In [1]:
```
import pandas as pd
import numpy as np
from sklearn import metrics
from sklearn.model_selection import train_test_split
from sklearn.tree import DecisionTreeClassifier
import matplotlib.pyplot as plt
import warnings
warnings.filterwarnings('ignore')
```

In [4]:
```
df_pill = pd.read_csv('C:/Users/Isaac/Desktop/IHD/EBAC DT/CIENCIA DE DATOS/M24 DS/drugs.csv')
df_pill.head()
```

Out[4]:

	Age	Sex	BP	Cholesterol	Na_to_K	Drug
0	23	F	HIGH	HIGH	25.355	drugY
1	47	M	LOW	HIGH	13.093	drugC
2	47	M	LOW	HIGH	10.114	drugC
3	28	F	NORMAL	HIGH	7.798	drugX
4	61	F	LOW	HIGH	18.043	drugY

In [5]:
```
# definimos columnas para 'x' y 'y'

feature_cols = ['Age','Sex','BP','Cholesterol','Na_to_K']
X = df_pill[feature_cols].values
y = df_pill.Drug
```

In [7]:
```
# convertimos variables categoricas en cuantitativas con 'preprocessing'

from sklearn import preprocessing

cod_sex = preprocessing.LabelEncoder()
cod_sex.fit(['F','M'])
X[:,1] = cod_sex.transform(X[:,1])

cod_bp = preprocessing.LabelEncoder()
cod_bp.fit(['HIGH','LOW','NORMAL'])
X[:,2] = cod_bp.transform(X[:,2])

cod_cho = preprocessing.LabelEncoder()
cod_cho.fit(['HIGH','NORMAL'])
X[:,3] = cod_cho.transform(X[:,3])
```

USAMOS RANDOM FOREST

```
from sklearn.ensemble import RandomForestClassifier
```

In [ ]:
```
# creamos grupos de entrenamiento y prueba

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.2, random_state = 1)
```

In [24]:
```
# inicializamos el metodo

rf = RandomForestClassifier(n_estimators = 100, random_state = 1)
```

In [25]:
```
# entrenamos el modelo

rf.fit(X_train, y_train)
```

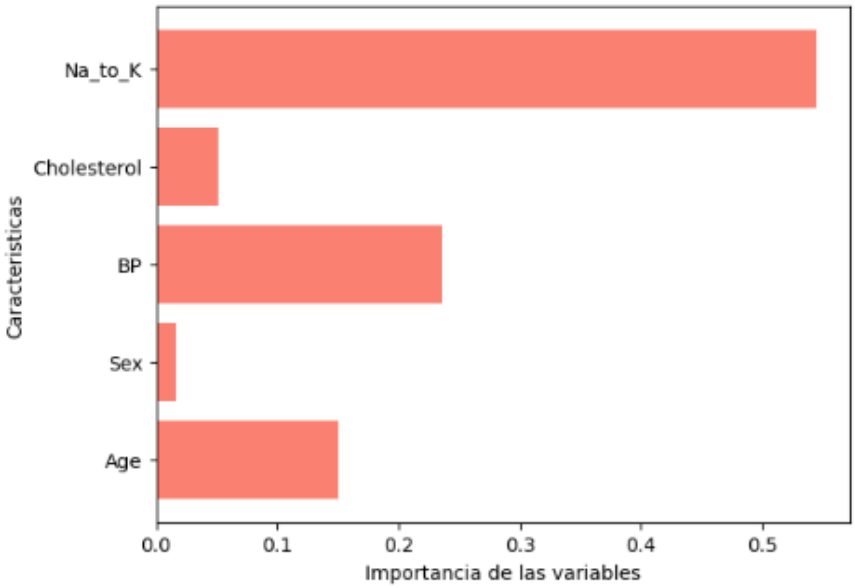
Out[25]:
```
RandomForestClassifier(random_state=1)
```

In [26]:
```
# realizamos predicciones

rf_pred = rf.predict(X_test)
```

In [27]:
```
# estadisticas de desempeño

from sklearn.metrics import classification_report
print(classification_report(y_test, rf_pred))
```

```
              precision    recall  f1-score   support

       drugA       1.00      1.00      1.00         4
       drugB       1.00      1.00      1.00         2
       drugC       1.00      0.75      0.86         4
       drugX       0.93      1.00      0.96        13
       drugY       1.00      1.00      1.00        17

    accuracy                           0.97        40
   macro avg       0.99      0.95      0.96        40
weighted avg       0.98      0.97      0.97        40
```

In [34]:
```
# creamos una funcion para imprimir las variables mas importantes

def plot_features_imp(df_pill, model):
    n_features = feature_cols
    plt.barh(n_features, model.feature_importances_, align = 'center', color = 'salmon')
    plt.xlabel('Importancia de las variables')
    plt.ylabel('Caracteristicas')
    plt.show()

plot_features_imp(df_pill, rf)
```



USAMOS GRADIENT BOOSTED TREE

In [18]:
```
from sklearn.ensemble import GradientBoostingClassifier
```

In [19]:
```
# creamos grupos de entrenamiento y pruebas

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.2, random_state = 1)
```

In [28]:
```
# inicalizamos el modelo

gbt = GradientBoostingClassifier(n_estimators = 100, random_state = 1)
```

In [29]:
```
# entrenamos el modelo

gbt.fit(X_train, y_train)
```

Out[29]:
```
GradientBoostingClassifier
GradientBoostingClassifier(random_state=1)
```

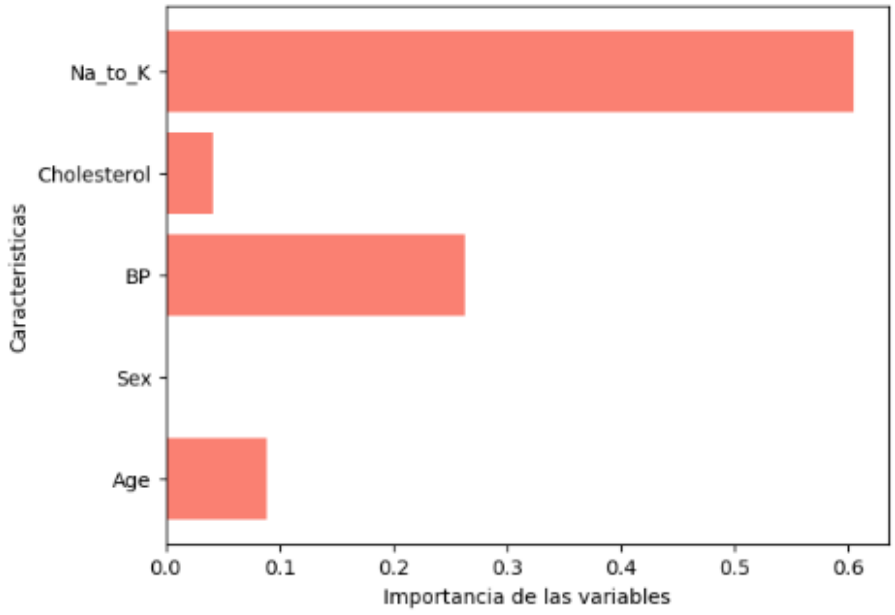
In [30]:
```
# realizamos predicciones

gbt_pred = gbt.predict(X_test)
```

In [33]:
```
# estadisticas de desempeño

print(classification_report(y_test, gbt_pred))
```

```
              precision    recall  f1-score   support

       drugA       1.00      1.00      1.00         4
       drugB       1.00      1.00      1.00         2
       drugC       1.00      1.00      1.00         4
       drugX       1.00      1.00      1.00        13
       drugY       1.00      1.00      1.00        17

    accuracy                           1.00        40
   macro avg       1.00      1.00      1.00        40
weighted avg       1.00      1.00      1.00        40
```

Con el Modelo GBT obtuvimos resultados excelentes, la Precision Global es de 1.0 y para los Score F1 en todos los medicamentos dio un valor de 1.0. Con estos resultados podemos recomedar cualquiera de los 5 medicamentos.

In [35]:
```
# graficamos

plot_features_imp(df_pill, gbt)
```



Probamos el modelo que mejor dio resultados con los valores indicados en la practica.

- En este caso es el modelo GBT

Variable a pronosticar:

Age	Sex	BP	Cholesterol	Na_to_K	Drug
23	F	HIGH	HIGH	25.355	drugY
47	M	LOW	HIGH	13.093	drugC
47	M	LOW	HIGH	10.114	drugC
28	F	NORMAL	HIGH	7.798	drugX
61	F	LOW	HIGH	18.043	drugY
22	F	NORMAL	HIGH	8.607	drugX
49	F	NORMAL	HIGH	16.275	drugY
41	M	LOW	HIGH	11.037	drugC

In [36]:
```
df_pronosticar = {'Age': 23,'Sex': 'F','BP': 'HIGH','Cholesterol': 'HIGH','Na_to_K': 25.355,
                  'Age': 47,'Sex': 'M','BP': 'LOW','Cholesterol': 'HIGH','Na_to_K': 13.093,
                  'Age': 47,'Sex': 'M','BP': 'LOW','Cholesterol': 'HIGH','Na_to_K': 10.114,
                  'Age': 28,'Sex': 'F','BP': 'NORMAL','Cholesterol': 'HIGH','Na_to_K': 7.798,
                  'Age': 61,'Sex': 'F','BP': 'LOW','Cholesterol': 'HIGH','Na_to_K': 18.043,
                  'Age': 22,'Sex': 'F','BP': 'NORMAL','Cholesterol': 'HIGH','Na_to_K': 8.607,
                  'Age': 49,'Sex': 'F','BP': 'NORMAL','Cholesterol': 'HIGH','Na_to_K': 16.275,
                  'Age': 41,'Sex': 'M','BP': 'LOW','Cholesterol': 'HIGH','Na_to_K': 11.037}

df_pronosticar['Sex'] = cod_sex.transform([df_pronosticar['Sex']])[0]
df_pronosticar['BP'] = cod_bp.transform([df_pronosticar['BP']])[0]
df_pronosticar['Cholesterol'] = cod_cho.transform([df_pronosticar['Cholesterol']])[0]
```

In [39]:
```
df_array = np.array([[df_pronosticar['Age'], df_pronosticar['Sex'],
                      df_pronosticar['BP'], df_pronosticar['Cholesterol'], df_pronosticar['Na_to_K']]])

df_array
```

Out[39]:
```
array([[41.   ,  1.   ,  1.   ,  0.   , 11.037]])
```

In [42]:
```
# realizamos las predicciones usando GBT

pred_drug = gbt.predict(df_array)
print('La recomendación para este grupo de personas es el Medicamento:' , pred_drug[0])
```

```
La recomendación para este grupo de personas es el Medicamento: drugC
```