APA-L4-python

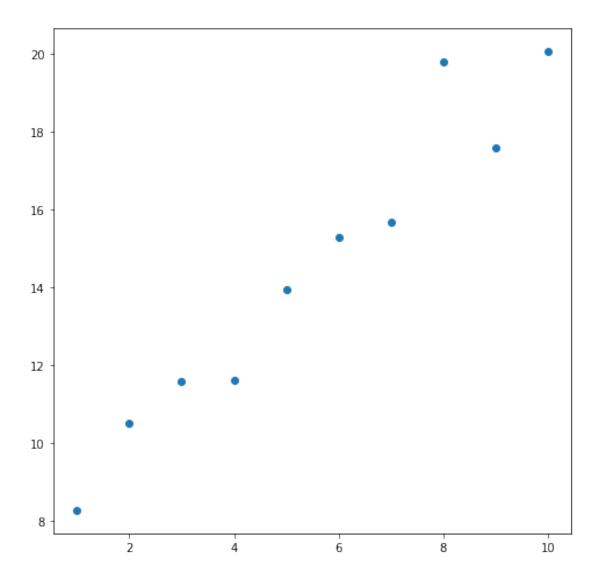
September 6, 2018

1 APA Laboratori 4 - Sistemes lineals (regularitzats)

```
In [1]: # Uncomment to upgrade packages
        # !pip install pandas --upgrade
        # !pip install numpy --upgrade
        # !pip install scipy --upgrade
        # !pip install statsmodels --upgrade
        # !pip install scikit-learn --upgrade
        %load_ext autoreload
In [2]: import numpy as np
        import matplotlib.pyplot as plt
        import seaborn as sn
        import pandas as pd
        pd.set_option('precision', 3)
        from IPython.core.interactiveshell import InteractiveShell
        InteractiveShell.ast_node_interactivity = "all"
In [3]: # Extra imports
        from numpy.random import normal
        from numpy.linalg import inv, svd, cond, pinv
        from statsmodels.genmod.generalized_linear_model import GLM
        from pandas import read_csv
        from scipy import stats
        from sklearn.linear_model import RidgeCV, Ridge
        from sklearn.linear_model import LassoCV, Lasso
   veiem que les matrius AA^T i A^TA són diferents
   1 j es la unitat imaginaria, definim la matriu
In [4]: A = np.array([[0,1j],[0,1]])
Out[4]: array([[0.+0.j, 0.+1.j],
               [0.+0.j, 1.+0.j]
   A \cdot A^T és la matriu (-1 i; i 1)
```

```
In [5]: A@A.T # el simbol @ es la multiplicació de matrius en numpy
Out[5]: array([[-1.+0.j, 0.+1.j],
               [ 0.+1.j, 1.+0.j]])
   A^T \cdot A és la matriu tot zeros
In [6]: A.T@A
Out[6]: array([[0.+0.j, 0.+0.j],
               [0.+0.j, 0.+0.j]
1.1 EXEMPLE 1
Resolució d'un problema artificial senzill
   Definició del sistema lineal a resoldre
   t = f(x) + \epsilon
   on f(x) = (1+1/9)(x-1) + 10 i \epsilon \sim N(0,1)
In [7]: N=10
        X=np.array([[1]*N,range(1,11)]).T
        Х
Out[7]: array([[ 1, 1],
               [1, 2],
               [1, 3],
               [1, 4],
               [1, 5],
               [1, 6],
               [1, 7],
               [1, 8],
               [1, 9],
               [ 1, 10]])
In [8]: t= np.linspace(9,20,num=N)+normal(size=N)
        t
Out[8]: array([ 8.27098422, 10.52270153, 11.57451043, 11.61698802, 13.93946336,
               15.27490323, 15.66396609, 19.78918239, 17.59525074, 20.07005656])
In [9]: fig, ax = plt.subplots(figsize=(8,8))
```

ax.plot(X[:,1], t, 'o');



1.1.1 Solució de problemes de mínims quadrats de l'estil

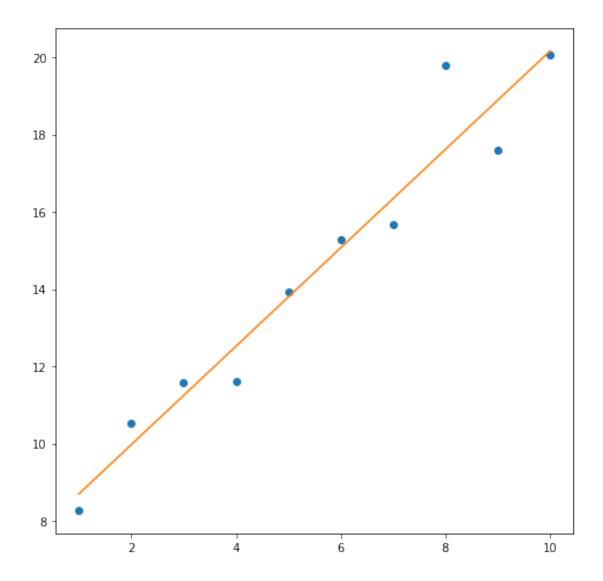
$$\min_{w} ||t - Xw||^2$$

1) Resolució mitjançant la pseudo-inversa

$$X^T\cdot X$$

In [10]:
$$C = X.T @ X$$
 C

$$(X^T \cdot X)^{-1} \cdot X^T$$



2) Resolució mitjançant la SVD

```
In [15]: u, d, v = svd(X, full_matrices=False)
         u,d,v
Out[15]: (array([[ 0.0571102 ,
                                0.58497262],
                 [ 0.10704739,
                                0.48685286],
                 [ 0.15698459,
                                0.38873309],
                                0.29061332],
                 [ 0.20692178,
                 [ 0.25685898,
                                0.19249355],
                 [ 0.30679617,
                                0.09437379],
                 [0.35673337, -0.00374598],
                 [0.40667056, -0.10186575],
                 [0.45660776, -0.19998551],
```

Les dues columnes d'X són linealment independents, i per tant els dos valors singulars són diferents de 0; en altres paraules, rang(X) = 2 = min(10,2), per tant X és "full rank" ara comprovem que $X = UDV^T$

Ara ho apliquem a la solució del problema de mínims quadrats $\min_{w} ||t - Xw||^2$

```
In [17]: D = np.diag(1/d)

w = v @ D @ u.T @ t

w
```

```
Out[17]: array([7.42349301, 1.27423775])
```

noteu que obtenim la mateixa solució

La rutina glm() implementa regressió lineal per mínims quadrats si li demanem mitjançant el paràmetre family = gaussian

```
In [18]: mostra = pd.DataFrame({'x1':X[:,0], 'x2':X[:,1],'t':t})
        mostra
Out[18]:
           x1 x2
               1 8.271
        0
            1
                2 10.523
        1
            1
        2
                3 11.575
            1
        3
          1
               4 11.617
        4
            1
                5 13.939
        5
                6 15.275
               7 15.664
        6
        7
          1
              8 19.789
        8
            1
              9 17.595
        9
            1 10 20.070
```

Noteu que glm sempre afegeix un terme intercept o offset (un regressor constant 1) per defecte, així que tenim dues opcions:

1) desactivar-lo (el "-1" a la fòrmula següent) i usar la nostra pròpia columna de 1's

```
In [19]: model1 = GLM.from_formula('t ~ x2 + x1 -1', mostra)
         result = model1.fit()
  2) usar la que glm ja posa (recomanat) i desactivar la nostra pròpia columna de 1's
In [20]: model2 = GLM.from_formula('t ~ x2', mostra)
         result = model2.fit()
   Els coefficients (el vector w)
In [21]: result.params
Out[21]: Intercept
                       7.423
         x2
                       1.274
         dtype: float64
   ** Per què la SVD?**
  a. En formar la matriu X^TX es pot perdre informació
In [22]: eps = 1e-3
         X_{eps} = np.array([[1,1],[eps,0],[0,eps]])
         X_eps
Out[22]: array([[1. , 1.
                 [0.001, 0.
                              ],
                 [0. , 0.001]])
In [23]: C_eps = X_eps.T @ X_eps
         C_eps
Out[23]: array([[1.000001, 1.
```

In [24]: inv(C_eps)# comencem a tenir problemes ...

, 1.000001]])

In [25]: eps = 1e-10 $X_{eps} = np.array([[1,1],[eps,0],[0,eps]])$

```
Out[25]: array([[1.e+00, 1.e+00],
                [1.e-10, 0.e+00],
                [0.e+00, 1.e-10]])
```

Г1.

```
In [26]: C_eps = X_eps.T @ X_eps
Out[26]: array([[1., 1.],
                [1., 1.]])
In [27]: inv(C_eps)# dóna error (la matriu 2x2 "tot uns" és singular)
        LinAlgError
                                                   Traceback (most recent call last)
        <ipython-input-27-3e489997295d> in <module>()
    ----> 1 inv(C_eps)# dóna error (la matriu 2x2 "tot uns" és singular)
        /usr/local/lib64/python3.6/site-packages/numpy/linalg/linalg.py in inv(a)
                signature = 'D->D' if isComplexType(t) else 'd->d'
        530
        531
                extobj = get_linalg_error_extobj(_raise_linalgerror_singular)
    --> 532
                ainv = _umath_linalg.inv(a, signature=signature, extobj=extobj)
                return wrap(ainv.astype(result_t, copy=False))
        533
        534
        /usr/local/lib64/python3.6/site-packages/numpy/linalg/linalg.py in _raise_linalgerror_si
         88 def _raise_linalgerror_singular(err, flag):
                raise LinAlgError("Singular matrix")
    ---> 89
         90
         91 def _raise_linalgerror_nonposdef(err, flag):
        LinAlgError: Singular matrix
  (el determinant és 1ů1 - 1ů1 = 0)
```

però no ho hauria de ser ... aquesta no és la nostra matriu ... el problema és que l'operacio X^T X fa perdre molta precissió numèrica (hem perdut epsilon)

b. El número de condició d'una matriu

El número de condició d'una matriu és el producte entre la norma de la matriu i la norma de la seva inversa Dóna una indicació de l'exactitud dels resultats de la inversió d'una matriu Valors prop d'1 indiquen una matriu ben condicionada

El número de condició de la matriu X^TX és el quadrat del de la matriu X

Incidentalment, el número de condició corresponent a usar la norma-2 equival al quocient entre el valor singular més gran i el més petit (no nul) de la matriu

La rutina cond() calcula el número de condició

```
In [28]: cond(X)
         cond(X.T @ X)
Out [28]: 13.679030222900371
Out [28]: 187.1158678390236
  veiem-ho amb un exemple:
In [29]: X= np.array([[1]*N, np.linspace(101,110,num=10)]).T
Out[29]: array([[ 1., 101.],
                  1., 102.],
                [ 1., 103.],
                [ 1., 104.],
                [ 1., 105.],
                [ 1., 106.],
                [ 1., 107.],
                [ 1., 108.],
                [ 1., 109.],
                [ 1., 110.]])
In [30]: cond(X)
         cond(X.T @ X)
Out[30]: 3878.275839190437
Out [30]: 15041023.484257316
  Una solució molt senzilla és centrar la segona columna:
In [31]: X= np.array([[1]*N, np.linspace(101,110,num=10)]).T
         X[:,1] = X[:,1] - np.mean(X[:,1])
         Х
Out[31]: array([[ 1. , -4.5],
                [1., -3.5],
                [1., -2.5],
                [ 1. , -1.5],
                [1., -0.5],
                [1., 0.5],
                [1., 1.5],
                [1., 2.5],
                [1., 3.5],
                [1., 4.5]])
In [32]: cond(X)
         cond(X.T @ X)
```

```
Out [32]: 2.8722813232690134
```

```
Out[32]: 8.25
```

Hi ha una relació senzilla entre els dos sistems lineals; en altres paraules, podem "postprocessar els coeficients de sortida perquè corresponguin a la matriu inicial

Nota: hi ha una rutina que calcula directament la pseudo-inversa (ho fa via la SVD):

1.2 EXEMPLE 2

Anem a analitzar dades de greix corporal mitjançant regressió normal i ridge (regularitzada)

```
In [34]: bodyfat_data = read_csv("bodyfatdata.txt",
                                delim_whitespace=True,
                                names=['triceps', 'thigh', 'midarm', 'bodyfat'])
        bodyfat_data.describe()
        N=bodyfat_data.shape[0]
Out [34]:
                        thigh midarm bodyfat
               triceps
                20.000 20.000 20.000
                                         20.000
        count
                25.305 51.170 27.620
                                         20.195
        mean
                 5.023
                        5.235
                                 3.647
                                          5.106
        std
                14.600 42.200 21.300
                                         11.700
        min
        25%
                21.500 47.775 24.750
                                         17.050
        50%
                25.550 52.000 27.900
                                         21.200
        75%
                29.900 54.625 30.025
                                         24.275
                31.400 58.600 37.000
                                         27.200
        max
```

let us start with standard linear regression

Dep. Variable: bodyfat No. Observations: 20
Model: GLM Df Residuals: 16
Model Family: Gaussian Df Model: 3

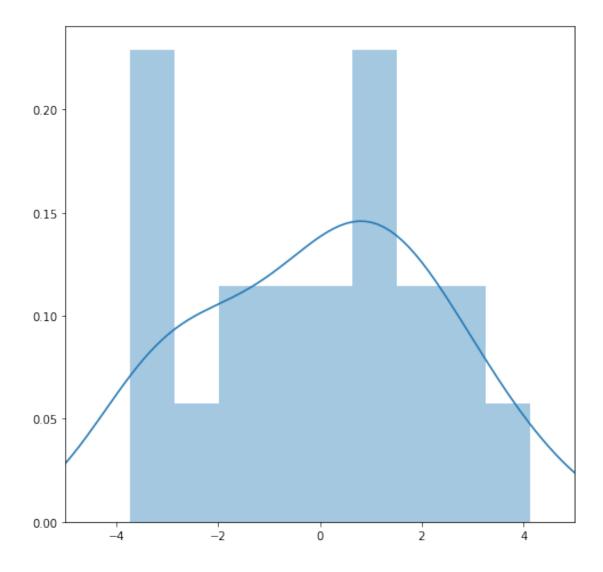
Method: Date: Time: No. Iterations:	Thu,	06 Sep 14:3	IRLS 2018 33:55 3	Devia: Pears	ikelihood: nce: on chi2: iance Type:		-44.312 98.405 98.4 nonrobust
C	oef s	std err		z	P> z	[0.025	0.975]
Intercept 117.0 triceps 4.3 thigh -2.8 midarm -2.1	3341 8568	99.782 3.016 2.582 1.595	-	1.173 1.437 1.106 1.370	0.241 0.151 0.269 0.171	-78.485 -1.576 -7.918 -5.313	312.655 10.244 2.204 0.941

11 11 11

How to read this output:

```
x = (1, triceps, thigh, midarm)^T w = (117.085, 4.334, -2.857, -2.186)^T the model is y(x; w) = w^T x = 117.085 + 4.334 * triceps - 2.857 * thigh - 2.186 * midarm The residuals are the differences (t_n - y(x_n; w)), n = 1, \dots N let's inspect model$residuals
```

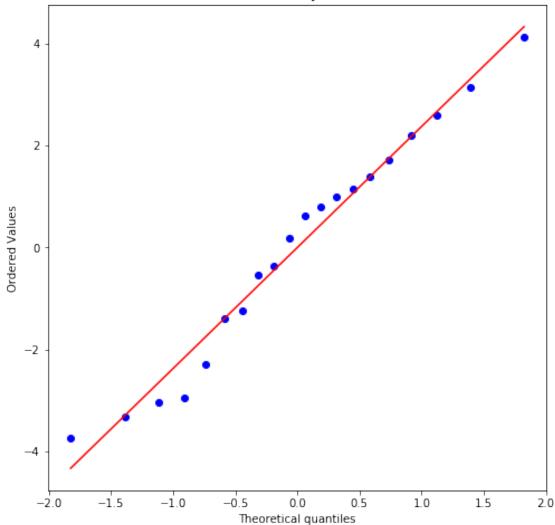
/usr/lib64/python3.6/site-packages/scipy/stats/stats.py:1706: FutureWarning: Using a non-tuple s return np.add.reduce(sorted[indexer] * weights, axis=axis) / sumval



Do the residuals look Gaussian? this is direct indication of model validity (since it was our departing assumption)

Let's do a more informative plot (a QQ-plot), which plots actual quantiles against theoretical quantiles of a comparison distribution (Gaussian in this case)





The solid line corresponds to the theoretical quantiles therefore in this case the residuals are not even close (the tails are heavier, the central part is flatter)

This is how we can compute the mean square error

Is this number large or small? it depends on the magnitude of the targets! a very good practice is to normalise it, by dividing by the variance of the target:

Out [39]: 0.2090962622501365

If we divide the mean square error by the variance of the targets t, we get the proportion of the variability of the target that is NOT explained by the model

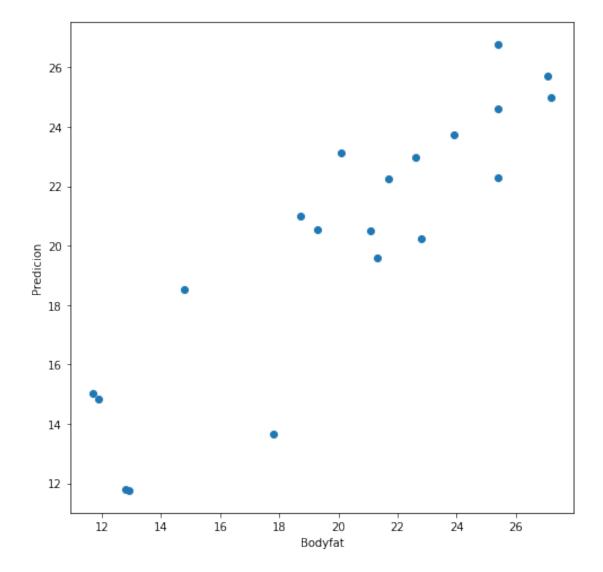
A model with 'norm.mse' equal to 1 is as good as the best constant model (namely, the model that always outputs the average of the target)

models with 'norm.mse' above 0.5 are so so, beyond 0.7 they begin to be quite bad models with 'norm.mse' below 0.2 are quite good

The Multiple R-squared (usually used by statisticians) is obtained by subtracting this quantity form one; that is, the proportion of the target variability that is explained by the model; in this case it reaches $\sim 80\%$

The "adjusted R-squared" is the same thing, but adjusted for the complexity of the model, i.e. the number of parameters (three in our case)

Now let us try to see how are the real predictions by plotting the real predictions against the targets:



It is difficult to see if the model is a good predictor; what we need is a numerical assessment of predictive ability. We compute the exact LOOCV as seen in class:

of predictive ability. We compute the exact LOOCV as section class:
$$LOOCV = \frac{1}{N} \sum_{i=1}^{N} \left(\frac{y_i - \hat{y}_i}{1 - h_i}\right)^2$$
 where $H = X(X^TX)^{-1}X^T$ and $h_i = diag(H)_i$ In [42]: H= np.diag(model.exog@inv(model.exog.T@model.exog)@model.exog.T)
$$LOOCV = \text{np.sum}(\text{ (result.resid_response/(1-H))**2}) / \text{N}$$

$$LOOCV$$
 Out [42]: 8.036828037162582

In [43]: R2_LOOCV = $(1 - LOOCV*N/((N-1)*np.var(bodyfat_data.bodyfat)))*100$ R2_LOOCV

and the corresponding predictive R-square

```
Out [43]: 65.8457880658071
```

we can see that prediction quality is not as good as it seemed (since CV error is worse than training error)

this last number is the one I recommend to do model selection!!!

Let us continue now with *regularized linear regression* (aka ridge regression) this time we need to use scikit-learn RidgeCV

We must first choose a value for lambda (the regularization constant) there are several criteria to do this, the most used of which is the GCV so we optimize the GCV for several values of lambda in a sequence

notice we start with a wide logarithmic search

```
In [44]: lambdas = 10**np.arange(-6,2,0.1)
         ridge = RidgeCV(alphas=lambdas,normalize=True)
         ridge.fit(bodyfat_data.loc[:,'triceps':'midarm'],
                   bodyfat_data.bodyfat)
         print('LAMBDA=',ridge.alpha_);
LAMBDA= 0.0019952623149688256
   best value (according to GCV) is 0.01995262
   we perform a finer search
In [45]: lambdas = np.arange(0.0001,1,0.0001)
         ridge = RidgeCV(alphas=lambdas,
                         normalize=True,
                          store_cv_values=True)
         ridge.fit(bodyfat_data.loc[:,'triceps':'midarm'],
                   bodyfat_data.bodyfat)
         print('LAMBDA=',ridge.alpha_);
LAMBDA= 0.00190000000000000000002
```

Definitely the best value is 0.019, so we refit the model with this precise value:

```
Out[46]: 0
Intercept 23.587
triceps 1.504
thigh -0.435
midarm -0.695
```

Now let us compare these results with those obtained by standard regression (without regularization)

Hand calculation of coefficients, since we know the theory:

they should coincide with the results of GLM

In [49]: R2_L00CV

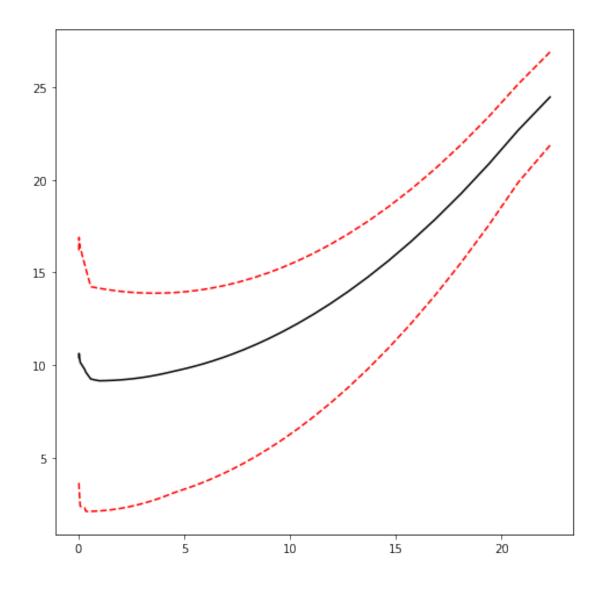
Out [50]: 8.422173377848805

Notice that the regularized weights are smaller (in absolute value), one by one Now we calculate the corresponding prediction errors First by standard regression (without regularization, we already did this)

Out[50]: 64.2081809933659

The prediction errors are quite close and the model is way simpler: we would probably prefer the regularized one

Now we use the LASSO: here the coefficients are penalized by the L1 norm. The optimal value for lambda is again chosen by cross-validation



Predictions can be made based on the fitted object; for instance, this would be the TR error with the *optimal* lambda as chosen by LOOCV

```
In [52]: bodyfat_lasso_reg =Lasso(alpha=1.0349, max_iter=5000)
        bodyfat_lasso_reg.fit(bodyfat_data.loc[:,'triceps':'midarm'],
                               bodyfat_data.bodyfat)
        print('Intercept:', bodyfat_lasso_reg.intercept_)
        print('triceps:', bodyfat_lasso_reg.coef_[0])
        print('thigh:', bodyfat_lasso_reg.coef_[1])
        print('midarm:', bodyfat_lasso_reg.coef_[2]);
Intercept: -17.803172901893376
triceps: 0.18928783908462435
thigh: 0.6489787792428563
midarm: 0.0
In [53]: pd.DataFrame(bodyfat_lasso_reg.predict(bodyfat_data.loc[:,'triceps':'midarm']))
Out [53]:
                  0
             13.859
        0
         1
            19.191
         2
            21.690
         3
             23.077
         4
            13.199
         5 22.023
         6
             26.106
         7
             21.290
         8
           18.764
        9
             21.744
         10 24.816
         11 24.748
         12 15.914
         13 14.611
         14 12.672
         15 23.085
         16 23.329
         17 25.943
         18 17.774
         19 20.065
```

And this would be corresponding LOOCV and the corresponding predictive R-square

Out[54]: 9.023634611567775

Out[54]: 61.652143418386096