

Lab04: Decision Tree and Naive Bayes

- Student ID:
- Student name:

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 0 point for the wrong submit.


Contents:

- Decision Tree
- Naive Bayes

Import library

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```
1 begin
2     using Distributions, Plots, LinearAlgebra, Random, Statistics
3 end
```

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```
1 Random.seed!(2022)
```

Load Iris dataset

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```
1 # If you use Linux, use this function to download Iris dataset
2 function download_dataset(save_path::String="data")
3     # setup directory
4     mkpath(joinpath(dirname(@__FILE__), save_path))
5     data_dir = joinpath(dirname(@__FILE__), save_path)
6     download("https://archive.ics.uci.edu/static/public
7 /53/iris.zip",joinpath(data_dir, "iris.zip"))
8     iris_file = joinpath(data_dir, "iris.zip")
9     cd(data_dir)
10    run(`unzip $iris_file -d $data_dir`)
11    rm(iris_file)
12    cd("..")
13 end
```


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

```
1 # If you don't use Linux, I have no solution for you. Please mkdir data, and goto
   https://archive.ics.uci.edu/dataset/53/iris for downloading
2 # Then, you can extract data to this dir by yourself.
3
4 # Structure:
5 # └─ data
6 #     └─ bezdekIris.data
7 #     └─ Index
8 #     └─ iris.data
9 #     └─ iris.names
10 # └─ Lab4.jl
```

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```
1 function iris_data_loader(data_path::String="data/iris.data")
2     # Initialize empty arrays to store data
3     sepal_length = Float64[]
4     sepal_width = Float64[]
5     petal_length = Float64[]
6     petal_width = Float64[]
7     classes = Int64[]
8
9     # open and read the data file
10    open(data_path, "r") do file
11        # read data each line
12        for line in eachline(file)
13            if line != ""
14                parts = split(line, ",")
15                push!(sepal_length, parse(Float64, parts[1]))
16                push!(sepal_width, parse(Float64, parts[2]))
17                push!(petal_length, parse(Float64, parts[3]))
18                push!(petal_width, parse(Float64, parts[4]))
19
20                if parts[5] == "Iris-setosa"
21                    push!(classes, 0)
22                elseif parts[5] == "Iris-versicolor"
23                    push!(classes, 1)
24                else
25                    push!(classes, 2)
26                end
27            end
28        end
29    end
30
31    # concat features
32    features = [sepal_length, sepal_width, petal_length, petal_width]
33    features = vcat(transpose.(features)...)
34    return features, classes
35 end
```

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

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```
1 function train_test_split(X, y, test_ratio=0.33)
2     X = X'
3     n = size(X)[1]
4     idx = shuffle(1:n)
5     train_size = 1 - test_ratio
6     train_idx = view(idx, 1:floor(Int, train_size*n))
7     test_idx = view(idx, (floor(Int, train_size*n)+1):n)
8
9     X_train = X[train_idx,:]
10    X_test = X[test_idx,:]
11
12    y_train = y[train_idx]
13    y_test = y[test_idx]
14
15    return X_train, X_test, y_train, y_test
16 end
```

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```
1 begin
2     # Load features, and labels for Iris dataset
3     iris_features, iris_labels = iris_data_loader("data/iris.data")
4
5     #split dataset into training data and testing data
6     X_train, X_test, y_train, y_test = train_test_split(iris_features, iris_labels,
7     0.33)
8
9     size(X_train), size(X_test), size(y_train), size(y_test)
10 end
```


1. Decision Tree: Iterative Dichotomiser 3 (ID3)

1.1 Information Gain

Expected value of the self-information (entropy):

$$Entropy = - \sum_i^n p_i \log_2(p_i)$$


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 an expression of the disorder, or randomness of a system, ...

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```
1 """
2 Parameters:
3 - 'counts': shape (n_classes): list number of samples in each class
4 - 'n_samples': number of data samples
5
6 Returns
7 - entropy
8 """
9 function entropy(counts, n_samples)
10     #TODO
11
12 end
```

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```
1 """
2 Returns entropy of a divided group of data
3
4 Data may have multiple classes
5 """
6 function entropy_of_one_division(division)
7
8     n_samples = size(division, 1)
9     n_classes = Set(division)
10
11     counts=[]
12
13     # count samples in each class then store it to list counts
14     #TODO:
15
16 end
```

 Code not executed in Safe preview

```
1 """
2 Returns entropy of a split
3
4 y_predict is the split decision by cutoff, True/Fasle
5 """
6 function get_entropy(y_predict, y)
7     n = size(y,1)
8     # left hand side entropy
9     entropy_true, n_true = entropy_of_one_division(y[y_predict])
10
11     # right hand side entropy
12     entropy_false, n_false = entropy_of_one_division(y[.~y_predict])
13
14     # overall entropy
15     #TODO s=?
16
17     return s
18 end
```

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

$$Gain(A) = Entropy(D) - Entropy_A(D)$$

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 ($\arg \min Entropy_A(D)$).


```
1 md"""
2 The information gain of classifying information set D by attribute A:
3
4 $$Gain(A)=Entropy(D)-Entropy_{\{A\}}(D)$$
5
6 At each node in ID3, an attribute is chosen if its information gain is highest
  compare to others.
7
8 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'.
9
10 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 $\left
  (\arg \min Entropy_{\{A\}}(D) \right)$.
11 """
```

1.2 Decision tree

```

1  """
2  Parameters:
3  - X: training data
4  - y: label of training data
5
6  Returns
7  - node
8
9  node: each node represented by cutoff value and column index, value and children.
10 - cutoff value is threshold where you divide your attribute.
11 - column index is your data attribute index.
12 - value of node is mean value of label indexes, if a node is leaf all data samples
    will have same label.
13
14 Note that: we divide each attribute into 2 part => each node will have 2 children:
    left, right.
15 """
16 function dtfit(X, y, node=Dict(), depth=0)
17     #Stop conditions
18
19     #if all value of y are the same
20     if all(y.==y[1])
21         return Dict("val"=>y[1])
22
23     else
24         # find one split given an information gain
25         col_idx, cutoff, entropy = find_best_split_of_all(X, y)
26
27         y_left = y[X[:,col_idx] .< cutoff]
28         y_right = y[X[:,col_idx] .>= cutoff]
29
30         node = Dict("index_col"=>col_idx,
31                     "cutoff"=>cutoff,
32                     "val"=> mean(y),
33                     "left"=> Any,
34                     "right"=> Any)
35
36         left = dtfit(X[X[:,col_idx] .< cutoff, :], y_left, Dict(), depth+1)
37         right = dtfit(X[X[:,col_idx] .>= cutoff, :], y_right, Dict(), depth+1)
38
39         push!(node, "left" => left)
40         push!(node, "right" => right)
41
42         depth += 1
43     end
44     return node
45 end

```

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```
1  """
2  Parameters:
3  - X: training data
4  - y: label of training data
5
6  Returns
7  - column index, cut-off value, and minimum entropy
8  """
9  function find_best_split_of_all(X, y)
10     col_idx = nothing
11     min_entropy = 1
12     cutoff = nothing
13
14     for i in 1:size(X,2)
15         col_data = X[:,i]
16         entropy, cur_cutoff = find_best_split(col_data, y)
17
18         # best entropy
19         if entropy == 0
20             return i, cur_cutoff, entropy
21         elseif entropy <= min_entropy
22             min_entropy = entropy
23             col_idx = i
24             cutoff = cur_cutoff
25         end
26     end
27     return col_idx, cutoff, min_entropy
28 end
```

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```
1  """
2  Parameters:
3  - col_data: data samples in column
4  - y: label of training data
5
6  Returns
7  - minimum entropy, and cut-off value
8  """
9  function find_best_split(col_data, y)
10     min_entropy = 10
11     cutoff = 0
12
13     #Loop through col_data find cutoff where entropy is minimum
14
15     for value in Set(col_data)
16         y_predict = col_data .< value
17         my_entropy = get_entropy(y_predict, y)
18
19         #TODO
20         #min entropy=?, cutoff=?
21
22     end
23     return min_entropy, cutoff
24 end
25 end
```


 Code not executed in Safe preview

```
1 function dtpredict(tree, data)
2   pred = []
3   n_sample = size(data, 1)
4   for i in 1:n_sample
5     push!(pred, dtpredict(tree, data[i,:]))
6   end
7   return pred
8 end
```

 Code not executed in Safe preview

```
1 function _dtpredict(tree, row)
2   cur_layer = tree
3   while haskey(cur_layer, "cutoff")
4     if row[cur_layer["index_col"]] < cur_layer["cutoff"]
5       cur_layer = cur_layer["left"]
6     else
7       cur_layer = cur_layer["right"]
8     end
9   end
10  if !haskey(cur_layer, "cutoff")
11    return get(cur_layer, "val", false)
12  end
13 end
```

1.3 Classification on Iris Dataset

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```
1 function tpfpnfn_cal(y_test, y_pred, positive_class=1)
2   true_positives = 0
3   false_positives = 0
4   true_negatives = 0
5   false_negatives = 0
6
7   # Calculate true positives, false positives, false negatives, and true negatives
8   for (true_label, predicted_label) in zip(y_test, y_pred)
9     if true_label == positive_class && predicted_label == positive_class
10      true_positives += 1
11    elseif true_label != positive_class && predicted_label == positive_class
12      false_positives += 1
13    elseif true_label == positive_class && predicted_label != positive_class
14      false_negatives += 1
15    elseif true_label != positive_class && predicted_label != positive_class
16      true_negatives += 1
17    end
18  end
19
20  return true_positives, false_positives, true_negatives, false_negatives
21 end
```

 Code not executed in Safe preview

```
1 tree = dtfit(X_train, y_train)
```

Code not executed in Safe preview

```
1 begin
2   pred = dtpredict(tree, X_test)
3
4   acc = 0
5   precision = 0
6   recall = 0
7   f1 = 0
8
9   for i ∈ [0, 1, 2]
10    # Calculate true positives, false positives, false negatives, and true
    negatives
11    true_positives, false_positives, true_negatives, false_negatives =
    tpfpntfn_cal(y_test, pred, i)
12
13    # Calculate precision, recall, and F1-score
14    acc += (true_positives + true_negatives) / (true_positives + false_positives
    + true_negatives + false_negatives)
15    precision += true_positives / (true_positives + false_positives)
16    recall += true_positives / (true_positives + false_negatives)
17  end
18
19  acc = acc / 3
20  precision = precision / 3
21  recall = recall / 3
22  f1 = 2 * precision * recall / (precision + recall)
23  print(" acc: $acc\n precision: $precision\n recall: $recall\n f1_score: $f1\n")
24 end
```

2. Bayes Theorem

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

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

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

Naïve Bayes

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


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

- d: number of features

2.1. Probability Density Function

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```
1 #update histogram for new data
2 function update(_hist, _mean, _std, data)
3     """
4     P(hypo/data)=P(data/hypo)*P(hypo)*(1/P(data))
5     """
6     hist = copy(_hist)
7     #P(hypo/data)=P(data/hypo)*P(hypo)*(1/P(data))
8
9     #Likelihood * Prior
10    #TODO
11
12    #Normalization
13
14    #TODO: s=P(data)
15    #s=?
16    s = 0
17
18
19    for hypo in keys(hist)
20        hist[hypo] = hist[hypo]/s
21    end
22    return hist
23 end
```

 Code not executed in Safe preview

```
1 function maxHypo(hist)
2     #find the hypothesis with maximum probability from hist
3     #TODO
4
5     return max_hypo
6 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

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

 Code not executed in Safe preview

```
1 function Gauss(std, mean, x)
2     #Compute the Gaussian probability distribution function for x
3     #TODO
4     return (1 ./ (std * sqrt( 2 * pi ))) * exp( -((x .- mean)^2) / (2 * std^2))
5 end
```

 Code not executed in Safe preview

```
1 function likelihood(_mean=nothing, _std=nothing, data=nothing, hypo=nothing)
2     """
3     Returns: res=P(data/hypo)
4     -----
5     Naive bayes:
6         Attributes are assumed to be conditionally independent given the class value.
7     """
8
9     std=_std[hypo]
10    mean=_mean[hypo]
11    res=1
12    #TODO
13    #res=res*P(x1/hypo)*P(x2/hypo)...
14
15    return res
16 end
```

 Code not executed in Safe preview

```
1 function gfit(X, y, _std=nothing, _mean=nothing, _hist=nothing)
2     """Parameters:
3     X: training data
4     y: labels of training data
5     """
6     n=size(X,1)
7     #number of iris species
8     #TODO
9     #n_species=???
10    n_species = length(Set(y))
11
12    hist=Dict()
13    mean=Dict()
14    std=Dict()
15
16    #separate dataset into rows by class
17    for hypo in Set(y)
18        #rows have hypo label
19        #TODO rows=
20
21        #histogram for each hypo
22        #TODO probability=?
23
24        hist[hypo]=probability
25
26        #Each hypothesis represented by its mean and standard derivation
27        """mean and standard derivation should be calculated for each column (or each
attribute)"""
28        #TODO mean[hypo]=?, std[hypo]=?
29
30    end
31    _mean=mean
32    _std=std
33    _hist=hist
34    return _hist, _mean, _std
```

Safe preview ⓘ

 Code not executed in Safe preview

```
1 function _gpredict(_hist, _mean, _std, data, plot=true)
2     """
3     Predict label for only 1 data sample
4     -----
5     Parameters:
6     data: data sample
7     plot: True: draw histogram after update new record
8     -----
9     return: label of data
10    """
11    hist = update(_hist, _mean, _std, data)
12    if (plot == true)
13        plt = bar(collect(keys(hist)), collect(values(hist)))
14    end
15    return maxHypo(hist)
16 end
```

 Code not executed in Safe preview

```
1 function plot_pdf(_hist)
2     bar(collect(keys(_hist)), collect(values(_hist)))
3 end
```

 Code not executed in Safe preview


```
1 function gpredict(_hist, _mean, _std, data)
2     """Parameters:
3     Data: test data
4     -----
5     return labels of test data
6     """
7     pred=[]
8     n_sample = size(data, 1)
9     for i in 1:n_sample
10        push!(pred, _gpredict(_hist, _mean, _std, data[i,:]))
11    end
12    return pred
13 end
```

Show histogram of training data

 Code not executed in Safe preview

```
1 begin
2     _hist, _mean, _std = gfit(X_train, y_train)
3     plt = plot_pdf(_hist)
4 end
```

Test with 1 data record

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```
1 begin
2     #label of test_y[10]
3     print("Label of X_test[10]: ", y_test[20])
4
5     #update model and show histogram with X_test[10]:
6     print("\nOur histogram after update X_test[10]: ", gpredict(_hist, _mean, _std,
7         X_test[20,:], true))
8 end
```

Evaluate your Gaussian Naive Bayes model

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```
1 begin
2     _pred = gpredict(_hist, _mean, _std, X_test)
3
4     _acc = 0
5     _p = 0
6     _r = 0
7     _f1 = 0
8
9     #TODO: Self-define and calculate accuracy, precision, recall, and f1-score
10
11     print(" acc: $_acc\n precision: $_p\n recall: $_r\n f1-score: $_f1\n")
12 end
```

TODO: F1, Recall and Precision report