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Importing libraries and setting seed for reproducibility

In [2]:
```
import sys
import time

import numpy as np
import pandas as pd
import statsmodels.api as st
import matplotlib.pyplot as plt

np.random.seed(1337)
```

Exercise 1

A. Direct approach using matrix inversion

In [3]:
```
A = [[2, 0, 1], [0, 4, 1], [1, -1, 4]]
b = [30, 40, 15]

def directMethod(A, b):
    """
    Solves the linear system directly by inversion.

    Arguments:
    A - coefficient matrix
    b - ordinate vector

    Returns:
    x - solution vector
    """
    return np.dot(np.linalg.inv(A), b)

xDir = directMethod(A, b)

print('Solution vector x: {}'.format(xDir))
print('Check if x is correct: {}'.format(np.round(np.dot(A, xDir), 0) =
= b))

print('\n\nCoefficient matrix inversion is a direct method. We may use
this method since the invertible of matrix A exists. Once this is not t
he case the solution to the system may be approximated with the help of
iterative methods')
```

```
Solution vector x: [13.66666667  9.33333333  2.66666667]
Check if x is correct: [ True  True  True]


Coefficient matrix inversion is a direct method. We may use this meth
od since the invertible of matrix A exists. Once this is not the case
the solution to the system may be approximated with the help of itera
tive methods
```

B. Iterative approch using Gauss-Seidel algorithm

In [5]:
```
def gaussSeidel(A, b, maxIter=10e3, tol=1/10e3):
    """
    Solves the linear system via Gauss-Seidel iterative method. The ini
tial guess is
    take as a null-vector of length of ordinate vector

    Arguments:
    A - coefficient matrix
    b - ardinate vector

    Returns:
    x - convergence vector
    """
    # check diagonal dominance of A
    for i in range (len(b)):
        diag = A[i][i]
        nondiag = 0
        for j in range(len(b)):
            nondiag += A[i][j] # sum of row elements

        if 2 * diag - nondiag < 0: # diag is multiplied by two since no
ndiag includes diag
            print('Matrix A is not strictly diagonally dominant at row:
{}'.format(i))

    # start iteration
    iteration = 0
    iterCond = 0
    error = 1
    errorCond = 0
    x0 = [0.0 for i in range(len(b))]
    L = np.tril(A) # lower triangular matrix
    U = A - L # upper triangular matrix

    while iterCond or errorCond != 1:
        x1 = np.dot(np.linalg.inv(L), b - np.dot(U, x0))
        error = np.linalg.norm(x1-x0)
        iteration += 1
        x0 = x1

        if error < tol:
            errorCond = 1
        elif iterCond > maxIter:
            iterCond = 1

    return x0, iteration

xConv, iteration = gaussSeidel(A, b)
print('Vector x {} converged at iteration {}'.format(xConv, iteration))

print('\n\n Since the matrix is strictly diagonally dominant we may use
the Gauss-Seidel method. The coefficient matrix is of shape (3,3) hence
the method converged relatively fast. Due to very low error tolerance o
f 1/10e3 convergence vector x is very close to solution vector x found
with the direct method of inversion of coefficient matrix')
```

```
Vector x [13.66666794  9.33333397  2.66666651] converged at iteration
6


 Since the matrix is strictly diagonally dominant we may use the Gaus
s-Seidel method. The coefficient matrix is of shape (3,3) hence the m
ethod converged relatively fast. Due to very low error tolerance of 1
/10e3 convergence vector x is very close to solution vector x found w
ith the direct method of inversion of coefficient matrix
```

C. Condition number calculation

In [4]:
```
def conditionNumber(A):
    return np.linalg.cond(A)

k = conditionNumber(A)

print('Condition number k(A): {}'.format(k))

print('\n\nThe condition number equals 2.8 which means this linear syst
em is well conditioned. For 1% change in ordinate vector the solution c
hanges by at most 3%')
```

```
Condition number k(A): 2.803427514506158


The condition number equals 2.8 which means this linear system is wel
l conditioned. For 1% change in ordinate vector the solution changes
by at most 3%
```

Exercise 2

A. Epsilon calculation via while and for loops

In [7]:
```
def epsilonWhileLoop(tol):
    """
    Calculates the lowest possible value (epsilon_m) for a 'em + 0 > to
l' condition in a while loop

    Arguments:
    tol - tolerance level. May take on any value in [0, 1]. Designed sp
ecifically for this function to converge faster. If set to zero, epsilo
n_m converges to the true epsilon of Python

    Returns:
    em - epsilon_m. The convergence function is epsilon_m = epsilon_m /
2
    """
    em = 1

    while em + 0 > tol:
        em = em/2 # convergence assumption

    return em, tol

emW, tolW = epsilonWhileLoop(1/10e4)

print('WHILE LOOP: e_m for a given tolerance level of {} is {}'.format
(tolW, emW))

def epsilonForLoop(tol, numIter):
    """
    Calculates the lowest possible value (epsilon_m) for a 'em + 0> tol
' condition in a for loop

    Arguments:
    tol - tolerance level. May take on any value in [0, 1]. Designed sp
ecifically for this function to converge faster. If set to zero, epsilo
n_m converges to the true epsilon of Python
    numIter - maximum number of iterations. If set to infinity, the arg
ument is ignored as a stopping condition.

    Returns:
    em - epsilon_m. The convergence function is epsilon = epsilon / 2
    """
    em = 1

    for i in range(numIter):
        if em + 0 > tol:
            em = em/2
        else:
            return em, tol, i

emF, tolF, iterationF  = epsilonForLoop(1/10e4, 1000)

print('FOR LOOP: e_m for a given tolerance level of {} is {}. For a def
ined convergence function it took {} iterations to reach the value belo
w the tolerance'.format(tolF, emF, iterationF))
```

```
print('\n\nThe system epsilon is given by {}. It is the lowest possible
value in Python which may be checked by the condition e + 0 > 0'.format
(sys.float_info.epsilon))
```

```
WHILE LOOP: e_m for a given tolerance level of 1e-05 is 7.62939453125
e-06
FOR LOOP: e_m for a given tolerance level of 1e-05 is 7.62939453125e-
06. For a defined convergence function it took 17 iterations to reach
the value below the tolerance


The system epsilon is given by 2.220446049250313e-16. It is the lowes
t possible value in Python which may be checked by the condition e +
0 > 0
```

B. Time measures for matrix additivity and product

In [8]:
```
A = np.random.rand(400, 600)
B = np.random.rand(400, 600)

def matrixSum(A, B):
    """
    Performs matrix summation operation

    Arguments:
    A - input matrix 1
    B - input matrix 2

    Returns:
    C - output matrix
    """
    C = np.zeros([400, 600]) # define a zero-matrix of shape (400,600)

    for i in range(A.shape[0]): # iterate over row values
        for ii in range(A.shape[1]): # iterate over column values
            C[i, ii] = A[i, ii] + B[i, ii]

    return C

startA = time.time()
C = A + B
endA = time.time()

startM = time.time()
C = matrixSum(A, B)
endM = time.time()

print('Time elapsed for an automatic summation: {}'.format(endA-start
A))
print('Time elapsed for a manual summation: {}'.format(endM-startM))

def matrixProd(A, B):
    C = np.zeros([A.shape[0], B.shape[0]]) # defines a zero-matrix of s
hape (A.shape[1], B.shape[0])

    for i in range(A.shape[0]):
        for ii in range(B.shape[0]):
            for iii in range(B.shape[1]):
                C[i, ii] += A[i, iii] * B[ii, iii]

    return C

startA = time.time()
CA = np.dot(A, np.transpose(B))
endA = time.time()

startM = time.time()
CM = matrixProd(A, B)
endM = time.time()

print('Time elapsed for an automatic product: {}'.format(endA-startA))
print('Time elapsed for a manual product: {}'.format(endM-startM))
print('\nCheck condition the manual function is correct {}'.format(
    np.round(CA, 2) == np.round(CM, 2)))
print('\n\n Put simply, legacy code and open-source code is much more e
fficient compared to our options. The reason behind this is that the co
re of such operators is written in C++ (which is much faster), and Pyth
on is just a wrapper')
```

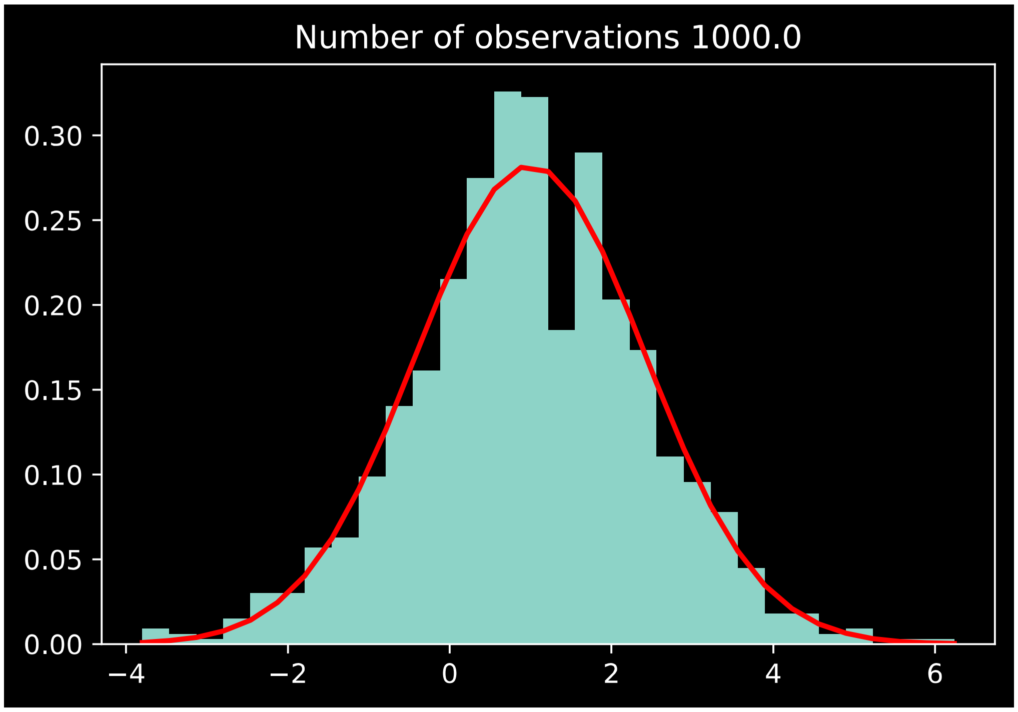
```
Time elapsed for an automatic summation: 0.0009992122650146484
Time elapsed for a manual summation: 0.1858675479888916
Time elapsed for an automatic product: 0.0039899349212646484
Time elapsed for a manual product: 95.35679531097412

Check condition the manual function is correct [[ True  True  True
...  True  True  True]
 [ True  True  True ...  True  True  True]
 [ True  True  True ...  True  True  True]
 ...
 [ True  True  True ...  True  True  True]
 [ True  True  True ...  True  True  True]
 [ True  True  True ...  True  True  True]]


 Put simply, legacy code and open-source code is much more efficient
compared to our options. The reason behind this is that the core of s
uch operators is written in C++ (which is much faster), and Python is
just a wrapper
```

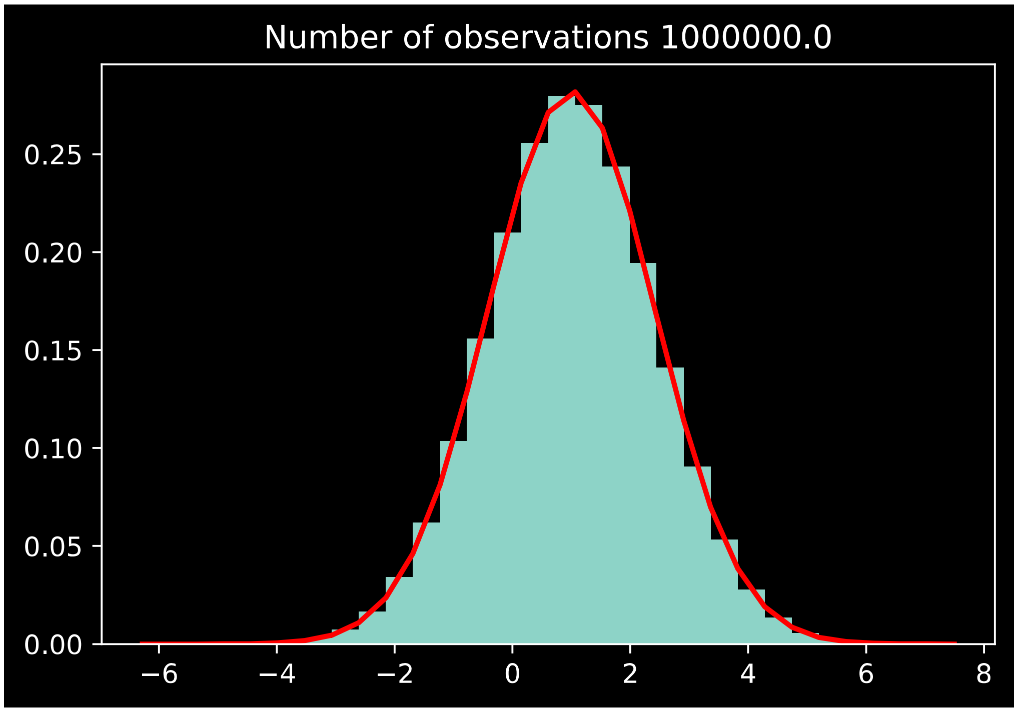
Exercise 3

```
In [9]: # a) Creating a vector of shape 10 filled with random numbers from a st
        andard normal distribution
        x = np.random.rand(10)
        print (x)

        # b) Calculating the mean and the standard deviation of x
        Ex = np.mean(x)
        Sx = np.std(x)

        # c) Creating a random variable z
        mu = 1
        sigma = np.sqrt(2)
        z = np.random.normal(mu, sigma, 10)

        # d) Calculating the mean and the standard deviation of z
        Ez = np.mean(z)
        Sz = np.std(z)

        # e) Increasing sample size for z
        numObs = [10e2, 10e5]


        for n in numObs:
            z = np.random.normal(mu, sigma, int(n))
            Ez = np.mean(z)
            Sz = np.std(z)

            print('The mean and the std of z are {} and {}'.format(np.round(Ez,
        5), np.round(Sz, 5)))
            fig, ax = plt.subplots()
            count, bins, ignored = ax.hist(z, 30, density=True)
            ax.plot(
                bins, 1/(sigma * np.sqrt(2 * np.pi)) * np.exp( - (bins - mu)**2
        / (2 * sigma**2)),
                linewidth=2, color='r')
            ax.set_title('Number of observations ' + str(n))

        print('\n\nIncreasing sample size from 1k to 1kk does contribute to a b
        etter precision of sample means and deviations to their corresponding t
        rue values. However, these adjustments are relatively weak compared to
        the increase of the sample size by 1k times')
```

```
[0.18813647 0.73559724 0.61380536 0.23062902 0.25430818 0.56762818
 0.81894421 0.44615588 0.48723152 0.42481824]
The mean and the std of z are 0.98079 and 1.44119
The mean and the std of z are 1.00049 and 1.4146
```

```
Increasing sample size from 1k to 1kk does contribute to a better pre
cision of sample means and deviations to their corresponding true val
ues. However, these adjustments are relatively weak compared to the i
ncrease of the sample size by 1k times
```





Exercise 4

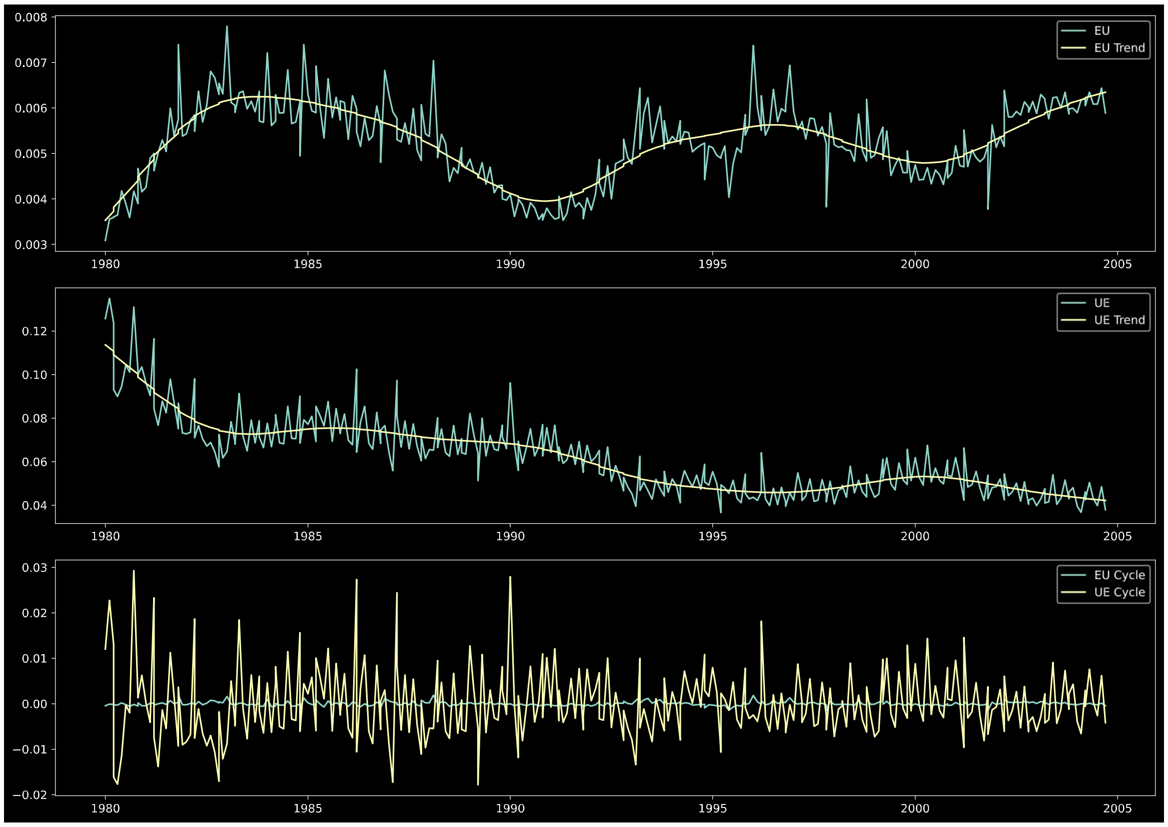
In [13]:
```
def olsEstimator(n):
    """
    Computes the estimator for beta using the standardazied OLS approac
h and setup from the problem 4.

    Arguments:
    X - matrix of covariates
    y - vector of dependables

    Returns:
    b - estimates of coefficient vector
    """
    mu = 0 # expected value of normal distribution
    sigma = 1 # variance = standard deviation of normal distribution
    low = 0 # lowest boundary of uniform distribution
    high = 100 # highest boundary of uniform distribution

    e = np.random.normal(mu, sigma, n) # normally distributed normalize
d error term
    x1 = np.random.uniform(low, high, n) # vector of features 1
    x2 = np.random.uniform(low, high, n) # vector of features 3
    X = np.transpose(np.matrix([np.ones(n), x1, x2])) # matrix of featu
res with intercept

    y = np.transpose(np.dot(X,bTrue) + e) # explained vector

    return np.dot(
        np.linalg.inv(np.dot(np.transpose(X), X)), np.dot(np.transpose
(X), y))

numObs = [10, 100000]
bTrue = np.array([2, 3, 5]) # true beta vector

for n in numObs:

    bStar = olsEstimator(n)

    print('n = {}: OLS estimates for beta are\n{}'.format(n, bStar))
    print('Difference between true values and estimated values is\n{}\
n\n'.format(
        bStar - bTrue.reshape(3, 1)))

print('The more observations we have the more closely the OLS estimatio
ns approach the true values of coefficient vector beta')
```

```
n = 10: OLS estimates for beta are
[[2.13578031]
 [3.01052757]
 [5.0020262 ]]
Difference between true values and estimated values is
[[0.13578031]
 [0.01052757]
 [0.0020262 ]]


n = 100000: OLS estimates for beta are
[[2.00437305]
 [2.99993455]
 [4.99995564]]
Difference between true values and estimated values is
[[ 4.37304652e-03]
 [-6.54482716e-05]
 [-4.43636395e-05]]


The more observations we have the more closely the OLS estimations ap
proach the true values of coefficient vector beta
```

Exercise 5

In [11]:
```
workerflows = pd.read_excel("../Helpers/workerflows.xlsx", usecols="A:
F", header=0)

lam = 14400
cycleEU, trendEU = st.tsa.filters.hpfilter(workerflows['EU'], lam) # cy
cle and trend component of log EU
cycleUE, trendUE = st.tsa.filters.hpfilter(workerflows['UE'], lam) # cy
cle and trend component of log UE

fig, (ax1, ax2, ax3) = plt.subplots(3, figsize=(14, 10))
fig.tight_layout()
ax1.plot(np.round(workerflows['Unnamed: 0'], 1), workerflows['EU'], lab
el='EU')
ax1.plot(np.round(workerflows['Unnamed: 0'], 1), trendEU, label='EU Tre
nd')
ax1.legend()
ax2.plot(np.round(workerflows['Unnamed: 0'], 1), workerflows['UE'], lab
el='UE')
ax2.plot(np.round(workerflows['Unnamed: 0'], 1), trendUE, label='UE Tre
nd')
ax2.legend()
ax3.plot(np.round(workerflows['Unnamed: 0'], 1), cycleEU, label='EU Cyc
le')
ax3.plot(np.round(workerflows['Unnamed: 0'], 1), cycleUE, label='UE Cyc
le')
ax3.legend()

print('As seen from first two graphs HP filter approximates the trend c
omponent of both time series pretty well. This trend may be used as inp
ut data for further nonlinear analysis. As seen from graph three the cy
clical component of the UE cycle is much stronger compared to the EU cy
cle.')
```

As seen from first two graphs HP filter approximates the trend compon ent of both time series pretty well. This trend may be used as input data for further nonlinear analysis. As seen from graph three the cyc lical component of the UE cycle is much stronger compared to the EU c ycle.


EU
EU Trend
UE
UE Trend
EU Cycle
UE Cycle