STAT406- Methods of Statistical Learning Lecture 22

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UBC - Sep / Dec 2019

- Dimension reduction
- For simplicity of model / interpretation
- Because of model requirements
- How can we find the **best** variables to use?

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(what do we mean by "best"?)
(which variables can I chose from?)
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- Two different ways to introduce them...
- but, at the end of the day, they are the same objects -
- linear combinations of the original variables that:
- are uncorrelated with each other;
- provide the "best lower-dimensional approximation" to the data.

PCA - Max variance

- Given a centered sample X_1, \ldots, X_n ,
- 1st PC: find $\|\mathbf{a}\| = 1$ such that

$$Var(Y_1, ..., Y_n) = \frac{1}{n-1} \sum_{i=1}^{n} (\mathbf{a}' \mathbf{X}_i)^2$$

is maximized, $Y_i = \mathbf{a}' \mathbf{X}_i$.

The solution is $\mathbf{a} = \mathbf{a}_0$ the eigenvector of \mathbf{S}_n associated with its largest eigenvalue $\tilde{\lambda}_1$.

• For the 2nd PC: find $\|\mathbf{a}\| = 1$ such that and, if $W_i = \mathbf{a}'\mathbf{X}_i$, i = 1, ..., n,

$$\operatorname{\mathsf{cov}}\left(Y_1,Y_2,\ldots,Y_n;W_1,W_2,\ldots,W_n\right) = \sum_{i=1}^n Y_i\,W_i = 0$$

and

$$Var(W_1,...,W_n) = \frac{1}{n-1} \sum_{i=1}^n (W_i)^2$$

is maximized.

- The solution is $\mathbf{a} = \mathbf{a}_1$ the eigenvector of \mathbf{S}_n associated with its **2nd largest** eigenvalue $\tilde{\lambda}_2$.
- etc.

PCA

Let $\mathbf{X}_1, \dots, \mathbf{X}_n \in \mathbb{R}^p$ be a sample.

Assume that $\bar{\mathbf{X}}_n = \mathbf{0}$

For a subspace \bot of dimension k let

$$P(\mathbf{X}_i, \mathbf{L})$$

be the orthogonal projection of X_i onto L

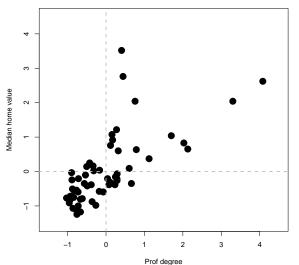
Dimension reduction

Find the "best" subspace \mathbf{L} of dimension k

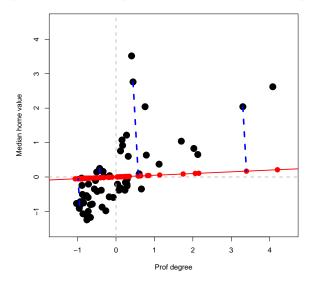
"Best" means: that best approximates the data

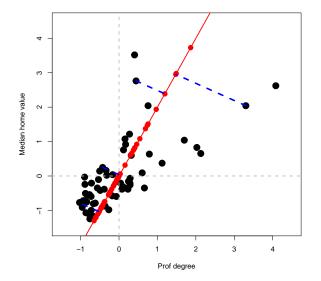
$$\min_{\mathbf{L}} \frac{1}{n} \sum_{i=1}^{n} \|\mathbf{X}_{i} - P(\mathbf{X}_{i}, \mathbf{L})\|^{2}$$

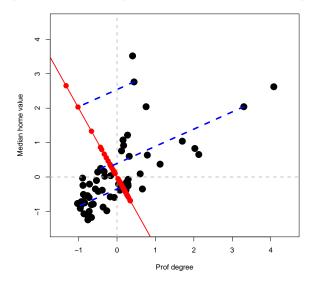
PCA - simple example

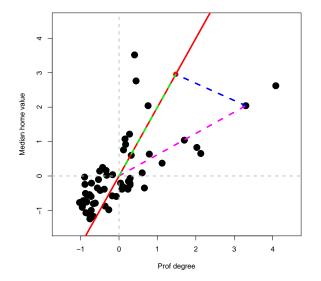


Census data - Percent of pop. with professional









$$\min_{\mathbf{L}} \frac{1}{n} \sum_{i=1}^{n} \|\mathbf{X}_{i} - P(\mathbf{X}_{i}, \mathbf{L})\|^{2} = \min_{\mathbf{L}} \frac{1}{n} \sum_{i=1}^{n} \left[\|\mathbf{X}_{i}\|^{2} - \|P(\mathbf{X}_{i}, \mathbf{L})\|^{2} \right]$$

We need to find

$$\max_{\mathbf{L}} \frac{1}{n} \sum_{i=1}^{n} \| P(\mathbf{X}_i, \mathbf{L}) \|^2$$

To fix ideas take k = 1. In this case $L = \langle a \rangle$ for some vector $a \in \mathbb{R}^p$ with $\|a\| = 1$. Thus

$$P(\mathbf{X}_i, \mathbf{L}) = \mathbf{a} (\mathbf{a}' \mathbf{X}_i)$$

hence

$$\sum_{i=1}^{n} \| P(\mathbf{X}_{i}, \mathbf{L}) \|^{2} = \sum_{i=1}^{n} \| \mathbf{a} (\mathbf{a}' \mathbf{X}_{i}) \|^{2}$$

$$\max_{\mathbf{L}} \frac{1}{n} \sum_{i=1}^{n} \| P(\mathbf{X}_i, \mathbf{L}) \|^2 =$$

$$\max_{\|\mathbf{a}\|=1} \frac{1}{n} \sum_{i=1}^{n} \| \mathbf{a} (\mathbf{a}' \mathbf{X}_i) \|^2 =$$

$$\max_{\|\mathbf{a}\|=1} \frac{1}{n} \sum_{i=1}^{n} \mathbf{X}_i' \mathbf{a} \mathbf{a}' \mathbf{a} \mathbf{a}' \mathbf{X}_i =$$

$$\max_{\|\mathbf{a}\|=1} \frac{1}{n} \sum_{i=1}^{n} \mathbf{X}_i' \mathbf{a} \mathbf{a}' \mathbf{X}_i$$

$$\max_{\mathbf{L}} \frac{1}{n} \sum_{i=1}^{n} \| P(\mathbf{X}_i, \mathbf{L}) \|^2 =$$

$$\max_{\|\mathbf{a}\|=1} \frac{1}{n} \sum_{i=1}^{n} \mathbf{a}' \mathbf{X}_i \mathbf{X}_i' \mathbf{a} =$$

$$\max_{\|\mathbf{a}\|=1} \mathbf{a}' \left[\frac{1}{n} \sum_{i=1}^{n} \mathbf{X}_i \mathbf{X}_i' \right] \mathbf{a} =$$

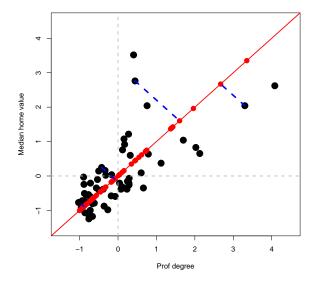
$$\max_{\|\mathbf{a}\|=1} \mathbf{a}' Q_n \mathbf{a}$$

- the "best" subspace L of dimension 1 is generated by the eigenvector \mathbf{a}_0 of Q_n associated with its largest eigenvalue λ_1 .
- The "scores" are the coefficients of the projections

$$y_i = \mathbf{X}_i' \mathbf{a_0}, \qquad i = 1, \dots, n$$

The projections are

$$\mathbf{v}_i = \mathbf{a}_0 \, \mathbf{v}_i = \mathbf{a}_0 \, (\mathbf{X}_i' \mathbf{a}_0) \,, \qquad i = 1, \dots, n$$



There is nothing special about L being of dimension k = 1

In general, let $\mathbf{B} \in \mathbb{R}^{p \times k}$ be an orthonormal $(\mathbf{B}' \mathbf{B} = \mathbf{I}_k)$ basis for \mathbf{L} , then

$$P(\mathbf{X}_i, \mathbf{L}) = \mathbf{B} (\mathbf{B}' \mathbf{X}_i)$$

and

$$\frac{1}{n}\sum_{i=1}^{n}\|P(\mathbf{X}_{i},\mathbf{L})\|^{2} = \frac{1}{n}\sum_{i=1}^{n}\|\mathbf{B}(\mathbf{B}'\mathbf{X}_{i})\|^{2} =$$

$$\frac{1}{n} \sum_{i=1}^{n} \mathbf{X}_{i}^{\prime} \mathbf{B} \mathbf{B}^{\prime} \mathbf{X}_{i}$$

Furthermore

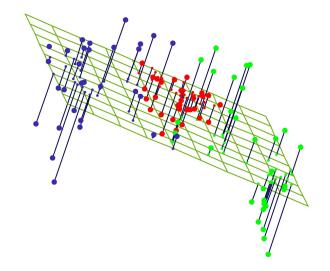
$$\frac{1}{n}\sum_{i=1}^{n}\mathbf{X}_{i}^{\prime}\mathbf{B}\mathbf{B}^{\prime}\mathbf{X}_{i}=\frac{1}{n}\sum_{i=1}^{n}\operatorname{trace}\left(\mathbf{B}^{\prime}\mathbf{X}_{i}\mathbf{X}_{i}^{\prime}\mathbf{B}\right)=$$

$$\operatorname{trace}(\mathbf{B}'Q_n\mathbf{B}) \leq \sum_{i=1}^k \lambda_i$$

and since

trace
$$(\mathbf{U}'_k Q_n \mathbf{U}_k) = \sum_{i=1}^k \lambda_i$$

the "best" subspace is generated by the k "largest" eigenvectors of Q_n © Matias Salibian-Barrera, 2019. All rights reserved. Cannot be copied, re-used, or edited.



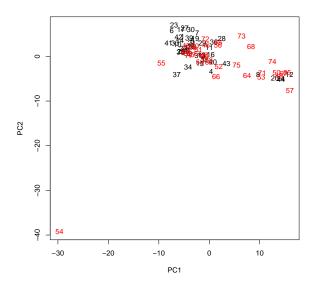
Breast Cancer Gene Expression

- Data on 78 patients
- 4751 measurements taken on each patient (4751 gene expression levels)
- For each patient we know whether the tumor metastasized or not
- Can we separate these groups using their gene expression measurements?

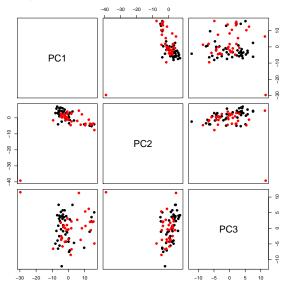
Breast Cancer Gene Expression

- Can't plot a 4751-dimensional space
- 78 observations are not too many to reveal structures on such a high-dimensional space
- We try to use fewer measurements, but in such a way that they remain close to the full 4751- dimensional observations

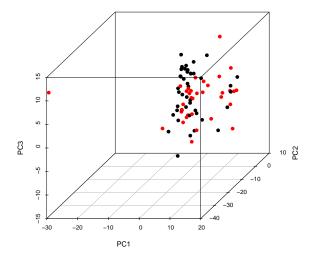
Gene Expression - Best 2D



Gene Expression - Best 3D



Gene Expression - Best 3D



How good is the **best k**-dimensional approximation?

$$\min_{\mathbf{L}} \frac{1}{n} \sum_{i=1}^{n} \|\mathbf{X}_{i} - P(\mathbf{X}_{i}, \mathbf{L})\|^{2} =$$

$$\min_{\mathbf{L}} \frac{1}{n} \sum_{i=1}^{n} \left[\|\mathbf{X}_{i}\|^{2} - \|P(\mathbf{X}_{i}, \mathbf{L})\|^{2} \right] =$$

$$\frac{1}{n} \sum_{i=1}^{n} \|\mathbf{X}_{i}\|^{2} - \max_{\mathbf{L}} \frac{1}{n} \sum_{i=1}^{n} \|P(\mathbf{X}_{i}, \mathbf{L})\|^{2} =$$

j=1 © Matias Salibian-Barrera, 2019. All rights reserved. Cannot be copied, re-used, of edited.

trace $(Q_n) - \sum_{i=1}^{n} \lambda_i = \sum_{i=1}^{p} \lambda_i$

- Important question: how many PC's should we use?
- The fewer we use the more we will have reduced the dimension
- The more we use the better the approximation to the full data
- There is a trade-off between goodness of the fit and number of principal components

We know that for the best subspace L
 of dimension k we have

$$\min_{\mathbf{L}} \frac{1}{n} \sum_{i=1}^{n} \|\mathbf{X}_{i} - P(\mathbf{X}_{i}, \mathbf{L})\|^{2} =$$

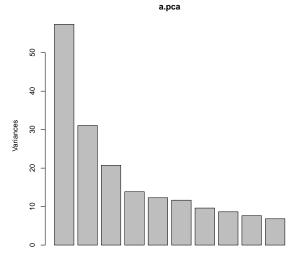
$$\log (\mathbf{k}) = \sum_{i=k+1}^{p} \lambda_{i}$$

hence, the gain obtained by using
 k + 1 PC's instead of using only k is

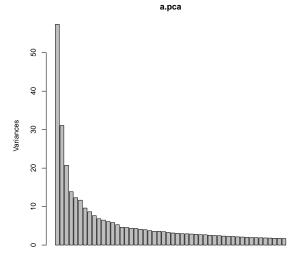
$$\mathsf{loss}\left(m{k}
ight) - \mathsf{loss}\left(m{k+1}
ight) \ = \ \lambda_{m{k+1}}$$
 for $m{k} = 0, 1, 2, \dots, p$

• the gain is decreasing...

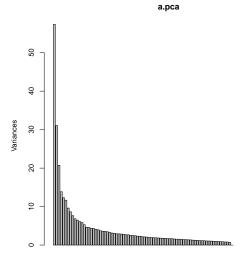
Breast cancer example - scree plot - first 10



Breast cancer example - scree plot - first 50



Breast cancer example - scree plot - first 100



PCA - summary

- Principal components (PCs) provide "best" lower-dimensional approximations
- The more PCs we use the better the approximation
- The gain in quality of the approximation decreases as we add more PCs
- These gains are the eigenvalues of the covariance matrix

- So, what about Statistics in all this?
- If X is a random vector with E[X] = 0 and cov (X) = cov (X, X) = Σ

$$\min_{\mathbf{L}} E \|\mathbf{X} - P(\mathbf{X}, \mathbf{L})\|^2 = \min_{\mathbf{L}} E \left[\|\mathbf{X}\|^2 - \|P(\mathbf{X}, \mathbf{L})\|^2 \right]$$

Hence, we need to find

$$\max E \| P(\mathbf{X}, \mathbf{L}) \|^2$$

For the case k = 1 We have

$$P(X, L) = a (a'X)$$

for some vector $\mathbf{a} \in \mathbb{R}^p$ with $\|\mathbf{a}\| = 1$ Hence

$$E \|P(\mathbf{X}, \mathbf{L})\|^2 = E \|\mathbf{a} (\mathbf{a}' \mathbf{X})\|^2$$

$$\max_{\mathbf{L}} E \| P(\mathbf{X}, \mathbf{L}) \|^2 = \max_{\|\mathbf{a}\|=1} E \| \mathbf{a} (\mathbf{a}' \mathbf{X}) \|^2$$

$$= \max_{\|\mathbf{a}\|=1} E [\mathbf{X}' \mathbf{a} \mathbf{a}' \mathbf{X}]$$

$$= \max_{\|\mathbf{a}\|=1} E [\mathbf{a}' \mathbf{X} \mathbf{X}' \mathbf{a}]$$

$$= \max_{\|\mathbf{a}\|=1} \mathbf{a}' E [\mathbf{X} \mathbf{X}'] \mathbf{a}$$

$$= \max_{\|\mathbf{a}\|=1} \mathbf{a}' \Sigma \mathbf{a}$$

Finding the "best" (in the L_2 sense) approximating 1-dimensional subspace is equivalent to finding the direction \mathbf{a}_0 such that

$$\mathbf{a_0}' \, \mathbf{\Sigma} \, \mathbf{a_0} = \max_{\|\mathbf{a}\|=1} \, \mathbf{a}' \, \mathbf{\Sigma} \, \mathbf{a}$$

Also note that, for any $\mathbf{a} \in \mathbb{R}^p$

$$\mathbf{a}' \, \mathbf{\Sigma} \, \mathbf{a} = \text{var} (\mathbf{a}' \, \mathbf{X})$$

Thus, the problem is equivalent to

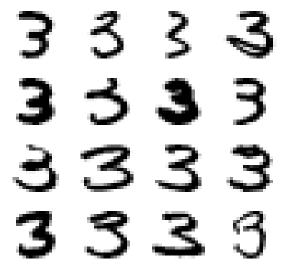
- finding the direction a₀ along which X
 has largest variability;
- finding the coefficients a₀ that produce the linear combination of components of X with maximum variance.

 The same approach we used for a sample applies to the population case.
 To find the 2nd PC we need to find

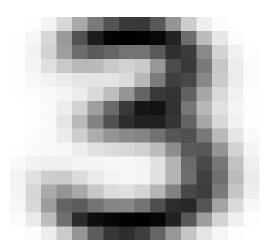
$$\max_{\|\boldsymbol{a}\|=1,\text{COV}\left(\boldsymbol{a}_0'\boldsymbol{X},\boldsymbol{a}'\boldsymbol{X}\right)=0}\text{Var}\left(\boldsymbol{a}'\boldsymbol{X}\right)\ =\ \boldsymbol{a}_1'\,\boldsymbol{\Sigma}\,\boldsymbol{a}_1$$

where \mathbf{a}_1 is the eigenvector of Σ associated with the second largest eigenvalue.

etc. etc.



$$egin{aligned} egin{aligned} (-1,-1,-0.989,-0.018,\cdots,-0.967,-1) \end{aligned} \ egin{aligned} egin{aligned} egin{aligned} egin{aligned} egin{aligned} i = 1,\ldots,658 \end{aligned} \end{aligned}$$



Picture of $\bar{\mathbf{X}}_n$ - the average "3" in the data

- The basic idea is to use PCA to obtain a (much) lower dimensional approximation to these
- Let $L \subset \mathbb{R}^{256}$ be a subspace of dimension k, generated by the vectors $\mathbf{b}_1, \dots, \mathbf{b}_k \in \mathbb{R}^{256}$, i.e.

$$L = < \mathbf{b}_1, \dots, \mathbf{b}_k >$$

If

$$\mathbf{B} = \begin{bmatrix} \vdots & \vdots & \vdots & \vdots \\ \mathbf{b}_1 & \mathbf{b}_2 & \vdots & \mathbf{b}_k \\ \vdots & \vdots & \vdots & \vdots \end{bmatrix} \in \mathbb{R}^{256 \times k}$$

then the orthogonal projection of $\mathbf{X}_i \in \mathbb{R}^{256}$ onto \boldsymbol{L} is

$$P(\mathbf{X}_i, \mathbf{L}) = \mathbf{B} (\mathbf{B}' \mathbf{X}_i)$$

• Let $S_n \in \mathbb{R}^{256 \times 256}$ be the sample covariance matrix of $\mathbf{X}_1, \dots, \mathbf{X}_n$, and let $\mathbf{u}_j, j = 1, \dots, 256$, be its eigenvectors, associated with decreasing eigenvalues:

$$S_n \, \mathbf{u}_j = \lambda_j \, \mathbf{u}_j \,, \qquad j = 1, \dots, 256 \,,$$
 with $\lambda_1 > \lambda_2 > \dots > \lambda_{256} > 0$.

Then, we have seen that the choice

$$\mathbf{b}_j = \mathbf{u}_j, \qquad j = 1, \dots, k$$

spans the subspace *L* that minimizes

$$\sum_{i=1}^{n} \|\mathbf{X}_{i} - P(\mathbf{X}_{i}, \mathbf{L})\|^{2}$$

over all possible subspaces $L \subset \mathbb{R}^{256}$ of dimension k.

• We first pick k = 2. Let

$$\mathbf{U}_2 = \left[egin{array}{ccc} \vdots & \vdots & \vdots \\ \mathbf{b}_1 & \mathbf{b}_2 & \vdots & \vdots \end{array}
ight] \in \mathbb{R}^{256 imes 2}$$

and let

$$V_i = U_2'X_i \in \mathbb{R}^2, \quad i = 1, \ldots, n$$

be the first 2 principal components. Note that

$$P(\mathbf{X}_i, \mathbf{L}) = \mathbf{U}_2 \mathbf{V}_i$$
.

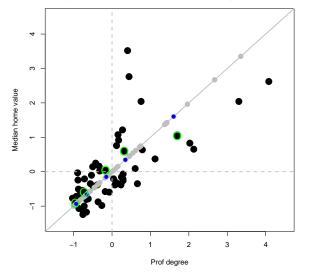
- Since it may be hard to interpret the 256 coefficients in each of the 2 principal components, we will instead find which images X_i are being approximated as we move along a grid on the 2-dimensional V_i-space.
- We illustrate this idea in the following slides. Here $\mathbf{X}_i \in \mathbb{R}^2$ and we use a single principal component (k = 1), represented by the **grey** line.

We select a grid of points (indicated in blue) along this 1-dimensional subspace of R², and find which points X_i are being approximated by them. These are the points in the sample closest to

$$P(\mathbf{X}_i, \mathbf{L}) = \mathbf{U}_1 \mathbf{V}_i$$

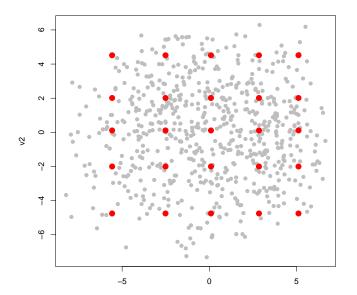
for each $V_i \in \mathbb{R}$ in the grid.

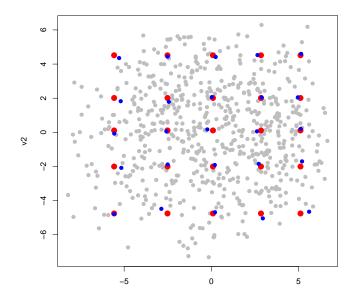
- The grid of points along the 1-dimensional principal component subspace are represented with blue dots. The corresponding closest points in the original sample are indicated by green circles.
- In our "images" application, we will see how these green points change as we move from one blue point to the next, along the grey line.



A simpler data set

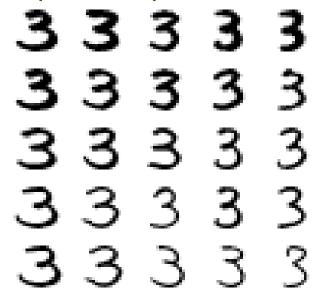
- Now, we calculate the first 2 principal components of our 256-dimensional images. These are vectors $\mathbf{V}_i \in \mathbb{R}^2$, i = 1, ..., n, pictured as **grey** points in the next 2 slides.
- Next, we select 25 of these vectors by overimposing a 5 × 5 grid over the V_i's, and selecting the closest V_j to each of these red points. These V_j's are indicated by blue points.
- The corresponding figures are in the next 2 slides.





- In the next slide we display the images closest to the 256-dimensional vector associated with each bivariate blue point in the previous plot.
- The images are arranged in a grid, and can be "read" left-right and top-bottom, corresponding to the same trajectories across the selected blue bivariate principal components in the previous plot.

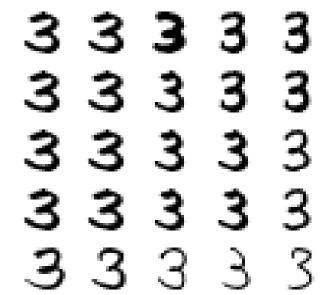
2 Principal Components



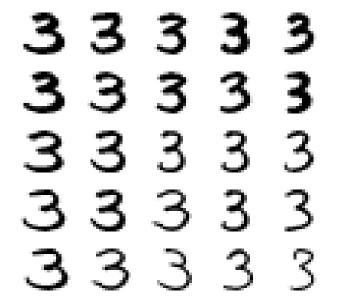
- Now we repeat the experiment but with 3 principal components.
- We have $V_i \in \mathbb{R}^3$, and select a 3-dimensional grid of dimension $75 = 5 \times 5 \times 3$; that is: 5 values for each of the first and second PCs, and 3 for the third one.
- As before, we select the V_j closest to each of the 75 points in the 3-dimensional grid.

- We now have 75 **blue** points in \mathbb{R}^{256} , and find the images closest to them.
- We represent this 3-dimensional array of images as 3 consecutive "slices" of 5 × 5. These are displayed in the next 3 slides.
- Further details can be found in the (somewhat commented) R code file

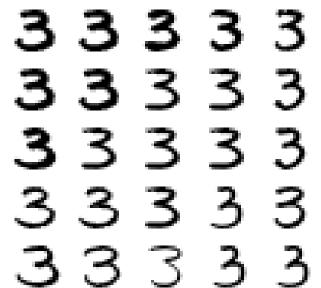
Low 3rd PC



Med 3rd PC



High 3rd PC



Another interesting PCA example

- PCs can be very sensitive to a few "outliers"
- These can sometimes be alleviated by using a "robust" covariance estimator $\hat{\Sigma}_n \neq S_n$
- However these robust covariance matrix estimators are very costly to compute (the complexity of the algorithms increases exponentially with the dimension).
- Sometimes,"n < p"

Application: Image processing

- Goal: to detect frames in a clip where "significant" changes occur
- Data: A 3-min scene with n=600 frames. Each frame is represented by a vector \mathbf{X}_i , $i=1,\ldots,600$.

Application: Image processing

 The idea is to identify "different" frames, by looking at their Mahalanobis distance to the "center" of the data, i.e.

$$d_i^2 = (\mathbf{X}_i - \hat{\mu})' \hat{\mathbf{\Sigma}}_n^{-1} (\mathbf{X}_i - \hat{\mu})$$

where $\hat{\mu}$ and $\hat{\Sigma}_n$ are "robust" estimators of the center and covariance matrix of the "good" frames.

- Each $X_i \in \mathbb{R}^{640 \times 479} = \mathbb{R}^{306560}$
- In this application the frames were reduced to $\mathbf{X}_i \in \mathbb{R}^{49152}$ before starting the analysis.
- Robust PCs were computed using projection-pursuit-type algorithms.
- The original clip, and results of the analysis

http://www.youtube.com/user/msalibian