Lab04: Decision Tree and Naive Bayes

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- Student name: Âu Dương Khang

```
md"""
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"""
```

How to do your homework

You will work directly on this notebook; the word TODO indicate the parts you need to do.

You can discuss ideas with classmates as well as finding information from the internet, book, etc...; but this homework must be your.

How to submit your homework

• Before submitting, save this file as <ID>.jl. For example, if your ID is 123456, then your file will be 123456.jl. And export to PDF with name 123456.pdf then submit zipped source code and pdf into 123456.zip onto Moodle.

Danger

Note that you will get o point for the wrong submit.

Contents:

- Decision Tree
- Naive Bayes

Import library

```
    begin
    using Distributions , Plots , LinearAlgebra , Random , Statistics
    end
```

```
MersenneTwister(2022)
```

Random.seed!(2022)

Load Iris dataset

download_dataset (generic function with 2 methods)

```
# If you use Linux, use this function to download Iris dataset
function download_dataset(save_path::String="data")
# setup directory
mkpath(joinpath(dirname(@__FILE__), save_path))
data_dir = joinpath(dirname(@__FILE__), save_path)
download("https://archive.ics.uci.edu/static/public/53/iris.zip",joinpath(data_dir, "iris.zip"))
iris_file = joinpath(data_dir, "iris.zip")
cd(data_dir)
run('unzip $iris_file -d $data_dir')
rm(iris_file)
cd("..")
end
```

```
# If you have downloaded the dataset yet, please uncomment this line below and run this cell. Otherwise, keep it in uncomment state.
# download_dataset()
```

iris_dataloader (generic function with 2 methods)

```
• function iris_dataloader(data_path::String="data/iris.data")
      # Initialize empty arrays to store data
      sepal_length = Float64[]
      sepal_width = Float64[]
      petal_length = Float64[]
      petal_width = Float64[]
     classes = Int64[]
      # open and read the data file
      open(data_path, "r") do file
          # read data each line
          for line in eachline(file)
              if line != ""
                  parts = split(line, ",")
                  push!(sepal_length, parse(Float64, parts[1]))
                  push!(sepal_width, parse(Float64, parts[2]))
                  push!(petal_length, parse(Float64, parts[3]))
                  push!(petal_width, parse(Float64, parts[4]))
                  if parts[5] == "Iris-setosa"
                      push!(classes, 0)
                  elseif parts[5] == "Iris-versicolor"
                      push!(classes, 1)
                  else
                      push!(classes, 2)
                  end
              end
         end
      end
      # concat features
      features = [sepal_length, sepal_width, petal_length, petal_width]
      features = vcat(transpose.(features)...)
      return features, classes
end
```

```
• # function change_class_to_num(y)
• # class = Dict("setosa"=> 0,"versicolor"=> 1, "virginica" => 2)
• # classnums = [class[item] for item in y]
• # return classnums
• # end
```

end

train_test_split (generic function with 2 methods)

function train_test_split(X, y, test_ratio=0.33)

X = X'
n = size(X)[1]
idx = shuffle(1:n)
train_size = 1 - test_ratio
train_idx = view(idx, 1:floor(Int, train_size*n))
test_idx = view(idx, (floor(Int, train_size*n)+1):n)

X_train = X[train_idx,:]
X_test = X[test_idx,:]

y_train = y[train_idx]
y_test = y[test_idx]

```
((100, 4), (50, 4), (100), (50))

• begin

• # Load features, and labels for Iris dataset

• iris_features, iris_labels = iris_dataloader("data/iris.data")

• #split dataset into training data and testing data

• X_train, X_test, y_train, y_test = train_test_split(iris_features, iris_labels, 0.33)

• size(X_train), size(X_test), size(y_train), size(y_test)

• end
```

1. Decision Tree: Iterative Dichotomiser 3 (ID3)

1.1 Information Gain

Expected value of the self-information (entropy):

return X_train, X_test, y_train, y_test

$$Entropy = -\sum_{i}^{n}p_{i}log_{2}(p_{i})$$

The entropy function gets the smallest value if there is a value of p_i equal to 1, reaches the maximum value if all p_i are equal. These properties of the entropy function make it is an expression of the disorder, or randomness of a system, ...

entropy

Parameters:

- counts: shape (n_classes): list number of samples in each class
- n_samples: number of data samples

Returns

entropy

```
Parameters:
- 'counts': shape (n_classes): list number of samples in each class
- 'n_samples:' number of data samples

Returns
- entropy
"""

function entropy(counts, n_samples)

#TODO
entropy = 0
for count in counts

p_i = count / n_samples
entropy -= p_i * log2(p_i)
end

return entropy

end
```

entropy_of_one_division

Returns entropy of a divided group of data

Data may have multiple classes

```
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Data may have multiple classes
"""

function entropy_of_one_division(division)

n_samples = size(division, 1)
n_classes = Set(division)

counts=[]

# count samples in each class then store it to list counts
#TODO:
counts = [count(x -> x == n_class, division) for n_class in n_classes]

return entropy(counts,n_samples),n_samples

end
```

get_entropy

Returns entropy of a split

y_predict is the split decision by cutoff, True/Fasle

```
Returns entropy of a split

y_predict is the split decision by cutoff, True/Fasle
"""

function get_entropy(y_predict, y)

n = size(y,1)

# left hand side entropy
entropy_true, n_true = entropy_of_one_division(y[y_predict])

# right hand side entropy
entropy_false, n_false = entropy_of_one_division(y[.~y_predict])

# overall entropy
#TODO s=?

s = entropy_true * n_true / n + entropy_false * n_false / n
return s
end
```

The information gain of classifying information set D by attribute A:

$$Gain(A) = Entrophy(D) - Entrophy_A(D)$$

At each node in ID3, an attribute is chosen if its information gain is highest compare to others.

All attributes of the Iris set are represented by continuous values. Therefore we need to represent them with discrete values. The simple way is to use a cutoff threshold to separate values of the data on each attribute into two part: <cutoff and > = cutoff.

To find the best cutoff for an attribute, we replace cutoff with its values then compute the entropy, best cutoff achieved when value of entropy is smallest $(\arg\min Entrophy_A(D))$.

```
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"""
```

1.2 Decision tree

dtfit

Parameters:

- X: training data
- y: label of training data

Returns

node

node: each node represented by cutoff value and column index, value and children.

- cutoff value is thresold where you divide your attribute.
- column index is your data attribute index.
- value of node is mean value of label indexes, if a node is leaf all data samples will have same label.

Note that: we divide each attribute into 2 part => each node will have 2 children: left, right.

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  will have same label.

    Note that: we divide each attribute into 2 part => each node will have 2 children:

  left, right.
 function dtfit(X, y, node=Dict(), depth=0)
      #Stop conditions
      #if all value of y are the same
      if all(y.==y[1])
          return Dict("val"=>y[1])
      else
          # find one split given an information gain
          col_idx, cutoff, entropy = find_best_split_of_all(X, y)
          y_left = y[X[:,col_idx] .< cutoff]</pre>
```

find_best_split_of_all

Parameters:

- X: training data
- y: label of training data

Returns

• column index, cut-off value, and minimum entropy

```
. . .
Parameters:
• - X: training data
• - y: label of training data

    Returns

    - column index, cut-off value, and minimum entropy

function find_best_split_of_all(X, y)
      col_idx = nothing
      min_entropy = 1
      cutoff = nothing
      for i in 1:size(X,2)
          col_data = X[:,i]
          entropy, cur_cutoff = find_best_split(col_data, y)
          # best entropy
          if entropy == 0
              return i, cur_cutoff, entropy
          elseif entropy <= min_entropy</pre>
              min_entropy = entropy
              col_idx = i
              cutoff = cur_cutoff
          end
      end
      return col_idx, cutoff, min_entropy
end
```

find_best_split

Parameters:

- col_data: data samples in column
- y: label of training data

Returns

• minimum entropy, and cut-off value

```
. . .
Parameters:
- col_data: data samples in column
• - y: label of training data

    Returns

- minimum entropy, and cut-off value

    function find_best_split(col_data, y)

      min_entropy = 10
      cutoff = 0
      #Loop through col_data find cutoff where entropy is minimum
      for value in Set(col_data)
          y_predict = col_data .< value</pre>
          my_entropy = get_entropy(y_predict, y)
          #TODO
          #min entropy=?, cutoff=?
          if my_entropy <= min_entropy</pre>
              min_entropy = my_entropy
              cutoff = value
          end
      end
      return min_entropy, cutoff
end
```

dtpredict (generic function with 1 method)

```
function dtpredict(tree, data)
pred = []
n_sample = size(data, 1)
for i in 1:n_sample
push!(pred, _dtpredict(tree, data[i,:]))
end
return pred
end
```

end

end

_dtpredict (generic function with 1 method)

• function _dtpredict(tree, row)

• cur_layer = tree

• while haskey(cur_layer, "cutoff")

• if row[cur_layer["index_col"]] < cur_layer["cutoff"]

• cur_layer = cur_layer["left"]

• else

• cur_layer = cur_layer["right"]

• end

• end

• if !haskey(cur_layer, "cutoff")

• return get(cur_layer, "val", false)</pre>

1.3 Classification on Iris Dataset

tpfptnfn_cal (generic function with 2 methods)

```
    function tpfptnfn_cal(y_test, y_pred, positive_class=1)

     true_positives = 0
     false_positives = 0
     true_negatives = 0
     false_negatives = 0
     # Calculate true positives, false positives, false negatives, and true negatives
     for (true_label, predicted_label) in zip(y_test, y_pred)
         if true_label == positive_class && predicted_label == positive_class
             true_positives += 1
         elseif true_label != positive_class && predicted_label == positive_class
             false_positives += 1
         elseif true_label == positive_class && predicted_label != positive_class
             false_negatives += 1
         elseif true_label != positive_class && predicted_label != positive_class
              true_negatives += 1
         end
     end
     return true_positives, false_positives, true_negatives, false_negatives
end
```

```
    begin

     pred = dtpredict(tree, X_test)
     acc = 0
     precision = 0
     recall = 0
     f1 = 0
     for i \in [0, 1, 2]
          # Calculate true positives, false positives, false negatives, and true
         negatives
          true_positives, false_positives, true_negatives, false_negatives =
     tpfptnfn_cal(y_test, pred, i)
          # Calculate precision, recall, and F1-score
         acc += (true_positives + true_negatives) / (true_positives + false_positives
         + true_negatives + false_negatives)
         precision += true_positives / (true_positives + false_positives)
         recall += true_positives / (true_positives + false_negatives)
     end
     acc = acc / 3
     precision = precision / 3
     recall = recall / 3
     f1 = 2 * precision * recall / (precision + recall)
     print(" acc: $acc\n precision: $precision\n recall: $recall\n f1_score: $f1\n")
end
```

```
acc: 0.96 ②
precision: 0.9523809523809524
recall: 0.923076923076923
f1_score: 0.9375
```

2. Bayes Theorem

Bayes formulation
$$P\left(A|B\right) = \frac{P\left(B|A\right)P\left(A\right)}{P\left(B\right)}$$

If \boldsymbol{B} is our data $\boldsymbol{\mathcal{D}}$, \boldsymbol{A} and \boldsymbol{w} are parameters we need to estimate:

$$\underbrace{P(w|\mathcal{D})}_{Posterior} = \underbrace{\frac{1}{P(\mathcal{D})}}_{Normalization} \underbrace{\underbrace{P(\mathcal{D}|w)P(w)}_{Likelihood} \underbrace{Prior}_{P(\mathcal{D}|w)P(w)}$$

Naive Bayes

To make it simple, it is often assumed that the components of the D random variable (or the features of the D data) are independent with each other, if w is known. It mean:

$$P(\mathcal{D}|w) = \prod_{i=1}^d P(x_i|w)$$

• d: number of features

2.1. Probability Density Function

```
update (generic function with 1 method)
```

```
    #update histogram for new data

function update(_hist, _mean, _std, data)
     P(hypo/data)=P(data/hypo)*P(hypo)*(1/P(data))
     hist = copy(_hist)
     #P(hypo/data)=P(data/hypo)*P(hypo)*(1/P(data))
     #Likelihood * Prior
     #TODO
     s = 0
     for hypo in keys(hist)
         hypo_likelihood = hist[hypo] * likelihood(_mean, _std, data, hypo)
         hist[hypo] = hypo_likelihood
          s+= hypo_likelihood
     end
     #Normalization
     #TODO: s=P(data)
     #s=?
     for hypo in keys(hist)
         hist[hypo] = hist[hypo]/s
     end
     return hist
end
```

maxHypo (generic function with 1 method)

```
function maxHypo(hist)
    #find the hypothesis with maximum probability from hist
    #TODO
    max_value_index = argmax(collect(values(hist)))
    max_keys = collect(keys(hist))
    return max_keys[max_value_index]
end
```

2.2 Classification on Iris Dataset

Gaussian Naive Bayes

- Naive Bayes can be extended to use on continuous data, most commonly by using a normal distribution (Gaussian distribution).
- This extension called Gaussian Naive Bayes. Other functions can be used to estimate data distribution, but Gauss (or the normal distribution) is the easiest to work with since we only need to estimate the mean and standard deviation from the training data.

Define Gauss function

$$f\left(x;\mu,\sigma
ight)=rac{1}{\sigma\sqrt{2\pi}}\mathrm{exp}\left(-rac{\left(x-\mu
ight)^{2}}{2\sigma^{2}}
ight)$$

Gauss (generic function with 1 method)

```
    function Gauss(std, mean, x)
    #Compute the Gaussian probability distribution function for x
    #TODO
    return (1.0 / (std * sqrt(2 * π))) * exp(-((x - mean)^2) / (2 * std^2))
    end
```

likelihood (generic function with 5 methods)

gfit (generic function with 4 methods)

```
function gfit(X, y, _std=nothing, _mean=nothing, _hist=nothing)
     """Parameters:
     X: training data
     y: labels of training data
     n=size(X,1)
     #number of iris species
     #TODO
     #n_species=???
     n_species = length(Set(y))
     hist_dict = Dict()
     mean_dict = Dict()
     std_dict = Dict()
     #separate dataset into rows by class
     for hypo in Set(y)
         #rows have hypo label
         #TODO rows=
         rows = findall(a->a==hypo,y)
         #histogram for each hypo
         #TODO probability=?
         probability = length(rows) / n
         hist_dict[hypo] = probability
         #Each hypothesis represented by its mean and standard derivation
         """mean and standard derivation should be calculated for each column (or each
 attribute)"""
         #TODO mean[hypo]=?, std[hypo]=?
         mean_dict[hypo] = mean(X[rows, :], dims=1)
         std_dict[hypo] = std(X[rows, :], dims=1)
     end
     _mean = mean_dict
     _std = std_dict
     _hist = hist_dict
     return _hist, _mean, _std
end
```

```
_gpredict (generic function with 2 methods)

    function _gpredict(_hist, _mean, _std, data, plot=true)

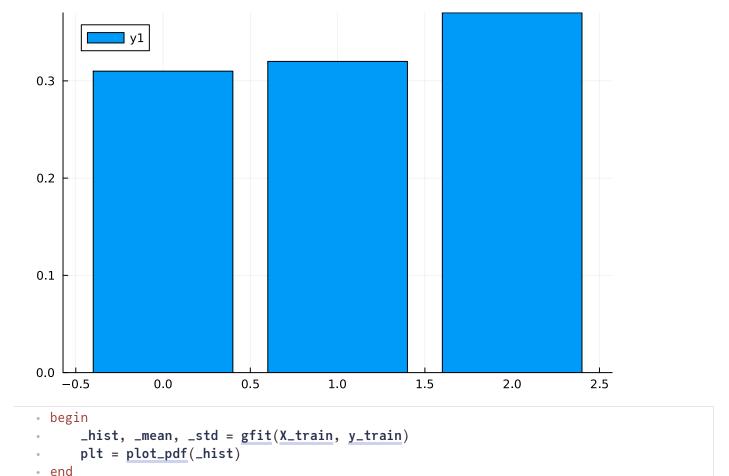
       Predict label for only 1 data sample
       Parameters:
       data: data sample
       plot: True: draw histogram after update new record
       return: label of data
       hist = update(_hist, _mean, _std, data)
       if (plot == true)
           plt = bar(collect(keys(hist)), collect(values(hist)))
       end
       return maxHypo(hist)
 end
plot_pdf (generic function with 1 method)
 function plot_pdf(_hist)
        bar(collect(keys(_hist)), collect(values(_hist)))
 end
gpredict (generic function with 1 method)

    function gpredict(_hist, _mean, _std, data)

       """Parameters:
       Data: test data
       return labels of test data
       \Pi \Pi \Pi
       pred=[]
       n_sample = size(data, 1)
       for i in 1:n_sample
           push!(pred, _gpredict(_hist, _mean, _std, data[i,:]))
       end
       return pred
```

Show histogram of training data

end



Test wih 1 data record

```
begin

#label of test_y[10]

print("Label of X_test[10]: ", y_test[20])

#update model and show histogram with X_test[10]:

print("\nOur histogram after update X_test[10]: ", _gpredict(_hist, _mean, _std, X_test[20,:], true))

end
```

Evaluate your Gaussian Naive Bayes model

```
    begin

      _pred = gpredict(_hist, _mean, _std, X_test)
      _{acc} = 0
      _{p} = 0
      _{r} = 0
      _{f1} = 0
      #TODO: Self-define and calculate accuracy, precision, recall, and f1-score
      # Calculate accuracy, precision, recall, and f1-score
      for i in 1:10
          _true_positives, _false_positives, _true_negatives, _false_negatives =
      tpfptnfn_cal(y_test, _pred)
          _acc += (_true_positives + _true_negatives) / (_true_positives +
      _false_positives + _true_negatives + _false_negatives)
          _p += _true_positives / (_true_positives + _false_positives)
          _r += _true_positives / (_true_positives + _false_negatives)
      end
      _acc /= 10
      _p /= 10
      _r /= 10
      _{f1} = 2 * _{p} * _{r} / (_{p} + _{r})
      print(" acc: $_acc\n precision: $_p\n recall: $_r\n f1_score: $_f1\n")
end
```

TODO: F1, Recall and Precision report