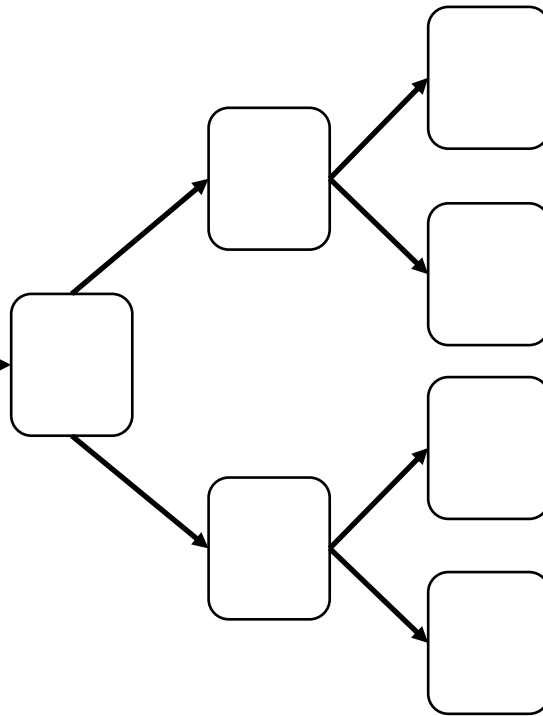


**$X, Y$**

Filtered and Normalized  
Single Cell RNA-Seq Dataset  
 $X$  = Gene expression  
 $Y$  = Cell types



`Sklearn.tree.DecisionTreeClassifier`

**$M(X)$**

$M(X)$  = Tree model for  $X$