# Data

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**ENIB** 

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- 2 Hyper Parameter tuning
- 3 Data preparation
- 4 Graphic tool for DataScientist
  - Introduction
  - Tell me everything, and I'll tell you who you are
  - A non-linear problem
- **5** Reduction of dimension
  - Iris
  - The theory behind principal component analysis

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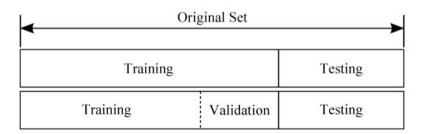
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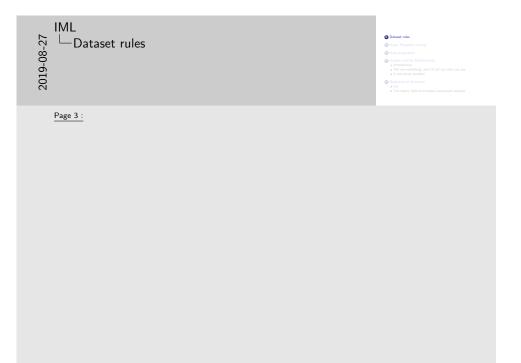
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#### Dataset rules or Parameter tuning Data preparation of for DataScientist

**Dataset** 



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#### Page 4:

How do you think about data? Think of a spreadsheet. You have columns, rows, and cells.

The statistical perspective of machine learning frames data in the context of a hypothetical function (f) that the machine learning algorithm aims to learn. Given some input variables (Input) the function answer the question as to what is the predicted output variable (Output).

Output = f(Input)

The inputs and outputs can be referred to as variables or vectors.

The computer science perspective uses a row of data to describe an entity (like a person) or an observation about an entity. As such, the columns for a row are often referred to as attributes of the observation and the rows themselves are called instances.

```
def split_data(data,prob):
        # split data into fractions [prob, 1 - prob]
        results=[],[]
        for row in data:
                results[0 if random.random() < prob else 1].append(row)
        return results
def train_test_split(x,y,test_pct):
        # pair corresponding values
        data = zip (x, y)
        # split the data set of pairs
        train , test = split_data ( data , 1 - test_pct )
        x_train , y_train = zip ( * train )
        x_test , y_test = zip ( * test )
        return x_train , x_test , y_train , y_test
model = SomeKindOfModel ()
x_{train} , x_{test} , y_{train} , y_{test} = train_{test_{split}} ( xs , ys , 0.33
model . train ( x_train , y_train )
performance = model . test ( x_{test} , y_{test} )
```

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Dataset rules

Hyper Parameter tuning

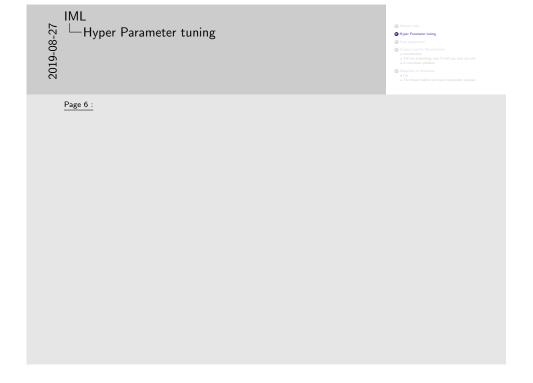
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Reduction of dimension

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IML
Dataset rules

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# Hyper Parameter tuning

- ▶ the parameters of the learning phase: hyper-parameters.
- example: maximum number of values that will be tested in a node of a decision tree, or the number of trees that will contain a random forest.
- ▷ no formal method to find the optimal values from the training data.
- ▶ often use exhaustive search on ranges defined by the developer: this requires in practice to make as many learnings as combinations of parameters. This technique is called *Grid Search*. It uses one of the model's quality metrics to select the best set of hyper-parameters.

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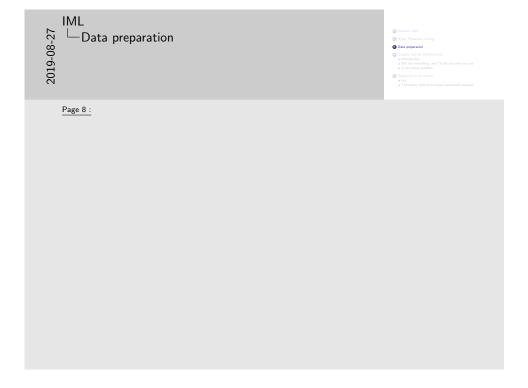
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Hyper Parameter tuning

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# Features and Label

- by the "features": we can measure them and it is from them that we will perform modeling and prediction.
- b the "label": the data that we are trying to predict: in the case of supervised learning, we have the explanatory variable in the learning data.

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☐ Data preparation

Features and Label

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# Preparation of more complex data

- ▶ images : Imagemagick, OpenCV2

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Graphic tool for DataScientist

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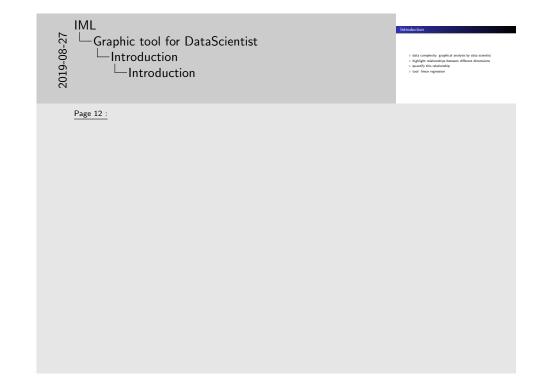
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Graphic tool for DataScientist

# Introduction

- ▶ data complexity: graphical analysis by data scientist
- ▶ highlight relationships between different dimensions
- quantify this relationship
- ▶ tool: linear regression





# NBA: size / weight relationship

- b it is hinted that the weight must increase with size, but to what extent?
- ▷ Is it possible to predict the weight of a player who knows his size?

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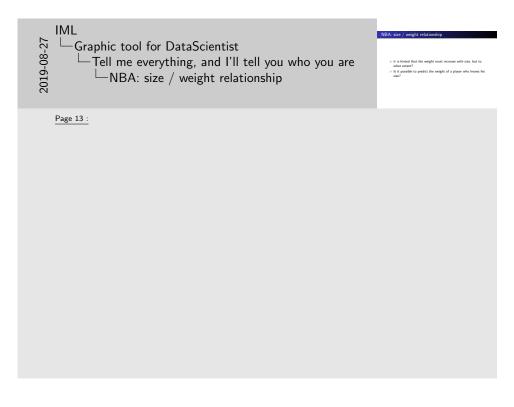
## **Pandas**

```
import pandas as pd
import matplotlib.pyplot as plt
from numpy.linalg import inv
import numpy as np
df = pd.read_csv('players_stats.csv')
height = df.dropna()['Height']
weight = df.dropna()['Weight']
plt.xlabel('Heightu(cm)')
plt.ylabel('Weightu(kg)')
plt.scatter(height, weight)
plt.show()
```

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#### inport punios an pi inport marpinility pypinn an pin form anapy, limaily inport into inpurt manys an sp all pintasi, mon'yingara, anananan'

#### Page 14 :

https://www.kaggle.com/drgilermo/nba-players-stats-20142015. Demo: players\_scatter.py

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# NBA: size / weight relationship

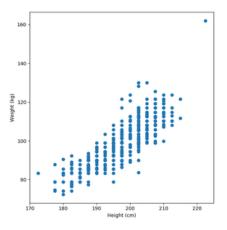


Figure: The weight of our players grows well with their size, and moreover linearly.

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Graphic tool for DataScientist

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# The mathematical tool

- ▶ establish a mathematical relationship between height and weight
- > regression: fit a mathematical model to a set of measures
- $\triangleright$  linear regression: y = a \* x + b where x is named predictor, while y is the variable to predict.
- ▶ NBA, x is the size of the players, while y is their weight.
- $\triangleright$  we have a set of samples of y values for various values of x
- ▶ link model and samples:

$$e = \sum_{i=0}^{n} (a * x_i + b - y_i)^2$$

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Graphic tool for DataScientist

Tell me everything, and I'll tell you who you are □NBA: size / weight relationship



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The vertical lines are artificial, and hold to the resolution of the sizes which are rounded to 2.5 cm. As for the general trend, it seems that weight is linearly related to size.

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Graphic tool for DataScientist

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The mathematical tool

- weight by expression: It is mathematical model to a set of measures beinger expression:  $p \to x + b$  when x is named predict while y is the variable to predict. b = b = b. The  $a \to b$  is the size of the players, while y is the various values of  $b \to b$  in  $b \to b$ . In the size of the players, while y is their weight.  $b \to b$  have a set of samples of y values for various values of  $b \to b$ . In  $b \to b$  in

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b is the value of the variable to predict for x = 0, which is the intercept.

If one represents the operation mentally, it is a question of sliding a rule vertically (which changes b), and of inclining it more or less (which changes a) until the points of our sampling seems to be regularly distributed on both sides of

In mathematical terms, we will derive the previous expression with respect to a and b, then we will seek to cancel this derivative. Indeed, remember your high school math class: a function reaches its extremum where its derivative vanishes.

# The mathematical tool

We will work in matrix form:  $e = (X * A - Y)^{T} (X * A - Y) = (X * A - Y)^{2}$ 

Y is a column vector containing yi

X is a matrix consisting of two columns. The first contains the predictors xi while the second contains only 1.

A meanwhile, is a line vector containing [ab]. The derivative of ewith respect to the parameters we wish to optimize, a and b, contained in A, is:

$$\frac{\partial e}{\partial A} = \frac{\partial (X*A - Y)^T}{\partial A} * (X*A - Y) = X^T (X*A - Y)$$

e reaches its minimum when this expression is null, that is:

$$X^{T}(X*A-Y)=0$$

$$X^{T}X*A=X^{T}Y$$

$$A=(X^{T}X)^{-1}X^{T}Y$$

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Hyper Parameter tuning Graphic tool for DataScientist

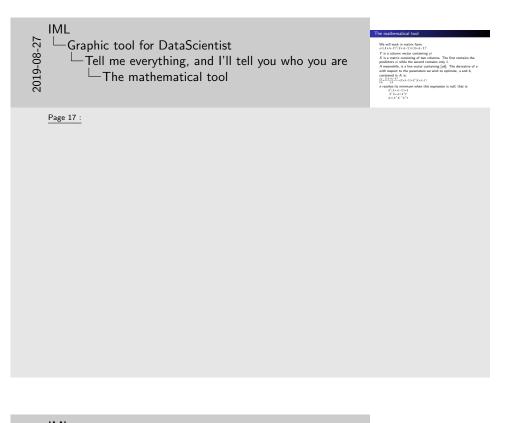
Tell me everything, and I'll tell you who you are

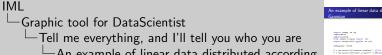
# An example of linear data distributed according to a Gaussian

```
import numpy as np
importmath
importrandom
from numpy.linalg import inv
import matplotlib.pyplot as plt
nbSamples =1000
X = np.matrix([[random.random(), 1] for x inrange(nbSamples)])
Y = np.matrix([3*x[0].item(0) + 0.666for x in X]).transpose()
Gnoise = np.random.normal(0.0,0.1,len(Y))
Ynoisy = np.matrix([Y[i].item(0)+ Gnoise[i]for i inrange(len(Y))]).transpose()
plt.scatter(np.asarray(X[:,0]), np.asarray(Ynoisy))
plt.show()
```

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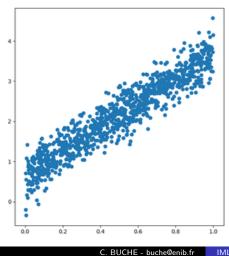
An example of linear data distributed according to a Gaussian

neighborhood of an equation line y = 3 \* x + 0.666. We added a Gaussian noise, of zero mean and with a standard deviation of 0.1

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# An example of linear data distributed according to a Gaussian.



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Tell me everything, and I'll tell you who you are An example of linear data distributed according

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An example of linear data distributed according to a Gaussian

```
A = inv(X.transpose()*X)*X.transpose()*Ynoisy
print(A)
>[[3.00512112]
>[0.66163949]]
```

2019-08-27 to a Gaussian. Page 19: IML Graphic tool for DataScientist Tell me everything, and I'll tell you who you are An example of linear data distributed according to a Gaussian. Page 20 : Let's see now if we fall back on our feet, and if by applying our formula, a = 3, b = 0.666 come out of the hat.

```
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```

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# An example of linear data distributed according to a Gaussian.

```
x = [0,1]
y = [[x[0],1],[x[1],1]] * A
plt.scatter(np.asarray(X[:,0]), np.asarray(Ynoisy))
plt.plot(x, y, color='r')
plt.show()
```

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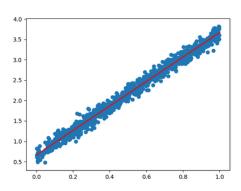
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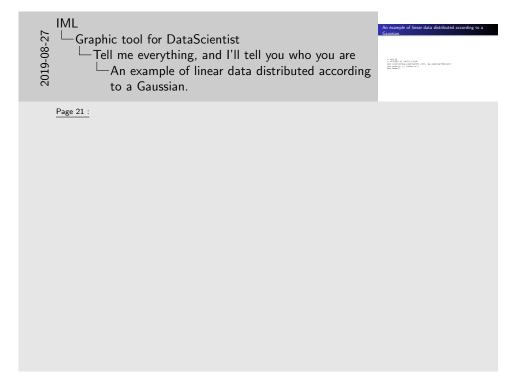
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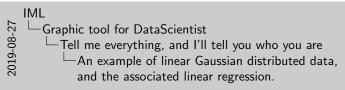
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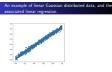
An example of linear Gaussian distributed data, and the associated linear regression.



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# **NBA**

```
import pandas as pd
import matplotlib.pyplot as plt
from numpy.linalg import inv
import numpy as np
df = pd.read_csv('players_stats.csv')
height = df.dropna()['Height']
weight = df.dropna()['Weight']
X = np.zeros((len(height),2))
X[:,0]= height
X[:,1]=1
Xm = np.matrix(X)
```

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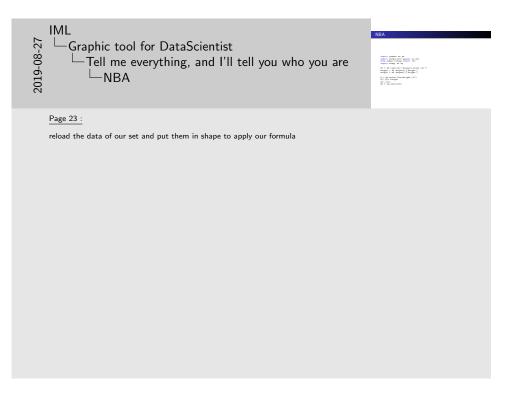
# **NBA**

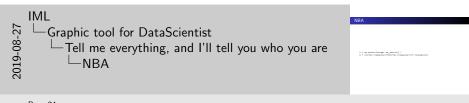
```
Y = np.matrix(weight.as_matrix())
A = inv(Xm.transpose()*Xm)*Xm.transpose()*Y.transpose()
```

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#### Page 24 :

We thus obtain A, which contains the coefficients a, b. It remains to be seen if they provide a good approximation of our data set, by drawing the corresponding line.

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# **NBA**

```
x =[160,230]
y =[[x[0],1],[x[1],1]]*A

plt.xlabel('Height_|(cm)')
plt.ylabel('Weight_|(kg)')
plt.scatter(height, weight)
plt.plot(x, y, color='r')
plt.show()
```

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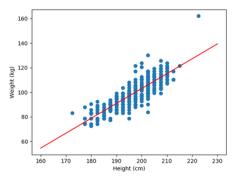
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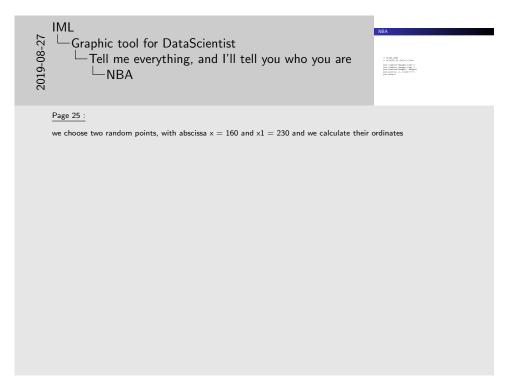
A non-linear problem

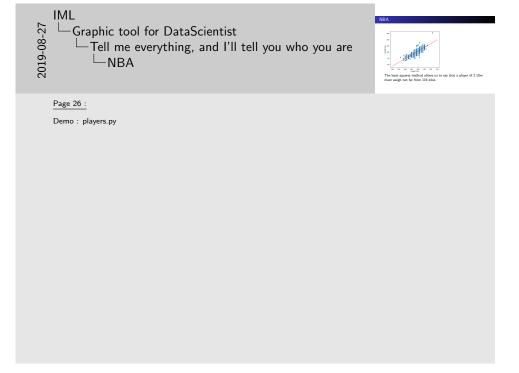
# **NBA**



The least squares method allows us to say that a player of 2.10m must weigh not far from 116 kilos

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# Computer tools

This method works very well, but may become impractical if the number of columns of X becomes too large, the cost of an inversion being in the general case in O(n3). The memory cost can also become prohibitive.

- work with a subset representative of the total ensemble
- develop an inversion algorithm
- $\odot$  opt for an iterative approach, where we start from (a, b) to converge progressively to.

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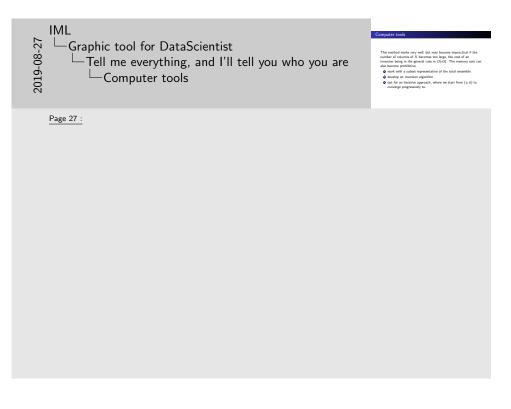
# Let's plot the error according to a

```
import autograd.numpy as np
from autograd import grad
import math
import random
from numpy.linalg import inv
import matplotlib.pyplot as plt
nbSamples =1000
X = np.matrix([[random.random(), 1] for x inrange(nbSamples)])
Y = np.matrix([3*x[0].item(0)+ 0.666for x in X]).transpose()
def error(X, Y, a):
   a = np.matrix([[a],[0.666]])
   e = X*a - Y
   return(e.transpose()* e).item(0)
def genError(X, Y):
   return lambda a : error(X, Y, a)
err = genError(X, Y)
xs = [x *6.0/ nbSamples for x inrange(nbSamples)]
e = [err(x)for x in xs]
plt.plot(xs, e)
```

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# IML

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Graphic tool for DataScientist

Tell me everything, and I'll tell you who you are Let's plot the error according to a

#### Let's plot the error according to a

f = sp.matrix([f=0]):itam(0)\* i.dkfor\*s in 1]) transpose()
def arror(i, Y, s):
 s = sp.matrix([(s], (0.666)])

a = sp.marin([(a),(0.665])) a = Xra - Y return(a transposal) = a).itum(E) def guillerer(E, Y): return landés a : seror(E, Y, a)

def gambrow(L, Y): recent lacks a : error(L, Y, a) err = gambrow(L, Y) err = (a + (a) + shimples for a inrange(shimples a = (arr(s)) for x in an) pls.pin(m, a)

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we capture X and Y to generate a function depending only on a

```
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```

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```
grad_err = grad(err)
def newtonStep(f0, df, x0):
   df0 = df(x0)
  x1 = x0 - f0/ df0
   return x1
def newtonSolver(f, df, x0):
   count =0
   f0 = f(x0)
   whileTrue:
      x0 = newtonStep(f0, df, x0)
     print("iteru%du:u%f"%(count, x0))
      count +=1
      f0 = f(x0)
      if f0< 1e-6:
         break
   return x0
newtonSolver(err, grad_err,0)
```

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```
iter 0 : 1.500000
iter 1 : 2.250000
iter 2 : 2.625000
iter 3 : 2.812500
iter 4 : 2.906250
iter 5 : 2.953125
iter 6 : 2.976562
iter 7 : 2.988281
iter 8 : 2.994141
iter 9 : 2.997070
iter 10 : 2.998535
iter 11: 2.999268
iter 12 : 2.999634
iter 13 : 2.999817
iter 14 : 2.999908
iter 15 : 2.999954
```

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# IML C7-80-6100 -Graphic tool for DataScientist -Tell me everything, and I'll tell you who you are

grad\_werr = grad(err)

del serrording((Gr, dr, dl))

del se d'(Gr, dr)

del se d'(Gr, dr)

rester si (Gr, dr)

del serrordinge((Gr, dr, dr))

serrordinge((Gr, dr, dr))

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The idea is to start from a value of a, say a=0. We calculate for this value err(a) as well as the derivative of the error in:  $\frac{\partial err}{\partial a}(a_0)$ 

to calculate the tangent, I use a little known method, which is the automatic differentiation, without us having to do the calculation of the derivative by hand. This is done by grad(), exported from the autograd module and generating a function of a giving the derivative in a.

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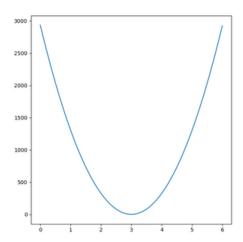
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Tell me everything, and I'll tell you who you are

There 0 : 1.500000 inter 0 : 2.200000 inter 0 : 2.2

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Demo : autodiff.py (ATTENTION MARCHE PAS)



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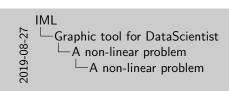
Introduction Tell me everything, and I'll tell you who you are  $\bf A$  non-linear problem

# A non-linear problem

- New York : 7 years of taxi and limousine journeys (1.1 billion trips)
- ▶ the FHV only have three measurements per way
- ▶ Yellow and GreenCabs:
  - the distance;
  - the collection point;
  - the drop point;
  - the price of the trip;
  - the amount of the tip;
  - the number of passengers.

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Tell me everything, and I'll tell you who you are

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Data are available here: https://www1.nyc.gov/site/tlc/about/tlc-trip-record-data.page

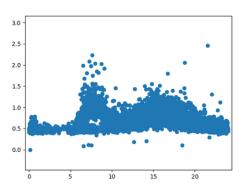
# from JFK Airport to Manhattan's UpperEastSide.

```
import pandas as pd
from dateutil importparser
import matplotlib.pyplot as plt
cols =['PULocationID','DOLocationID','tpep_pickup_datetime','
     tpep_dropoff_datetime','trip_distance']
dfJ = pd.read_csv('yellow_tripdata_2017-01.csv', usecols=cols)
dfF = pd.read_csv('yellow_tripdata_2017-02.csv', usecols=cols)
dfM = pd.read_csv('yellow_tripdata_2017-03.csv', usecols=cols)
dfA = pd.read_csv('yellow_tripdata_2017-04.csv', usecols=cols)
dfMy = pd.read_csv('yellow_tripdata_2017-05.csv', usecols=cols)
df = dfJ.append(dfF).append(dfM).append(dfA).append(dfMy)
#236 manhattan upper east side
JFK_MU = df[(df['PULocationID']==132)&(df['DOLocationID']==236)]
JFK_MU.to_csv("JFKraw.csv", columns=cols)
pu = [parser.parse(dt)for dt in JFK_MU['tpep_pickup_datetime'].values]
do = [parser.parse(dt)for dt in JFK_MU['tpep_dropoff_datetime'].values]
dur = [(b -a).total_seconds()/ 3600.0for a, b inzip(pu, do)]
startTime = [dt.hour+ dt.minute/ 60.0for dt in pu]
plt.scatter(startTime, dur)
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```

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Tell me everything, and I'll tell you who you are
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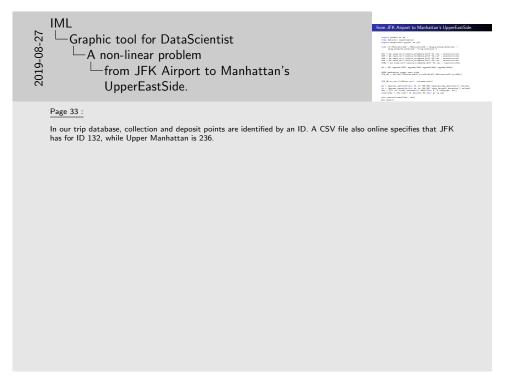
Travel time between JFK and Upper East Side depending on time of departure.



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Graphic tool for DataScientist

A non-linear problem

Travel time between JFK and Upper East Side depending on time of departure.

#### Travel time between JFK and Upper East Side depending on time of departure.



#### Page 34 :

Demo : JFK.py

# Cleaning

- b two peaks are around 7am and 4pm
- b the peak of 7am is not always a real one
- ▶ It's a safe bet that these easy-going points are just weekend days (and probably holidays)

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A non-linear problem

```
import pandas as pd
from dateutil importparser
import matplotlib.pyplot as plt
cols =['PULocationID','DOLocationID','tpep_pickup_datetime','
     tpep_dropoff_datetime','trip_distance']
dfJ = pd.read_csv('yellow_tripdata_2017-01.csv', usecols=cols)
dfF = pd.read_csv('yellow_tripdata_2017-02.csv', usecols=cols)
dfM = pd.read_csv('yellow_tripdata_2017-03.csv', usecols=cols)
dfA = pd.read_csv('yellow_tripdata_2017-04.csv', usecols=cols)
dfMy = pd.read_csv('yellow_tripdata_2017-05.csv', usecols=cols)
df = dfJ.append(dfF).append(dfM).append(dfA).append(dfMy)
JFK_MU = df[(df['PULocationID']==132)&(df['DOLocationID']==236)]
JFK_MU['weekday'] = JFK_MU['tpep_pickup_datetime'].apply(lambda x :parser.parse(x
     ).weekday())
JFK_MU = JFK_MU[JFK_MU['weekday']<5]</pre>
pu = [parser.parse(dt)for dt in JFK_MU['tpep_pickup_datetime'].values]
do = [parser.parse(dt)for dt in JFK_MU['tpep_dropoff_datetime'].values]
dur = [(b -a).total_seconds()/ 3600.0for a, b inzip(pu, do)]
startTime = [dt.hour+ dt.minute/ 60.0for dt in pu]
plt.scatter(startTime, dur)
plt.show()
```

**IML** 2019-08-27 Graphic tool for DataScientist A non-linear problem └─Cleaning

- two peaks are around 7am and 4pm
  the peak of 7am is not always a real one
  It's a safe bet that these easy-going points are just weekend
  days (and probably holidays)

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**IML** 2019-08-27 Graphic tool for DataScientist ─A non-linear problem

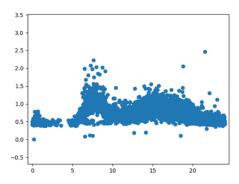
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ys = [parast-paras(ds)dor dt in JE\_NG['tpsy\_pinksy\_datation'].valuas] dt = [parast-paras(ds)dor dt in JE\_NG['tpsy\_dropoff\_datation'].valuas] dur = [(h = 0.0000\_assisting)]. Nddd ddar dt in psy\_pinksy\_datation'] thatTime = [dh.kmar\* dt.winter | dh.dir dt in ps]

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Introduction Tell me everything, and I'll tell you who you are  $\bf A$  non-linear problem

# All aberrations (7am) are almost disappeared.



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IML

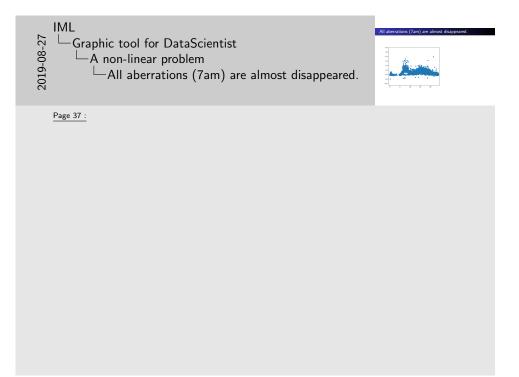
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Data preparation
Graphic tool for DataScientist

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Tell me everything, and I'll tell you who you are
A non-linear problem

# Cerce

- ▷ example of data that clearly does not fit into a linear model
- ▶ use a linear regression: splines
  - $\diamond$  interval [xmin, xmax] on which the spline is defined is divided into n control points  $x_i$ .
  - ♦ At each of these points of control, we add a new line, which alters the pace of the curve defined at this point.
  - $\diamond$  we build a series of functions, generally noted  $I_{plus}^{i}(x)$  which are zero until  $x_i$  and the value is  $x x_i$  from  $x_i$ .

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```
Graphic tool for DataScientist
```

A non-linear problem

```
def Iplus(xi, x):
        if x>= xi: return x - xi
        else: return 0.0
```

This allows you to start a new line at each control point. Once this function has been defined, the calculation of the ordinate of this spline for a given abscissa is straightforward:  $y = S(x) = \sum_{i=0}^{n-1} a_i I_{plus}^i(x) + b$ 

$$y = S(x) = \sum_{i=0}^{n-1} a_i I_{plus}^i(x) + b$$

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A non-linear problem

```
def splinify(xMin, xMax, step, x):
  a = [Iplus(xMin + i *step, x)for i inrange(int((xMax - xMin) / step))]
  a.reverse()
  return a +[1]
np.dot(x, A)
```

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#### Page 39

y is therefore expressed in linear form. We will therefore be able to reuse our linear regression by simply extending it to a dimension greater than 1. Concretely, the matrix X, which up to now consisted of two columns, will henceforth contain n+1. The last column, corresponding b is always filled with 1. The first n, for their part, contain the result of the application of liplus(x) on the abscissa of the current sample.

# IML Graphic tool for DataScientist ☐A non-linear problem

#### Page 40 :

xMin and xMax specify the bounds of the interval including all values of x, while step specifies the distance between each node of our spline. On an interval of [0, 1] and step = 0.1 the spline is based on 10 nodes.

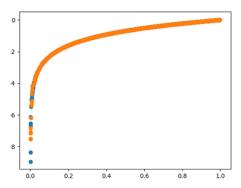
Introduction
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# Case study

```
import numpy as np
import math
import random
from numpy.linalg import inv
import matplotlib.pyplot as plt
nbSamples =1000
X = np.matrix([[random.random(), 1] for x inrange(nbSamples)])
Y = np.matrix([math.log(x[0].item(0))for x in X]).transpose()
def Iplus(xi, x):
        if x>= xi: return x - xi
        else: return 0.0
def splinify(xMin, xMax, step, x):
        a = [Iplus(xMin + i *step, x) for i inrange(int((xMax - xMin) / step))]
        a.reverse()
        return a +[1]
Xm = np.matrix([splinify(0.0, 1.0, 0.01, x[0].item(0))for x in X])
A = inv(Xm.transpose()*Xm)*Xm.transpose()*Y
Yreg = np.matrix([[np.dot(x, A).item(0)]for x in Xm])
plt.scatter(np.asarray(X[:,0]), np.asarray(Y))
plt.scatter(np.asarray(X[:,0]), np.asarray(Yreg))
plt.show()
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```

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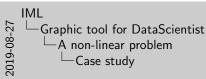
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# Case study

whitepine sides

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T = qp\_natris([[rank.lag(n[0].inra(b)]for = in k]).transpose()

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#### Page 41:

We start with the construction of our dataset by filling in X with values drawn at random in [0, 1]. From there, we populate Y by applying the logarithm function.

Then, in the same way as in the case of the right, we fill Xm with the terms of our polynomial of degree 1, using the splinify() function. A is then calculated with the same formula, and we evaluate in the process our spline for all the abscissae of our sample using a simple scalar product. The result is stored in Yreg.

The last three lines generate the figure, where we see that our modeling by a linear spline of our test set works very well. It is possible to degrade the quality of this modeling by playing on the step parameter of the *splinify()* function.

# IML Craphic tool for DataScientist A non-linear problem



#### Page 42 :

The logarithm function on the interval [0, 1], in blue, and its modeling by the spline, in orange. The two overlap almost perfectly.

Demo : spline.py

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# $\mathsf{JFK} \to \mathsf{Upper} \ \mathsf{Manhattan}$

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Reduction of dimension

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# $\mathsf{JFK} \to \mathsf{Upper} \ \mathsf{Manhattan}$

```
pu = [parser.parse(dt)for dt in JFK_MU['tpep_pickup_datetime'].values]
do = [parser.parse(dt)for dt in JFK_MU['tpep_dropoff_datetime'].values]
dur = [(b -a).total_seconds()/ 3600.0for a, b inzip(pu, do)]
startTime = [dt.hour+ dt.minute/ 60.0for dt in pu]
X = startTime
Y = dur
def Iplus(xi, x):
        if x>= xi:
                        return x - xi
        else: return 0.0
def splinify(xMin, xMax, step, x):
        a = [Iplus(xMin + i *step, x)for i inrange(int((xMax - xMin) / step))]
        a.reverse()
        return a +[1]
Xm = np.matrix([[Iplus(0.5, x), Iplus(0, x), 1]for x in X])
Xm = np.matrix([splinify(np.min(X), np.max(X), 0.1, x)for x in X])
A = inv(Xm.transpose()*Xm)*Xm.transpose()*np.matrix(Y).transpose()
Yreg = np.matrix([[np.dot(x, A).item(0)]for x in Xm])
plt.scatter(X, np.asarray(Y))
plt.scatter(X, np.asarray(Yreg))
plt.show()
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```

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JFK → Upper Manhattan

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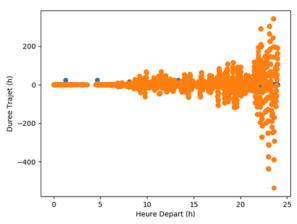
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# $\mathsf{JFK} \to \mathsf{Upper}\ \mathsf{Manhattan}$



overfitting: essential distinction between learning set and validation set !!

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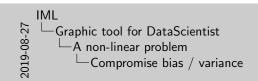
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# Compromise bias / variance

- step = 0.1 (arbitrary)
- b abscissa extending to [0.25]
- > our spline is found with no less than 250 nodes.
- $\triangleright$  large number of degrees of freedom: allows to deform a lot.
- principle of understood bias / variance. That is to say that the data scientist, when he chooses a model for these data, must arbitrate between a too simple model, which would lead to a significant bias, and a model that is too complex, too flexible, that generates too much variance. That's what we just did.

 $\begin{array}{c} IML \\ Graphic tool for DataScientist \\ -A non-linear problem \\ -JFK \rightarrow Upper Manhattan \\ \end{array}$ 

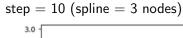


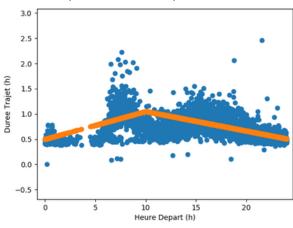
#### Compromise bias / variance

- step = 0.1 (arbitrary)
- abscissa extending to [0.25]
   our soline is found with no less than 250 nodes.
- our spline is found with no less than 250 nodes.
   large number of degrees of freedom: allows to deform a lo
- large number of degrees of freedom: allows to deform a lot. b principle of understood biss; / variance. That is to say that th data scientist, when he chooses a model for these data, must arbitrate between a too simple model, which would lead to a significant bias, and a model that is too complex, too flexible

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# Compromise bias / variance





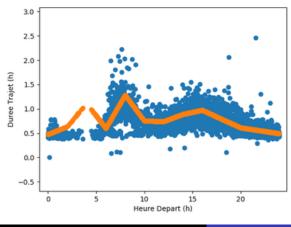
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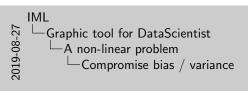
# Compromise bias / variance

step = 2



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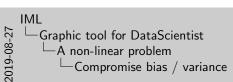
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Demo: splineJFK.py splineJFKVar.py





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To choose the value of our step parameter, we proceeded by iteration, evaluating the quality of the obtained result. This method has the merit of making use of the expertise of the data scientist, but in order to obtain the best result, it is necessary to rely on more scientific criteria.

For this, it is necessary as detailed in the previous box, to have a set of learning and validation. Given these sets, it is then possible to calculate several metrics, to quantify how well the solution models the reality.

These metrics are often measures of errors between the actual values and their prediction using the model. We can cite for example the Mean Absolute Error (MAE) or the Root Mean Square Error (RMSE).

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# Aberrant points

modeling error around 4:20. This error is due to the presence of outliers, which are either measurement errors or extraordinary cases of plugs, failures, etc.

```
# Find a and b
Xm = np.matrix([splinify(np.min(X), np.max(X), 1.0, x)for x in X])
A = inv(Xm.transpose()*Xm)*Xm.transpose()*np.matrix(Y).transpose()
Yreg = np.matrix([[np.dot(x, A).item(0)]for x in Xm])
Yfiltered = [Y[i]for i in range(len(Y)) if ((math.fabs((Y[i]-Yreg[i]) / Y[i]) <
      0.9) and (Y[i] > 0.2) and(Y[i] < 2.5))]
Xfiltered = [X[i]for i in range(len(Y)) if ((math.fabs((Y[i]-Yreg[i]) / Y[i]) <</pre>
      0.9) and (Y[i] > 0.2) and (Y[i] < 2.5)
Xm = np.matrix([splinify(np.min(Xfiltered), np.max(X), 1.0, x)for x in Xfiltered
     ])
 \texttt{A} \ = \ \texttt{inv}(\texttt{Xm.transpose}() * \texttt{Xm}) * \texttt{Xm.transpose}() * \texttt{np.matrix}(\texttt{Yfiltered}). \texttt{transpose}() 
Yfilteredreg = np.matrix([[np.dot(x, A).item(0)]for x in Xm])
plt.xlabel('Heure_Depart_(h)')
plt.ylabel('Duree_Trajet_(h)')
plt.scatter(X, np.asarray(Y))
plt.scatter(Xfiltered, np.asarray(Yfilteredreg))
plt.show()
```

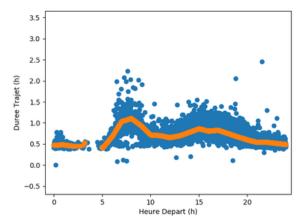
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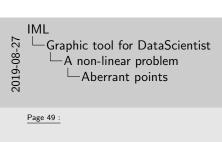
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#### Aberrant point

modeling error around 4:20. This error is due to the presence outliers, which are either measurement errors or extraordinary of plurs. failures, etc.

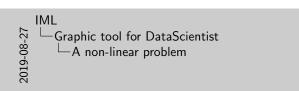
of plugs, failures, etc.

# Find a and h

a reparatio((splinity(sp.min(1), sp.man(1), i.0, s)for a in 1))

 $\begin{aligned} & \text{frag } \times \text{ ap. matrix} \left( \left[ (p, \text{dat}(x, k), \text{turn}(k) \right] / \text{for } x \text{ in } 2k \right] \right) \\ & \text{ With turnd } \times \left\{ \left[ \left( \left[ (k + 1, \text{in } \text{range}(lim(k)) \right], i \right] \left( \text{leach. } \text{fails} \left( \left( \left[ (k - 1, \text{range}(k)) \right], i \right] \right) \right. \\ & \text{ $0, 0$ and } \left( \left[ \left( \left[ (k - 1, \text{in}) \right], \text{sup} \left( \left[ \left( \left[ (k - 1, \text{range}(lim(k)) \right], i \right] \right] \right) \right] \right) \right] \\ & \text{ $0, 1 \text{ and } } \left\{ \left[ \left[ \left( \left[ (k - 1, \text{in}) \right], \text{sup} \left( \left[ \left( \left[ (k - 1, \text{in}) \right], \text{sup} \left( \left[ \left( \left[ (k - 1, \text{in}) \right], \text{sup} \left( \left[ \left( \left[ (k - 1, \text{in}) \right], \text{sup} \left( \left[ \left( \left[ (k - 1, \text{in}) \right], \text{sup} \left( \left[ \left( \left[ (k - 1, \text{in}) \right], \text{sup} \left( \left[ \left( \left[ (k - 1, \text{in}) \right], \text{sup} \left( \left[ \left( \left[ (k - 1, \text{in}) \right], \text{sup} \left( \left[ \left( \left[ (k - 1, \text{in}) \right], \text{sup} \left( \left[ \left( \left[ (k - 1, \text{in}) \right], \text{sup} \left( \left[ \left( \left[ (k - 1, \text{in}) \right], \text{sup} \left( \left[ \left( \left[ (k - 1, \text{in}) \right], \text{sup} \left( \left[ \left( \left[ (k - 1, \text{in}) \right], \text{sup} \left( \left[ \left( \left[ (k - 1, \text{in}) \right], \text{sup} \left( \left[ \left( \left[ (k - 1, \text{in}) \right], \text{sup} \left( \left[ \left( \left[ (k - 1, \text{in}) \right], \text{sup} \left( \left[ \left( \left[ (k - 1, \text{in}) \right], \text{sup} \left( \left[ \left( \left[ (k - 1, \text{in}) \right], \text{sup} \left( \left[ \left( \left[ (k - 1, \text{in}) \right], \text{sup} \left( \left[ \left( \left[ (k - 1, \text{in}) \right], \text{sup} \left( \left[ \left( \left[ (k - 1, \text{in}) \right], \text{sup} \left( \left[ \left( \left[ (k - 1, \text{in}) \right], \text{sup} \left( \left[ (k - 1, \text{in}) \right], \text{sup} \left( \left[ \left( \left[ (k - 1, \text{in}) \right], \text{sup} \left( \left[ \left( \left[ (k - 1, \text{in}) \right], \text{sup} \left( \left[ \left( \left[ (k - 1, \text{in}) \right], \text{sup} \left( (k - 1, \text{in}) \right], \text{sup} \left( (k - 1, \text{in}) \right), \text{sup} \left( (k - 1, \text{$ 

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The code was developed under Ubuntu, and is available on GitHub: https://github.com/kayhman/SmartLinearReg

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- 2 Hyper Parameter tuning
- 3 Data preparation
- 4 Graphic tool for DataScientist
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  - A non-linear problem
- **5** Reduction of dimension
  - Iris
  - The theory behind principal component analysis

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Reduction of dimension

The theory behind principal component analysi

# Introduction

- > number of variables in a dataset becomes too large.
- precise analysis in each of the dimensions, it takes a set of measures quite gigantic
- b difficult for a human to understand the relationships between so many variables.

IML
—Reduction of dimension

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# Example

3 different iris species, brings together four different measures:

- ▶ the length of the sepals;
- ▶ the width of the sepals;
- ▶ the length of the petals;
- ▶ the width of the petals

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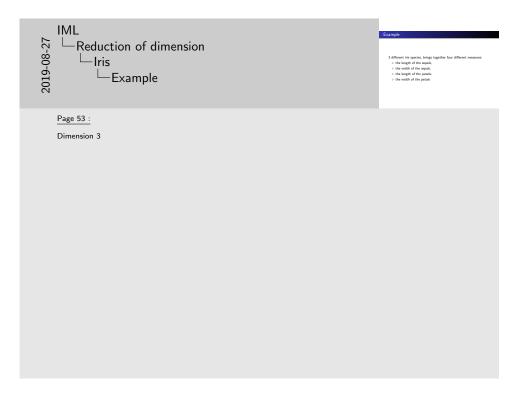
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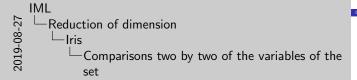
# Comparisons two by two of the variables of the set

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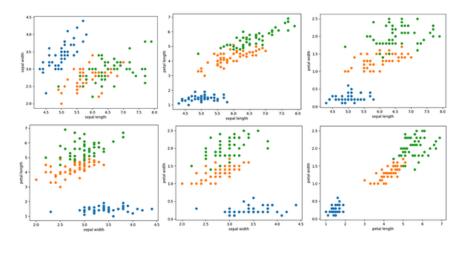
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The dimension of this set, n = 4, being reduced, the number of graphs to be plotted does not exceed n (n-1) / 2 = 6. This remains analysable by a human, and it is also easy to generate automatically these analyzes



The theory behind principal component analysis

# Comparisons two by two of the variables of the set



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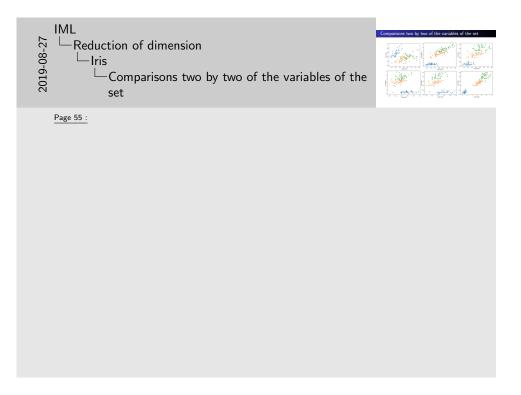
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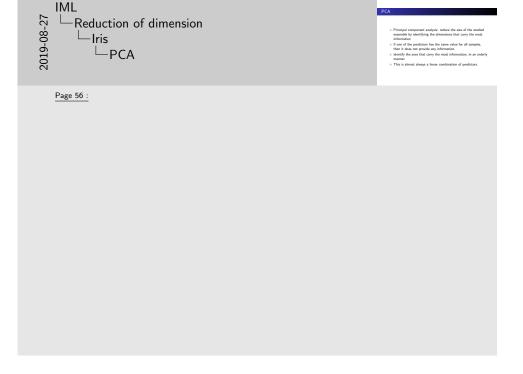
Dataset rules Hyper Parameter tuning Data preparation Graphic tool for DataScientist Reduction of dimension

The theory behind principal component analysi

# **PCA**

- ▶ Principal component analysis: reduce the size of the studied ensemble by identifying the dimensions that carry the most information
- if one of the predictors has the same value for all samples, then it does not provide any information
- identify the axes that carry the most information, in an orderly manner
- ▶ This is almost always a linear combination of predictors.





# a simple 2D case

```
import matplotlib.pyplot as plt
from sklearn import datasets
from sklearn.decomposition import PCA
from random importrandom
import numpy as np

nbSamples =1000
X0 = [random()for x inrange(nbSamples)]
X1 = [3.1416*x for x in X0]

plt.scatter(X0, X1)
plt.show()
```

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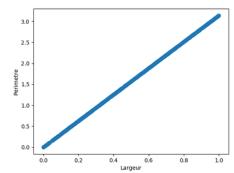
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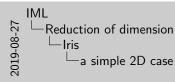
The relationship between our

two predictors is clearly linear. By identifying the relationship between them, it is possible to reduce our set to one dimension.

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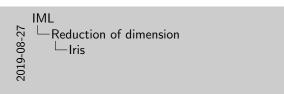


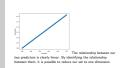
O case

import marginatile popiet as pix from ablance import factories from ablance import factories from ablance. Interpretable import margin and ablance import margin and ablance with the control of the control of the from a for a large (ablancies ii s [0.1660 et a la 20] pix. secure (Qs. 13)

#### Page 57 :

In this example, we collect the width of an object and its perimeter. Now, it turns out that all these objects are disks. Given their width d, which is none other than their diameter, it is easy to calculate their perimeter  $p=d*\pi$ .





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```
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```

```
import matplotlib.pyplot as plt
from sklearn import datasets
from sklearn.decomposition import PCA
from random importrandom
import numpy as np

nbSamples =1000
X0 = [random()for x inrange(nbSamples)]
X1 = [3.1416*x for x in X0]

X = np.matrix((X0, X1)).transpose()
pca = PCA(n_components=2)
pca.fit(X)
print(pca.components_[0])
print(pca.components_variance_)
```

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```
[[ 0.30331383 0.95289072]
[-0.95289072 0.30331383]]
[ 3.04402295e+01 2.11846137e-15]

>>> pca.components_[0][1]/ pca.components_[0][0]
3.1416000000000022

>>> np.dot(pca.components_[0], pca.components_[1])
0.0

>>> np.linalg.norm(pca.components_[0])
1.0

>>> np.linalg.norm(pca.components_[1])
1.0
```

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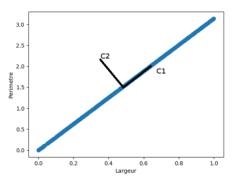


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Note that if we do the ratio between the two coordinates of the first vector, we fall well on  $\pi$ . Very important point too, if we have fun making the scalar product between these two vectors, we discover that they are orthogonal



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The first axis, the one with the greatest eigenvalue, is enough to capture our whole

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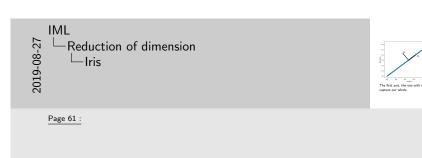
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the matrix presented above can be considered, in the case 2D at least, as a rotation matrix.

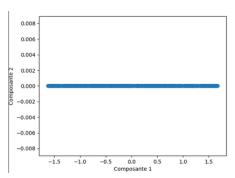
```
import matplotlib.pyplot as plt
from sklearn import datasets
from sklearn.decomposition import PCA
from random importrandom
import numpy as np
nbSamples =1000
X0 = [random() for x inrange(nbSamples)]
X1 = [3.1416*x for x in X0]
X = np.matrix((X0, X1)).transpose()
pca = PCA(n_components=2)
X_r = pca.fit(X).transform(X)
print(pca.components_)
print(pca.singular_values_)
plt.scatter(X_r[:,0], X_r[:,1])
plt.xlabel("Composante_1")
plt.ylabel("Composante_2")
plt.show()
```

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No doubt, the second dimension of our 2D case definitely does not help.

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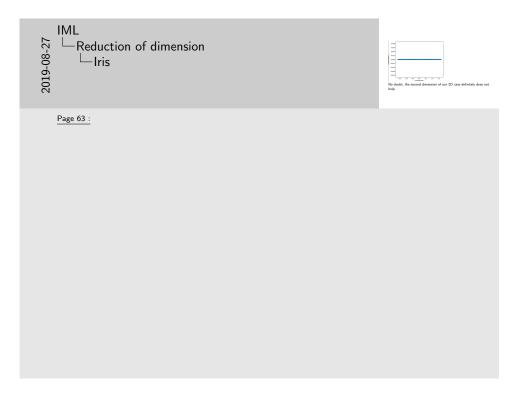
Iris
The theory behind principal component analysi

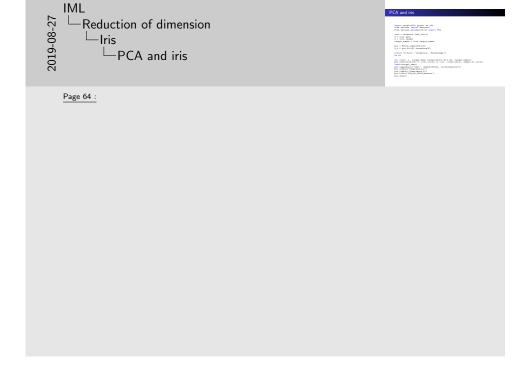
# PCA and iris

```
import matplotlib.pyplot as plt
from sklearn import datasets
from sklearn.decomposition import PCA
iris = datasets.load_iris()
X = iris.data
y = iris.target
target_names = iris.target_names
pca = PCA(n_components=4)
X_r = pca.fit(X).transform(X)
colors =['navy','turquoise','darkorange']
for color, i, target_name inzip(colors,[0,1,2], target_names):
plt.scatter(X_r[y == i,0], X_r[y == i,1], color=color, alpha=.8, lw=lw,
label=target_name)
plt.legend(loc='best', shadow=False, scatterpoints=1)
plt.xlabel("Composante_1")
plt.ylabel("Composanteu2")
plt.title('PCA_of_IRIS_dataset')
plt.show()
```

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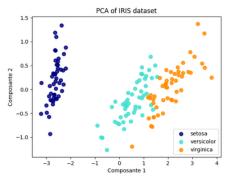
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The theory behind principal component analysis



Principal component analysis automatically provides a representation that separates the different types of iris.

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# PCA et iris

>>> print(pca.components\_)
[[0.36158968-0.082268890.856572110.35884393]
[0.656539880.72971237-0.1757674-0.07470647]
[-0.580997280.596418090.072524080.54906091]
[0.31725455-0.32409435-0.479718990.75112056]]
>>> print(pca.exaplained\_variances\_)
[25.089863986.007852543.420535381.87850234]

a lot of the information is contained in the first dimension

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# **BIPLOT**

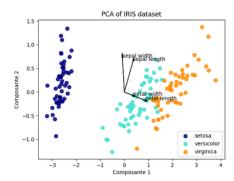
```
import matplotlib.pyplot as plt
from sklearn import datasets
from sklearn.decomposition import PCA
iris = datasets.load_iris()
X = iris.data
y = iris.target
target_names = iris.target_names
pca = PCA(n_components=4)
X_r = pca.fit(X).transform(X)
colors =['navy','turquoise','darkorange']
for color, i, target_name inzip(colors,[0,1,2], target_names):
  plt.scatter(X_r[y == i,0], X_r[y == i,1], color=color, alpha=.8, lw=lw,
label=target_name)
plt.legend(loc='best', shadow=False, scatterpoints=1)
plt.xlabel("Composante_1")
plt.ylabel("Composante_2")
plt.title('PCA_of_IRIS_dataset')
props =["sepal_length", "sepal_width", "petal_length", "petal_width"]
for i inrange(4):
   x = pca.components_[0][i]
   y = pca.components_[1][i]
   plt.arrow(0,0, x, y, head_width=0.05, head_length=0.1, fc='k', ec='k')
   plt.text(x, y, props[i])
   plt.show()
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```

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# **BIPLOT**

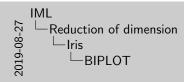


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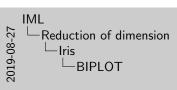


# BPLOT The second secon

#### Page 67:

biplot: display on a 2D graph the maximum of information on all dimensions of the problem. This tool allows to display several dimensions in only two dimensions.

For this, we start from the projection of our data in the 2D plane described by the first two main components of our analysis. Then we display in the form of 2D vectors the initial dimensions of the problem considered.





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# Reduction of dimension

# **BIPLOT**

```
# moyenne de la longueur du petale - setosa
np.std(iris.data[y==0][:,2])
# -> 0.17176728442867112
# moyenne de la longueur du petale - versicolor
np.std(iris.data[y==1][:,2])
# -> 0.4651881339845203
# moyenne de la longueur du petale - virginica
np.std(iris.data[y==2][:,2])
# -> 0.54634787452684397
```

The length of the petals of the setosa is clearly smaller than for versicolor and virginica.

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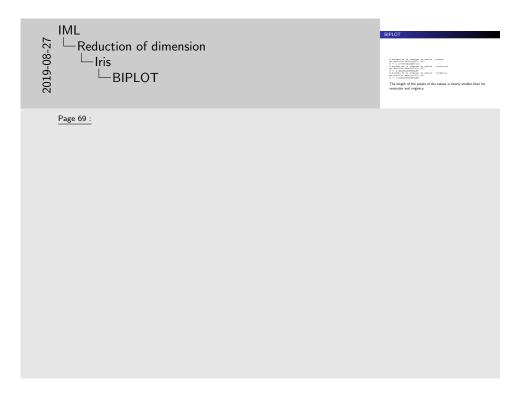
Reduction of dimension

# **BIPLOT**

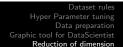
```
# moyenne de la Largeur du sepale - setosa
np.std(iris.data[y==0][:,1])
# -> 0.37719490982779713
# moyenne de la Largeur du sepale - versicolor
np.std(iris.data[y==1][:,1])
# -> 0.31064449134018135
# moyenne de la Largeur du sepale - virginica
np.std(iris.data[y==2][:,1])
# -> 0.31925538366643091
```

In this case, the values are very close: it is not a good parameter to distinguish the different species.

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The theory behind principal component analysis

# Normalization

- ▶ Principal component analysis provides a series of analysis axes that capture the variability of the data studied, in descending order.
- ▶ The data thus spread widely along the first axis, while they are fairly condensed around the last one.
- ▷ If the data are not normalized, that is, if they have not been reworked in such a way that their averages are zero, and their standard deviations are 1.0, then the analysis may be skewed by differences in units used.

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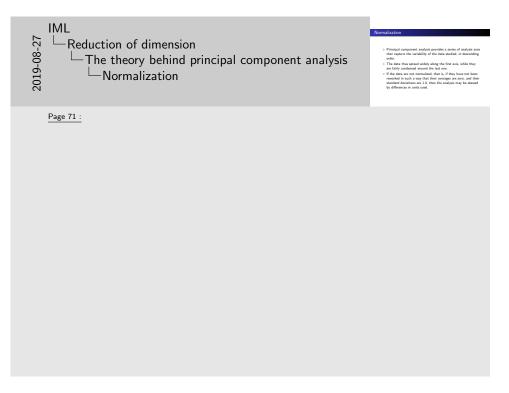
The theory behind principal component analysis

## Raw data

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The theory behind principal component analysis
Raw data

#### Raw data

from ablesce import propressuring import marphable, pypint as pix

min "['prin', 'armin\_prin', 'dainr,am','equa', 'plinder', 'herspoor di pa'rmi, me'(dainr,de. ver, 'me'), 'me'(dainr,am', 'me'), 'me'(dainr') pa " (da'rmi, me'(dainr,de. ver, 'me'), 'me'(dainr') pa " (da'('prin', 'prin')) (da'('aqua')) pa " (da'('prin', 'me'), 'da'('aqua'))

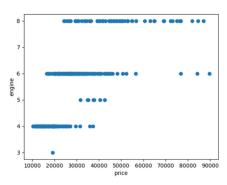
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To illustrate the importance of standardization, we will focus on two variables: price and engine capacity. The price is given in dollars, while the cubic capacity is in liters. Without normalization, we compare data that have very different scales, which bias the result.

The theory behind principal component analysis

# **BIPLOT**



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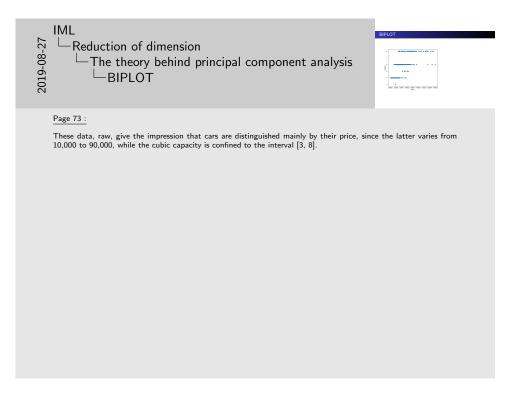
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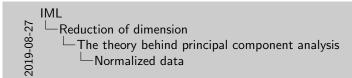
# Normalized data

Let's normalize our data: a zero mean and a standard deviation of  $\boldsymbol{1}$ 

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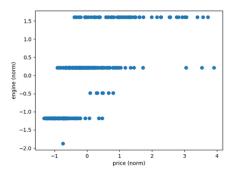




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# Normalized data



Price and displacement of cars, once standardized. These two axes now seem to contain information.

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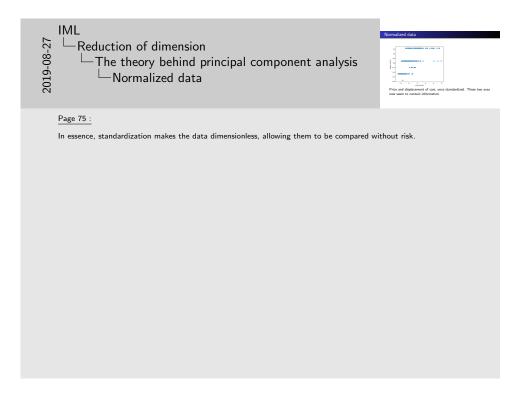
# **PCA**

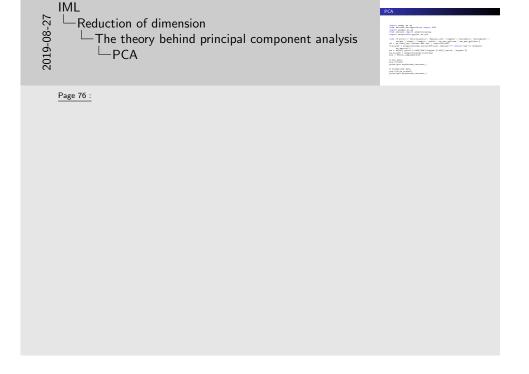
```
import numpy as np
from sklearn.decomposition import PCA
import pandas as pd
from sklearn import preprocessing
import matplotlib.pyplot as plt
cols =['price','invoiceuprice','dealerucost','engine','cylinders','horsepower','
weight','wheel','length','width','cmuperugallons','hmuperugallons']
df = pd.read_csv('04cars.dat.txt', usecols=cols)
X_scaled = preprocessing.scale(df[cols].replace('*',float('nan')).dropna().
      as_matrix())
pe = df[df['price']>1000][df['engine']<10][['price', 'engine']]</pre>
pe_scaled = preprocessing.scale(pe)
pca = PCA(n_components=2)
# raw data
pca.fit(pe)
print(pca.explained_variance_)
# normalized data
pca.fit(pe_scaled)
print(pca.explained_variance_)
```

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The theory behind principal component analysis

# **PCA**

# raw data [ 2.32179369e+08 1.08822536e+00]

# normalized data [ 1.69570742 0.31072345]

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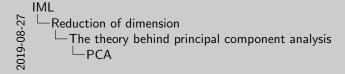
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The theory behind principal component analysis

# Correlation matrix

- ▷ in Python: C = pe\_scaled.transpose()\*pe\_scaled
- ▶ This matrix contains valuable information: each element Cij quantifies the relationship between the variables i and j. If Cij is positive, then when i grows, then j as well. If, on the other hand, it is negative, then j decreases while i increases.
- ▷ In the case where Cij is zero, and that's where it gets interesting, then the variables i and j are not correlated. They therefore vary independently of each other.
- ▶ The particular case where the matrix is diagnonal is therefore particularly sympathetic, because in this case, the variables are all independent of each other.

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f raw data ( 1.55/FERGU-OR 1.08820036a-0 f normalised data

#### Page 77 :

The principal component analysis therefore makes the same observations as we do. In the first case, that of raw data, it is fooled by the difference in unity between price and engine capacity, and unduly believes that most of the information is carried by a single axis.

In the second case, the analysis is more measured because the variance of the data is not clearly driven by a single

# 2019-08-27 T T \_\_\_

# Reduction of dimension

The theory behind principal component analysis

Correlation matrix

#### Correlation matrix

- in Python: C = pea-scaled.transpose()\*pea-scaled
  This matrix contains valuable information: each element Cji
  quantifies the relationship between the variables i and j. W Cij
  is positive, then when i grows, then j as well. M, on the other
- In the case where Cij is zero, and that's where it gets interesting, then the variables i and j are not correlated. The therefore vary intersection to deach other.
- therefore vary independently of each other.

  The particular case where the matrix is diagnonal is therefo particularly sympathetic, because in this case, the variables

#### Page 78:

It is precisely in this particular case that the analysis in principal components is reduced. Indeed, the correlation matrix C is symmetric, square, and contains real values. It is therefore possible to diagonalize it, that is to say to find a change of reference making the directions orthogonal.

This is precisely what principal component analysis does, by calculating the eigenvectors and the eigenvalues of C. The eigenvectors are then the new axes of analysis, while the eigenvalues make it possible to classify these axes by variance decreasing.

Note that for reasons of performance, we do not always proceed directly to the diagonalization of C, but rather to the decomposition of singular values.

The theory behind principal component analysis

# Data

Cédric Buche

**ENIB** 

August 27, 2019

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