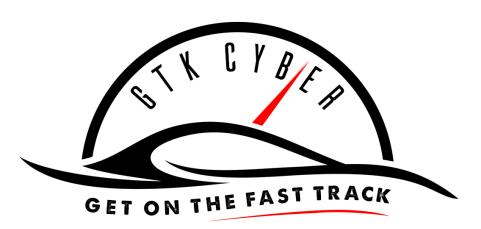


### Machine Learning for Security Professionals - Day 3

Unsupervised Learning: Clustering

Clustering

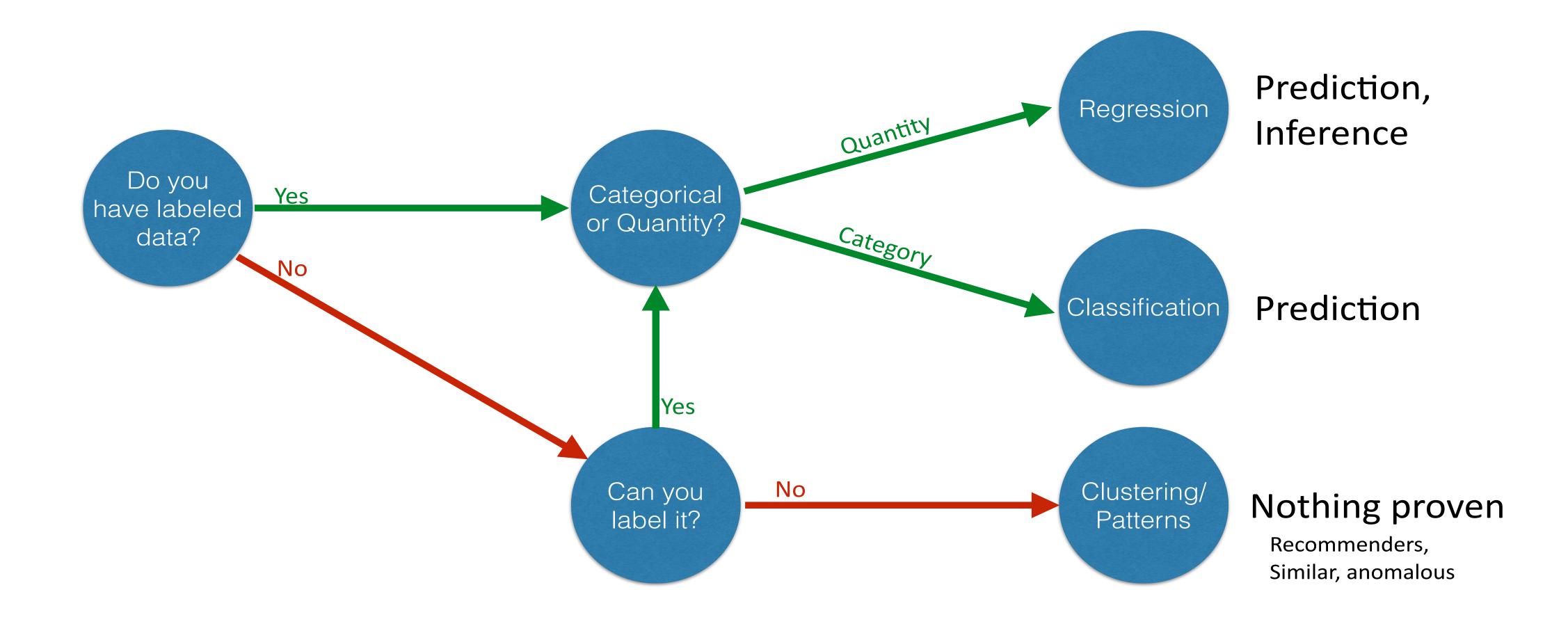
Clustering



### Agenda for Today

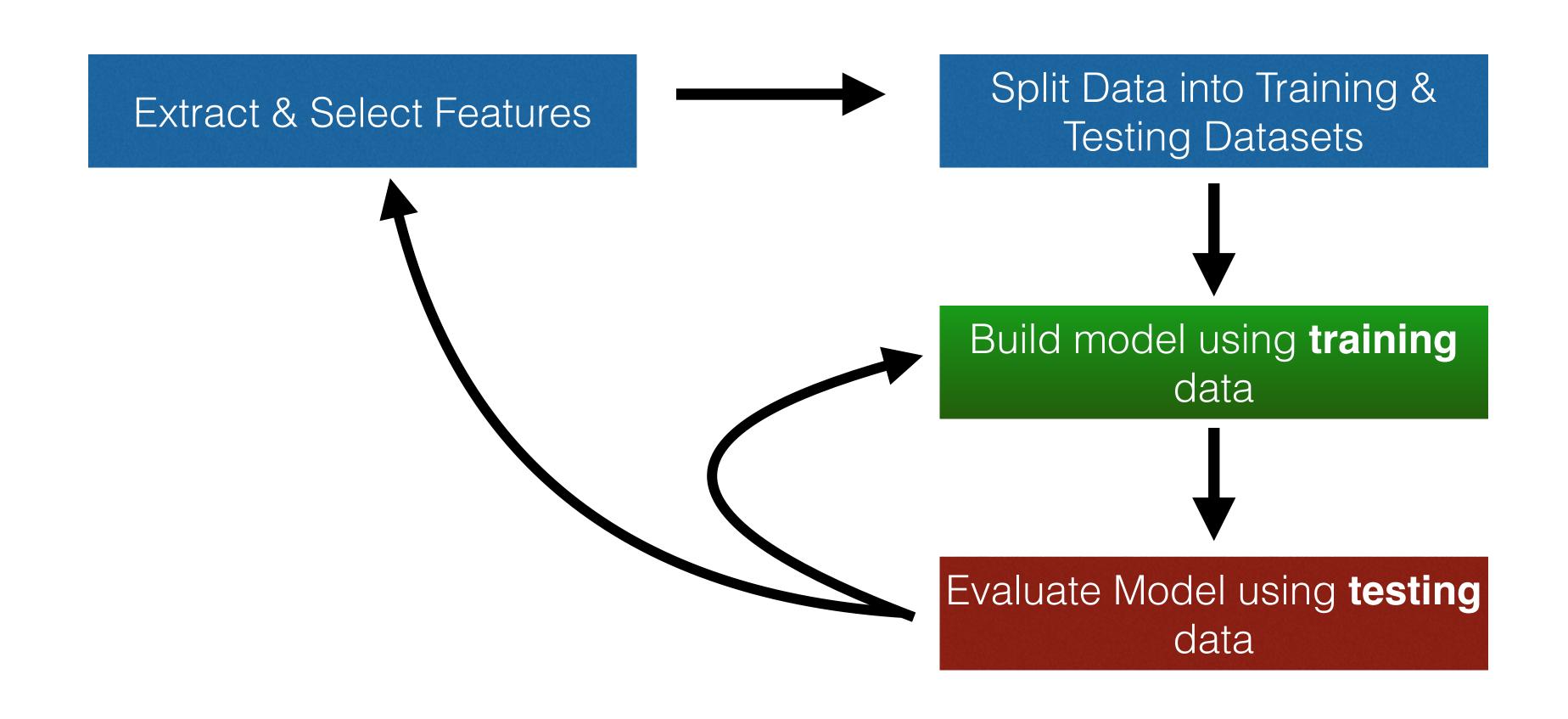
- Measuring Distances
- Math free overview of clustering techniques
- Pipelines and pickles





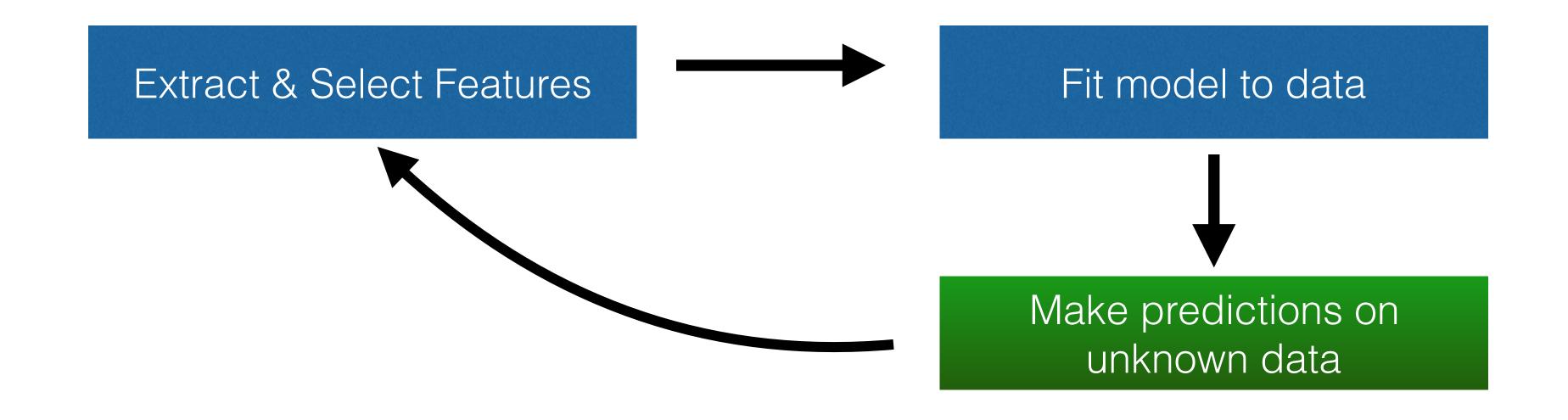


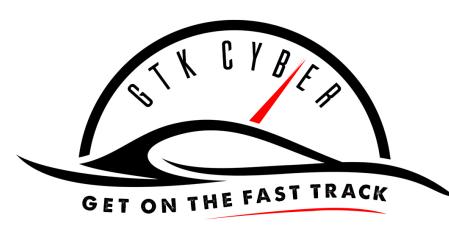
#### Supervised ML Process





### Unsupervised ML Process





#### Unsupervised Clustering Algorithm

- 1. Select Features
- 2. Calculate a distance measure
- 3. Apply a clustering algorithm
- 4. Validate?



	Malware events	
Dept1	6	
Dept2	1	
Dept3	8	



	Malware events	Phishing
Dept1	6	6
Dept2	1	2
Dept3	8	1



	Malware events	Phishing	Open Tickets
Dept1	6	6	3
Dept2	1	2	1
Dept3	8	1	9



### Computing Distance

	Malware events	
Dept1	6	
Dept2	1	
Dept3	8	

Compare:

Dept1 to Dept2: | 6 - 8 | = 5

Dept2 to Dept3: | 1 - 8 | = 7

Dept1 to Dept3: | 6 - 8 | = 2

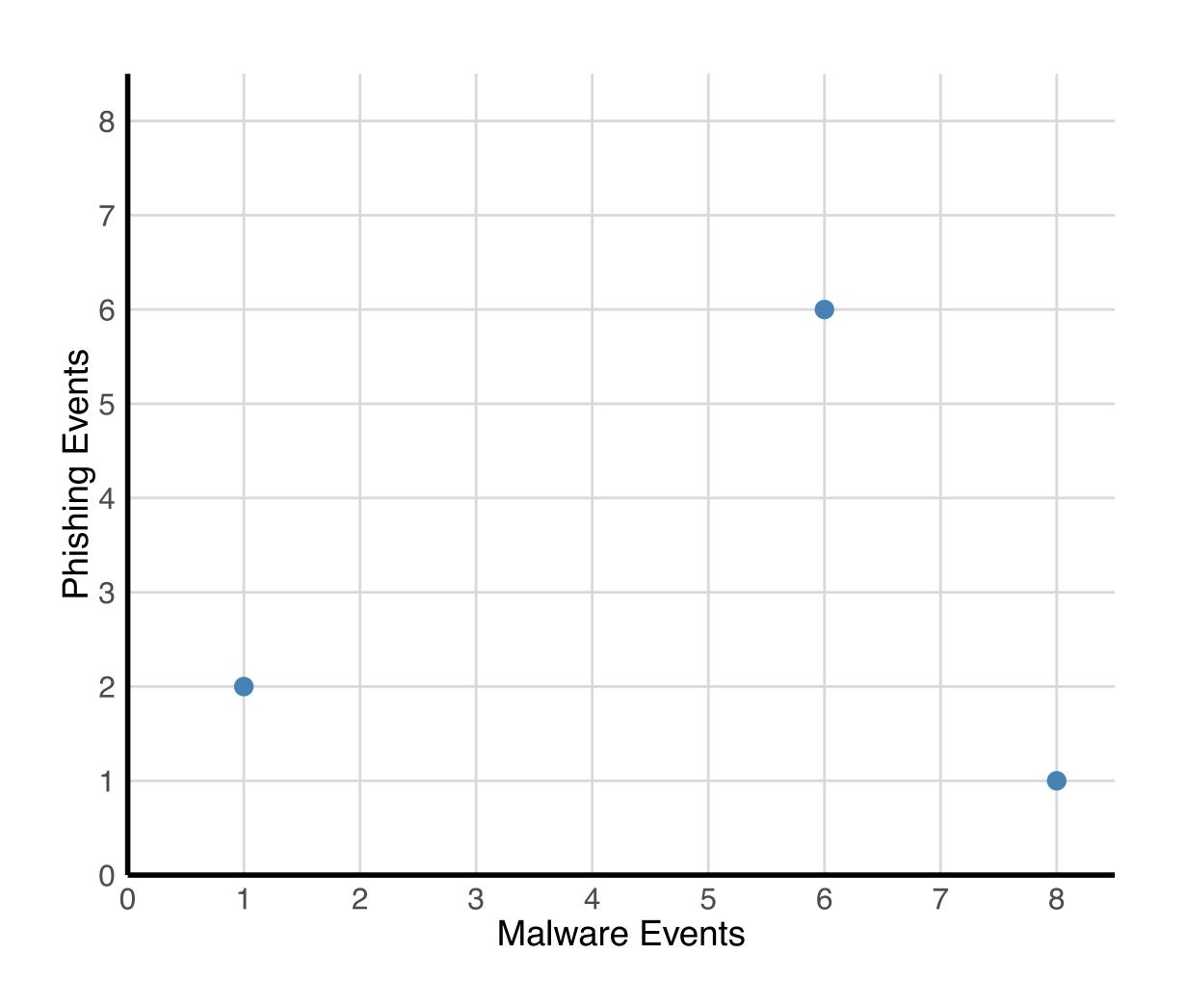


	Malware events	Phishing
Dept1	6	6
Dept2	1	2
Dept3	8	1

#### Multiple Distance methods

- Euclidean
- Manhattan
- Maximum
- Canberra
- Binary
- Minkowski
- ... (to name a few)

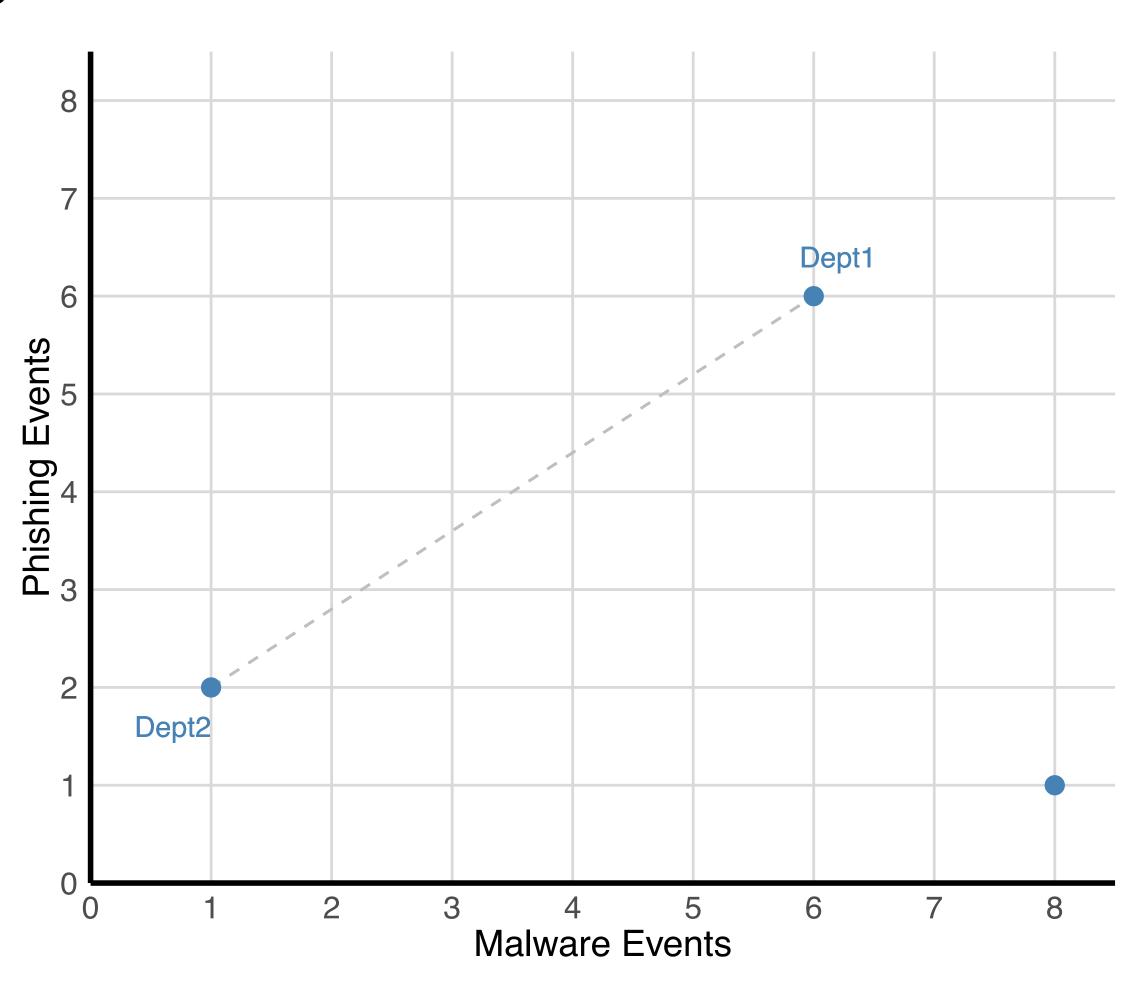
	Malware events	Phishing
Dept1	6	6
Dept2	1	2
Dept3	8	1





Euclidean very common and easy to understand

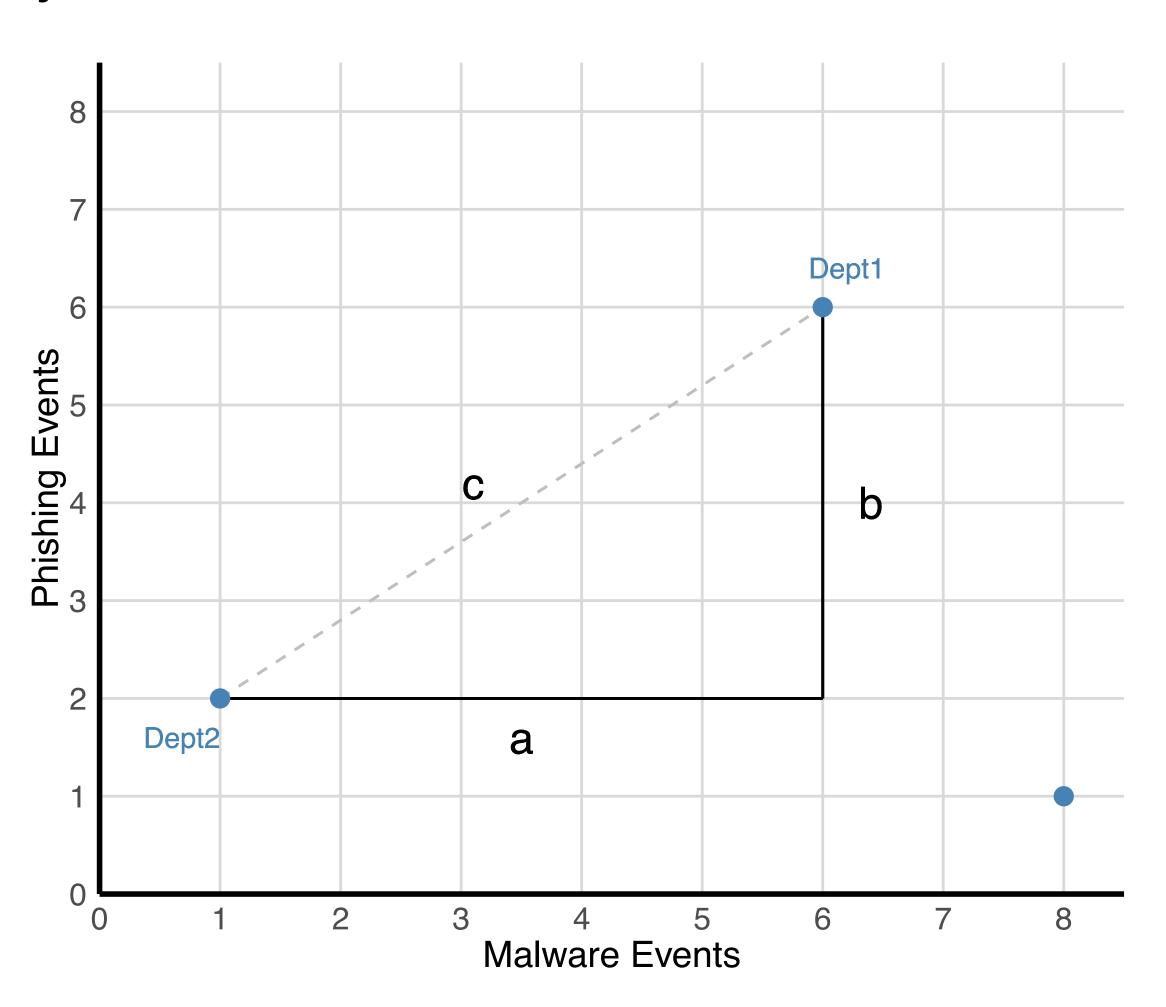
	Malware events	Phishing
Dept1	6	6
Dept2	1	2
Dept3	8	1





Euclidean very common and easy to understand:  $a^2 + b^2 = c^2$ 

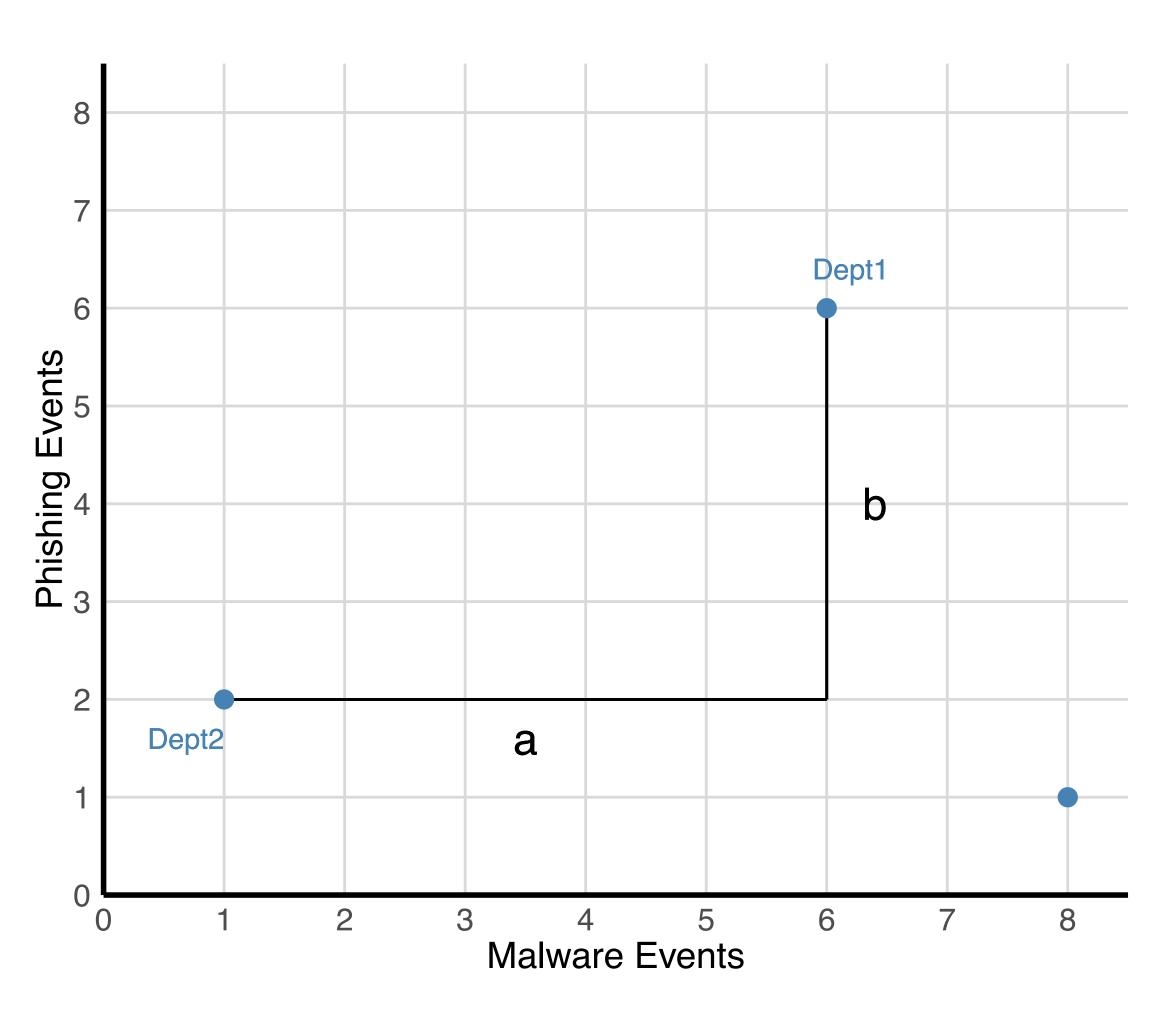
	Malware events	Phishing
Dept1	6	6
Dept2	1	2
Dept3	8	1





Manhattan also easy to comprehend: a + b

	Malware events	Phishing
Dept1	6	6
Dept2	1	2
Dept3	8	1





### Computing Distance

	Malware events	Phishing
Dept1	6	6
Dept2	1	2
Dept3	8	1

Compare:

Dept1 to Dept2:  $sqrt((6-1)^2 + (6-2)^2) = 6.4$ 

Dept2 to Dept3: ... = **7.1** 

Dept1 to Dept3: ... = **5.4** 



#### Euclidean Distance calculations

```
def dist(x,y):
    return np.sqrt(np.sum((x-y)**2))

> mat = np.array([[ 6,6,3 ], [1,2,1], [8,1,9]])
> dist(mat[0], mat[1])
6.7082039324993694

> dist(mat[1], mat[2])
10.677078252031311

> dist(mat[0], mat[2])
8.0622577482985491
```



	Malware events	Phishing	Open Tickets	
Dept1	6	6	3	67
Dept2	1	2	1	8.1
Dept3	8	1	9	)10.7

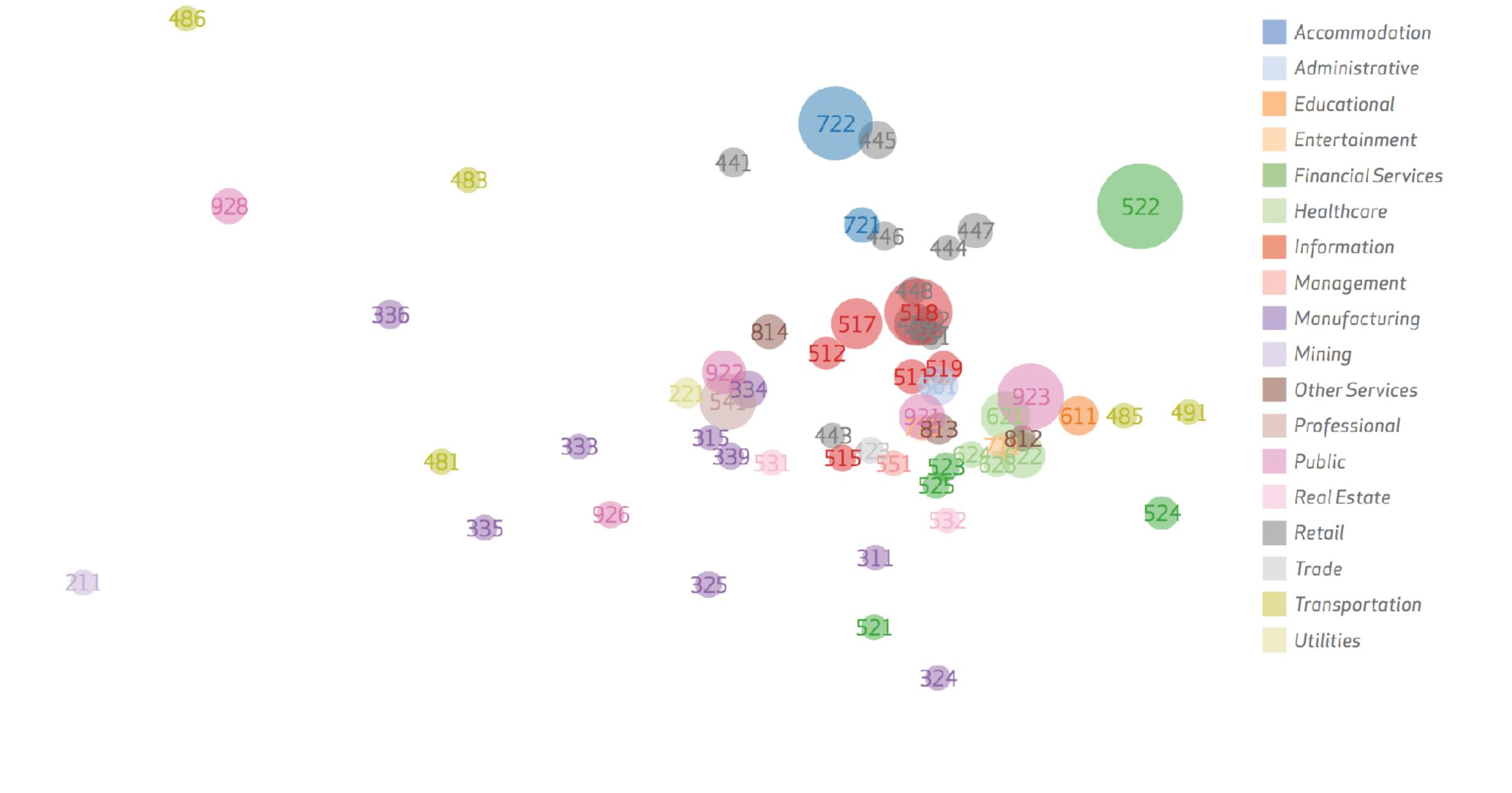


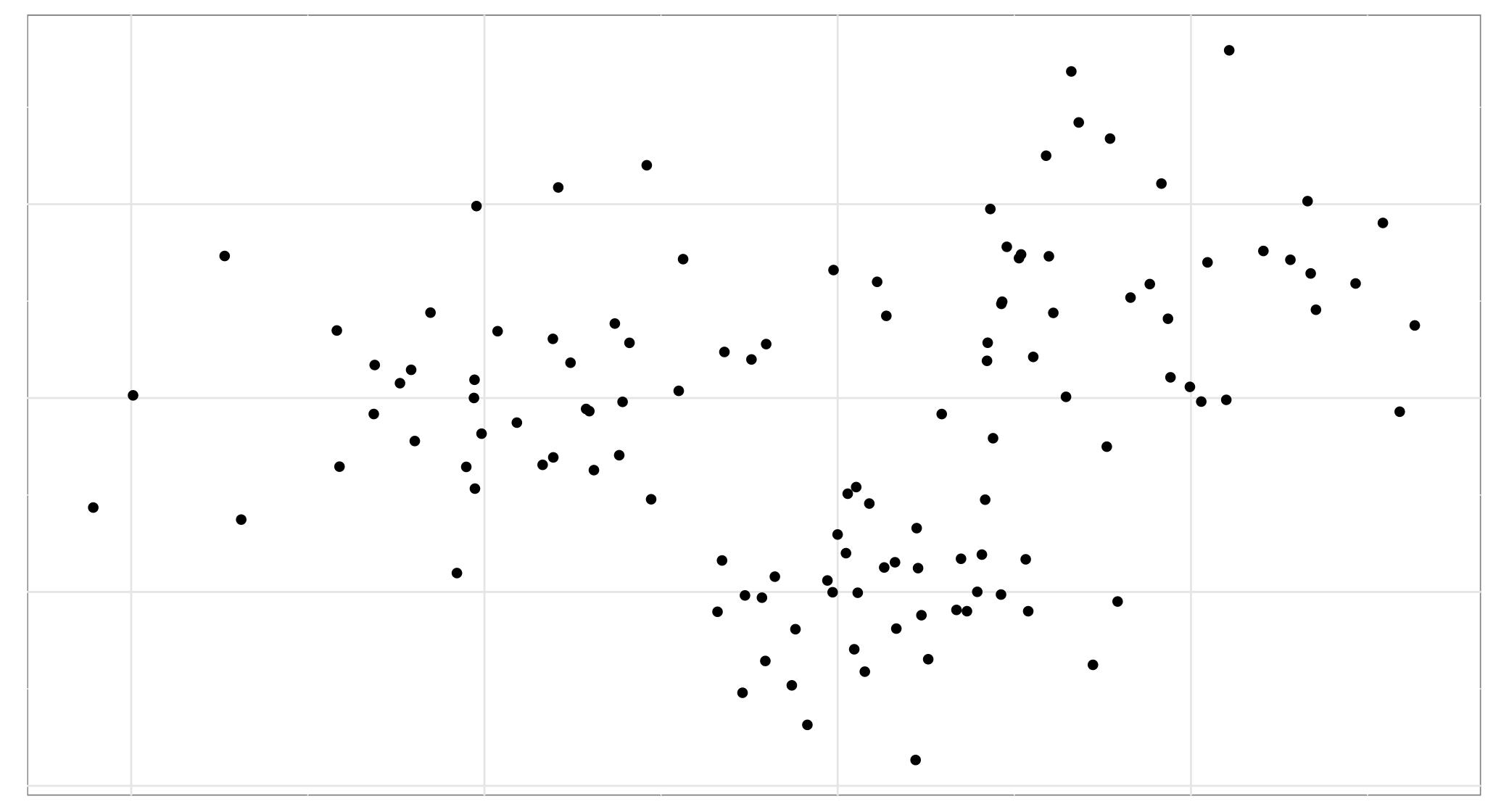
Figure 19.

Clustering on breach data across industries

213

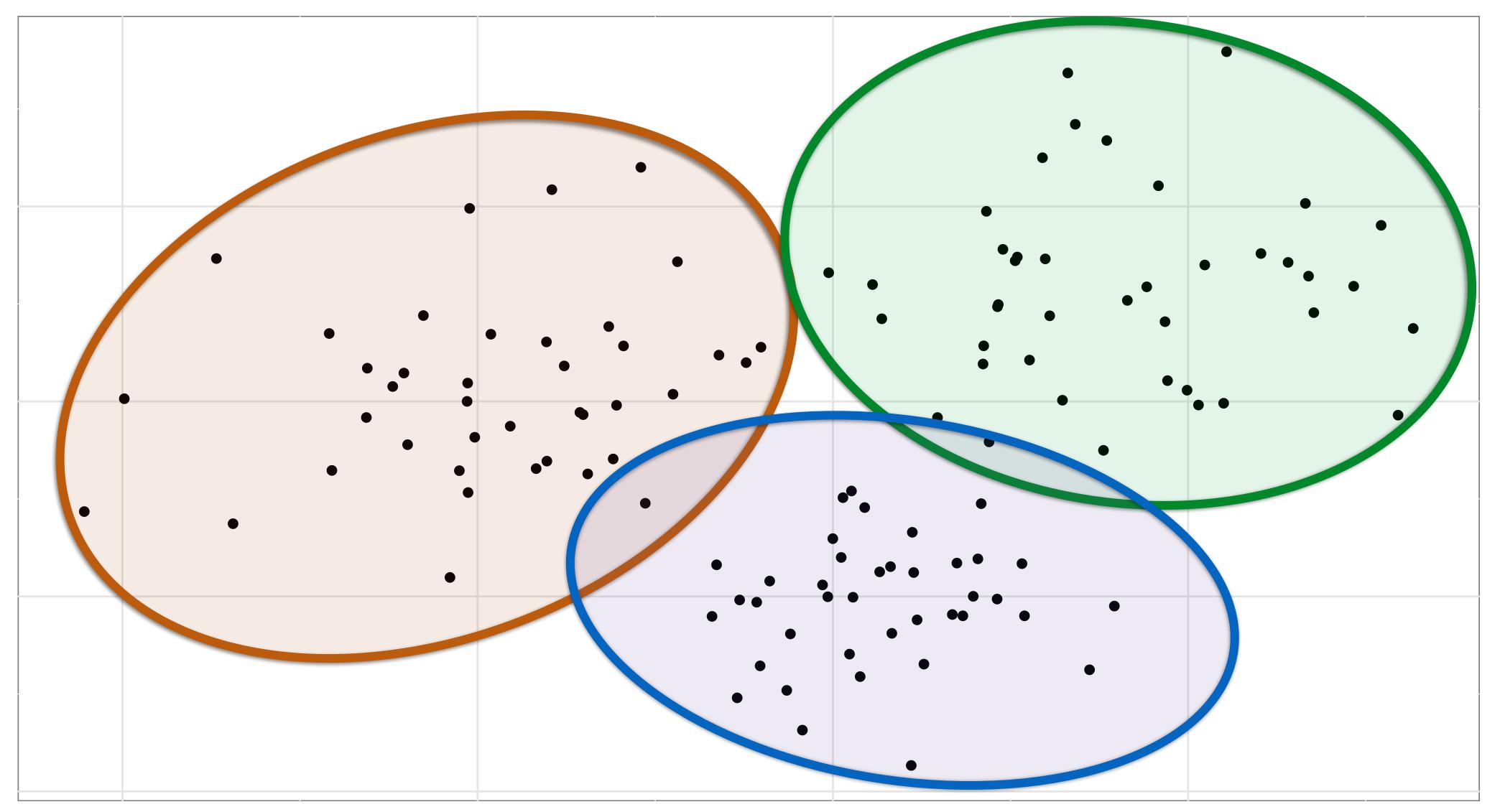


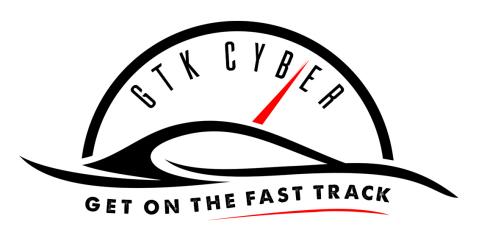
### Clustering...



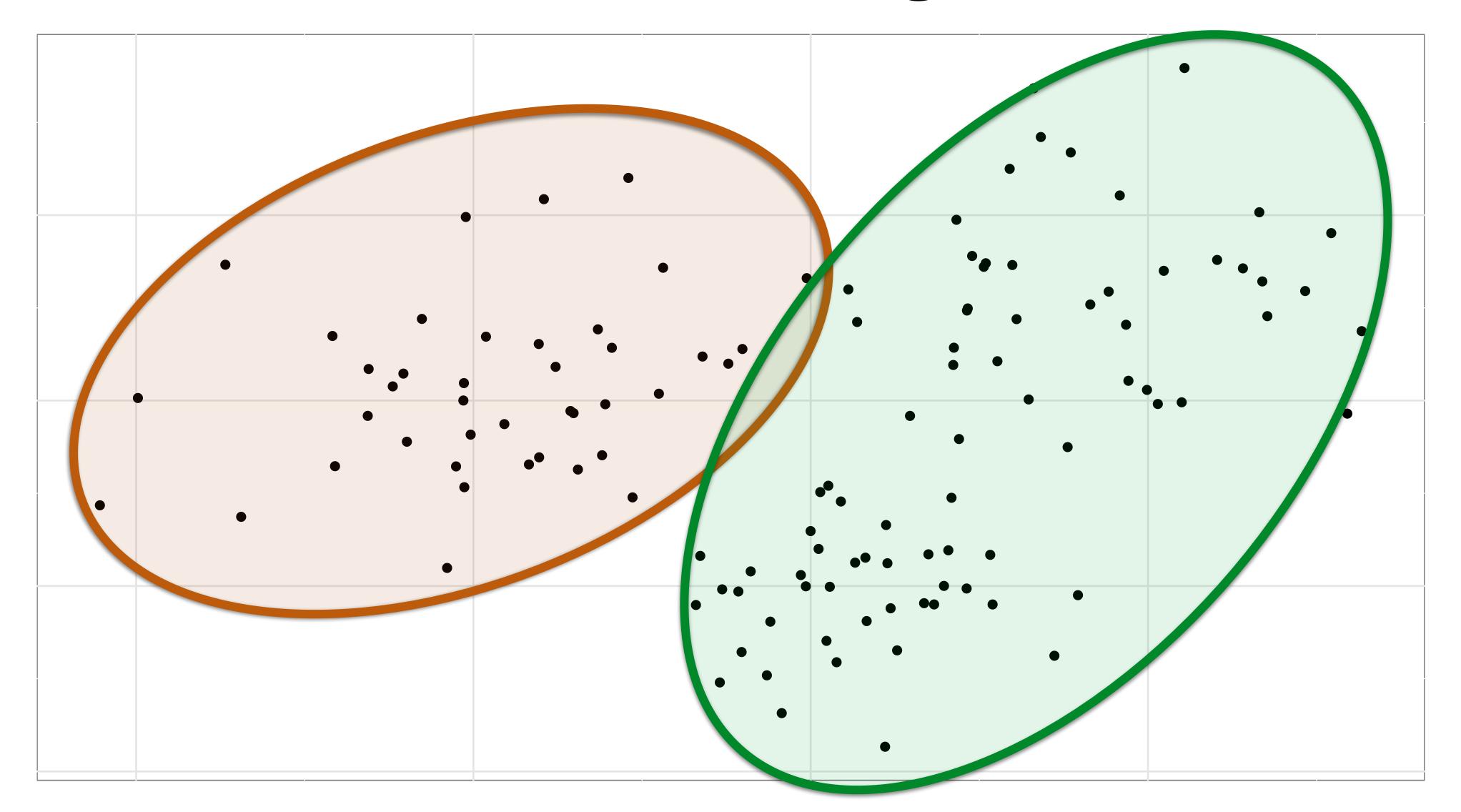


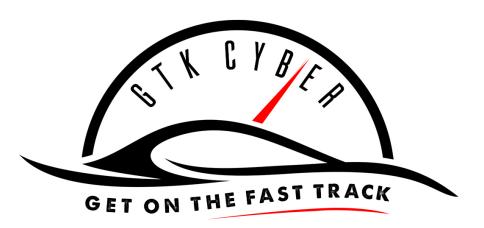
### Clustering...





### Clustering...





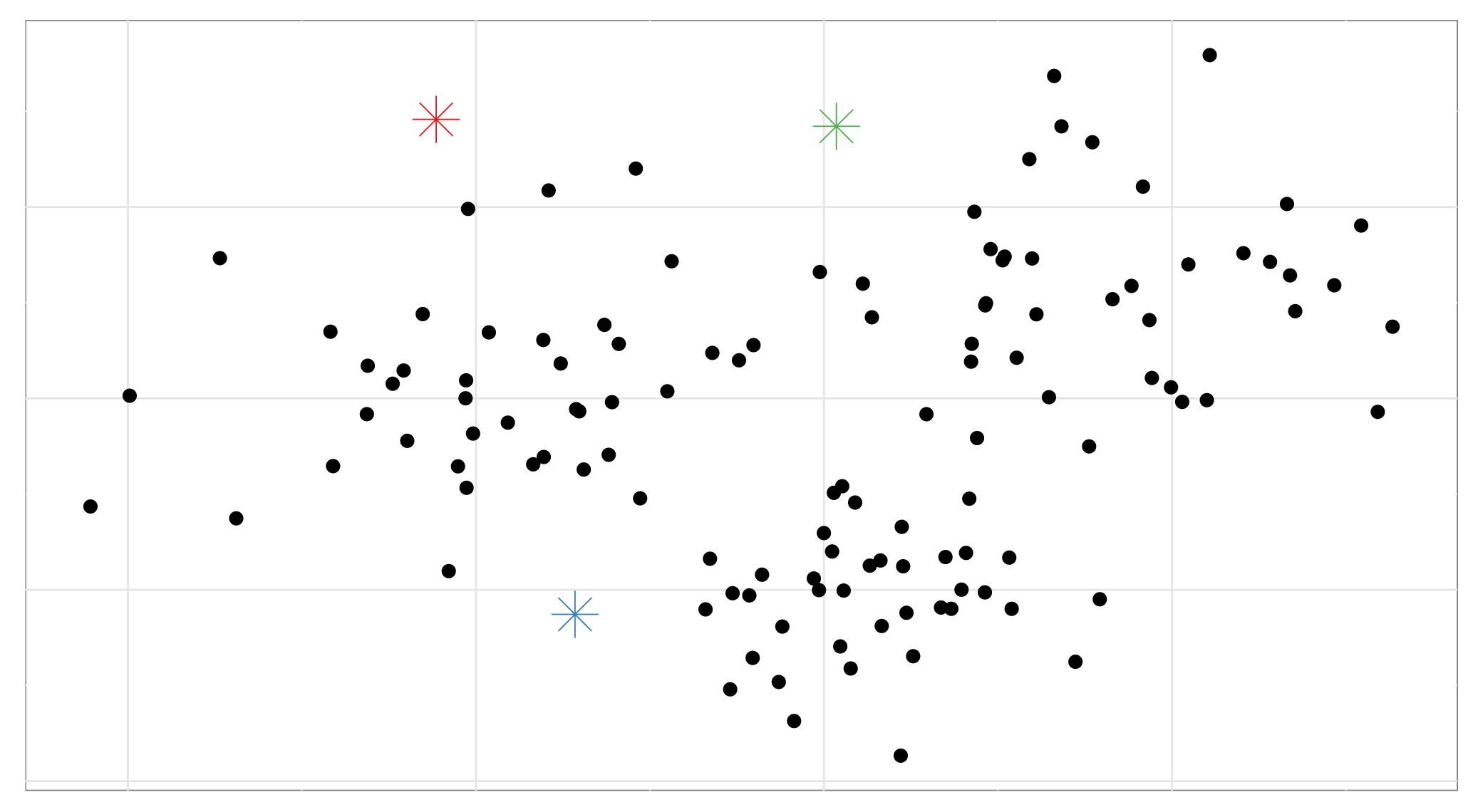
#### K-Means

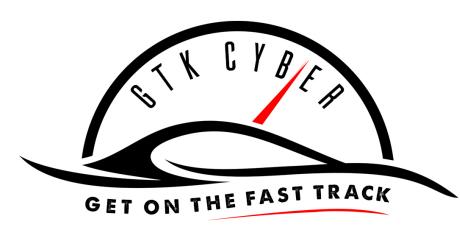
Before starting, pick the number of clusters, K

- 1. Pick K random centroids within data range
- 2. Assign each data point to the nearest centroid
- 3. Move centroid to center of assigned points
- 4. Repeat steps 2 and 3 until centroid stops shifting

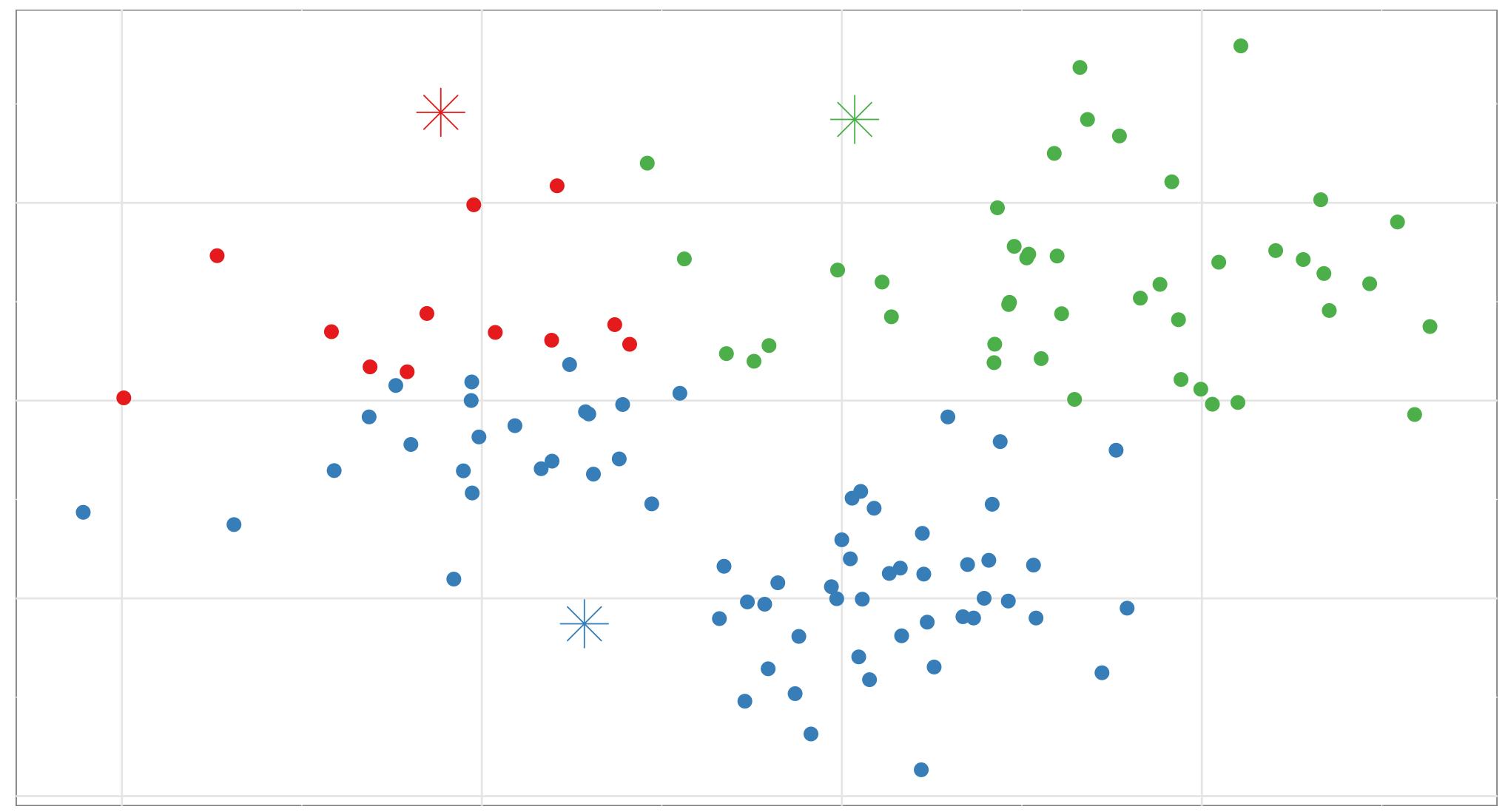


Step 1: Pick 3 random centroids within data range



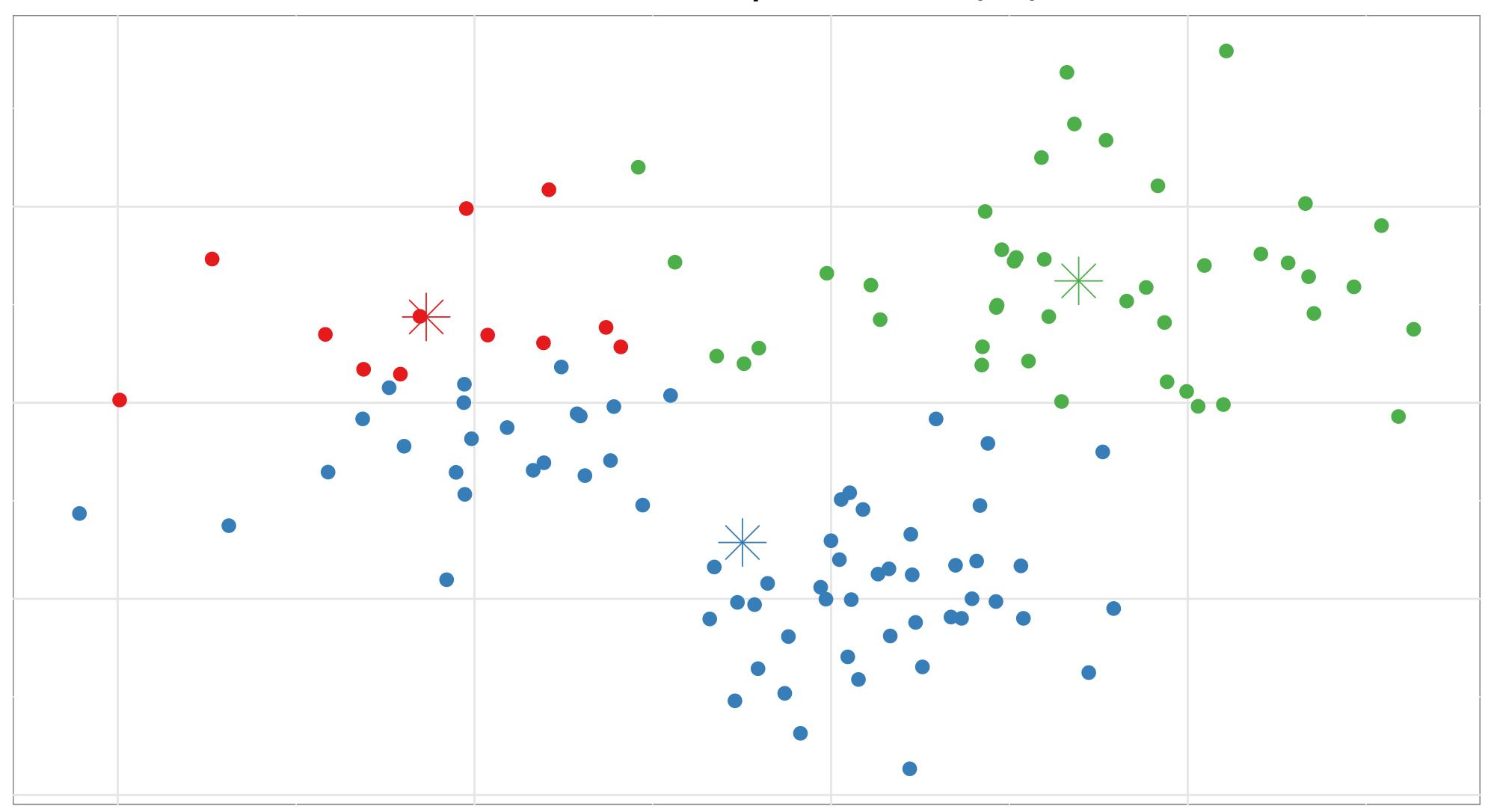


### Step 2: Assign each data point to the nearest centroid (1)



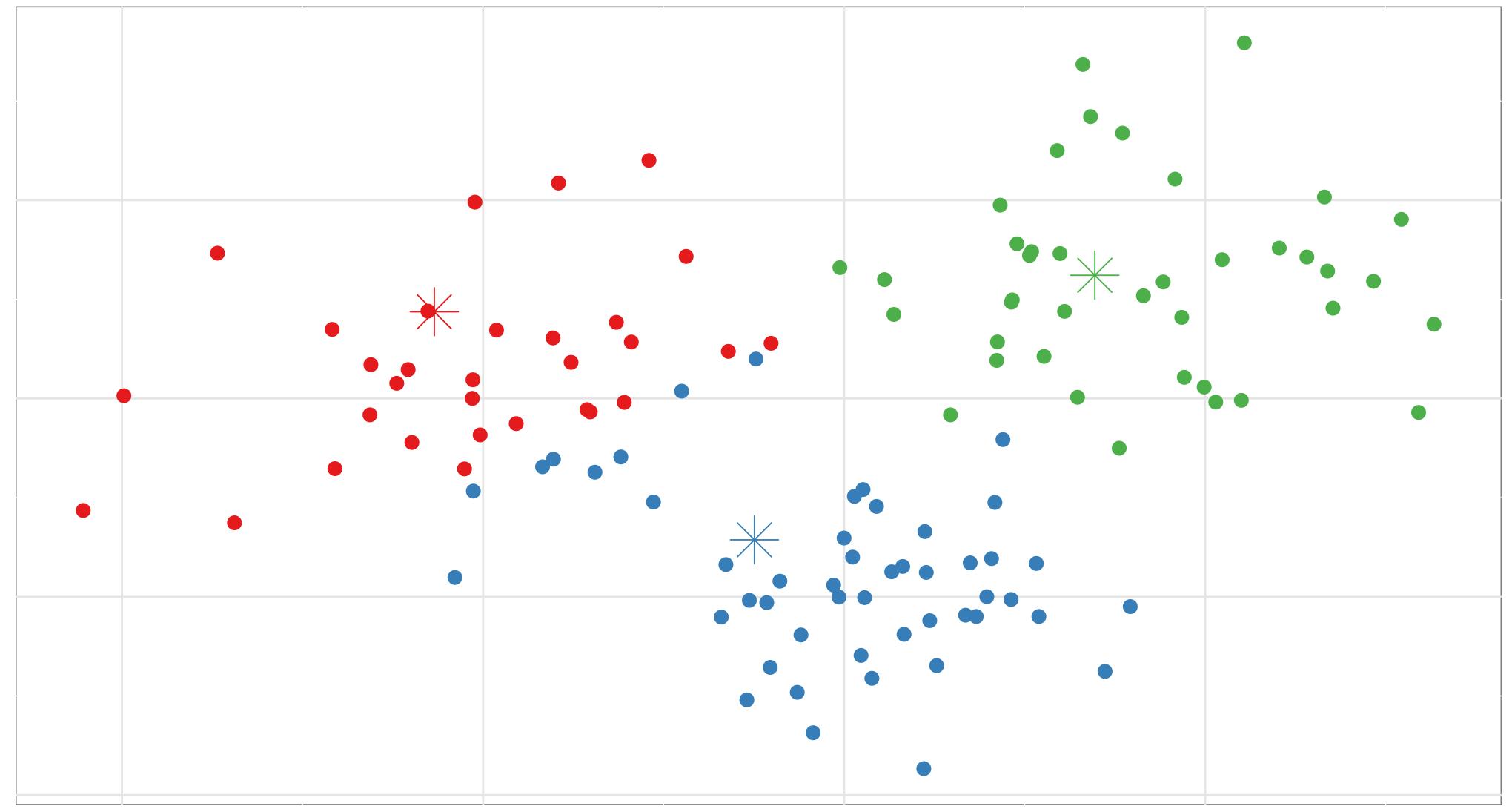


## Step 3: Move centroid to center of assigned points (1)



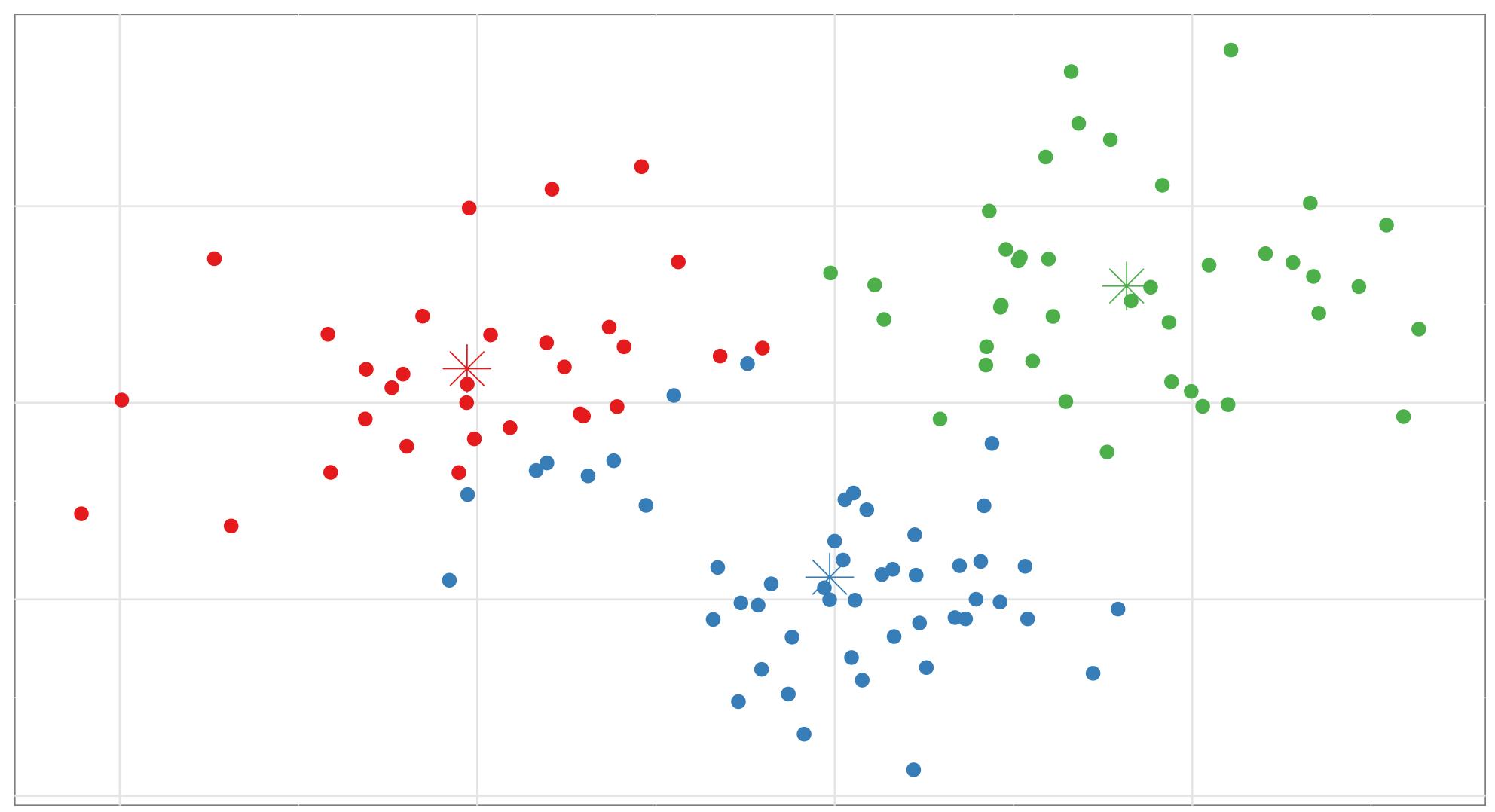


## Step 2: Assign each data point to the nearest centroid (2)



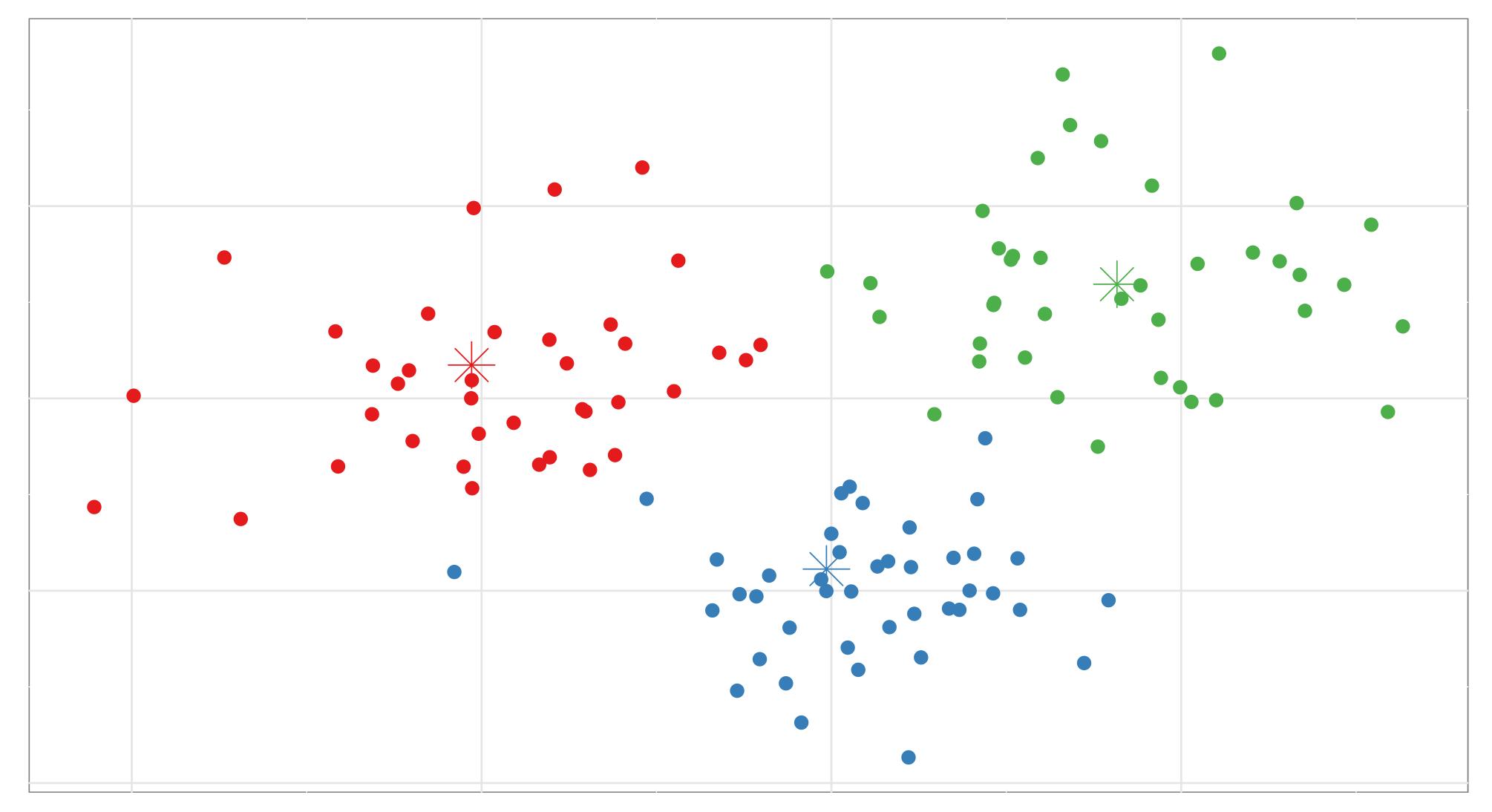


## Step 3: Move centroid to center of assigned points (2)



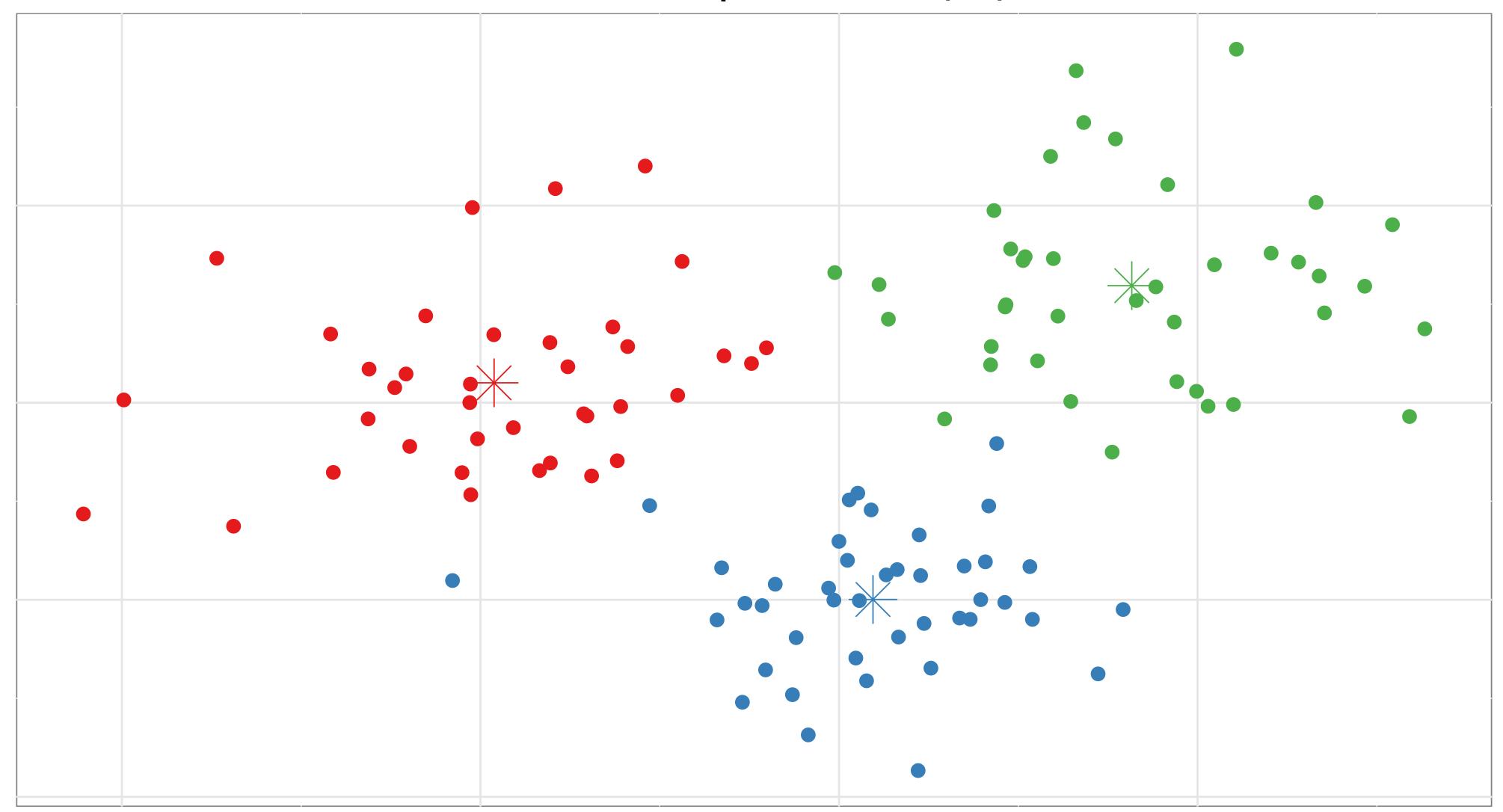


## Step 2: Assign each data point to the nearest centroid (3)



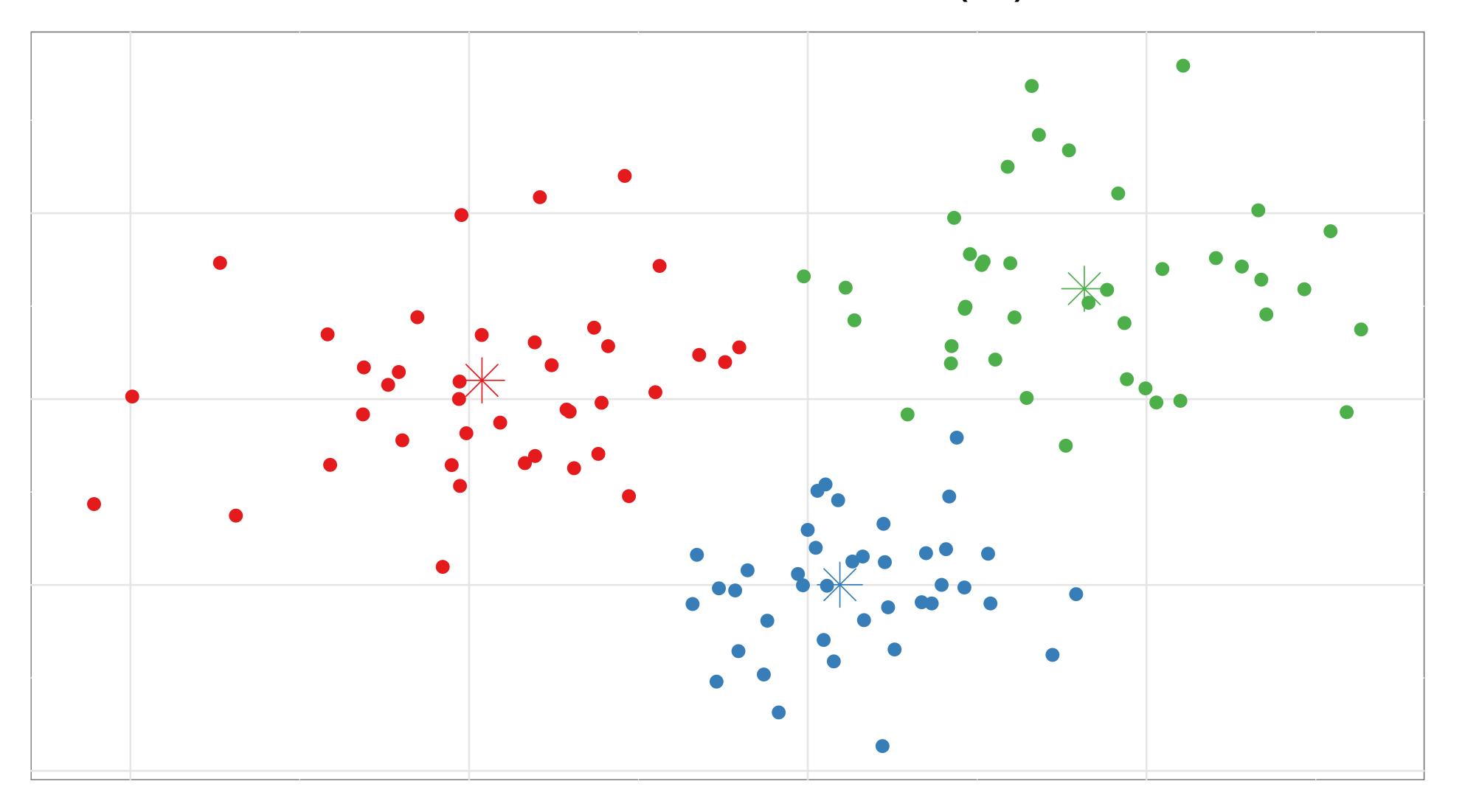


## Step 3: Move centroid to center of assigned points (3)



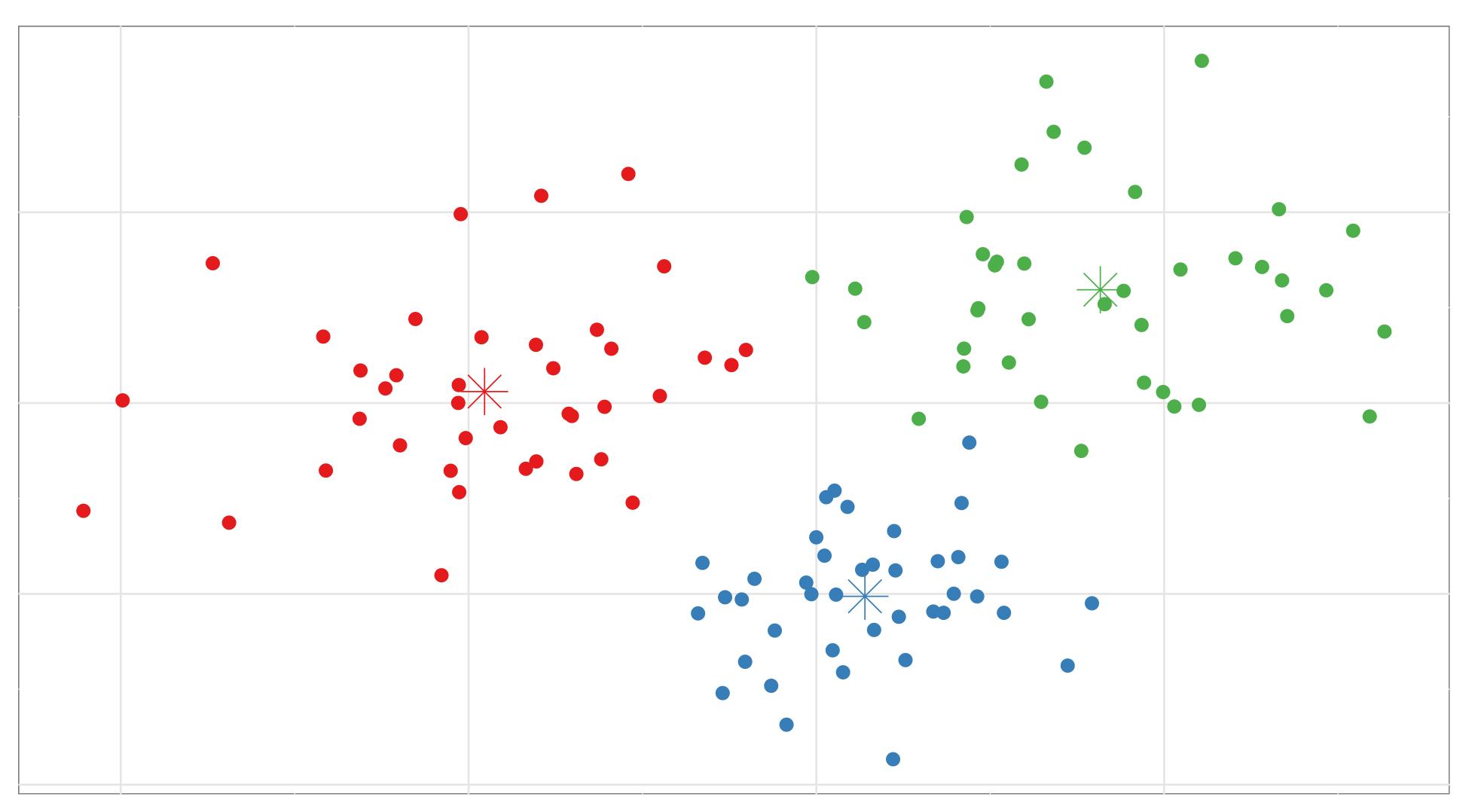


### Step 2: Assign each data point to the nearest centroid (4)



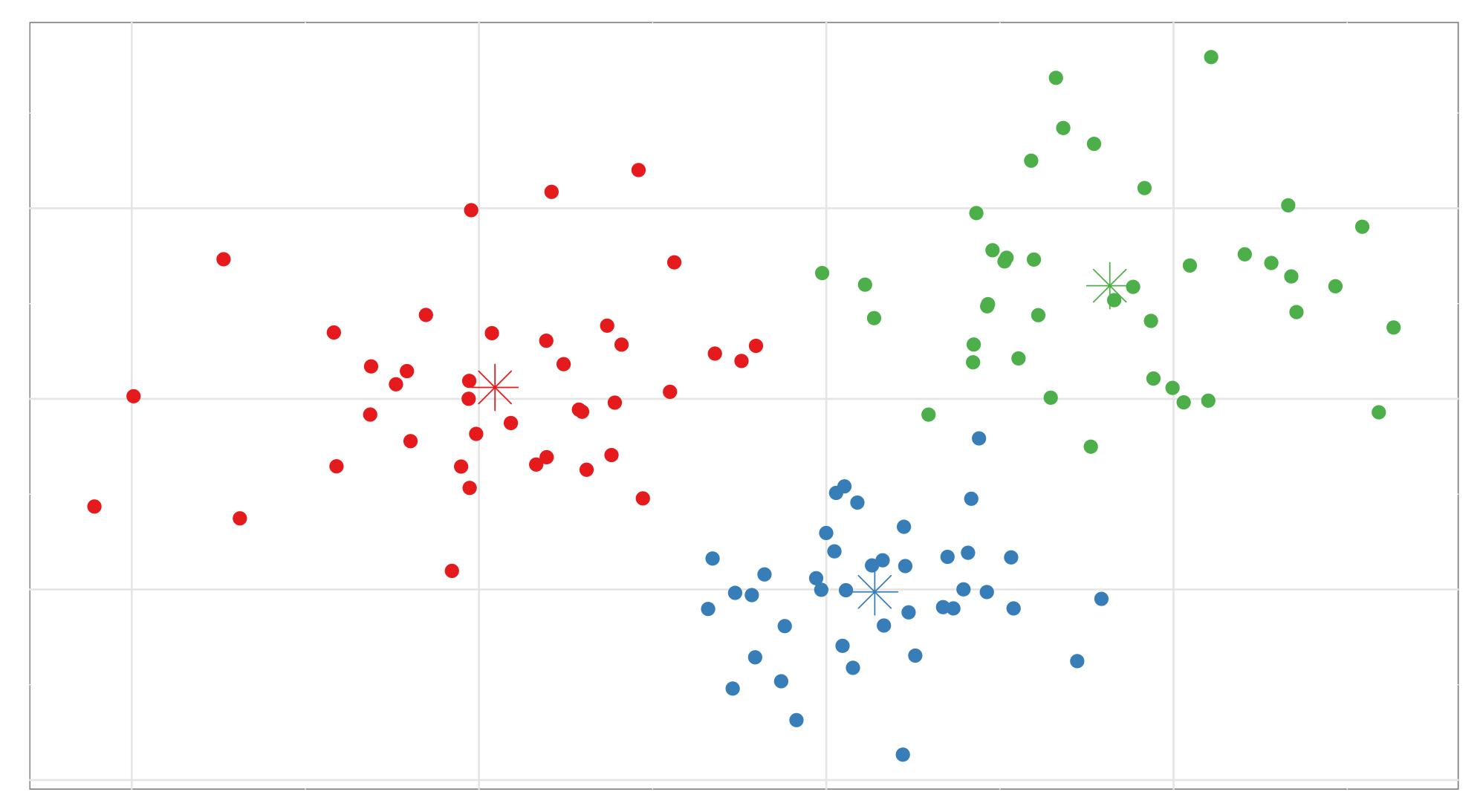


## Step 3: Move centroid to center of assigned points (4)



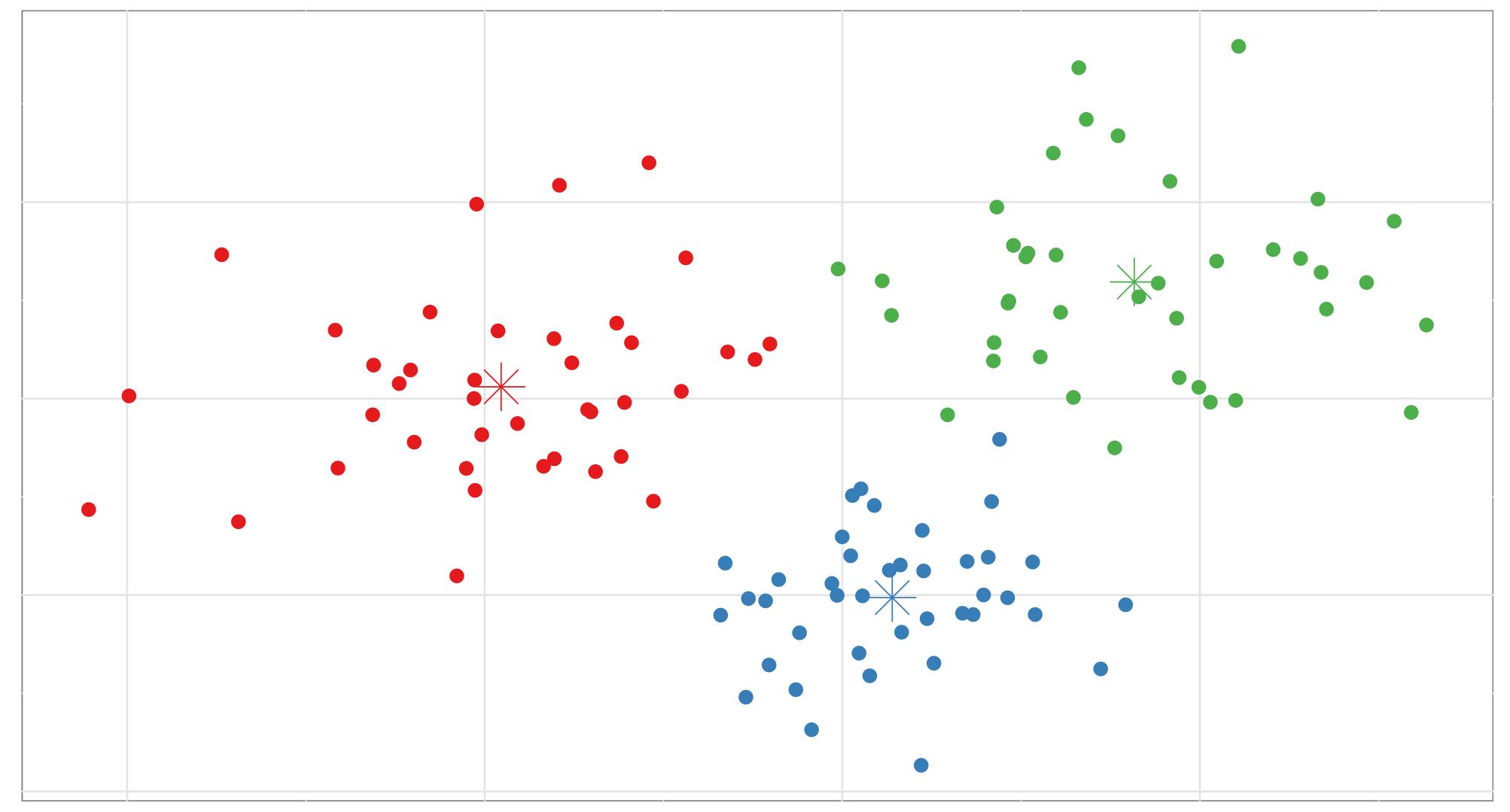


## Step 2: Assign each data point to the nearest centroid (5)



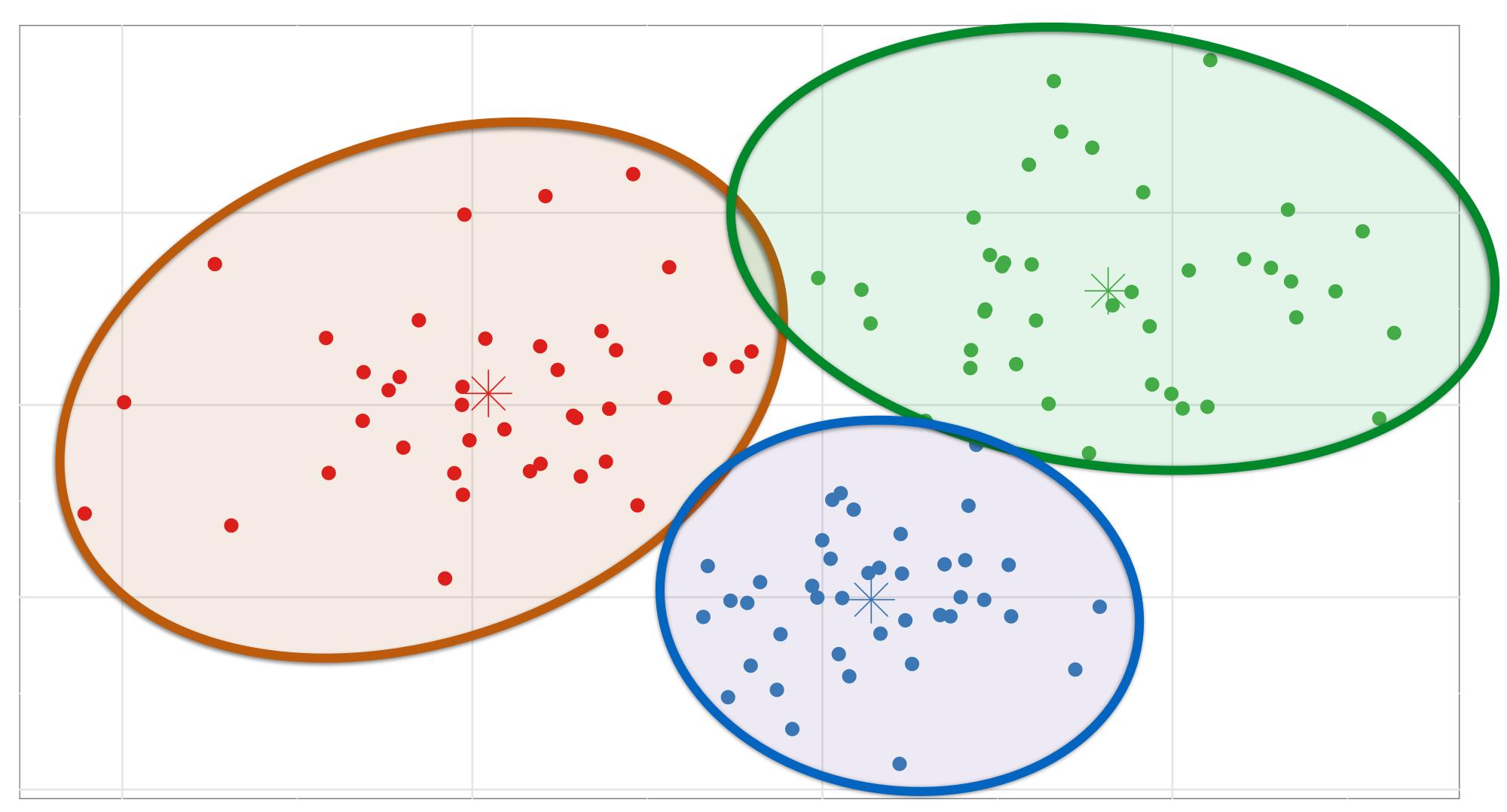


# Step 3: Move centroid to center of assigned points (5)





## Step 3: Move centroid to center of assigned points (5)





## K-Means: Got a problem with it?

Before starting, pick the number of clusters, K

- 1. Pick K random centroids within data range
- 2. Assign each data point to the nearest centroid
- 3. Move centroid to center of assigned points
- 4. Repeat steps 2 and 3 until centroid stops shifting



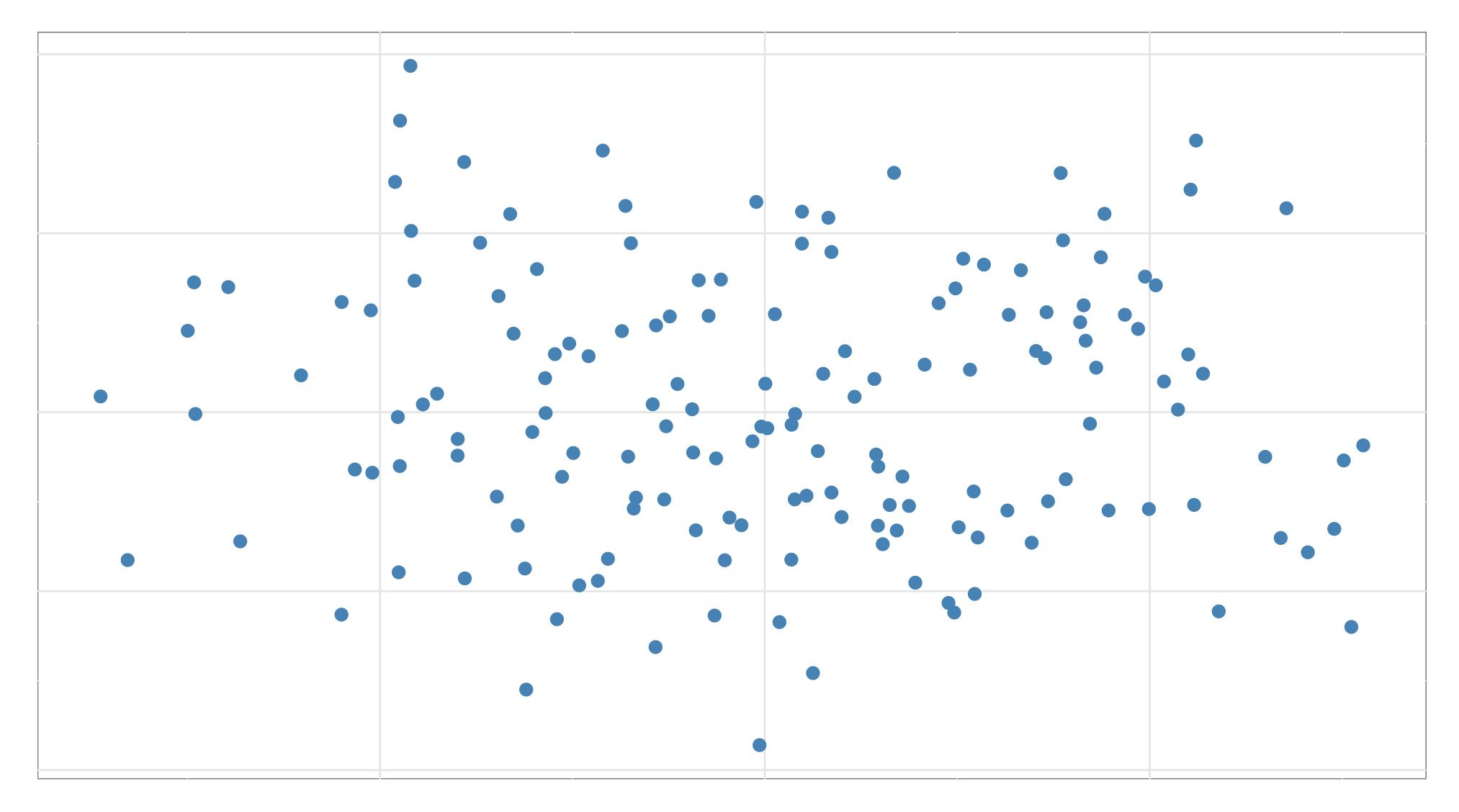
## K-Means: Got a problem with it?

Before starting, pick the number of clusters, K Subjective

- 1. Pick K random centroids within data range Not Repeatable
- 2. Assign each data point to the nearest centroid Sensitive to Scale
- 3. Move centroid to center of assigned points
- 4. Repeat steps 2 and 3 until centroid stops shifting

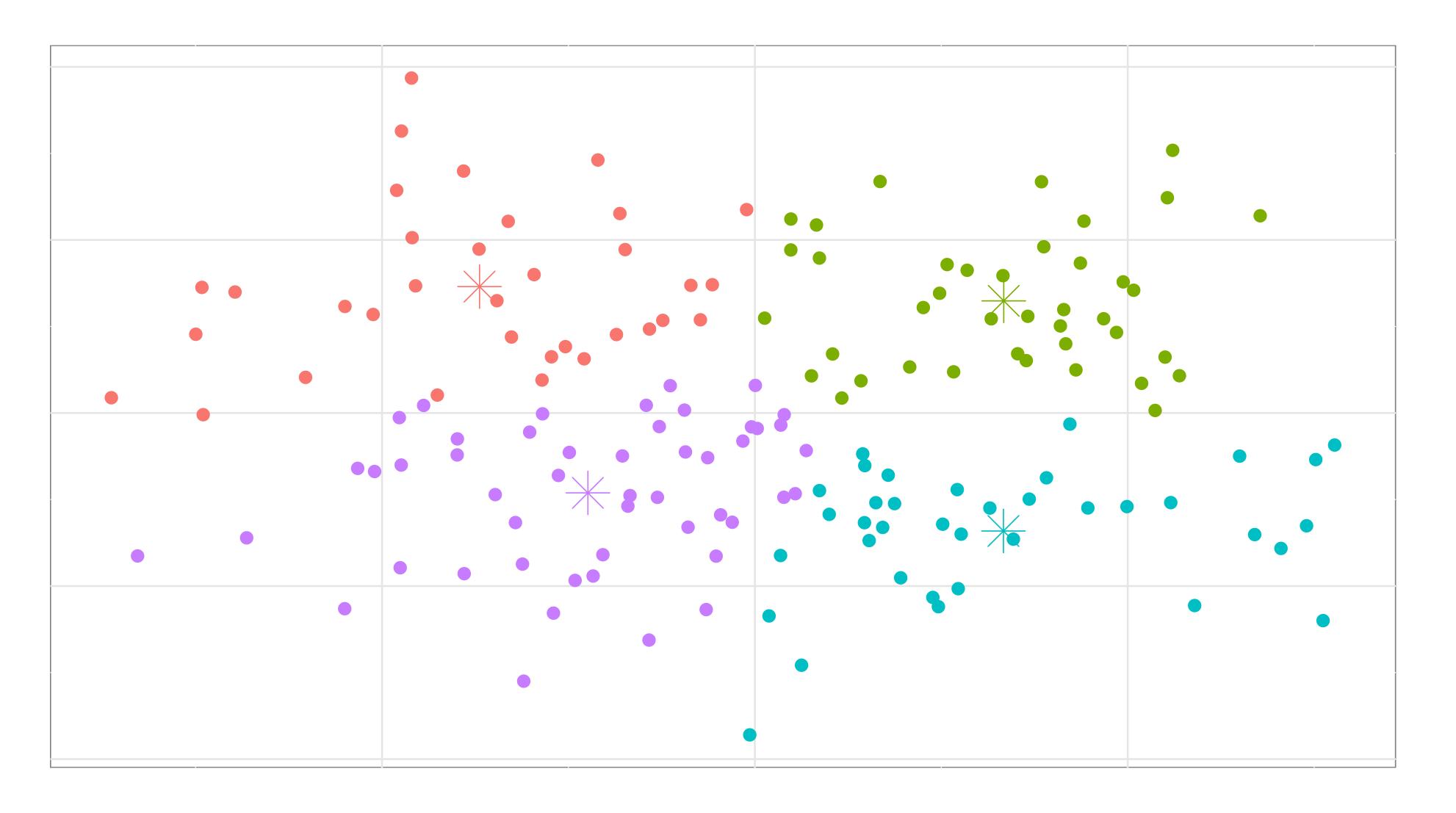


# How many clusters?



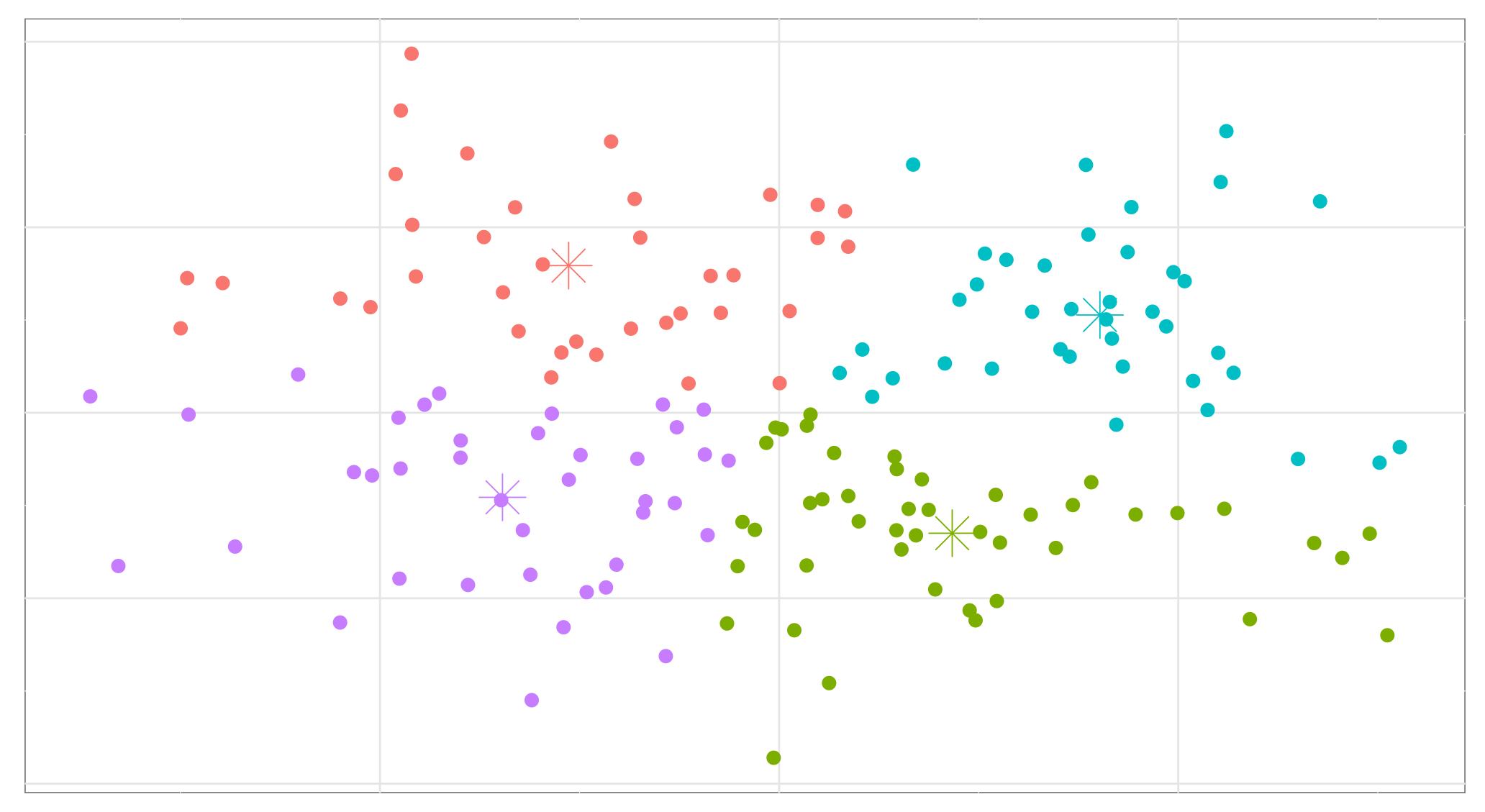


## Random Start...



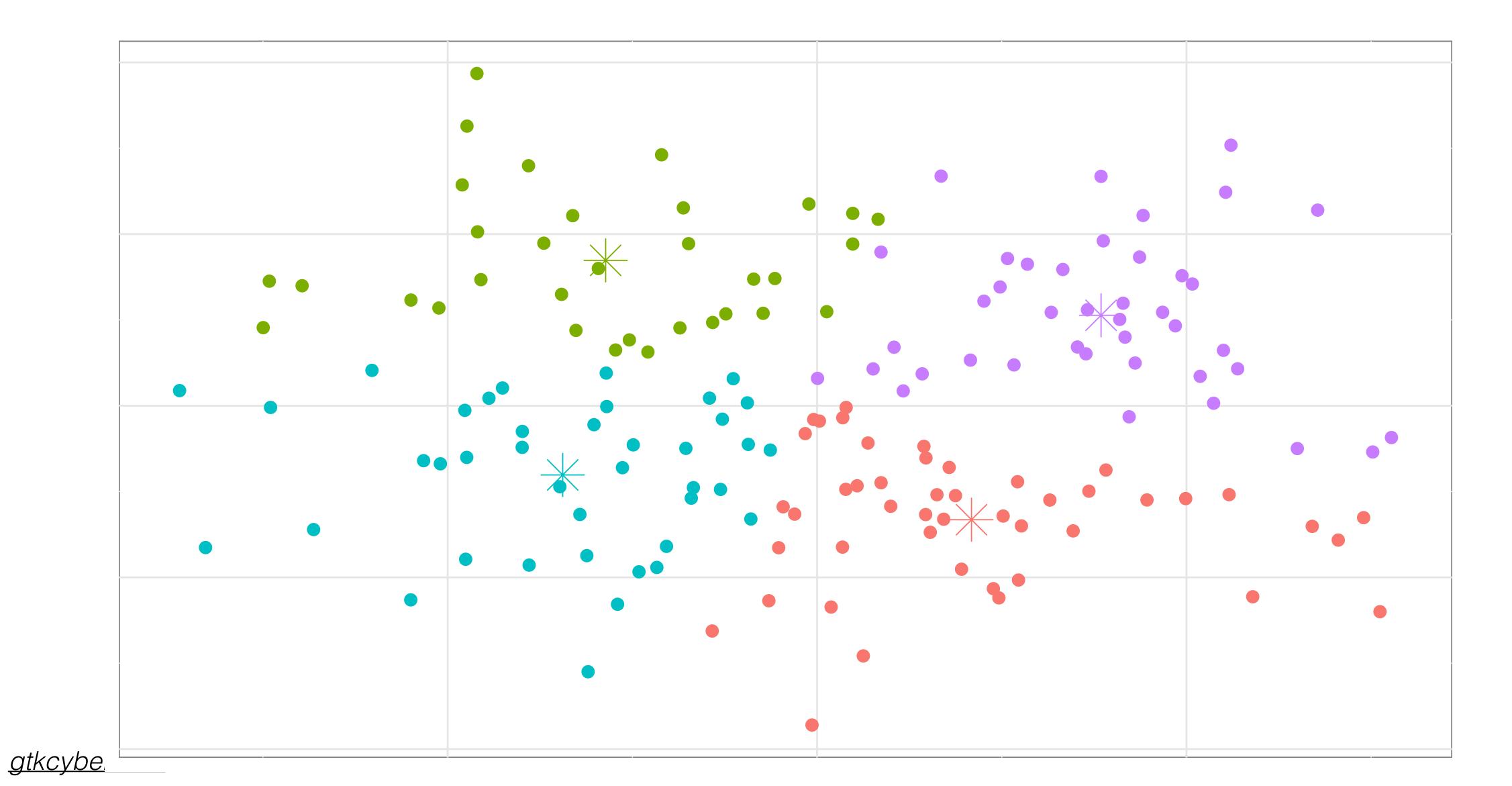


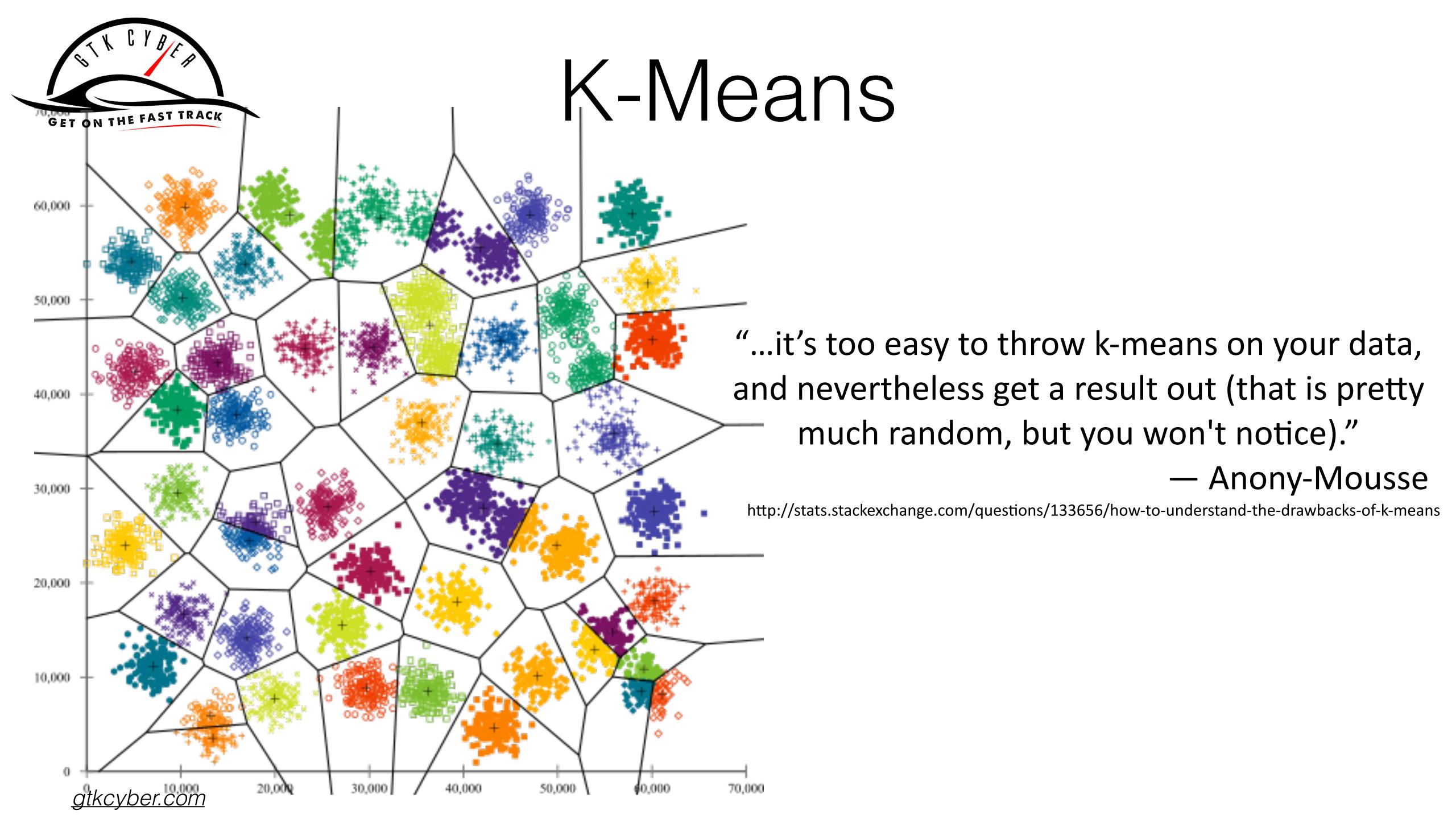
## Random Start...





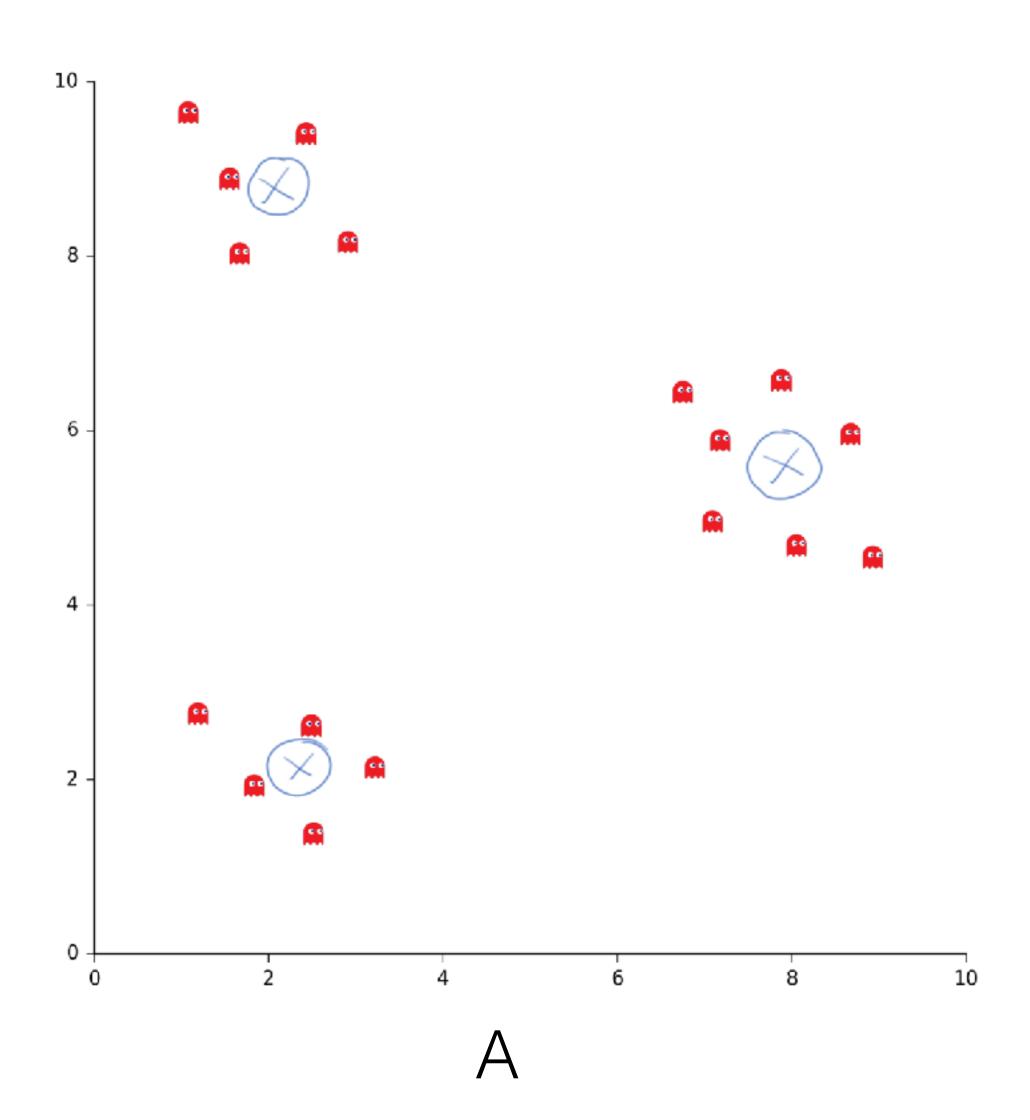
## Random Start...

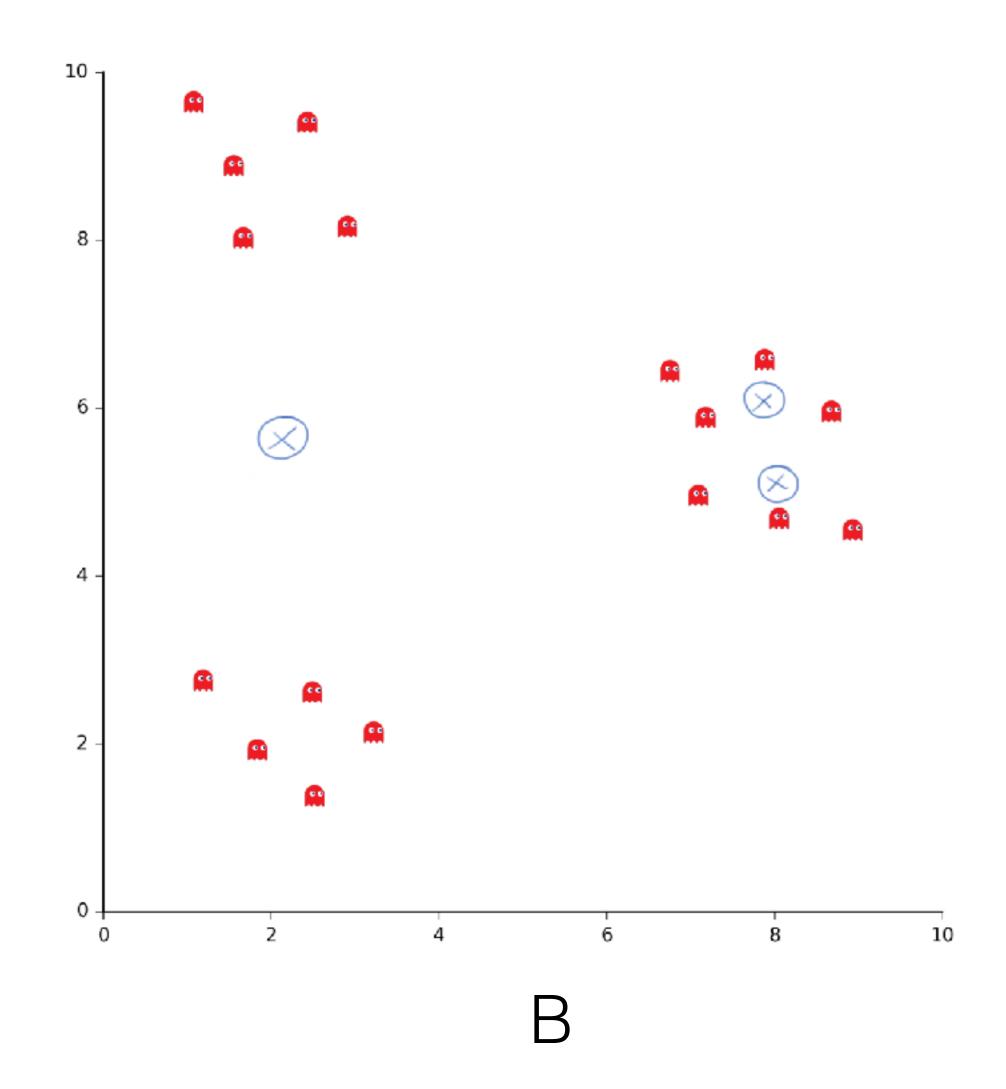


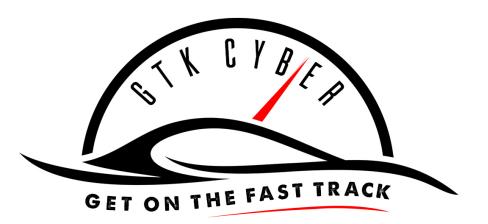




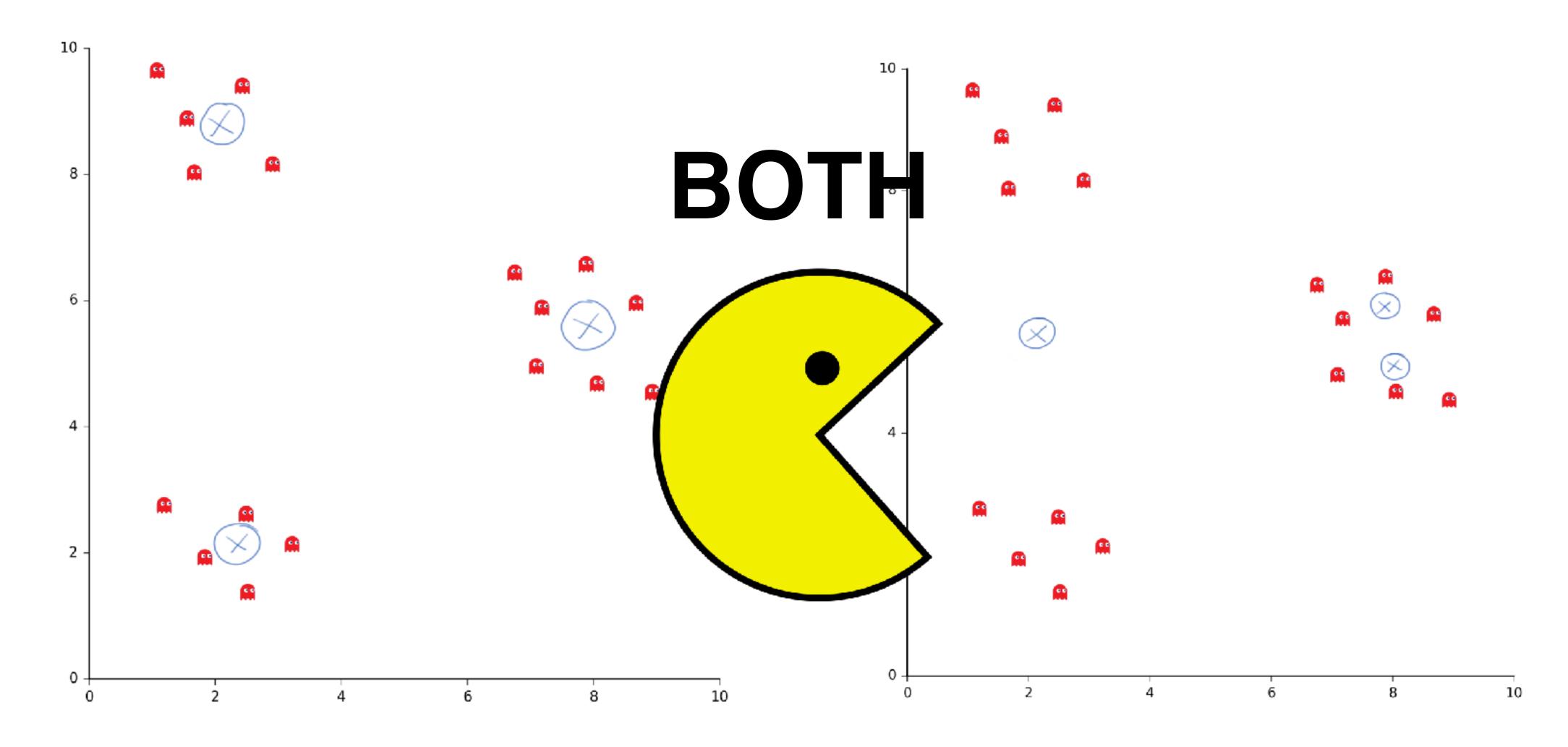
#### Which one is correct?





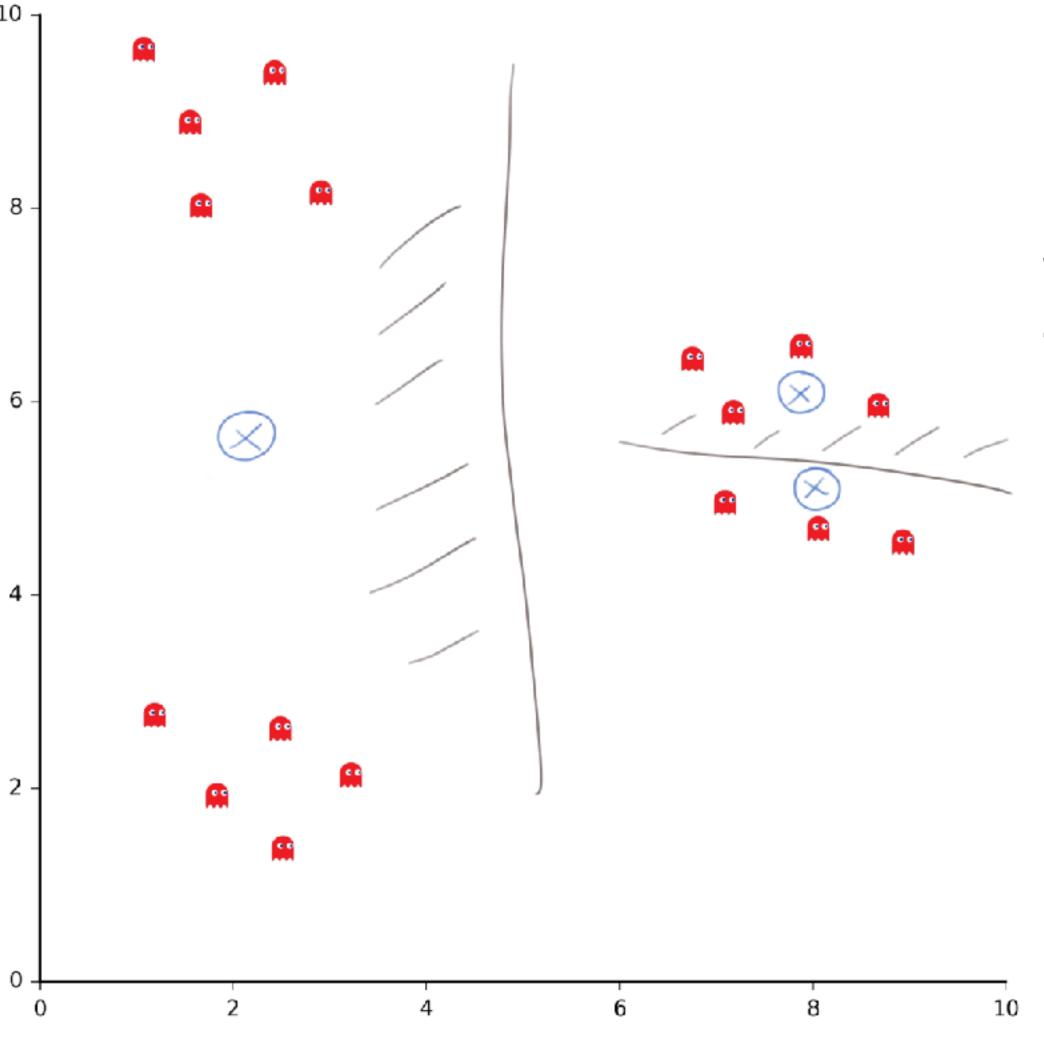


#### Which one is correct?





# Pain of optimization...Being stuck at sub-optimal local minimum...



Initial guess matters!
Same outcome
cannot be guaranteed

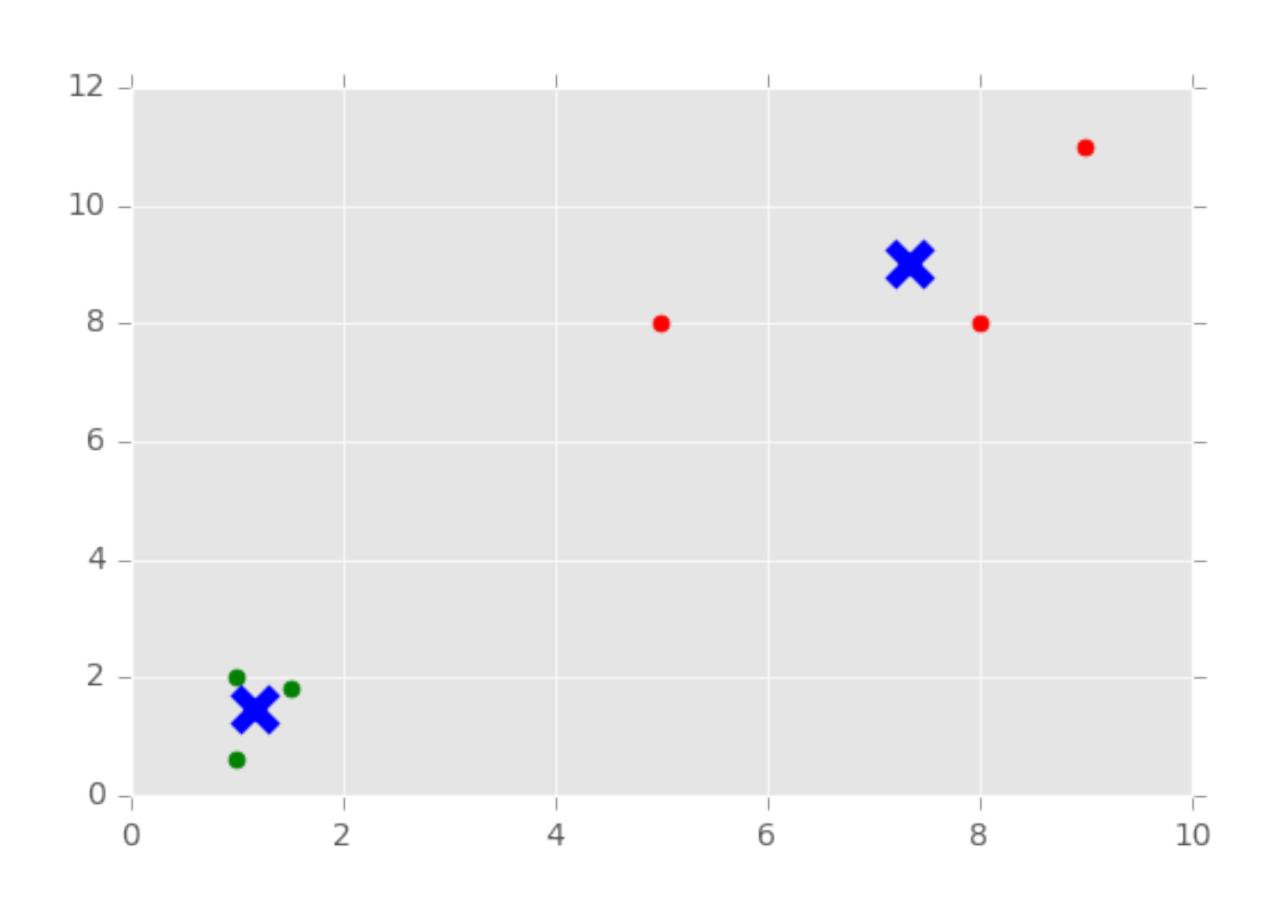


#### K-Means in practice (Python version)

```
#Import from Scikit-learn
from sklearn.cluster import KMeans
```

```
kmeans = KMeans(n_clusters=2)
kmeans.fit(data)
```

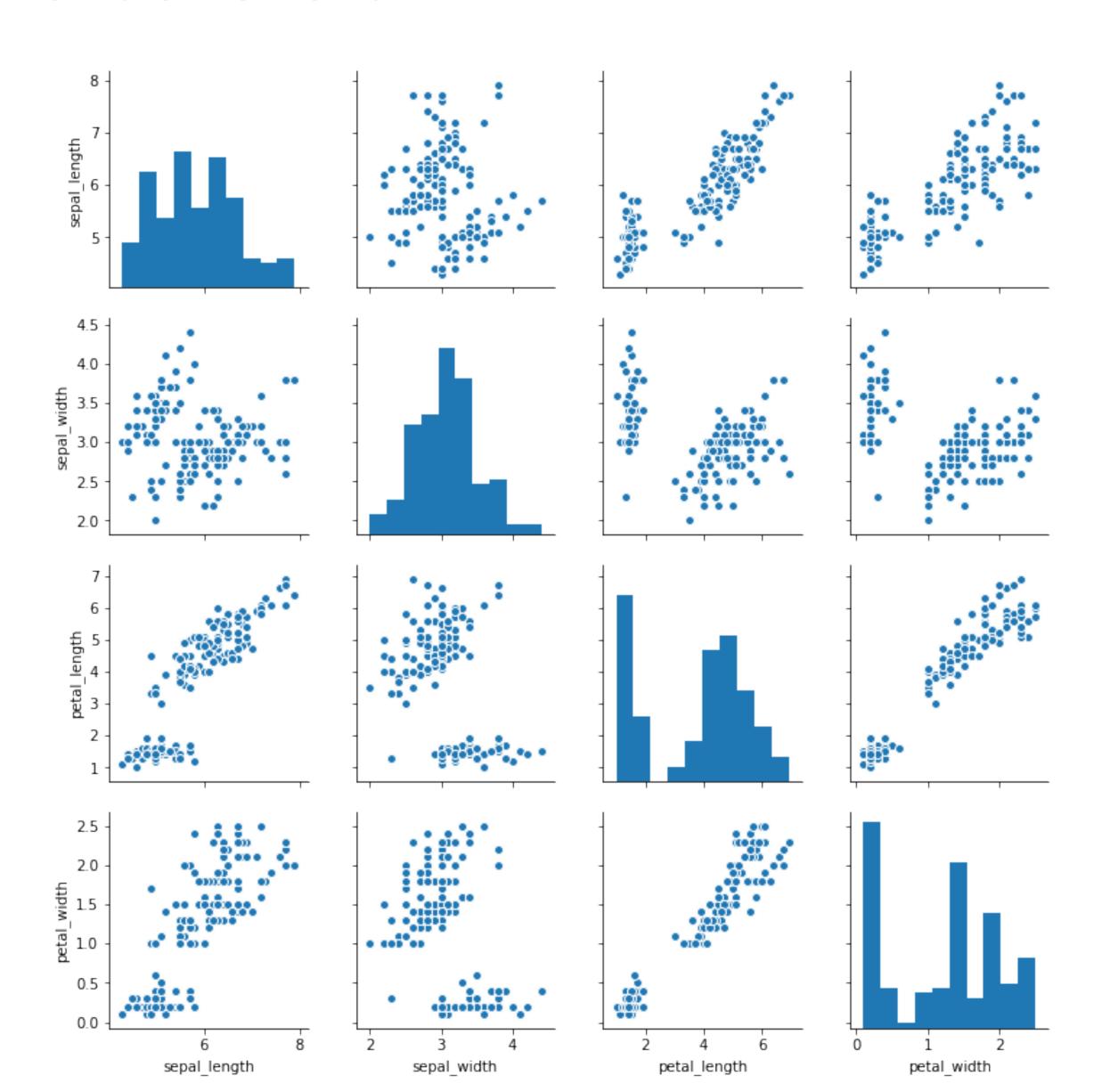
centroids = kmeans.cluster\_centers\_
labels = kmeans.labels f





### The Dataset

sns.pairplot(<data>)





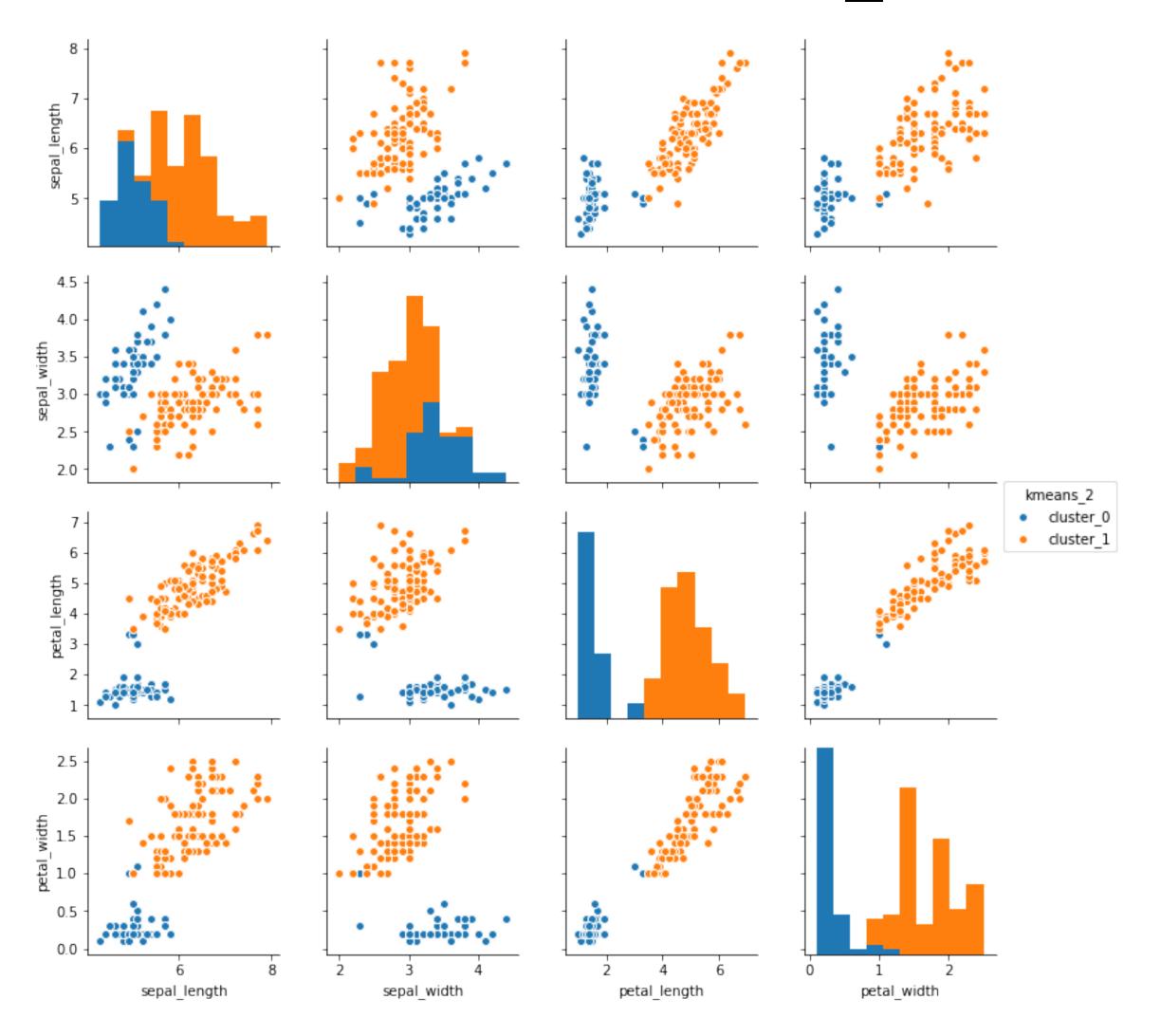
## K-Means Clustering

```
kmeans = KMeans( n_clusters=2 )
kmeans.fit( <data> )
```



## K-Means Clustering

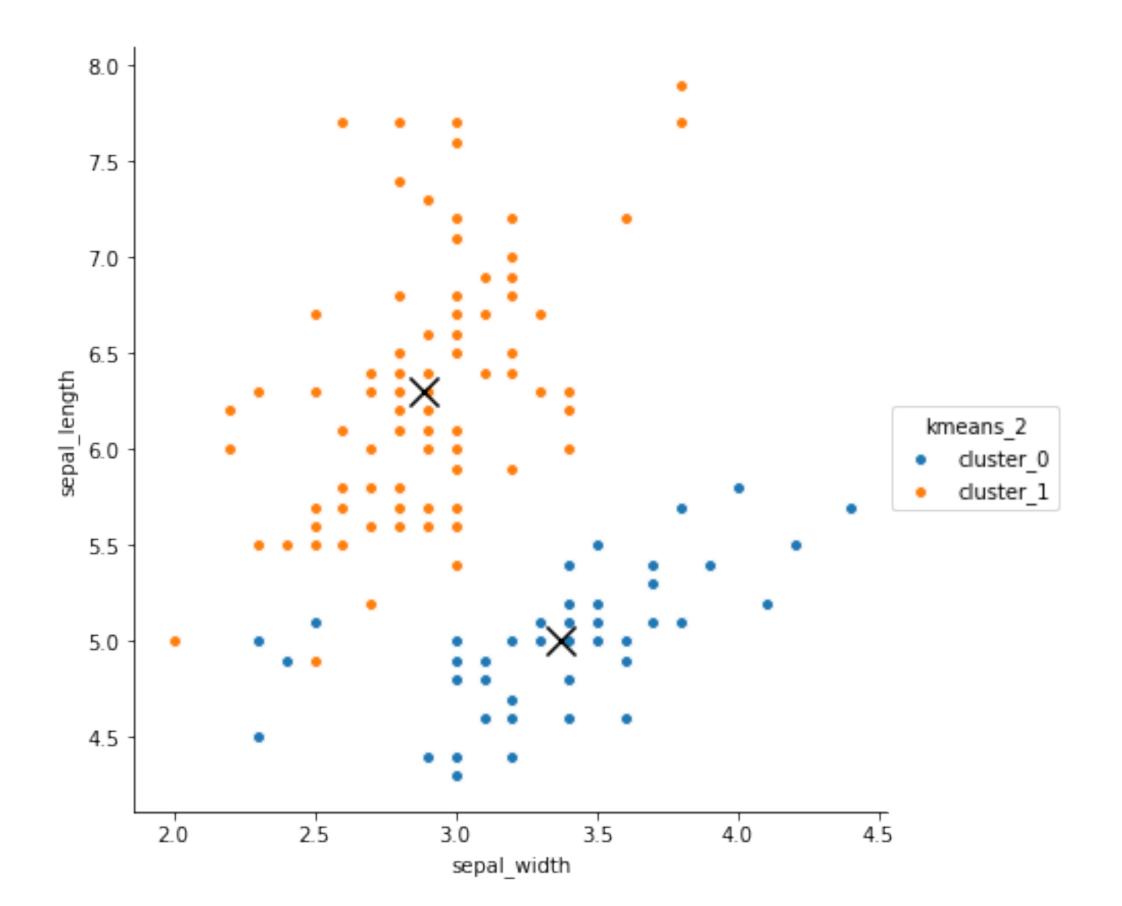
sns.pairplot(<data>,hue="kmeans\_2")





## K-Means Clustering

sns.pairplot(<data>,x\_vars="col\_1",y\_vars="col\_2",hue="kmeans\_2",size=6)
plt.scatter(<cluster\_centers>,<col\_2>, linewidths=3, marker='x', s=200,
c='black')





# K-Means is affected by the scale of every feature.



For k-means clustering, features must be scaled to the same ranges of values to contribute "equally" to the euclidean distance calculation.

Each row is transformed per-column by:

- Subtracting from the element in each row the mean for each feature (column) and then taking this value and
- Dividing by that feature's (column's) standard deviation.



```
# center and scale the data
scaler = StandardScaler()

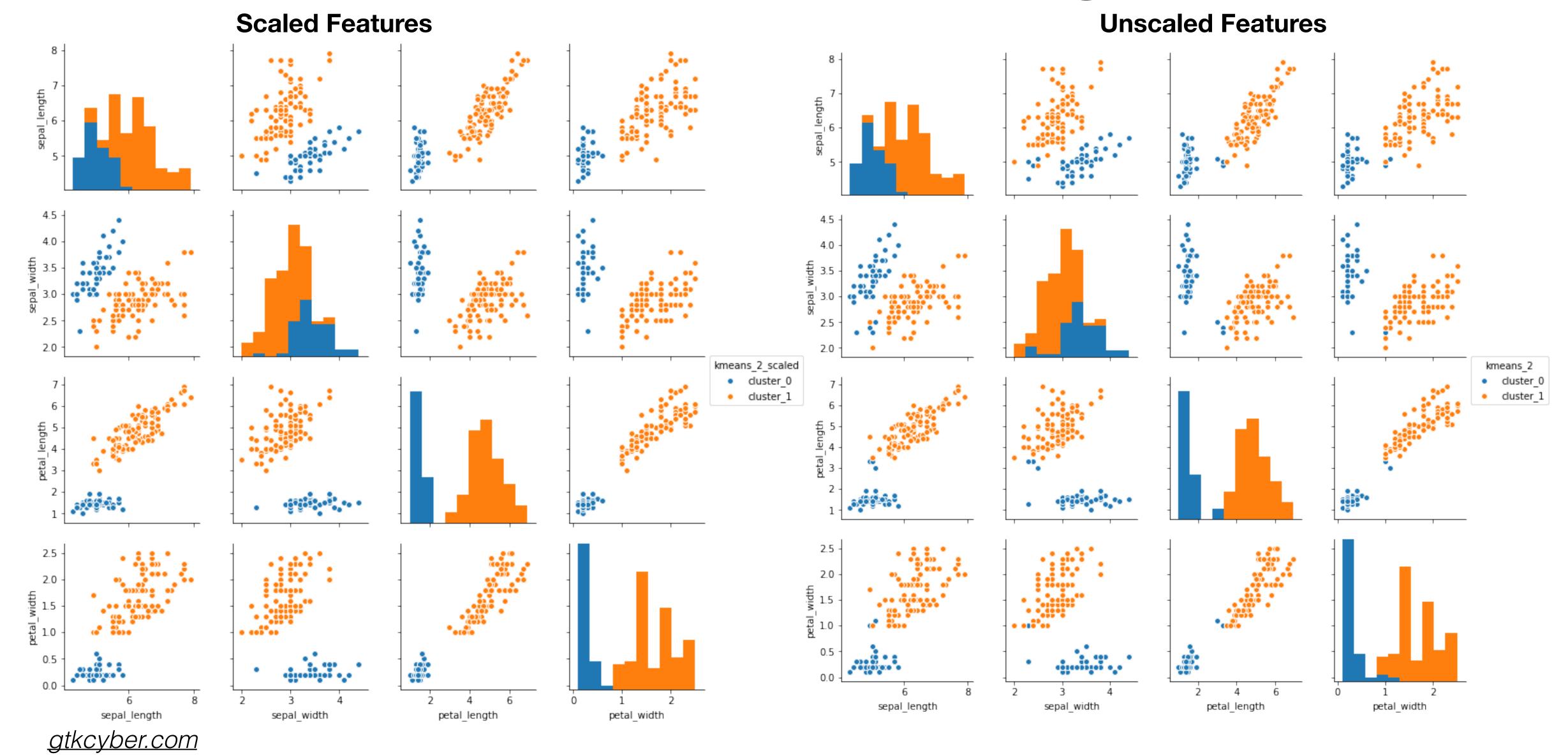
raw_data_scaled = scaler.fit_transform( <data> )

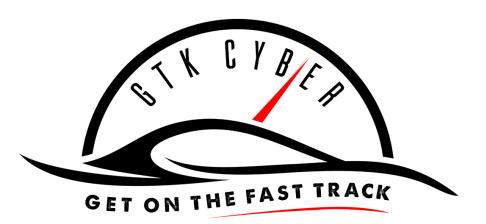
data_scaled = pd.DataFrame( raw_data_scaled, columns=features )
```



```
# K-means on scaled data
km = KMeans( n_clusters=2 )
km.fit( <scaled_data> )
```

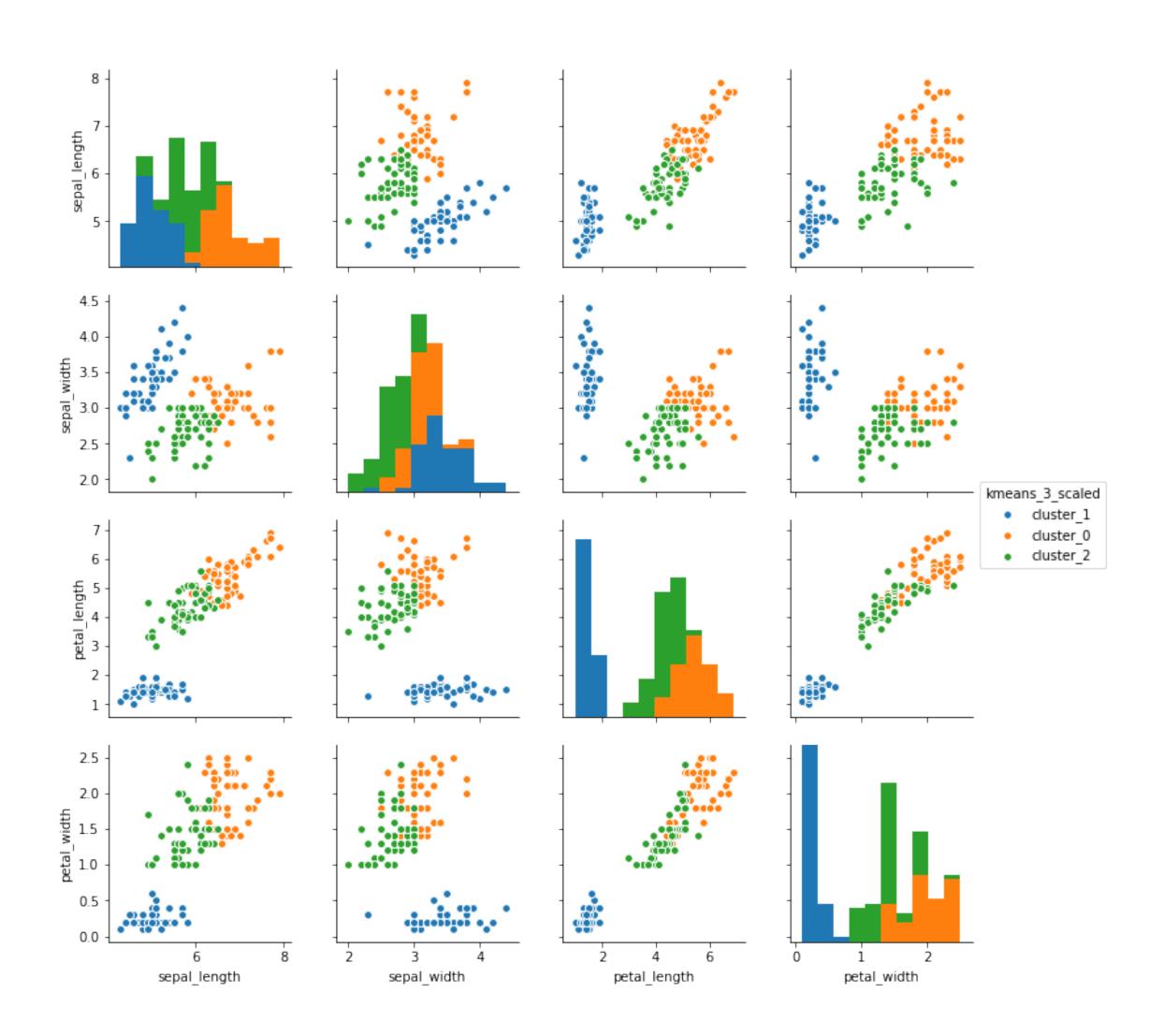






### More Clusters

```
km3 = KMeans(n_clusters=3)
km3.fit(scaled_data)
```

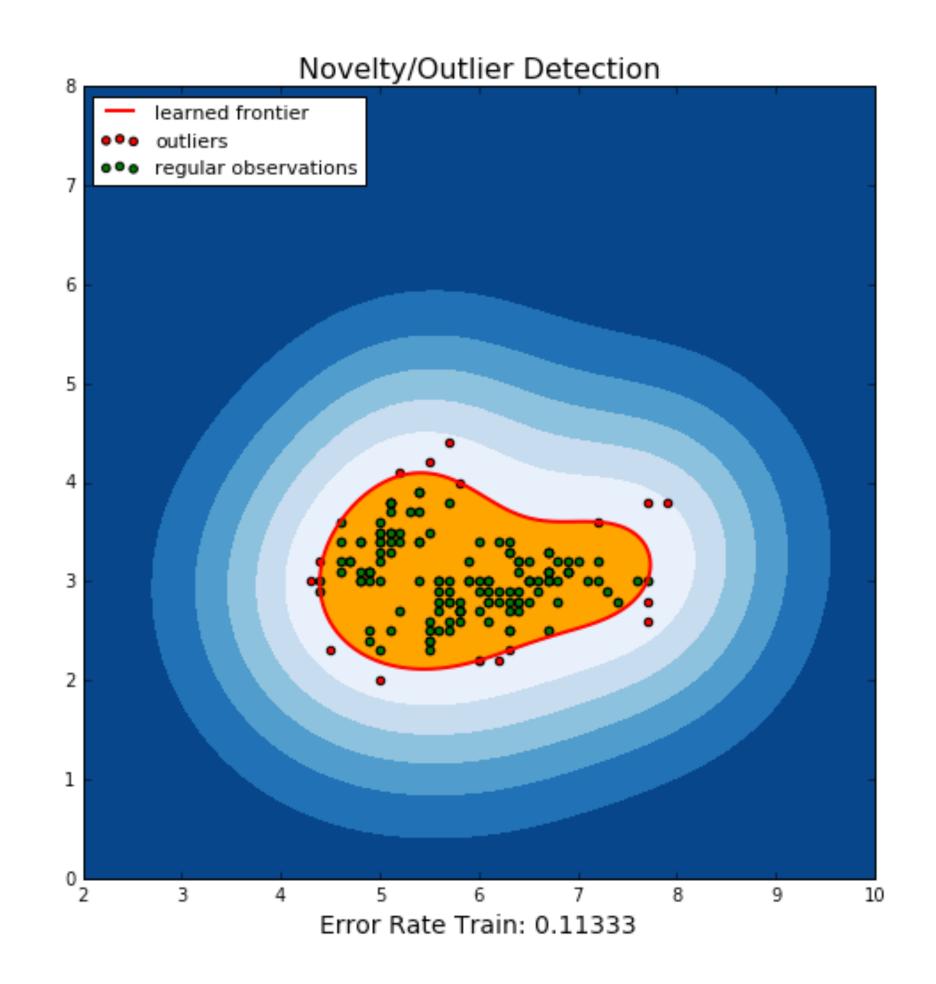




#### Outlier Detection

```
clf = svm.OneClassSVM( tol=0.001, nu=0.1)
clf.fit(X)
target_pred_outliers=clf.predict(X)
```

Delete n% of "outlier data", here ~10%





The Silhouette Coefficient is a common metric for evaluating clustering "performance" in situations when the "true" cluster assignments are not known.

b = mean distance to next nearest cluster

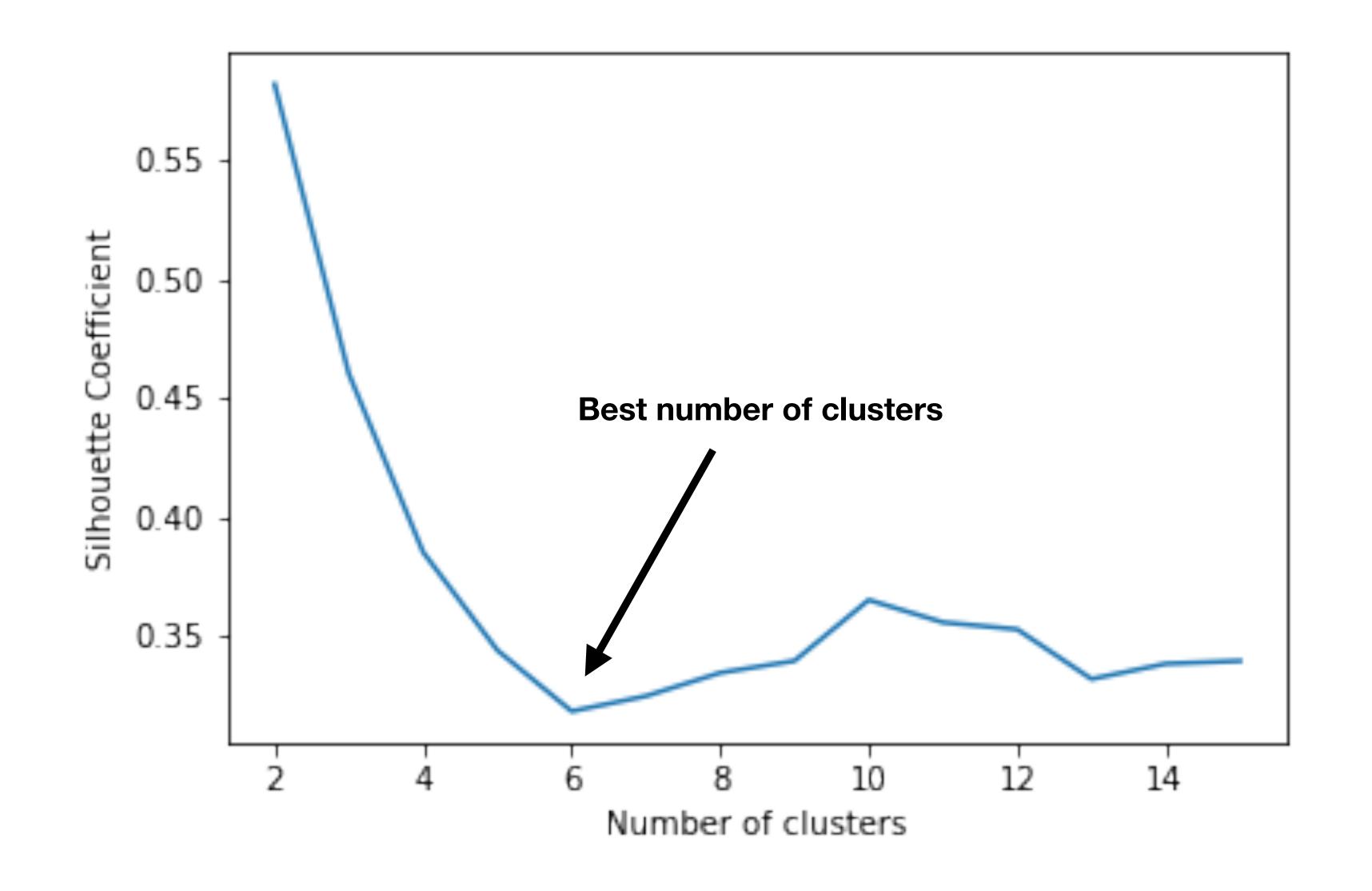
a = mean distance to other points in cluster

silhouette\_coeff = (b - a) / max(a,b)



```
k_range = range(2,16)
scores = []
for k in k_range:
    km_ss = KMeans(n_clusters=k, random_state=1)
    km_ss.fit(iris_data_scaled)
    scores.append(silhouette_score(<data>,
km_ss.labels_))
```

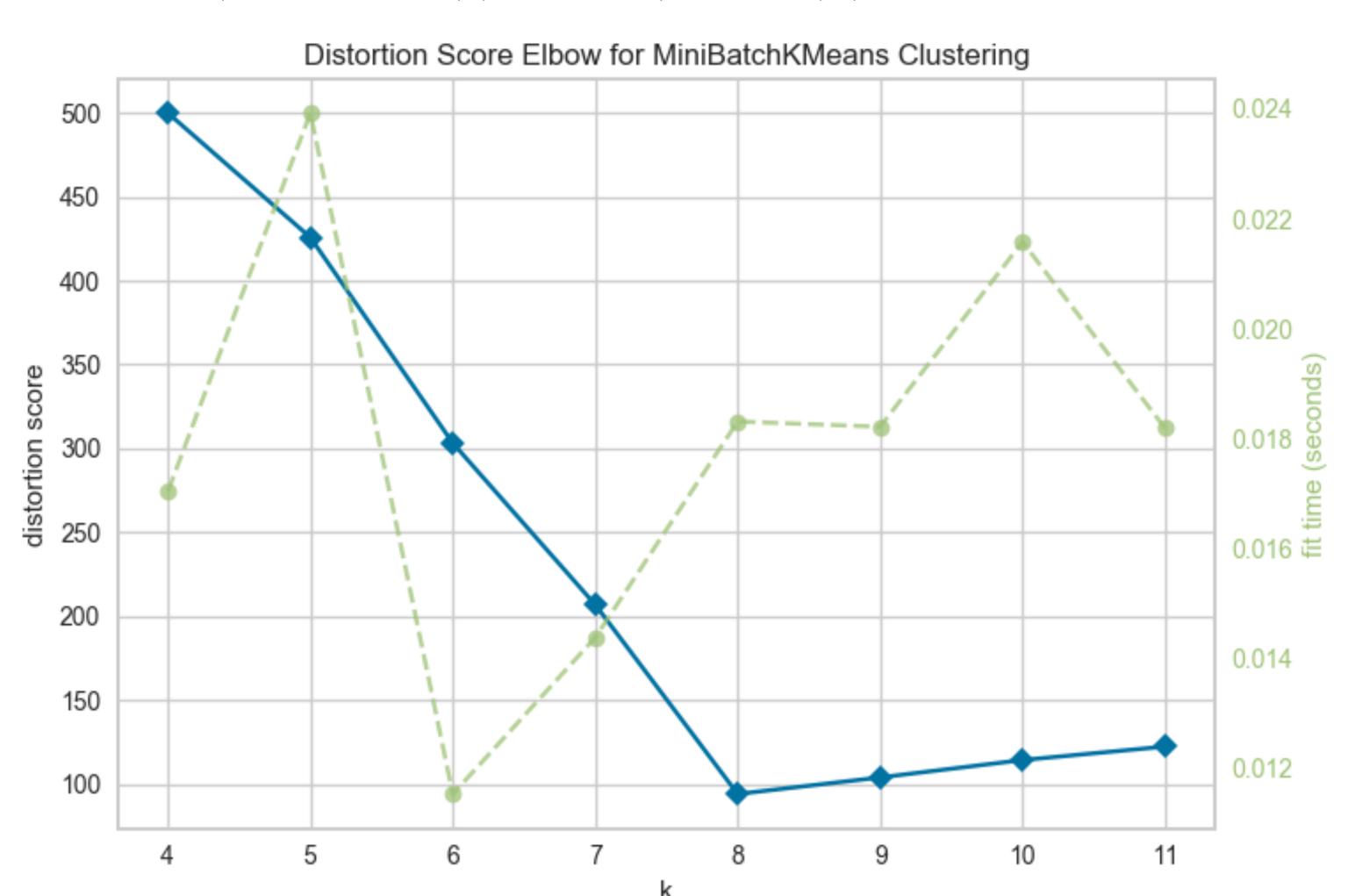






from yellowbrick.cluster import KElbowVisualizer
visualizer = KElbowVisualizer(KMeans(), k=(4,12))

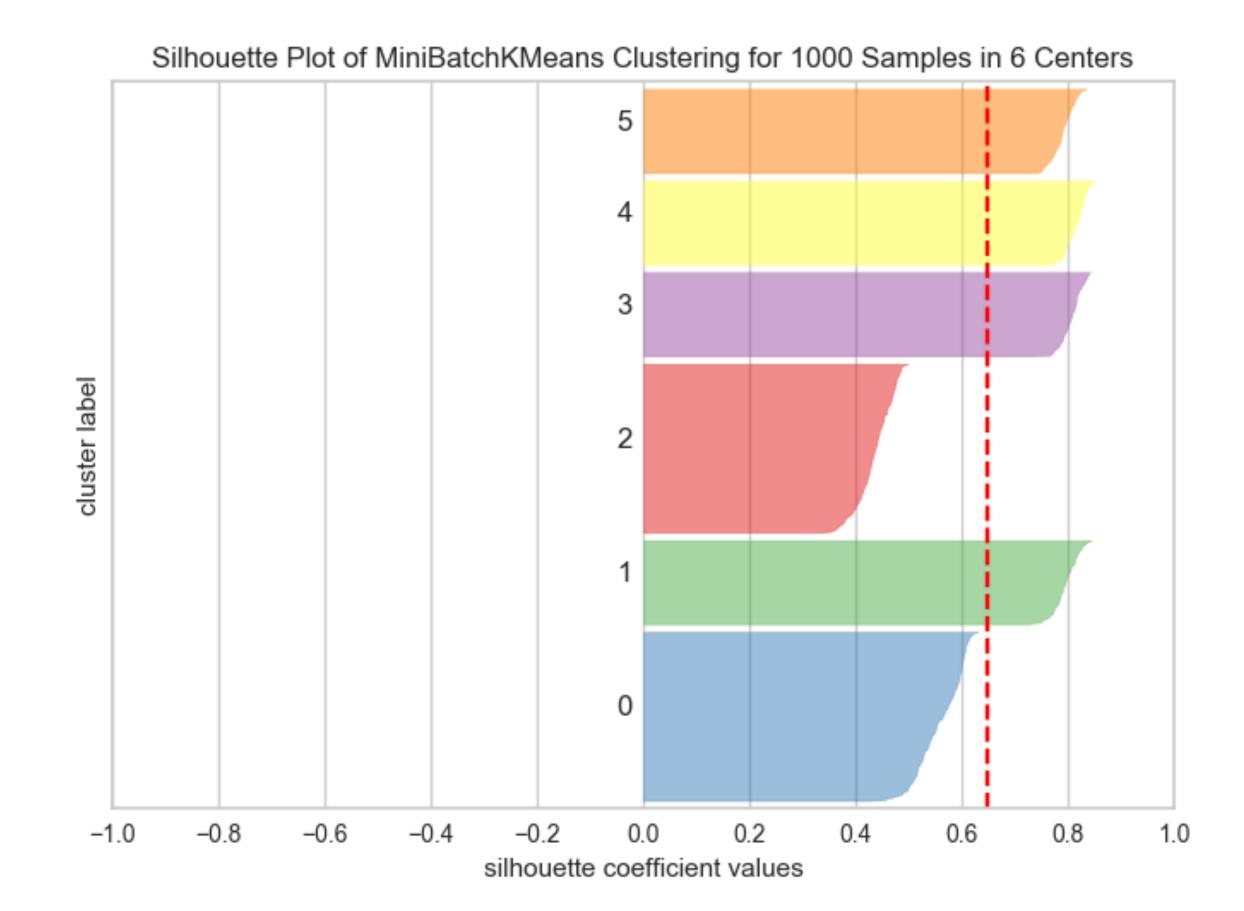
```
visualizer.fit(X)
visualizer.poof()
```





```
from yellowbrick.cluster import SilhouetteVisualizer
model = MiniBatchKMeans(6)
visualizer = SilhouetteVisualizer(model)
```

```
visualizer.fit(X)
visualizer.poof()
```





DBSCAN stands for **D**ensity-**B**ased **S**patial **C**lustering of **A**pplications with **N**oise.

Whereas K-means does not care about the density of data, DBSCAN does, under the assumption that regions of high density in your data should be treated as clusters.



DBSCAN does not allow you to specify how many clusters you want. Instead, you specify 2 parameters:

- **c (epsilon)**: This is the maximum distance between two points to allow them to be neighbors
- min\_samples: The number of neighbors a given point is allowed to have to be able to be part of a cluster

Any points that don't satisfy the criteria of being close enough to other points are labeled outliers and all fall into a single "cluster" (their cluster label by default is -1).

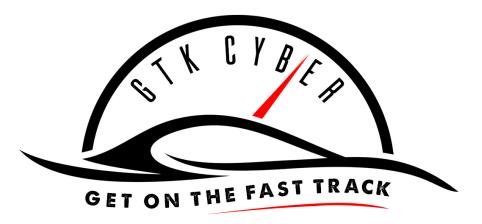


#### DBSCAN works as follows:

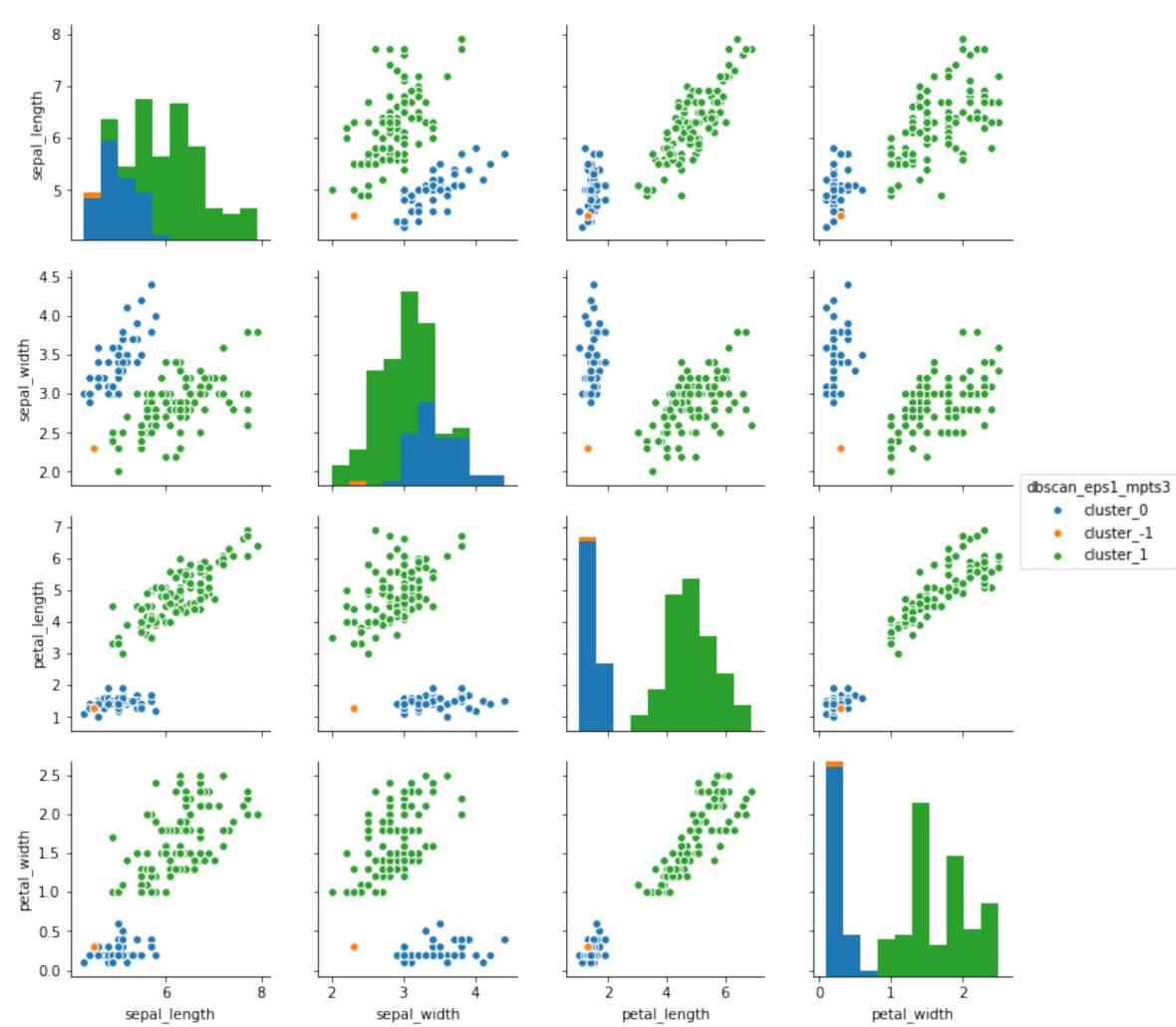
- 1. Choose an arbitrary starting point in your dataset that has not been seen.
- 2. Retrieve this point's  $\epsilon$ -neighborhood (all points that are within a distance  $\epsilon$  from it), and if it contains at least \*min\_samples, a cluster is started.
- 3. Otherwise, the point is labeled as an outlier (-1). Note: This point might later be found in a sufficiently sized  $\varepsilon$ -environment of a different point and hence be made part of a cluster.
- 4. If a point is found to be a dense part of a cluster, its  $\epsilon$ -neighborhood is also part of that cluster. All points that are found within the  $\epsilon$ -neighborhood are added, as is their own  $\epsilon$ -neighborhood when they are also dense.
- 5. Continue until the density-connected cluster is completely found.
- 6. Find a new unvisited point to process and repeat.



```
db = DBSCAN(eps=1, min_samples=3)
db.fit(<scaled_data>)
```

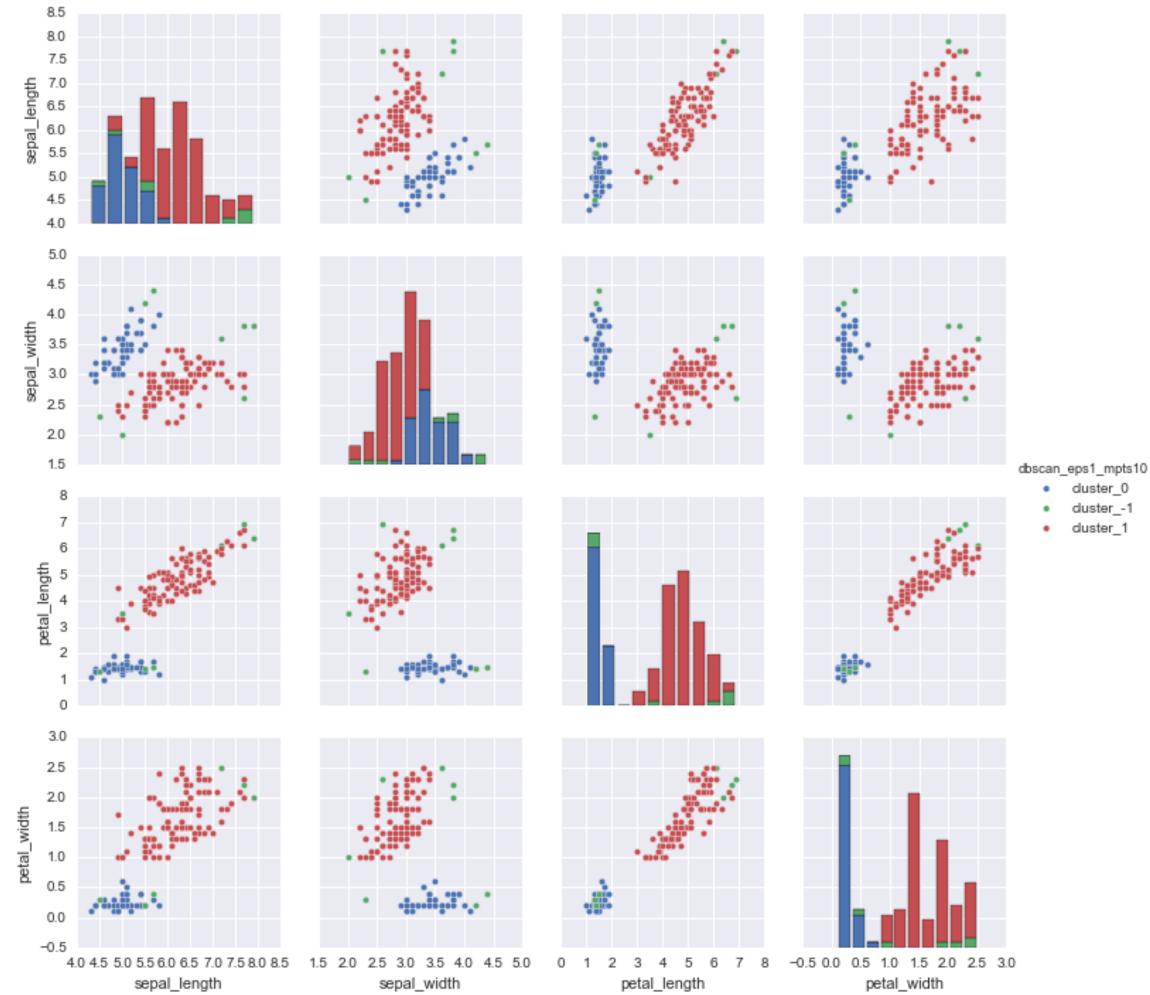


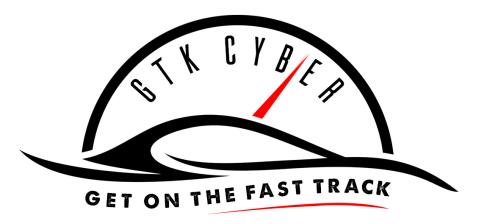
data\_no\_names['dbscan\_eps1\_mpts3'] = [ "cluster\_" + str(label) for label in db.labels\_ ]
sns.pairplot(data\_no\_names, hue="dbscan\_eps1\_mpts3")





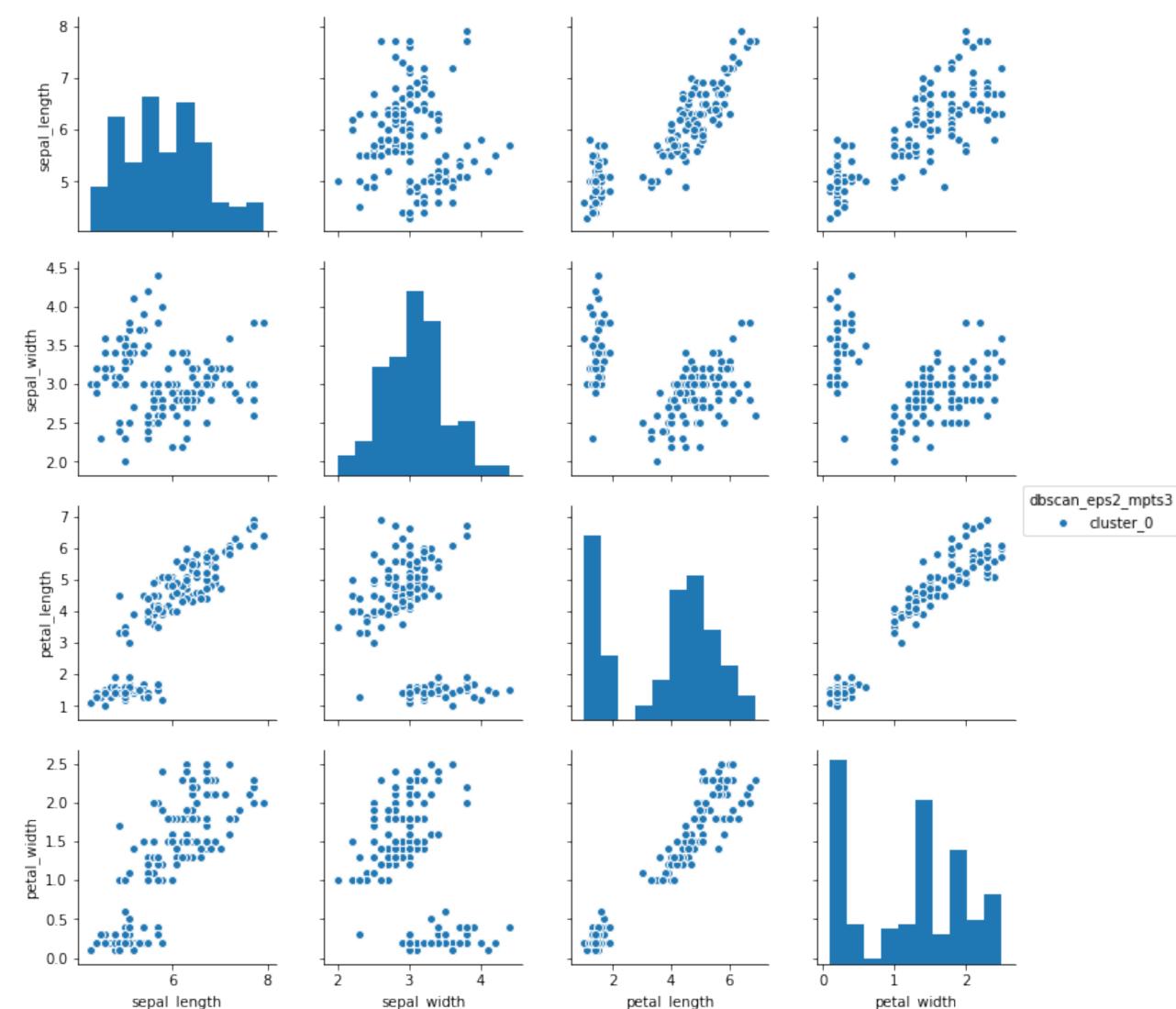
db2 = DBSCAN(eps=1, min\_samples=10)
db2.fit(data\_scaled)





db2 = DBSCAN(eps=2, min\_samples=3)

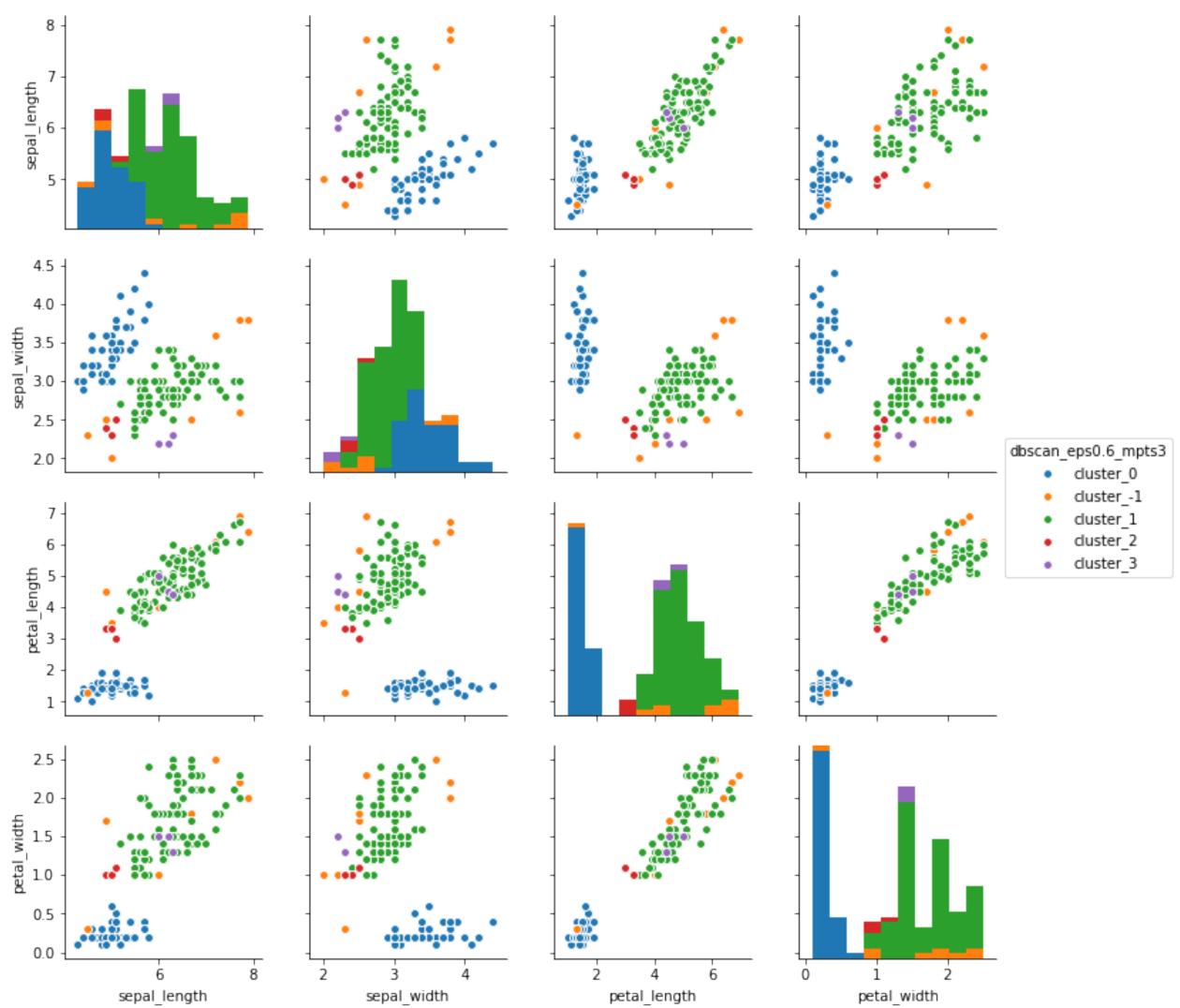
db2.fit(iris\_data\_scaled)





db2 = DBSCAN(eps=0.6, min\_samples=3)

db2.fit(iris\_data\_scaled)





### In Class Exercise

Please take 30 minutes and complete

Day 3: Clustering Worksheet



# Questions?



# Tuning Hyperparameters



#### Grid Search

```
RandomForestClassifier(bootstrap=True,
class_weight=None,
criterion='gini',
max depth=None,
max features='auto',
max leaf nodes=None,
min impurity decrease=0.0,
min_impurity_split=None,
min samples leaf=1,
min samples_split=2,
min_weight_fraction_leaf=0.0,
n estimators=10,
n_jobs=1,
oob score=False
<u>átkcyber.com</u>
```

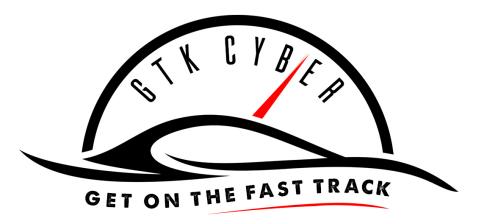
# Tuning these parameters

- GridSearchCV: You provide a list of possible parameters
- RandomizedSearchCV: Random combinations are searched



#### Grid Search

```
param_grid = [
    {'C': [1, 10, 100, 1000], 'kernel': ['linear']},
    {'C': [1, 10, 100, 1000], 'gamma': [0.001, 0.0001],
'kernel': ['rbf']},
]
```



#### Grid Search

```
# use a full grid over all parameters
param grid = {"max depth": [3, None],
              "max features": [1, 3, 10],
              "min samples split": [2, 3, 10],
              "min samples leaf": [1, 3, 10],
              "bootstrap": [True, False],
              "criterion": ["gini", "entropy"]}
# run grid search
grid search = GridSearchCV(clf, param grid=param grid)
start = time()
grid search.fit(X, y)
print("GridSearchCV took %.2f seconds for %d candidate parameter settings."
     % (time() - start, len(grid search.cv results ['params'])))
report(grid search.cv results )
```

http://scikit-learn.org/stable/auto\_examples/model\_selection/plot\_randomized\_search.html



#### Random Search

```
# specify parameters and distributions to sample from
param dist = {"max depth": [3, None],
              "max features": sp randint(1, 11),
              "min samples split": sp randint(2, 11),
              "min samples leaf": sp randint(1, 11),
              "bootstrap": [True, False],
              "criterion": ["gini", "entropy"]}
# run randomized search
n iter search = 20
random_search = RandomizedSearchCV(clf, param_distributions=param_dist,
                                   n iter=n iter search)
start = time()
random search.fit(X, y)
print("RandomizedSearchCV took %.2f seconds for %d candidates"
        parameter settings." % ((time() - start), n_iter_search))
report(random search.cv results )
```



# What is a pipeline?





# Why use a pipeline?

- It makes code more readable
- You don't have to worry about keeping track data during intermediate steps, for example between transforming and estimating.
- It makes it trivial to move ordering of the pipeline pieces, or to swap pieces in and out.
- It allows you to do GridSearchCV on your workflow



# Without Pipeline

```
#get categorical features
#drop off last column because its unnecessary
X categorical =
pd.get dummies(df[categorical columns]).astype(int).iloc[:,:-1]
#get and transform numeric features
X numeric = df[numeric columns]
X numeric[numeric columns] =
StandardScaler().fit transform(X numeric)
#get outcome variable
y = df[target]
#combine transformed categorical and numeric features
X final = pd.concat((X numeric, X categorical), axis=1)
```



# Without Pipeline

```
#create rf regressor and check 10-fold RMSE
rf = RandomForestRegressor()
cross_val_scores =
np.abs(cross_val_score(rf,X_final,y,scoring =
"neg_mean_squared_error", cv=10))
rmse_cross_val_scores = np.sqrt(cross_val_scores)
```



# With Pipeline



# With Pipeline

```
cross_val_scores =
np.abs(cross_val_score(full_pipeline,X,y,cv=10,scoring="n
eg_mean_squared_error"))
rmse_cross_val_scores = np.sqrt(cross_val_scores)
```



# With Pipeline

#### full\_pipeline.steps

```
[('all features', FeatureUnion(n jobs=1,
         transformer list=[('categoricals', Pipeline(memory=None,
       steps=[('selector', ItemSelector(key=['rbc', 'pc', 'pcc', 'ba', 'htn',
'dm', 'cad', 'appet', 'pe', 'ane'])), ('imputer', Imputer(axis=0, copy=True,
missing values=0, strategy='most frequent',
      verbose=0)), ('encoder', OneHotEncoder(cat ... tegy='median', verbose=0)),
('scaler', StandardScaler(copy=True, with mean=True, with std=True))]))],
         transformer weights=None)),
 ('rf classifier',
  RandomForestClassifier(bootstrap=True, class weight=None, criterion='gini',
              max depth=None, max features='auto', max leaf nodes=None,
              min impurity decrease=0.0, min impurity split=None,
              min samples leaf=1, min samples split=2,
              min weight fraction leaf=0.0, n estimators=10, n jobs=1,
              oob_score=False, random_state=None, verbose=0,
              warm start=False))]
```



# Pipelines

```
from sklearn.feature selection import SelectKBest
from sklearn.ensemble import RandomForestClassifier
from sklearn.pipeline import Pipeline
select = SelectKBest(k=100)
clf = RandomForestClassifier()
steps = [('feature selection', select),
        ('random forest', clf)]
pipeline = Pipeline(steps)
```



# Pipelines

```
pipeline.fit( X_train, y_train )

y_prediction = pipeline.predict( X_test )

report = classification_report( y_test, y_prediction )

print(report)
```



### In Class Exercise

Please take 30 minutes and complete

Day 3: Optimizing your Model



# Pickling Your Model

 Pickling your model allows you to preserve your model to be used later.



# Pickling Your Model

In order to rebuild a similar model with future versions of scikit-learn, additional metadata should be saved along the pickled model:

- The training data, e.g. a reference to a immutable snapshot
- The python source code used to generate the model
- The versions of scikit-learn and its dependencies
- The cross validation score obtained on the trained ata



# Pickling Your Model

```
#Saving your model
from sklearn.externals import joblib
joblib.dump(clf, 'filename.pkl')

#Loading your model
clf = joblib.load('filename.pkl')
```



# Case Studies in Machine Learning & Cyber Security

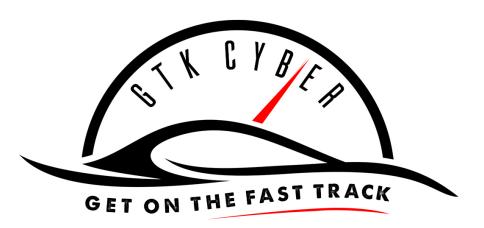
# Finding SQL Injection Attempts

GETONTHE FASTIRACK

# What is SQL injection?

GETONTHE FASITRACK

SQL Injection is a vulnerability, most commonly in web applications in which an attacker can execute malicious queries on **YOUR** server



# A normal SQL Query

```
SELECT *
FROM users
WHERE username=charles AND
password=pass1234
```



# Pseudo Code for Web App Authentication

```
username = <from user>
password = <from user>
query = "SELECT * FROM users WHERE username =
username AND password = password"
query result = db.execute(query)
if len( query result > 0 )
   //Authenticate user
else
   //Boot them out
```



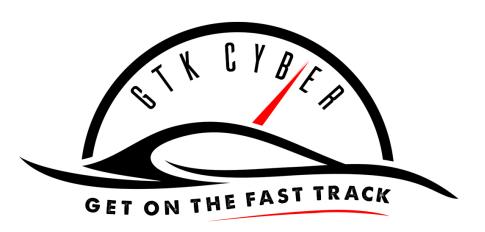
# Pseudo Code for Web App Authentication

```
username = "charles"
password = "12345" //Combination an idiot would use on their luggage
query = "SELECT *
FROM users
WHERE username = charles AND
password = 12345"
query result = db.execute(query)
if len( query result > 0 )
   //Authenticate user
else
   //Boot them out
gtkcyber.com
```



# Pseudo Code for Web App Authentication

```
username = "charles"
password = "12345 OR 1=1" //Combination an idiot would use on
their luggage
query = "SELECT *
FROM users
WHERE username = charles AND
password = 12345 OR 1=1"
query result = db.execute(query)
if len( query result > 0 )
   //Authenticate user
else
atkcyber. Lo Boot them out
```



# Legit vs. Malicious

```
SELECT count(category) FROM Product WHERE price >
'$20'
SELECT ctid, xmin, * FROM lockdemo
SELECT current_date FROM dual
```



# Legit vs. Malicious

```
' or 'unusual' = 'unusual'
' or 'something' = 'some'+'thing'
' or 'text' = n'text'
' or 'something' like 'some%'
```

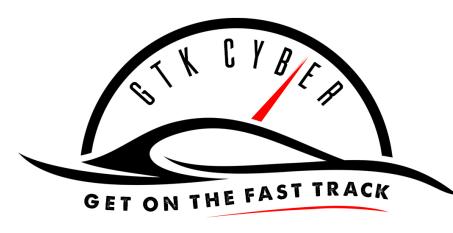


# Step 1: Tokenize SQL

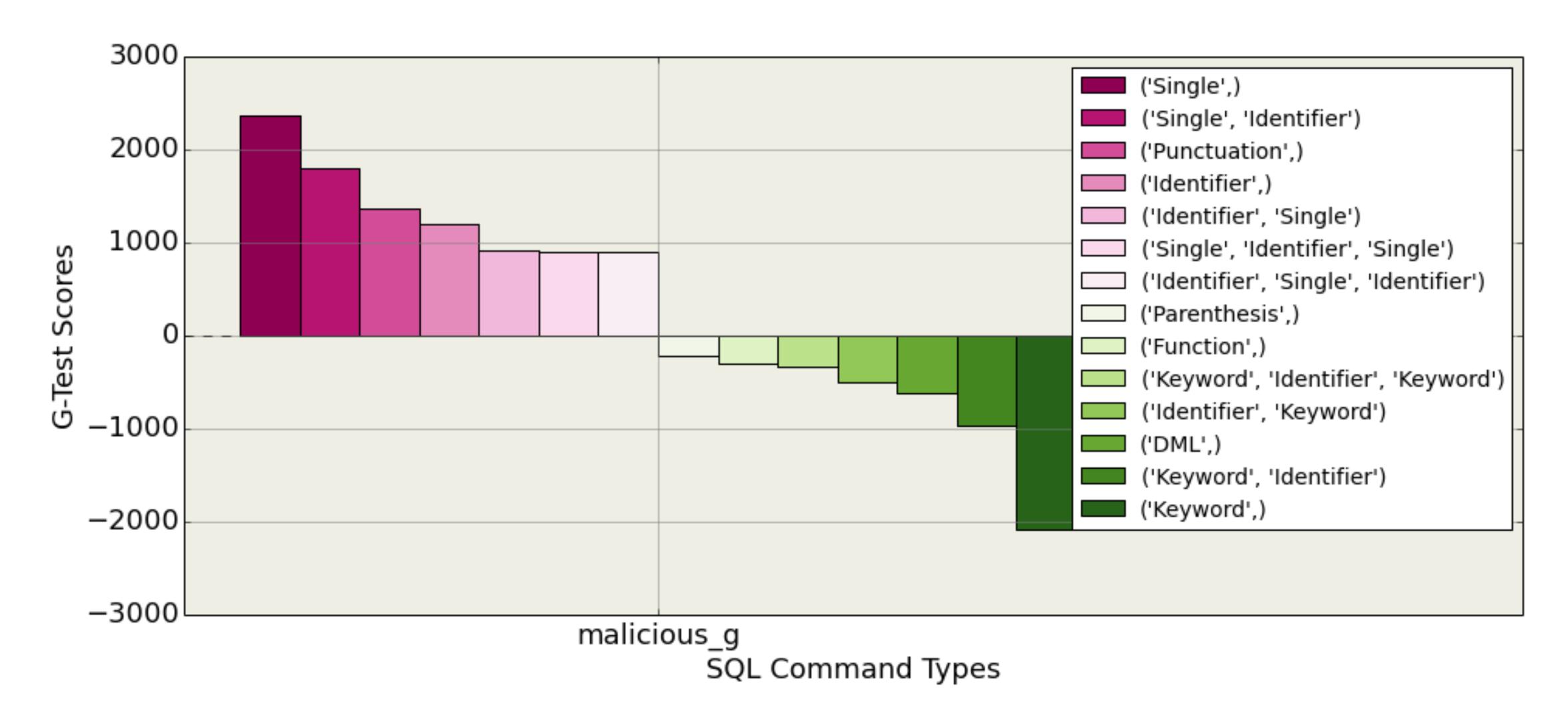
```
import sqlparse
def parse_it(raw_sql):
    parsed = sqlparse.parse(unicode(raw_sql,'utf-8'))
    return [token._get_repr_name() for parse in parsed for token in
parse.tokens if token._get_repr_name() != 'Whitespace']

dataframe['parsed sql'] = dataframe['raw sql'].map(lambda x: parse_it(x))
```

	raw_sql	type	parsed_sql
0	; exec masterxp_cmdshell 'ping	malicious	[Single, Identifier, Float, Float, Float,
1	create user name identified by	malicious	[DDL, Keyword, Identifier, Keyword,
2	create user name identified by pass123	malicious	[DDL, Keyword, Identifier, Keyword,
3	exec sp_addlogin 'name' , 'password'	malicious	[Keyword, Identifier, IdentifierList]
4	exec sp_addsrvrolemember 'name',	malicious	[Keyword, Identifier, IdentifierList]



# Step 2: Create N-Grams



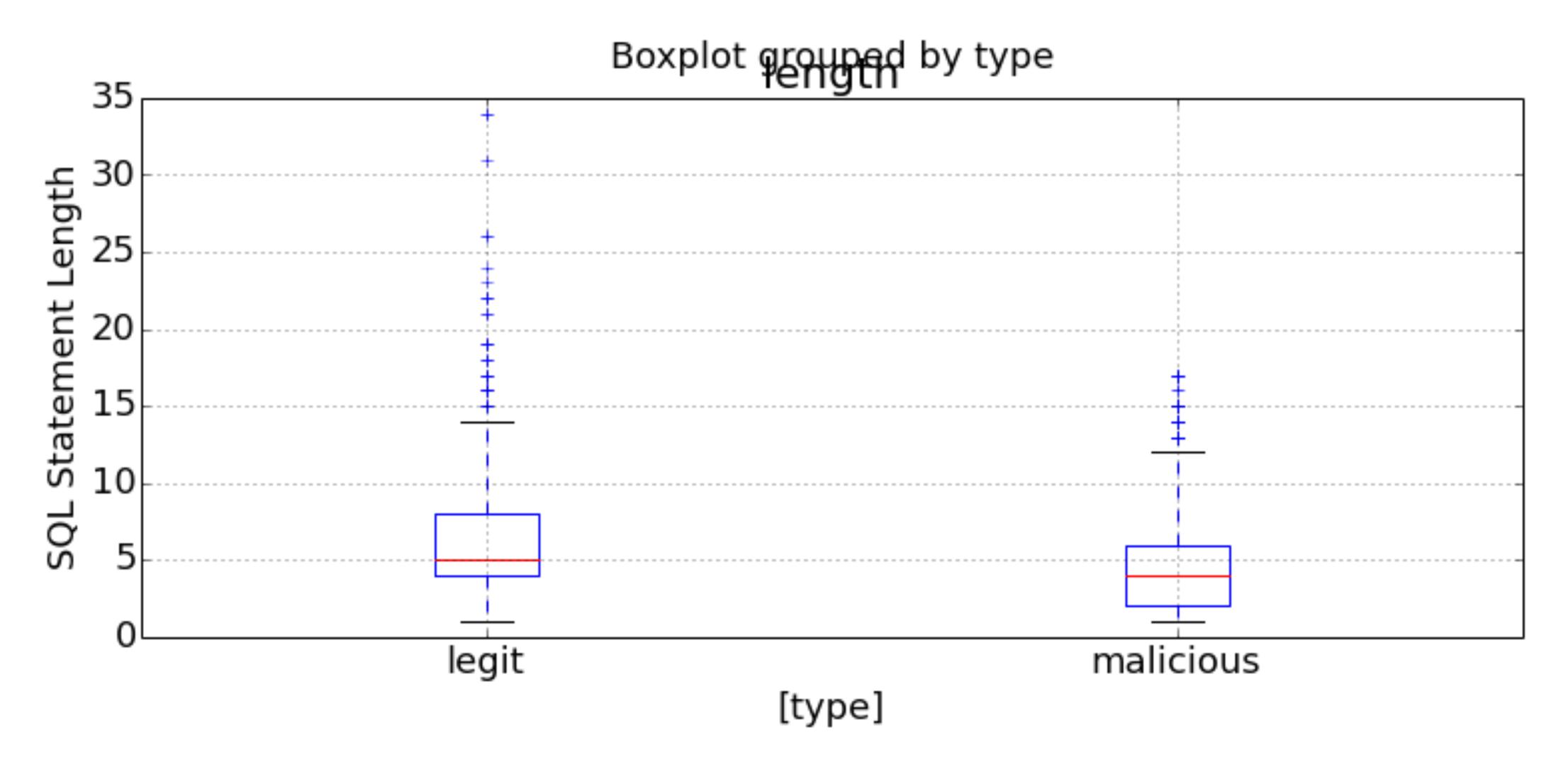
# Step 2: Create N-Grams

	raw_sql	type	parsed_sql	sequences
0	; exec masterxp_cmdshell 'ping 10.10.1.2'	malicious	[Single, Identifier, Float, Float, Float, Erro	[('Single',), ('Identifier',), ('Float',), ('F
44	anything' or 'x'='x	malicious	[Identifier, Single, Identifier, Single, Ident	[('Identifier',), ('Single',), ('Identifier',)
	; exec masterxp_cmdshell 'ping aaa.bbb.ccc	malicious	[Single, Identifier, Error, Single]	[('Single',), ('Identifier',), ('Error',), ('S
54	; if not(select system_user) <> 'sa' waitfor	malicious		[('Single',), ('Identifier',), ('Single',), ('
55	; if is_srvrolemember('sysadmin') > 0 waitfor	malicious	[Single, Identifier, Single, Integer, Placehol	[('Single',), ('Identifier',), ('Single',), ('

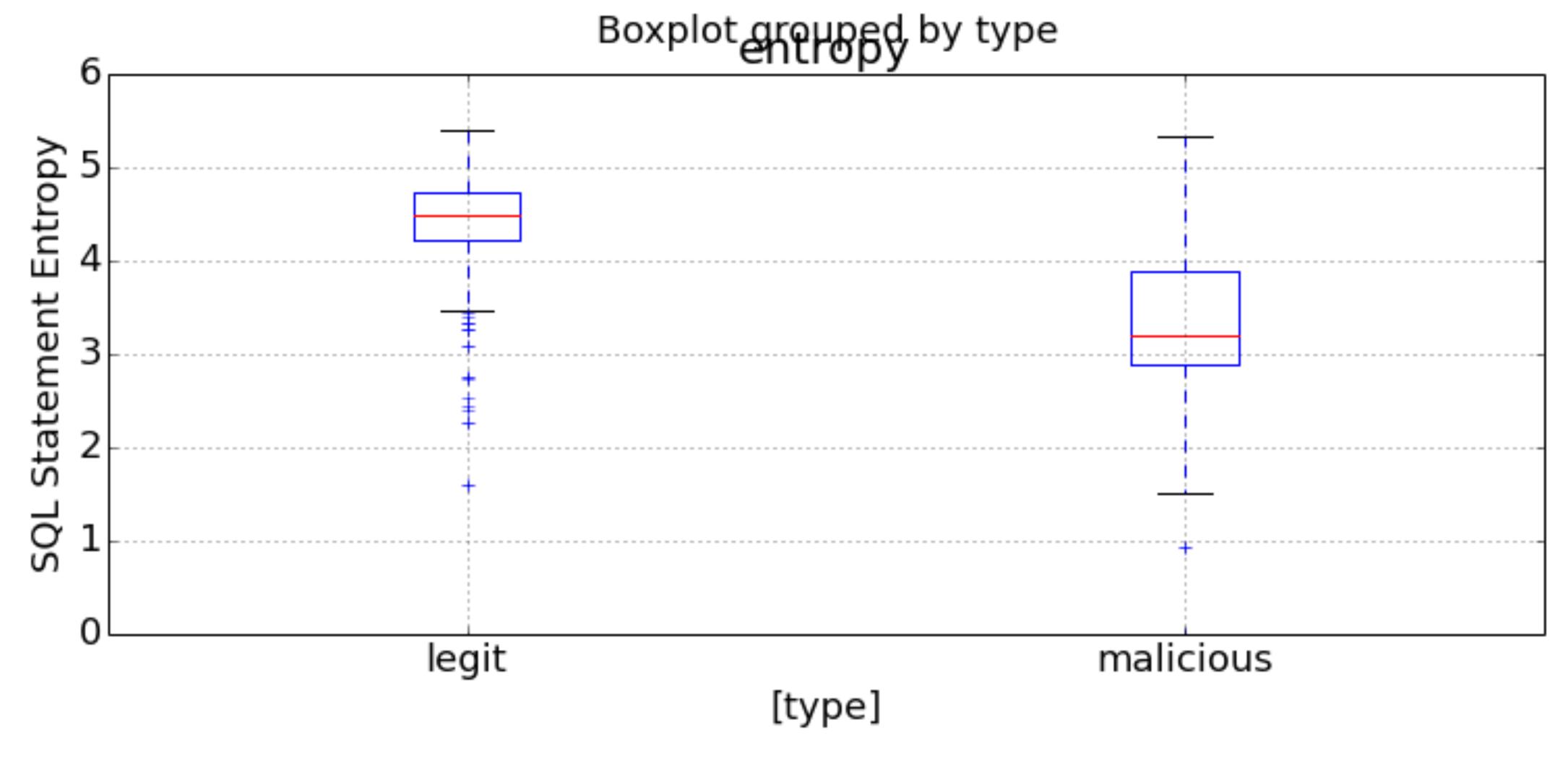


- Entropy
- Length
- G-Score Test

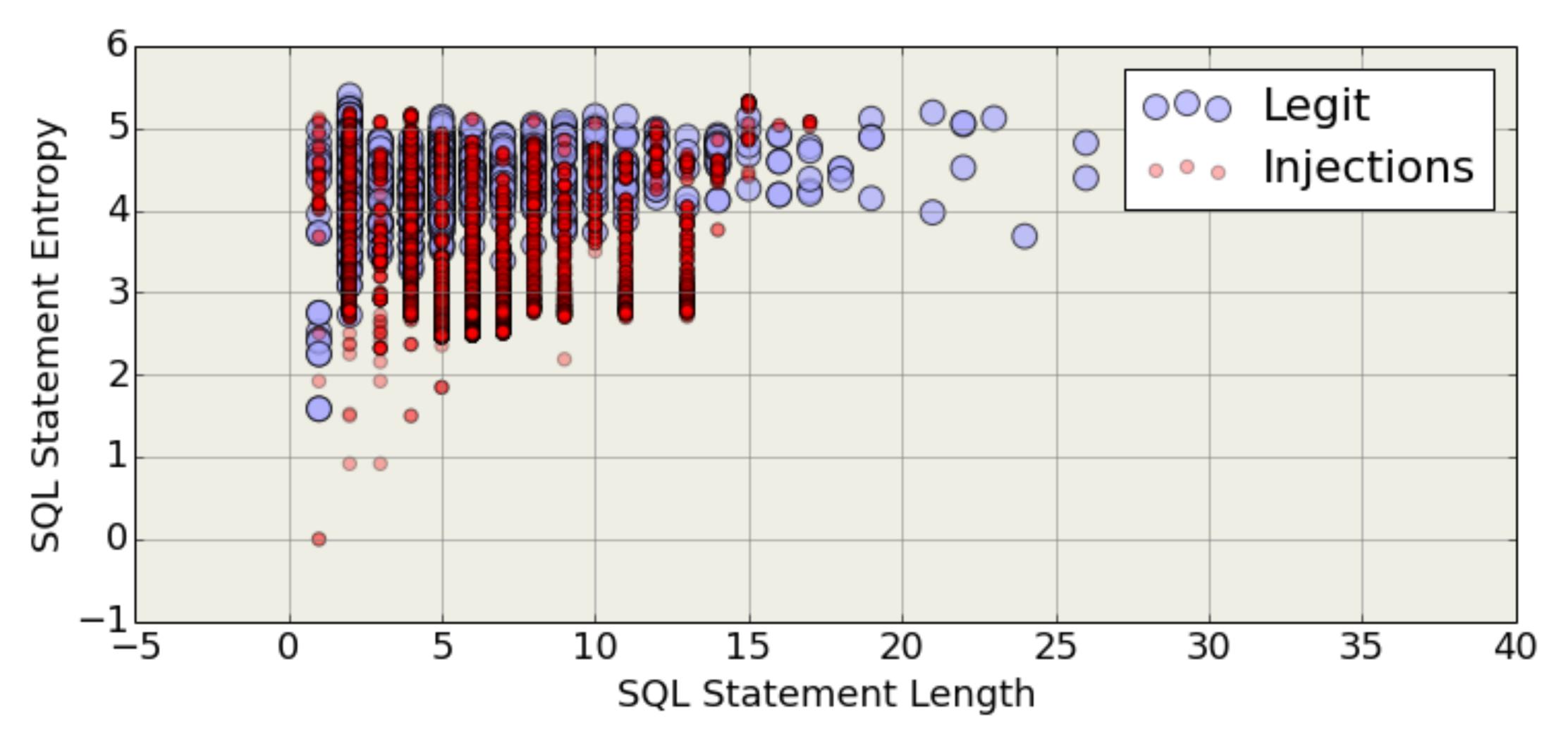




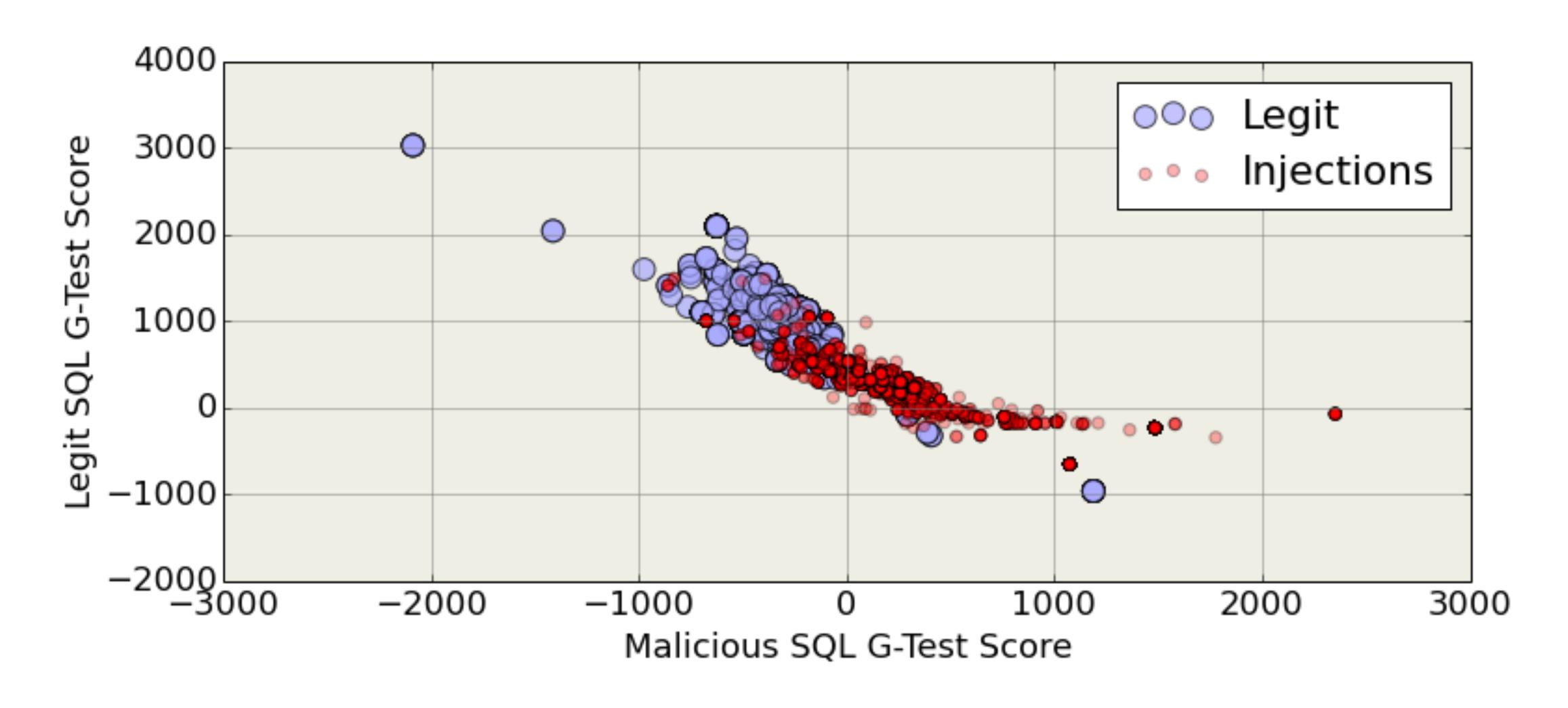














# Step 4: Train Classifier

```
import sklearn.ensemble
clf =
sklearn.ensemble.RandomForestClassifier(n_estimators=20)
scores = sklearn.cross_validation.cross_val_score(clf, X, y, cv=10, n_jobs=4)
print scores
```

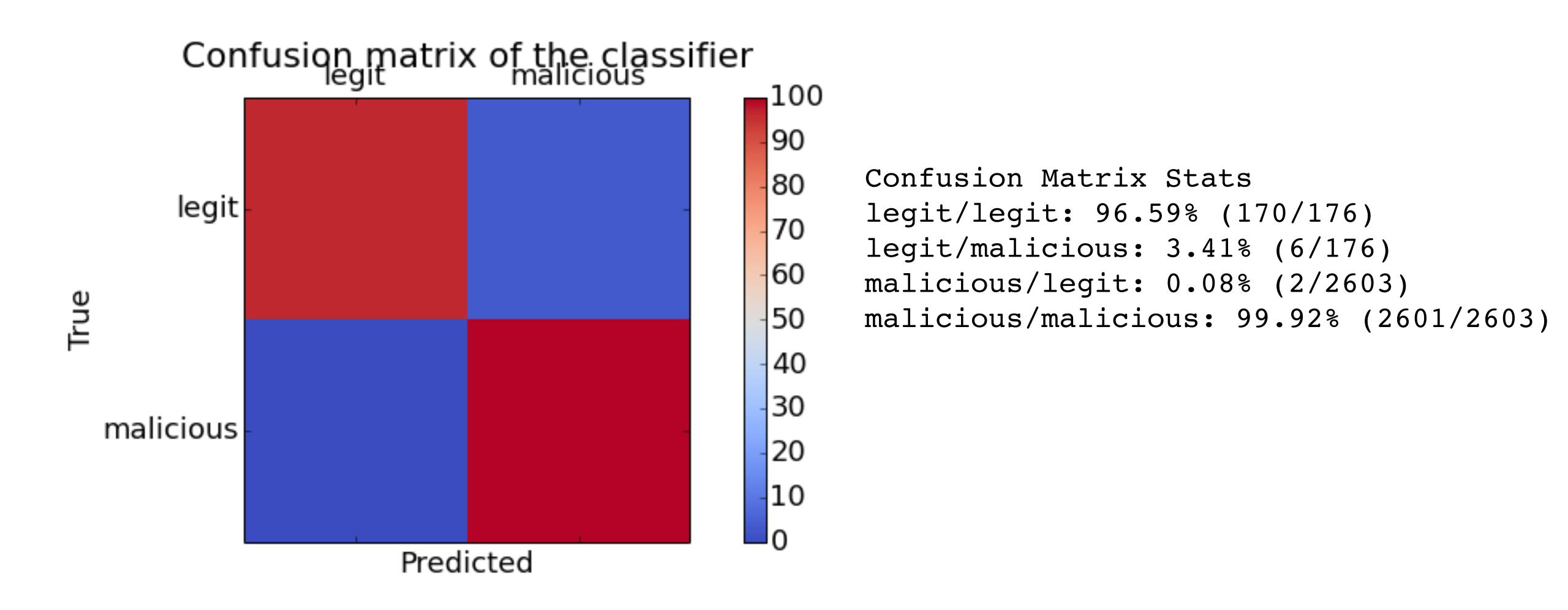


# Step 5: Evaluate Model

```
scores = sklearn.cross_validation.cross_val_score(clf, X, y,
cv=10, n_jobs=4)
```



## Step 5: Evaluate Model





# Thank you!