VLSI Signed Processing Architecture

# Structured Analysis of High Dimensional FMR Model

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## CONTENTS

## INTRODUCTION TO FMR

➤Popular tool for accommodating data heterogeneity

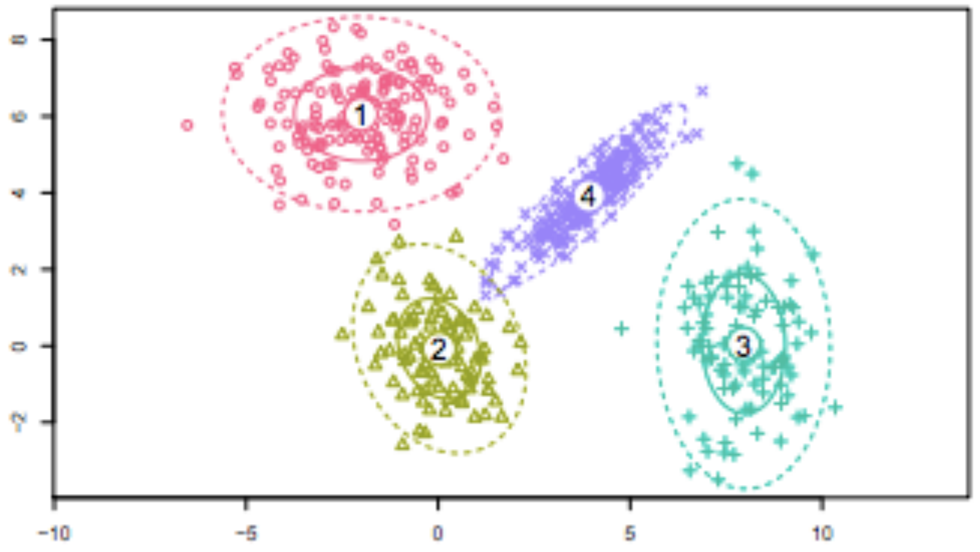
➤In the analysis of FMR models with high-dimensional covariates, it is necessary to conduct regularized estimation and identify important covariates rather than noises.

➤Specifically, important covariates can be classified into two types: those that behave the same in different subpopulations and those that behave differently. It is of interest to conduct structured analysis to identify such structures, which will enable researchers to better understand covariates and their associations with outcomes.

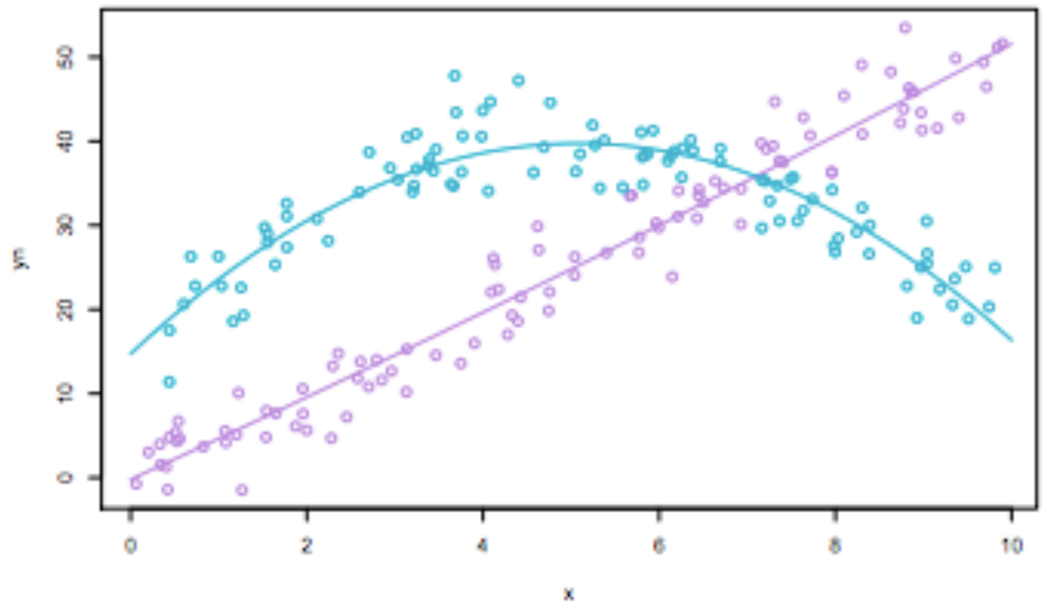
## METHODS FOR ANALYSIS OF FMR

➤ Structured Analysis Method: When , the FMR model with high-dimensional covariates is considered a structured penalization approach is developed for regularized estimation, selection of important variables, and, equally importantly, identification of the underlying covariate effect structure. lternatives.

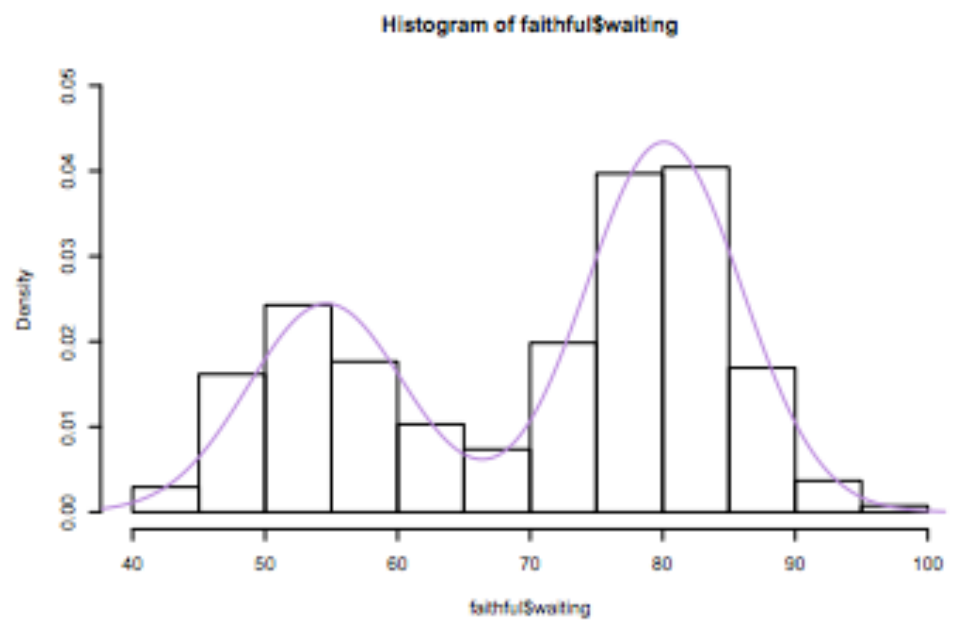
➤After analyzing FMR using Structured Analysis output should look like:



➤ Component specific method: This method is presented using a combination of the random forest learner and a penalized linear FMR. The performance of the new method is assessed by predictive log-likelihood in extensive simulation studies. After analyzing FMR using Component specific method output should look like:



➤Concomitant variable method: For this method component sizes are assumed to be constant. After analyzing FMR using Concomitant variable method: output should look like:



## HETEROGENEOUS AND HOMOGENEOUS COVARIATES

➤In data analysis, a set of data is considered homogeneous if the variables are one type (i.e. binary or categorical)

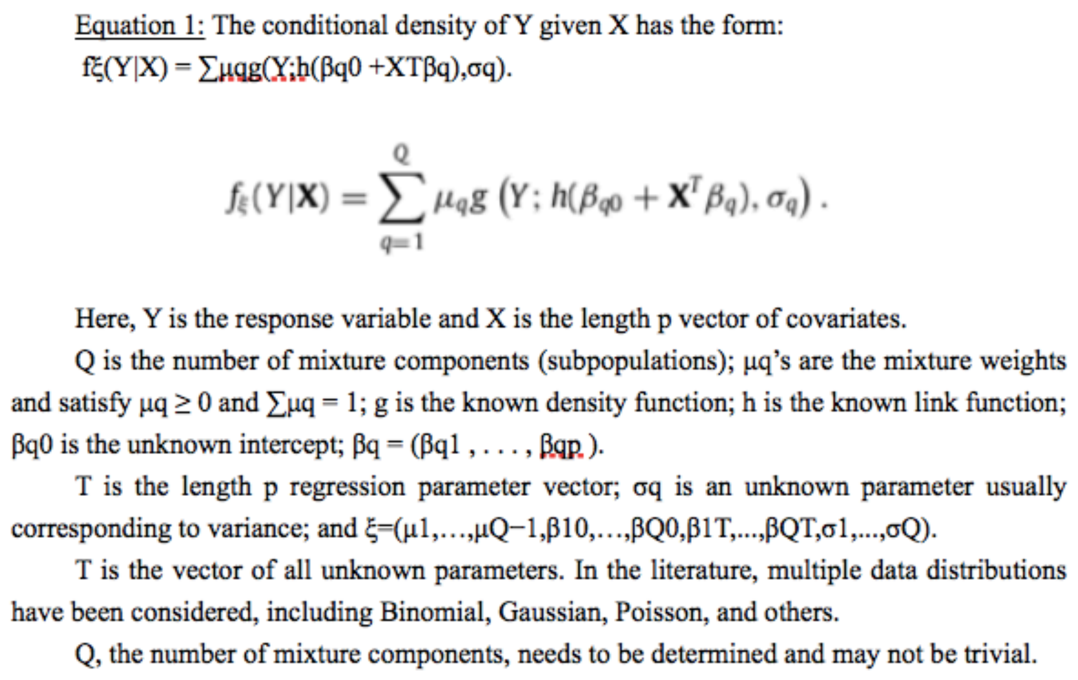
➤ if the variables are mixed (i.e. binary + categorical), then the data set is heterogeneous.

# FMR IMPLEMENTATION USING STRUCTURED ANALYSIS

- Implementing Equations

Equation

Implementation



Equation 1: The conditional density of Y given X has the form:

$f\xi(Y|X) = \sum\mu q g(Y;h(\beta q0 + XT\beta q),\sigma q)$.

$$f_{\xi}(Y|\mathbf{X}) = \sum_{q=1}^{Q} \mu_q g\left(Y; h(\beta_{q0} + \mathbf{X}^T\beta_q), \sigma_q\right).$$

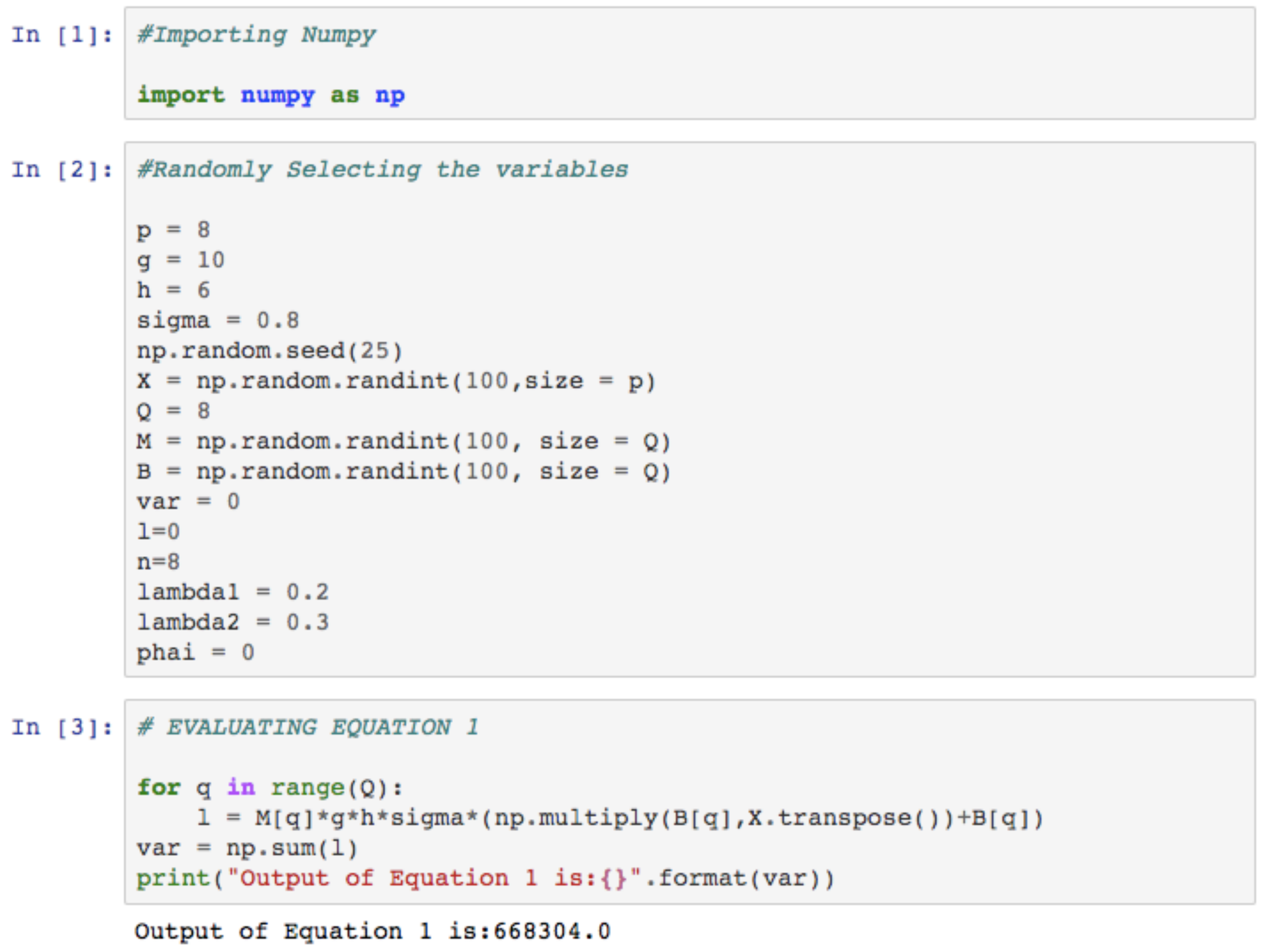
Here, Y is the response variable and X is the length p vector of covariates.

Q is the number of mixture components (subpopulations); $\mu q$'s are the mixture weights and satisfy $\mu q \geq 0$ and $\sum\mu q = 1$; g is the known density function; h is the known link function; $\beta q0$ is the unknown intercept; $\beta q = (\beta q1, \ldots, \beta qp)$.

T is the length p regression parameter vector; $\sigma q$ is an unknown parameter usually corresponding to variance; and $\xi=(\mu 1,\ldots,\mu Q-1,\beta 10,\ldots,\beta Q0,\beta 1T,\ldots,\beta QT,\sigma 1,\ldots,\sigma Q)$.

T is the vector of all unknown parameters. In the literature, multiple data distributions have been considered, including Binomial, Gaussian, Poisson, and others.

Q, the number of mixture components, needs to be determined and may not be trivial.



```
In [1]: #Importing Numpy

        import numpy as np
```

```
In [2]: #Randomly Selecting the variables

        p = 8
        g = 10
        h = 6
        sigma = 0.8
        np.random.seed(25)
        X = np.random.randint(100,size = p)
        Q = 8
        M = np.random.randint(100, size = Q)
        B = np.random.randint(100, size = Q)
        var = 0
        l=0
        n=8
        lambda1 = 0.2
        lambda2 = 0.3
        phai = 0
```

```
In [3]: # EVALUATING EQUATION 1

        for q in range(Q):
            l = M[q]*g*h*sigma*(np.multiply(B[q],X.transpose())+B[q])
        var = np.sum(l)
        print("Output of Equation 1 is:{}".format(var))

        Output of Equation 1 is:668304.0
```

## Equation

## Implementation

Equation 2:

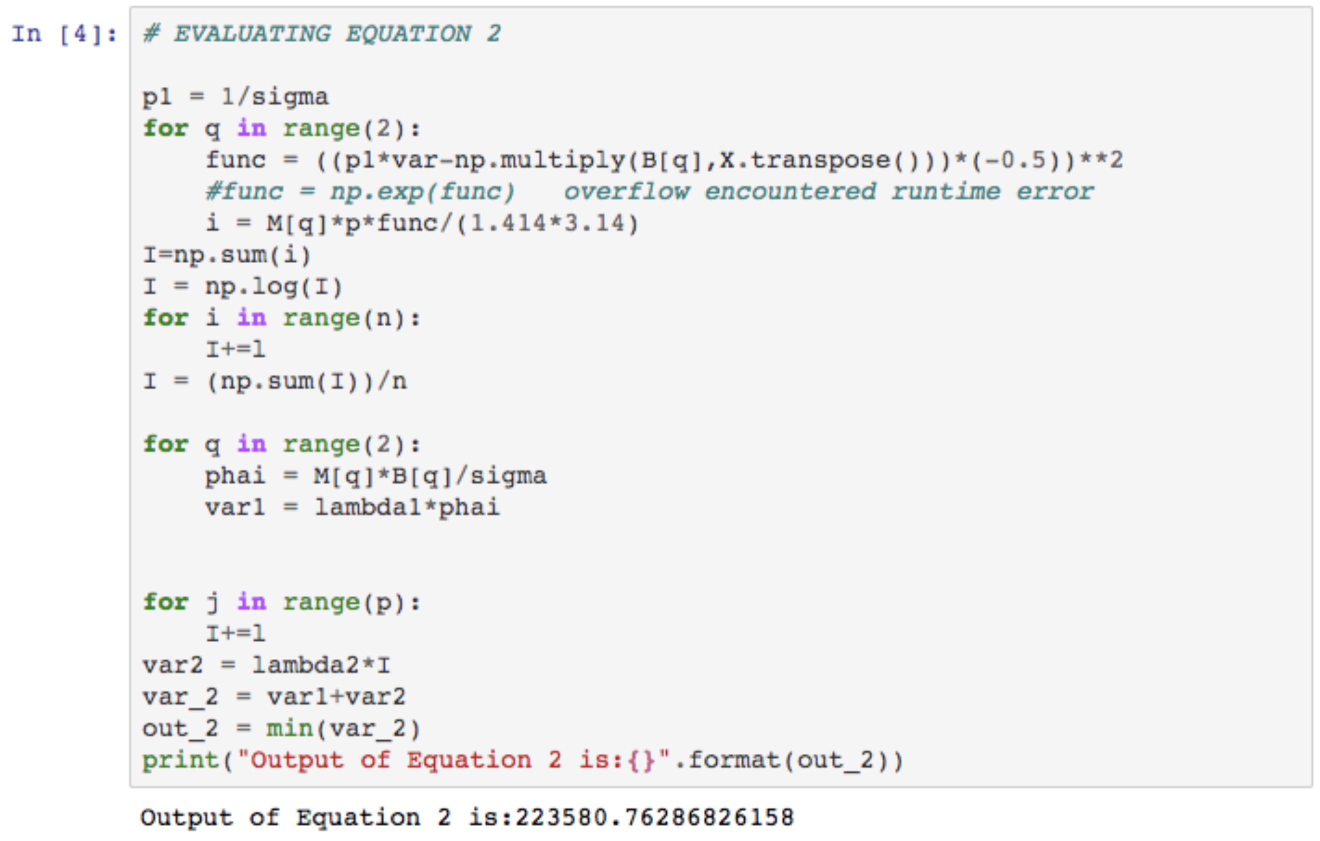
Denote the new vector of unknown parameters as θ = (φ1,φ2,ρ1,ρ2,μ1). Assume n independent observations Z = {(xi, yi) : i = 1, . . . , n}. Then the log-likelihood function is:

$$l(\theta;\mathbb{Z}) = n^{-1}\sum_{i=1}^{n} log\left(\sum_{q=1}^{2}\mu_q\frac{\rho_q}{\sqrt{2\pi}}e^{-\frac{1}{2}(\rho_q y_i-\mathbf{x}_i^T\phi_q)^2}\right).$$

We propose the penalized estimate

$$\check{\theta}_\lambda^\gamma = \arg\min\left\{-l(\theta;\mathbb{Z}) + \lambda_1\sum_{q=1}^{2}\mu_q^\gamma\left\|\phi_q\right\|_1 + \lambda_2\sum_{j=1}^{p}I(\phi_{1j}\neq\phi_{2j})\right\}. \quad (2)$$

where λ = (λ1, λ2) are data-dependent tunings, γ is a parameter designed to accommodate unbalance in data, μ2 = 1 − μ1, ‖·‖1 is the l1 norm, and I(·) is the indicator function. Important and unimportant covariates correspond to the nonzero and zero components of φˇq's, respectively. If φˇ1j = φˇ2j/= 0, then covariate j is a homogeneous one.



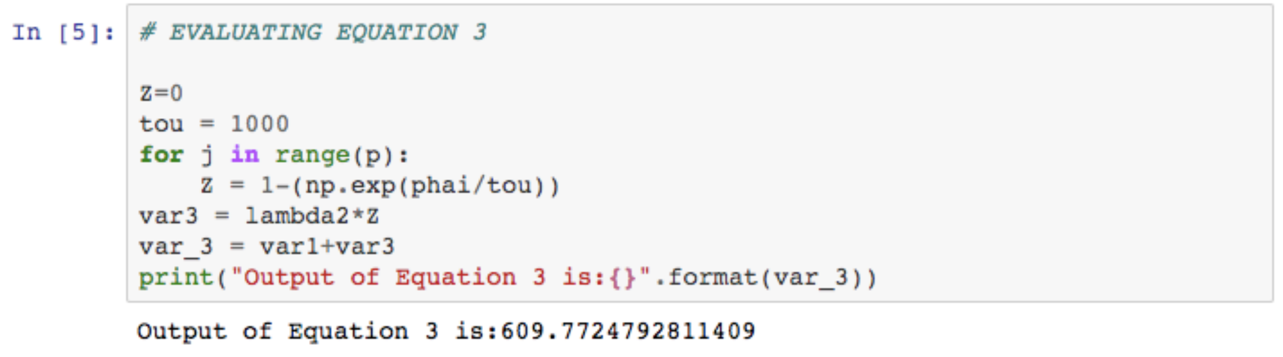
```
In [4]: # EVALUATING EQUATION 2

        p1 = 1/sigma
        for q in range(2):
            func = ((p1*var-np.multiply(B[q],X.transpose()))*(-0.5))**2
            #func = np.exp(func)   overflow encountered runtime error
            i = M[q]*p*func/(1.414*3.14)
        I=np.sum(i)
        I = np.log(I)
        for i in range(n):
            I+=1
        I = (np.sum(I))/n

        for q in range(2):
            phai = M[q]*B[q]/sigma
            var1 = lambda1*phai


        for j in range(p):
            I+=1
        var2 = lambda2*I
        var_2 = var1+var2
        out_2 = min(var_2)
        print("Output of Equation 2 is:{}".format(out_2))

        Output of Equation 2 is:223580.76286826158
```

Equation 3:

The indicator function is not continuous, making optimization challenging. To simplify computation, we further propose the estimate:

$$\hat{\theta}_\lambda^\gamma = \arg\min\left\{-l(\theta;\mathbb{Z}) + \lambda_1\sum_{q=1}^{2}\mu_q^\gamma\left\|\phi_q\right\|_1 + \lambda_2\sum_{j=1}^{p}\left[1-e^{-\frac{(\phi_{1j}-\phi_{2j})^2}{\tau}}\right]\right\}$$

here τ is a small positive number that controls the goodness of the approximation.



```
In [5]: # EVALUATING EQUATION 3

        Z=0
        tou = 1000
        for j in range(p):
            Z = 1-(np.exp(phai/tou))
        var3 = lambda2*Z
        var_3 = var1+var3
        print("Output of Equation 3 is:{}".format(var_3))

        Output of Equation 3 is:609.7724792811409
```

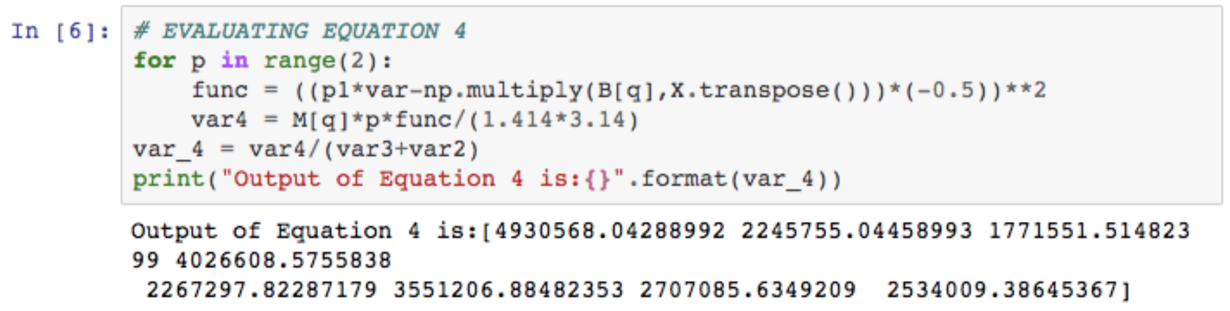
We conclude that a covariate is homogeneous if its estimates in the two subpopulations are sufficiently close.

Equation

Implementation

$$l_c(\theta;\mathbb{Z},\Delta)=\sum_{i=1}^{n}\sum_{q=1}^{2}\left\{\Delta_{i,q}\log\left(\frac{\rho_q}{\sqrt{2\pi}}e^{-\frac{1}{2}(\rho_q y_i-\mathbf{x}_i^T\phi_q)^2}\right)+\Delta_{i,q}\log(\mu_q)\right\}$$

$$\hat{\delta}_{i,q}=E_{\theta^{(m)}}[\Delta_{i,q}|\mathbb{Z}]=\frac{\mu_q^{(m)}\rho_q^{(m)}e^{-\frac{1}{2}\left(\rho_q^{(m)}y_i-\mathbf{x}_i^T\phi_q^{(m)}\right)^2}}{\mu_1^{(m)}\rho_1^{(m)}e^{-\frac{1}{2}\left(\rho_1^{(m)}y_i-\mathbf{x}_i^T\phi_1^{(m)}\right)^2}+\mu_2^{(m)}\rho_2^{(m)}e^{-\frac{1}{2}\left(\rho_2^{(m)}y_i-\mathbf{x}_i^T\phi_2^{(m)}\right)^2}}.$$



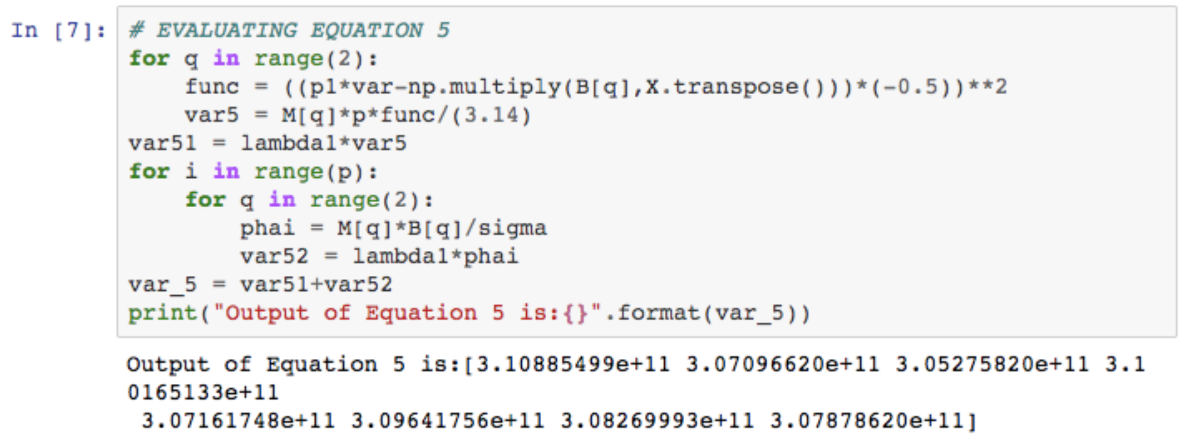
```
In [6]: # EVALUATING EQUATION 4
        for p in range(2):
            func = ((p1*var-np.multiply(B[q],X.transpose()))*(-0.5))**2
            var4 = M[q]*p*func/(1.414*3.14)
        var_4 = var4/(var3+var2)
        print("Output of Equation 4 is:{}".format(var_4))
```

```
Output of Equation 4 is:[4930568.04288992 2245755.04458993 1771551.514823
99 4026608.5755838
 2267297.82287179 3551206.88482353 2707085.6349209  2534009.38645367]
```

Equation 5:

Generalized M-Step: Optimizes (θ|θ(m)) with respect to θ. (a) Optimize with respect to

$$-n^{-1}\sum_{i=1}^{n}\sum_{q=1}^{2}\hat{\delta}_{i,q}\log(\mu_q)+\lambda_1\sum_{q=1}^{2}\mu_q^{\gamma}\left\|\phi_q^{(m)}\right\|_1.$$



```
In [7]: # EVALUATING EQUATION 5
        for q in range(2):
            func = ((p1*var-np.multiply(B[q],X.transpose()))*(-0.5))**2
            var5 = M[q]*p*func/(3.14)
        var51 = lambda1*var5
        for i in range(p):
            for q in range(2):
                phai = M[q]*B[q]/sigma
                var52 = lambda1*phai
        var_5 = var51+var52
        print("Output of Equation 5 is:{}".format(var_5))
```

```
Output of Equation 5 is:[3.10885499e+11 3.07096620e+11 3.05275820e+11 3.1
0165133e+11
 3.07161748e+11 3.09641756e+11 3.08269993e+11 3.07878620e+11]
```

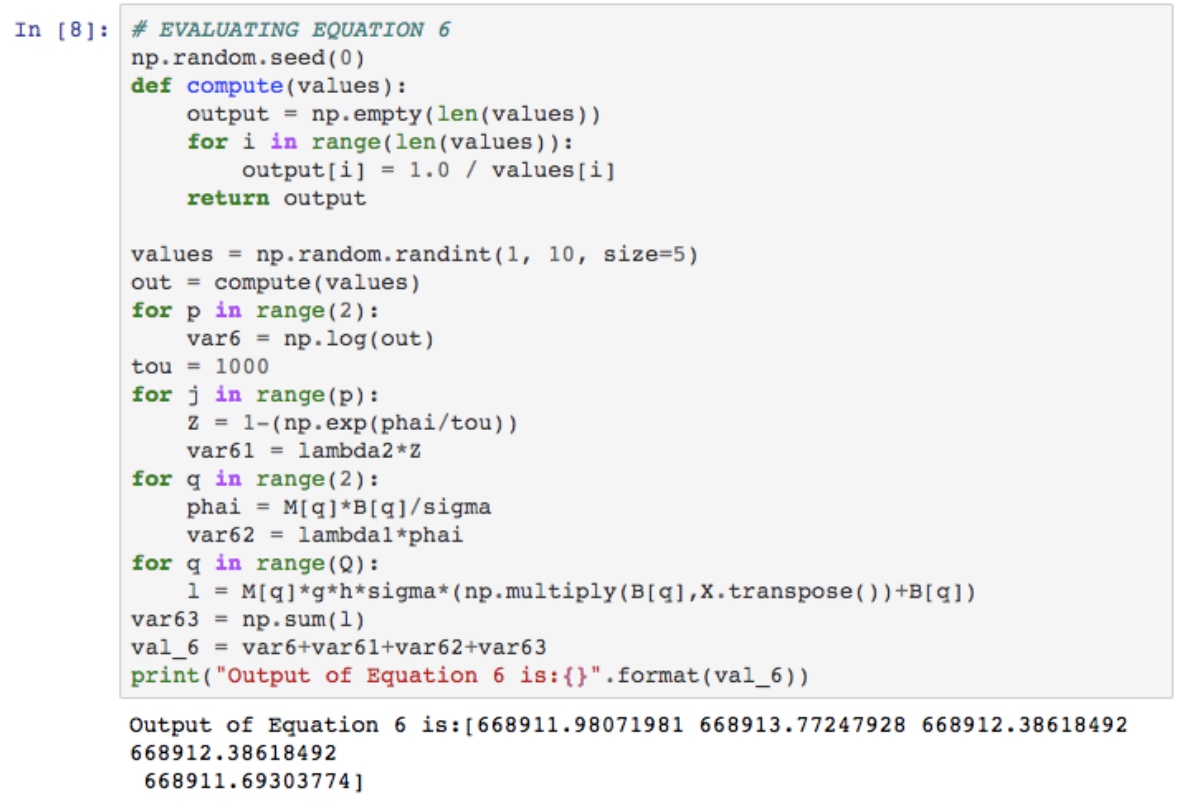
## Equation

## Implementation

Equation 6:

$$\sum_{q=1}^{2} -\frac{n_q}{n}\log(\rho_q) + \frac{1}{2n}\left\|\rho_q\tilde{y} - \tilde{\mathbf{x}}^T\phi_q\right\|^2 + \lambda_1\sum_{q=1}^{2}\mu_q^{\gamma}\left\|\phi_q\right\|_1 + \lambda_2\sum_{j=1}^{p}\left[1 - e^{-\frac{(\phi_{1j}-\phi_{2j})^2}{\tau}}\right],$$

where y˜ and x˜ are composed of (y˜i,x˜i)’s and (y˜i,x˜i) = √δˆi,q(yi,xi).



```
In [8]: # EVALUATING EQUATION 6
        np.random.seed(0)
        def compute(values):
            output = np.empty(len(values))
            for i in range(len(values)):
                output[i] = 1.0 / values[i]
            return output

        values = np.random.randint(1, 10, size=5)
        out = compute(values)
        for p in range(2):
            var6 = np.log(out)
        tou = 1000
        for j in range(p):
            Z = 1-(np.exp(phai/tou))
            var61 = lambda2*Z
        for q in range(2):
            phai = M[q]*B[q]/sigma
            var62 = lambda1*phai
        for q in range(Q):
            l = M[q]*g*h*sigma*(np.multiply(B[q],X.transpose())+B[q])
        var63 = np.sum(l)
        val_6 = var6+var61+var62+var63
        print("Output of Equation 6 is:{}".format(val_6))
```

```
Output of Equation 6 is:[668911.98071981 668913.77247928 668912.38618492
668912.38618492
 668911.69303774]
```

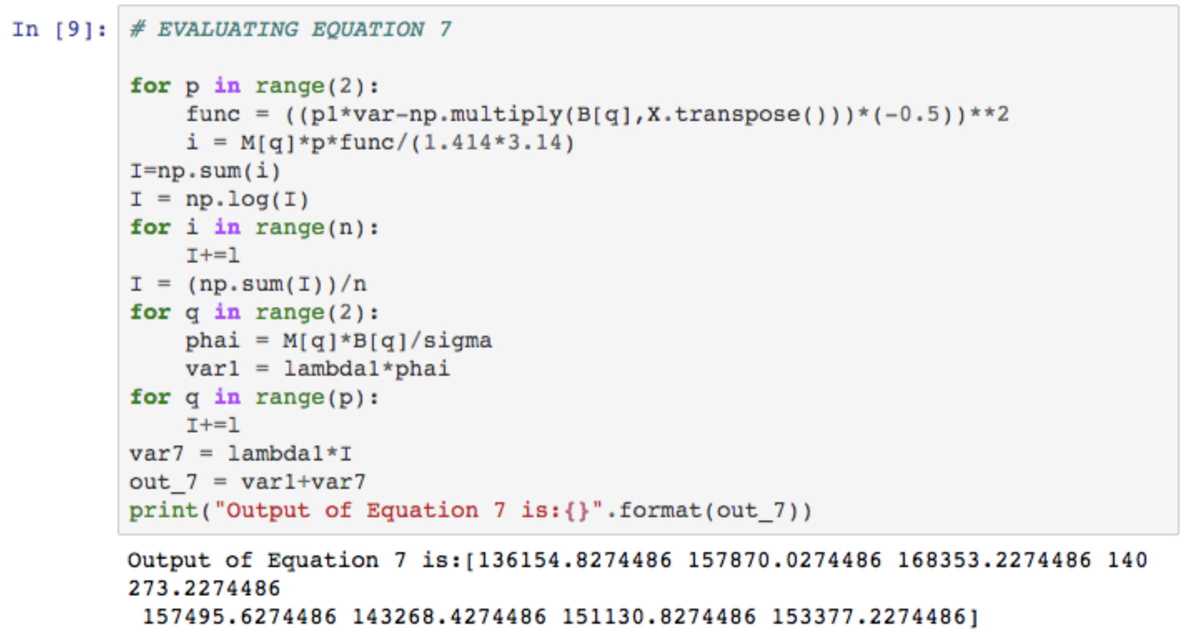
Equation 7:

As opposed to fully optimizing (6), we minimize it in a coordinate-wise manner, update one coordinate, and hold the q=1 q=1 j=1 other coordinates at their current estimates. The closed-form coordinate updates can be obtained as:

$$\rho_q^{(m+1)} = \frac{\left\langle\tilde{y}, \tilde{\mathbf{x}}^T\phi_q^{(m)}\right\rangle + \sqrt{\left\langle\tilde{y}, \tilde{\mathbf{x}}^T\phi_q^{(m)}\right\rangle^2 + 4\left\|\tilde{y}\right\|^2 n_q}}{2\left\|\tilde{y}\right\|^2}, \quad q = 1, 2,$$

$$\phi_{1,j}^{(m+1)} = \begin{cases} (-M_{1,j} - n\lambda_1(\mu_1^{(m+1)})^{\gamma} + L\phi_{2,j}^{(m)})/(\left\|\tilde{\mathbf{x}}_j\right\|^2 + L) & \text{if} \quad L\phi_{2,j}^{(m)} > M_{1,j} + n\lambda_1(\mu_1^{(m+1)})^{\gamma}, \\ (-M_{1,j} + n\lambda_1(\mu_1^{(m+1)})^{\gamma} + L\phi_{2,j}^{(m)})/(\left\|\tilde{\mathbf{x}}_j\right\|^2 + L) & \text{if} \quad L\phi_{2,j}^{(m)} < M_{1,j} - n\lambda_1(\mu_1^{(m+1)})^{\gamma}, \\ 0 & \text{otherwise}, \end{cases}$$

$$\phi_{2,j}^{(m+1)} = \begin{cases} (-M_{2,j} - n\lambda_1(\mu_1^{(m+1)})^{\gamma} + L\phi_{1,j}^{(m)})/(\left\|\tilde{\mathbf{x}}_j\right\|^2 + L), & \text{if} \quad L\phi_{1,j}^{(m)} > M_{2,j} + n\lambda_1(\mu_1^{(m+1)})^{\gamma} \\ (-M_{2,j} + n\lambda_1(\mu_1^{(m+1)})^{\gamma} + L\phi_{1,j}^{(m)})/(\left\|\tilde{\mathbf{x}}_j\right\|^2 + L), & \text{if} \quad L\phi_{1,j}^{(m)} < M_{2,j} - n\lambda_1(\mu_1^{(m+1)})^{\gamma} \\ 0 & \text{otherwise}, \end{cases}$$



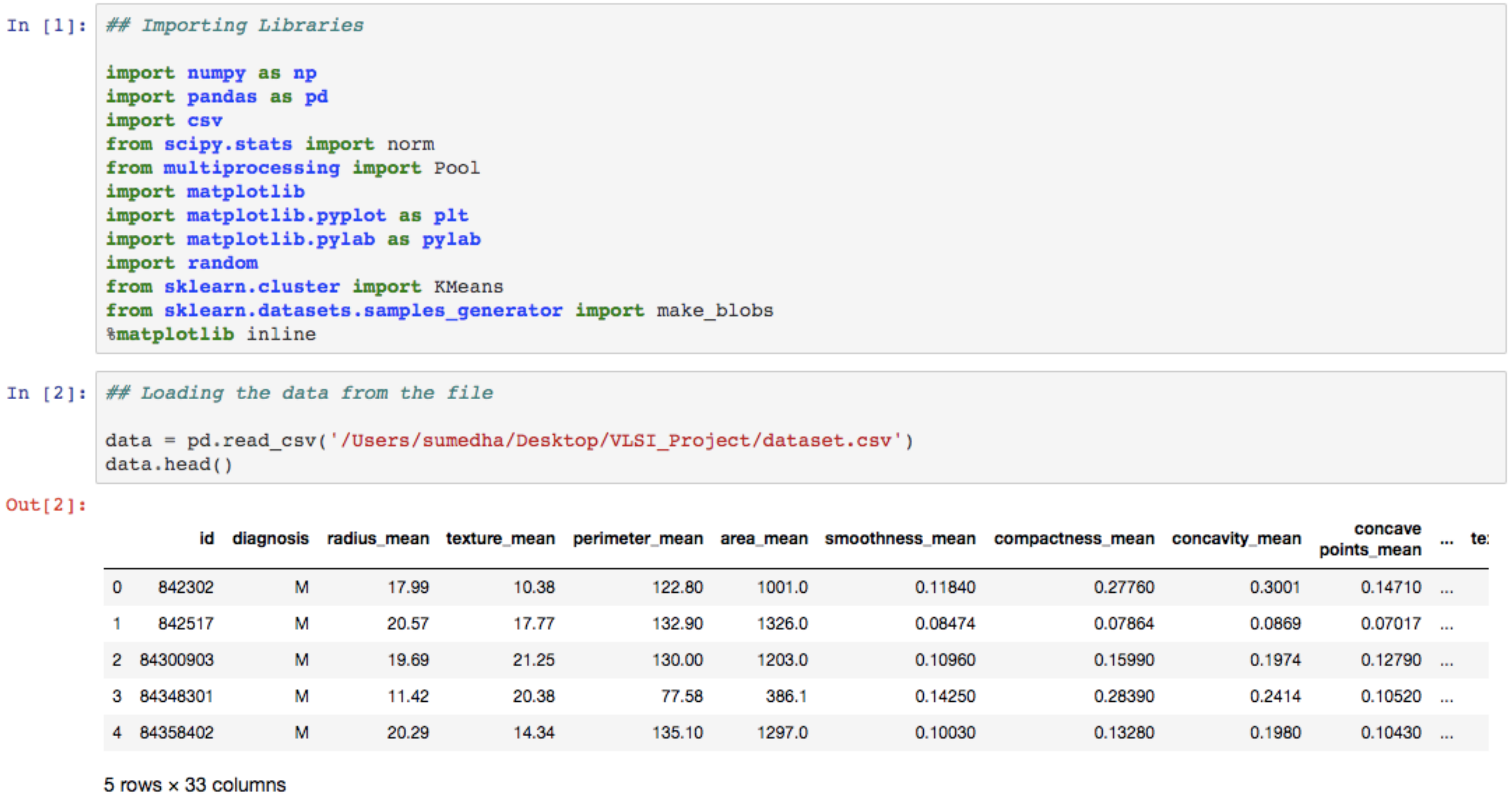
```
In [9]: # EVALUATING EQUATION 7

        for p in range(2):
            func = ((p1*var-np.multiply(B[q],X.transpose()))*(-0.5))**2
            i = M[q]*p*func/(1.414*3.14)
        I=np.sum(i)
        I = np.log(I)
        for i in range(n):
            I+=1
        I = (np.sum(I))/n
        for q in range(2):
            phai = M[q]*B[q]/sigma
            var1 = lambda1*phai
        for q in range(p):
            I+=1
        var7 = lambda1*I
        out_7 = var1+var7
        print("Output of Equation 7 is:{}".format(out_7))
```

```
Output of Equation 7 is:[136154.8274486 157870.0274486 168353.2274486 140
273.2274486
 157495.6274486 143268.4274486 151130.8274486 153377.2274486]
```

## FMR IMPLEMENTATION USING STRUCTURED ANALYSIS

Implementing on Dataset

**Dataset used**:
Breast Cancer dataset from kaggle.



```
In [1]: ## Importing Libraries

        import numpy as np
        import pandas as pd
        import csv
        from scipy.stats import norm
        from multiprocessing import Pool
        import matplotlib
        import matplotlib.pyplot as plt
        import matplotlib.pylab as pylab
        import random
        from sklearn.cluster import KMeans
        from sklearn.datasets.samples_generator import make_blobs
        %matplotlib inline
```

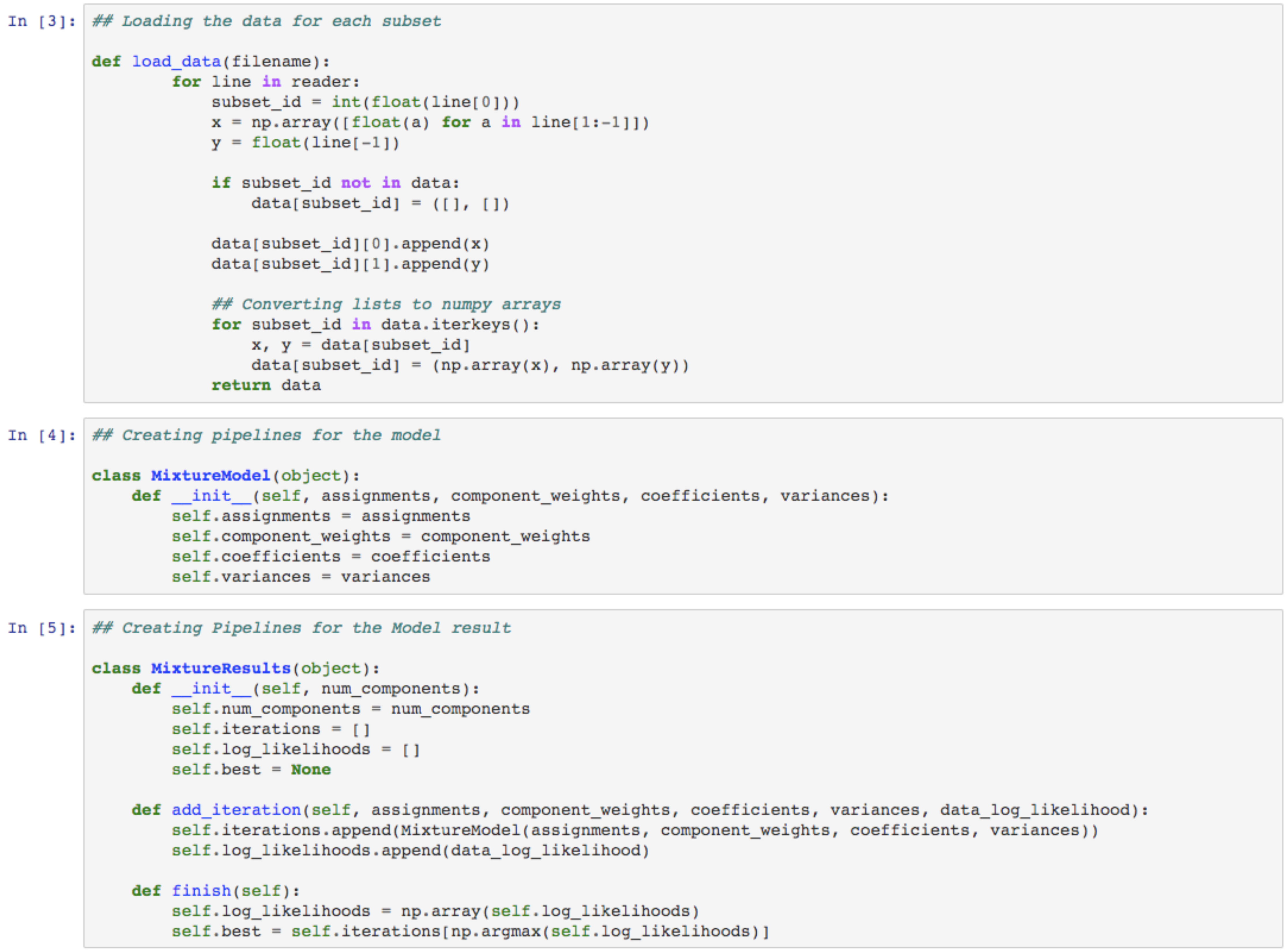
```
In [2]: ## Loading the data from the file

        data = pd.read_csv('/Users/sumedha/Desktop/VLSI_Project/dataset.csv')
        data.head()
```

Out[2]:

| | id | diagnosis | radius_mean | texture_mean | perimeter_mean | area_mean | smoothness_mean | compactness_mean | concavity_mean | concave points_mean | ... | te |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 0 | 842302 | M | 17.99 | 10.38 | 122.80 | 1001.0 | 0.11840 | 0.27760 | 0.3001 | 0.14710 | ... | |
| 1 | 842517 | M | 20.57 | 17.77 | 132.90 | 1326.0 | 0.08474 | 0.07864 | 0.0869 | 0.07017 | ... | |
| 2 | 84300903 | M | 19.69 | 21.25 | 130.00 | 1203.0 | 0.10960 | 0.15990 | 0.1974 | 0.12790 | ... | |
| 3 | 84348301 | M | 11.42 | 20.38 | 77.58 | 386.1 | 0.14250 | 0.28390 | 0.2414 | 0.10520 | ... | |
| 4 | 84358402 | M | 20.29 | 14.34 | 135.10 | 1297.0 | 0.10030 | 0.13280 | 0.1980 | 0.10430 | ... | |

5 rows × 33 columns

# Implementing on Dataset

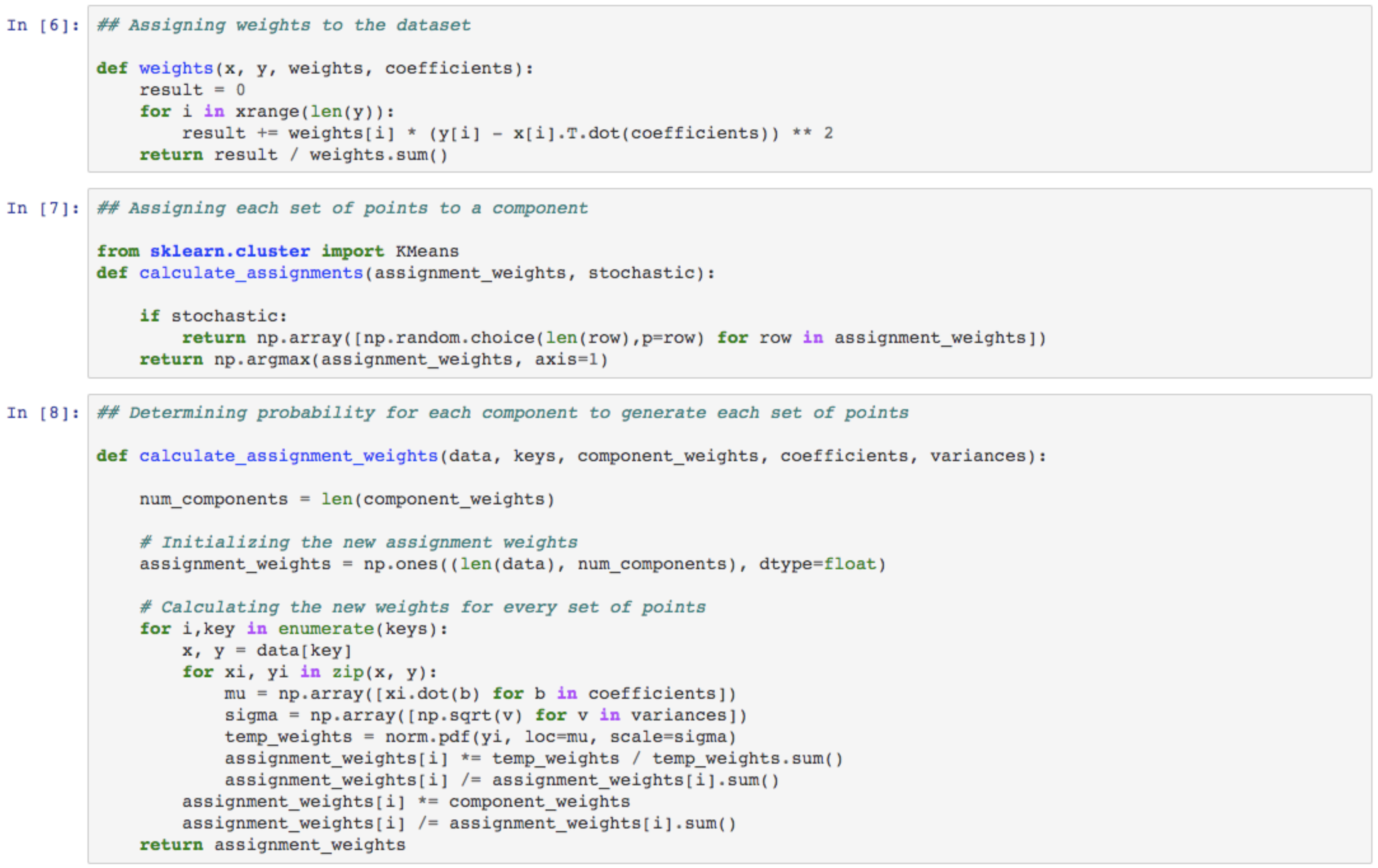


```
In [3]: ## Loading the data for each subset

        def load_data(filename):
                for line in reader:
                    subset_id = int(float(line[0]))
                    x = np.array([float(a) for a in line[1:-1]])
                    y = float(line[-1])

                    if subset_id not in data:
                        data[subset_id] = ([], [])

                    data[subset_id][0].append(x)
                    data[subset_id][1].append(y)

                    ## Converting lists to numpy arrays
                    for subset_id in data.iterkeys():
                        x, y = data[subset_id]
                        data[subset_id] = (np.array(x), np.array(y))
                    return data
```

```
In [4]: ## Creating pipelines for the model

        class MixtureModel(object):
            def __init__(self, assignments, component_weights, coefficients, variances):
                self.assignments = assignments
                self.component_weights = component_weights
                self.coefficients = coefficients
                self.variances = variances
```

```
In [5]: ## Creating Pipelines for the Model result

        class MixtureResults(object):
            def __init__(self, num_components):
                self.num_components = num_components
                self.iterations = []
                self.log_likelihoods = []
                self.best = None

            def add_iteration(self, assignments, component_weights, coefficients, variances, data_log_likelihood):
                self.iterations.append(MixtureModel(assignments, component_weights, coefficients, variances))
                self.log_likelihoods.append(data_log_likelihood)

            def finish(self):
                self.log_likelihoods = np.array(self.log_likelihoods)
                self.best = self.iterations[np.argmax(self.log_likelihoods)]
```

## Implementing on Dataset



In [6]:
```python
## Assigning weights to the dataset

def weights(x, y, weights, coefficients):
    result = 0
    for i in xrange(len(y)):
        result += weights[i] * (y[i] - x[i].T.dot(coefficients)) ** 2
    return result / weights.sum()
```

In [7]:
```python
## Assigning each set of points to a component

from sklearn.cluster import KMeans
def calculate_assignments(assignment_weights, stochastic):

    if stochastic:
        return np.array([np.random.choice(len(row),p=row) for row in assignment_weights])
    return np.argmax(assignment_weights, axis=1)
```

In [8]:
```python
## Determining probability for each component to generate each set of points

def calculate_assignment_weights(data, keys, component_weights, coefficients, variances):

    num_components = len(component_weights)

    # Initializing the new assignment weights
    assignment_weights = np.ones((len(data), num_components), dtype=float)

    # Calculating the new weights for every set of points
    for i,key in enumerate(keys):
        x, y = data[key]
        for xi, yi in zip(x, y):
            mu = np.array([xi.dot(b) for b in coefficients])
            sigma = np.array([np.sqrt(v) for v in variances])
            temp_weights = norm.pdf(yi, loc=mu, scale=sigma)
            assignment_weights[i] *= temp_weights / temp_weights.sum()
            assignment_weights[i] /= assignment_weights[i].sum()
        assignment_weights[i] *= component_weights
        assignment_weights[i] /= assignment_weights[i].sum()
    return assignment_weights
```

## Implementing on Dataset

```
In [9]: ## Calculating the parameter values that maximize the likelihood of the data

def maximum_likelihood_parameters(data, keys, num_components, num_features, assignments, assignment_weights):
    # Calculating the weight of each component in the mixture
    component_weights = np.array([(assignments == i).sum() for i in xrange(num_components)]) / float(len(assignments))

    # Calculating the regression coefficients and variance for each component
    coefficients = np.zeros((num_components, num_features))
    variances = np.zeros(num_components)
    for i in xrange(num_components):
        points = np.where(assignments == i)[0]
        subset_weights = assignment_weights[points][:,i]
        if len(points) == 0:
            points = np.random.choice(len(assignments), size=np.random.randint(1, len(assignments)), replace=False)
            subset_weights = np.ones(len(points)) / float(len(points))
        component_x = []
        component_y = []
        weights = []
        for key, subset_weight in zip(keys[points], subset_weights):
            x, y = data[key]
            component_x.extend(x)
            component_y.extend(y)
            weights.extend([subset_weight / float(len(y))] * len(y))
        component_x = np.array(component_x)
        component_y = np.array(component_y)
        weights = np.array(weights)
        coefficients[i] = weighted_linear_regression(component_x, component_y, weights)
        variances[i] = weighted_regression_variance(component_x, component_y, weights, coefficients[i])
    return (component_weights, coefficients, variances)
```

```
In [10]: ## Fitting the Mixture Model

def fit_with_restarts_worker(worker_params):
    data, keys, num_components, max_iterations, num_restarts, stochastic, verbose = worker_params
    return fit_with_restarts(data, keys, num_components, max_iterations, num_restarts, stochastic=stochastic, verbose=
verbose)
```

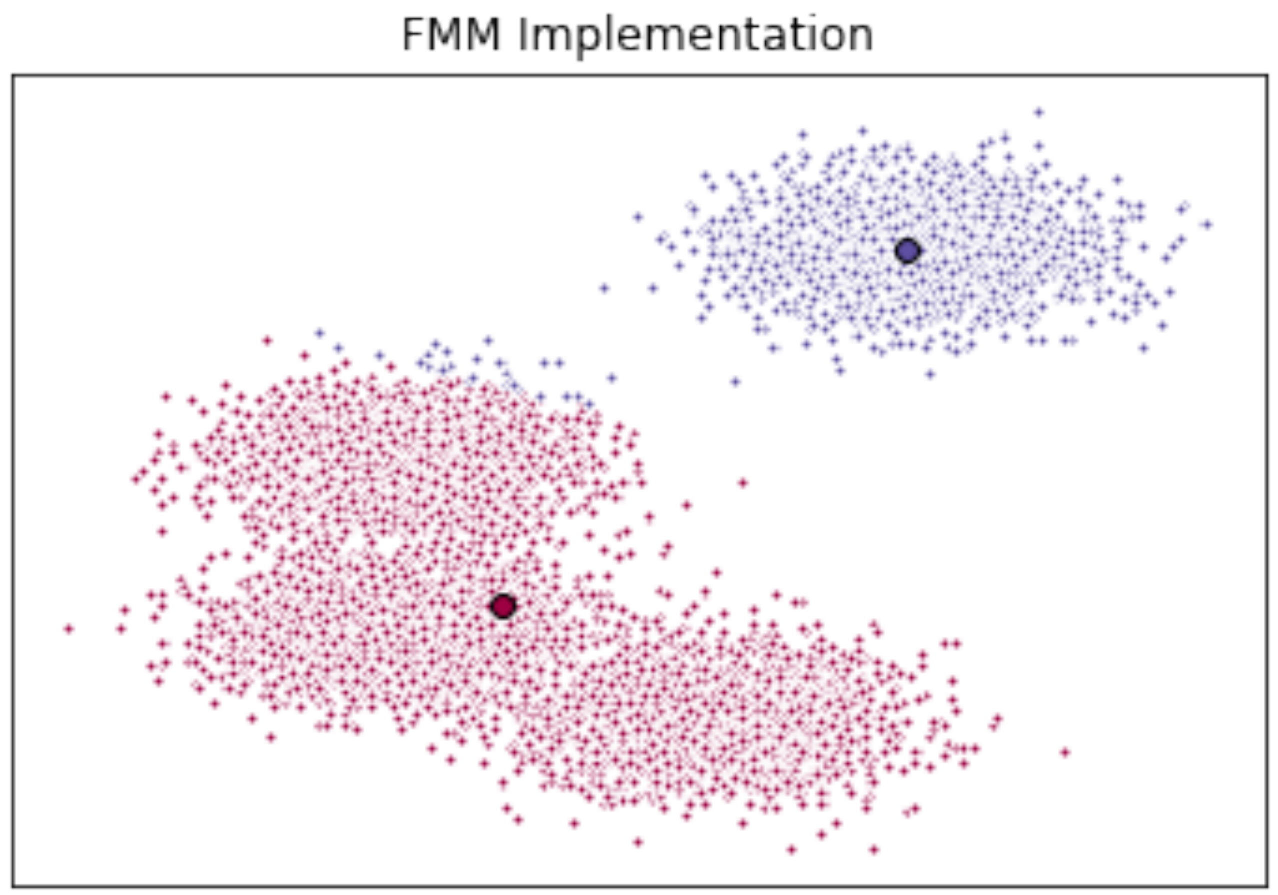
# Implementing on Dataset

```
In [11]: ## Saving the result

         def save_results(results, keys, filename):
             with open(filename, 'wb') as f:
                 writer = csv.writer(f)
                 writer.writerow([results.num_components])
                 best = results.best
                 print('component_weights: {0} coefficients: {1} variances: {2}'.format(best.component_weights.shape, best.coef
         ficients.shape, best.variances.shape))
                 rows = np.zeros((results.num_components, best.coefficients.shape[1] + 2))
                 rows[:,0] = best.component_weights
                 rows[:,1:1+best.coefficients.shape[1]] = best.coefficients
                 rows[:,1+best.coefficients.shape[1]] = best.variances
                 writer.writerows(rows)
                 for key, assignment in zip(keys, best.assignments):
                     writer.writerow([key, assignment])
```

```
In [12]: ## Chooseing parameter values for the algorithm

         # Number of mixture components
         num_components = 3
         # Maximum iterations per run
         max_iterations = 20
         # Number of random restarts to try
         num_restarts = 5
         # Using stochastic process
         stoachastic = False
         # Number of worker processes to use
         num_workers = 4
```

```
In [13]: X, y = make_blobs(n_samples=8000, centers=[[-1,3], [4, 8], [2, -3], [-1, -1]], cluster_std=0.9)
         fmm = KMeans(init = "k-means++", n_clusters = 2, n_init = 100)
         fmm.fit(X)
         fmm_labels = fmm.labels_
         fmm_labels
         fmm_centers = fmm.cluster_centers_
         fmm_centers
         fig = plt.figure(figsize=(6, 4))
         colors = plt.cm.Spectral(np.linspace(0, 1, len(set(fmm_labels))))

         # Create a plot
         ax = fig.add_subplot(1, 1, 1)
         for k, col in zip(range(len([[4,4], [-2, -1], [2, -3], [1, 1]])), colors):
             my_members = (fmm_labels == k)
             cluster_center = fmm_centers[k]
             ax.plot(X[my_members, 0], X[my_members, 1], 'w', markerfacecolor=col, marker='.')
             ax.plot(cluster_center[0], cluster_center[1], 'o', markerfacecolor=col,  markeredgecolor='k', markersize=6)

         # Title of the plot
         ax.set_title('FMM Implementation')
         ax.set_xticks(())
         ax.set_yticks(())

         # Show the plot
         plt.show()
```

## OUTPUT AFTER IMPLEMENTATION OF DATASET



- **<u>Points with Red colour represent Heterogeneous Covariates</u>**
- **<u>Points with Blue colour represent Homogeneous Covariates</u>**

## APPLICATIONS

•The problem of feature selection in finite mixture of regression models is used when the number of parameters in the model can increase with the sample size. A penalized likelihood approach for feature selection in these models is used. Under certain regularity conditions, our approach leads to consistent variable selection.

•It is also applied for tele-monitoring of Parkinson's disease (PD), where the problem concerns whether dysphoric features extracted from the patients' speech signals recorded at home can be used as surrogates to study PD severity and progression.

•Another is on breast cancer prognosis, in which one is interested in assessing whether cell nuclear features may offer prognostic values on long−term survival of breast cancer patients.

## ADVANTAGES

- Most people understand structured methods better than object oriented methods. As one of main reasons of modelling a system is for communication with users and customers, there is a benefit in providing structured models for information exchange with customers or user groups.
- Specifications are typically in form of a simple English language statement of Work. Thus, the system to be built, understood in terms of requirements (functions the system has to perform), which is why this naturally leads to a structured analysis, at least at the upper most level.
- Specially structured methods (functional decomposition) provide a natural vehicle for modelling, discussing and deriving the requirements of the system.

## DISADVANTAGES

- The difficulty with structured methods is that they do not readily support use of reusable modules.
- It procedure works well for new development, but does not provide mechanisms for designing in use of existing components.
- This does not lead to a set of requirements which map well to existing component, which does not lead to a good successful system.

## CONCLUSION

Structured Analysis of High Dimensional FMR Models can be used to fit finite mixtures of regressions to datasets used in the literature to illustrate these models. The results can be reproduced and additional insights can be gained using visualization methods available in python. A suitable methods have been implemented for objects of class which are returned.

## FUTURE SCOPE

In the future it would be desirable to have more diagnostic tools available to analyze the model fit and compare different models. The use of resampling methods would be convenient as they can be applied to all kinds of mixtures models and would therefore suit well the purpose of the package which is flexible modelling of various finite mixture models. Furthermore, an additional visualization method for the fitted coefficients of the mixture would facilitate the comparison of the components.

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