Linstat Rec 1

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Problem 1

a)

```
A <- matrix(c(9,-2,-2,6),nrow=2,ncol=2)
print(A)
```

```
##      [,1] [,2]
## [1,]    9   -2
## [2,]   -2    6
```

b)

```
print(A-t(A))
```

```
##      [,1] [,2]
## [1,]    0    0
## [2,]    0    0
```

We see that the difference between A and its transposed is the (2×2) zero matrix. Thus, A is symmetric. This is also easily verifiable by hand, since A^T would be

$$\begin{bmatrix} 9 & -2 \\ -2 & 6 \end{bmatrix},$$

which is the same as A.

c)

To find out if A is positive definite, we check if A is diagonal-dominant. From **a)**, we see that its diagonals, 9 and 6, are both positive and greater than the absolute value of non-diagonal entries, $|-2|$. Hence, A is positive definite.

d)

By hand, we solve the system

$$\det(A - \lambda I) = 0 \iff (9-\lambda)(6-\lambda) - 4 = 0$$

for λ, which simply factors to $(\lambda - 10)(\lambda - 5)$. In R, we use `eigen()`:

```
tmp <- eigen(A)
eVecs <- tmp$vectors
eVals <- tmp$values
print(eVecs)
```

```
##             [,1]       [,2]
## [1,] -0.8944272 -0.4472136
## [2,]  0.4472136 -0.8944272
```

```r
print(eVals)
```

```
## [1] 10  5
```

e)

We already have all we need to find the orthogonal diagonalization $A = V\Lambda V^{-1}$, we simply need to find the eigenvector matrix's inverse (using `solve()`) and Λ using `diag`(λ)

```r
eVecsInv <- solve(eVecs)
Lmbd <- diag(eVals)
print(eVecs%*%Lmbd%*%eVecsInv)
```

```
##      [,1] [,2]
## [1,]    9   -2
## [2,]   -2    6
```

f)

```r
A_inv <- solve(A)
```

g)

```r
print(eigen(A_inv))
```

```
## eigen() decomposition
## $values
## [1] 0.2 0.1
##
## $vectors
##           [,1]       [,2]
## [1,] 0.4472136 -0.8944272
## [2,] 0.8944272  0.4472136
```

The relationship between $\lambda(A)$ and $\lambda(A-1)$ is clearly that $\lambda(A^{-1}) = 1/\lambda(A)$, i.e. $\frac{1}{5}$ and $\frac{1}{10}$. As a consequence, the eigenvectors, which can freely be scaled, will be the same.

h)

We've seen in the lectures that a covariance matrix must be symmetric and positive semi-definite. We've already shown that it's symmetric, and that it's positive defininte, thus it can represent some covariance matrix.

i)

```r
corrMatrix <- rbind(c(0,0), c(0,0))
for (i in 1:nrow(A)){
    for (j in 1:ncol(A)){
        corrMatrix[i,j] = A[i,j]/sqrt(A[i,i]*A[j,j])
    }
}
print(corrMatrix)
```

```
##             [,1]       [,2]
## [1,]  1.0000000 -0.2721655
## [2,] -0.2721655  1.0000000
```

Check with built-in function:

```r
print(cov2cor(A))
```

```
##             [,1]       [,2]
## [1,]  1.0000000 -0.2721655
## [2,] -0.2721655  1.0000000
```

j)