In [1]:

```python
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
plt.style.use('fivethirtyeight')
import warnings
warnings.filterwarnings('ignore')
%matplotlib inline
```

In [2]:

```python
import os
# 운영체제별 한글 폰트 설정
if os.name == 'posix': # Mac 환경 폰트 설정
    plt.rc('font', family='AppleGothic')
elif os.name == 'nt': # Windows 환경 폰트 설정
    plt.rc('font', family='Malgun Gothic')

plt.rc('axes', unicode_minus=False) # 마이너스 폰트 설정


# 글씨 선명하게 출력하는 설정
%config InlineBackend.figure_format = 'retina'
```

In [3]:

```python
data1 = pd.read_csv('NHIS_OPEN_GJ_2017_100.csv',encoding='euc-kr')
data2 = pd.read_csv('NHIS_OPEN_GJ_2018_100.csv')
```

In [4]:

```python
# 데이터 묶기 + 사용 컬럼만 빼내기
data = pd.concat([data1,data2])
column_m, column_n,column_o, column_z  = '수축기혈압','이완기혈압','식전혈당(공복혈당)'
data = data[[column_m, column_n,column_o, column_z]]
```

In [5]:

```python
data
```

Out[5]:

	수축기혈압	이완기혈압	식전혈당(공복혈당)	흡연상태
0	120.0	80.0	99.0	1.0
1	130.0	82.0	106.0	3.0
2	120.0	70.0	98.0	1.0
3	145.0	87.0	95.0	1.0
4	138.0	82.0	101.0	1.0
...	...	...	...	...
999995	110.0	70.0	107.0	1.0
999996	136.0	88.0	114.0	1.0
999997	162.0	90.0	98.0	2.0
999998	140.0	98.0	94.0	2.0
999999	120.0	80.0	85.0	1.0

2000000 rows × 4 columns

Null 개수 확인

In [6]:

```
data.isnull().sum()
notnull_data = data.dropna(axis =0)

print(data)
print(notnull_data)
```

```
         수축기혈압  이완기혈압  식전혈당(공복혈당)  흡연상태
0        120.0   80.0        99.0   1.0
1        130.0   82.0       106.0   3.0
2        120.0   70.0        98.0   1.0
3        145.0   87.0        95.0   1.0
4        138.0   82.0       101.0   1.0
...        ...    ...         ...   ...
999995   110.0   70.0       107.0   1.0
999996   136.0   88.0       114.0   1.0
999997   162.0   90.0        98.0   2.0
999998   140.0   98.0        94.0   2.0
999999   120.0   80.0        85.0   1.0

[2000000 rows x 4 columns]
         수축기혈압  이완기혈압  식전혈당(공복혈당)  흡연상태
0        120.0   80.0        99.0   1.0
1        130.0   82.0       106.0   3.0
2        120.0   70.0        98.0   1.0
3        145.0   87.0        95.0   1.0
4        138.0   82.0       101.0   1.0
...        ...    ...         ...   ...
999995   110.0   70.0       107.0   1.0
999996   136.0   88.0       114.0   1.0
999997   162.0   90.0        98.0   2.0
999998   140.0   98.0        94.0   2.0
999999   120.0   80.0        85.0   1.0

[1993626 rows x 4 columns]
```

이상치 제거

- 식전혈당 300 이상 데이터 제거
- 혈당 300이상 + 220 /60 수축기, 140/40 이완기 데이터 제거

In [7]:

```
notnull_lower_300_data = notnull_data[notnull_data[column_o]<=300]
sys_cut_data = notnull_lower_300_data[(notnull_lower_300_data[column_m] >= 60
dias_cut_data = sys_cut_data[(sys_cut_data[column_n] >= 40) & (sys_cut_data[c
print(notnull_lower_300_data)
data = dias_cut_data
print(data)
```

```
         수축기혈압  이완기혈압  식전혈당(공복혈당)  흡연상태
0        120.0   80.0        99.0   1.0
1        130.0   82.0       106.0   3.0
2        120.0   70.0        98.0   1.0
3        145.0   87.0        95.0   1.0
4        138.0   82.0       101.0   1.0
...        ...    ...         ...   ...
999995   110.0   70.0       107.0   1.0
999996   136.0   88.0       114.0   1.0
999997   162.0   90.0        98.0   2.0
999998   140.0   98.0        94.0   2.0
999999   120.0   80.0        85.0   1.0

[1990562 rows x 4 columns]
```

```
        수축기혈압  이완기혈압  식전혈당(공복혈당)  흡연상태
0        120.0   80.0      99.0   1.0
1        130.0   82.0     106.0   3.0
2        120.0   70.0      98.0   1.0
3        145.0   87.0      95.0   1.0
4        138.0   82.0     101.0   1.0
...        ...    ...       ...   ...
999995   110.0   70.0     107.0   1.0
999996   136.0   88.0     114.0   1.0
999997   162.0   90.0      98.0   2.0
999998   140.0   98.0      94.0   2.0
999999   120.0   80.0      85.0   1.0

[1990388 rows x 4 columns]
```

In [8]:

```
diabetes = data[data[column_o] >= 126]
diabetes
```

Out[8]:

	수축기혈압	이완기혈압	식전혈당(공복혈당)	흡연상태
11	109.0	69.0	137.0	2.0
37	167.0	84.0	128.0	1.0
75	149.0	90.0	155.0	1.0
76	130.0	80.0	160.0	2.0
85	120.0	74.0	140.0	3.0
...	...	...	...	...
999936	114.0	62.0	137.0	2.0
999940	146.0	101.0	143.0	1.0
999942	132.0	66.0	150.0	1.0
999977	132.0	96.0	160.0	2.0
999991	110.0	76.0	217.0	1.0

152785 rows × 4 columns

전체 인원(널제거, 공복혈당 300이상 제거) : 1990388 당뇨 인원 : 152785

In [9]:

```
total_people = 1990388
total_dia = 152785

p_diabetes = total_dia/total_people
p_not_diabetes = (total_people - total_dia)/total_people

print("당뇨 확률 : %f, 당뇨x 확률 : %f" % (p_diabetes,p_not_diabetes))
P = np.array([p_diabetes,p_not_diabetes])
```

```
당뇨 확률 : 0.076761, 당뇨x 확률 : 0.923239
```

H(parent) 계산

In [10]:

```
h_parent = - ((P[0]*np.log2(P[0]))+ (P[1] * np.log2(P[1])))

print("H(parent) (당뇨병 엔트로피) : %f"%(h_parent))
h_parent
```

```
H(parent) (당뇨병 엔트로피) : 0.390664
```

Out[10]:
```
0.39066374732574616
```

In [11]:
```python
# Function compute Entropy
def H(p):
    id_p = np.where(p != 0)
    return -np.sum(p[id_p]*np.log2(p[id_p]))




# Compute H(X)
# Expected result: H = 1.27985422583
print ("H = ", H(P))
```

```
H =  0.39066374732574616
```

흡연 여부 엔트로피

In [12]:
```python
z1_people = len(data[data[column_z] == 1])
z2_people = len(data[data[column_z] == 2])
z3_people = len(data[data[column_z] == 3])
```

In [13]:
```python
print( "흡연1 : %d 흡연2 : %d 흡연3 : %d 흡연 총 인원 : %d" % (z1_people,z2_people,
```

```
흡연1 : 1209391 흡연2 : 352982 흡연3 : 428015 흡연 총 인원 : 1990388
```

In [14]:
```python
z1_dia = len(data[(data[column_z] == 1) & (data[column_o] >= 126)])
z1_not_dia = len(data[(data[column_z] == 1) & (data[column_o] < 126)])
z2_dia = len(data[(data[column_z] == 2) & (data[column_o] >= 126)])
z2_not_dia = len(data[(data[column_z] == 2) & (data[column_o] < 126)])
z3_dia = len(data[(data[column_z] == 3) & (data[column_o] >= 126)])
z3_not_dia = len(data[(data[column_z] == 3) & (data[column_o] < 126)])
```

In [15]:
```python
print("흡연여부:1, 당뇨인 사람 = %d, 당뇨x인 사람 = %d" %(z1_dia, z1_not_dia))
print("흡연여부:2, 당뇨인 사람 = %d, 당뇨x인 사람 = %d" %(z2_dia, z2_not_dia))
print("흡연여부:3, 당뇨인 사람 = %d, 당뇨x인 사람 = %d" %(z3_dia, z3_not_dia))
```

```
흡연여부:1, 당뇨인 사람 = 75897, 당뇨x인 사람 = 1133494
흡연여부:2, 당뇨인 사람 = 37179, 당뇨x인 사람 = 315803
흡연여부:3, 당뇨인 사람 = 39709, 당뇨x인 사람 = 388306
```

H(children) 계산

In [16]:
```python
p_z1_dia = z1_dia/z1_people
p_z1_not_dia = (z1_people - z1_dia) / z1_people
p_z2_dia = z2_dia/z2_people
p_z2_not_dia = (z2_people - z2_dia) / z2_people
p_z3_dia = z3_dia/z3_people
p_z3_not_dia = (z3_people - z3_dia) / z3_people

p_z1 = z1_people/total_people
p_z2 = z2_people/total_people
p_z3 = z3_people/total_people
```

In [17]:
```
h_z1 = - ((p_z1_dia*np.log2(p_z1_dia))+ (p_z1_not_dia* np.log2(p_z1_not_dia))
h_z2 = - ((p_z2_dia*np.log2(p_z2_dia))+ (p_z2_not_dia* np.log2(p_z2_not_dia))
h_z3 = - ((p_z3_dia*np.log2(p_z3_dia))+ (p_z3_not_dia* np.log2(p_z3_not_dia))

print("H(z1): %f"%(h_z1))
print("H(z2): %f"%(h_z2))
print("H(z3): %f"%(h_z3))
```

```
H(z1): 0.338291
H(z2): 0.485662
H(z3): 0.445664
```

IG(Information Gain) 계산

: 질문) 계산할 때 확률 부분이 'z1 && 당뇨/z1인 사람' 이게 맞을까요? 'z1인 사람/ 전체 사람' 이게 맞을까요? 둘 다 해볼께요.. 두번째가 맞는듯

In [18]:
```
z_IG_1 = h_parent - ((p_z1_dia *h_z1) + (p_z2_dia *h_z2) +(p_z2_dia *h_z2))
z_IG_2 = h_parent - ((p_z1 * h_z1) +(p_z2 * h_z2)+(p_z3 * h_z3))

print(z_IG_1, z_IG_2)
```

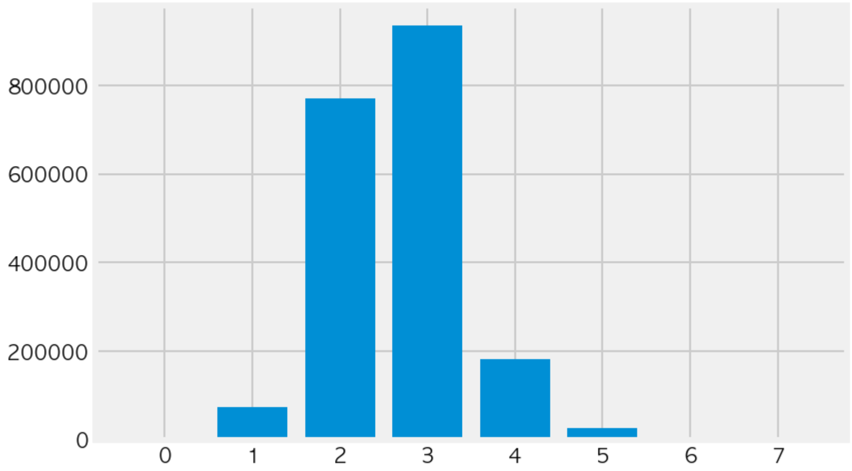
```
0.2671259330594141 0.003147859406958775
```

수축/이완 혈압 엔트로피

~혈압 기준은 두 세가지 정도 있는데 추후에 다른 기준으로 분리해서 해보려고 함~ 일단 그냥 +20 씩 분류할께요

In [19]:
```
# 고혈합 분류법
# only_bp = data[(data[column_m] >= 140) & (data[column_n] < 90)]

# lv2_bp = data[(data[column_m] >= 160) | (data[column_n] >= 100)]

# lv1_bp = data[((data[column_m] >= 140) & (data[column_m] <= 159)) |
#                ((data[column_n] >= 90) & (data[column_n] <= 99))]

# lv0_bp = data[((data[column_m] >= 130) & (data[column_m] <= 139)) |
#                ((data[column_n] >= 80) & (data[column_n] <= 89))]

# warn_bp = data[((data[column_m] >= 120) & (data[column_m] <= 129)) &
#                (data[column_n] < 80)]

# normal_bp = data[((data[column_m] >= 90) & (data[column_m] < 120)) &
#                ((data[column_n] >= 60) & (data[column_n] < 80))]

# low_bp = data[(data[column_m] < 90) & (data[column_n] < 60)]

# 단순히 범위로 수축기: 60~220(+20) , 이완기: 40~140 (+15, 마지막만 +10)
sys_lv0 = data[(data[column_m] >= 60) & (data[column_m] < 80)]
sys_lv1 = data[(data[column_m] >= 80) & (data[column_m] < 100)]
sys_lv2 = data[(data[column_m] >= 100) & (data[column_m] < 120)]
sys_lv3 = data[(data[column_m] >= 120) & (data[column_m] < 140)]
sys_lv4 = data[(data[column_m] >= 140) & (data[column_m] < 160)]
sys_lv5 = data[(data[column_m] >= 160) & (data[column_m] < 180)]
sys_lv6 = data[(data[column_m] >= 180) & (data[column_m] < 200)]
sys_lv7 = data[(data[column_m] >= 200) & (data[column_m] <= 220)]

sys_len = np.array([len(sys_lv0),len(sys_lv1),len(sys_lv2),len(sys_lv3),
                   len(sys_lv4),len(sys_lv5),len(sys_lv6),len(sys_lv7)])
```

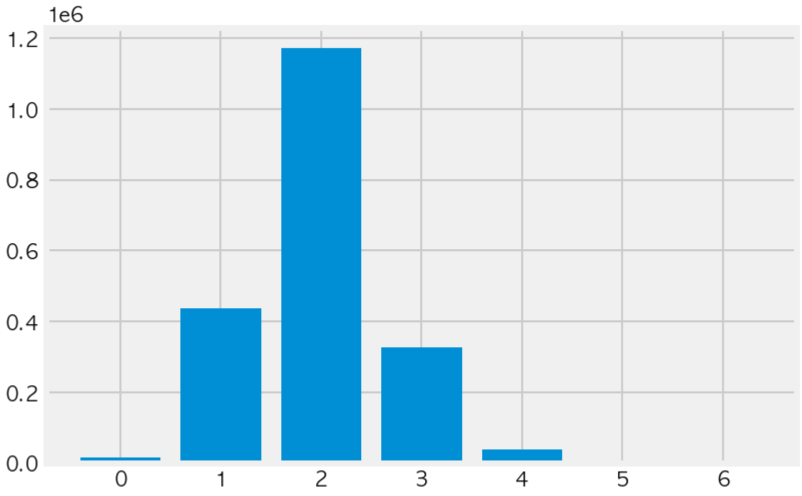
```
sys_x = range(len(sys_len))
plt.bar(sys_x,sys_len)
plt.show()
print("수축기혈압 전체 인원 분포",sys_len, sys_len.sum() == total_people)
```



```
수축기혈압 전체 인원 분포 [    103   73036 770312 934401 181663   27103    3349     421]
True
```

In [20]:

```
dias_lv0 = data[(data[column_n] >= 40) & (data[column_n] < 55)]
dias_lv1 = data[(data[column_n] >= 55) & (data[column_n] < 70)]
dias_lv2 = data[(data[column_n] >= 70) & (data[column_n] < 85)]
dias_lv3 = data[(data[column_n] >= 85) & (data[column_n] < 100)]
dias_lv4 = data[(data[column_n] >= 100) & (data[column_n] < 115)]
dias_lv5 = data[(data[column_n] >= 115) & (data[column_n] < 130)]
dias_lv6 = data[(data[column_n] >= 130) & (data[column_n] <= 140)]


dias_len = np.array([len(dias_lv0),len(dias_lv1),len(dias_lv2),len(dias_lv3),
                   len(dias_lv4),len(dias_lv5),len(dias_lv6)])
dias_x = range(len(dias_len))
plt.bar(dias_x,dias_len)
plt.show()
print("이완기혈압 전체 인원 분포",dias_len, dias_len.sum() == total_people)
```



```
이완기혈압 전체 인원 분포 [  14482  437070 1171540  326398    38031    2500     367]
True
```

In [21]:

```
sys_lv0_diab = sys_lv0[sys_lv0[column_o]>=126]
sys_lv1_diab = sys_lv1[sys_lv1[column_o]>=126]
sys_lv2_diab = sys_lv2[sys_lv2[column_o]>=126]
sys_lv3_diab = sys_lv3[sys_lv3[column_o]>=126]
sys_lv4_diab = sys_lv4[sys_lv4[column_o]>=126]
```

```
sys_lv5_diab = sys_lv5[sys_lv5[column_o]>=126]
sys_lv6_diab = sys_lv6[sys_lv6[column_o]>=126]
sys_lv7_diab = sys_lv7[sys_lv7[column_o]>=126]

dias_lv0_diab = dias_lv0[dias_lv0[column_o]>=126]
dias_lv1_diab = dias_lv1[dias_lv1[column_o]>=126]
dias_lv2_diab = dias_lv2[dias_lv2[column_o]>=126]
dias_lv3_diab = dias_lv3[dias_lv3[column_o]>=126]
dias_lv4_diab = dias_lv4[dias_lv4[column_o]>=126]
dias_lv5_diab = dias_lv5[dias_lv5[column_o]>=126]
dias_lv6_diab = dias_lv6[dias_lv6[column_o]>=126]


sys_diab_len = np.array([len(sys_lv0_diab),len(sys_lv1_diab),len(sys_lv2_diab
                         len(sys_lv3_diab), len(sys_lv4_diab),len(sys_lv5_dia
                         len(sys_lv6_diab),len(sys_lv7_diab)])
dias_diab_len = np.array([len(dias_lv0_diab),len(dias_lv1_diab),
                          len(dias_lv2_diab),len(dias_lv3_diab),
                          len(dias_lv4_diab),len(dias_lv5_diab),len(dias_lv6_

print(sys_len)
print(sys_diab_len, sys_diab_len.sum())
print(dias_len)
print(dias_diab_len, dias_diab_len.sum())
## sys_diab_len.sum() == dias_diab_len.sum() == 당뇨병 인원
```

```
[    103   73036  770312  934401  181663   27103    3349     421]
[      3    1821  35449  83416  26611   4763    653     69] 152785
[  14482  437070 1171540  326398   38031    2500     367]
[   655  21343  91270  34202   4883    380    52] 152785
```

확률 구하기

In [22]:

```
px1=[0 for _ in range(len(sys_len))]
py1=[0 for _ in range(len(sys_len))]
for i in range(len(sys_len)):
    px1[i] = sys_diab_len[i] / sys_len[i]
    py1[i] = (sys_len[i] - sys_diab_len[i]) / sys_len[i]

print("수축기 당뇨 확률: ",px1)
print("수축기 정상 확률: ",py1)

px2=[0 for _ in range(len(dias_len))]
py2=[0 for _ in range(len(dias_len))]
for i in range(len(dias_len)):
    px2[i] = dias_diab_len[i] / dias_len[i]
    py2[i] = (dias_len[i] - dias_diab_len[i]) / dias_len[i]

print("이완기 당뇨 확률: ",px2)
print("이완기 정상 확률: ",py2)
```

```
수축기 당뇨 확률:  [0.02912621359223301, 0.024932909797907882, 0.0460190156715720
4, 0.08927216473441274, 0.1464855253959254, 0.17573700328376932, 0.19498357718
722006, 0.16389548693586697]
수축기 정상 확률:  [0.970873786407767, 0.9750670902020921, 0.9539809843284279, 0.
9107278352655872, 0.8535144746040746, 0.8242629967162307, 0.80501642281278, 0.
836104513064133]
이완기 당뇨 확률:  [0.04522855959121668, 0.04883199487496282, 0.0779060040630281
5, 0.10478618128787553, 0.12839525650127528, 0.152, 0.14168937329700274]
이완기 정상 확률:  [0.9547714404087834, 0.9511680051250372, 0.9220939959369718,
0.8952138187121245, 0.8716047434987247, 0.848, 0.8583106267029973]
```

In [23]:

```
sys_entropy = []
```

```
for x,y in zip(px1,py1):
    P = np.array([x,y])
    print(P)
    print(H(P))
    sys_entropy.append(H(P))


print("수축기혈압 엔트로피 : ")
for i in range(len(sys_len)):
    print("lv%d = %f" % (i,sys_entropy[i]))
```

```
[0.02912621 0.97087379]
0.18999075553626754
[0.02493291 0.97506709]
0.1683061994731502
[0.04601902 0.95398098]
0.26923904364961826
[0.08927216 0.91072784]
0.4340357206412661
[0.14648553 0.85351447]
0.6009749954631391
[0.175737 0.824263]
0.6706618294011848
[0.19498358 0.80501642]
0.7117810758706125
[0.16389549 0.83610451]
0.6435478784630176
수축기혈압 엔트로피 :
lv0 = 0.189991
lv1 = 0.168306
lv2 = 0.269239
lv3 = 0.434036
lv4 = 0.600975
lv5 = 0.670662
lv6 = 0.711781
lv7 = 0.643548
```

In [24]:

```
dias_entropy = []
for x,y in zip(px2,py2):
    P = np.array([x,y])
    print(P)
    print(H(P))
    dias_entropy.append(H(P))


print("이완기혈압 엔트로피 : ")
for i in range(len(dias_len)):
    print("lv%d = %f" % (i,dias_entropy[i]))
```

```
[0.04522856 0.95477144]
0.26577153576502643
[0.04883199 0.95116801]
0.28141448371513106
[0.077906 0.922094]
0.3947575435909049
[0.10478618 0.89521382]
0.48398636839174347
[0.12839526 0.87160474]
0.5530206875307276
[0.152 0.848]
0.6148227571490692
[0.14168937 0.85831063]
0.5886460862619332
이완기혈압 엔트로피 :
lv0 = 0.265772
lv1 = 0.281414
lv2 = 0.394758
```

```
lv3 = 0.483986
lv4 = 0.553021
lv5 = 0.614823
lv6 = 0.588646
```

In [25]:

```
p_sys = []
p_dias = []


for i in range(len(sys_len)):
    p_sys.append(sys_len[i] / total_people)


for i in range(len(dias_len)):
    p_dias.append(dias_len[i] / total_people)


print(p_sys)
print(p_dias)

arr_p_sys = np.array(p_sys)
arr_p_dias = np.array(p_dias)
# bp_arr = np.array([len(low_bp),len(normal_bp),len(warn_bp),len(lv0_bp),len(
# px = np.array(bp_arr/total_people)
# print (px)
```

```
[5.174870427273476e-05, 0.03669435306081025, 0.38701599889066857, 0.4694567089
431809, 0.09127014431357103, 0.013616943028193497, 0.0016825865107707642, 0.00
021151654853224596]
[0.007275968303667425, 0.21959035122800177, 0.5885988058609678, 0.163987122108
85516, 0.01910732982714928, 0.0012560365114741448, 0.00018438615988440444]
```

In [26]:

```
sys_IG = h_parent - sum(arr_p_sys * sys_entropy)
print("수축기혈압 정보증가량 : ", sys_IG)

dias_IG = h_parent - sum(arr_p_dias * dias_entropy)
print("이완기혈압 정보증가량 : ", dias_IG)
```

```
수축기혈압 정보증가량 :  0.011200037300218568
이완기혈압 정보증가량 :  0.003765219580828927
```

: 다음과 같은 정보증가량을 구할 수 있고, 이를 기반으로 수축기 혈압의 정보가 더 중요하다고 고려할 수 있다.

In [ ]: