

# Lab2\_2

2024-04-12

```
# 5: import code
all.data <- read.csv("cell_infectivity_wide.csv")
# 6: view the data, also done in console
View(all.data)
```

```
# 8,9
f.WT <- all.data$Wild.type.Finch
f.hLDLR <- all.data[, "hLDLR.Finch"]
c.WT <- all.data[["Wild.type.Chicken"]]
c.hLDLR <- all.data[[4]]
# 10
c.WT[5]
```

```
## [1] 1.343797
```

```
c.WT
```

```
## [1] 4.076517 2.046030 3.952518 3.067056 1.343797 4.398596 4.416107 3.243844
## [9] 5.772721
```

```
# second value of f.WT
f.WT[2]
```

```
## [1] 0.197452
```

```
# Section 3, number 11
mean(f.WT)
```

```
## [1] 0.2536965
```

```
# mean of f.hLDLR
mean(f.hLDLR)
```

```
## [1] 2.143759
```

```
# 12
data.means <- colMeans(all.data) # create a vector of group means.
data.means # print the vector
```

| ## | Wild.type.Finch | hLDLR.Finch | Wild.type.Chicken | hLDLR.Chicken |
|----|-----------------|-------------|-------------------|---------------|
| ## | 0.2536965       | 2.1437594   | 3.5907984         | 3.7064355     |

```
# 13, 14
apply(all.data, 2, mean)
```

| ## | Wild.type.Finch | hLDLR.Finch | Wild.type.Chicken | hLDLR.Chicken |
|----|-----------------|-------------|-------------------|---------------|
| ## | 0.2536965       | 2.1437594   | 3.5907984         | 3.7064355     |

```
# 15
# sd function
apply(all.data,2, sd)
```

| ## | Wild.type.Finch | hLDLR.Finch | Wild.type.Chicken | hLDLR.Chicken |
|----|-----------------|-------------|-------------------|---------------|
| ## | 0.07997842      | 1.23324550  | 1.33656421        | 0.88193124    |

```
# var function
apply(all.data,2, var)
```

| ## | Wild.type.Finch | hLDLR.Finch | Wild.type.Chicken | hLDLR.Chicken |
|----|-----------------|-------------|-------------------|---------------|
| ## | 0.006396548     | 1.520894451 | 1.786403894       | 0.777802718   |

```
# min function
apply(all.data,2, min)
```

| ## | Wild.type.Finch | hLDLR.Finch | Wild.type.Chicken | hLDLR.Chicken |
|----|-----------------|-------------|-------------------|---------------|
| ## | 0.1458407       | 0.4487605   | 1.3437965         | 2.4873307     |

```
# max function
apply(all.data,2, max)
```

| ## | Wild.type.Finch | hLDLR.Finch | Wild.type.Chicken | hLDLR.Chicken |
|----|-----------------|-------------|-------------------|---------------|
| ## | 0.3737137       | 4.1256479   | 5.7727210         | 4.8716014     |

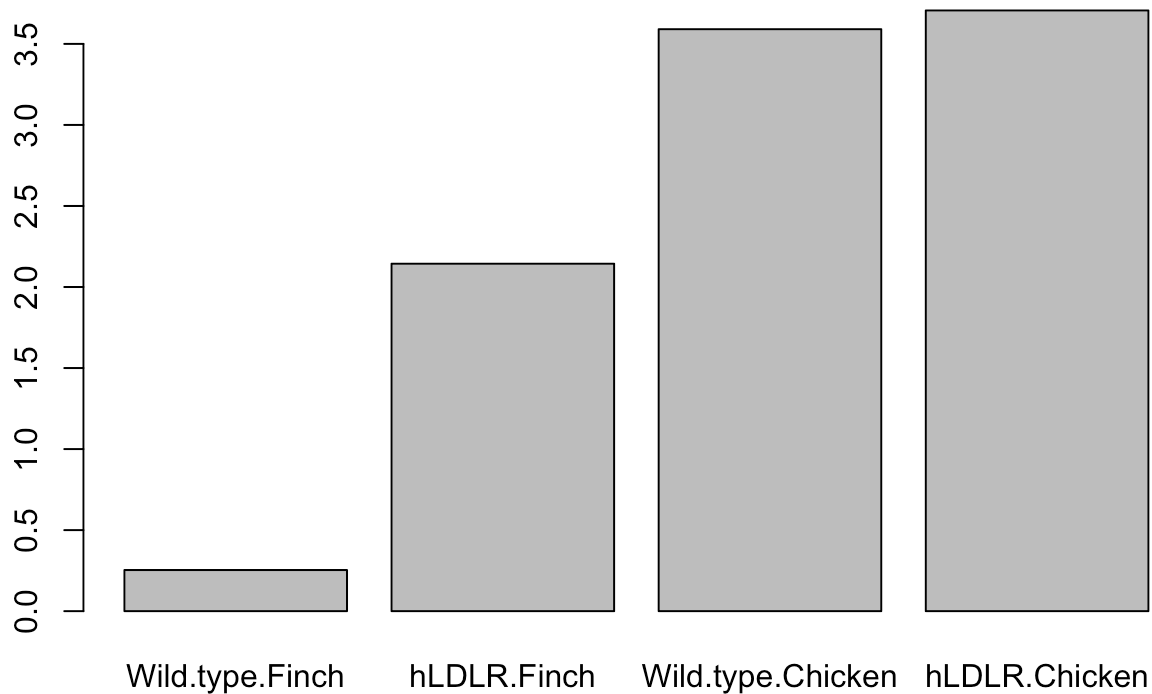
```
# median function
apply(all.data, 2, median)
```

| ## | Wild.type.Finch | hLDLR.Finch | Wild.type.Chicken | hLDLR.Chicken |
|----|-----------------|-------------|-------------------|---------------|
| ## | 0.239245        | 2.067363    | 3.952518          | 3.622098      |

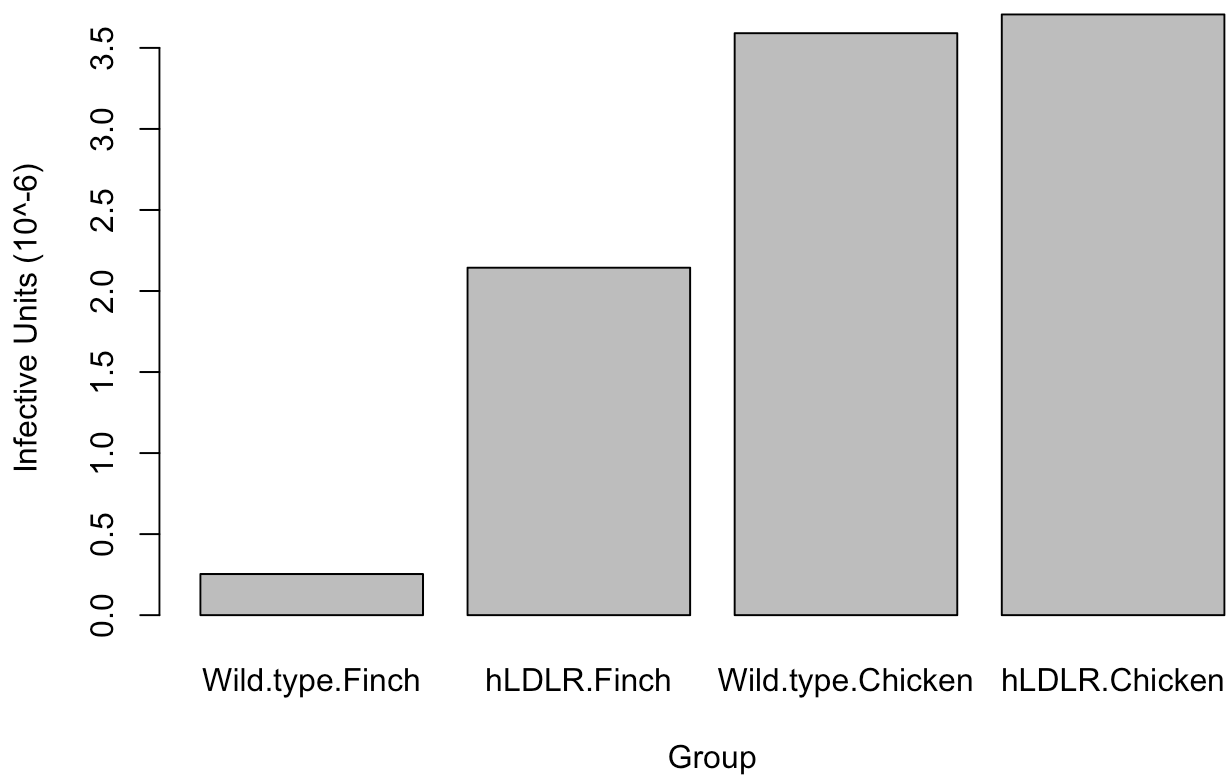
```
# summary function
apply(all.data,2, summary)
```

```
##           Wild.type.Finch hDLR.Finch Wild.type.Chicken hDLR.Chicken
## Min.      0.1458407      0.4487605      1.343797      2.487331
## 1st Qu.    0.1974520      1.4996970      3.067056      3.136610
## Median     0.2392450      2.0673629      3.952518      3.622098
## Mean       0.2536965      2.1437594      3.590798      3.706436
## 3rd Qu.    0.3229060      3.2264398      4.398596      4.596712
## Max.       0.3737137      4.1256479      5.772721      4.871601
```

```
# 16
barplot(data.means)
```



```
# 17
barplot(data.means, ylab = "Infective Units (10^-6)", xlab = "Group")
```



```
# 18
finch <- data.means[1:2]
chicken <- data.means[3:4]
print(finch)
```

```
## Wild.type.Finch    hLDLR.Finch
##      0.2536965      2.1437594
```

```
print(chicken)
```

```
## Wild.type.Chicken    hLDLR.Chicken
##      3.590798        3.706436
```

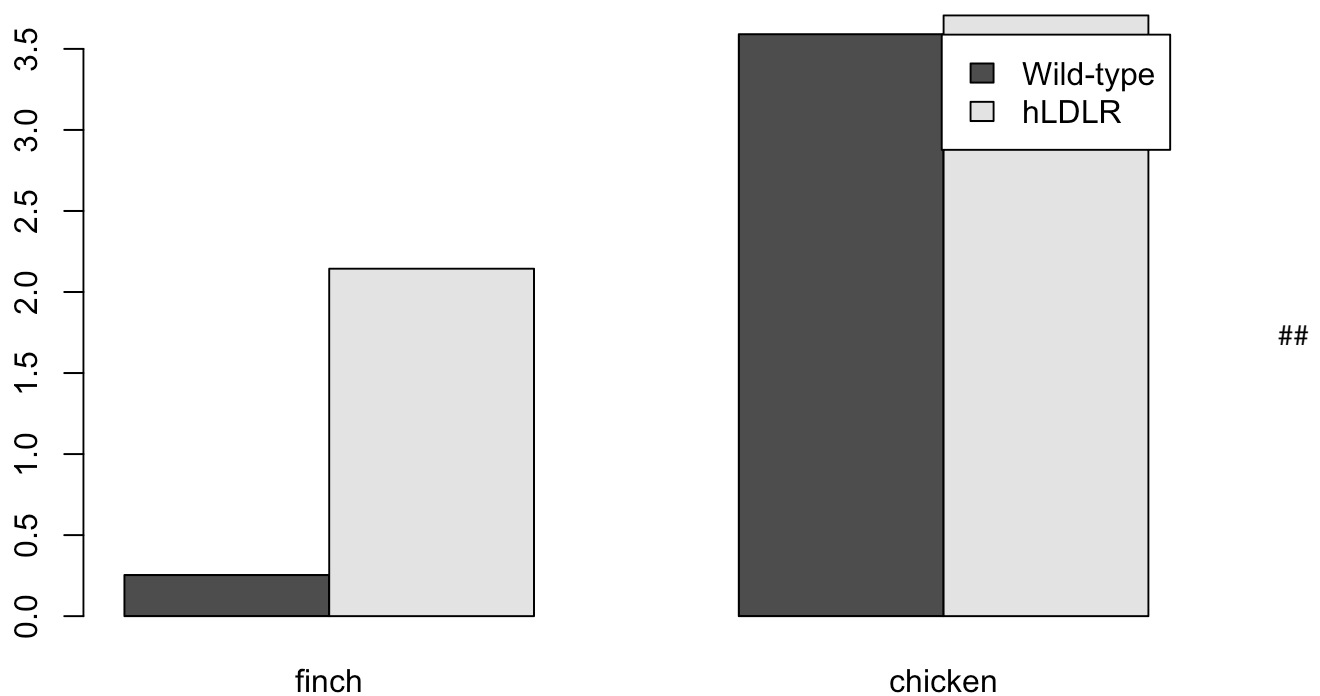
```
# 19
bar.data <- data.frame(finch, chicken)
bar.data
```

```
##              finch  chicken
## Wild.type.Finch 0.2536965 3.590798
## hLDLR.Finch    2.1437594 3.706436
```

```
# 20
rownames(bar.data) <- c("Wild-type", "hLDLR")
bar.data
```

```
##           finch  chicken
## Wild-type 0.2536965 3.590798
## hLDLR     2.1437594 3.706436
```

```
# 21
barplot( as.matrix(bar.data), legend= rownames(bar.data), beside = TRUE)
```



## Section 5: Assessment

### Q1:

1. `all.data$Wild.type.Finch`
2. `all.data[, "Wild.type.Finch"]` or `all.data[ , 1 ]`
3. `all.data[["Wild.type.Finch"]]` or `all.data[[ 1 ]]`
4. `all.data["Wild.type.Finch"]` or `all.data[ 1 ]`

Try out by code:

```
a <- all.data$Wild.type.Finch
b1 <- all.data[, "Wild.type.Finch"]
b2 <- all.data[, 1]
c1 <- all.data[["Wild.type.Finch"]]
c2 <- all.data[[1]]
d1 <- all.data["Wild.type.Finch"]
d2 <- all.data[1]
a == b1
```

```
## [1] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
```

```
a == b2
```

```
## [1] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
```

```
a == c1
```

```
## [1] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
```

```
a == c2
```

```
## [1] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
```

```
a == d1
```

```
##      Wild.type.Finch
## [1,]              TRUE
## [2,]              TRUE
## [3,]              TRUE
## [4,]              TRUE
## [5,]              TRUE
## [6,]              TRUE
## [7,]              TRUE
## [8,]              TRUE
## [9,]              TRUE
```

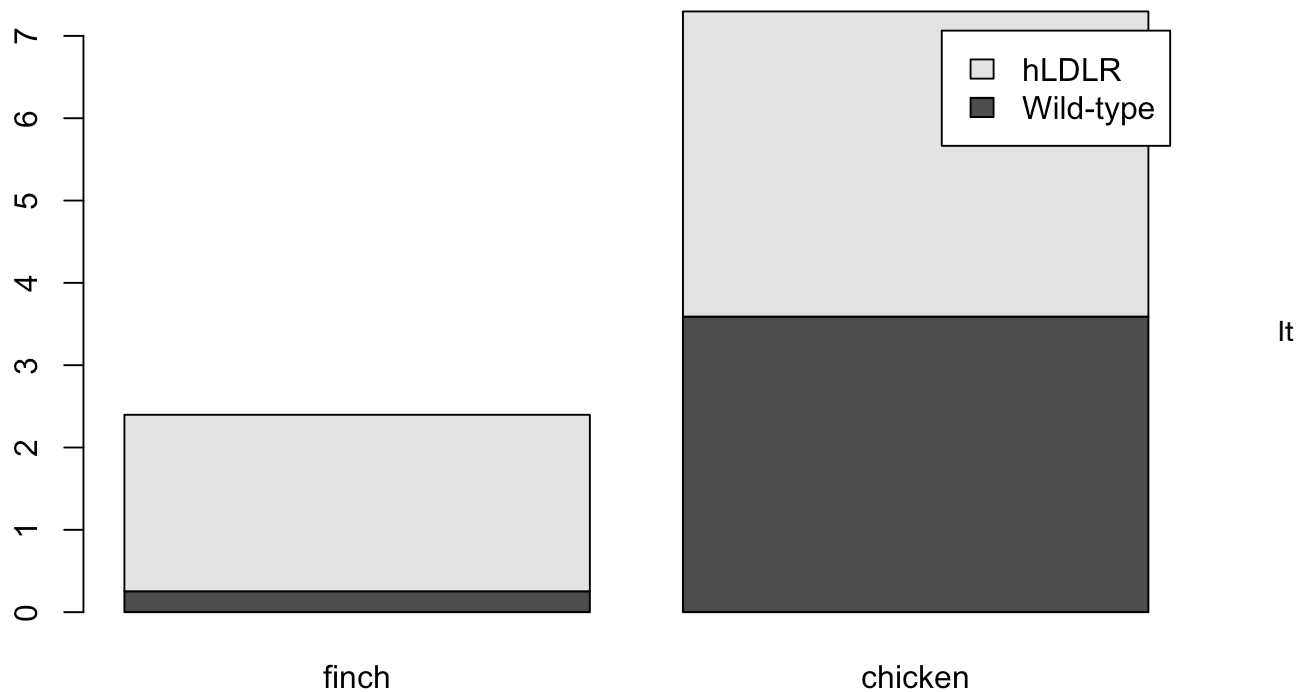
```
a == d2
```

```
##      Wild.type.Finch
## [1,]              TRUE
## [2,]              TRUE
## [3,]              TRUE
## [4,]              TRUE
## [5,]              TRUE
## [6,]              TRUE
## [7,]              TRUE
## [8,]              TRUE
## [9,]              TRUE
```

```
# note only d1 and d2 are in the dataframe format
```

## Q2:

```
barplot( as.matrix(bar.data), legend= rownames(bar.data))
```



seems like instead of having 4 column, we now get 2 columns in total but each column contain 2 different color represent the wild type or hLDLR. Without this code, there seems to have a sub-bars. Thus, the code beside = TRUE will put the value in each column juxtapose instead of stack together.

## Q3:

Null hypothesis[H0]: There is no difference in infectivity (number of infective units) between wildtype and hLDLR zebra finch cells.

Alternative hypothesis[H1]: There is a difference in infectivity (number of infective units) between wildtype and hLDLR zebra finch cells.

## Q4:

1. mean for both finch group

```
finch
```

```
## Wild.type.Finch      hLDLR.Finch
##           0.2536965      2.1437594
```

It is clear that wild type finch has a much smaller mean value compare to the hLDLR finch. Thus, this support that idea that cell type has an effect on infective in zebra finch cells.

2. standard deviation for both finch group

```
apply(all.data,2, sd)
```

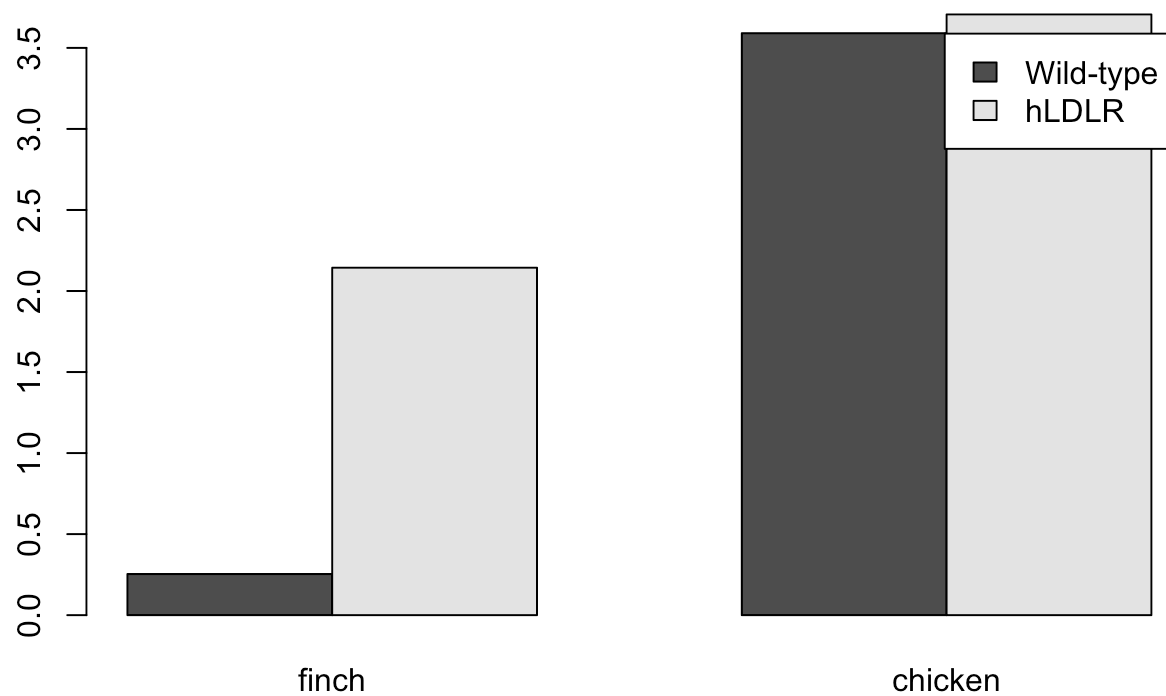
```
##      Wild.type.Finch      hLDLR.Finch Wild.type.Chicken      hLDLR.Chicken
##           0.07997842           1.23324550           1.33656421           0.88193124
```

From here, we get to see that even though the standard deviation for hLDLR group is a little bit higher than the wild type finch, the standard deviation is still very small. Hence, it is a support evident that to reject the null hypothesis.

3. By looking at this barplot:

```
barplot( as.matrix(bar.data), legend= rownames(bar.data), beside = TRUE)
```





We can see that the infective units for hLDLR finch is much higher than the wild type finch.

Therefore, the null hypothesis from Q3 will be rejected since there is a clear connection between cell type and the infective unit in zebra finch.

## Q5:

Null hypothesis[H0]: There is no difference in infectivity (number of infective units) between wildtype and hLDLR chicken cell .

Alternative hypothesis[H1]: There is a difference in infectivity (number of infective units) between wildtype and hLDLR chicken cell.

## Q6:

The null hypothesis from Q5 will not be rejected. 1. mean for both chicken group:

chicken

| ## | Wild.type.Chicken | hLDLR.Chicken |
|----|-------------------|---------------|
| ## | 3.590798          | 3.706436      |

We can see that both group has a very similar mean value. It is a good support that there is no connection between cell type and the infectivity in the chicken cell.

By using the same code from Q4, for the standard derivation, as both group has a similar number of standard derivation and the value is relative small. We will say the data is highly conserves and convince.

From the barplot we used for Q4, since the level of the infecivity unit for both wildtype and hLDLR chicken cell are very close and there is no big difference, we can conclude that there is no clear connection between the cell type and infecitviy in chicken cell. In other word, wide-type or hLDLR cell type does not affected the infectivity units in chicken cells.

Therefore, we will not rejected the null hypothesis from Q5.