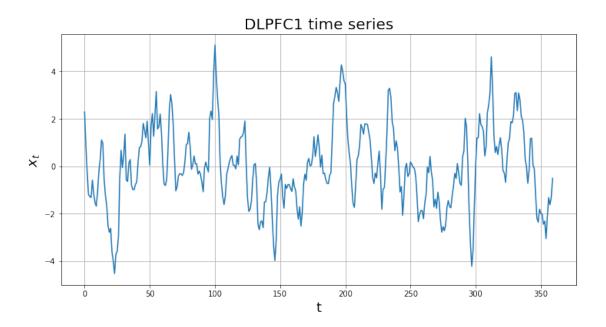
### Time Series Analysis and Recurrent Neural Network Giacomo Barzon - 3626438 Exercise 3

November 12, 2019

### 1 Task 1

#### 1.0.1 Consider the first time series of DLPFC

```
In [1]: import pandas as pd
        import matplotlib.pyplot as plt
        import numpy as np
        from scipy.io import loadmat
                                                    #import mat data
        from sklearn.linear_model import LinearRegression
        from scipy.stats import chi2
        from scipy import special
        from mpl_toolkits.mplot3d import Axes3D
In [2]: mat_file = loadmat('ex3file1.mat')
        data = mat_file['DLPFC1'].ravel()
In [3]: # Plot data
       plt.figure(figsize=[12,6])
       plt.plot(np.arange(0,len(data)), data)
       plt.xlabel('t', fontsize = 18)
       plt.ylabel(r'$x_t$', fontsize = 18)
       plt.grid()
       plt.title('DLPFC1 time series', fontsize = 20)
Out[3]: Text(0.5, 1.0, 'DLPFC1 time series')
```



### 1.0.2 1) Compute the log-likelihood of an AR(4) model

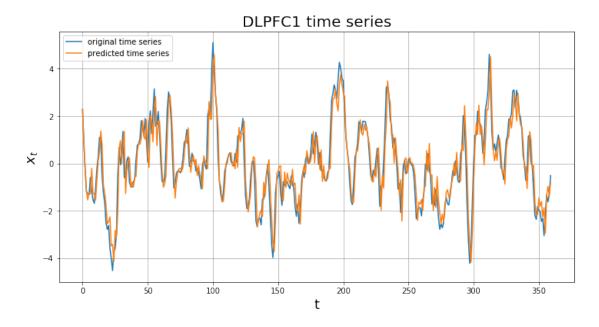
```
In [4]: # Coefficient estimation for AR(p) model
        def coeff_AR(data, p):
            xT = data[p:]
            Xp = np.zeros((len(data)-p,p+1))
            Xp[:,0] = 1
            for i in range(1,p+1):
                Xp[:,i] = data[p-i:-i]
            temp = np.matmul(np.transpose(Xp),Xp)
            temp = np.linalg.inv(temp)
            a = np.matmul(np.transpose(Xp),xT)
            a = np.matmul(temp,a)
            return a
        # Inferred time series
        def pred(data, p):
            a = coeff_AR(data, p)
            T = len(data)
            # predictions
            x_new = np.zeros(T)
            x_new[:p] = data[:p]
```

```
for i in range(p,T):
                x_new[i] = a[0] + np.dot(a[1:],np.flip(data[i-p:i]))
            return x_new
        # Residuals of the AR(p) model
        def res(data, p):
            return pred(data,p)[p:] - data[p:]
        # Std of the residuals
        def sigma(data, p):
            return np.std(res(data, p))
        # Log-likelihood for AR(p) model
        def log_likelihood(data, p):
            T = len(data)
            sigma1 = sigma(data, p)
            square_res = res(data, p)**2
            t1 = - (T-p)/2. * np.log(2*np.pi)
            t2 = - (T-p)/2. * np.log(sigma1**2)
            t3 = -np.sum(square_res) / sigma1**2 / 2.
            return t1 + t2 + t3
        # Likelihood for AR(p) model
        def likelihood(data, p):
            return np.exp(log_likelihood(data, p))
In [5]: # Coefficient estimation for AR(4) model
        a = coeff_AR(data,4)
        print("Estimated vector of coefficients: ")
        print(a)
        # Predicted time series
        pred_data = pred(data,4)
        # Plot predicted series vs. real series
        plt.figure(figsize=[12,6])
        plt.plot(np.arange(0,len(data)), data, label='original time series')
        plt.plot(np.arange(0,len(pred_data)), pred_data, label='predicted time series')
        plt.xlabel('t', fontsize = 18)
        plt.ylabel(r'$x_t$', fontsize = 18)
        plt.grid()
        plt.legend()
        plt.title('DLPFC1 time series', fontsize = 20)
```

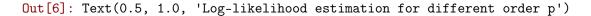
```
Estimated vector of coefficients:

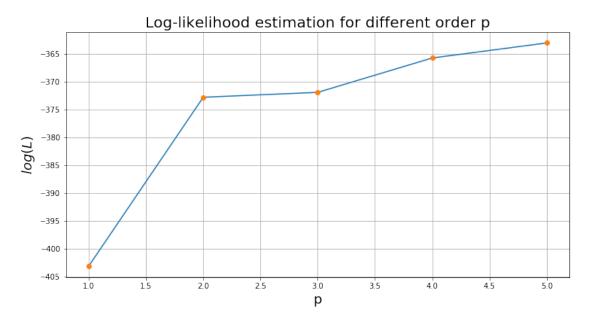
[-4.55062900e-04 1.24878325e+00 -4.83247551e-01 2.42845690e-01 -1.69905103e-01]
```

Out[5]: Text(0.5, 1.0, 'DLPFC1 time series')



Log-likelihood for AR(4) model: -365.77319316608975





## 1.0.3 2) Determine the optimal order p of the AR model by computing the log-likelihood-ratio test statistic

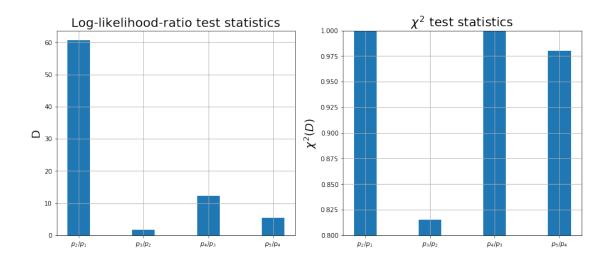
```
In [7]: def D(data, p1,p2):
            return -2 * (log_likelihood(data, p1) - log_likelihood(data, p2))
In [8]: # Log-likelihood-ratio test statistics
       Di = np.zeros(k-2)
        for i in range(1,k-1):
            Di[i-1] = D(data, i, i+1)
        print('Log-likelihood-ratio values:\n',Di)
        print('Respective chi-square values:\n',chi2.cdf(Di,1))
        # Plots
        fig1 = plt.subplots(figsize=[15,6])
        plt.subplot(1,2,1)
        plt.bar(np.arange(0,len(Di)), Di, width=0.35)
        plt.xticks(np.arange(0,len(Di)),(r'$p_2/p_1$',r'$p_3/p_2$',r'$p_4/p_3$',r'$p_5/p_4$'))
        plt.ylabel('D', fontsize = 18)
        plt.grid()
       plt.title('Log-likelihood-ratio test statistics', fontsize = 20)
       plt.subplot(1,2,2)
```

```
plt.bar(np.arange(0,len(Di)), chi2.cdf(Di,1), width=0.35)
    plt.xticks(np.arange(0,len(Di)),(r'$p_2/p_1$',r'$p_3/p_2$',r'$p_4/p_3$',r'$p_5/p_4$' ))
    plt.ylabel(r'$\chi^2(D)$', fontsize = 18)
    plt.ylim([0.8, 1])
    plt.grid()
    plt.title(r'$\chi^2$ test statistics', fontsize = 20)

    plt.show(fig1)

Log-likelihood-ratio values:
    [60.64193308 1.75847012 12.34423505 5.40117097]

Respective chi-square values:
    [1. 0.81518455 0.99955765 0.97987675]
```



It can be noticed that the log-likelihood-ratio of the fifth-order model respect to the fourth-order model is smaller than the previous value; this is reflected also in the respective chi-square value, which is smaller than the previous (0.979 compared to 0.999) and it means a loss of significance of the model. For these reasons the optimal order of the AR model is p=4.

### 2 Task 2

### 2.0.1 Use all four time series contained in the data file

```
In [9]: keys = list(mat_file.keys())
    keys = keys[-4:]

multiple_data = mat_file[keys[0]]

for i in range(1,len(keys)):
    multiple_data = np.append(multiple_data, mat_file[keys[i]], axis = 1)
```

```
print(multiple_data.shape)

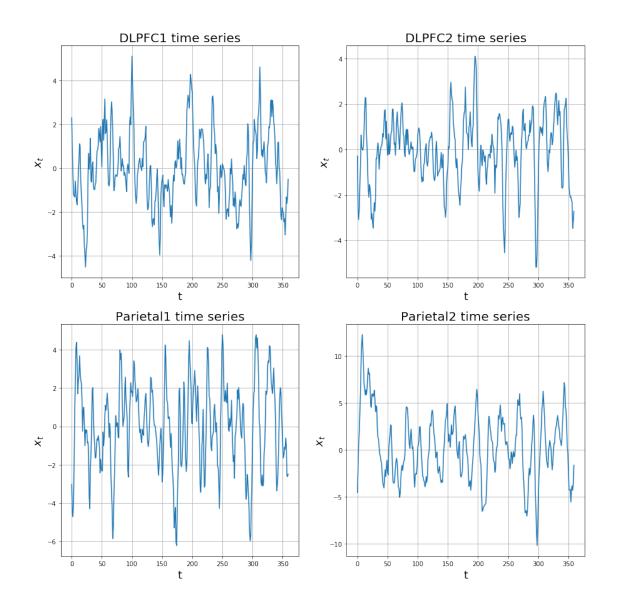
# Plot the time series
fig1 = plt.subplots(figsize=[15,15])

for i in range(len(keys)):

    plt.subplot(2,2,i+1)
    plt.plot(np.arange(0,len(data)), multiple_data[:,i])
    plt.xlabel('t', fontsize = 18)
    plt.ylabel(r'$x_t$', fontsize = 18)
    plt.grid()
    plt.title(keys[i]+" time series", fontsize = 20)

plt.show(fig1)

(360, 4)
```



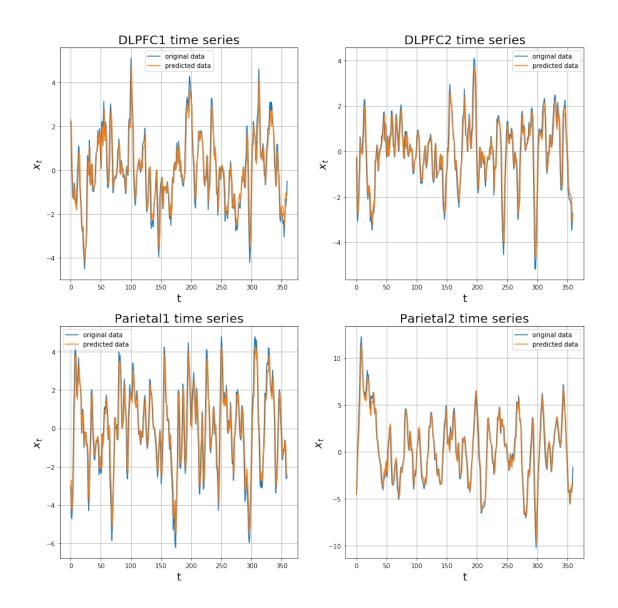
# 2.0.2 1) Estimate a VAR(1) model by performing multivariate regression on the 4-variate time series

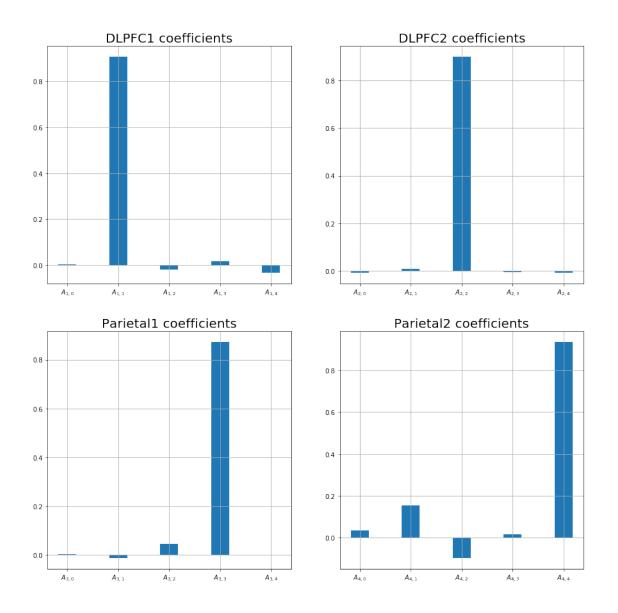
```
In [10]: # coefficient estimation for VAR(p)
    def coeff_VAR(data, p):
        T = data.shape[0]
        n = data.shape[1]

# define empty matrix
    A = np.zeros(( n, n*p+1 ))
        xT = np.zeros(T-p)
        Xp = np.zeros(( (T-p), n*p+1 ))
```

```
Xp[:,0] = np.zeros(T-p) + 1
            # fill matrix Xp
            for i in range(n):
                for k in range(1,p+1):
                    Xp[:, i*p +k] = data[p-k:-k, i]
            # compute coefficients
            for i in range(n):
                xT = data[p:, i]
                temp = np.matmul(np.transpose(Xp),Xp)
                temp = np.linalg.inv(temp)
                a = np.matmul(np.transpose(Xp),xT)
                a = np.matmul(temp,a)
                A[i] = a
            return A
        # inferred time series
        def pred(data, p):
            T = data.shape[0]
            n = data.shape[1]
            A = coeff_VAR(data, p)
            # define empty array
            x_new = np.zeros((data.shape[0],data.shape[1]))
            # set first p values
            x_new[:p] = multiple_data[:p]
            for i in range(p,T):
                x_new[i] = A[:,0] + np.dot(A[:,1:], np.flip(data[i-p:i],0).T).T
            return x_new
In [11]: # coefficient estimation for VAR(1)
        A = coeff_VAR(multiple_data, 1)
        print('Intercepts:\n', A[:,0])
        print('Coefficients:\n', A[:,1:])
Intercepts:
 [ 0.0024904 -0.00690006 0.00287008 0.03277537]
Coefficients:
 [0.00975233 \quad 0.89853182 \quad -0.00518382 \quad -0.00724422]
 [-0.01223154  0.04526295  0.87266454  0.00158463]
```

# add column of 1s





# 2.0.3 What do the coefficients in matrix A tell you about the coupling between the DLPFC and parietal cortex?

By looking at the plots above, it can be noticed that the biggest coefficient in all the plots is the one related to the considered time series: this means that the new outcomes are strongly related to the values of the same time series while weakly related to the other time series. The most relevant relations are the negative dependency of the values of the DLPFC1 time series respect to the Parietal2 ones, the positive dependency of the values of the Parietal time series respect to the DLPFC2 ones and the positive dependency of the values of the Parietal time series respect to the DLPFC1 ones and the negative dependency respect to the DLPFC2 ones.

### 2.0.4 Is the resulting VAR(1) model stationary or not?

Since the modulus of the biggest eigenvalue of the coefficient matrix A is lower than 1, the VAR(1) model is stationary.

### 2.0.5 2) Determine the log-likelihood of this model

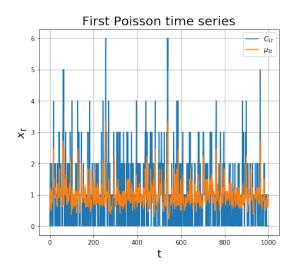
```
In [15]: # Residuals of the VAR(p) model
         def res(data, p):
             return pred(data,p)[p:] - data[p:]
         # Covariance matrix of the residuals
         def sigma(data, p):
             return np.cov(res(data, p).T)
         # Log-likelihood for VAR(p) model
         def log_likelihood(data, p):
             T = data.shape[0]
             n = data.shape[1]
             res1 = res(data, p)
             sigma1 = sigma(data, p)
             det = np.linalg.det(sigma1)
             square_res = res1**2
             t1 = - (T-p)*n/2. * np.log(2*np.pi)
             t2 = - (T-p)/2. * np.log(det)
             t3 = 0.
             for i in range(T-p):
                 temp = np.dot(np.linalg.inv(sigma1), res1[i].T)
                 t3 += np.dot(res1[i], temp)
             t3 = -t3 / 2.
             return t1 + t2 + t3
         # Likelihood for VAR(p) model
```

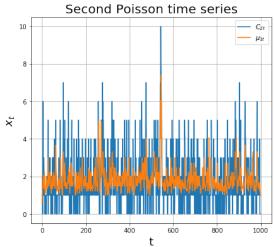
### 3 Task 3

### 3.0.1 1) Create your own order 2 Poisson time series (assume no base rate)

```
In [17]: # parameters
         T = 1000
         A1 = np.array(([0.2, -0.1], [0.1, 0.1]))
         A2 = np.array(([0.1, -0.1], [0.1, 0.1]))
        np.random.seed(0)
         # define empty array
         mu_t = np.zeros((2,T), dtype=np.float64)
         mu_t[:,0] = [0.5, 0.5]
         data = np.zeros((2,T), dtype=np.float64)
         data[:,0] = np.random.poisson(mu_t[:,0])
In [18]: # loop over each timestep
         mu_t[:,1] = np.exp( np.dot(A1, data[:,0]) )
         data[:,1] = np.random.poisson(mu_t[:,1])
         for i in range(2,T):
             mu_t[:,i] = np.exp(np.dot(A1, data[:,i-1]) + np.dot(A2, data[:,i-2]))
             data[:,i] = np.random.poisson(mu_t[:,i])
In [19]: # Plot the generated TS
         fig1 = plt.subplots(figsize=[15,6])
        plt.subplot(1,2,1)
         plt.plot(np.arange(T), data[0,:], label=r'$C_{1t}$')
        plt.plot(np.arange(T), mu_t[0,:], label=r'$\mu_{1t}$')
        plt.xlabel('t', fontsize = 18)
         plt.ylabel(r'$x_t$', fontsize = 18)
         plt.grid()
         plt.legend()
         plt.title('First Poisson time series', fontsize = 20)
```

```
plt.subplot(1,2,2)
plt.plot(np.arange(T), data[1,:], label=r'$C_{2t}$')
plt.plot(np.arange(T), mu_t[1,:], label=r'$\mu_{1t}$')
plt.xlabel('t', fontsize = 18)
plt.ylabel(r'$x_t$', fontsize = 18)
plt.grid()
plt.legend()
plt.legend()
plt.title('Second Poisson time series', fontsize = 20)
plt.show(fig1)
```





### 3.0.2 2) Given the data generated in (1), vary the parameters A1(1,1) and A2(2,1) between 0 and 0.4 with 0.01 increments.

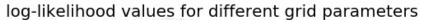
```
In [20]: # Compute log-likelihood for a Poisson model
    def poi_log_like(data, A1, A2):
        T = data.shape[1]

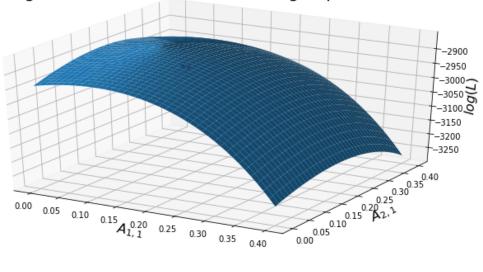
    # define empty matrix
        mu_t = np.zeros((2,T), dtype=np.float64)

# compute mean series
        mu_t[:,0] = data[:,0]
        mu_t[:,1] = np.exp( np.dot(A1, data[:,0]) )
        for i in range(2,T):
            mu_t[:,i] = np.exp( np.dot(A1, data[:,i-1]) + np.dot(A2, data[:,i-2]) )

# compute log-likelihood
```

```
111 = \text{np.sum}(\text{data}[0,2:]*\text{np.log}(\text{mu_t}[0,2:]) - \text{mu_t}[0,2:] -
                                          np.log(special.factorial(data[0,2:])) )
                                          112 = \text{np.sum}(\text{data}[1,2:]*\text{np.log}(\text{mu_t}[1,2:]) - \text{mu_t}[1,2:] -
                                          np.log(special.factorial(data[1,2:])) )
                                          return 111 + 112
In [21]: # evaluate log-likelihood for the parameter grid
                             par = np.arange(0., 0.41, 0.01)
                             11 = np.zeros(( len(par), len(par) ))
                             for i in range(len(par)):
                                          for j in range(len(par)):
                                                       A1[0,0] = par[i]
                                                       A2[1,0] = par[j]
                                                       ll[i,j] = poi_log_like(data, A1, A2)
In [22]: # Maximum value of log-likelihood in the parameter grid
                            \max_{1} = \min_{1 \le 1} \max_{1 \le 1} \min_{1 \le
                             max_par = np.where(11 == max_11)
                             print('Maximum value of the log-likelihood:', max_ll)
                             print('Parameters related to the maximum:')
                             print('A11 = ',par[max_par[0]][0])
                             print('A21 = ',par[max_par[1]][0])
Maximum value of the log-likelihood: -2871.458687410929
Parameters related to the maximum:
A11 = 0.19
A21 = 0.1
In [23]: # 3-D plot of the log-likelihood values respect to the parameter grid
                             fig = plt.figure(figsize=[12,6])
                             X, Y = np.meshgrid(par, par)
                             ax = fig.gca(projection='3d')
                             ax.plot_surface(X, Y, 11)
                             ax.scatter(0.2, 0.1,11[20,10],color='r')
                             ax.scatter(par[max_par[0]][0], par[max_par[1]][0], ll[max_par],color='b')
                             ax.set_xlabel(r'$A_{1,1}$', fontsize = 16)
                             ax.set_ylabel(r'$A_{2,1}$', fontsize = 16)
                             ax.set_zlabel(r'$log(L)$', fontsize = 16)
                             ax.set_title('log-likelihood values for different grid parameters', fontsize = 20)
                             plt.show()
```





As we can notice from the calculations and the plot above, the model that best describes the Poisson generated time series (which corresponds to the one with the higher value of likelihood) is the one with parameters [A11 = 0.19, A21 = 0.10], that is very close to the original parameters in the parameter grid.