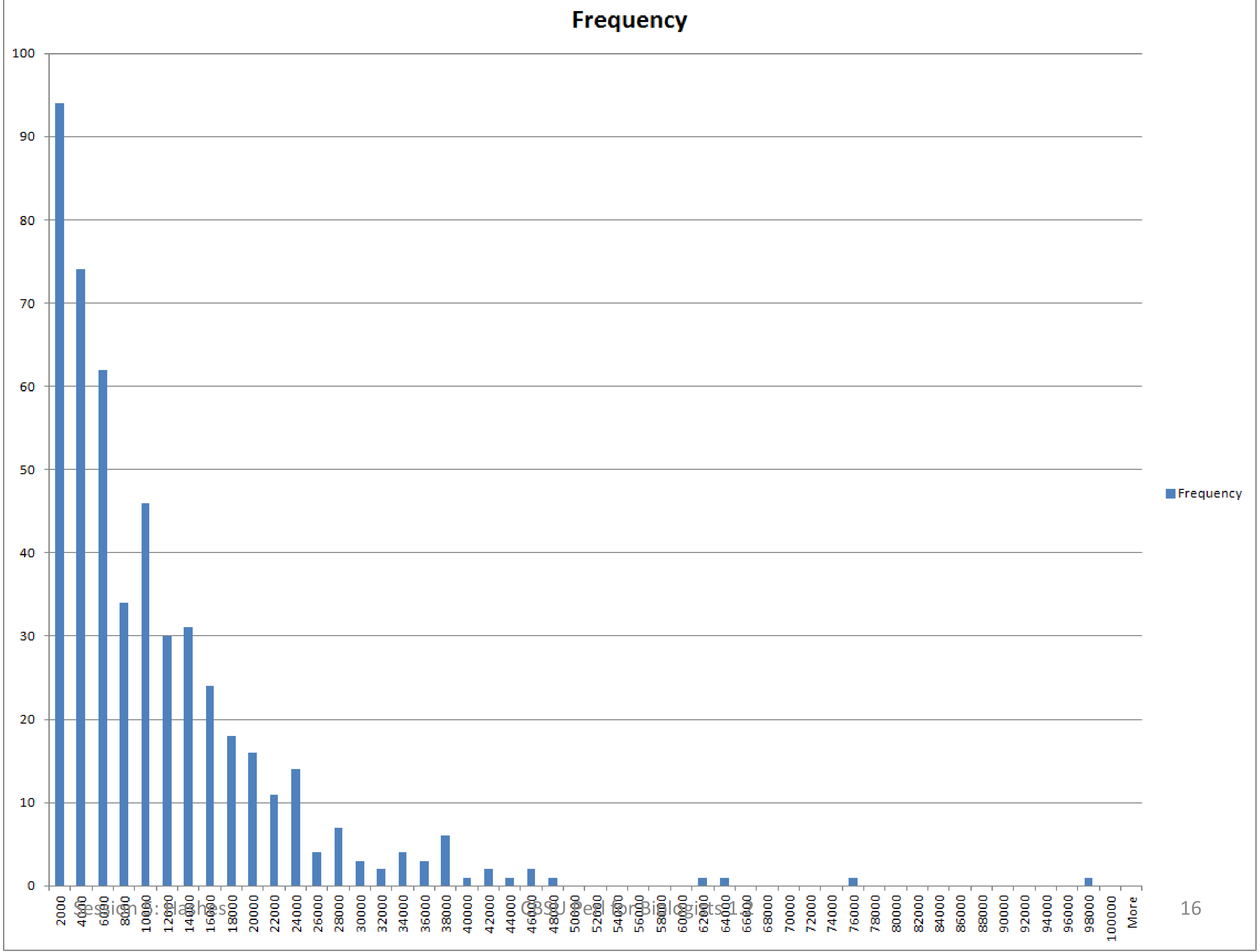
Exercise Review

```
$n=0;
foreach $frg (@fragments)
{
    if($n==0)
    {
        $fraglen[$n] = length($frg) + 1;
    }
    elsif($n==$#fragments)
    {
        $fraglen[$n] = length($frg) + 5;
    }
    else
    {
        $fraglen[$n] = length($frg) + 6;
    }
    $n++;
}
```

Exercise Review

D. Sort the lengths array. Remember that `sort` function by default sorts in string context (in alphabetical order i.e. 123 comes before 99), you need to provide sorting function to sort numerically :
`sort {$a <=> $b} @array`
Print out the sorted fragment lengths.

```
@fraglen = sort {$a <=> $b} @fraglen;
foreach $frag (@fraglen)
{
    print "$frag\n";
}
```


Frequency
100
90
80
70
60
50
40
30
20
10
0
2000
4000
6000
8000
10000
12000
14000
16000
18000
20000
22000
24000
26000
28000
30000
32000
34000
36000
38000
40000
42000
44000
46000
48000
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52000
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56000
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62000
64000
66000
68000
70000
72000
74000
76000
78000
80000
82000
84000
86000
88000
90000
92000
94000
96000
98000
100000
More
Frequency

What is a Hash?

Array

Index	Value
0	apple
1	banana
2	cranberry
3	daikon
4	eggplant
5	81

Hash

Key	Value
red fruit	apple
yellow fruit	banana
red berry	cranberry
white tuber	daikon
purple veggie	eggplant
nine squared	81

What is a Hash?

- Data structure similar to an Array.
  - Use to be known as “Associative Arrays”
- Indexed by an arbitrary unique string, the **Key**
- Each **Key** points to an element, the **Value**
- Each **Value** is an arbitrary scalar
- Establish relationship between **Key** and **Value**

What is a Hash?

- **Keys** must be UNIQUE!
- **Keys** are strings!
- Only one **Value** per **Key**!

THERE IS NO "ORDER"!

Hash Syntax

- Declaring a variable to be a Hash, use “%”

```
%hash;
```

- Can initialize a hash using an Array

```
%hash = ('red fruit', 'apple',
  'yellow fruit', 'banana', 'nine
  squared', 81);
```

Hash Syntax

- Accessing individual Hash element

```
$hash{'red fruit'};
```

- Equivalently

```
$key = 'red fruit';
$hash{$key};
```

Hash Syntax

- Assigning individual Hash element

```
$hash{'purple veggie'} =
  'eggplant';
```

- Can initialize a array using a Hash

```
@array = %hash;
```

The Big Arrow

=>

- Also known as “The Fat Comma”
- A way to “spell” a comma
- Simplifies Hash Declaration

The Big Arrow

```
%hash = (
        'red fruit'       => 'apple',
        'yellow fruit'    => 'banana',
        'red berry'       => 'cranberry',
        'white tuber'     => 'daikon',
        'purple veggie'   => 'eggplant',
        'nine squared'    => 81,
        );
```

Hash Functions

- keys(%hash): returns an Array of the Keys

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

- values(%hash): returns an Array of the Values

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

Hash Functions

- Order of elements is consistent between arrays returned for Keys and Values
- First element of Keys will be the key to the hash that returns the first element of Values

Hash Functions

- exists($hash{$key}): returns true if $key exists in the hash

```
exists ($hash{$key1});
exists $hash{$key1};
```

- defined($hash{$key}): returns true if $key has a defined Value in the hash

```
defined ($hash{$key1});
defined $hash{$key1};
```

Hash Functions

- delete($hash{$key}): deletes $key and associated Value from the hash

```
$hash{'green fruit'} = 'kiwi';
delete ($hash{'green fruit'});
```

- reverse(%hash): returns Hash with Keys and Values swapped

```
%reverse_hash = reverse (%hash);
%reverse_hash = reverse %hash;
```

Hash Functions

- each(%hash): returns the next Key Value pair as a 2 element array

```
@pair = each (%hash);
print "$pair[0] = $pair[1]\n";
```

Hash Functions

- Lets use a while loop to go through the rest of the hash using the Each function

```
while (@pair = each (%hash))
{
    print "$pair[0] = $pair[1]\n";
}
```

Hash Foreach

- Just like for an array, you can use a foreach loop to look through a hash

```
foreach $key (keys %hash)
{
    print "$key = $hash{$key}\n";
}
```

Hash Sort

- What if we want to order a hash? Sort the keys!

```
foreach $key (sort keys (%hash))
{
    print "$key = $hash{$key}\n";
}
```

Hash Sort

- More likely we'll want to sort by value

```
foreach $key (sort {$hash{$a} <=> $hash{$b}} keys (%hash))
{
    print "$key = $hash{$key}\n";
}
```

Hash Nuances

- **Keys** are strings, perl will convert if otherwise

```
%hash = (
      'red fruit'     => 'apple',
      'yellow fruit'  => 'banana',
      'nine squared'  => 81,
      5/2             => '5 over 2',
      );
print "->$hash{'5/2'}<-\n";
print "$hash{'2.5'}\n";
```

Hash Nuances

- **Keys** are unique, you will lose data if you try to assign more than one **Value** to a **Key**

```
$hash{'red fruit'} = 'cherry';

print "$hash{'red fruit'}\n";
```

Hash Nuances

- Declare a new **Key** and modify it in one line

```
$hash{'test int'} += 1;
print "$hash{'test int'}\n";

$hash{'test string'} .= 'Hello
  World!';
print "$hash{'test string'}\n";
```

Hash Nuances

- Reverse function can cause you to lose data

```
%hash = (
      'red fruit'              => 'apple',
      'technology company' => 'apple',
      );
%reverse_hash = reverse (%hash);
while (@pair = each (%reverse_hash))
{
    print "$pair[0] = $pair[1]\n";
}
```

The Environment Hash

- Perl runs in a certain environment
- Most cases this will be linux
- %ENV hash contains information about the environment that the perl program is running in

The Environment Hash

```
foreach $key (keys %ENV)
{
    print "$key\n";
}

print "$ENV{'PATH'}\n";
```

- Now lets set a new environment variable and try to access it

Hash Example

- Lets redo part D of last week's exercise with hashes
- List out the steps that we need to take to make bins to use in Excel to make a histogram
  - Create a hash where Keys are bins and values are bin counts
  - Go through the list of fragment lengths adding one to the correct bin
  - Print out results in order of bin

Hash Example

- Creating a the hash table with correct bin values
- Bin values are multiples of 2000 up to 100,000

Hash Example

```
$bin = 2000;
while ($bin <= 100000)
{
    $bin_counts{$bin} = 0;
    $bin += 2000;
}
```

Hash Example

- Traverse through the fragment length array, adding to the correct bin

```
foreach $element (@fraglen)
{
    $this_bin = 2000 * int($element/2000) + 2000;
    $bin_counts{$this_bin}++;
}
```

Hash Example

- Print the results in order of bin

```
foreach $key (sort {$a <=> $b} keys %bin_counts)
{
    print "$key\t$bin_counts{$key}\n";
}
```

Exercises

1. Modify the code from session 3 exercise 3 to generate a 9kb long random DNA sequence. Save this sequence to a variable.
2. Create a hash where the keys are unique sequences of 3 base pairs and the values are the counts of how often the key appeared in the randomly generated sequence. Print out/save to a file these keys and values

- There are numerous ways to accomplish creating the hash from the string, a few hints:
  – Look at the substring function from Session 2
  – Modify the creation of the sequence string, look at the split function from Session 4, and the % (mod) operator

Exercises

- Bonus: Print out/save keys and values sorted by values in decreasing order

- Person with the most number (at least 3) of distinct methods of populating a hash from a string wins 50 FREE CBSU computing hours!