

Homework due May 4, 2021 15:01 +03

For the following questions, use the data loaded with:

```
library(tissuesGeneExpression)
data(tissuesGeneExpression)
```

## MDS Exercises #1

1/1 point (graded)

In these exercise we will demonstrate the relationship between the SVD and the output of `cmdscale()`, the function in R that performs MDS.

Using the `z` we computed in [SVD Exercises #4](#):

```
y = e - rowMeans(e)
s = svd(y)
z = s$d * t(s$v)
```

we can make an MDS plot:

```
library(rafalib)
ftissue = factor(tissue)
mypar(1,1)
plot(z[1,],z[2,],col=as.numeric(ftissue))
legend("topleft",levels(ftissue),col=seq_along(ftissue),pch=
```

Now run the function `cmdscale()` on the original data:

```
d = dist(t(e))
mds = cmdscale(d)
```

What is the correlation between the first row of `z` and the first column in `mds` ?

-1

✓ Answer: -1

-1

### Explanation

```
cor(z[1,],mds[,1])
```

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You have used 1 of 5 attempts

**i** Answers are displayed within the problem

## MDS Exercises #2

1/1 point (graded)

What is the correlation between the second row of `z` and the second column of `mds` ?

-1

✓ Answer: -1

-1

### Explanation

```
cor(z[2,],mds[,2])
```

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You have used 1 of 5 attempts

**i** Answers are displayed within the problem

## MDS Exercises #3

1/1 point (graded)

Note that the MDS plot is not the same:

```
library(rafalib)
ftissue = factor(tissue)
mypar(1,2)
plot(z[1,],z[2,],col=as.numeric(ftissue))
legend("topleft",levels(ftissue),col=seq_along(ftissue),pch=
plot(mds[,1],mds[,2],col=as.numeric(ftissue))
```

Given the answer to MDS Exercises #1 and #2, what do we have to do to `z[1,]` and `z[2,]` to get a practically identical plot?

- ☐ It is impossible
- ☐ Use the columns instead `z[,1]` and `z[,2]`
- ☐ Remove the row means from `e` before computing the distance
- ☒ multiply `z[1,]` and `z[2,]` by -1



### Explanation

From the answer to the previous question we see that we have a flipped sign in both dimensions.

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You have used 1 of 2 attempts

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**i** Answers are displayed within the problem

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## MDS Exercises #4

1/1 point (graded)

Load the following dataset:

```
library(GSE5859Subset)
data(GSE5859Subset)
```

Compute the SVD and compute `z`:

```
s = svd(geneExpression-rowMeans(geneExpression))  
z = s$d * t(s$v)
```

Which dimension of `z` most correlates with the outcome `sampleInfo$group`?

✓ Answer: 1

### Explanation

```
which.max(cor(sampleInfo$g,t(z)))
```

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You have used 1 of 5 attempts

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**i** Answers are displayed within the problem

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## MDS Exercises #5

1/1 point (graded)

Continue working with the `z` calculated from the **GSE5859Subset** data.

What is this max correlation?

✓ Answer: 0.6236858

### Explanation

```
max(cor(sampleInfo$g,t(z)))
```

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You have used 1 of 5 attempts

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**i** Answers are displayed within the problem

## MDS Exercises #6

1/1 point (graded)

Continue working with the `z` calculated from the **GSE5859Subset** data.

Which dimension of `z` has the *second highest* correlation with the outcome `sampleInfo$group`?

✓ Answer: 6

### Explanation

```
which.max(cor(sampleInfo$g,t(z))[-1])) + 1
```

We add 1 because we took out the first.

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You have used 1 of 5 attempts

**i** Answers are displayed within the problem

## MDS Exercises #7

2/2 points (graded)

Note these measurements were made during two months:

```
sampleInfo$date
```

We can extract the month this way:

```
month = format( sampleInfo$date, "%m")
month = factor( month)
```

Which dimension of `z` has the highest correlation with the outcome `month`?



What is this correlation?



You have used 2 of 5 attempts

✓ Correct (2/2 points)

## MDS Exercises #8 (ADVANCED)

1/1 point (graded)

Note: this is an advanced question. Please feel free to research this question online.

In MDS Exercises #7 we saw that that one of the dimensions was highly correlated to the `sampleInfo$group`. Now take the 5th column of `U` and stratify by the gene chromosome. Remove `chrUn` and make a boxplot of the values of `U6` stratified by chromosome.

Which chromosome looks different from the rest?

Copy and paste the name as it appears in `geneAnnotation`.



**Answer:** chrY

### Explanation

```
result = split(s$u[,6],geneAnnotation$CHR)
result = result[ which(names(result)!="chrUn") ]
boxplot(result,range=0)
boxplot(result,range=0,ylim=c(-0.025,0.025))
medians = sapply(result,median)
names(result)[ which.max(abs(medians)) ]
```

Given the answer to this question, any guesses as to what `sampleInfo$group` represents?

Submit

You have used 1 of 10  
attempts

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**i** Answers are displayed within the problem