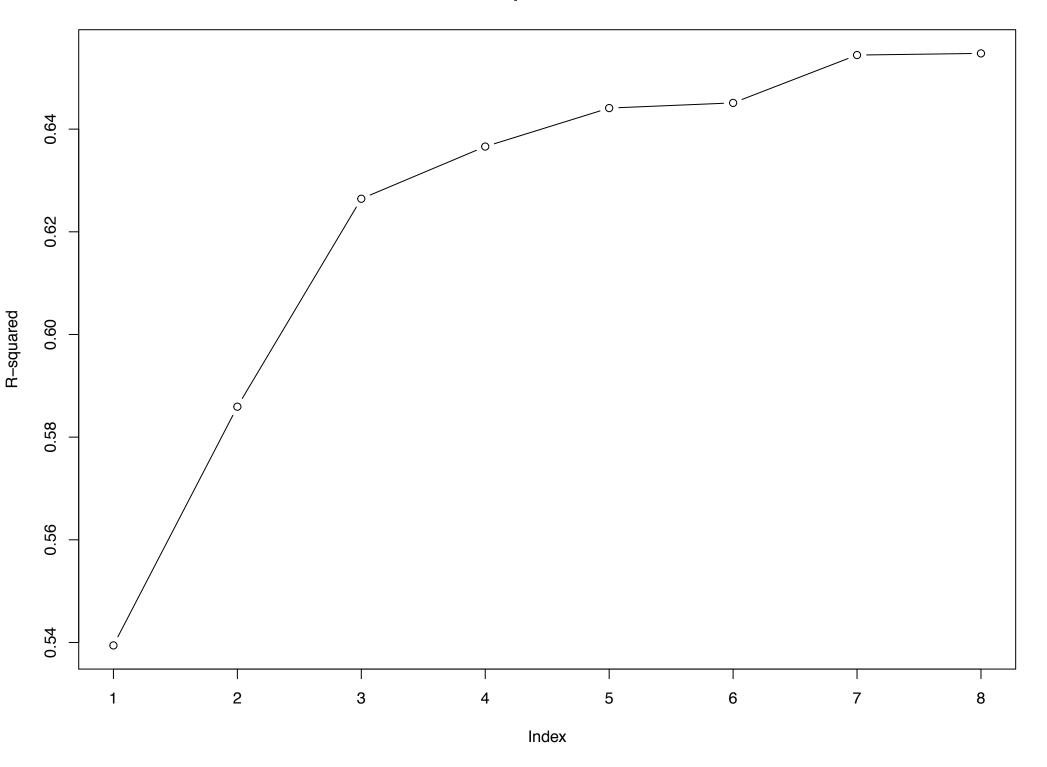
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# title: "MSDS596 - HW1"
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# date: "09/18/2018"
#Problem 1
#Part a
  # \lambda is eigenvalue of A => Ax = \lambdax
  # A is idemponent => A^2x = \lambda x => A(Ax) = \lambda x
  # x is eigenvector of A => A(\lambda x) = \lambda x => \lambda(Ax) = \lambda x
  # x is eigenvector of A => \lambda(\lambda x) = \lambda x => \lambda^2 x = \lambda x
  # \lambda^2 x - \lambda x = 0 \Rightarrow x(\lambda^2 - \lambda) = 0
  \# \Rightarrow \lambda = 0 \text{ or } \lambda = 1
#Part b
  # *1
  # Ax = \lambdax => rank(A) = \sum \lambda i, \lambda i != 0 # (sum from i to n of \lambda sub i)
  # *2
  # Spectral decomposition A = Q\Lambda Q'
  # tr(A) = tr(Q\Lambda Q') = tr(QQ'\Lambda) #trace properties
  # QQ' = I => tr(QQ'\Lambda) = tr(\Lambda) = \sum \lambda i
  # *3
  # using part a) \lambda = 0 or \lambda = 1
  # because of *1, *2 and *3 \Rightarrow tr(A) = rank(A)
# Part c
  # A is idemponent => (I-A)^2 = I^2 - 2IA + A^2 = I - 2A + A = I-A => I-A is
idemponent
  # using part b
  \# \operatorname{rank}(I-A) = \operatorname{tr}(I-A)
  # tr(I-A) = tr(I) - tr(A) # trace properties
  \# tr(I) - tr(A) = n - rank(A)
  \# \Rightarrow rank(I-A) = n - rank(A) \Rightarrow rank(A) + rank(I-A) = n
# Problem 2
# (I-P)^2 = I^2 - 2IP + P^2 = I - 2P + P = I-P => I-P is idemponent
# I-P is also symmetric
# so I-P = In - 1/n(1n)(1n') is a projection matrix
# and P = 1/n(1n)(1n')
# A projection matrix is a square matrix that does a linear transformation of
a vector onto a subspace
#install.packages("faraway")
library(faraway)
#Problem 5
data(teengamb)
head(teengamb)
```

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#using linear model function
aux <- lm(gamble ~ sex+status+income+verbal)</pre>
#part a
print("Part a")
#getting summary of the model
print(summary(aux))
#part b
print("Part b")
#getting the r-square value from the summary
print(summary(aux)$r.squared)
#part c
print("Part c")
#max:
print("max:")
#getting the max value of all model's residuals
print(which.max(aux$residuals))
print("min:")
#min:
#getting the min value of all model's residuals
print(which.min(aux$residuals))
#part d
print("Part d")
print("Mean:")
#mean
#getting the mean value of all model's residuals
print(mean(aux$residuals))
print("Median:")
#median
#getting the median value of all model's residuals
print(median(aux$residuals))
#part e
print("Part e")
#getting the correlation between the residuals and the fitted values of the
model
print(cor(aux$residuals,aux$fitted.values))
#part f
print("Part f")
#getting the correlation between the residuals and the income
print(cor(aux$residuals,income))
#part g
print("Part g")
       'Based on the summary, the fitted model can be explicitly written as:
gamble = 22.55565 - 22.11833 \times \text{sex} + 0.05223 \times \text{status} + 4.96198 \times \text{income} -
2.95949 \times verbal")
# from
https://www.rdocumentation.org/packages/faraway/versions/1.0.7/topics/teengamb
# sex is 0 for man and 1 for female
print("If all the predictors except sex continue to be constant, the
difference in predicted
```

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expenditure on gambling between male and female will be equal to the
regression
coefficient of sex (-22.11833). So if sex changes from male (0) to female
the value of gamble decreases by 22.11833.")
#Problem 6
data(prostate)
head(prostate)
# creating vectors to save r-square and standard error values from different
r squared trend <- c()
se trend <- c()
#part a
# creating the model with lpsa as the response and lcavol as the predictor
prostate.lm1=lm(lpsa~lcavol, data=prostate);
lm1.rsquared <-summary(prostate.lm1)$r.squared</pre>
lm1.sigma <-summary(prostate.lm1)$sigma</pre>
#adding r-square and standard error values to the vectors
r_squared_trend <- c(r_squared_trend, lm1.rsquared)</pre>
se trend <- c(se trend, lm1.sigma)</pre>
#part b
#adding lweight
prostate.lm2=lm(lpsa~lcavol+lweight, data=prostate);
#getting the r-square value
lm2.rsquared <-summary(prostate.lm2)$r.squared</pre>
#getting the standard error value
lm2.sigma <-summary(prostate.lm2)$sigma</pre>
#adding r-square and standard error values to the vectors
r squared trend <- c(r squared trend, lm2.rsquared)</pre>
se trend <- c(se trend, lm2.sigma)
#adding svi
prostate.lm3=lm(lpsa~lcavol+lweight+svi, data=prostate);
lm3.rsquared <-summary(prostate.lm3)$r.squared</pre>
lm3.sigma <-summary(prostate.lm3)$sigma</pre>
#adding r-square and standard error values to the vectors
r_squared_trend <- c(r_squared_trend, lm3.rsquared)</pre>
se_trend <- c(se_trend, lm3.sigma)</pre>
#adding lbph
prostate.lm4=lm(lpsa~lcavol+lweight+svi+lbph, data=prostate);
lm4.rsquared <-summary(prostate.lm4)$r.squared</pre>
lm4.sigma <-summary(prostate.lm4)$sigma</pre>
#adding r-square and standard error values to the vectors
r_squared_trend <- c(r_squared_trend, lm4.rsquared)</pre>
se_trend <- c(se_trend, lm4.sigma)</pre>
#adding age
prostate.lm5=lm(lpsa~lcavol+lweight+svi+lbph+age, data=prostate);
lm5.rsquared <-summary(prostate.lm5)$r.squared</pre>
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lm5.sigma <-summary(prostate.lm5)$sigma</pre>
#adding r-square and standard error values to the vectors
r_squared_trend <- c(r_squared_trend, lm5.rsquared)</pre>
se trend <- c(se trend, lm5.sigma)
#adding lcp
prostate.lm6=lm(lpsa~lcavol+lweight+svi+lbph+age+lcp, data=prostate);
lm6.rsquared <-summary(prostate.lm6)$r.squared</pre>
lm6.sigma <-summary(prostate.lm6)$sigma</pre>
#adding r-square and standard error values to the vectors
r squared trend <- c(r squared trend, lm6.rsquared)</pre>
se trend <- c(se trend, lm6.sigma)
#adding pgg45
prostate.lm7=lm(lpsa~lcavol+lweight+svi+lbph+age+lcp+pgg45, data=prostate);
lm7.rsquared <-summary(prostate.lm7)$r.squared</pre>
lm7.sigma <-summary(prostate.lm7)$sigma</pre>
#adding r-square and standard error values to the vectors
r_squared_trend <- c(r_squared_trend, lm7.rsquared)</pre>
se trend <- c(se trend, lm7.sigma)</pre>
#adding gleason
prostate.lm8=lm(lpsa~lcavol+lweight+svi+lbph+age+lcp+pgg45+gleason,
data=prostate);
lm8.rsquared <-summary(prostate.lm8)$r.squared</pre>
lm8.sigma <-summary(prostate.lm8)$sigma</pre>
#adding r-square and standard error values to the vectors
r_squared_trend <- c(r_squared_trend, lm8.rsquared)</pre>
se_trend <- c(se_trend, lm8.sigma)</pre>
#Plot R-Square
plot(r squared trend, type="b", main="R-Squared Trend", ylab="R-squared")
#R-Squared: when adding more variables to model, it is closer to 1. So we can
conclude the more
#variables we include in the model, it better fits.
#Plot Standard Error
plot(se_trend, type="b", main="Residual Standard Error Trend", ylab="Standard
Error")
#Residual Standard Error: Contrary to R-Squared, when adding more variables
to the model, it is closer
#to 0, which is good, because it means that as we aggregate variable, the
model fits better.
```



Residual Standard Error Trend

