Fáza 2

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In [1]:

```
import pandas as pd
import numpy as np
import category_encoders as ce
from sklearn.impute import KNNImputer
from sklearn.impute import SimpleImputer
from numpy import asarray
from sklearn.preprocessing import MinMaxScaler
from sklearn.preprocessing import RobustScaler
```

Načítanie súboru "labor.csv" a "profiles.csv" po identifikácií a riešení problémov v dátach v 1. fáze projektu.

In [2]:

```
filename = "phase1_labor.csv"
labor = pd.read_csv(filename)
labor.head()
```

Out[2]:

	Unnamed: 0	hemoglobin	etytr	hbver	smoker	alt	trombocyty	erytrocyty	leukocyty	name	ssn
0	0	8.04859	8.33134	6.92033	no	5.32060	9.02598	7.77355	6.19725	Alicia White	269-22-8465
1	1	6.51314	9.25854	9.38356	yes	4.11257	7.37351	7.33091	8.58102	Tanner Nunez	006-24-1461
2	2	7.67594	9.79867	6.90776	no	18.41131	6.92801	9.53044	6.70686	Kenneth Edwards	118-32-9149
3	3	6.38250	9.62834	7.70289	no	1.68916	8.64702	6.15432	7.33775	Peter Cobb	564-32-8668
4	4	7.81369	7.62289	9.16622	no	2.30729	7.42597	4.52950	5.23373	Kenneth Deleon	092-44-7767

In [3]:

```
filename = "phase1_profiles.csv"
profiles = pd.read_csv(filename)
profiles.head()
```

Out[3]:

	Unnamed: 0	blood_group	company	race	sex	address	job	ssn	name	birthdate
0	0	AB-	Lewis Group	black	F	145 Nicole Square\nBradleyborough, MT 98980	Minerals surveyor	111-68-5386	Katherine Ortega	1998-11-17
1	1	AB+	Krueger-Herman	black	F	7144 Luis Junction Suite 705\nPriceborough, IA...	Surveyor, building control	034-30-4283	Amanda Frank	2018-10-03
2	2	A+	Rhodes-Lynch	black	F	24781 Lee Walk\nNorth Amy, MT 75915	Manufacturing systems engineer	376-24-8085	Ann Gray	1957-06-10

	Unnamed: 0	blood_group	company	race	sex	address	job	ssn	name	birthdate
3	3	B+	Chung-Osborne	black	F	54505 Anderson Parkways\nNorth David, NC 59887	Designer, blown glass/stained glass	259-78-9704	Stephanie Baker	1984-04-18
4	4	B-	Gibson-Berg	black	F	731 James Streets\nCalvinberg, NC 37619	Advertising account planner	353-69-9598	Brenda Price	1966-04-27

1. Integrácia a čistenie dát

Pre správne fungovanie strojového učenia je potrebné transformovať včetky atribúty do numerického formátu. V textovom formáte v súbore "phase1_labor.csv" sú atribúty 'smoker', 'name' a 'relationship'. S určitosťou vieme povedať, že meno neovplyvňuje hodnotu indikátora a nebudeme s ním pracovať, z toho dôvodu ho nie je potrebné transformovať na numerickú hodnotu.

Ak atribút 'smoker' má hodnotu 'no', jeho numerická hodnota bude 0 a ak je hodnota 'yes', zmenená hodnota bude 1. Atribút 'relationship' transformujeme pomocou ordinal encoding. Číselné hodnoty sú priradené takto: 1: 'widowed', 2: 'separated', 3: 'married', 4: 'single', 5: 'divoced', 6: 'nop'.

In [4]:
```
# transform smoker
map_dict = {'no':0, 'yes':1}
labor["smoker"] = labor["smoker"].map(map_dict)

# transform relationship ordinal encoding
ce_relationship = ce.OrdinalEncoder(cols=['relationship'])
labor = ce_relationship.fit_transform(labor)
labor.head()
```

Out[4]:

	Unnamed: 0	hemoglobin	etytr	hbver	smoker	alt	trombocyty	erytrocyty	leukocyty	name	ssn
0	0	8.04859	8.33134	6.92033	0	5.32060	9.02598	7.77355	6.19725	Alicia White	269-22-8465
1	1	6.51314	9.25854	9.38356	1	4.11257	7.37351	7.33091	8.58102	Tanner Nunez	006-24-1461
2	2	7.67594	9.79867	6.90776	0	18.41131	6.92801	9.53044	6.70686	Kenneth Edwards	118-32-9149
3	3	6.38250	9.62834	7.70289	0	1.68916	8.64702	6.15432	7.33775	Peter Cobb	564-32-8668
4	4	7.81369	7.62289	9.16622	0	2.30729	7.42597	4.52950	5.23373	Kenneth Deleon	092-44-7767

V súbore "profiles.csv" transformujeme atribúty 'blood-group', 'race' a 'sex'. Zvyšné atribúty nebudeme brať do úvahy. Atribút 'blood_group' bude zmenený takto: 1: 'AB-', 2: 'AB+', 3: 'A+', 4: 'B+', 5: 'B-', 6: 'O-', 7: 'A-', 8: 'O+'. Atribút 'sex' bude zmenený takto: 0: 'F', 1: 'M'. Atribút 'race' bude zmenený takto: 1: 'black', 2: 'white', 3: 'asian', 4: 'hawaiian', 5: 'indian'.

In [5]:
```
# transform blood_group, race ordinal encoding
ce_ordinal = ce.OrdinalEncoder(cols=['blood_group', 'race'])
profiles = ce_ordinal.fit_transform(profiles)

# transform sex
map_dict = {'F':0, 'M':1}
profiles["sex"] = profiles["sex"].map(map_dict)

profiles.head()
```

Out[5]:

	Unnamed: 0	blood_group	company	race	sex	address	job	ssn	name	birthdate
0	0	1	Lewis Group	1	0	145 Nicole Square\nBradleyborough, MT 98980	Minerals surveyor	111-68-5386	Katherine Ortega	1998-11-17
1	1	2	Krueger-Herman	1	0	7144 Luis Junction Suite 705\nPriceborough, IA...	Surveyor, building control	034-30-4283	Amanda Frank	2018-10-03
2	2	3	Rhodes-Lynch	1	0	24781 Lee Walk\nNorth Amy, MT 75915	Manufacturing systems engineer	376-24-8085	Ann Gray	1957-06-10
3	3	4	Chung-Osborne	1	0	54505 Anderson Parkways\nNorth David, NC 59887	Designer, blown glass/stained glass	259-78-9704	Stephanie Baker	1984-04-18
4	4	5	Gibson-Berg	1	0	731 James Streets\nCalvinberg, NC 37619	Advertising account planner	353-69-9598	Brenda Price	1966-04-27

Z dát odstraníme atribúty, o ktorých už teraz vieme povedať, že nebudú mať vplyv na indikátor.

In [6]:
```
labor = labor.drop(columns=['indicator_str', 'weight', 'weight', 'Unnamed: 0', 'name'])
profiles = profiles.drop(columns=['company', 'address', 'job', 'Unnamed: 0', 'name'])
```

Jedno pozorovanie musí byť reprezentované jedným riadkom tabuľky. Na základe 'ssn' spojíme tabuľky 'labor' a 'profiles'.

In [7]:
```
data = pd.merge(labor, profiles, on=['ssn'])
```

Na ďalšie fázy už nie je potrebný atribút 'ssn', stĺpec odstraníme.

In [8]:
```
data = data.drop(columns=['ssn'])
```

Posledná nenumerická hodnota v tabuľke je 'birthdate'.

In [9]:
```
from datetime import datetime
birthdates = data['birthdate']

date_1900 = datetime.strptime('1900-01-01', '%Y-%m-%d')

birthdates_new = []
for birthdate in birthdates:
    birth = datetime.strptime(birthdate,'%Y-%m-%d')
    delta = birth - date_1900
    birthdates_new.append(delta.days)
```

```
data['birthdate'] = birthdates_new
#data['birthdate'] = data['birthdate'].str.replace("-","").astype(int)
```

In [10]:
```
data.head()
```

Out[10]:

	hemoglobin	etytr	hbver	smoker	alt	trombocyty	erytrocyty	leukocyty	relationship	indicator	hem
0	8.04859	8.33134	6.92033	0	5.32060	9.02598	7.77355	6.19725	1	1.0	
1	7.06975	5.87075	7.55645	1	3.00974	8.16432	6.61407	8.12903	3	0.0	
2	7.99925	8.50456	8.74478	1	6.86390	7.41719	8.10390	9.39205	3	1.0	
3	6.51314	9.25854	9.38356	1	4.11257	7.37351	7.33091	8.58102	1	1.0	
4	6.47968	5.81228	10.71625	0	2.88381	6.21111	5.73826	7.38472	5	1.0	

Všetky typy atribútov v tabuľke 'data' sú numerické.

In [11]:
```
data.dtypes
```

Out[11]:
```
hemoglobin      float64
etytr           float64
hbver           float64
smoker            int64
alt             float64
trombocyty      float64
erytrocyty      float64
leukocyty       float64
relationship      int32
indicator       float64
hematokrit      float64
alp             float64
ast             float64
er-cv           float64
blood_group       int32
race              int32
sex               int64
birthdate         int64
dtype: object
```

1.1 Chýbajúce hodnoty

Prvým spôsobom je odstránenie pozorovaní s chýbajúcimi údajmi.

In [12]:
```
data.isna().sum()
```

Out[12]:
```
hemoglobin      30
etytr           31
hbver           30
smoker           0
alt             30
trombocyty      30
erytrocyty      30
leukocyty       30
relationship     0
indicator        0
hematokrit      30
alp             30
ast             31
er-cv           31
blood_group      0
```

```
race             0
sex              0
birthdate        0
dtype: int64
```

In [13]:

```
def delete_nan(data):
 return data.dropna(axis=0)

data_nan = delete_nan(data)
print(f'Tvar pred odstránením NaN hodnôt: {data.shape}, po odstránení: {data_nan.shape}, r
data = data_nan
```

```
Tvar pred odstránením NaN hodnôt: (10000, 18), po odstránení: (9673, 18), rozdiel: 327 ria
dkov.
```

Druhým spôsobom je nahradenie chýbajúcej hodnoty mediánom.

In [14]:

```
def median_nan(data):
    imputer_median = SimpleImputer(missing_values = np.nan, strategy ='mean')
    imputer_median = imputer_median.fit(data)
    return pd.DataFrame(imputer_median.transform(data), columns = data.columns)
data_median = median_nan(data)
```

Tretím spôsobom je nahradenie chýbajúcej hodnoty priemerom.

In [15]:

```
def mean_nan(data):
    imputer_mean = SimpleImputer(missing_values = np.nan, strategy ='mean')
    imputer_mean = imputer_mean.fit(data)
    return pd.DataFrame(imputer_mean.transform(data), columns = data.columns)
data_mean = mean_nan(data)
```

štvrtým spôsobom je nahradenie chýbajúcej hodnoty pomocou k-nearest neighbors (KNN) algoritmu.

In [16]:

```
def knn_nan(data):
    imputer = KNNImputer()
    imputer.fit(data)
    return pd.DataFrame(imputer.transform(data), columns = data.columns)
data_knn = knn_nan(data)
```

1.2 Vychýlené hodnoty

Identifikácia vychýlených hodnôt prostredníctvom 3-násobku štandardnej odchýlky od priemeru.

In [17]:

```
mean, std = np.mean(data), np.std(data)
out_range = 3 * std
lower, upper = mean - out_range, mean + out_range
```

Nájdenie všetkých vychýlených hodnôt a ošetrenie dvomi metódamy, odstránenením týchto hodnôt z dát a nahradenie týchto hodnôt hraničnýými hodnotami. DataFrame data_border predstavuje dáta bez vychýlených hodnôt v DataFrame data_border sa nachádzajú záznamy v pôovodnom poradí so zmenenými vychýlenými hodnotami na hraničné hodnoty. DataFrame otliers obsahuje iba záznamy s vychýlenými hodnotami.

In [18]:

```
outliers = []
data_out = []
data_border = []

def manage(row):
    for i in range(len(row)):
            if row[i] < lower.values[i]:
                row[i] = lower.values[i]
            elif  row[i] > upper.values[i]:
                row[i] = upper.values[i]
        return row

def outOutliers(data):
    for row in data.values:
        for i in range(len(row)):
            if row[i] < lower.values[i] or row[i] > upper.values[i]:
                outliers.append(row)
                data_border.append(manage(row))
                break
            else:
                if i == len(row) - 1:
                    data_out.append(row)
                    data_border.append(row)

outOutliers(data)
outliers = pd.DataFrame(outliers, columns = data.columns)
data_out = pd.DataFrame(data_out, columns = data.columns)
data_border = pd.DataFrame(data_border, columns = data.columns)
print(f'Počet vychýlených hodnôt: {outliers.shape[0]}, počet záznamov po odstránení vychý
data = data_out
```

```
Počet vychýlených hodnôt: 400, počet záznamov po odstránení vychýlených hodnôt: 9273.
```

2. Realizácia predspracovania dát

2.1 Testovacia a trénovacia množina

In [19]:
```
x = data.drop('indicator', axis=1)
x
```

Out[19]:

	hemoglobin	etytr	hbver	smoker	alt	trombocyty	erytrocyty	leukocyty	relationship	hematokrit
0	8.04859	8.33134	6.92033	0.0	5.32060	9.02598	7.77355	6.19725	1.0	8.42675
1	7.06975	5.87075	7.55645	1.0	3.00974	8.16432	6.61407	8.12903	3.0	5.20481
2	7.99925	8.50456	8.74478	1.0	6.86390	7.41719	8.10390	9.39205	3.0	8.05943
3	6.51314	9.25854	9.38356	1.0	4.11257	7.37351	7.33091	8.58102	1.0	8.36402
4	6.47968	5.81228	10.71625	0.0	2.88381	6.21111	5.73826	7.38472	5.0	9.81301
...	...	...	...	...	...	...	...	...	...	...
9268	7.41285	5.46108	10.35929	0.0	3.02486	7.47343	6.65908	6.40945	5.0	9.18126
9269	6.75718	9.15128	7.57213	1.0	2.68629	6.79721	6.25926	8.51760	1.0	7.98747
9270	6.87349	7.08973	9.70552	0.0	1.58039	6.94379	5.56571	6.31337	1.0	7.75174
9271	6.23404	8.61925	7.80780	0.0	2.05330	7.43009	6.52320	7.15476	1.0	8.46357
9272	7.50848	5.87947	9.29240	0.0	3.38950	7.18074	7.12375	5.89864	3.0	10.48685

9273 rows × 17 columns

In [20]:
```
y = data['indicator']
y
```

```
Out[20]: 0       1.0
         1       0.0
         2       1.0
         3       1.0
         4       1.0
                ...
         9268    1.0
         9269    1.0
         9270    0.0
         9271    1.0
         9272    0.0
         Name: indicator, Length: 9273, dtype: float64
```

```
In [21]:
from sklearn.model_selection import train_test_split

x_train,x_test,y_train,y_test=train_test_split(x,y,test_size=0.2)
```

2.2 Transformácia atribútov

Na transformáciu atribútov dát pre strojové učenie je použitá technika scaling. Pomocou škálovania predchádzame rozdielom v škálovaní a distribúcii, ktoré môžu byť príčinou slabého výkonu modelu a vysokej citlivosti pre vstupné údaje a teda vyššej chybovosti.

Data Normalization

```
In [22]:
scaler = MinMaxScaler()

scaled = scaler.fit_transform(x_train)
data_mm_scaled = pd.DataFrame(scaled, columns = x_train.columns)
print(x_train)
print(data_mm_scaled)
```

```
      hemoglobin    etytr     hbver  smoker       alt  trombocyty  erytrocyty  \
5752     8.05211  5.08009   7.39627     0.0  11.63109     6.75524     8.94419
7276     8.20383  8.83966   7.53826     0.0   4.19382     7.48624     7.03347
7354     7.44860  5.33211  11.02218     1.0   3.00469     6.91420     7.36460
2131     6.26165  6.30979   6.90382     0.0   2.39050     8.05212     6.65065
1814     7.87260  6.39549   7.66717     0.0   3.30393     7.27744     6.16535
...          ...      ...       ...     ...       ...         ...         ...
7833     6.63464  7.05545   9.05441     0.0   8.29911     8.05224     8.49669
8279     5.67241  4.81312   8.12398     0.0   4.41652     5.43467     7.43306
811      6.67368  6.89389  10.23336     1.0   3.24527     7.17276     7.12247
7088     7.68289  5.80737   7.67200     1.0   2.33105     6.49525     5.60131
6329     7.62628  6.93177   7.58441     1.0   4.48579     7.35496     7.95759

      leukocyty  relationship  hematokrit       alp       ast     er-cv  \
5752    8.18671           6.0     7.19419  34.14363  82.58028  62.88254
7276    9.56309           4.0     7.63773  25.50572  64.39503  58.09717
7354    8.08583           5.0     8.52006  58.83208  75.48976  51.73403
2131    9.99156           1.0     6.72792  83.08067  72.50356  82.03240
1814    5.36521           4.0     7.29848  40.48462  80.80694  52.44928
...         ...           ...         ...       ...       ...       ...
7833    8.14712           3.0     8.26528  78.04706  66.40972  48.02453
8279    8.63932           2.0     6.93304  71.28264  72.62223  44.99081
811     8.29327           6.0     9.17199  78.30990  68.12942  30.71926
7088    5.41456           1.0     7.29989  50.81377  67.38004  82.12984
6329    8.70491           5.0     5.75289  54.94712  71.07149  73.73175

      blood_group  race  sex  birthdate
5752          2.0   1.0  0.0    22136.0
7276          4.0   2.0  1.0    29462.0
7354          7.0   2.0  1.0     8102.0
2131          5.0   2.0  1.0     5707.0
```

```
1814          8.0   2.0  0.0    17759.0
...           ...   ...  ...        ...
7833          6.0   3.0  0.0    26529.0
8279          8.0   1.0  0.0    30258.0
811           7.0   2.0  0.0    32874.0
7088          3.0   2.0  1.0    26446.0
6329          1.0   2.0  0.0    25701.0

[7418 rows x 17 columns]
      hemoglobin     etytr     hbver  smoker       alt  trombocyty  \
0       0.648236  0.275791  0.359728     0.0  0.745950    0.426840
1       0.674171  0.672484  0.379499     0.0  0.268967    0.550106
2       0.545069  0.302383  0.864608     1.0  0.192703    0.453645
3       0.342168  0.405543  0.291158     0.0  0.153313    0.645528
4       0.617549  0.414586  0.397449     0.0  0.211895    0.514896
...          ...       ...       ...     ...       ...         ...
7413    0.405928  0.484222  0.590611     0.0  0.532256    0.645548
7414    0.241441  0.247621  0.461056     0.0  0.283250    0.204157
7415    0.412602  0.467175  0.754771     1.0  0.208133    0.497245
7416    0.585120  0.352530  0.398121     1.0  0.149500    0.382999
7417    0.575443  0.471172  0.385925     1.0  0.287692    0.527968

      erytrocyty  leukocyty  relationship  hematokrit       alp       ast  \
0       0.911709   0.617579           1.0    0.412484  0.341436  0.794944
1       0.544761   0.756475           0.6    0.462984  0.255057  0.375096
2       0.608354   0.607399           0.8    0.563445  0.588321  0.631243
3       0.471242   0.799714           0.0    0.359395  0.830807  0.562300
4       0.378042   0.332851           0.6    0.424358  0.404846  0.754003
...          ...        ...           ...         ...       ...       ...
7413    0.825768   0.613584           0.4    0.534436  0.780471  0.421610
7414    0.621501   0.663254           0.2    0.382750  0.712826  0.565040
7415    0.561853   0.628333           1.0    0.637672  0.783099  0.461313
7416    0.269720   0.337831           0.0    0.424518  0.508138  0.444012
7417    0.722235   0.669873           0.8    0.248380  0.549471  0.529237

         er-cv  blood_group  race  sex  birthdate
0     0.628156     0.142857  0.00  0.0   0.472964
1     0.566922     0.428571  0.25  1.0   0.646021
2     0.485499     0.857143  0.25  1.0   0.141450
3     0.873197     0.571429  0.25  1.0   0.084875
4     0.494652     1.000000  0.25  0.0   0.369570
...        ...          ...   ...  ...        ...
7413  0.438033     0.714286  0.50  0.0   0.576737
7414  0.399213     1.000000  0.00  0.0   0.664824
7415  0.216595     0.857143  0.25  0.0   0.726620
7416  0.874444     0.285714  0.25  1.0   0.574776
7417  0.766982     0.000000  0.25  0.0   0.557178

[7418 rows x 17 columns]
```

Robust Scaling

In [23]:
```
scaler = RobustScaler()

scaled = RobustScaler().fit_transform(x_train)
data_rb_scaled = pd.DataFrame(scaled, columns = x_train.columns)
print(data_rb_scaled)
```

```
      hemoglobin     etytr     hbver  smoker       alt  trombocyty  \
0       0.658691 -0.854834 -0.616625     0.0  3.345538   -0.327138
1       0.774506  0.653603 -0.527755     0.0  0.150368    0.214161
2       0.198004 -0.753717  1.652789     1.0 -0.360502   -0.209429
3      -0.708049 -0.361446 -0.924843     0.0 -0.624367    0.633190
4       0.521663 -0.327061 -0.447072     0.0 -0.231943    0.059547
...          ...       ...       ...     ...       ...         ...
```

```
7413   -0.423329 -0.062268  0.421185     0.0  1.914066    0.633279
7414   -1.157843 -0.961949 -0.161160     0.0  0.246043   -1.305008
7415   -0.393528 -0.127090  1.159076     1.0 -0.257145   -0.017968
7416    0.376848 -0.563030 -0.444049     1.0 -0.649908   -0.519658
7417    0.333635 -0.111892 -0.498870     1.0  0.275803    0.116949

      erytrocyty  leukocyty  relationship  hematokrit       alp       ast  \
0       1.324775   0.383777           1.0   -0.554911 -0.981985  1.263269
1      -0.127780   0.925945           0.0   -0.300027 -1.242285 -0.568022
2       0.123949   0.344040           0.5    0.207012 -0.238008  0.549240
3      -0.418805   1.094723          -1.5   -0.822857  0.492714  0.248523
4      -0.787737  -0.727636           0.0   -0.494980 -0.790901  1.084690
...          ...        ...           ...         ...       ...       ...
7413    0.984579   0.368182          -0.5    0.060601  0.341028 -0.365139
7414    0.175993   0.562064          -1.0   -0.704983  0.137185  0.260473
7415   -0.060121   0.425752           1.0    0.581650  0.348949 -0.191962
7416   -1.216528  -0.708196          -1.5   -0.494169 -0.479636 -0.267426
7417    0.574748   0.587901           0.5   -1.383167 -0.355080  0.104311

         er-cv  blood_group  race  sex  birthdate
0     0.562934        -0.50  -1.0 -1.0  -0.083741
1     0.296346         0.00   0.0  0.0   0.263352
2    -0.058139         0.75   0.0  0.0  -0.748647
3     1.629756         0.25   0.0  0.0  -0.862118
4    -0.018293         1.00   0.0 -1.0  -0.291115
...        ...          ...   ...  ...        ...
7413 -0.264792         0.50   1.0 -1.0   0.124391
7414 -0.433798         1.00  -1.0 -1.0   0.301065
7415 -1.228853         0.75   0.0 -1.0   0.425006
7416  1.635184        -0.25   0.0  0.0   0.120459
7417  1.167334        -0.75   0.0 -1.0   0.085162

[7418 rows x 17 columns]
```

Druhou technikou je transformácia, ktorá zabezpečí, aby boli dáta vo viac normálnom (gausovom) tvare.

Power transformer

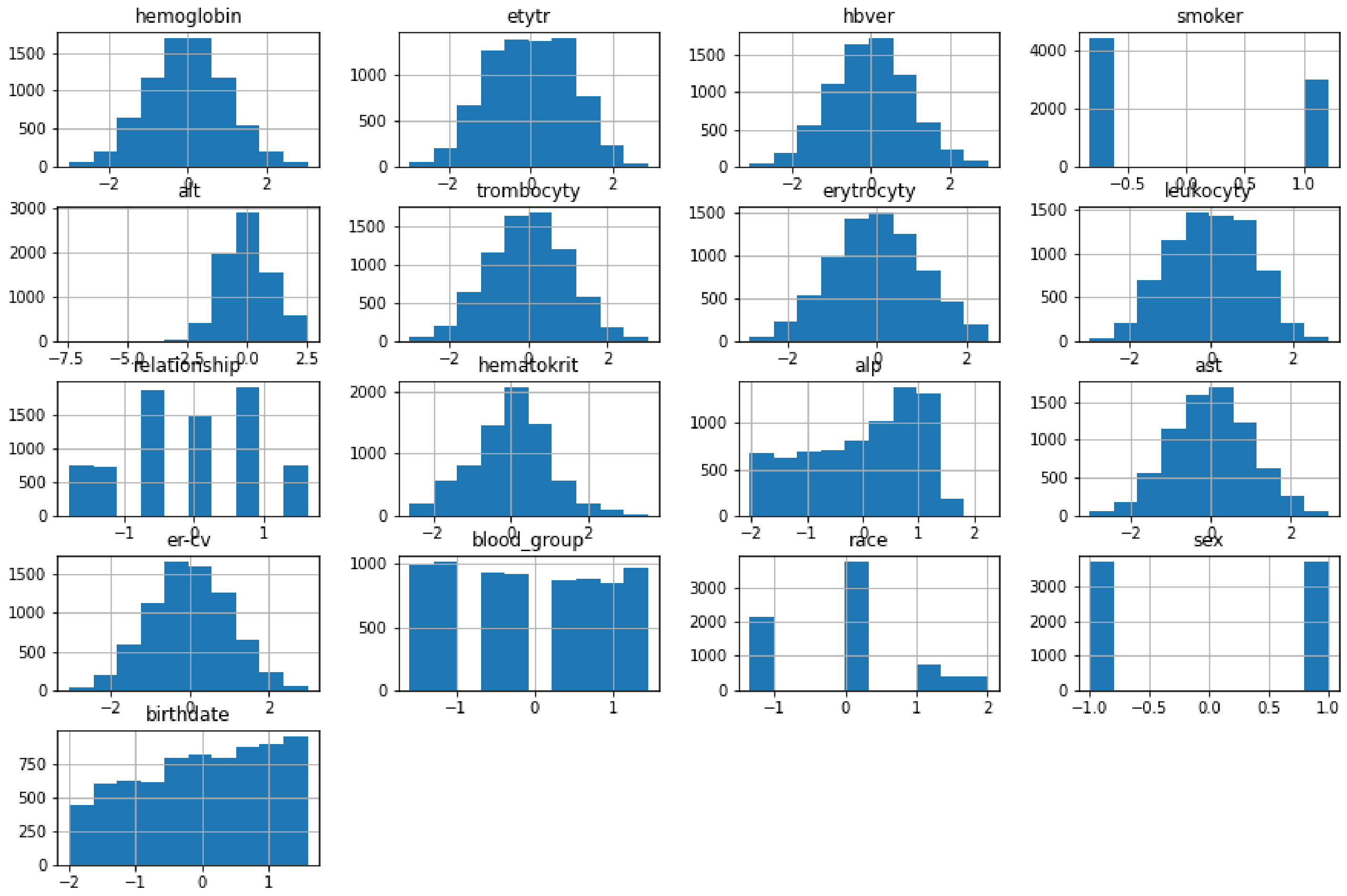
In [24]:
```python
from matplotlib import pyplot as plt
from pandas import read_csv
from pandas import DataFrame
from sklearn.preprocessing import PowerTransformer

plt.rcParams['figure.figsize'] = [15, 10]

data_power = x_train.values[:, :]

pt = PowerTransformer(method='yeo-johnson')
data_power = pt.fit_transform(data_power)

data_power = pd.DataFrame(data_power, columns = x_train.columns)
fig = data_power.hist()
```



Quantile Transformer

```
In [25]:
from matplotlib import pyplot
import numpy as np
from sklearn.preprocessing import QuantileTransformer

qt = QuantileTransformer()
X_t = qt.fit_transform(x_train)
data_quantile = pd.DataFrame(X_t, columns = x_train.columns)
print(data_quantile)
print(data)
```

```
      hemoglobin     etytr     hbver  smoker       alt  trombocyty  \
0       0.817842  0.100987  0.205245     0.0  0.978485    0.329457
1       0.855719  0.824843  0.240004     0.0  0.581448    0.621111
2       0.604556  0.134874  0.985517     1.0  0.263004    0.385430
3       0.173246  0.319484  0.108346     0.0  0.106239    0.806210
4       0.764870  0.336820  0.275823     0.0  0.350540    0.532647
...          ...       ...       ...     ...       ...         ...
7413    0.284793  0.471504  0.717100     0.0  0.921508    0.806235
7414    0.059950  0.070899  0.419077     0.0  0.623063    0.038071
7415    0.298328  0.438443  0.937498     1.0  0.333932    0.488458
7416    0.692238  0.215499  0.277368     1.0  0.094493    0.244381
7417    0.670649  0.446185  0.252472     1.0  0.638738    0.565595

      erytrocyty  leukocyty  relationship  hematokrit       alp       ast  \
0       0.973831   0.689268      1.000000    0.256120  0.160774  0.955384
1       0.434068   0.921906      0.545045    0.353434  0.101903  0.221935
2       0.566800   0.671035      0.771271    0.624038  0.392908  0.776054
3       0.290557   0.961698      0.000000    0.186001  0.895802  0.632063
4       0.144157   0.158578      0.545045    0.274386  0.202761  0.929863
...          ...        ...           ...         ...       ...       ...
7413    0.912904   0.681497      0.321321    0.536201  0.735712  0.316518
7414    0.596089   0.780770      0.148148    0.211214  0.580646  0.638803
```

```
7415    0.470662   0.711329      1.000000    0.820897  0.744638  0.396662
7416    0.057383   0.166432      0.000000    0.274688  0.305280  0.360084
7417    0.782557   0.792171      0.771271    0.087858  0.348263  0.553894

         er-cv  blood_group      race  sex  birthdate
0     0.773595     0.202202  0.000000  0.0   0.455453
1     0.650141     0.457958  0.543043  1.0   0.631362
2     0.467661     0.812312  0.543043  1.0   0.134262
3     0.990058     0.578579  0.543043  1.0   0.073858
4     0.489554     1.000000  0.543043  0.0   0.351351
...        ...          ...       ...  ...        ...
7413  0.355275     0.696196  0.845846  0.0   0.558187
7414  0.275485     1.000000  0.000000  0.0   0.649440
7415  0.042092     0.812312  0.543043  0.0   0.711695
7416  0.990297     0.333333  0.543043  1.0   0.556385
7417  0.946988     0.000000  0.543043  0.0   0.538614

[7418 rows x 17 columns]
      hemoglobin    etytr     hbver  smoker      alt  trombocyty  erytrocyty  \
0        8.04859  8.33134   6.92033     0.0  5.32060     9.02598     7.77355
1        7.06975  5.87075   7.55645     1.0  3.00974     8.16432     6.61407
2        7.99925  8.50456   8.74478     1.0  6.86390     7.41719     8.10390
3        6.51314  9.25854   9.38356     1.0  4.11257     7.37351     7.33091
4        6.47968  5.81228  10.71625     0.0  2.88381     6.21111     5.73826
...          ...      ...       ...     ...      ...         ...         ...
9268     7.41285  5.46108  10.35929     0.0  3.02486     7.47343     6.65908
9269     6.75718  9.15128   7.57213     1.0  2.68629     6.79721     6.25926
9270     6.87349  7.08973   9.70552     0.0  1.58039     6.94379     5.56571
9271     6.23404  8.61925   7.80780     0.0  2.05330     7.43009     6.52320
9272     7.50848  5.87947   9.29240     0.0  3.38950     7.18074     7.12375

      leukocyty  relationship  indicator  hematokrit       alp       ast  \
0       6.19725           1.0        1.0     8.42675  40.67505  65.03438
1       8.12903           3.0        0.0     5.20481  80.56262  78.69936
2       9.39205           3.0        1.0     8.05943  41.70678  73.50396
3       8.58102           1.0        1.0     8.36402  83.65217  69.74486
4       7.38472           5.0        1.0     9.81301  85.75254  57.14540
...         ...           ...        ...         ...       ...       ...
9268    6.40945           5.0        1.0     9.18126  60.15868  71.03993
9269    8.51760           1.0        1.0     7.98747  77.81515  70.81704
9270    6.31337           1.0        0.0     7.75174  78.37399  83.00607
9271    7.15476           1.0        1.0     8.46357  77.31291  77.37206
9272    5.89864           3.0        0.0    10.48685  50.29070  64.58161

         er-cv  blood_group  race  sex  birthdate
0     57.03521          2.0   2.0  0.0    34593.0
1     49.12368          2.0   2.0  0.0    34593.0
2     23.21061          2.0   2.0  0.0    34593.0
3     59.63760          3.0   1.0  1.0    37513.0
4     52.17063          3.0   1.0  1.0    37513.0
...        ...          ...   ...  ...        ...
9268  65.99197          4.0   2.0  0.0    14612.0
9269  52.71076          4.0   2.0  0.0    14612.0
9270  70.10314          8.0   2.0  1.0     6210.0
9271  46.87337          8.0   2.0  1.0     6210.0
9272  62.56574          8.0   2.0  1.0     6210.0

[9273 rows x 18 columns]
```

3. Výber atribútov pre strojové učenie

In [26]:
```
from sklearn.feature_selection import SelectKBest
from sklearn.feature_selection import mutual_info_regression
```

Pri výbere atribútov na strojové učenie sme vyskúšali niekoľko techník, každú techniko pre rôzne spôsoby transformácie dát, a porovnali ich výsledky. Prvou technikou je mutual information regression.

Mutual information regression pre MinMaxScaler:

In [27]:
```
r = mutual_info_regression(data_mm_scaled, y_train)
result = pd.DataFrame({"atribut":list(x_train.columns), "vysledok": r})
result = result.sort_values("vysledok", ascending=0)
result
```

Out[27]:

	atribut	vysledok
9	hematokrit	0.116765
0	hemoglobin	0.020085
1	etytr	0.013979
7	leukocyty	0.009320
15	sex	0.008399
10	alp	0.008322
3	smoker	0.007752
16	birthdate	0.007448
12	er-cv	0.006284
5	trombocyty	0.003931
4	alt	0.003179
11	ast	0.000135
6	erytrocyty	0.000000
13	blood_group	0.000000
14	race	0.000000
2	hbver	0.000000
8	relationship	0.000000

Mutual information regression pre Robust Scaling:

In [28]:
```
r = mutual_info_regression(data_rb_scaled, y_train)
result = pd.DataFrame({"atribut":list(x_train.columns), "vysledok": r})
result = result.sort_values("vysledok", ascending=0)
result
```

Out[28]:

	atribut	vysledok
9	hematokrit	0.116580
0	hemoglobin	0.020202
1	etytr	0.014198
7	leukocyty	0.009482
10	alp	0.008322
16	birthdate	0.008273

	atribut	vysledok
12	er-cv	0.006329
5	trombocyty	0.004100
4	alt	0.003307
11	ast	0.000017
6	erytrocyty	0.000000
3	smoker	0.000000
2	hbver	0.000000
13	blood_group	0.000000
14	race	0.000000
15	sex	0.000000
8	relationship	0.000000

Mutual information regression pre Power Transformer:

In [29]:
```
r = mutual_info_regression(data_power, y_train)
result = pd.DataFrame({"atribut":list(x_train.columns), "vysledok": r})
result = result.sort_values("vysledok", ascending=0)
result
```

Out[29]:

	atribut	vysledok
9	hematokrit	0.116768
0	hemoglobin	0.020545
3	smoker	0.015145
1	etytr	0.013898
7	leukocyty	0.009565
10	alp	0.008327
16	birthdate	0.006809
12	er-cv	0.006299
13	blood_group	0.004418
5	trombocyty	0.004068
4	alt	0.002953
11	ast	0.000121
6	erytrocyty	0.000000
2	hbver	0.000000
14	race	0.000000
15	sex	0.000000
8	relationship	0.000000

Mutual information regression pre Quantile Transformer:

In [30]:
```
r = mutual_info_regression(data_quantile, y_train)
result = pd.DataFrame({"atribut":list(x_train.columns), "vysledok": r})
result = result.sort_values("vysledok", ascending=0)
result
```

Out[30]:

	atribut	vysledok
9	hematokrit	0.117653
0	hemoglobin	0.020667
1	etytr	0.014588
7	leukocyty	0.011107
12	er-cv	0.006379
16	birthdate	0.006194
10	alp	0.005029
5	trombocyty	0.002570
4	alt	0.002548
11	ast	0.000678
6	erytrocyty	0.000000
3	smoker	0.000000
2	hbver	0.000000
13	blood_group	0.000000
14	race	0.000000
15	sex	0.000000
8	relationship	0.000000

Ďalšou metódou výberu atribútov pre strojové učenie je chi-squared štatistika. Predpokladajú sa nezáporné hodnoty, čiže možno použiť iba ak sme pri transformácii použili MinMaxScaling alebo Quantile Transformer

In [31]:
```
from sklearn.feature_selection import chi2

r1, r2 = chi2(data_mm_scaled, y_train)
result = pd.DataFrame({"atribut":list(data_mm_scaled.columns), "vysledok": r1, "p value":
result = result.sort_values("vysledok", ascending=0)
result
```

Out[31]:

	atribut	vysledok	p value
9	hematokrit	59.787727	1.056602e-14
15	sex	0.910669	3.399370e-01
13	blood_group	0.627575	4.282461e-01
7	leukocyty	0.401204	5.264679e-01
8	relationship	0.352164	5.528905e-01
14	race	0.164493	6.850530e-01
3	smoker	0.040459	8.405866e-01
0	hemoglobin	0.030579	8.611826e-01

	atribut	vysledok	p value
1	etytr	0.024141	8.765262e-01
10	alp	0.013293	9.082124e-01
2	hbver	0.006697	9.347796e-01
4	alt	0.003232	9.546652e-01
5	trombocyty	0.001351	9.706815e-01
12	er-cv	0.001100	9.735381e-01
6	erytrocyty	0.000416	9.837190e-01
11	ast	0.000116	9.913885e-01
16	birthdate	0.000026	9.959571e-01

In [32]:
```
r1, r2 = chi2(data_quantile, y_train)
result = pd.DataFrame({"atribut":list(data_mm_scaled.columns), "vysledok": r1, "p value":
result = result.sort_values("vysledok", ascending=0)
result
```

Out[32]:

	atribut	vysledok	p value
9	hematokrit	158.794556	2.075054e-36
7	leukocyty	2.131568	1.442931e-01
15	sex	0.910669	3.399370e-01
13	blood_group	0.568131	4.510027e-01
8	relationship	0.351028	5.535319e-01
14	race	0.217087	6.412687e-01
10	alp	0.060123	8.063017e-01
2	hbver	0.043904	8.340324e-01
3	smoker	0.040459	8.405866e-01
12	er-cv	0.030083	8.623013e-01
0	hemoglobin	0.021391	8.837186e-01
4	alt	0.012118	9.123446e-01
1	etytr	0.005110	9.430103e-01
5	trombocyty	0.003464	9.530666e-01
16	birthdate	0.000260	9.871332e-01
6	erytrocyty	0.000234	9.877964e-01
11	ast	0.000002	9.987629e-01

Feature selection podľa f regresie:

Pre MinMaxScaler:

In [33]:
```
from sklearn.feature_selection import f_regression

r1, r2 = f_regression(data_mm_scaled, y_train)
```

```
result = pd.DataFrame({"atribut":list(x_train.columns), "vysledok": r1, "p value": r2})
result = result.sort_values("vysledok", ascending=0)
result
```

Out[33]:

	atribut	vysledok	p value
9	hematokrit	1300.898370	1.278384e-262
7	leukocyty	7.076351	7.827594e-03
13	blood_group	2.776251	9.571413e-02
8	relationship	2.261748	1.326469e-01
15	sex	1.822277	1.770837e-01
14	race	0.662690	4.156381e-01
0	hemoglobin	0.561047	4.538626e-01
1	etytr	0.405459	5.243029e-01
10	alp	0.164503	6.850557e-01
2	hbver	0.121178	7.277705e-01
3	smoker	0.068022	7.942465e-01
4	alt	0.040773	8.399820e-01
5	trombocyty	0.024629	8.752983e-01
12	er-cv	0.020034	8.874452e-01
6	erytrocyty	0.007082	9.329340e-01
11	ast	0.002102	9.634355e-01
16	birthdate	0.000159	9.899323e-01

Pre Robust Scaling:

In [34]:
```
r1, r2 = f_regression(data_rb_scaled, y_train)
result = pd.DataFrame({"atribut":list(x_train.columns), "vysledok": r1, "p value": r2})
result = result.sort_values("vysledok", ascending=0)
result
```

Out[34]:

	atribut	vysledok	p value
9	hematokrit	1300.898370	1.278384e-262
7	leukocyty	7.076351	7.827594e-03
13	blood_group	2.776251	9.571413e-02
8	relationship	2.261748	1.326469e-01
15	sex	1.822277	1.770837e-01
14	race	0.662690	4.156381e-01
0	hemoglobin	0.561047	4.538626e-01
1	etytr	0.405459	5.243029e-01
10	alp	0.164503	6.850557e-01
2	hbver	0.121178	7.277705e-01

	atribut	vysledok	p value
3	smoker	0.068022	7.942465e-01
4	alt	0.040773	8.399820e-01
5	trombocyty	0.024629	8.752983e-01
12	er-cv	0.020034	8.874452e-01
6	erytrocyty	0.007082	9.329340e-01
11	ast	0.002102	9.634355e-01
16	birthdate	0.000159	9.899323e-01

Pre Power Transformer:

In [35]:
```
r1, r2 = f_regression(data_power, y_train)
result = pd.DataFrame({"atribut":list(x_train.columns), "vysledok": r1, "p value": r2})
result = result.sort_values("vysledok", ascending=0)
result
```

Out[35]:

	atribut	vysledok	p value
9	hematokrit	1151.737710	8.391033e-235
7	leukocyty	7.022972	8.064135e-03
13	blood_group	2.985910	8.403370e-02
8	relationship	2.122337	1.452072e-01
15	sex	1.822277	1.770837e-01
14	race	0.869762	3.510517e-01
0	hemoglobin	0.556369	4.557507e-01
1	etytr	0.474283	4.910448e-01
10	alp	0.320965	5.710452e-01
2	hbver	0.154795	6.940057e-01
3	smoker	0.068022	7.942465e-01
4	alt	0.063926	8.004019e-01
5	trombocyty	0.024021	8.768365e-01
12	er-cv	0.020592	8.859002e-01
6	erytrocyty	0.008716	9.256208e-01
16	birthdate	0.004779	9.448902e-01
11	ast	0.002441	9.606007e-01

Pre Quantile Transformer:

In [36]:
```
r1, r2 = f_regression(data_quantile, y_train)
result = pd.DataFrame({"atribut":list(data_quantile.columns), "vysledok": r1, "p value": 
result = result.sort_values("vysledok", ascending=0)
result
```

Out[36]:

	atribut	vysledok	p value

	atribut	vysledok	p value
9	hematokrit	1092.546381	1.252459e-223
7	leukocyty	12.805002	3.479006e-04
13	blood_group	2.885797	8.940570e-02
8	relationship	1.964209	1.611057e-01
15	sex	1.822277	1.770837e-01
14	race	0.936788	3.331367e-01
10	alp	0.360566	5.482104e-01
2	hbver	0.263288	6.078858e-01
12	er-cv	0.180411	6.710322e-01
0	hemoglobin	0.128276	7.202362e-01
4	alt	0.072667	7.875002e-01
3	smoker	0.068022	7.942465e-01
1	etytr	0.030646	8.610365e-01
5	trombocyty	0.020774	8.854013e-01
16	birthdate	0.001560	9.684996e-01
6	erytrocyty	0.001403	9.701217e-01
11	ast	0.000014	9.969705e-01

Použili sme aj wrapper feature selection metódy pomocou SelectFromModel, znovu pre všetky použité metódy transformácie dát:

Pre MinMaxScaler:

In [37]:
```
from sklearn.feature_selection import SelectFromModel
from sklearn.linear_model import LogisticRegression

selector = SelectFromModel(estimator=LogisticRegression()).fit(data_mm_scaled, y_train)
print(selector.estimator_.coef_)
print(selector.threshold_)
selected = pd.DataFrame({"attribute":list(data_mm_scaled.columns), "selected": selector.ge
print(selected)

X_new = selector.transform(data_mm_scaled)
print(X_new.shape)
X_new
```

```
[[ 5.36499281e-01 -1.38113077e+00 -1.93156404e+00  5.22516785e-03
  -9.71550535e-02 -7.27708254e-03  5.81473011e-02  1.47367272e+00
   1.43108310e-01  6.53430965e+00  4.09760904e-01 -3.39705045e-02
  -3.03548340e-02 -1.36420336e-01 -1.24586737e-01 -1.05419307e-01
   3.26686136e-03]]
0.7654040505473184
       attribute  selected
0     hemoglobin     False
1          etytr      True
2          hbver      True
3         smoker     False
4            alt     False
5     trombocyty     False
6     erytrocyty     False
```

```
7      leukocyty      True
8   relationship     False
9     hematokrit      True
10           alp     False
11           ast     False
12         er-cv     False
13   blood_group     False
14          race     False
15           sex     False
16     birthdate     False
(7418, 4)
```

Out[37]:
```
array([[0.27579068, 0.35972809, 0.61757942, 0.41248362],
       [0.67248445, 0.37949909, 0.7564754 , 0.4629842 ],
       [0.30238276, 0.86460783, 0.60739921, 0.56344452],
       ...,
       [0.46717511, 0.75477079, 0.62833281, 0.63767197],
       [0.35253016, 0.39812134, 0.33783073, 0.42451841],
       [0.47117205, 0.38592512, 0.66987304, 0.24838009]])
```

Pre Robust Scaling:

In [38]:
```
selector = SelectFromModel(estimator=LogisticRegression()).fit(data_rb_scaled, y_train)
print(selector.estimator_.coef_)
print(selector.threshold_)
selected = pd.DataFrame({"attribute":list(data_rb_scaled.columns), "selected": selector.ge
print(selected)


X_new = selector.transform(data_rb_scaled)
print(X_new.shape)
X_new
```

```
[[ 0.13501707 -0.40085561 -0.46657343  0.00560401 -0.01871989 -0.00172928
   0.02007418  0.4141388   0.05719545  1.36098487  0.15237189 -0.00847773
  -0.00722293 -0.07902444 -0.0319813  -0.10843656  0.00181579]]
0.192366072274719
       attribute  selected
0      hemoglobin     False
1           etytr      True
2           hbver      True
3          smoker     False
4             alt     False
5      trombocyty     False
6      erytrocyty     False
7       leukocyty      True
8    relationship     False
9      hematokrit      True
10            alp     False
11            ast     False
12          er-cv     False
13    blood_group     False
14           race     False
15            sex     False
16      birthdate     False
(7418, 4)
```

Out[38]:
```
array([[-0.85483352, -0.61662484,  0.38377727, -0.55491082],
       [ 0.65360276, -0.527755  ,  0.92594518, -0.30002658],
       [-0.7537166 ,  1.65278864,  0.34403977,  0.20701228],
       ...,
       [-0.12709026,  1.15907569,  0.42575217,  0.5816497 ],
       [-0.56303006, -0.44404874, -0.70819645, -0.49416937],
       [-0.11189183, -0.49887027,  0.5879007 , -1.3831668 ]])
```

Pre Power Transformer:

In [39]:
```
selector = SelectFromModel(estimator=LogisticRegression()).fit(data_power, y_train)
print(selector.estimator_.coef_)
print(selector.threshold_)
selected = pd.DataFrame({"attribute":list(data_power.columns), "selected": selector.get_su
print(selected)

X_new = selector.transform(data_power)
print(X_new.shape)
X_new
```

```
[[ 0.10514965 -0.24032302 -0.34084142  0.00343983 -0.04497061 -0.00114434
   0.03761873  0.25895445  0.03897593  1.09120677  0.10995248 -0.00602025
  -0.00461926 -0.04734615 -0.03551946 -0.05416788  0.00171449]]
0.14246851329472457
       attribute  selected
0      hemoglobin     False
1           etytr      True
2           hbver      True
3          smoker     False
4             alt     False
5      trombocyty     False
6      erytrocyty     False
7       leukocyty      True
8    relationship     False
9      hematokrit      True
10            alp     False
11            ast     False
12          er-cv     False
13    blood_group     False
14           race     False
15            sex     False
16      birthdate     False
(7418, 4)
```

Out[39]:
```
array([[-1.30366073, -0.82164294,  0.58331037, -0.59327311],
       [ 0.9977348 , -0.70068246,  1.40417432, -0.29391114],
       [-1.1474497 ,  2.1918131 ,  0.52341353,  0.33365411],
       ...,
       [-0.1861741 ,  1.54828884,  0.646621  ,  0.82414268],
       [-0.85373929, -0.58700114, -1.04718543, -0.52292463],
       [-0.16299099, -0.66142687,  0.89157979, -1.489029  ]])
```

Pre Quantile Transformer:

In [40]:
```
selector = SelectFromModel(estimator=LogisticRegression()).fit(data_quantile, y_train)
print(selector.estimator_.coef_)
print(selector.threshold_)
selected = pd.DataFrame({"attribute":list(data_quantile.columns), "selected": selector.get
print(selected)


X_new = selector.transform(data_quantile)
print(X_new.shape)
X_new
```

```
[[ 0.33165184 -0.84019455 -1.15281076  0.01231275 -0.16089729  0.0179818
   0.13300028  0.72642416  0.11267988  3.4725106   0.37201793 -0.02939289
   0.00734216 -0.14156375 -0.11303467 -0.098753    0.00557737]]
0.45459680525952845
       attribute  selected
0      hemoglobin     False
1           etytr      True
2           hbver      True
3          smoker     False
4             alt     False
5      trombocyty     False
```

```
6     erytrocyty     False
7      leukocyty      True
8   relationship     False
9     hematokrit      True
10           alp     False
11           ast     False
12         er-cv     False
13   blood_group     False
14          race     False
15           sex     False
16     birthdate     False
(7418, 4)
```

Out[40]:

```
array([[0.10098735, 0.2052453 , 0.68926781, 0.25612033],
       [0.82484262, 0.2400035 , 0.92190639, 0.35343387],
       [0.13487358, 0.98551686, 0.67103549, 0.62403841],
       ...,
       [0.43844271, 0.93749846, 0.71132943, 0.82089739],
       [0.21549929, 0.27736837, 0.16643239, 0.27468819],
       [0.44618495, 0.25247166, 0.79217147, 0.08785775]])
```

SelectFromModel s L1 based feature selection:

Pre MinMaxScaler:

In [41]:

```
from sklearn.svm import LinearSVC
from sklearn.feature_selection import SelectFromModel

lsvc = LinearSVC(C=0.01, penalty="l1", dual=False).fit(data_mm_scaled, y_train)
selector = SelectFromModel(estimator=lsvc, prefit=True)
selected = pd.DataFrame({"attribute":list(data_mm_scaled.columns), "selected": selector.ge
print(selected)

X_new = selector.transform(data_mm_scaled)
print(X_new.shape)
X_new
```

```
       attribute  selected
0     hemoglobin     False
1          etytr      True
2          hbver      True
3         smoker     False
4            alt     False
5     trombocyty     False
6     erytrocyty     False
7      leukocyty     False
8   relationship     False
9     hematokrit      True
10           alp     False
11           ast     False
12         er-cv     False
13   blood_group      True
14          race     False
15           sex      True
16     birthdate     False
(7418, 5)
```

Out[41]:

```
array([[0.27579068, 0.35972809, 0.41248362, 0.14285714, 0.        ],
       [0.67248445, 0.37949909, 0.4629842 , 0.42857143, 1.        ],
       [0.30238276, 0.86460783, 0.56344452, 0.85714286, 1.        ],
       ...,
       [0.46717511, 0.75477079, 0.63767197, 0.85714286, 0.        ],
       [0.35253016, 0.39812134, 0.42451841, 0.28571429, 1.        ],
       [0.47117205, 0.38592512, 0.24838009, 0.        , 0.        ]])
```

Pre Robust Scaling:

```
In [42]: lsvc = LinearSVC(C=0.01, penalty="l1", dual=False).fit(data_rb_scaled, y_train)
         selector = SelectFromModel(estimator=lsvc, prefit=True)
         selected = pd.DataFrame({"attribute":list(data_rb_scaled.columns), "selected": selector.ge
         print(selected)

         X_new = selector.transform(data_rb_scaled)
         print(X_new.shape)
         X_new
```

```
        attribute  selected
0       hemoglobin     False
1            etytr      True
2            hbver      True
3           smoker     False
4              alt     False
5       trombocyty     False
6       erytrocyty     False
7        leukocyty      True
8     relationship      True
9       hematokrit      True
10             alp     False
11             ast     False
12           er-cv     False
13     blood_group      True
14            race      True
15             sex      True
16       birthdate     False
(7418, 8)
Out[42]: array([[-0.85483352, -0.61662484,  0.38377727, ..., -0.5       ,
                 -1.        , -1.        ],
                [ 0.65360276, -0.527755  ,  0.92594518, ...,  0.        ,
                  0.        ,  0.        ],
                [-0.7537166 ,  1.65278864,  0.34403977, ...,  0.75      ,
                  0.        ,  0.        ],
                ...,
                [-0.12709026,  1.15907569,  0.42575217, ...,  0.75      ,
                  0.        , -1.        ],
                [-0.56303006, -0.44404874, -0.70819645, ..., -0.25      ,
                  0.        ,  0.        ],
                [-0.11189183, -0.49887027,  0.5879007 , ..., -0.75      ,
                  0.        , -1.        ]])
```

Pre Power Transformer:

```
In [43]: lsvc = LinearSVC(C=0.01, penalty="l1", dual=False).fit(data_power, y_train)
         selector = SelectFromModel(estimator=lsvc, prefit=True)
         selected = pd.DataFrame({"attribute":list(data_power.columns), "selected": selector.get_su
         print(selected)

         X_new = selector.transform(data_power)
         print(X_new.shape)
         X_new
```

```
        attribute  selected
0       hemoglobin      True
1            etytr      True
2            hbver      True
3           smoker     False
4              alt     False
5       trombocyty     False
6       erytrocyty     False
7        leukocyty      True
8     relationship      True
9       hematokrit      True
10             alp      True
```

```
11          ast     False
12        er-cv     False
13  blood_group      True
14         race      True
15          sex      True
16    birthdate     False
(7418, 10)
```

Out[43]:
```
array([[ 0.90084997, -1.30366073, -0.82164294, ..., -1.03340363,
        -1.34475447, -1.00053937],
       [ 1.05880558,  0.9977348 , -0.70068246, ..., -0.09278226,
         0.1932455 ,  0.99946092],
       [ 0.2736398 , -1.1474497 ,  2.1918131 , ...,  1.08458915,
         0.1932455 ,  0.99946092],
       ...,
       [-0.5289725 , -0.1861741 ,  1.54828884, ...,  1.08458915,
         0.1932455 , -1.00053937],
       [ 0.51691705, -0.85373929, -0.58700114, ..., -0.54101816,
         0.1932455 ,  0.99946092],
       [ 0.45811031, -0.16299099, -0.66142687, ..., -1.59221293,
         0.1932455 , -1.00053937]])
```

Pre Quantile Transformer:

lsvc = LinearSVC(C=0.01, penalty="l1", dual=False).fit(data_quantile, y_train) selector = SelectFromModel(estimator=lsvc, prefit=True) selected = pd.DataFrame({"attribute":list(data_quantile.columns), "selected": selector.get_support()}) print(selected)

X_new = selector.transform(data_quantile) print(X_new.shape) X_new

Všetky metódy sa zhodujú, že hematokrit je najdôležitejší atribút. Leukocyty boli medzi niekoľkými atribútmi s najväčšou váhou pri takmer všetkých testoch. Často boli vybrané taktiež napr. hbver, etytr, blood_group. Presný výber atribútov záleží na výbere metódy pre výber atribútov pre strojové učenie.

4. Replikovateľnosť predspracovania

Aby bolo možné kód použiť znova na spracovanie dát, významné časti kódu sú vo formáte funkcií a je možné ich volať z rôznych miest v rámci notebooku.

Nasledujúca funkcia vykoná predspracovanie dát (transformáciu dát a feature selection) na testovacej množine, alebo na akejkoľvek inej množine dát. Predpokladá sa, že čistenie a integrácia dát (prvý bod zadania) už boli vykonané.

Na transformáciu dát sa aplikuje MinMaxScaler, následne sa vykoná feature selection pomocou SelectFromModel s logistickou regresiou. Funkcia zároveň vypíše, ktoré atribúty boli zvolené vo feature selection.

In [44]:
```python
from sklearn.pipeline import Pipeline

def predspracuj(data_x, data_y):
    pipe = Pipeline([('mm', MinMaxScaler()), ('lr', SelectFromModel(estimator=LogisticRegr
    selector = pipe.fit(data_x, data_y)

    selected = pd.DataFrame({"attribute":list(data_x.columns), "selected": selector.named_
    print(selected)
    selected = selected[selected["selected"] == True]

    new_data_x = selector.transform(data_x)
    return new_data_x, selected['attribute']

predspracuj(x_test, y_test)
```

```
        attribute  selected
0      hemoglobin     False
1           etytr      True
2           hbver      True
3          smoker     False
4             alt     False
5      trombocyty     False
6      erytrocyty     False
7       leukocyty      True
8    relationship     False
9      hematokrit      True
10            alp     False
11            ast     False
12          er-cv     False
13    blood_group     False
14           race     False
15            sex     False
16      birthdate     False
```

Out[44]:

```
(array([[0.22509558, 0.5034429 , 0.26446319, 0.43008949],
        [0.37152839, 0.36188088, 0.38197471, 0.5127333 ],
        [0.29532261, 0.62567789, 0.55808103, 0.37621049],
        ...,
        [0.5279106 , 0.69499551, 0.61921986, 0.13330305],
        [0.64541249, 0.47518789, 0.44438607, 0.5915333 ],
        [0.32014191, 0.26797194, 0.14122885, 0.43606303]]),
 1          etytr
 2          hbver
 7      leukocyty
 9     hematokrit
 Name: attribute, dtype: object)
```

Výstupom je upravená trénovacia dátová sada so zvolenými atribútmy pre strojové učenie.

In [45]:

```
new_frame, new_columns = predspracuj(x_train, y_train)
new_frame = pd.DataFrame(new_frame, columns = new_columns)
print(new_frame.head())
new_frame.to_csv("phase2_result.csv", index=False)
```

```
        attribute  selected
0      hemoglobin     False
1           etytr      True
2           hbver      True
3          smoker     False
4             alt     False
5      trombocyty     False
6      erytrocyty     False
7       leukocyty      True
8    relationship     False
9      hematokrit      True
10            alp     False
11            ast     False
12          er-cv     False
13    blood_group     False
14           race     False
15            sex     False
16      birthdate     False
attribute     etytr     hbver  leukocyty  hematokrit
0          0.275791  0.359728   0.617579    0.412484
1          0.672484  0.379499   0.756475    0.462984
2          0.302383  0.864608   0.607399    0.563445
3          0.405543  0.291158   0.799714    0.359395
4          0.414586  0.397449   0.332851    0.424358
```