Basketball Player Positions

Find natural groupings in basketball player data based on height, weight, and various statistics per game.

Import data

Read file of basketball player data containing per game statistics.

```
data = readtable("basketballDataProcessed.csv");
posnames = ["G","G-F","F-G","F","F-C","C-F","C"];
data.pos = categorical(data.pos,posnames);
```

Extract numeric data (and their names) and normalize data to mean 0 and standard deviation 1. Set random seed.

```
labels = data.Properties.VariableNames(4:end);
stats = data{:,4:end};
statsNorm = normalize(stats);
rng(0)
```

Dimensionality Reduction

Perform multidimensional scaling

```
d = pdist(statsNorm);
[X,e] = cmdscale(d);
```

Perform PCA

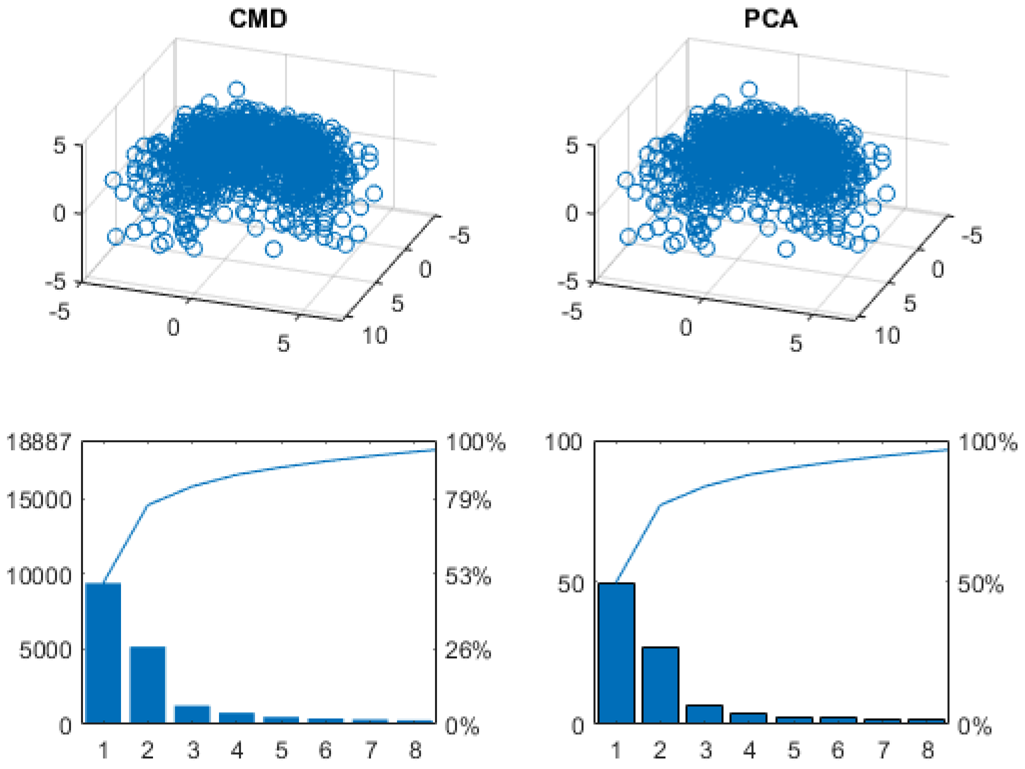
```
[pcs,scrs,~,~,pexp] = pca(statsNorm);
```

Compare PCA and CMD scaling

Note that CMD scaling is the same as PCA when using the 2-norm as the distance metric (within a potential minus sign). In this case, it turns out that the 3rd component is flipped:

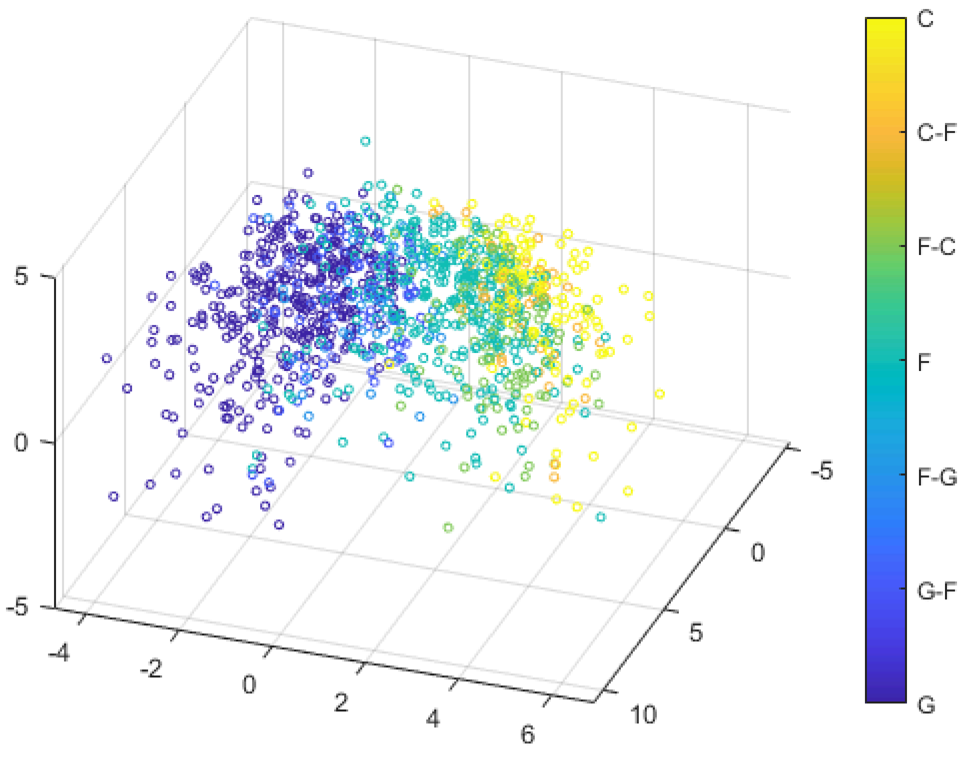
```
clf
tiledlayout(2,2);

% CMD scatter
nexttile
scatter3(X(:,1),X(:,2),-X(:,3))   % flip 3rd component
view(110,40)
title("CMD")

% PCA scatter
nexttile
scatter3(scrs(:,1),scrs(:,2),scrs(:,3))
view(110,40)
title("PCA")

% CMD pareto
```

```
nexttile
pareto(e)

% PCA pareto
nexttile
pareto(pexp)
```



Look for correlation with player position

```
clf
scatter3(scrs(:,1),scrs(:,2),scrs(:,3),10,data.pos)
view(110,40)
c = colorbar;
c.TickLabels = posnames;
```



Clustering Algorithms

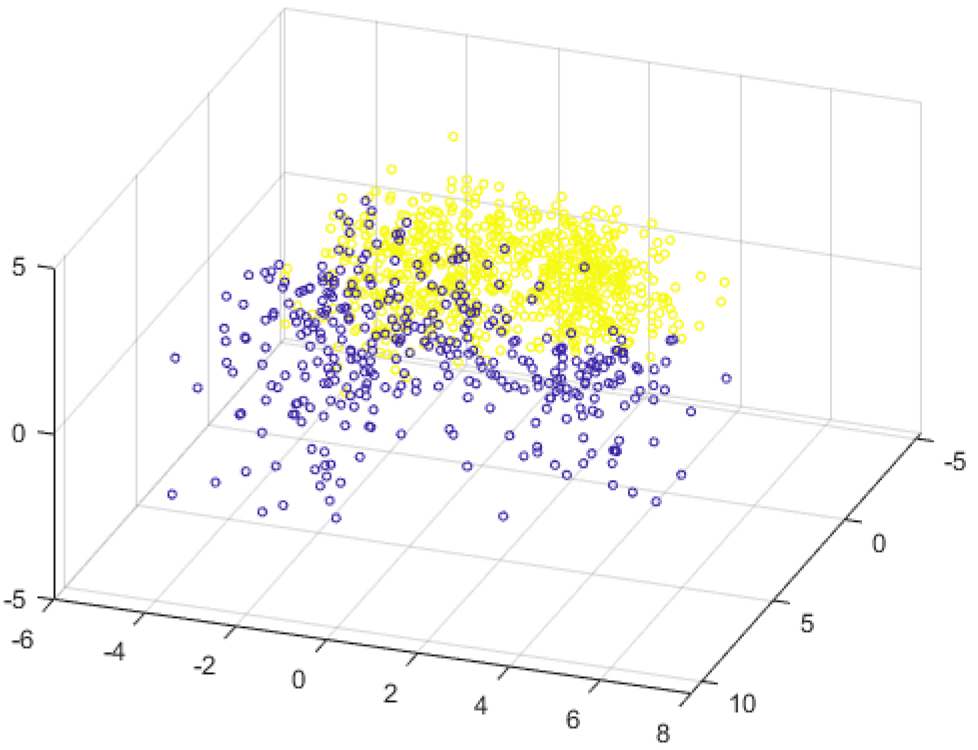
Cluster data into *k* groups using different methods and plot transformed (PCA) data by group for each method.

```
rng(0)
k = 2
```

```
k = 2
```

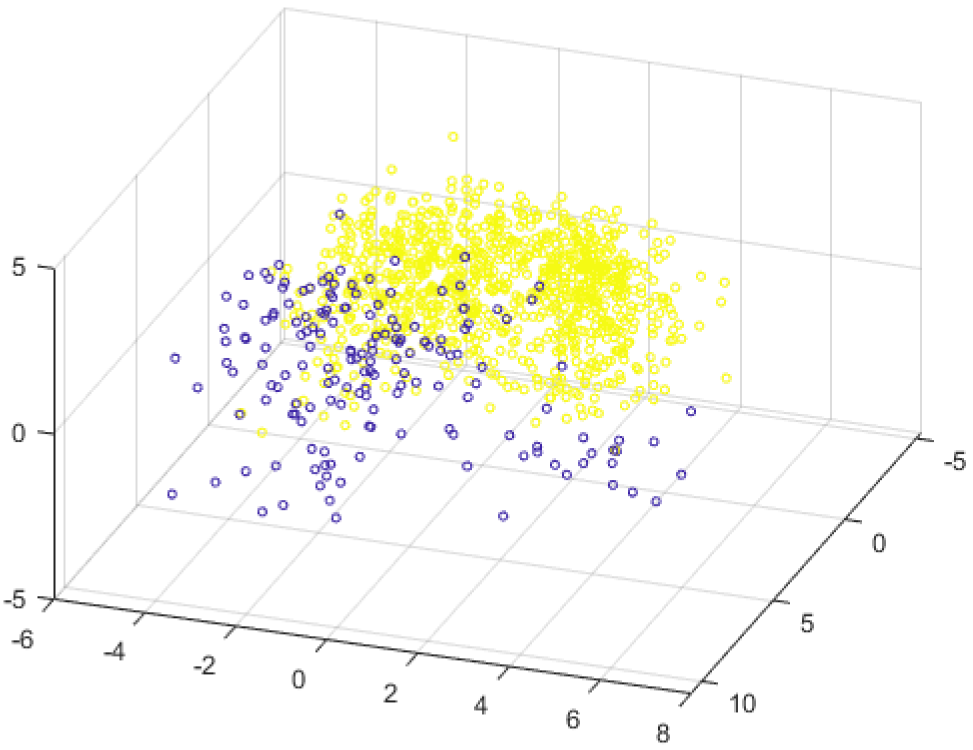
Perform k-means clustering

```
grpKM = kmeans(statsNorm,k,"Replicates",5);
scatter3(scrs(:,1),scrs(:,2),scrs(:,3),10,grpKM)
view(110,40)
```



Perform hierarchical clustering

```
Z = linkage(statsNorm,"ward");
grpHC = cluster(Z,"maxclust",k);
scatter3(scrs(:,1),scrs(:,2),scrs(:,3),10,grpHC)
view(110,40)
```

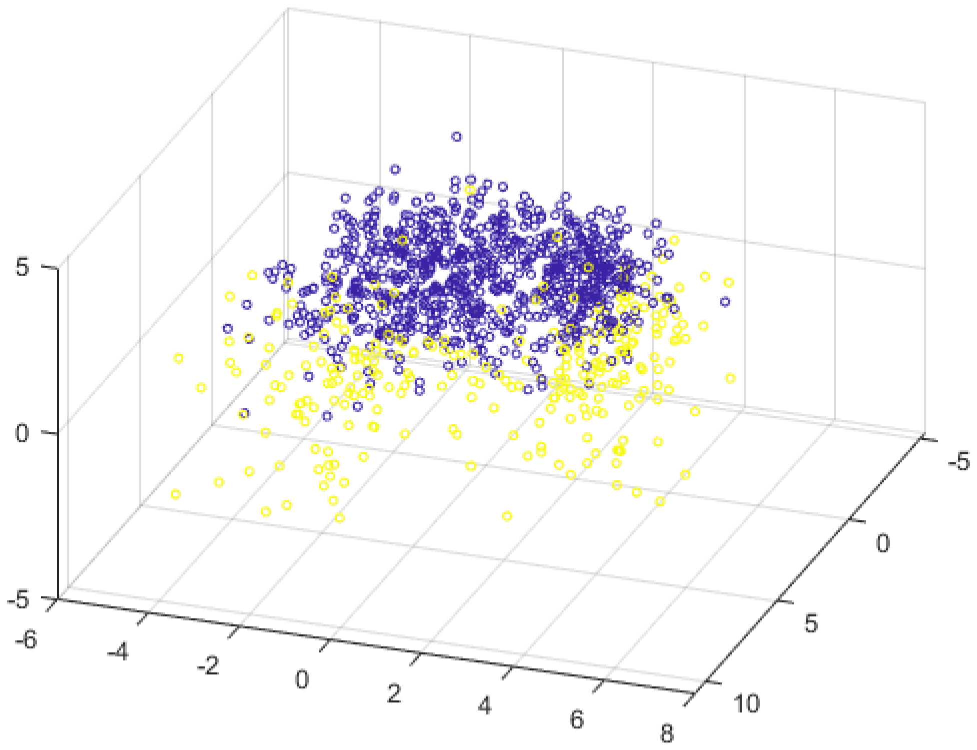


Fit a Gaussian mixture model

```
gmModel = fitgmdist(statsNorm,k,"Replicates",5,"RegularizationValue",0.02);
```

```
Warning: Failed to converge in 100 iterations during replicate 3 for gmdistribution with 2 components
```

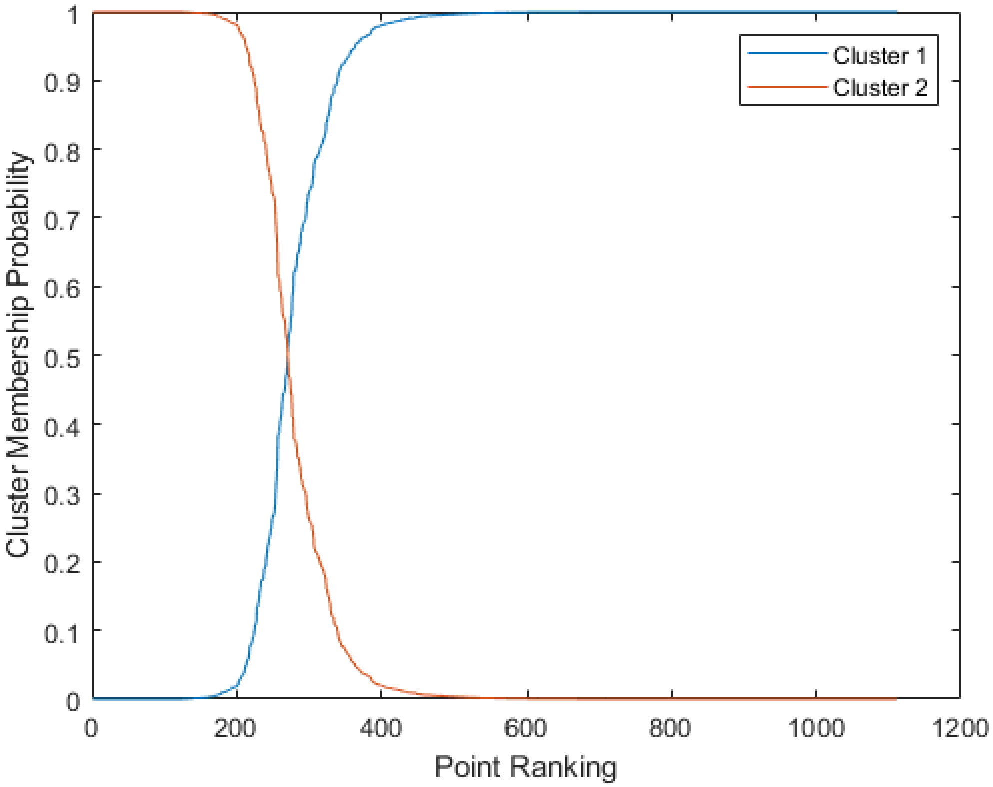
```
grpGM = cluster(gmModel,statsNorm);
scatter3(scrs(:,1),scrs(:,2),scrs(:,3),10,grpGM)
view(110,40)
```



Interpret Clusters

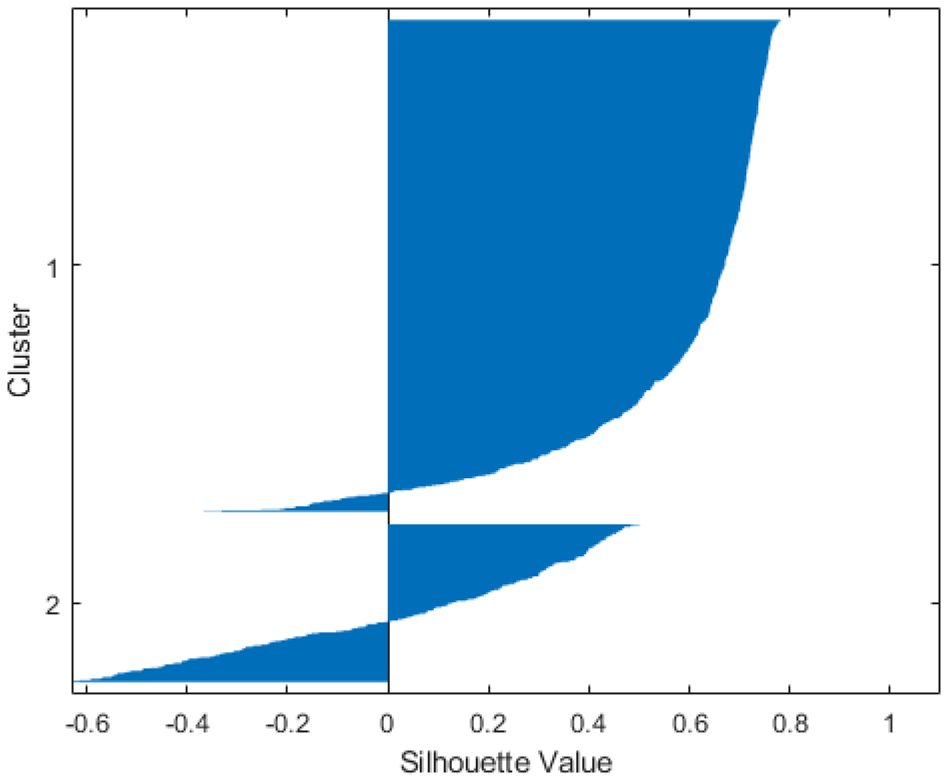
Visualize group separation for GMM.

```
[grpGM,~,gprob] = cluster(gmModel,statsNorm);
gpsort = sortrows(gprob,1:k-1);
plot(gpsort)
xlabel("Point Ranking")
ylabel("Cluster Membership Probability")
legend("Cluster "+ (1:k))
```



Create a silhouette plot

```
silhouette(statsNorm,grpGM)
```

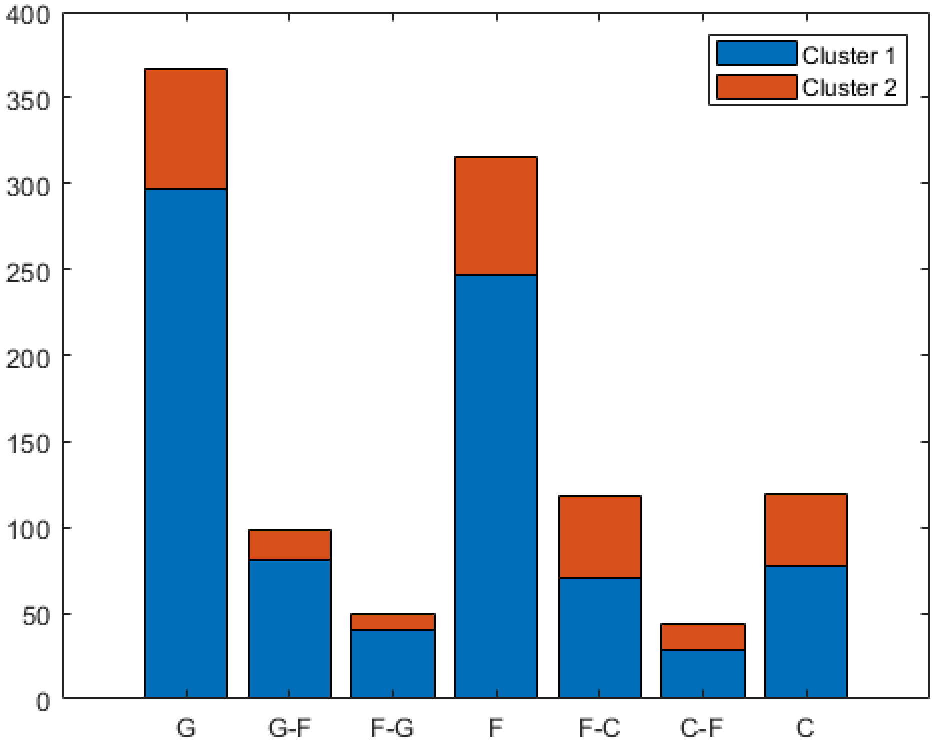


Visualize cluster membership by position.

```
ct = crosstab(data.pos,grpGM)
```

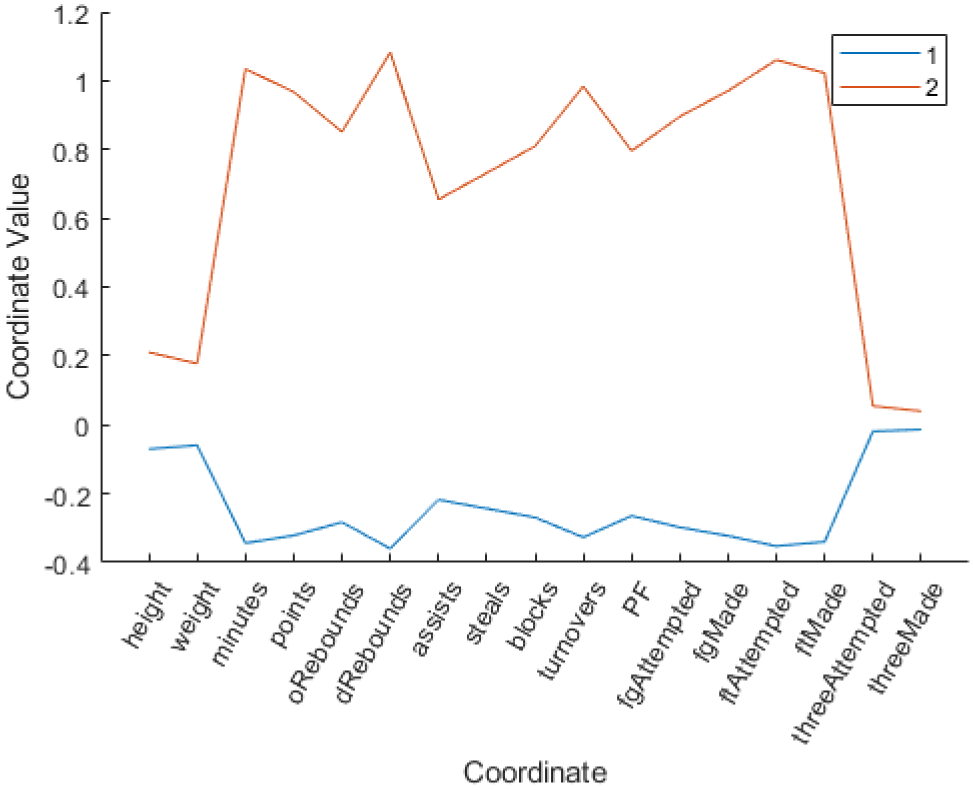
```
ct = 7×2
   297    70
    81    18
    40     9
   247    69
    70    48
    29    15
    78    41
```

```
bar(ct,"stacked")
legend("Cluster "+ (1:k))
xticklabels(categories(data.pos))
```



Create parallel coordinates plot of group mean.

```
parallelcoords(gmModel.mu,"Group",1:k)
xticklabels(labels)
xtickangle(60)
```



Evaluate optimal number of clusters

```
cev = evalclusters(statsNorm,"gmdistribution","DaviesBouldin","KList",2:6)
```

```
Warning: Failed to converge in 100 iterations during replicate 5 for gmdistribution with 2 components
Warning: Failed to converge in 100 iterations during replicate 2 for gmdistribution with 3 components
Warning: Failed to converge in 100 iterations during replicate 4 for gmdistribution with 3 components
Warning: Terminating replicate 3 for gmdistribution with 5 components.
Warning: Failed to converge in 100 iterations during replicate 2 for gmdistribution with 6 components
cev = 
  DaviesBouldinEvaluation with properties:

    NumObservations: 1112
         InspectedK: [2 3 4 5 6]
    CriterionValues: [1.6949 1.4852 1.6345 1.8583 1.5947]
           OptimalK: 3
```

```
optK = cev.OptimalK
```

```
optK = 3
```

Clusters within a Player Position

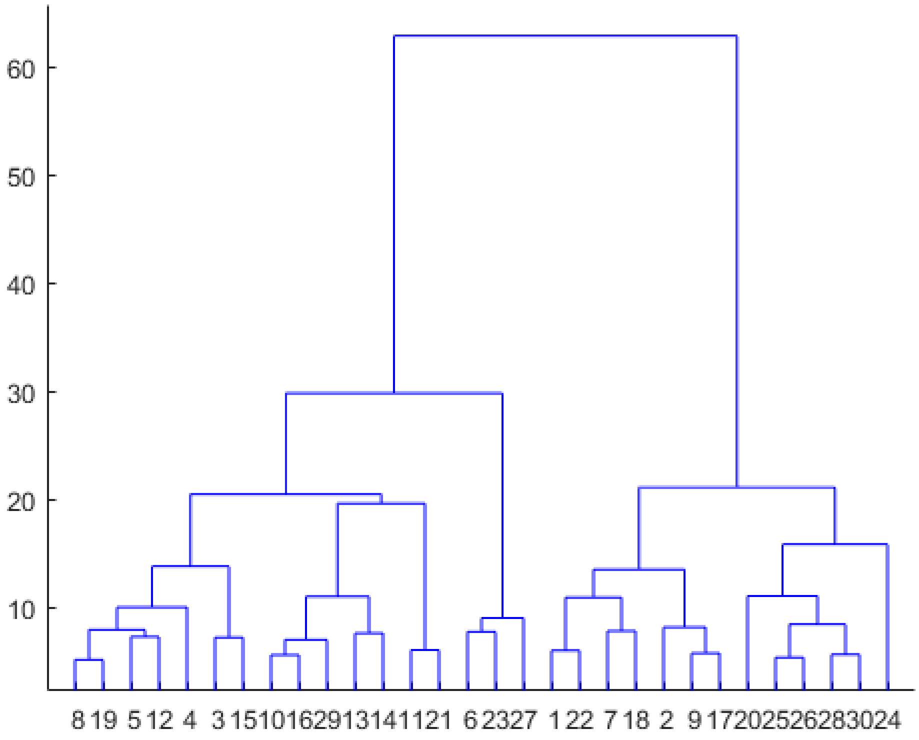
Extracts the data for the guard position (`G`). Can change to other positions.

```
posStats = statsNorm(data.pos == "G",:);
```

Create and visualize hierarchical tree.

```
Z = linkage(posStats,"ward");
```

```
dendrogram(Z)
```

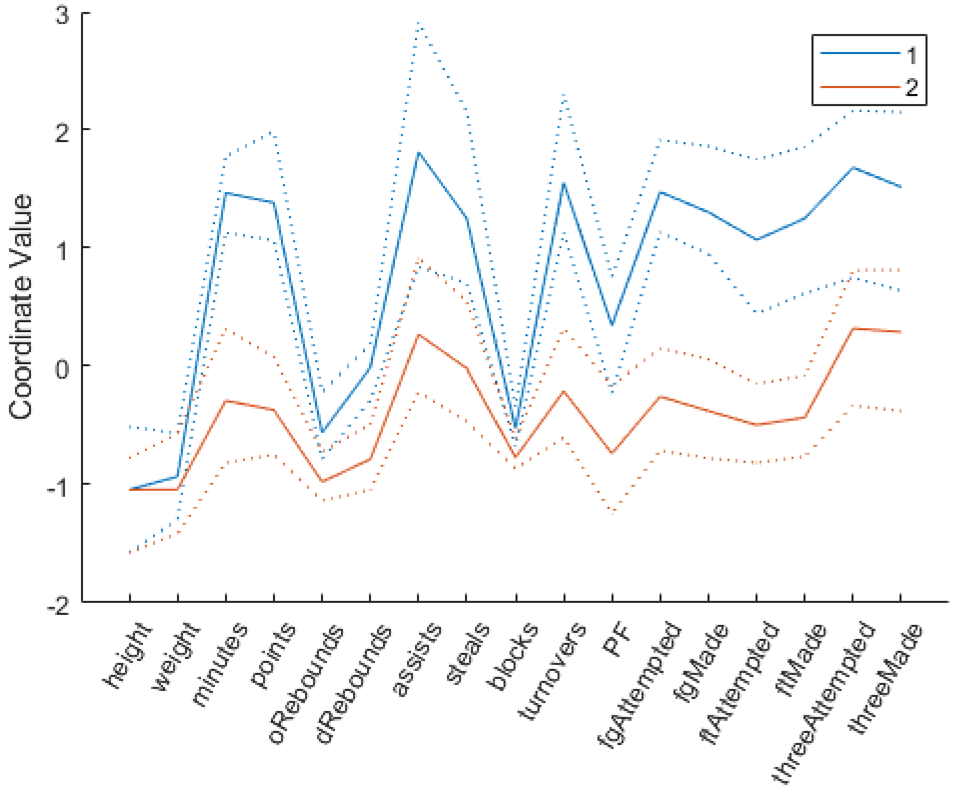


Cluster into 2 and 3 clusters.

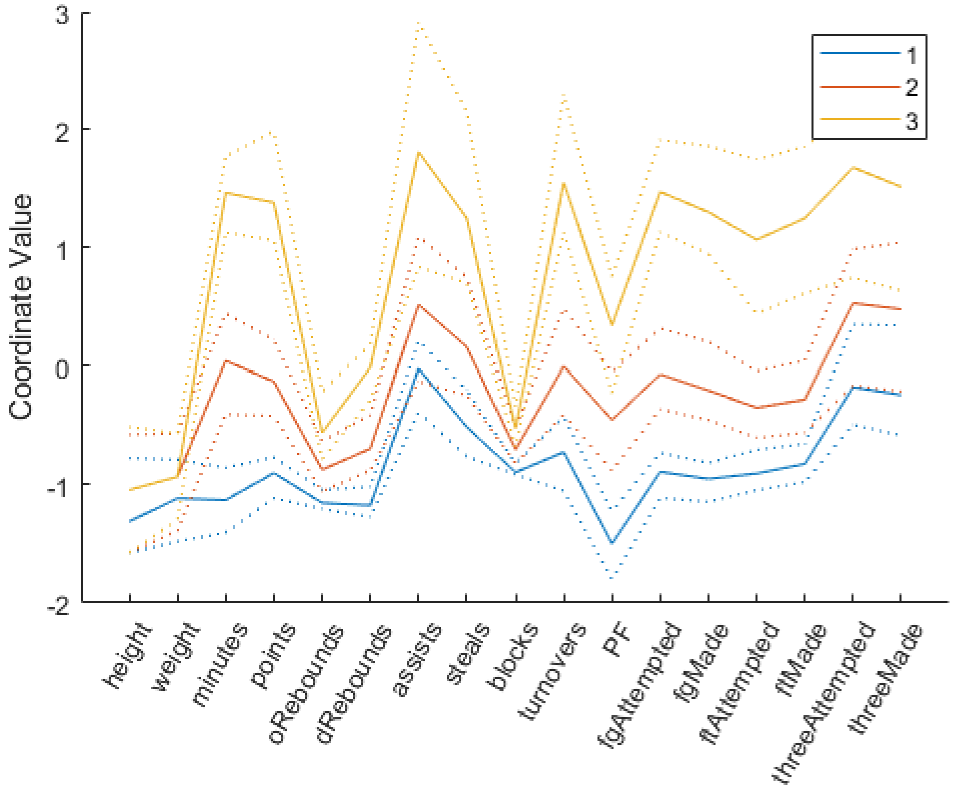
```
gc2 = cluster(Z,"maxclust",2);
gc3 = cluster(Z,"maxclust",3);
```

Visualize clusters (middle 50% of each cluster)

```
parallelcoords(posStats,"Group",gc2,"Quantile",0.25,"Labels",labels)
xtickangle(60)
```



```
parallelcoords(posStats,"Group",gc3,"Quantile",0.25,"Labels",labels)
xtickangle(60)
```



Evaluate optimal number of clusters.

```
ec = evalclusters(posStats,"linkage","silhouette","KList",2:8)
```

```
ec = 
  SilhouetteEvaluation with properties:

    NumObservations: 367
         InspectedK: [2 3 4 5 6 7 8]
    CriterionValues: [0.6281 0.2870 0.2611 0.2034 0.2294 0.2390 0.2299]
           OptimalK: 2
```