

Learning outcomes:

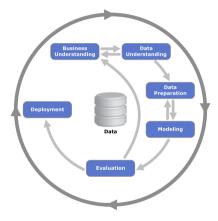


Figure: The <u>CRISP-DM</u> process.

 Summarize the argument for dimensionality reduction;

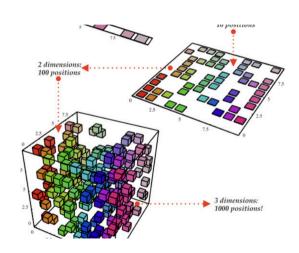
Describe the problem PCA is trying to solve;

Define the PCA algorithm;

► State at least one criteria for deciding how many components to use.

Dimensionality Reduction: what and why?

- In high-dimensional spaces, data points appear to be sparse and not very similar;
- Curse of dimensionality: the number of observations needed to cover feature space increases exponentially;
 - ► Three features with 10 categories has 1000 possibilities;
 - Two features with 10 categories has 100 possibilities;
 - One features with 10 categories has 10 possibilities;
- One way to address this: represent a vector of m features with a vector of d features. d << m.</p>



Principal Components Analysis (PCA)

Assumption: the data lie within or close to a much lower dimensional subspace of the high-dimensional space (ex: hyperplane);

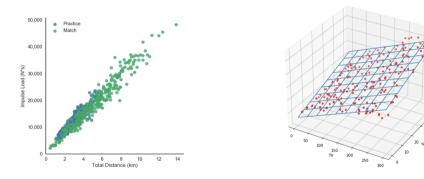
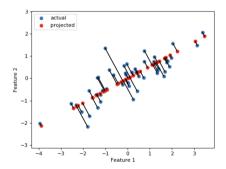


Figure: On the left the data is two dimensional but looks like there is a 1d latent dimension. On the right the data is three dimensional but looks like there is a 2d latent dimension.

Principal Components Analysis (PCA)

Goal of PCA: identify this hyperplane and then project data onto this lower dimensional subspace;





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- 5. Multiply our standardized feature matrix X_s by the eigenvectors vectors to project them.

Step 1: start with X

- Example data:
 - One hundred observations;
 - Two numerical variables;
 - $x_2 = 2x_1 3 + ε;$
- ▶ x_1 has mean ≈ 0.54 and standard deviation ≈ 0.28 :
- ▶ x_2 has mean ≈ -1.91 and standard deviation ≈ 0.56 ;

	x_1	x_2
0	0.873429	-1.237948
1	0.968541	-1.062855
2	0.869195	-1.228109
3	0.530856	-1.900809
4	0.232728	-2.463162
95	0.298625	-2.196156
96	0.138385	-2.620040
97	0.635398	-1.754138
98	0.008308	-3.180289
99	0.788583	-1.455530

100 rows × 2 columns

Step 2: standardize X to make X_s

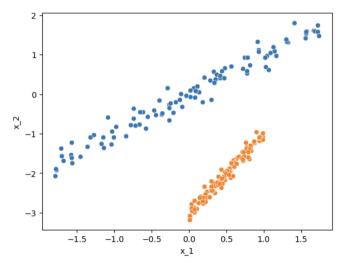
- For each column:
 - Compute the mean and standard deviation;
 - For each entry in the column subtract the mean and divide by the standard deviation;
- ► After this x_1 and x_2 will have mean 0 and standard deviation 1:
- ► Easy to do manually, or can use StandardScaler from sklearn.

	x_1	x_2
0	1.322987	1.310675
1	1.665125	1.615516
2	1.307753	1.327807
3	0.090668	0.156623
4	-0.981766	-0.822445
95	-0.744720	-0.357583
96	-1.321143	-1.095573
97	0.466731	0.411980
98	-1.789058	-2.070977
99	1.017775	0.931861

100 rows x 2 columns

Step 2: standardize X to make X_s

The original data X is in orange and the standardized data X_s is in blue.



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- ▶ But what if we have multiple features how do we measure how one feature varies with another? **Covariance** is a measure of between feature variation!

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- ▶ Variance = square root of standard deviation describes within feature variation;
- ▶ But what if we have multiple features how do we measure how one feature varies with another? **Covariance** is a measure of between feature variation!
- ▶ But didn't we already have correlation to do this job? We did it is a standardized version of covariance:

$$Cov(x,y) = \frac{\sum_{j}(x_{j} - \overline{x})(y_{j} - \overline{y})}{n-1}$$
 and $Corr(x,y) = \frac{Cov(x,y)}{\sigma_{x}\sigma_{y}}$.

Step 3: compute the covariance matrix – wait, but why?!

- ▶ Remember that we want our features to collectively predict our response variable;
- ► The amount our feature varies with our response can be thought of as the information encoded in our feature that is able to predict our response;

Step 3: compute the covariance matrix – wait, but why?!

- Remember that we want our features to collectively predict our response variable;
- ► The amount our feature varies with our response can be thought of as the information encoded in our feature that is able to predict our response;
- Covariance is a way to measure how much information is available in our data across features;
 - ML (and hypothesis testing) is all about separating our observations;
 - ▶ The features that describe our observations provide this separation;
- We want to minimize the correlation between our features;
 - ► If the features contain the same information (covary highly) then adding more won't improve our ability to separate observations;
 - ► Additionally, we may not know or be able to clearly solve for which feature is important for our response.



Step 3: compute the covariance matrix

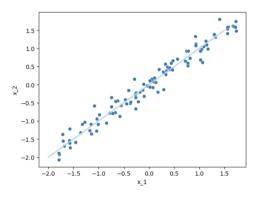
Compute the **covariance matrix** for your scaled features $Cov(X_s) = \frac{1}{n-1}(X_s)^T X_s$:

$$\frac{1}{n-1} \times \overbrace{\left(\begin{array}{ccc}
1.322987 & 1.665125 & 1.307753 & \dots \\
1.310675 & 1.615516 & 1.327807 & \dots
\end{array}\right)}_{X_s} \times \overbrace{\left(\begin{array}{ccc}
1.322987 & 1.310675 \\
1.665125 & 1.615516 \\
1.307753 & 1.327807 \\
0.090668 & 0.156623 \\
\vdots & \vdots & \vdots
\end{array}\right)}_{X_s}$$

$$= \left(\begin{array}{ccc}
1.0000 & 0.9821 \\
0.9821 & 1.0000
\end{array}\right) = Cov(X_s)$$

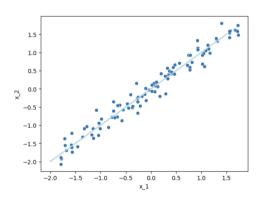
Before we get to step 4...

- ► Looks like we don't really have two dimensions of information here...
- So, what if we put a line through the point cloud? Looks like this line:
 - Was described by a combination of x₁ and x₂;
 - Went along the axis of highest variance;
- If we had a new feature along this line, we might be able to get away with only using it...



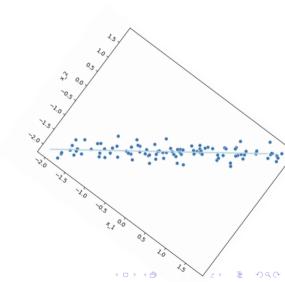
Before we get to step 4...

- We think in Euclidean space the axes are orthogonal;
- ▶ When we plot features, we represent them on these orthogonal axes;
- The axes on which we operate are basis vectors;
- There is nothing stopping us from describing our original features in a new basis...



Before we get to step 4...

- We think in Euclidean space the axes are orthogonal;
- ▶ When we plot features, we represent them on these orthogonal axes;
- The axes on which we operate are basis vectors;
- There is nothing stopping us from describing our original features in a new basis... what if we rotate the space to make new axes?



Step 4: Solve for the eigenvectors and eigenvalues of $Cov(X_s)$ – what?

ightharpoonup If we have a matrix M then the Eigenvalues and Eigenvectors will satisfy:

$$MU = \lambda U$$

- \triangleright λ is the **Eigenvalue**;
- *U* is the **Eigenvector**;

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- Properties of Eigenvalues and Eigenvectors:
 - 1. Each Eigenvalue has an associated Eigenvector;
 - 2. Each pair of Eigenvectors for a symmetric matrix are orthogonal;
 - 3. Any symmetric matrix M is a sum of Eigenvectors weighted by Eigenvalues:

$$M = \sum_{i} \lambda_{i} U_{i} U_{i}^{T}.$$

Step 4: Solve for the eigenvectors and eigenvalues of $Cov(X_s)$ – why?

We can represent all the information in the covariance matrix with a bunch of orthogonal vectors (the Eigenvectors):

$$Cov(X_s) = \sum_i \lambda_i U_i U_i^T;$$

- ► The Eigenvectors are a new basis (new axes) in which feature variance is maximized along the each dimension:
- The Eigenvalues are the importance (explained variance) of each axis;

Our covariance matrix:

$$Cov(X_s) = \left(egin{array}{ccc} 1.0000 & 0.9821 \\ 0.9821 & 1.0000 \end{array}
ight)$$

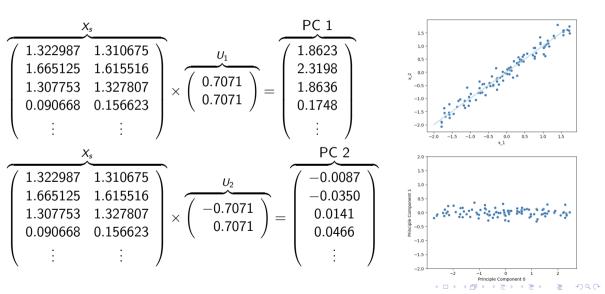
has Eigenvalues/vectors of:

$$\lambda_1 = 1.9821, U_1 = \begin{pmatrix} 0.7071 \\ 0.7071 \end{pmatrix}$$

$$\lambda_2 = 0.0179, U_2 = \begin{pmatrix} -0.7071 \\ 0.7071 \end{pmatrix}$$



Step 5: Multiply X_s by the eigenvectors vectors to project

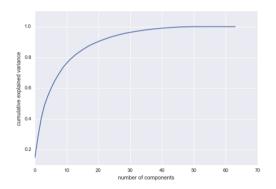


So, how do we use this?

- Now that you have these principal components you can:
 - use them as new features;
 - use them for visualization;
 - use them to compress the data.
- How many components should you use? Compute cumulative explained variance:
 - Sort Eigenvalues largest to smallest;
 - Compute:

$$\frac{\sum_{i=1}^{k} \lambda_i}{\sum_{i} \lambda_i}$$

Choose the number of components that explains a large portion of the variance, e.g. 95%.



PCA – summary

- PCA gives us principal components that we can use as new features;
 - Mixtures of our previous features hard to interpret;
 - Governed by the data that we have (unsupervised);
 - ▶ The information is distilled into the basis vectors with the largest eigenvalues;
 - ► The noise in our data becomes concentrated in the basis vectors with the smallest eigenvalues;
 - ▶ We can use fewer features (principal components) to describe the relationships in our data – Dimensionality Reduction;

- ► IRL we don't perform PCA this way:
 - Covariance matrix will be very large;
 - ▶ We use randomized algorithms or SVD to avoid computing the covariance matrix;
 - ► Good libraries (e.g., scikit-learn) should provide implementations.