CANB7640
Practical Workshop
Class 01

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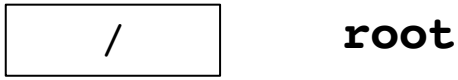
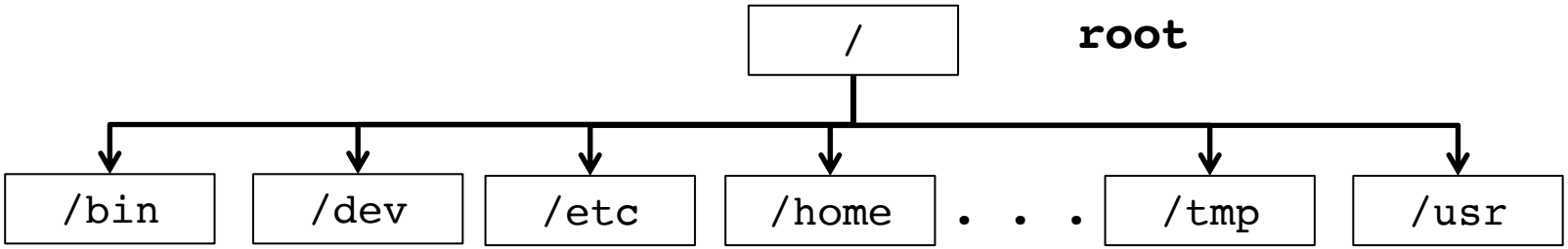
http://tanlab.ucdenver.edu/labHomePage/teaching/CANB7640/

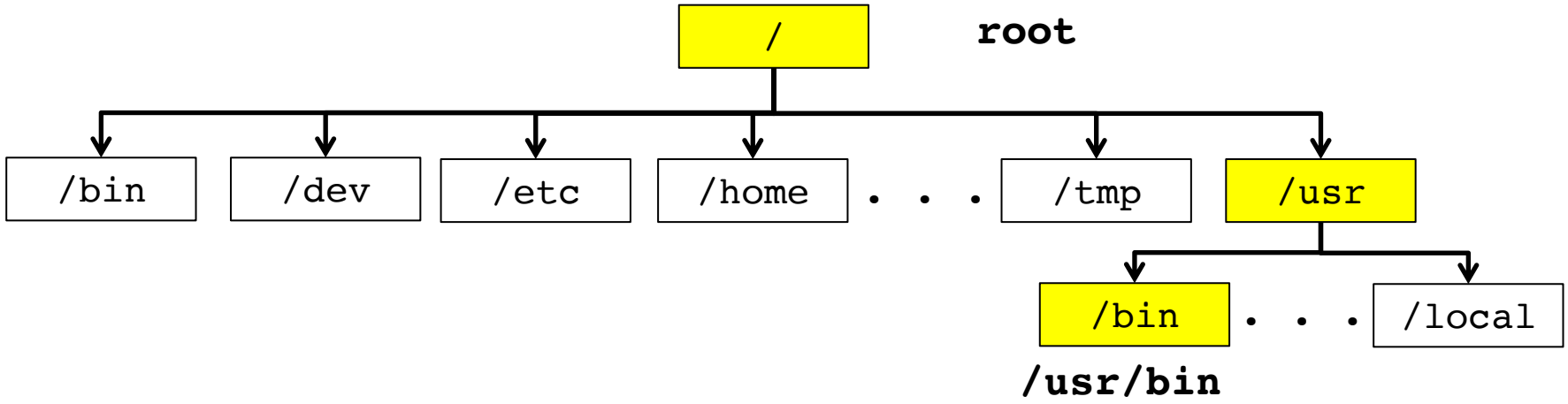
Unix Directory Structure



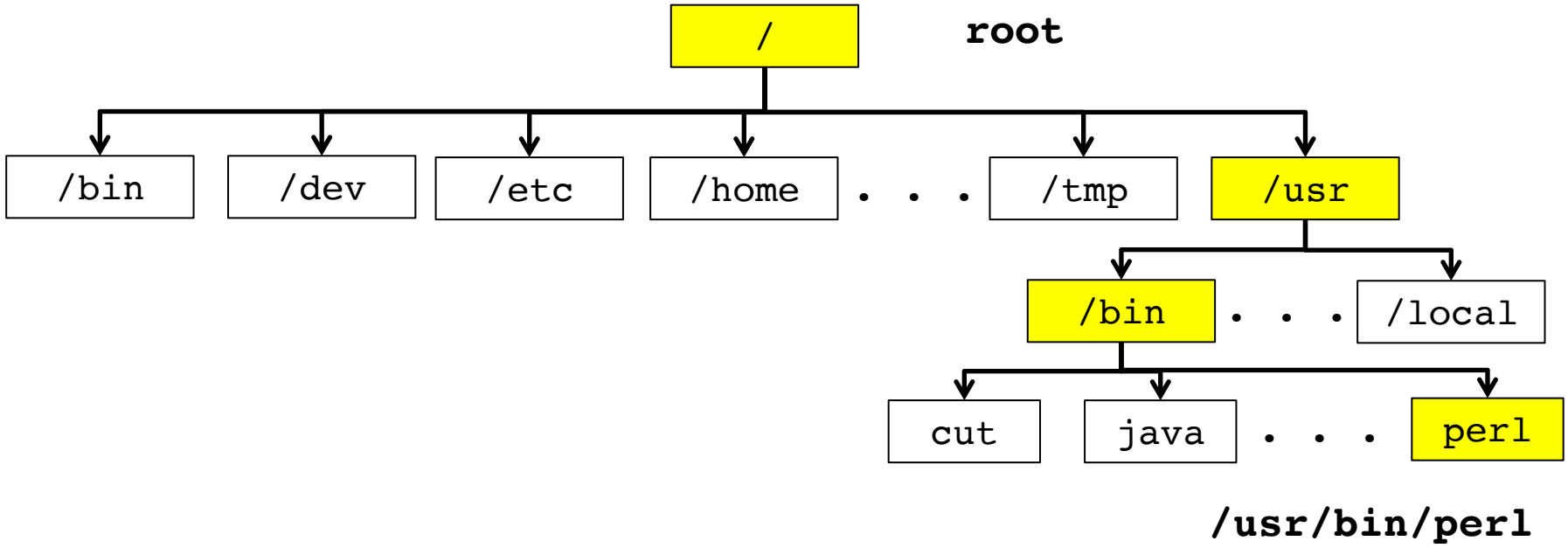
Unix Directory Structure



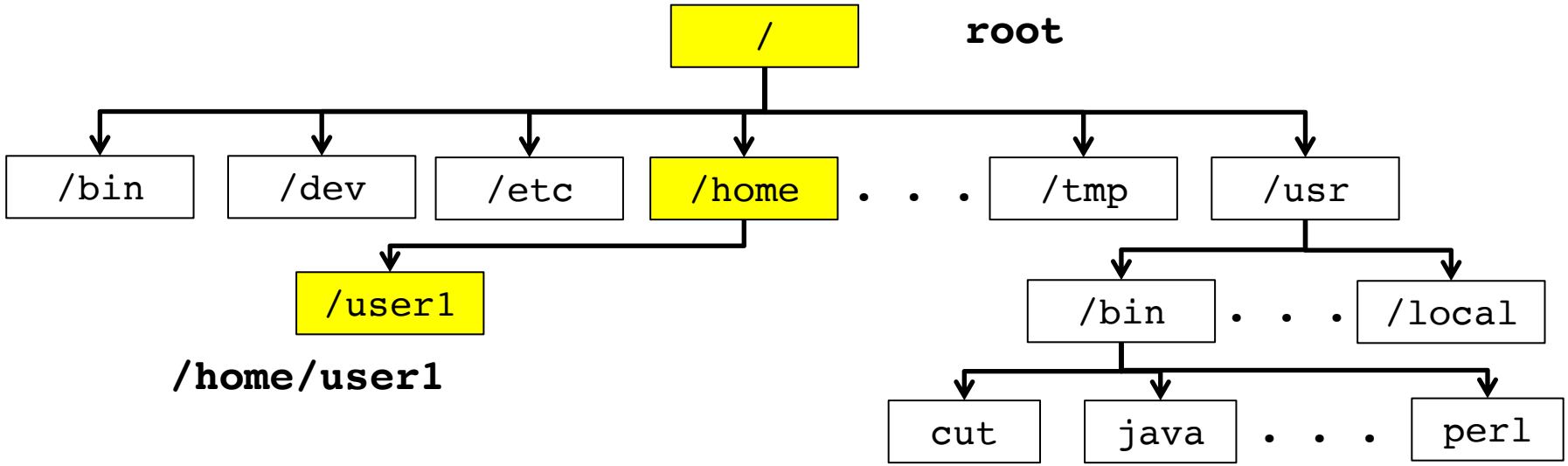
Unix Directory Structure



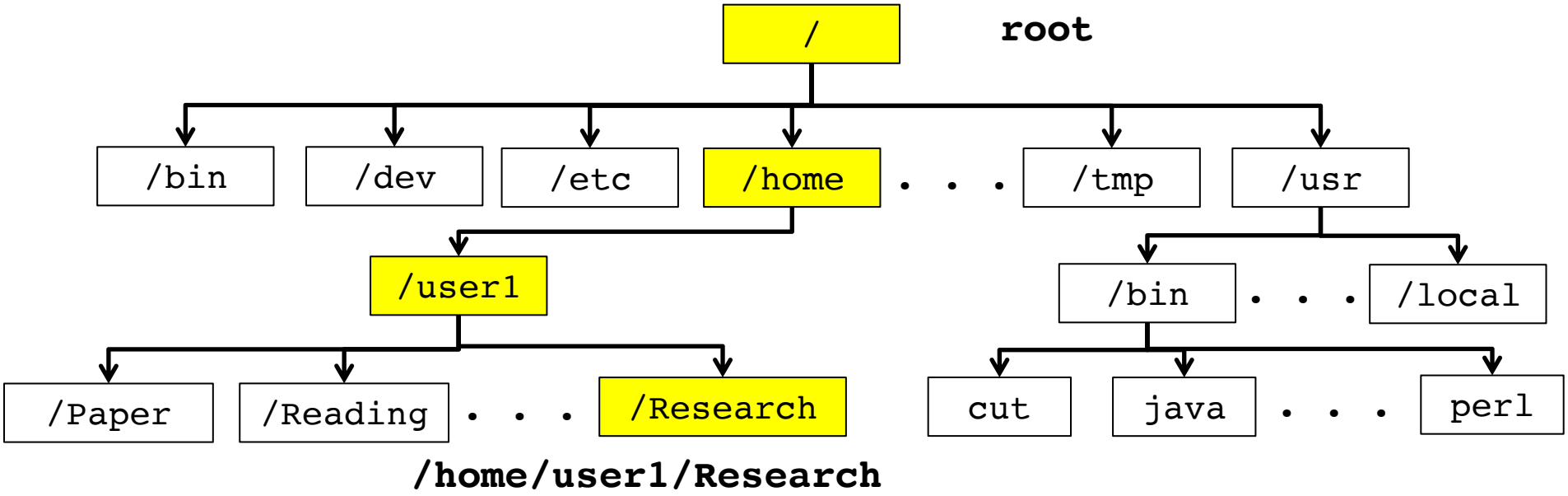
Unix Directory Structure



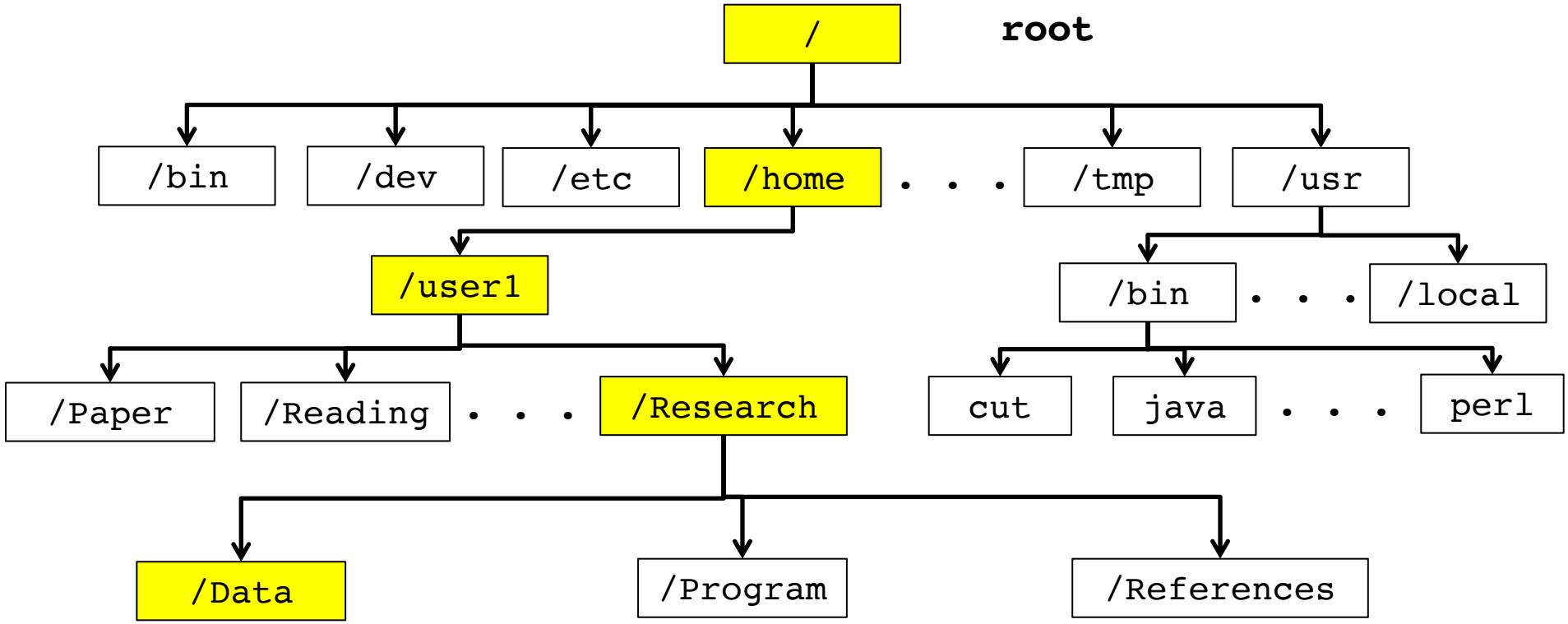
Unix Directory Structure



Unix Directory Structure

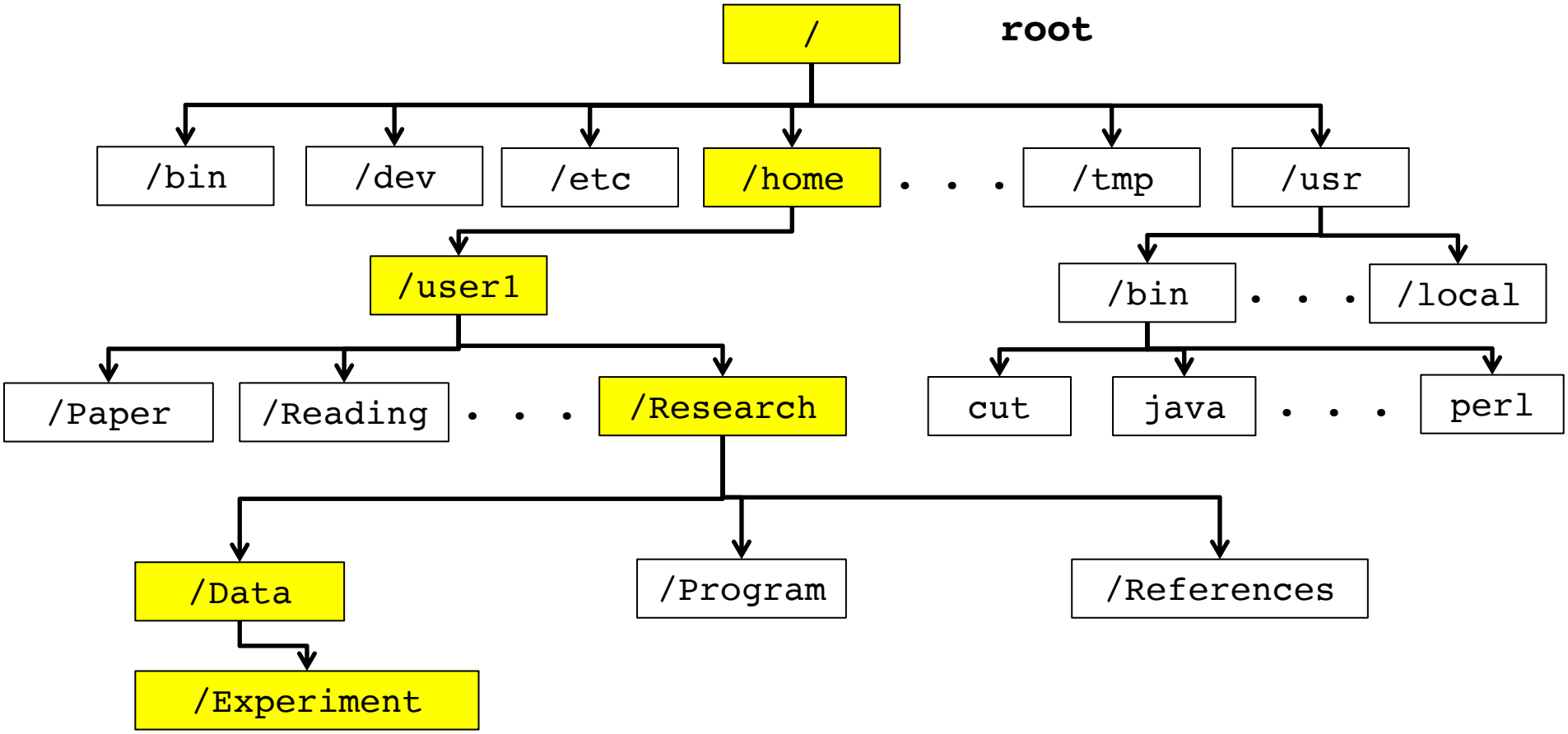


Unix Directory Structure



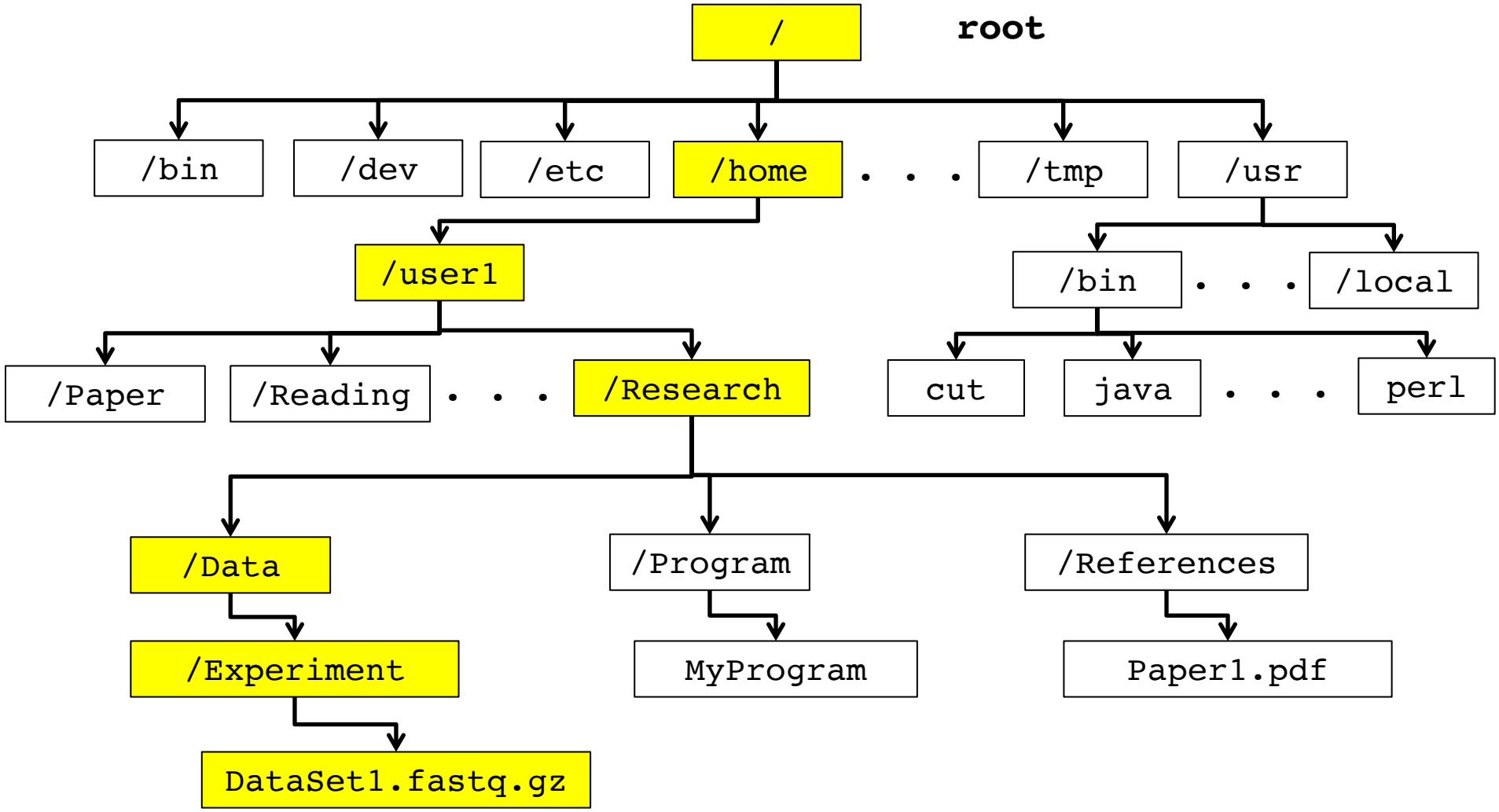
/home/user1/Research/Data

Unix Directory Structure



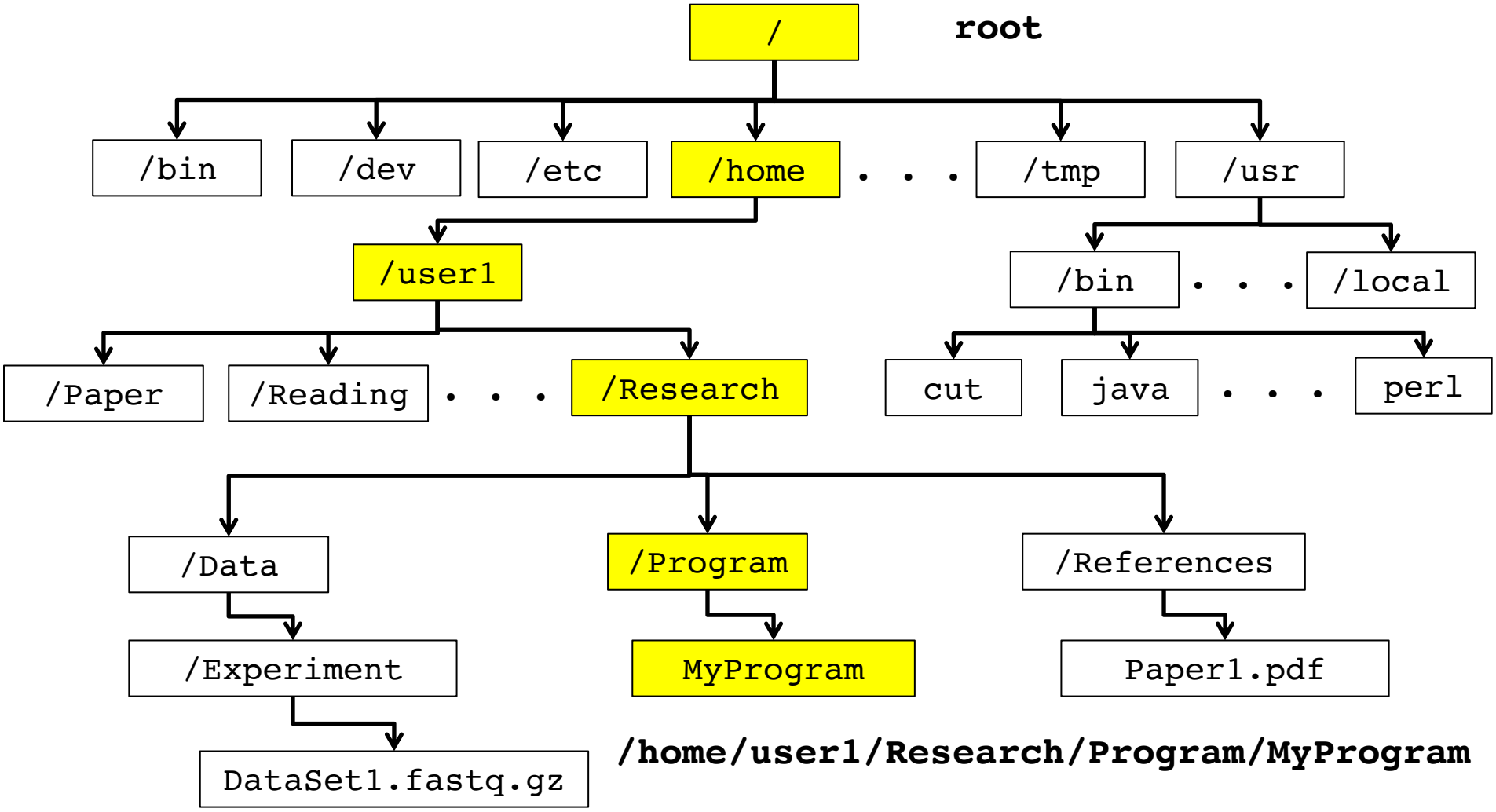
/home/user1/Research/Data/Experiment

Unix Directory Structure

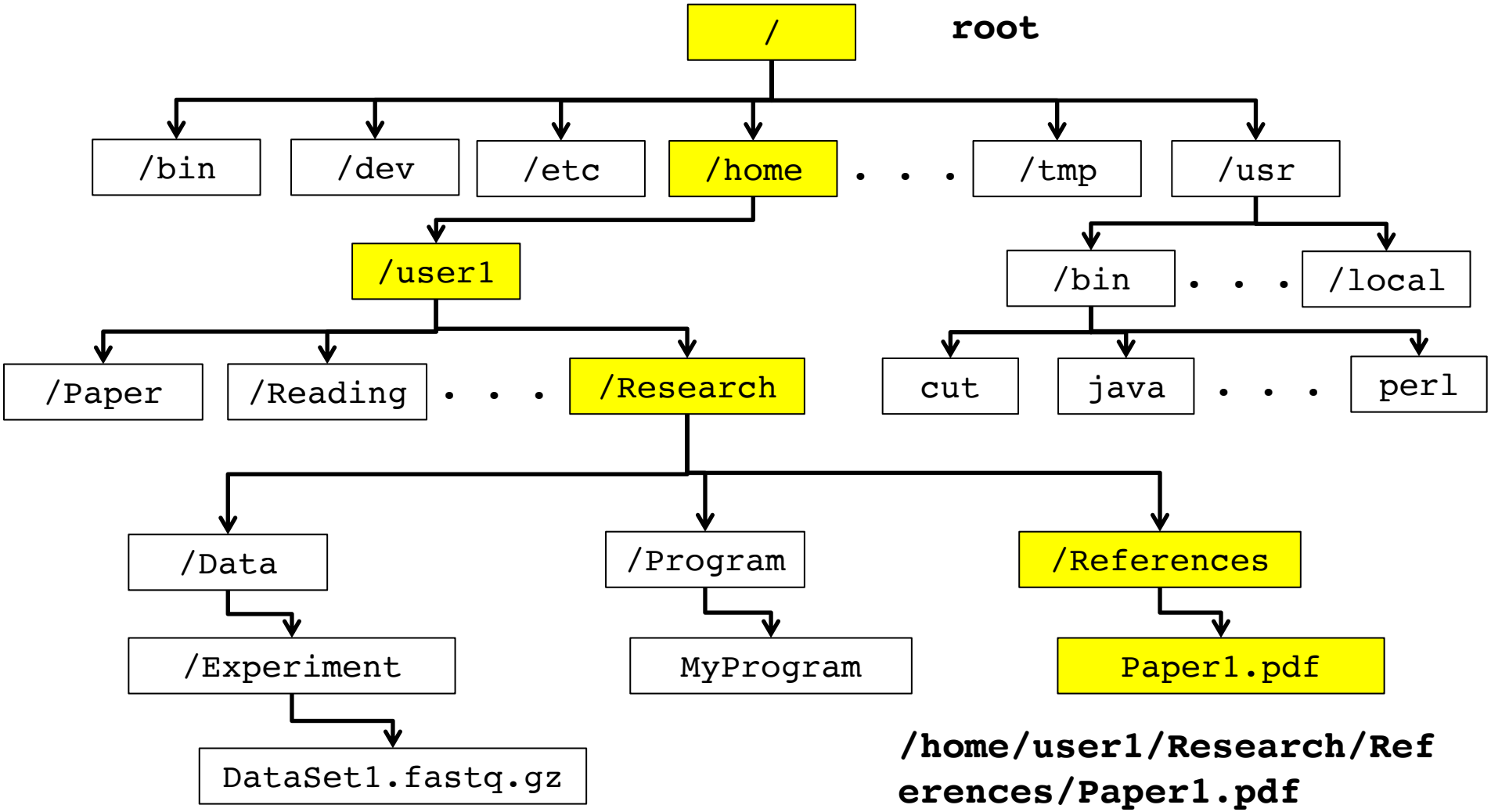


/home/user1/Research/Data/Experiment/DataSet1.fastq.gz

Unix Directory Structure



Unix Directory Structure



Practical

- In your terminal, type

```
pwd
```

What is your current working directory?

Practical

- change your directory to root

```
cd /
```

- List out the contents in root

```
ls
```

- Now, change your directory to `/bin`

- List out the contents in `/bin`

Practical

- change your directory back to your working directory

```
cd
```

- List out the contents in your directory

```
ls
```

- Now, make a new directory name **CANB7640** using `mkdir`

- Make a new directory **CLASS01** in **CANB7640** folder using `mkdir`

Practical

- change your directory back to your working directory

```
cd
```

- List out the contents in your directory

```
ls
```

- Now, make a new directory name **CANB7640** using `mkdir`

- Make a new directory **CLASS01** in **CANB7640** folder using `mkdir`

Practical

- Copy **HG-U133_Plus_2.na32.chip** to **CLASS01** folder

Use `cp`

- Count how many lines in **HG-U133_Plus_2.na32.chip** file

Use `wc`

- Check the **HG-U133_Plus_2.na32.chip** file

Use `more`

- how many columns in **HG-U133_Plus_2.na32.chip** ?

Practical

- Print out the top 5 lines of **HG-U133_Plus_2.na32.chip** file

Use `head`

- Print out the last 15 lines of **HG-U133_Plus_2.na32.chip** file

Use `tail`

Practical

- Extract the GeneSymbol column of **HG-U133_Plus_2.na32.chip** file and output to **Gene.txt**

Use `cut`

- Sort the file in **Gene.txt** (ascending, A - Z)

Use `sort`

- Then sort the file in **Gene.txt** (descending, Z - A)

Use `sort`

Practical

- Extract the *Gene Symbol* column of **HG-U133_Plus_2.na32.chip** file and output to **Gene.txt**

Use `cut`

- Sort the file in **Gene.txt** (ascending, A - Z)

Use `sort`

- Then sort the file in **Gene.txt** (descending, Z - A)

Use `sort`

Practical

- Count the unique *Gene Symbol* in **Gene.txt** and output as **UniqueGene.txt**

Use `sort` and `uniq`

- How many unique Gene Symbols?

Practical

- Count the unique *Gene Symbol* in **Gene.txt** and output as **UniqueGene.txt**

Use `sort` and `uniq`

- How many unique Gene Symbols?

Practical

- Print out WNT-family genes from **UniqueGene.txt** and output as **GREP_WNT.txt**

Use `grep`

- How many WNT-family genes ?

Practical

- Now write a perl script to print out WNT-family genes from **UniqueGene.txt** and save as **PERL_WNT.txt**

PrintGene.pl

```
#! /usr/bin/perl -w


while (<>)
{
        @temp = split(/\t/);
        chomp @temp;

        if ($temp[0] =~ "WNT*")
        {

                print "$temp[0]\n";
        }
}
```

Practical

- Compare the output from **GREP_WNT.txt** and **PERL_WNT.txt**

Use `comm`

- Do both files contain the same WNT-family genes?

Practical

- Now write a perl script to randomly print out 500 genes from **UniqeGene.txt** and save as **A_LIST.txt**

PrintRandomGene.pl

```
#! /usr/bin/perl -w

@mygenes = (<>);
chomp @mygenes;

$range = 21000;

for ($i = 1; $i <= 500; $i++)
{
$random_number = rand($range);

$int_random_number = int($random_number);

print "$int_random_number\t$mygenes[$int_random_number]\n";
}
```

Practical

- Use the same perl script to randomly print out another 500 genes from **UniqeGene.txt** and save as **B_LIST.txt**

- Compare the two gene lists, **A_LIST.txt** and **B_LIST.txt** and print out the common genes between the two lists (overlapping genes).

Use `comm`

*__HINT:__ need to sort the two lists before you can use `comm` for finding the common genes between the two lists.

Practical

- Try another approach using `cat` and `uniq` commands to find out the common genes between the two lists

Use `cat` and `uniq` (with option –d)

*__HINT:__ need to sort the combined list before you can use `uniq –d` for finding the common genes between the two lists.

Practical

- What about comparing more than two gene lists?
- You need a program

- Write out the pseudocode for finding the common gene lists from two or more files

- **HINT:** need to think about the inputs and outputs, and the data structures (how to store the inputs)

Practical

- Assume these are your three gene lists (A, B, C)

A

GENE1
GENE2
GENE3
GENE4
GENE5

B

GENE1
GENE2
GENE5
GENE6
GENE7
GENE8
GENE9

C

GENE1
GENE10
GENE11
GENE2
GENE4
GENE7

Practical

Data Preprocessing

1. label the source
   - Write a program to do this?

2. combine the lists
   - Write a program to do this?
   - Use command ?

3. Sort
   - Write a program to do this?
   - Use command?

Practical

Label the Source

PrintLabel.pl

```
#! /usr/bin/perl -w

$label = "A";

while (<>)
{
        @tmp = split (/\t/);
        chomp @tmp;

        print "$tmp[0]\t$label\n";

}
```

```
perl PrintLabel.pl < Gene_A_List.txt > Gene_A_List_Label.txt
```

Practical

Label the Source

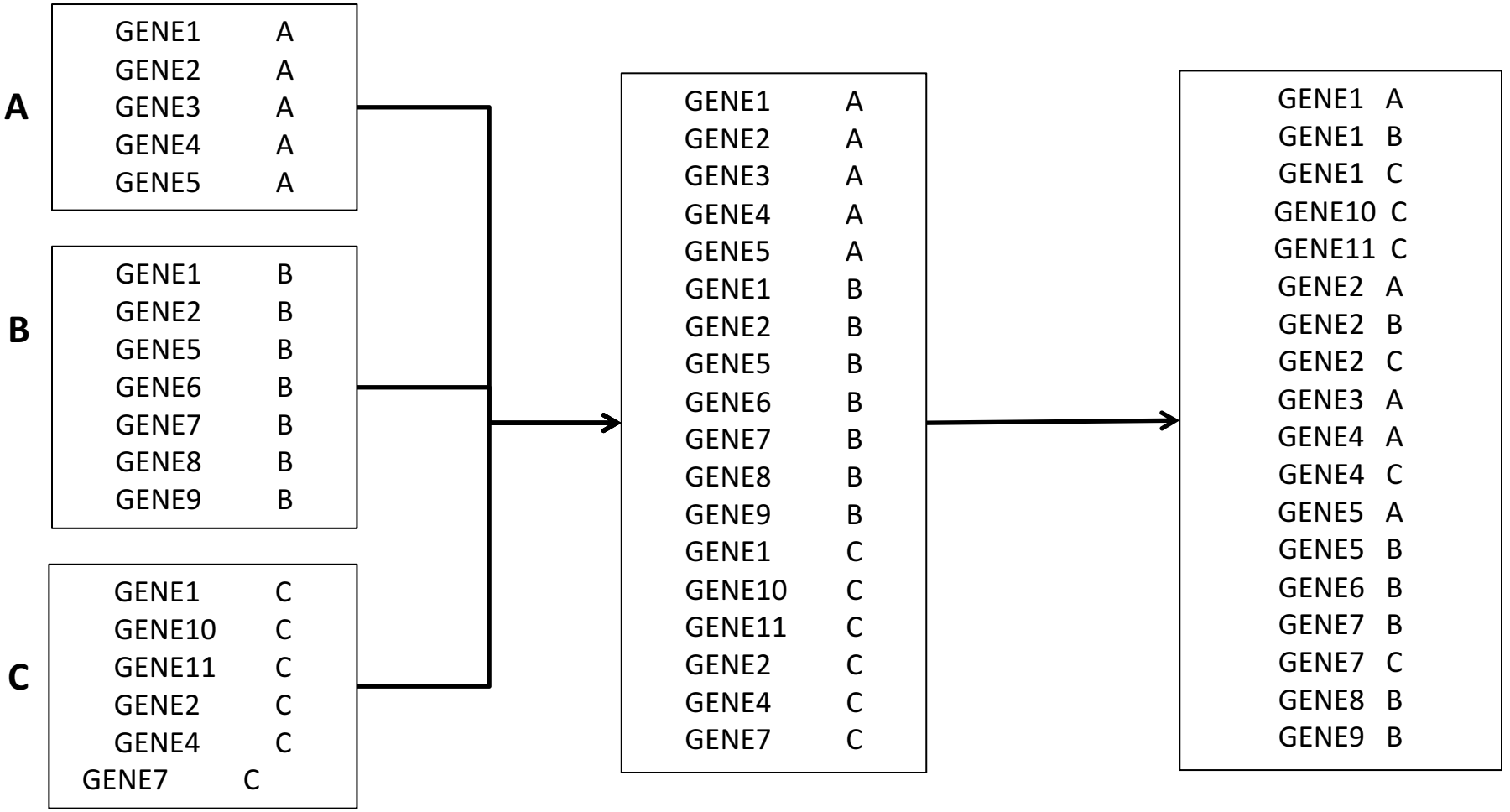
PrintLabel2.pl

```
#! /usr/bin/perl -w

$label = "A";

@list = (<>);

foreach $list(@list)
{
        chomp $list;
        print "$list\t$label\n”;
}
```

```
perl PrintLabel2.pl < Gene_A_List.txt > Gene_A_List_Label.txt
```

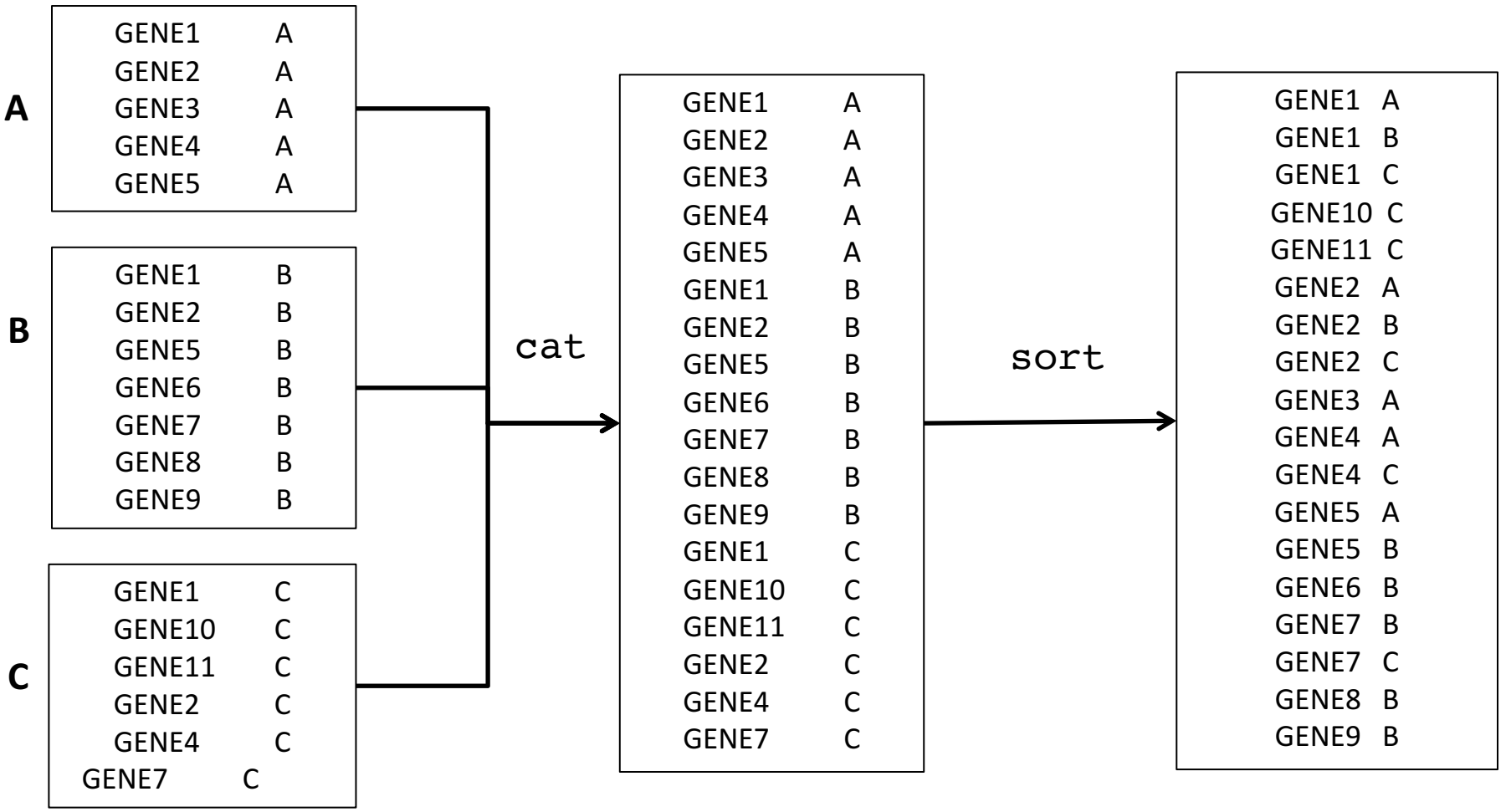
Practical

- label the source, combine the lists and sort



Practical

- labeled the source, combined the lists and sort



Practical

FindCommonGenes.pl

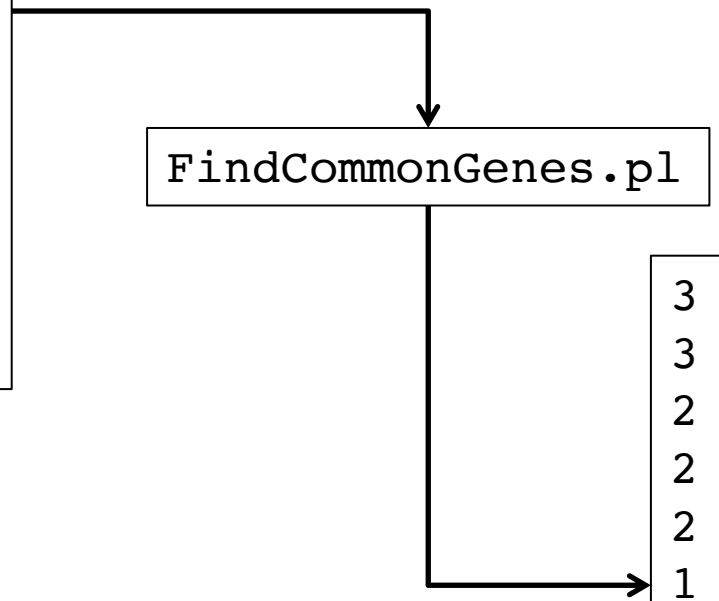
```
#! /usr/bin/perl -w

$count = 0;
while (<>)
{
@data = (split /\t/);
chomp @data;
                $gene_new = $data[0];
                $class_new = $data[1];
                if (exists $gene{$gene_new})
                {
                        push (@class, $class_new);
                        $count++;
                }
                else
                {
                        if ($count == 0)
                        {
                                $gene{$gene_new} = $gene_new;
                                $gene_old = $gene_new;
                                push (@gene, $gene_new);
                                push (@class, $class_new);
                                $count++;
                        }
                        else
                        {
                                print "$count\t$gene_old\t@class\n";
                                @class = ();
                                $gene{$gene_new} = $gene_new;
                                $gene_old = $gene_new;
                                push (@gene, $gene_new);
                                push (@class, $class_new);
                                $count = 1;
                        }
                }
}
```

Practical

input

```
GENE1   A
GENE1   B
GENE1   C
GENE10  C
GENE11  C
GENE2   A
GENE2   B
GENE2   C
GENE3   A
GENE4   A
GENE4   C
GENE5   A
GENE5   B
GENE6   B
GENE7   B
GENE7   C
GENE8   B
GENE9   B
```

```
perl FindCommonGenes.pl < genes_A_B_C | sort -r
```



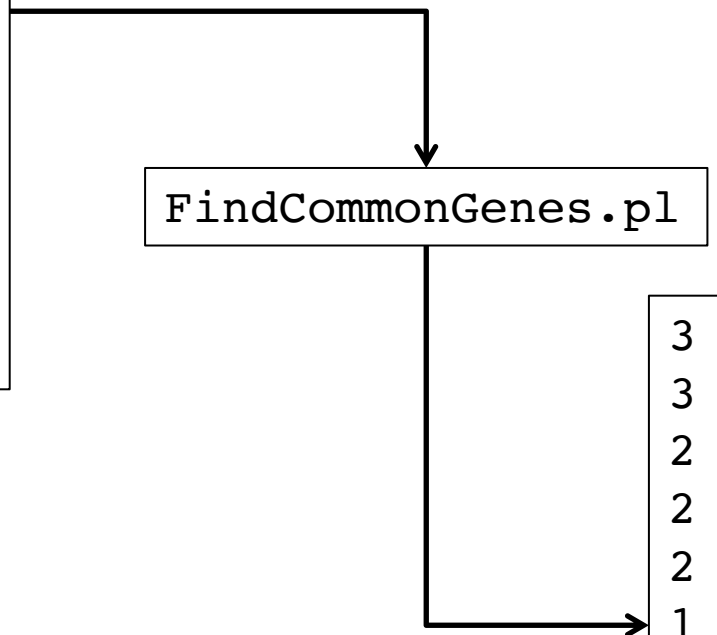
output

```
3   GENE2  A B C
3   GENE1  A B C
2   GENE7  B C
2   GENE5  A B
2   GENE4  A C
1   GENE9  B
1   GENE8  B
1   GENE6  B
1   GENE3  A
1   GENE11 C
1   GENE10 C
```

Practical

```
GENE1   A
GENE1   B
GENE1   C
GENE10  C
GENE11  C
GENE2   A
GENE2   B
GENE2   C
GENE3   A
GENE4   A
GENE4   C
GENE5   A
GENE5   B
GENE6   B
GENE7   B
GENE7   C
GENE8   B
GENE9   B
```

```
perl FindCommonGenes.pl < genes_A_B_C | sort -r
```




```
3   GENE2  A B C
3   GENE1  A B C
2   GENE7  B C
2   GENE5  A B
2   GENE4  A C
1   GENE9  B
1   GENE8  B
1   GENE6  B
1   GENE3  A
1   GENE11 C
1   GENE10 C
```

Practical

Table (List)

3	GENE2	A B C
3	GENE1	A B C
2	GENE7	B C
2	GENE5	A B
2	GENE4	A C
1	GENE9	B
1	GENE8	B
1	GENE6	B
1	GENE3	A
1	GENE11	C
1	GENE10	C

Practical

Table (List)

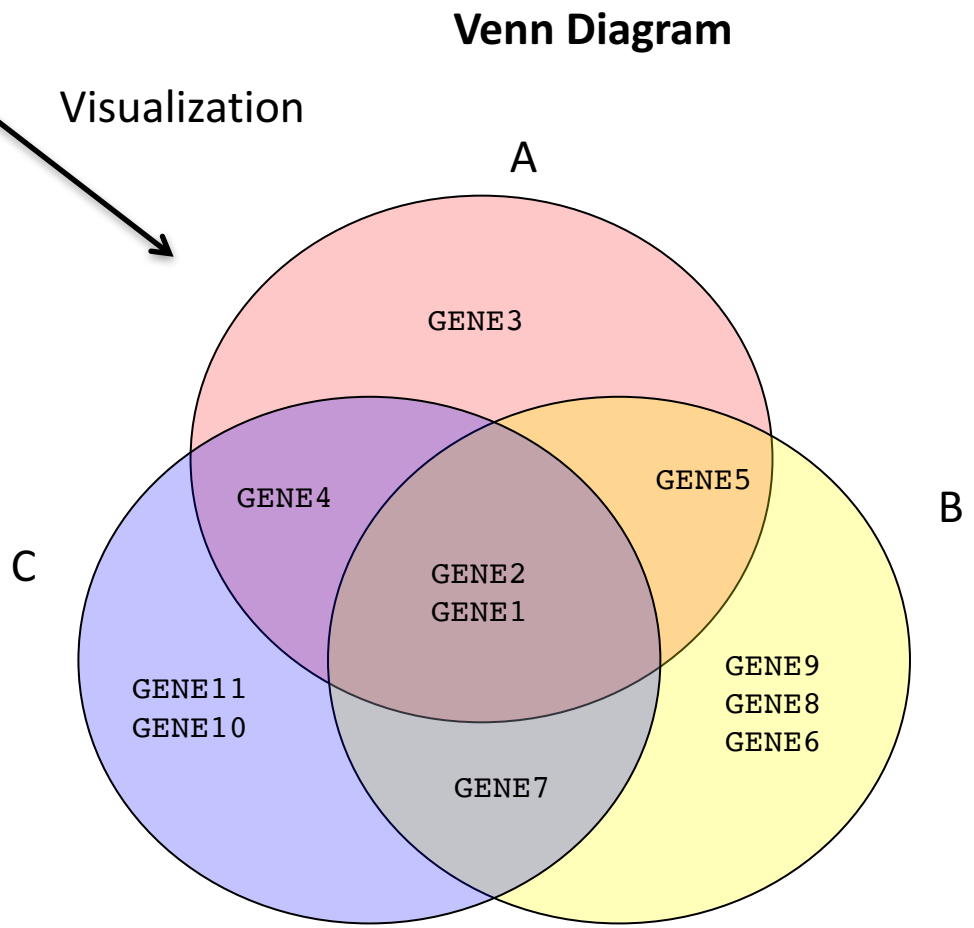
3	GENE2	A B C
3	GENE1	A B C
2	GENE7	B C
2	GENE5	A B
2	GENE4	A C
1	GENE9	B
1	GENE8	B
1	GENE6	B
1	GENE3	A
1	GENE11	C
1	GENE10	C

BORING

Practical

3	GENE2	A B C
3	GENE1	A B C
2	GENE7	B C
2	GENE5	A B
2	GENE4	A C
1	GENE9	B
1	GENE8	B
1	GENE6	B
1	GENE3	A
1	GENE11	C
1	GENE10	C

Visualization

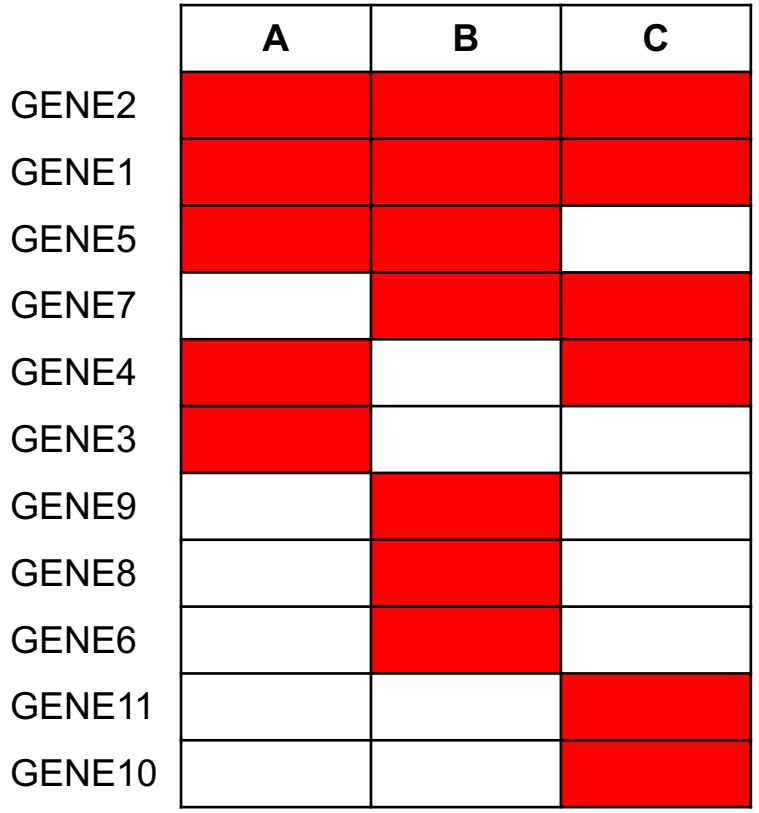


Practical

```
3   GENE2  A B C
3   GENE1  A B C
2   GENE7  B C
2   GENE5  A B
2   GENE4  A C
1   GENE9  B
1   GENE8  B
1   GENE6  B
1   GENE3  A
1   GENE11 C
1   GENE10 C
```

Visualization

Heatmap



Practical

- Try to get the probe sets covering the following genes from the **U133_Plus_2.na32.chip** and output into **MY_PROBESETS.txt**

KRAS

BRAF

MAP2K1

MAK2K2

PIK3CA

- **HINT:** use `grep`

Practical

- Try to get the probe sets covering the following genes from the **HG-U133_Plus_2.na32.chip** and output into **MY_PROBESETS.txt**

KRAS

BRAF

MAP2K1

MAP2K2

PIK3CA

- **HINT:** use `grep`

Practical

RUN_GREP_GENES

```
grep "\bKRAS\b" HG-U133_Plus_2.na32.chip
grep "\bBRAF\b" HG-U133_Plus_2.na32.chip
grep "\bMAP2K1\b" HG-U133_Plus_2.na32.chip
grep "\bMAP2K2\b" HG-U133_Plus_2.na32.chip
grep "\bPIK3CA\b" HG-U133_Plus_2.na32.chip
```

Practical

-rw-r--r-- 1 aikchoontan staff 211 Sep 4 10:20 RUN_GREP_GENES

chmod 777 RUN_GREP_GENES

-rwxrwxrwx 1 aikchoontan staff 211 Sep 4 10:20 RUN_GREP_GENES

./RUN_GREP_GENES

Practical

1559203_s_at	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	KRAS
1559204_x_at	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	KRAS
204009_s_at	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	KRAS
204010_s_at	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	KRAS
214352_s_at	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	KRAS
206044_s_at	v-raf murine sarcoma viral oncogene homolog B1	BRAF
236402_at	v-raf murine sarcoma viral oncogene homolog B1	BRAF
243829_at	v-raf murine sarcoma viral oncogene homolog B1	BRAF
202670_at	mitogen-activated protein kinase kinase 1	MAP2K1
202424_at	mitogen-activated protein kinase kinase 2	MAP2K2
213487_at	Mitogen-activated protein kinase kinase 2	MAP2K2
213490_s_at	mitogen-activated protein kinase kinase 2	MAP2K2
204369_at	phosphoinositide-3-kinase, catalytic, alpha polypeptide	PIK3CA
231854_at	phosphoinositide-3-kinase, catalytic, alpha polypeptide	PIK3CA
235980_at	phosphoinositide-3-kinase, catalytic, alpha polypeptide	PIK3CA

Assignment #1

- Write a **perl** script to do the same

  - Use these in the program:

    `@array`

    `foreach` loop

    `if` loop