# Principal Component Regression 

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Math 243: Stat Learning

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## Outline

In today's class, we will...

- Discuss Principal Component Analysis as a means of dimensionality reduction for regresion
- Implement PCR in R


## Section 1

## Principal Component Regression

## Dimensionality Reduction

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- But dropping variables completely loses possible valauable information.
- Instead, we can combine variables into new ones that adequately describe the variance in the data, and drop those that have limited utility in explaining that variance.


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```
## sd_Pop sd_Ad
## 1 8.981994 7.418227
```


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$\left.\begin{array}{lr}\text { \#\# } & \text { R_sq } \\ \text { \#\# } & 1\end{array}\right)$

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How much variation occurs perpendicular to this line?


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- Alternatively, we could express $Z_{1}$ as an affine linear combination of the predictors themselves (affine meaning including a constant term)


## PCA Example

The first principal component


$$
Z_{1}=0.8(\operatorname{Pop}-41.1)+0.6(\mathrm{Ad}-40.4)
$$

## PCA Example

What is leftover?


## Other Principal Components

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Generally, the $k$ th principal component is obtained by finding a linear combination of centered variables that is uncorrelated with all previous principal components, and has the largest variance subject to this constraint.

## PCA Example

The second principal component


## Principal Comoponent Regression

The PCR approach to linear regression constructs the first $M$ principal components $Z_{1}, \ldots, Z_{M}$ of a data set with $p$ predictors (so $M \leq p$ ), and then uses these as predictors in a linear regression model.

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In general, PCR tends to produce linear models with higher accuracy than models fit with the original predictors.


## Principal Component Regression in R

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The Hitters data set from the ISLR package contains Salary and 18 other predictors for 263 baseball players
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my_pcr <- pcr( Salary ~ ., data = Hitters, scale = T, validation = "CV")

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- Setting scale $=\mathrm{T}$ standardizes each predictor
- Setting validation $=$ "CV" causes pcr to compute the 10 -fold CV error for each value of $M$ (number of principal components used)


## PCR Results

```
summary(my_pcr)
## Data: X dimension: 263 19
## Y dimension: 263 1
## Fit method: svdpc
## Number of components considered: 19
##
## VALIDATION: RMSEP
## Cross-validated using 10 random segments.
```



```
## TRAINING: % variance explained
\begin{tabular}{lrrrrrrrrrr} 
\#\# & 1 comps & 2 comps & 3 comps & 4 comps & 5 & comps & 6 & comps & 7 comps & 8 comps \\
\#\# X & 38.31 & 60.16 & 70.84 & 79.03 & 84.29 & 88.63 & 92.26 & 94.96 \\
\#\# Salary & 40.63 & 41.58 & 42.17 & 43.22 & 44.90 & 46.48 & 46.69 & 46.75 \\
\#\# & 9 comps & 10 comps & 11 comps & 12 comps & 13 & comps & 14 comps & 15 & comps \\
\#\# X & 96.28 & 97.26 & 97.98 & 98.65 & 99.15 & 99.47 & 99.75 \\
\#\# Salary & 46.86 & 47.76 & 47.82 & 47.85 & 48.10 & 50.40 & 50.55 \\
\#\# & 16 comps & 17 comps & 18 comps & 19 comps & & & & \\
\#\# X & 99.89 & 99.97 & 99.99 & 100.00 & & & & \\
\#\# Salary & 53.01 & 53.85 & 54.61 & 54.61 & & & &
\end{tabular}
```


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- Note: pcr reports RSE, so values need to be squared to get MSE.


## Validation Plot

validationplot(my_pcr, val.type = "MSEP")
Salary


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- Note: The smallest CV error occurs at $M=16$ (which is close to the maximum number of predictors $p=19$.)


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Salary


- Note: The smallest CV error occurs at $M=16$ (which is close to the maximum number of predictors $p=19$.)
- However, a relatively low CV error is also obtained at $M=6$, suggesting fewer components are sufficient


## Comparative Performance

Live coding. A .Rmd file will be available on course website after class

