Project 5: Comparison of K-Means and LCA Clustering

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Introduction

Objectives

Clustering, also known as unsupervised classification, by grouping data with similar properties, has been broadly used as an independent tool to obtain intuitive understanding of relevant aspects of a dataset and a preprocessing step for other algorithms. Well-performed clustering methods should produce clusters with low inter-class and high intra-class similarity. Among various methods, K-Means and Latent Class Analysis (LCA) have been time-tested tools used for normally or elliptically distributed data, however, their performances in data with non-normal features are somewhat less understood. To evaluate their power for non-normal data, this project primarily focuses on comparing their clustering results by simulation with different scenarios in which data are skewed or heavy-tailed in bivariate case.

Statistical Methods to Be Studied

K-Means Categorized as a partitioning algorithm, k-means aims to partition n observations into a set of k clusters where the total within-cluster variances are minimized. The algorithm starts with a prespecified number of clusters (k) and places the centroids of the clusters at

some random locations. Then, each data point is assigned to its closest centroid with the least squared Euclidean distance. The next step is to update the centroid of the cluster by averaging the data points assigned to that cluster. Steps of assigning points to the closest centroid and updating the centroid are repeated until no further assignments can be performed.

Latent Class Analysis Unlike K-means which uses mean and distances to classify observations into groups, LCA is based on similarity in data patterns using probability and it belongs to the mixture models family which recovers hidden groups from observed data (Ferguson, et al, 2019). In our project, we consider the case where the observed variable is continuous. As a model-based method, LCA estimates parameters that best characterize different distributions and seeks to assign probability that each observation is a sample from the distribution of a class is assigned. Retention of fitted models with different classes can be decided by using criteria such as BIC (Masyn, 2013).

Data Generating Methods

In order to conduct the comparison between the above two statistical methods, we first need to generate non-normal bivariate data since real life data often has the unnormal feature. Here, we consider the bivariate distribution as a combination of a marginal distribution and a conditional distribution, then we can transform the problem into generating two univariate distributions. Next, focus on four other common characteristics including kurtosis, skewness, multimodality and outliers. During the data generation process, we realized that the outliers can be obtained by creating tails, that is changing the kurtosis of the distribution. And for multimodality, we combine it into the data by shifting the distribution to generate different clusters. Therefore, our main focus becomes simulating bivariate distributions with different kurtosis and skewness. To compare the performance of K-Means and LCA under different scenarios, we decide to visualize the performance measure by changing the kurtosis and

skewness parameters respectively.

To change the kurtosis, we first induce an algorithm to generate data from a mixture univariate distribution that combines a student-t distribution with probability p and a standard normal distribution with probability (1 - p). Here, let the degree of freedom be 2 to obtain a heavy tail. We use this algorithm to generate one univariate sample. Based on the univariate data, we generate the other sample with the conditional distribution by adding a correlation factor ρ. The conditional distribution of the second variable is the same mixture distribution but the mean and the variance of the normal distribution depend on a function of the first variable and rho. Combine these two samples together, we get the bivariate data. Considering p as the kurtosis parameter and with its value increasing, the tails become heavier.

Next, to change the skewness, we use the skew normal distribution as the distribution to generate the univariate sample instead. The density function of skew normal distribution is $f(x) = 2 \times \phi(x) \times \psi(\alpha x)$, where ϕ and ψ are the pdf and cdf of the standard Normal distribution respectively, and parameter alpha is the skewness coefficient. Then we write a function called rsnorm using accept/reject algorithm $f(x) < Mg(x)$ with $g(x)$ being the standard normal distribution, $M = 2$. Using rsnorm to generate an univariate sample and the bivariate sample by conditional distribution similar as in the kurtosis case. For both cases, we use multinomial distribution with k = 3 and p = 0.25, 0.35 and 0.4 respectively to decide the cluster of each sample and shift its mean based on the cluster. Then, we get bivariate data that have three clusters with different means for further testing on the classification methods.

Simulation Settings

The simulating scenarios depend on sample size, kurtosis parameters p and skewness parameter alpha. Sample size is taken as 300, 900 and 1500. The kurtosis parameter p can

take any values in [0, 1] and we use every 0.1 unit change in p combined with the change of sample size. alpha can be any real number. Here, we use alpha within the range [-10, 10] for every 2 unit changes and combine with the change of sample size. We explore the change of sample size combined with various kurtosis and skewness separately.

Selection of Performance Measures

Adjusted Random Index (ARI) When we have the true clustering assignment of the data, the similarity of true clusters and estimated clusters could determine the performance of the clustering. Random Index is one of the external criteria that assesses the agreement between two clustering assignments. It calculates the percentage of pairs that are in the same cluster in both clusterings and pairs that are in the different clusters in both clusterings among the total number of pairs of the data. The adjusted random index corrects the random index by considering the chance of random guess. Random Index is bounded between 0 and 1 and ARI closer to 1 usually implies higher similarity.

Misclassification Rate (MR) The other performance measure is the misclassification rate that is commonly used in classification. Classification has defined response, but clustering is unsupervised learning, so we could not directly measure the error rate. We compute the misclassification rate with each permutation of the estimated clusters. The permutation with the lowest misclassification rate should be the actual estimated clustering and then we could figure out the actual misclassification rate.

For each simulation scenario, we run the simulation a hundred times and calculate the summary statistics of each measure of performance, especially the average and standard deviation. We also add up the square of average value from the best performance value with the variance as the mean square error (MSE) of the performance measure of the scenario.

Simulation Results

Data Visualization

True cluster

We make some simulation examples with $p = 0, 0.5, 1$ and alpha $= -10, 0, 10$ to visualize change of kurtosis and skewness of the data. We utilize the scatter plot to visualize the data. The series of scatter plots shows the data for each pair of variables with different kurtosis and skewness results in different clusters shown in different colors. Data is concentrated into three clusters after shifting. Marginal density reflects the distribution of each data which is multimodial. The unsmooth contour line indicates the data is non-normal, non-ellipse, and satisfied the requirement of our research. When kurtosis parameter p = 0 (Fig 1), the plot reflects a flatter top with fat tails. Clusters are well separated, data share high similarities in each cluster but are different from other clusters. There is no outlier. When kurtosis parameter p = 0.5 (Fig 2), data are not well separated and there are three extreme outlier with heavier tails. When kurtosis parameter p = 1 (Fig 3), there are more outliers and heavier tails than p = 0.5. As the kurtosis parameter p gets larger, the value of kurtosis becomes larger. The data tend to have heavier tails and more outliers. The similarities among different clusters get higher and the similarity of each point in a cluster gets lower (Fig 4). Therefore, data becomes more scattered. As for the skewness, when the skewness parameter alpha = 0 (Fig 5), the three clusters are overlapped, the points are concentrated but evenly distributed within the cluster. When skewness parameter alpha = 10 (Fig 6), three clusters are well separated, each cluster having higher density in the left part. When skewness parameter alpha = −10 (Fig 7), similar to the plot when alpha = 10, but the data concentrated in the right part of each cluster due to the change sign of parameter alpha. When the skewness parameter moves away from 0, points would be concentrated in some

part within the cluster instead of evenly distributed.

Estimated cluster

To have some senses about how the clustering methods work in variation of p and alpha, we apply the clustering on the data from simulation examples generated previously, and draw a series of scatter plots. The plots show the clusters estimated by K-Means and LCA with variation of p (fig 4) and alpha (fig 8). From the Fig 4, we can figure out that both two methods divide points into 3 clusters but LCA does not cluster the data well when p is equal to 1.

In the figure 8 showing the change in skewness, both clustering methods have roughly similar results compared with the true clusters.

Comparison

In order to compare the performance between LCA and K-Means, we consider the misclassification rate (MR) and adjusted random index (ARI) of the two clustering methods LCA and K-Means by comparing the mean, standard deviation and MSE in different kurtosis and skewness. After obtaining the performance measures in different scenario, we plot those performance over the change in kurtosis and skewness respectively to visualize the outcomes and do the comparison in different sample sizes 300, 900 and 1500 by drawing a grid of plots. The trend of ARI and MR of the two methods is very similar. Regardless of the performance measures, we can see in this figure (fig 9) that when kurtosis parameter is below 0.5 (light-tails), LCA has better performance, but when kurtosis increases, the performance of LCA getting worse and it is worse than that of K-Means when kurtosis parameter is higher than 0.5 (heavy tail). However, K-means always has higher variability than LCA, which might be not preferable when we need precise outcome. The

LCA showed higher MSE when kurtosis is high so we might prefer K-Means for heavy tail data.

In the figure 10 about the change in skewness, we can observe that when the skewness parameter is below zero (left-skewed), the mean performance of LCA is obviously better than K-Means. When the skewness is close to zero, the performances of these two methods are becoming closer and maintain this trend for the situation of skewness parameter larger than zero (right-skewed). LCA always has lower variance than K-Means and has better average performance in most of the cases.

Besides, we can figure out that the performance of LCA and K-Means have similar trends in different sample size 300, 900, 1500.

Conclusion

To evaluate the performance of K-Means and LCA for data with non-normal features which mimics real-world situations, bivariate data with varied skewness and tail behavior are generated using combination of distributions and sampling method such as acceptance/rejection algorithm. With known true cluster assignments from the data generation process, the clustering results of K-Means and LCA are evaluated by two criteria, Adjusted Random Index (ARI) and misclassification rate. Based on the simulation results with varied sample size and parameter values for skewness and kurtosis, we observe that, regardless of variation in sample size, as data becomes heavy-tailed or contains large quantity of outliers, the performance of K-Means is relatively more stable and better than LCA with higher average ARI score and similar misclassification rate. In terms of skewness, when data is highly right-skewed, LCA outperforms K-Means under both criteria. In the right-skewed situation, two methods show equally desired performance. In both scenarios, K-Means always has

higher variability than LCA, so we might prefer LCA when we need precise outcomes. It is also worthy to address that the performance of both methods are more prone to be influenced or relatively poorer in heavy-tails/outliers situations than the skewed case.

Limitation of our work includes but not limited to the fact that as only bivariate data is considered for evaluation, clustering results of both methods would likely to be different in more complex cases for data with non-normal features. To conclude, our work has shown that the performance of K-Means is more stable to the variations of data characteristics including sample size, skewness, and kurtosis. Compared to K-Means, when data is heavily right-skewed, LCA would be a preferable tool for clustering, whereas when data contains heavy-tails/outliers, K-means is recommended.

Contribution

Xiao Ma is responsible for data generating methods and true cluster visualization group working with Hao. Generating the data, regulating the skewness and kurtosis then shifting to check the changes. Did the corresponding part for the report and presentation. Yida Wang writes the code of LCA and K-Means performance visualization in the simulation part based on Ruiqi's work and response for the sample clustering outputs and performance plots of report and slide. Ruiqi Yan writes the rsnorm function for generating skew normal data, find estimated cluster function to find the actual estimated clusters, compare function to calculate the performance measure, the for loop to do simulation in each scenario and writes selection the performance measure part in the report. Hao Zheng is responsible for the data generating including the univariate, conditional distribution, adjusting the kurtosis and skewness, initial visualization, simulation settings and corresponding report with Xiao. Peilin Zhou is responsible for objectives, statistical methods to be studied, conclusion of the report, and visualization of the sample clustering outputs of the two methods based on generated data in r.

References

1. Ferguson, S. L., G. Moore, E. W., & Hull, D. M. (2019). Finding latent groups in observed data: A Primer on Latent Profile Analysis in mplus for applied researchers. International Journal of Behavioral Development, 44(5), 458–468. https://doi.org/10.1177/0165025419881721/
2. Masyn, K. E. (2013). Latent class analysis and finite mixture modeling. In T. Little (Eds), The Oxford Handbook of Quantitative Methods (551-611). New York, NY: Oxford University Press.

Appendix I Figures and Tables

Fig1: Scatter Plot with Contour when p = 0

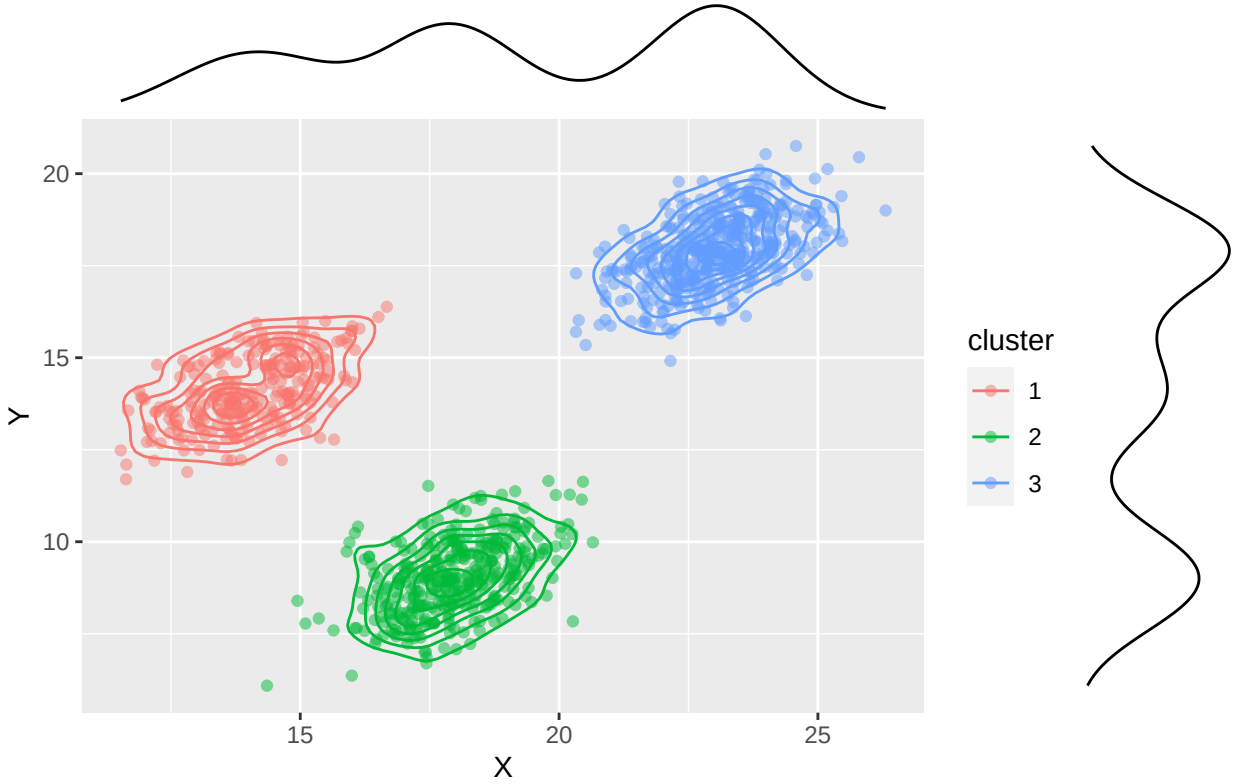


Fig2: Scatter Plot with Contour when p = 0.5

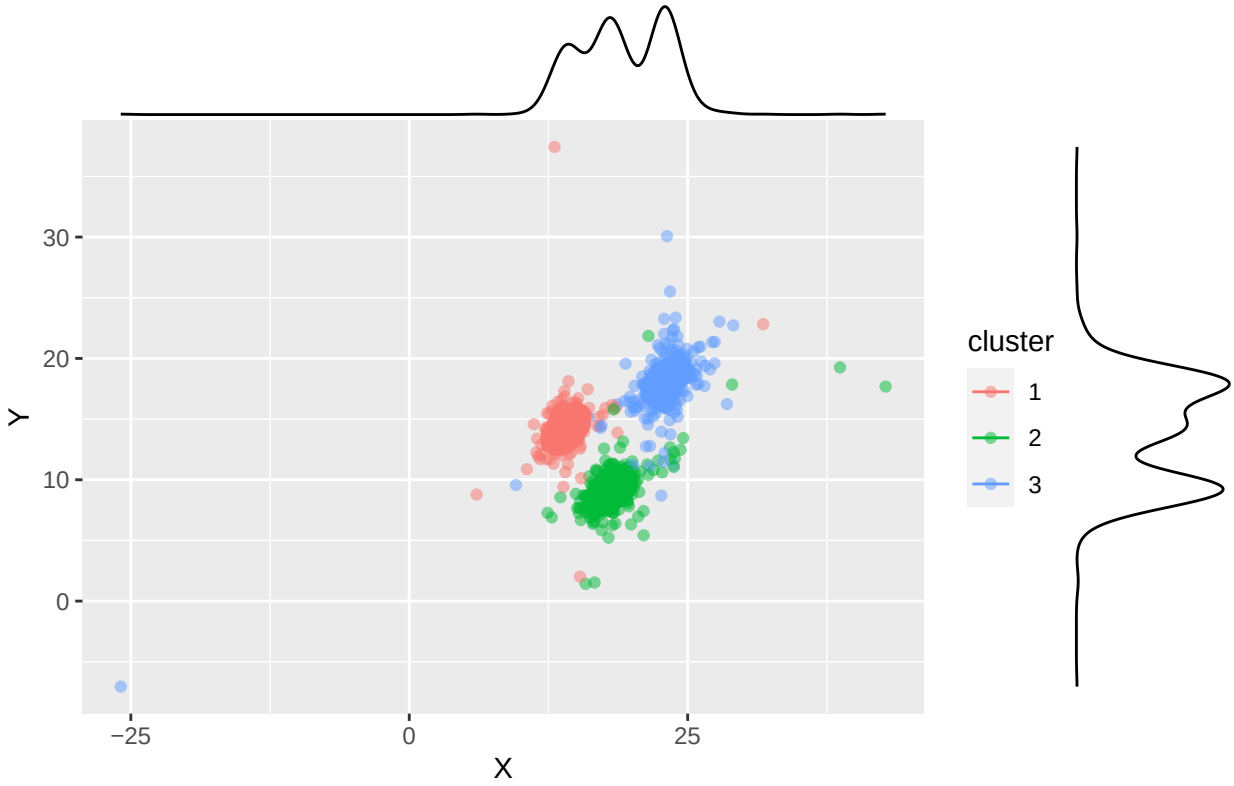


Fig3: Scatter Plot with Contour when p = 1

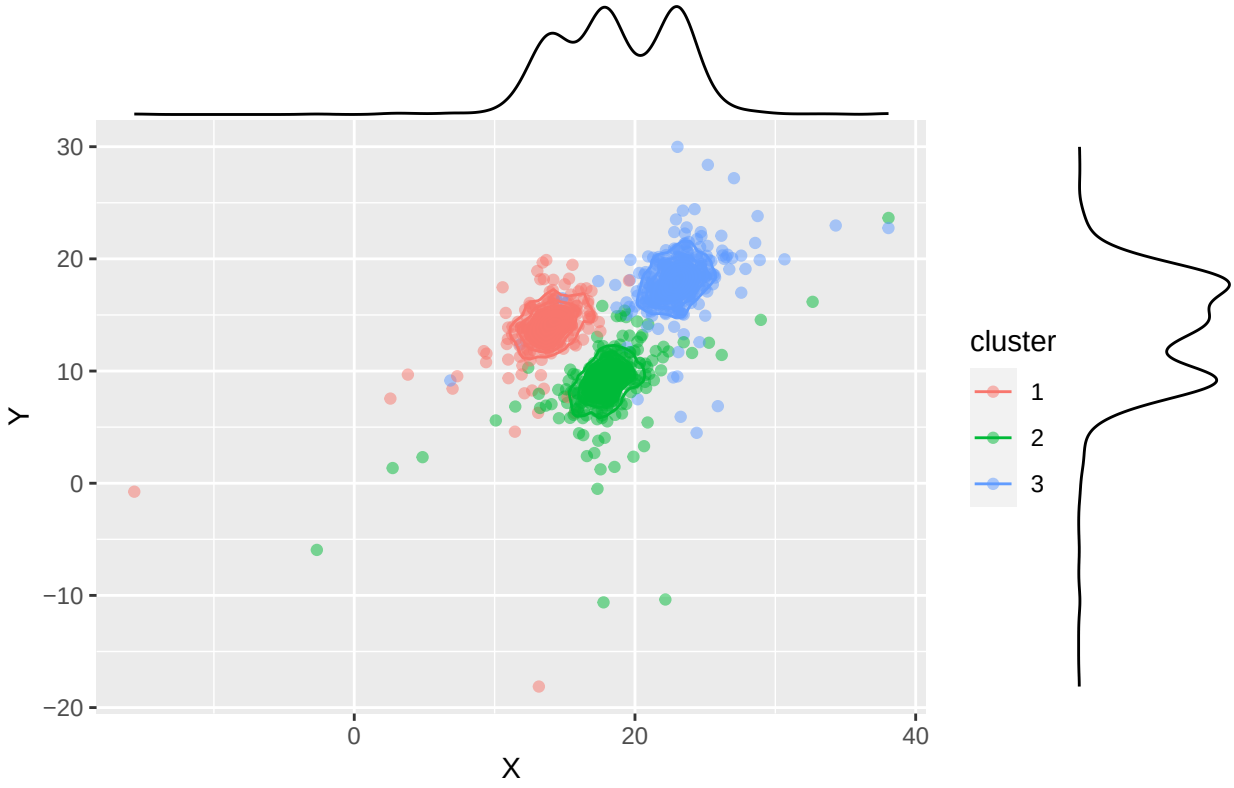


Fig11: Comparison Between Different Kurtosis

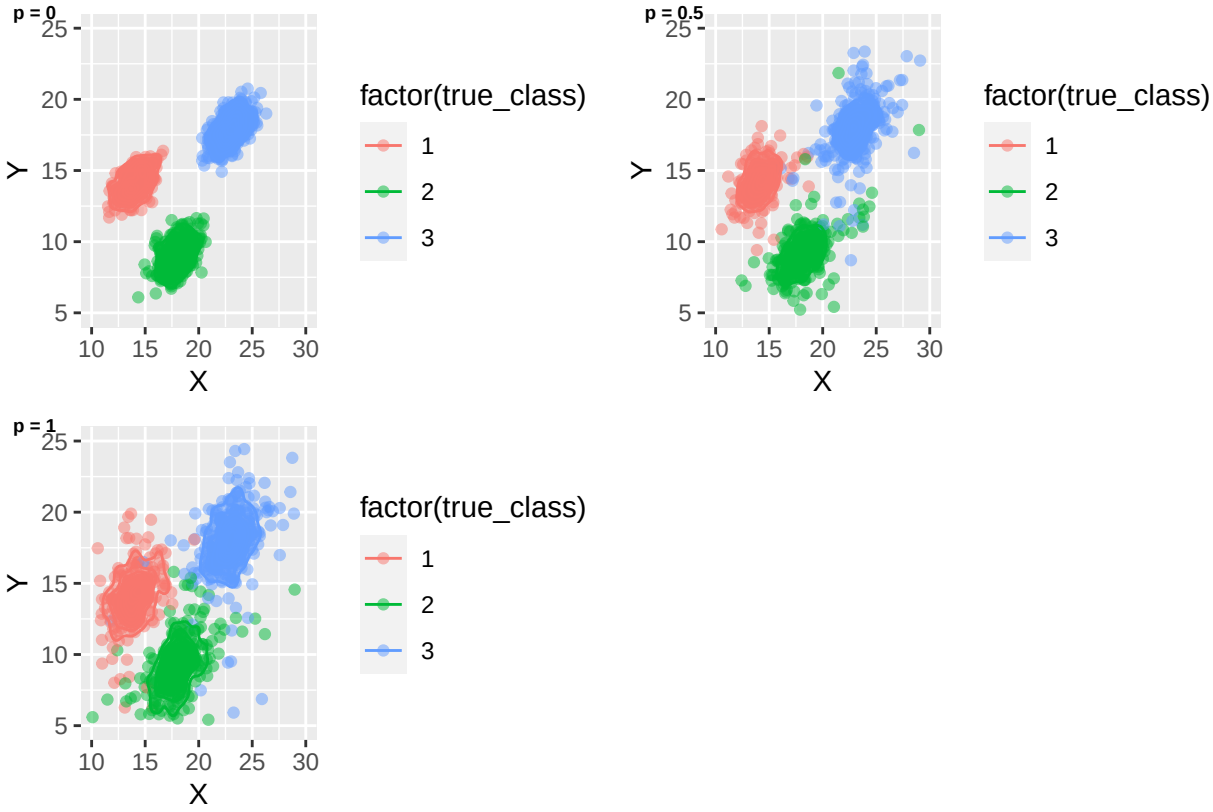


Fig4: Cluster Plots with Variation of P

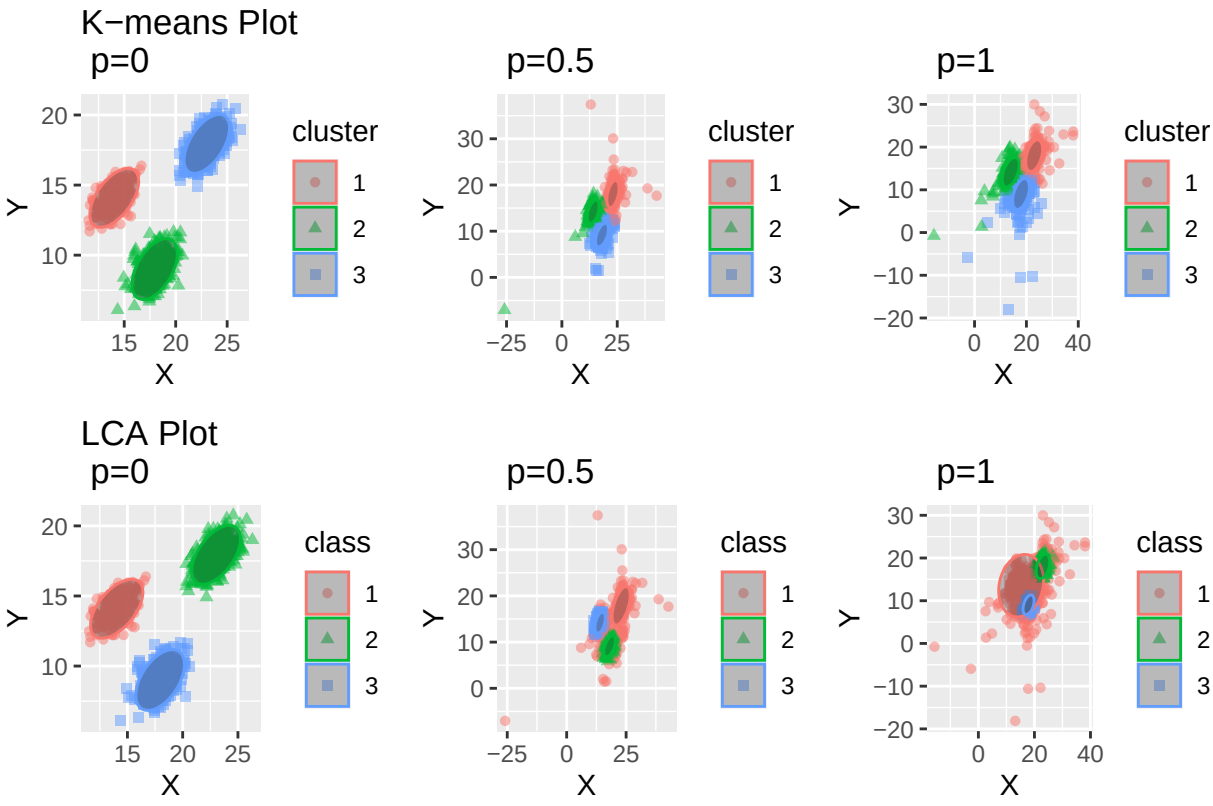


Fig5: Scatter Plot when alpha = 0

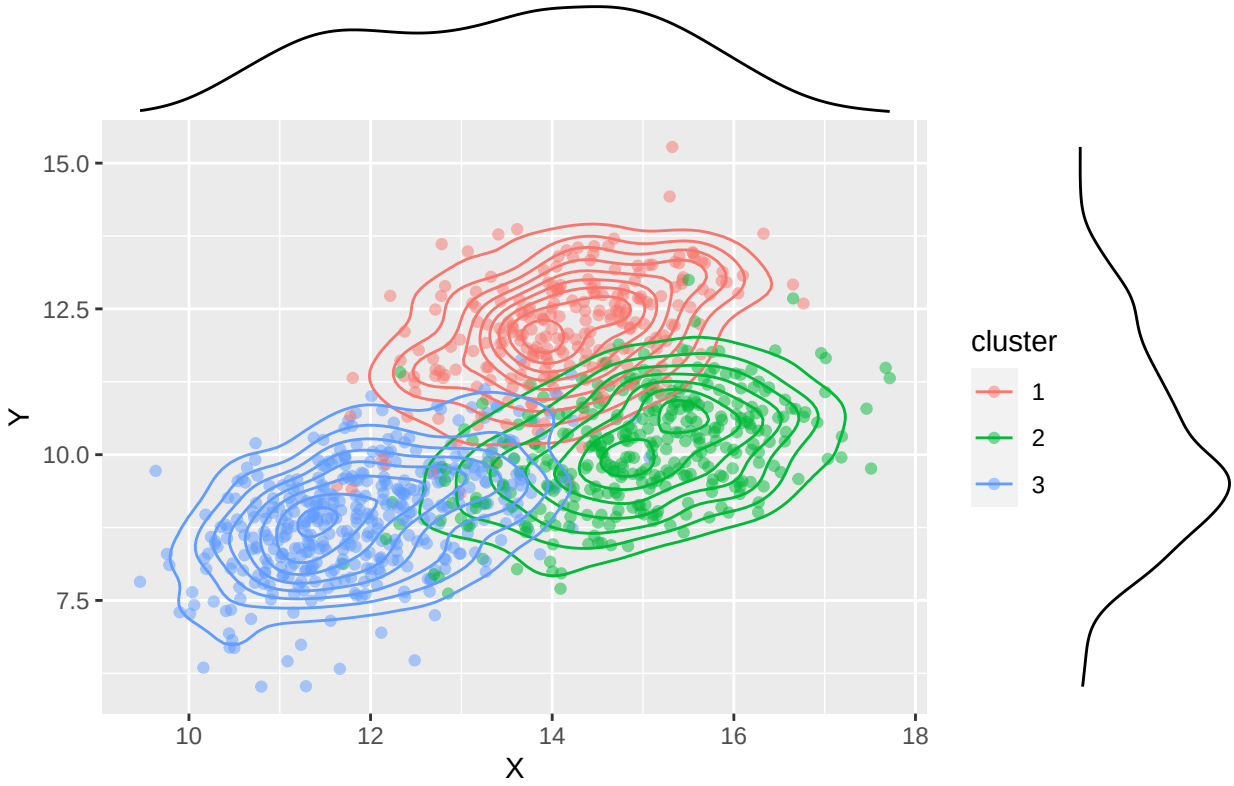


Fig6: Scatter Plot when alpha = 10

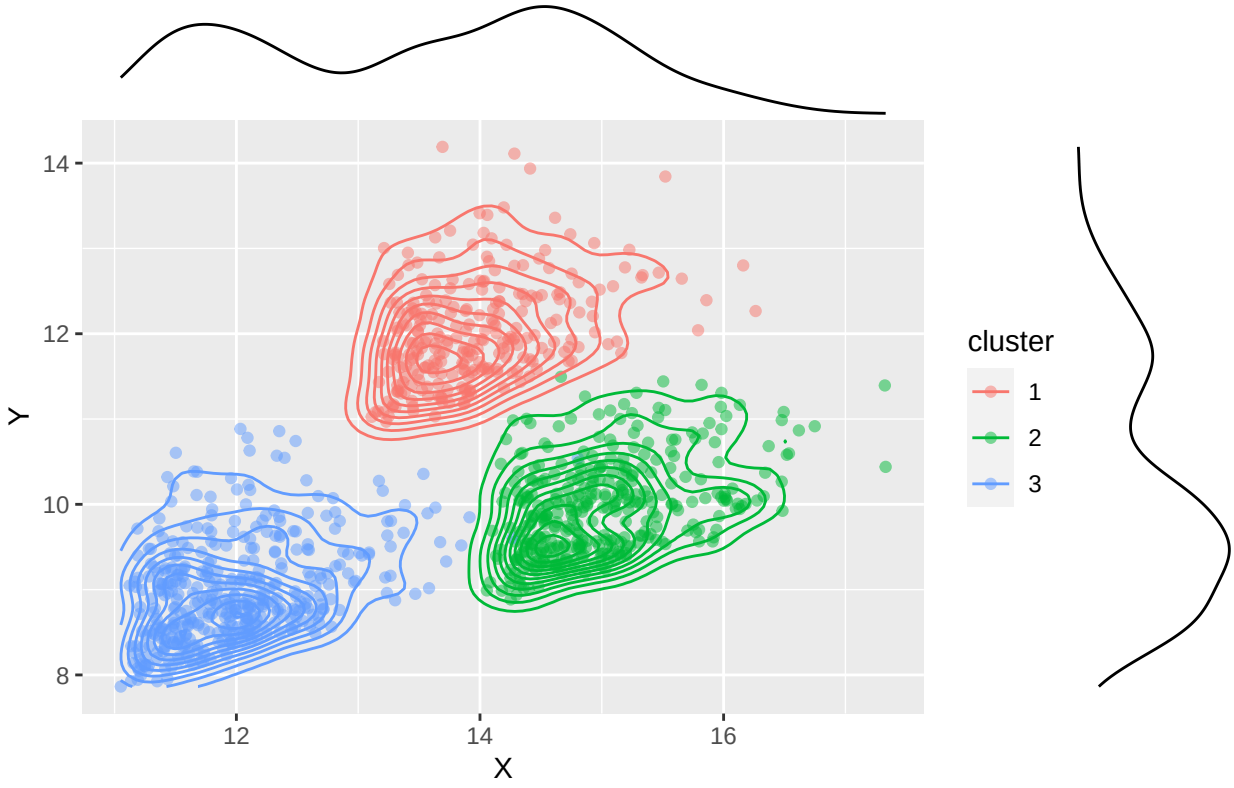


Fig7: Scatter Plot when alpha = −10

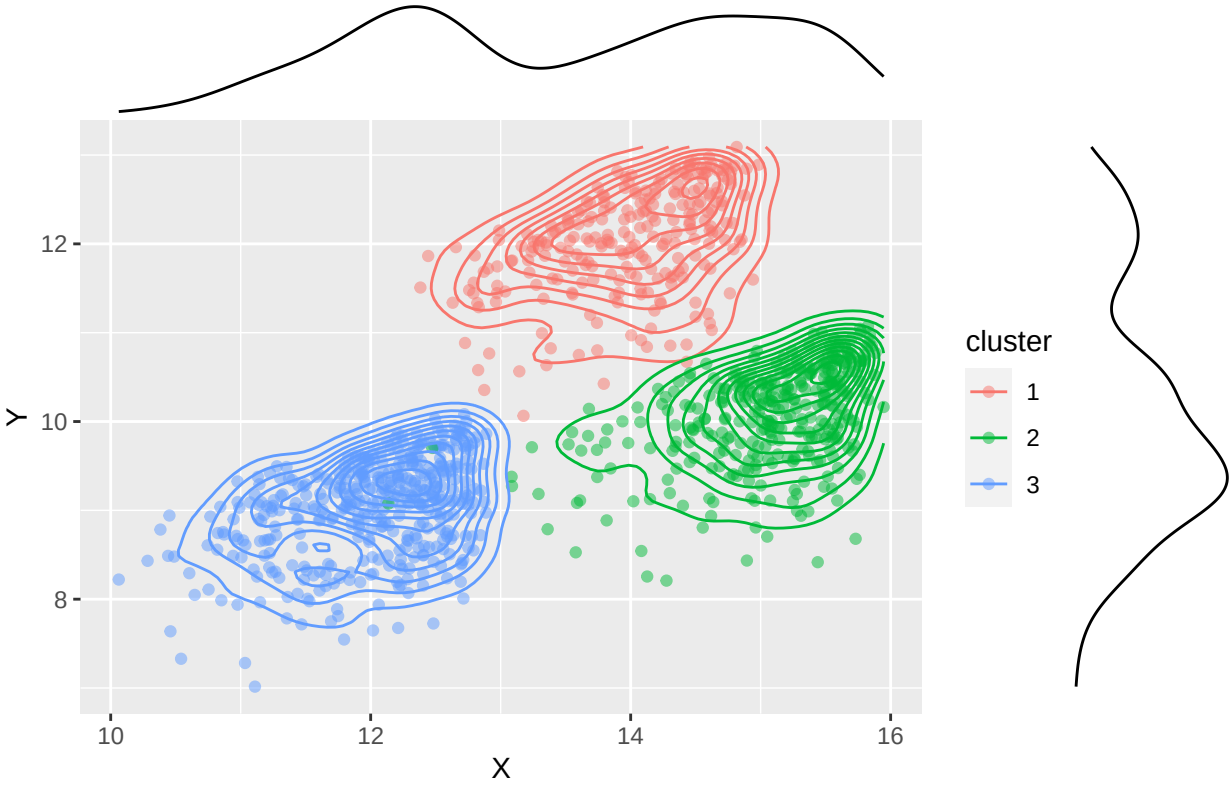


Fig12: Comparison between Different Skewness

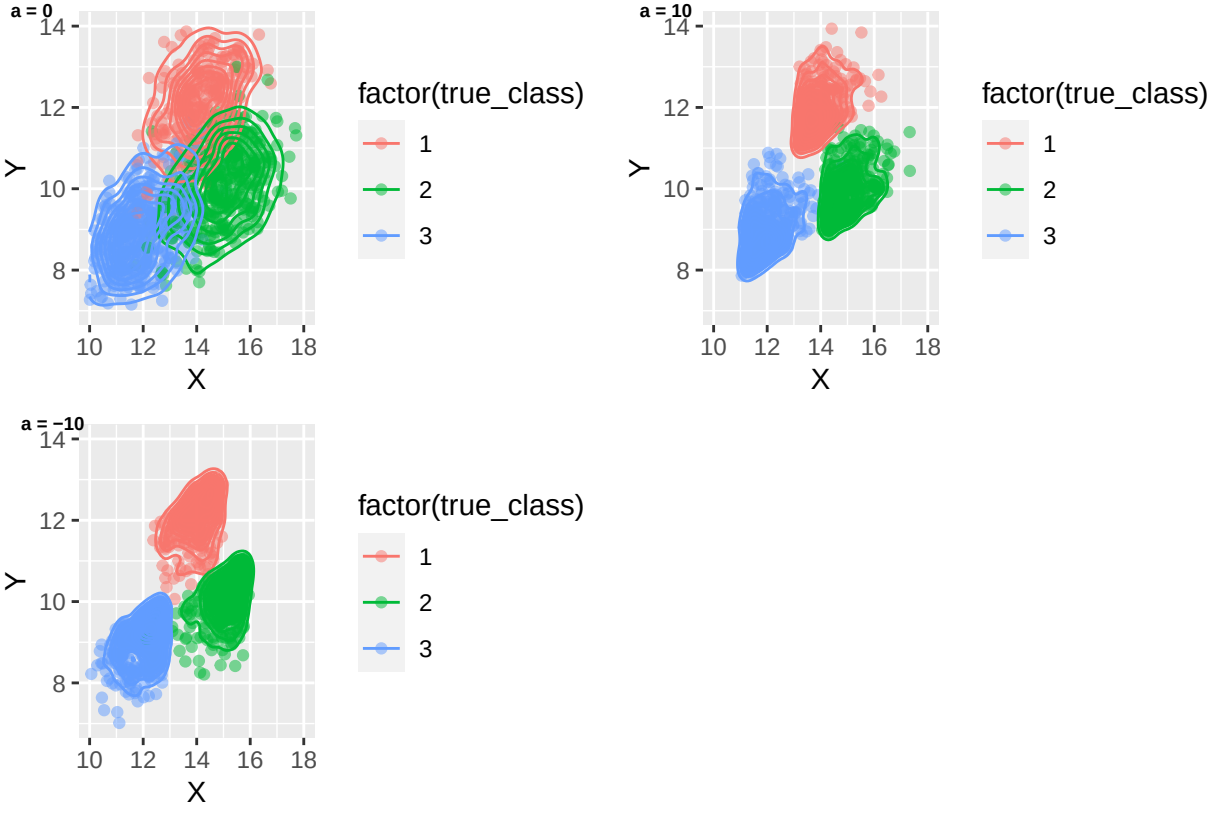


Fig8: Cluster Plots with Variation of Alpha

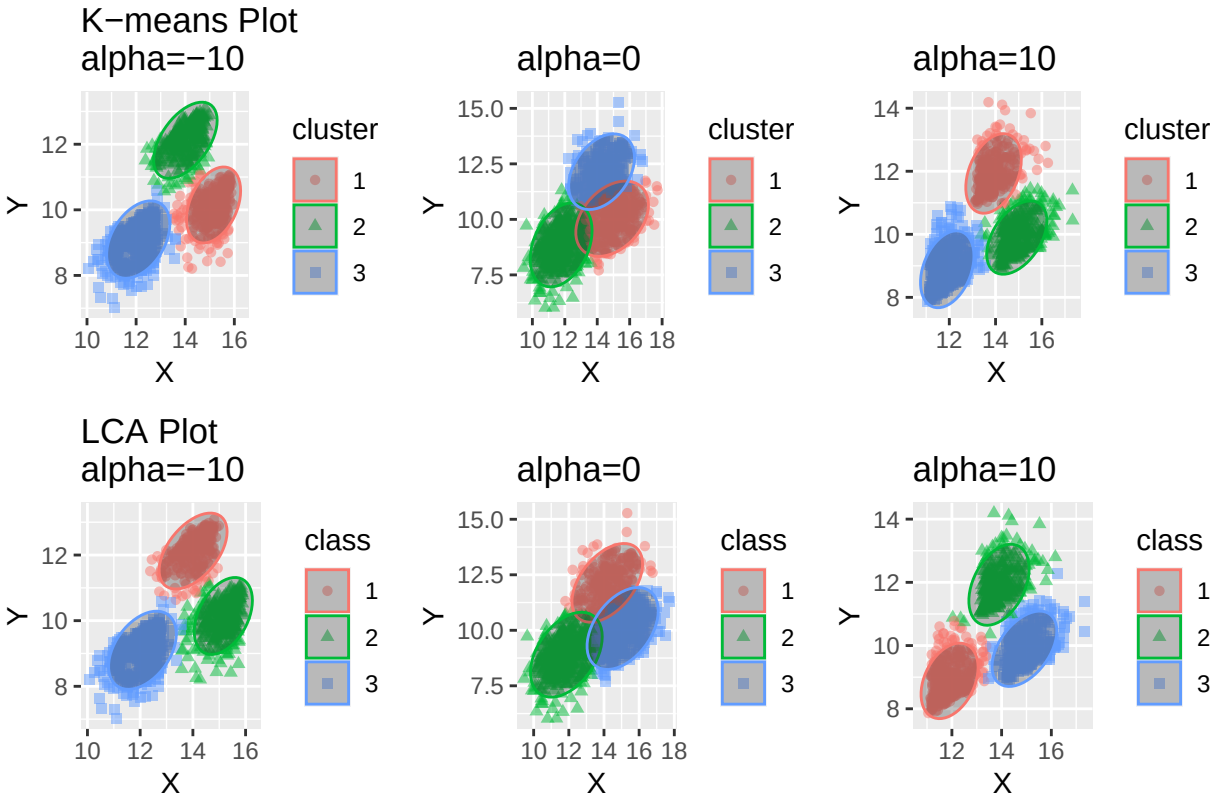


Fig9: Comparing the performance in different Sample Sizes

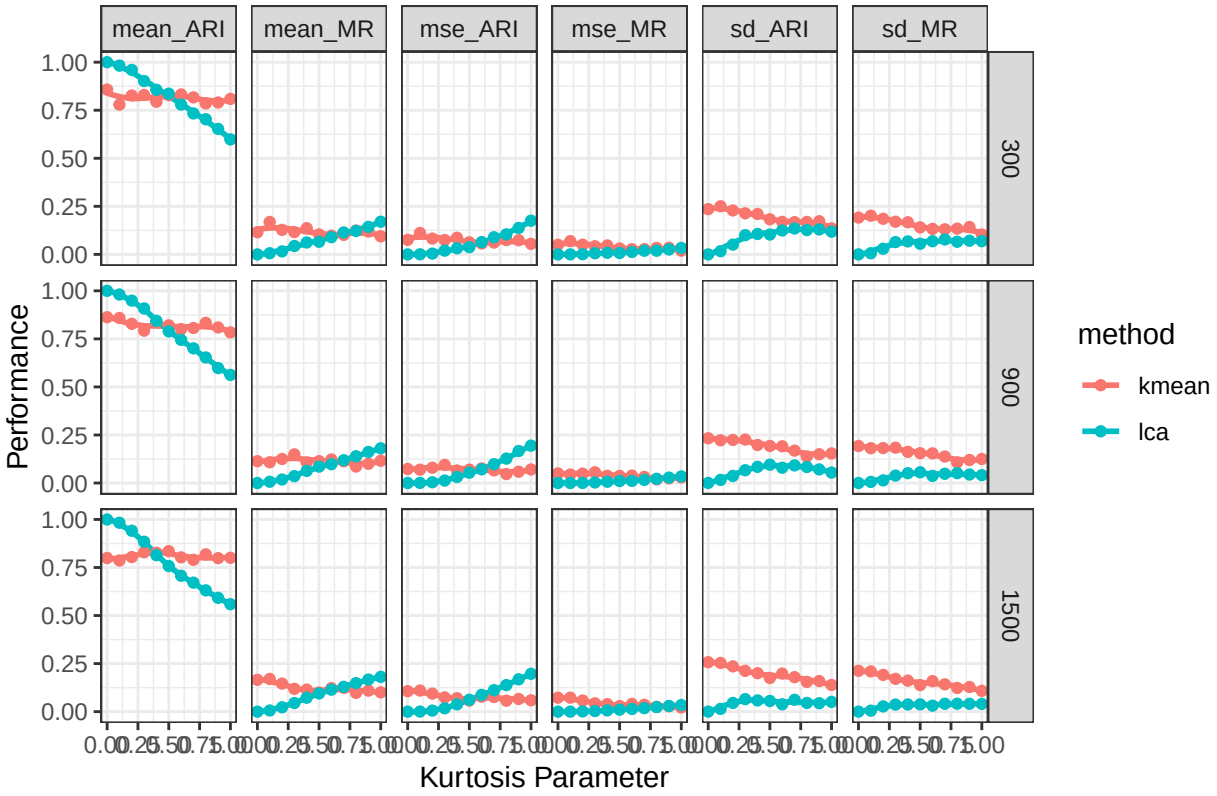
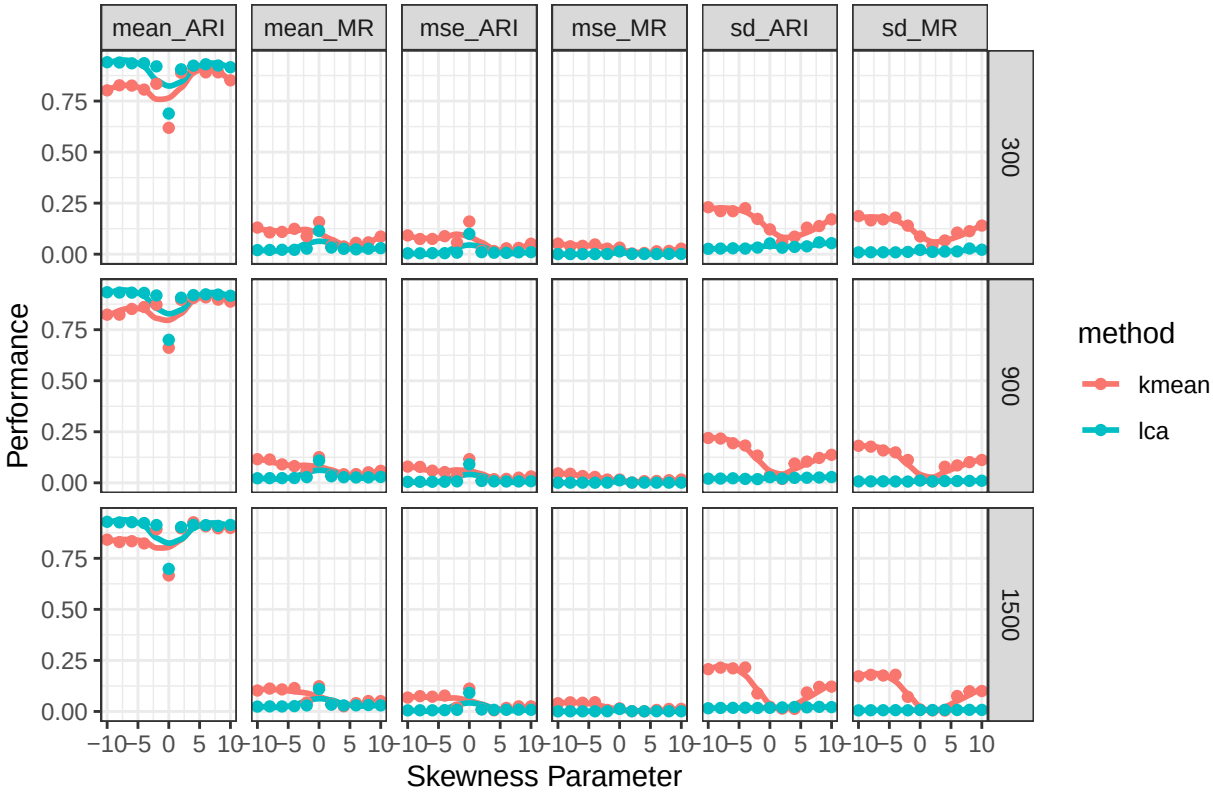


Fig10: Comparing the performance in different Sample Sizes



Appendix II R code

```
## Kurtosis


kurdata <- function(N, mu1, s1, mu2, s2, rho, p){
  true_cluster = rmultinom(n = N, size = 1, prob = c(0.25,0.35,0.4))


  usenorm <- runif(N) < (1-p)
  X <- usenorm*rnorm(N, mean = mu1, sd = s1) + (1-usenorm)*(rt(N, df = 2)+mu1)
  con_muy = mu2+rho*s2*(X-mu1)/s1
  con_sigmay = sqrt(1-rho^2)*s2
  usenorm <- runif(N) < (1-p)
  Y <- usenorm*rnorm(N, mean = con_muy, sd = con_sigmay) + (1-usenorm)*(rt(N, df = 2)+co


  kurxy = as.data.frame(cbind(X,Y))


  # shifting data
  data_mod = kurxy %>% mutate(true_class =
                        true_cluster[1,]*1+true_cluster[2,]*2+true_cluster[3,]*3,
                      X = case_when(true_class == 1 ~ X+14,
                                    true_class == 2 ~ X+18,
                                    true_class == 3 ~ X+23),
                      Y = case_when(true_class == 1 ~ Y+14,
                                    true_class == 2 ~ Y+9,
                                    true_class == 3 ~ Y+18))
  return(data_mod)
}
```

```
######
## skewed normal distribution, use alpha to change the skewness of the distribution
rsnorm <-function(N, mu, sigma, alpha){
  mu_diff = mu - alpha*sqrt(2/pi)/sqrt(1+alpha^2)
  x = NULL
  while (length(x)<N){
   g = rnorm(N)
   x = c(x,g[runif(N) < pnorm(alpha*g)])
   }
  return((x[1:N]+mu_diff)*sigma)
}


skewdata <- function(N, mu1, s1, mu2, s2, rho, alpha){
  true_cluster = rmultinom(n = N, size = 1, prob = c(0.25,0.35,0.4))

  X = rsnorm(N, mu1, s1, alpha)
  Y = rsnorm(N, mu2 + (s2/s1)*rho*(X - mu1), sqrt((1-rho^2)*s2^2), alpha)
  skewxy = as.data.frame(cbind(X,Y))
  data_mod = skewxy %>% mutate(true_class =
                       true_cluster[1,]*1+true_cluster[2,]*2+true_cluster[3,]*3,
                     X = case_when(true_class == 1 ~ X+14,
                                   true_class == 2 ~ X+15,
                                   true_class == 3 ~ X+12),
                     Y = case_when(true_class == 1 ~ Y+12,
                                   true_class == 2 ~ Y+10,
                                   true_class == 3 ~ Y+9))
```

```
  return(data_mod)
}



#Find the permutation of cluster with lowest MR
find_true_estimate_class <- function(true_class, estimate_class){
  per_df = data_frame(per1 = estimate_class,
                      per2 = case_when(
                        estimate_class == 1 ~ 1,
                        estimate_class == 2 ~ 3,
                        estimate_class == 3 ~ 2
                      ),
                      per3 = case_when(
                        estimate_class == 1 ~ 2,
                        estimate_class == 2 ~ 1,
                        estimate_class == 3 ~ 3,
                      ),
                      per4 = case_when(
                        estimate_class == 1 ~ 2,
                        estimate_class == 2 ~ 3,
                        estimate_class == 3 ~ 1
                      ),
                      per5 = case_when(
                        estimate_class == 1 ~ 3,
                        estimate_class == 2 ~ 1,
                        estimate_class == 3 ~ 2
                      ),
```

```
                      per6 = case_when(
                        estimate_class == 1 ~ 3,
                        estimate_class == 2 ~ 2,
                        estimate_class == 3 ~ 1
                      )) %>% as.matrix()
   return(per_df[,which.max(colMeans(per_df == true_class))])
}


#Compare two clustering methods using simulated data
compare <- function(N, data_mod, p){
  kmean_mod = kmeans(data_mod[,-3], 3)
  mclust_mod = Mclust(data_mod[,-3], G = 3, verbose = FALSE)
  ARI_kmean = adjustedRandIndex(kmean_mod$cluster, data_mod$true_class)
  ARI_lca = adjustedRandIndex(mclust_mod$classification, data_mod$true_class)
  mr_kmean = 1 - mean(data_mod$true_class == find_true_estimate_class(data_mod$true_clas
  mr_lca = 1 - mean(data_mod$true_class == find_true_estimate_class(data_mod$true_class,
  return(data_frame(N = c(N,N),
                    p = c(p,p),
                    method = c("kmean","lca"),
                    ARI = c(ARI_kmean, ARI_lca),
                    MR = c(mr_kmean, mr_lca)))
}
```

Data Visualization

Kurtosis

```
## Scatter plot with contour for p = 0, 0.5, 1
# p = 0
set.seed(2022)
kurtosis_data_p0 = kurdata(1000, 0, 1, 0, 1, 0.5, 0)


p0 = ggplot(kurtosis_data_p0, aes(x = X, y = Y, color = factor(true_class))) +
  geom_point(alpha = .5) +
  geom_density_2d() +
  labs(title = "Fig1: Scatter Plot with Contour when p = 0",
       x = "X",
       y = "Y",
       color = "cluster")
dp0 = ggMarginal(p0, type = "density")
dp0
```

```
# p = 0.5
kurtosis_data_p0.5 = kurdata(1000, 0, 1, 0, 1, 0.5, 0.5)


p0.5 = ggplot(kurtosis_data_p0.5, aes(x = X, y = Y, color = factor(true_class))) +
  geom_point(alpha = .5) +
  geom_density_2d() +
  labs(title = "Fig2: Scatter Plot with Contour when p = 0.5",
       x = "X",
       y = "Y",
       color = "cluster")
dp0.5 = ggMarginal(p0.5, type = "density")
```

```r
dp0.5
```

```r
# p = 1
kurtosis_data_p1 = kurdata(1000, 0, 1, 0, 1, 0.5, 1)
p1 = ggplot(kurtosis_data_p1, aes(x = X, y = Y, color = factor(true_class))) +
  geom_point(alpha = .5) +
  geom_density_2d() +
  labs(title = "Fig3: Scatter Plot with Contour when p = 1",
       x = "X",
       y = "Y",
       color = "cluster")
dp1 = ggMarginal(p1, type = "density")
dp1
```

```r
# Compare with Different Kurtosis
a = ggplot(kurtosis_data_p0, aes(x = X, y = Y, color = factor(true_class))) +
  geom_point(alpha = .5) +
  geom_density_2d() + lims(x = c(10, 30), y = c(5, 25))
b = ggplot(kurtosis_data_p0.5, aes(x = X, y = Y, color = factor(true_class))) +
  geom_point(alpha = .5) +
  geom_density_2d() + lims(x = c(10, 30), y = c(5, 25))
c = ggplot(kurtosis_data_p1, aes(x = X, y = Y, color = factor(true_class))) +
  geom_point(alpha = .5) +
  geom_density_2d() + lims(x = c(10, 30), y = c(5, 25))
figure11 = ggarrange(a, b, c, ncol = 2, nrow = 2, labels = c("p = 0","p = 0.5","p = 1"),
annotate_figure(figure11,top = text_grob("Fig11: Comparison Between Different Kurtosis",
```

Perform k-means and LCA

```
kmeans_cluster_plot = function(data, title){
  k = kmeans(data[,1:2], centers = 3, nstart = 10)
  data = data %>%
  mutate(cluster = as.factor(k$cluster))
  data %>%
    ggplot(aes(x = X, y = Y, shape = cluster, color = cluster)) +
    geom_point(alpha = .5) +
    stat_ellipse(type = "t",geom = "polygon",alpha = .3) +
    labs(title = title)
}


lca_plot = function(data, title){
  BIC = mclustBIC(data[,1:2])
  lca = Mclust(data[,1:2], 3, x = BIC)
  data = data %>%
  mutate(class = as.factor(lca$classification))
  data %>%
    ggplot(aes(x = X, y = Y, shape = class, color = class)) +
    geom_point(alpha = .5) +
    stat_ellipse(type = "t",geom = "polygon",alpha = .3) +
    labs(title = title)
}


list = c("kurtosis_data_p0","kurtosis_data_p0.5","kurtosis_data_p1")
kurt_title_kmeans = c("K-means Plot \n p=0", " \n p=0.5","\n p=1")
```

```
kurt_kmeans_plot = list()

for(i in seq_along(list)){
  kurt_kmeans_plot[[i]] = kmeans_cluster_plot(get(list[i]), kurt_title_kmeans[i])
}

kurt_title_lca = c("LCA Plot \n p=0 ", " \n p=0.5","\n p=1")
kurt_lca_plot = list()

for(i in seq_along(list)){
  kurt_lca_plot[[i]] = lca_plot(get(list[i]), kurt_title_lca[i])
}

kurt_plot.list = c(kurt_kmeans_plot, kurt_lca_plot)
grid.arrange(grobs = kurt_plot.list, ncol = 3, top=textGrob("Fig4: Cluster Plots with Va
```

Skewness

```
#scatter plot with 2d joint density plot

#alpha1 = 0
set.seed(2022)
skewed_data_0 = skewdata(1000, 0, 1, 0, 1, 0.5, 0)

alpha_0 =
  ggplot(skewed_data_0, aes(x = X, y = Y, color = factor(true_class))) +
  geom_point(alpha = .5) +
```

```
  geom_density_2d() +
  labs(title = "Fig5: Scatter Plot when alpha = 0",
       x = "X",
       y = "Y",
       color = "cluster")
dalpha_0 = ggMarginal(alpha_0, type = "density")
dalpha_0
```

```
#alpha2 = 10
skewed_data_10 = skewdata(1000, 0, 1, 0, 1, 0.5, 10)


alpha_10 =
  ggplot(skewed_data_10, aes(x = X, y = Y, color = factor(true_class))) +
  geom_point(alpha = .5) +
  geom_density_2d() +
  labs(title = "Fig6: Scatter Plot when alpha = 10",
       x = "X",
       y = "Y",
       color = "cluster")
dalpha_10 = ggMarginal(alpha_10, type = "density")
dalpha_10
```

```
#alpha3 = -10
skewed_data_n10 = skewdata(1000, 0, 1, 0, 1, 0.5, -10)


alpha_n10 =
  ggplot(skewed_data_n10, aes(x = X, y = Y, color = factor(true_class))) +
  geom_point(alpha = .5) +
```

```
  geom_density_2d() +
  labs(title = "Fig7: Scatter Plot when alpha = -10",
       x = "X",
       y = "Y",
       color = "cluster")
dalpha_n10 = ggMarginal(alpha_n10, type = "density")
dalpha_n10
```

```
#Compare with Different Skewness
d = ggplot(skewed_data_0, aes(x = X, y = Y, color = factor(true_class))) +
  geom_point(alpha = .5) +
  geom_density_2d() + lims(x = c(10, 18), y = c(7,14 ))
e = ggplot(skewed_data_10, aes(x = X, y = Y, color = factor(true_class))) +
  geom_point(alpha = .5) +
  geom_density_2d() + lims(x = c(10, 18), y = c(7,14 ))
f = ggplot(skewed_data_n10, aes(x = X, y = Y, color = factor(true_class))) +
  geom_point(alpha = .5) +
  geom_density_2d() + lims(x = c(10, 18), y = c(7,14 ))
figure12 = ggarrange(d,e,f,
                     labels = c("a = 0","a = 10","a = -10"),font.label=list(color="black
                     = 2, nrow = 2)
annotate_figure(figure12,top = text_grob("Fig12: Comparison between Different Skewness",
```

Perform k-means and LCA

```
skew_list = c("skewed_data_n10", "skewed_data_0", "skewed_data_10")
skew_title_kmeans = c("K-means Plot\nalpha=-10", "\nalpha=0", "\nalpha=10")
skew_kmeans_plot = list()
```

```
for(i in seq_along(list)){
  skew_kmeans_plot[[i]] = kmeans_cluster_plot(get(skew_list[i]), skew_title_kmeans[i])
}

skew_title_lca = c("LCA Plot\nalpha=-10 ", "\nalpha=0","\nalpha=10")
skew_lca_plot = list()

for(i in seq_along(list)){
  skew_lca_plot[[i]] = lca_plot(get(skew_list[i]), skew_title_lca[i])
}

skew_plot.list = c(skew_kmeans_plot, skew_lca_plot)
grid.arrange(grobs = skew_plot.list, ncol = 3, top=textGrob("Fig8: Cluster Plots with Va
```

Heavy-tail/Outiers

```
contaminate_rate = seq(0,1,by = 0.1)
sampleN = c(300,900,1500)
simluation_results_1 = NULL
set.seed(2022)
for(i in 1:length(sampleN)) {
  for(j in  1:length(contaminate_rate)){
    for(k in 1:100) {
      sim_data = kurdata(sampleN[i], 0, 1, 0, 1, 0.3, contaminate_rate[j])
      simluation_results_1 = rbind(simluation_results_1, compare(sampleN[i], sim_data,co
    }
```

```
  }
}
```

```
simulation_df = simluation_results_1 %>% group_by(N,p,method) %>%
  summarise(
    mean_ARI = mean(ARI),
    mean_MR = mean(MR),
    sd_ARI = sd(ARI),
    sd_MR = sd(MR),
  ) %>%
  mutate(mse_MR = mean_MR^2+sd_MR^2,
         mse_ARI = (1 - mean_ARI)^2+sd_ARI^2)
```

```
result_df = simulation_df %>%
  pivot_longer(
    cols = c("sd_ARI", "sd_MR", "mse_MR", "mean_ARI", "mean_MR", "mse_ARI")
  )
```

```
result_df %>%
  ggplot(aes(x = p,y = value)) +
  geom_smooth(aes(color = method), se = FALSE) +
  geom_point(aes(color = method)) +
  facet_grid(N ~ name, margins = FALSE) +
  labs(
    title = "Fig9: Comparing the performance in different Sample Sizes",
    x = "Kurtosis Parameter",
```

```
    y = "Performance"
   ) +
  theme(axis.text.x = element_text(angle = 90))
```

Skewness

```
skewness_parameter = seq(-10,10,by = 2)
simluation_results_2 = NULL
set.seed(2022)
for(i in 1:length(sampleN)) {
  for(j in  1:length(skewness_parameter)){
    for(k in 1:100) {
      sim_data = skewdata(sampleN[i], 0, 1, 0, 1, 0.5, skewness_parameter[j])
      simluation_results_2 = rbind(simluation_results_2, compare(sampleN[i], sim_data,sk
    }

  }
}

simulation_df_2 = simluation_results_2 %>% rename(skew = p) %>%
  group_by(N,skew,method) %>%
  summarise(
    mean_ARI = mean(ARI),
    mean_MR = mean(MR),
    sd_ARI = sd(ARI),
    sd_MR = sd(MR),
  ) %>%
```

```
  mutate(mse_MR = mean_MR^2+sd_MR^2,
         mse_ARI = (1-mean_ARI)^2+sd_ARI^2)


result_df_2 = simulation_df_2 %>%
  pivot_longer(
    cols = c("sd_ARI", "sd_MR", "mse_MR", "mean_ARI", "mean_MR", "mse_ARI")
  )


result_df_2 %>%
  ggplot(aes(x = skew,y = value)) +
  geom_smooth(aes(color = method), se = FALSE) +
  geom_point(aes(color = method)) +
  facet_grid(N ~ name, margins = FALSE) +
  labs(
    title = "Fig10: Comparing the performance in different Sample Sizes",
    x = "Skewness Parameter",
    y = "Performance"
   ) +
  theme_bw()
```