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1 task2/README.txt

```
1  README.txt
2  USERS.txt
3  project.pdf
4
5  task2/part1/classifier.py
6  task2/part1/predictions.csv
7  task2/part1/requirements.txt
8
9  task2/part2/regression.py
10 task2/part2/predictions.csv
11 task2/part2/requirements.txt
```

2 task2/USERS.txt

```
1 aviram.aloni,208377598
2 roizhv22,208648154
3 assafine,319091773
4 omerfree,208966820
```

IML Hackathon 2022

Aviram Aloni, Assaf Fine, Roi Zehavi, Omer Freeman

Describing the dataset

In our project, we decided to work on the second challenge: [Detecting Attributes of Breast Cancer](#). The data given to us in this challenge is an actual medical data, provided by medical centers. As such, it has many missing values, free-text categories, and obviously contain a decent amount of noise. The training dataset contains 65,798 entries (across train and test), each with 34 features.

Cleaning and preprocessing

After taking a brief look at the data, we decided to brainstorm together, in order to analyze and better understand each and every feature given. Some features were easy to figure out, some were unclear and required some medical background to understand. We checked, for each feature, its unique values in the dataset, and its distribution. This helped us with understanding the feature, its valid values (or values range), how a missing value of this feature looks like, and most importantly, how should we categorize this feature values, and how to treat a new value of this feature, when preprocessing new data. Generally, we decided to categorize the values in each feature using different techniques, such as dummy nodes, detecting regular expressions and categorizing accordingly, averaging for multi-decimal value features, and many more. As the dataset contains quite a lot of features, we decided to give up on some features that we thought were irrelevant for the prediction, or to merge some together in order to create new features, which we believe describe all merged features better. In some features, there were unique values that stood out for being extra uncommon - in those cases we usually decided to give up on all specific samples containing them.

Part 1: Predicting Metastases

Exploring data analysis

Our main effort was trying to figure out the relationships and correlation between different features, in order to choose a general agenda for our learning algorithm. Measuring the Pearson correlation between the different features made us realize that many features have a distinct linkage to other features, so we decided to go for a complex multi label model - instead of a simple one which do not assume connection between the different features.

Considerations that guided our design of the learning systems

When first reading the challenge, we realized that we're facing a multi-label, multi-class categories learning problem. So, our main consideration was how to train our model. As multi-label problems were not discussed in class, we tried to figure out ourselves what solutions may target the problem most precisely. Eventually, 3 main approaches came into consideration: the first one, was to train 11 different models, as each model is linked to a specific breast cancer type, and after that - to combine all predictions, to create a multi label prediction for each sample. We eventually rejected this approach as many links were found among different features. The second approach was fitting a model over the power set of all breast cancer types, and the third one was training a neural network, which outputs a 11 entries vector, using the SoftMax function, to show the probability risk for each type of cancer - and then using thresholds to derive labels in the expected format.

After careful thought, we decided to use scikit's Multilabel k Nearest Neighbors model. The reason for giving up on the second approach was mainly because we believed that the power set was a bit too big, which might

cause some samples to be misclassified. As for the third approach - even though we thought that targeting our learning problem with neural networks is the best option, we had to give up on it due to technical issues and lack of knowledge in the neural networks field.

Baseline

In order to understand how our dataset behaves, and to get a sense of the problem's complexity (after it was preprocessed), we decided to use a baseline - a naive approach against which we'll compare more complex models. Our chosen baseline was decision stamp. We've decided to split our training data into train and validation sets, and with that to fit and test our stamp with. Unsurprisingly, we got high accuracy value, which implies some overfit of the model over the training set. In order to handle this issue we decided to drop off duplicate samples in our dataset.

Our learning system

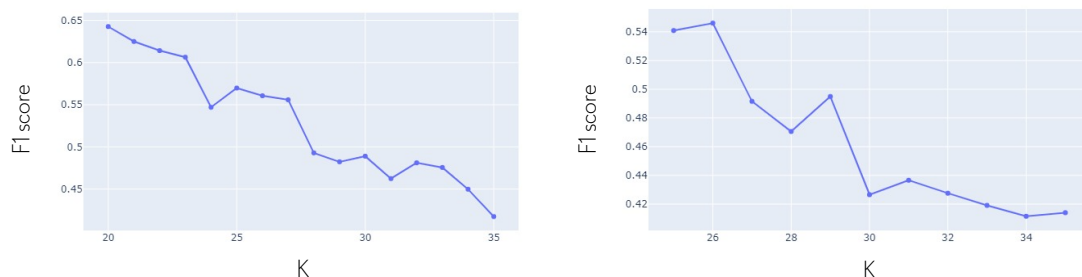
We decided to use the KNN model to target our learning problem for several reasons, the main one was that KNN is a learning model which is fast and simple - but yet strong and powerful. Also, as it is obvious that our learning problem has non-linear decision boundaries, when using KNN, we can come up with a highly flexible decision boundary adjusting the value of k .

Choosing hyperparameters

In the graphs below, we can see the f1 score error as a function of k - the number of neighbors used by the algorithm. We tried to find a spot where k is large enough to allow a good expressivity of our data, and on the other hand, a k small enough to not cause our model to underfit the data.

Eventually, we decided to choose $k=25$, which had a f1 score value of 0.56989. The use of this k value shows nice f1 scores, and its large enough to express our data well.

Figure 1.1 & Figure 1.2: The F1 score as a function of K (number of neighbors)



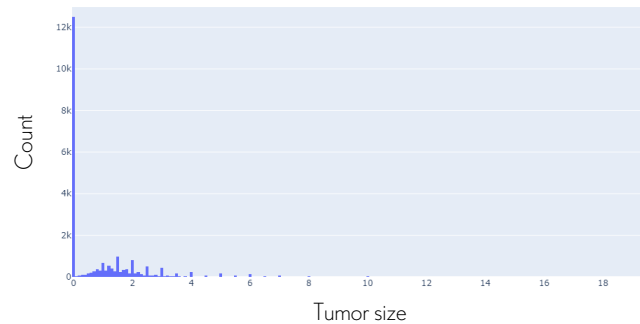
FINAL RESULTS: Micro f1: 0.6575 Macro f1: 0.4917

Part 2: Predicting Tumor Size

Exploring data analysis

In this part, we were asked to predict the diagnosed tumor size of patients. We tried to understand better the distribution and scale of the labels - to do so, we plotted a histogram of the tumor size (attached below).

Figure 2: Tumor size histogram



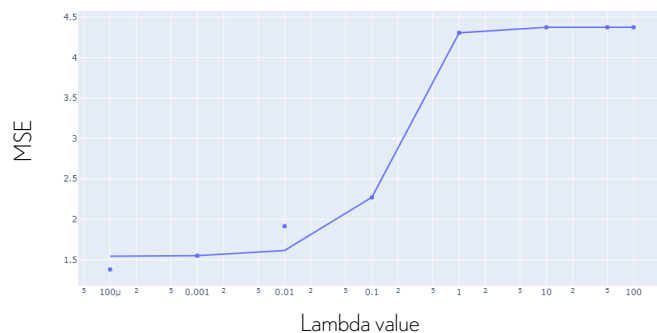
Considerations that guided our design of the learning systems

As the second learning problem we were required to handle was a regression problem, we decided to consider some regression models which we thought suite the problem best: linear regression, ridge regression and decision tree regressor. We trained and tested each and every model described before, and evaluated their behavior on our data. We also tried to enhance the models' performances, using kernels and ensemblers like random forest.

Our learning system

After examination all 3 regression models on our data, we decided to choose random forest regressor as our learning model. In the graph below (figure 3) we can see the MSE value as a function of the regularization parameter value (lambda).

Figure 3: MSE as a function of the RF regularization parameter



FINAL RESULTS: MSE: 0.7018

4 task2/part1/classifier.py

```
1 import ast
2 import re
3 import pandas as pd
4 import numpy as np
5 from skmultilearn.adapt import MLkNN
6
7 BASIC_STAGE = 'אבחנה-Basic stage'
8 DIAGNOSTIC_DATE = 'אבחנה-Diagnosis date'
9 LYMPHOVASCULAR = 'אבחנה-Ivi -Lymphovascular invasion'
10 METASTASES_MARK = 'אבחנה-M -metastases mark (TNM)'
11 MARGIN_TYPE = 'אבחנה-Margin Type'
12 SIDE_TYPE = 'אבחנה-Side'
13 STAGE = 'אבחנה-Stage'
14 POSITIVE_NODES = 'אבחנה-Positive nodes'
15 TUMOR_DEPTH = 'אבחנה-Tumor depth'
16 TUMOR_WIDTH = 'אבחנה-Tumor width'
17 FROM_NAME = 'Form Name'
18 LABEL_DICT = {}
19 TRAIN_LABELS = {'LYM - Lymph nodes', 'BON - Bones', 'SKI - Skin',
20                'HEP - Hepatic',
21                'PLE - Pleura', 'PUL - Pulmonary', 'BRA - Brain',
22                'MAR - Bone Marrow',
23                'ADR - Adrenals', 'OTH - Other', 'PER - Peritoneum'}
24
25 """
26 Parsing function for different features
27 """
28
29 def parse_HER2(word):
30     neg_set = {"eg", "-", "akhkh", "ne", "שלי", "_", "no"}
31     pos_set = {"pos", "os", "+", "י", "po", "yes", "amp"}
32     for n in neg_set:
33         if n in word.lower():
34             return -1
35     for p in pos_set:
36         if p in word.lower():
37             return 1
38     return 0
39
40
41 def parse_Histopatological_degree(word):
42     word = word.lower()
43     regex = [["g4", "gx", "un", "not"], ["g3", "poor"], ["g2", "mod"],
44             ["g1", "well"]]
45     for i in range(len(regex)):
46         for pattern in regex[i]:
47             if pattern in word:
48                 return i
49     return -1
50
51
52 def parse_KI67(word):
53     regx1 = re.match(".*?(\\d+).*(\\d+).*", word)
54     regx2 = re.match(".*?(\\d+).*", word)
55     if regx1:
56         return np.average([int(i) for i in regx1.groups()])
57     elif regx2:
58         return regx2.groups()[0]
59     if "low" in word.lower():
```

```

60         return 10
61     if "high" in word.lower():
62         return 90
63     return -1
64
65
66 def parse_TNM(word):
67     if "1" in word:
68         return 1
69     elif "2" in word:
70         return 2
71     elif "3" in word:
72         return 3
73     elif "0" in word:
74         return 0
75     elif "4" in word:
76         return 4
77     elif "x" in word.lower():
78         return 5
79     return -1
80
81
82 def parse_Nodes_exam(word):
83     if word == "":
84         return 6
85     return int(word)
86
87
88 def parse_Nodes_exam_pos(word):
89     if word == "":
90         return 1
91     return int(word)
92
93
94 def is_surgery(col1, col2, col3):
95     res = []
96     for i in range(len(col1)):
97         if col1[i] == "" and col2[i] == "" and col3[i] == "":
98             res.append(0)
99         else:
100             res.append(1)
101     return pd.Series(data=res)
102
103
104 def parse_er_pr(word):
105     word = word.lower()
106     strong = {"st"}
107     weak = {"שׁוּׁ", "we"}
108     if "eg" in word or "-" in word:
109         return 0
110     for st in strong:
111         if st in word:
112             return 3
113     for w in weak:
114         if w in word:
115             return 1
116
117     return 2
118
119
120 def extract_labels(labels_set):
121     res = set()
122     for lst in labels_set:
123         if lst == "":
124             continue
125         lst = ast.literal_eval(lst)
126         for v in lst:
127             res.add(v)

```



```

128     return res
129
130
131 def preprocess_basic_stage(df):
132     df[df[BASIC_STAGE] == 'Null'] = np.NaN
133     return pd.get_dummies(df, columns=[BASIC_STAGE], prefix='stage') # here
134
135
136 def preprocess_diagnosis_date(df):
137     df['diagnosis_date'] = pd.to_datetime(df[DIAGNOSTIC_DATE])
138     return df.drop(columns=DIAGNOSTIC_DATE)
139
140
141 def preprocess_lymphovascular_invasion(df):
142     return df.drop(columns=LYMPHOVASCULAR)
143
144
145 def preprocess_metastases_mark(df):
146     return pd.get_dummies(df, columns=[METASTASES_MARK],
147                             prefix='metastases_mark')
148
149
150 def preprocess_form_name(df):
151     return pd.get_dummies(df, columns=[FROM_NAME],
152                             prefix='form_name') # HERE
153
154
155 def preprocess_margin_type(df):
156     return pd.get_dummies(df, columns=[MARGIN_TYPE], prefix='margin_type')
157
158
159 def preprocess_side_type(df):
160     return pd.get_dummies(df, columns=[SIDE_TYPE], prefix='side')
161
162
163 def preprocess_stage(df):
164     df.loc[df[STAGE].isna() & ~(df[POSITIVE_NODES].astype('float').notna() & (
165         df[POSITIVE_NODES] > 0.5)), STAGE] = 'Stage1'
166     df.loc[df[STAGE].isna() & (df[POSITIVE_NODES].astype('float').notna() & (
167         df[POSITIVE_NODES] > 0.5)), STAGE] = 'Stage2a'
168     return pd.get_dummies(df, columns=[STAGE], prefix='stage')
169
170
171 def preprocess(df, preprocessors):
172     for preprocessor in preprocessors:
173         df = preprocessor(df)
174     return df
175
176
177 def parse_age(word):
178     if word == "":
179         return 55
180     return float(word)
181
182
183 def update_label_row(df):
184     for i, row in df.iterrows():
185         my_label = row["metastases_sites_raw"]
186         # print(row.index)
187         for col in row.index:
188             if col in my_label:
189                 df.at[i, col] = 1
190             else:
191                 df.at[i, col] = 0
192
193
194 def match_columns(df, expected_columns):
195     missing_columns = list(set(expected_columns) - set(df.columns))

```

```

196     excess_columns = list(set(df.columns) - set(expected_columns))
197     df[missing_columns] = [0] * len(missing_columns)
198     return df.drop(columns=excess_columns)
199
200
201 def parse_data(file_to_be_parsed: str, train_mode: bool):
202     """
203     file_to_be_parsed : .csv path to be parsed.
204     This is the main parsing function - this creates the train, test,
205     and label that were used during development.
206     """
207     pd.set_option('display.max_columns', None)
208     train = pd.read_csv(file_to_be_parsed, encoding="UTF-8")
209     train.drop_duplicates()
210
211     # parse data
212     train = preprocess(train, [preprocess_basic_stage,
213                               preprocess_lymphovascular_invasion,
214                               preprocess_metastases_mark,
215                               preprocess_margin_type,
216                               preprocess_side_type,
217                               preprocess_stage,
218                               preprocess_form_name
219                               ])
220
221     train = train.fillna("")
222     train["אבחנה-Her2"] = train["אבחנה-Her2"].apply(parse_HER2)
223     # delete the col diagnosis.
224     train['אבחנה-Histopatological degree'] = train[
225         'אבחנה-Histopatological degree']. \
226         apply(parse_Histopatological_degree)
227     train['אבחנה-KI67 protein'] = train['אבחנה-KI67 protein'].apply(parse_KI67)
228     train['אבחנה-N -lymph nodes mark (TNM)'] = train[
229         'אבחנה-N -lymph nodes mark (TNM)'].apply(parse_TNM)
230     train['אבחנה-Nodes exam'] = train['אבחנה-Nodes exam']. \
231         apply(parse_Nodes_exam)
232     train['אבחנה-Positive nodes'] = train['אבחנה-Positive nodes']. \
233         apply(parse_Nodes_exam_pos)
234     train['אבחנה-Age'] = train['אבחנה-Age'].apply(parse_age)
235     train['אבחנה-Surgery sum'] = train['אבחנה-Surgery sum'].apply(
236         lambda x: 0 if x == "" else x)
237
238     train.drop(columns=['אבחנה-Surgery date1', 'אבחנה-Lymphatic penetration',
239                       'אבחנה-Surgery name3',
240                       'surgery before or after-Activity date',
241                       'id-hushed_internalpatientid', ' Hospital',
242                       DIAGNOSTIC_DATE,
243                       'אבחנה-Surgery date2', 'אבחנה-Surgery date3',
244                       'אבחנה-Surgery name1', 'User Name',
245                       'אבחנה-Histological diagnosis',
246                       'אבחנה-Surgery name2', 'אבחנה-Surgery name2', 'אבחנה-Tumor depth',
247                       'אבחנה-Tumor width'], inplace=True)
248
249     # if train_mode:
250     #     # 'Unnamed: 0'
251     #     train.drop(columns=['Unnamed: 0'], inplace=True)
252
253     train['אבחנה-T -Tumor mark (TNM)'] = train['אבחנה-T -Tumor mark (TNM)'] \
254         .apply(parse_TNM)
255
256     train['אבחנה-er'] = train['אבחנה-er'].apply(parse_er_pr)
257     train['אבחנה-pr'] = train['אבחנה-pr'].apply(parse_er_pr)
258
259     # make sure dummies cover all possible features in the train
260     surgery_before_or_after_activity = {'בלוטות+למפקטומי-שד-כירו',
261                                         'כריתה בגישה זעירה דרך העטרה-שד',
262                                         'בלוטות+כריתה בגישה זעירה-שד',
263                                         'שד למפקטומי-כירורגיה',
264                                         'בלוטות+מסטקטומי-שד-כירו',

```

```

264         'קרינה תוך +בלוטות+למפקטומי-שד-כיר'
265         'ניתוחית(intrabeam)',
266         'הוצאת בלוטות לימפה-כירור',
267         'בלוטות בית שח.הוצ-שד-כיר',
268         'שד מסטקטומי-כירורגיה',
269         'שנוי מי/הוצ טבעת-לאפ-כיר'}
270
271 intersect_sur = surgery_before_or_after_activity. \
272     difference(train['surgery before or after-Actual activity'].unique())
273 if len(intersect_sur) != 0:
274     for val in intersect_sur:
275         train.loc[len(train.index)] = \
276             {'surgery before or after-Actual activity': val}
277
278 sub_df = pd.get_dummies(train['surgery before or after-Actual activity'])
279 train = pd.concat((train, sub_df), axis=1)
280 train.drop(columns=['surgery before or after-Actual activity'],
281             inplace=True)
282 train.drop(train.tail(len(intersect_sur)).index, inplace=True)
283
284 if train_mode:
285     # Change labels the matrix
286     label_df = pd.DataFrame(data=train['metastases_sites_raw'])
287     labels = extract_labels(train['metastases_sites_raw'].unique())
288     for label in TRAIN_LABELS:
289         label_df[label] = [0 for _ in label_df.index]
290     update_label_row(label_df)
291     label_df.drop(columns=['metastases_sites_raw', ], inplace=True)
292     train.drop(columns=['metastases_sites_raw'],
293                inplace=True)
294
295     return train, label_df, list(labels)
296
297 else:
298     return train, None, None
299
300
301 def extract_output(arr):
302     prediction = []
303     for i in range(len(arr)):
304         val = []
305         for j in range(len(arr[0])):
306             if arr[i][j] == 1:
307                 val.append(LABEL_DICT[j])
308             # if val != "[:":
309             #     val = val[:-2]
310             # val += "]"
311         prediction.append(val)
312     res = pd.DataFrame()
313     res['מיקום-Location of distal metastases'] = prediction
314     # res.reset_index(drop=True, inplace=True)
315     return res
316
317
318
319 if __name__ == "__main__":
320     # X, y, labels = parse_data("train_data.csv", True)
321
322
323     # test_X, test_y, test_labels = parse_data("test_data.csv", True)
324     model = MLkNN(k=25)
325
326     all_data, all_test, labels = parse_data("train.feats.csv", True)
327     LABEL_DICT = {i: labels[i] for i in range(len(labels))}
328
329     real_test, _1, _2 = parse_data("test.feats.csv", False)
330     to_drop = list(set(all_data.columns).difference(set(real_test.columns)))
331     all_data.drop(columns=to_drop, inplace=True)

```

```
332     model.fit(all_data, all_test.to_numpy())
333     pred = model.predict(real_test)
334     # create predictions
335     extract_output(pred.toarray()).to_csv("prediction.csv", index=False)
```

5 task2/part1/predictions.csv

```
1  אבחנה-Location of distal metastases
2  []
3  []
4  []
5  []
6  []
7  []
8  []
9  []
10 []
11 []
12 []
13 []
14 []
15 []
16 ['BON - Bones']
17 []
18 []
19 []
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22 []
23 []
24 []
25 []
26 []
27 []
28 []
29 []
30 []
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10002 *****
10003 *** THIS FILE HAD TOO MANY LINES AND WAS TRUNCATED ***
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6 task2/part1/requirements.txt

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2 anyio==3.5.0
3 argon2-cffi==21.3.0
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36 kiwisolver==1.3.1
37 MarkupSafe==2.1.0
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39 matplotlib-inline==0.1.3
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59 Pygments==2.11.2
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67 pywin32-ctypes==0.2.0
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88 pandas==1.4.2
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7 task2/part2/predictions.csv

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9806	0.011481114039242811
9807	0.011481114039242811
9808	0.011481114039242811
9809	0.011481114039242811
9810	0.7010276124203368
9811	0.6879238003687813
9812	0.6879238003687813
9813	0.6879238003687813
9814	0.011481114039242811
9815	0.4634526889552007
9816	0.4634526889552007
9817	0.4634526889552007
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9826	0.4634526889552007
9827	1.2932599899562094
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9998 1.0658304014626747
9999 1.0658304014626747
10000 1.0658304014626747
10001
10002 *****
10003 *** THIS FILE HAD TOO MANY LINES AND WAS TRUNCATED ***
10004 *****
```

8 task2/part2/regression.py

```
1  import ast
2  import re
3
4  import pandas as pd
5  import sklearn
6  import itertools
7  import numpy as np
8  from sklearn.metrics import f1_score
9  import plotly.graph_objects as go
10 from sklearn.metrics import mean_squared_error as mse
11 from sklearn.ensemble import RandomForestRegressor
12
13 BASIC_STAGE = 'אבחנה-Basic stage'
14 DIAGNOSTIC_DATE = 'אבחנה-Diagnosis date'
15 LYMPHOVASCULAR = 'אבחנה-Ivi -Lymphovascular invasion'
16 METASTASES_MARK = 'אבחנה-M -metastases mark (TNM)'
17 MARGIN_TYPE = 'אבחנה-Margin Type'
18 SIDE_TYPE = 'אבחנה-Side'
19 STAGE = 'אבחנה-Stage'
20 POSITIVE_NODES = 'אבחנה-Positive nodes'
21 TUMOR_DEPTH = 'אבחנה-Tumor depth'
22 TUMOR_WIDTH = 'אבחנה-Tumor width'
23 FROM_NAME = 'Form Name'
24 LABEL_DICT = {}
25 TRAIN_LABELS = {'LYM - Lymph nodes', 'BON - Bones', 'SKI - Skin',
26                'HEP - Hepatic',
27                'PLE - Pleura', 'PUL - Pulmonary', 'BRA - Brain',
28                'MAR - Bone Marrow',
29                'ADR - Adrenals', 'OTH - Other', 'PER - Peritoneum'}
30
31
32 def parse_HER2(word):
33     neg_set = {"eg", "-", "akhkh", "ne", "שלי", "_", "no"}
34     pos_set = {"pos", "os", "+", "י", "po", "yes", "amp"}
35     for n in neg_set:
36         if n in word.lower():
37             return -1
38     for p in pos_set:
39         if p in word.lower():
40             return 1
41     return 0
42
43
44 def parse_Histopatological_degree(word):
45     word = word.lower()
46     regex = [["g4", "gx", "un", "not"], ["g3", "poor"], ["g2", "mod"],
47             ["g1", "well"]]
48     for i in range(len(regex)):
49         for pattern in regex[i]:
50             if pattern in word:
51                 return i
52     return -1
53
54
55 def parse_KI67(word):
56     regx1 = re.match(".*?(\\d+).*(\\d+).*", word)
57     regx2 = re.match(".*?(\\d+).*", word)
58     if regx1:
59         return np.average([int(i) for i in regx1.groups()])
```

```

60     elif regx2:
61         return regx2.groups()[0]
62     if "low" in word.lower():
63         return 10
64     if "high" in word.lower():
65         return 90
66     return -1
67
68
69 def parse_TNM(word):
70     if "1" in word:
71         return 1
72     elif "2" in word:
73         return 2
74     elif "3" in word:
75         return 3
76     elif "0" in word:
77         return 0
78     elif "4" in word:
79         return 4
80     elif "x" in word.lower():
81         return 5
82     return -1
83
84
85 def parse_Nodes_exam(word):
86     if word == "":
87         return 6
88     return int(word)
89
90
91 def parse_Nodes_exam_pos(word):
92     if word == "":
93         return 1
94     return int(word)
95
96
97 def is_surgery(col1, col2, col3):
98     res = []
99     for i in range(len(col1)):
100         if col1[i] == "" and col2[i] == "" and col3[i] == "":
101             res.append(0)
102         else:
103             res.append(1)
104     return pd.Series(data=res)
105
106
107 def parse_er_pr(word):
108     word = word.lower()
109     strong = {"st"}
110     weak = {"שָׁלָה", "we"}
111     if "eg" in word or "-" in word:
112         return 0
113     for st in strong:
114         if st in word:
115             return 3
116     for w in weak:
117         if w in word:
118             return 1
119
120     return 2
121
122
123 def extract_labels(labels_set):
124     res = set()
125     for lst in labels_set:
126         if lst == "":
127             continue

```



```

128         lst = ast.literal_eval(lst)
129         for v in lst:
130             res.add(v)
131     return res
132
133
134 def preprocess_basic_stage(df):
135     df[df[BASIC_STAGE] == 'Null'] = np.NaN
136     return pd.get_dummies(df, columns=[BASIC_STAGE], prefix='stage') # here
137
138
139 def preprocess_diagnosis_date(df):
140     df['diagnosis_date'] = pd.to_datetime(df[DIAGNOSTIC_DATE])
141     return df.drop(columns=DIAGNOSTIC_DATE)
142
143
144 def preprocess_lymphovascular_invasion(df):
145     return df.drop(columns=LYMPHOVASCULAR)
146
147
148 def preprocess_metastases_mark(df):
149     return pd.get_dummies(df, columns=[METASTASES_MARK],
150                             prefix='metastases_mark')
151
152
153 def preprocess_form_name(df):
154     return pd.get_dummies(df, columns=[FROM_NAME],
155                             prefix='form_name') # HERE
156
157
158 def preprocess_margin_type(df):
159     return pd.get_dummies(df, columns=[MARGIN_TYPE], prefix='margin_type')
160
161
162 def preprocess_side_type(df):
163     return pd.get_dummies(df, columns=[SIDE_TYPE], prefix='side')
164
165
166 def preprocess_stage(df):
167     df.loc[df[STAGE].isna() & ~(df[POSITIVE_NODES].astype('float').notna() & (
168         df[POSITIVE_NODES] > 0.5)), STAGE] = 'Stage1'
169     df.loc[df[STAGE].isna() & (df[POSITIVE_NODES].astype('float').notna() & (
170         df[POSITIVE_NODES] > 0.5)), STAGE] = 'Stage2a'
171     return pd.get_dummies(df, columns=[STAGE], prefix='stage')
172
173
174 def preprocess(df, preprocessors):
175     for preprocessor in preprocessors:
176         df = preprocessor(df)
177     return df
178
179
180 def parse_age(word):
181     if word == "":
182         return 55
183     return float(word)
184
185
186 def update_label_row(df):
187     for i, row in df.iterrows():
188         my_label = row["metastases_sites_raw"]
189         # print(row.index)
190         for col in row.index:
191             if col in my_label:
192                 df.at[i, col] = 1
193             else:
194                 df.at[i, col] = 0
195

```

```

196
197 def match_columns(df, expected_columns):
198     missing_columns = list(set(expected_columns) - set(df.columns))
199     excess_columns = list(set(df.columns) - set(expected_columns))
200     df[missing_columns] = [0] * len(missing_columns)
201     return df.drop(columns=excess_columns)
202
203
204 def parse_data(df_to_parse, training_df=True):
205     """
206     file_to_be_parsed : .csv path to be parsed.
207     """
208     if training_df:
209         df_to_parse.drop_duplicates()
210
211     # parse data
212     df_to_parse = preprocess(df_to_parse, [preprocess_basic_stage,
213                                           preprocess_lymphovascular_invasion,
214                                           preprocess_metastases_mark,
215                                           preprocess_margin_type,
216                                           preprocess_side_type,
217                                           preprocess_stage,
218                                           preprocess_form_name
219                                           ])
220
221     df_to_parse = df_to_parse.fillna("")
222     df_to_parse["אבחנה-Her2"] = df_to_parse["אבחנה-Her2"].apply(parse_HER2)
223     # delete the col diagnosis.
224     df_to_parse['אבחנה-Histopatological degree'] = df_to_parse[
225         'אבחנה-Histopatological degree']. \
226         apply(parse_Histopatological_degree)
227     df_to_parse['אבחנה-KI67 protein'] = df_to_parse[
228         'אבחנה-KI67 protein'].apply(parse_KI67)
229     df_to_parse['אבחנה-N -lymph nodes mark (TNM)'] = df_to_parse[
230         'אבחנה-N -lymph nodes mark (TNM)'].apply(parse_TNM)
231     df_to_parse['אבחנה-Nodes exam'] = df_to_parse['אבחנה-Nodes exam']. \
232         apply(parse_Nodes_exam)
233     df_to_parse['אבחנה-Positive nodes'] = df_to_parse['אבחנה-Positive nodes']. \
234         apply(parse_Nodes_exam_pos)
235     df_to_parse['אבחנה-Age'] = df_to_parse['אבחנה-Age'].apply(parse_age)
236     df_to_parse['אבחנה-Surgery sum'] = df_to_parse['אבחנה-Surgery sum'].apply(
237         lambda x: 0 if x == "" else x)
238
239     df_to_parse.drop(
240         columns=['אבחנה-Surgery date1', 'אבחנה-Lymphatic penetration',
241                 'אבחנה-Surgery name3',
242                 'surgery before or after-Activity date',
243                 'id-hushed_internalpatientid', 'Hospital',
244                 # 'Unnamed: 0', DIAGNOSTIC_DATE,
245                 'אבחנה-Surgery date2', 'אבחנה-Surgery date3',
246                 'אבחנה-Surgery name1', 'User Name',
247                 'אבחנה-Histological diagnosis'
248                 , 'אבחנה-Surgery name2', 'אבחנה-Surgery name2',
249                 'אבחנה-Tumor depth',
250                 'אבחנה-Tumor width'], inplace=True)
251     df_to_parse['אבחנה-T -Tumor mark (TNM)'] = df_to_parse[
252         'אבחנה-T -Tumor mark (TNM)'] \
253         .apply(parse_TNM)
254
255     df_to_parse['אבחנה-er'] = df_to_parse['אבחנה-er'].apply(parse_er_pr)
256     df_to_parse['אבחנה-pr'] = df_to_parse['אבחנה-pr'].apply(parse_er_pr)
257
258     # make sure dummies cover all possible features in the df_to_parse
259     surgery_before_or_after_activity = {'בלוטות+למפקטומי-שד-כירו',
260                                         'כריתה בגישה זעירה דרך העטרה-שד',
261                                         'בלוטות+כריתה בגישה זעירה-שד',
262                                         'שד למפקטומי-כירורגיה',
263                                         'בלוטות+מסטקטומי-שד-כירו',
264                                         'קרונה תוך +בלוטות+למפקטומי-שד-כירו'

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```

264         'ניתוחית(intrabeam)',
265         'הוצאת בלוטות לימפה-כירור',
266         'בלוטות בית שח.הוצ-שד-כיר',
267         'שד מסטקטומי-כירורגיה',
268         'שנוי מי/הוצ טבעת-לאפ-כיר'}
269
270 intersect_sur = surgery_before_or_after_activity. \
271     difference(
272         df_to_parse['surgery before or after-Actual activity'].unique())
273 if len(intersect_sur) != 0:
274     for val in intersect_sur:
275         df_to_parse.loc[len(df_to_parse.index)] = \
276             {'surgery before or after-Actual activity': val}
277
278 sub_df = pd.get_dummies(
279     df_to_parse['surgery before or after-Actual activity'])
280 df_to_parse = pd.concat((df_to_parse, sub_df), axis=1)
281 df_to_parse.drop(columns=['surgery before or after-Actual activity'],
282                  inplace=True)
283 df_to_parse.drop(df_to_parse.tail(len(intersect_sur)).index, inplace=True)
284
285 # Change labels the matrix
286 # label_df = pd.DataFrame(data=df_to_parse['metastases_sites_raw'])
287 # labels = extract_labels(df_to_parse['metastases_sites_raw'].unique())
288 # for label in TRAIN_LABELS:
289 #     label_df[label] = [0 for _ in label_df.index]
290 # update_label_row(label_df)
291 # label_df.drop(columns=['metastases_sites_raw', ], inplace=True)
292 # df_to_parse.drop(columns=['metastases_sites_raw', 'is_malignant'], inplace=True)
293
294 # return df_to_parse, label_df, list(labels)
295 if training_df:
296     df_to_parse = df_to_parse[
297         ['אבחנה-Age', 'אבחנה-Her2', 'אבחנה-Histopatological degree',
298          'אבחנה-KI67 protein', 'אבחנה-N -lymph nodes mark (TNM)',
299          'אבחנה-Nodes exam', 'אבחנה-Positive nodes', 'אבחנה-Surgery sum',
300          'אבחנה-T -Tumor mark (TNM)', 'אבחנה-er', 'אבחנה-pr',
301          'אבחנה-Tumor size',
302          'stage_c - Clinical', 'stage_p - Pathological',
303          'metastases_mark_M0',
304          'metastases_mark_M1', 'metastases_mark_M1b',
305          'metastases_mark_MX', 'metastases_mark_Not yet Established',
306          'margin_type_ללא', 'margin_type_נגועים', 'margin_type_נקיים',
307          'side_דו צדדי', 'side_ימין', 'side_שמאל', 'stage_LA',
308          'stage_Stage0', 'stage_Stage0is',
309          'stage_Stage1', 'stage_Stage1b', 'stage_Stage1c',
310          'stage_Stage2', 'stage_Stage2a', 'stage_Stage2b', 'stage_Stage3',
311          'stage_Stage3a', 'stage_Stage3b', 'stage_Stage3c', 'stage_Stage4',
312          'form_name_סימפטומים ודיווח סיעודי',
313          'form_name_אנמנזה סיעודית',
314          'form_name_קצרה סיעודית', 'form_name_רפואית',
315          'form_name_ביקור במרפאה',
316          'form_name_אונקולוגית-ביקור במרפאה המטו',
317          'form_name_קרינה ביקור במרפאה קרינה', 'form_name_דיווח סיעודי',
318          'בלוטות בית שח.הוצ-שד-כיר', 'שנוי מי/הוצ טבעת-לאפ-כיר',
319          'בלוטות+למפקטומי-שד-כיר',
320          'ניתוחית תוך קרינה +בלוטות+למפקטומי-שד-כיר',
321          'הוצאת בלוטות לימפה-כירור', 'בלוטות+מסטקטומי-שד-כיר',
322          'שד מסטקטומי-כירורגיה', 'שד מסטקטומי-כירורגיה',
323          'בלוטות+כריתה בגישה זעירה-שד', 'כריתה בגישה זעירה דרך העטרה-שד']]
324 else:
325     df_to_parse = df_to_parse[
326         ['אבחנה-Age', 'אבחנה-Her2', 'אבחנה-Histopatological degree',
327          'אבחנה-KI67 protein', 'אבחנה-N -lymph nodes mark (TNM)',
328          'אבחנה-Nodes exam', 'אבחנה-Positive nodes', 'אבחנה-Surgery sum',
329          'אבחנה-T -Tumor mark (TNM)', 'אבחנה-er', 'אבחנה-pr',
330          'stage_c - Clinical', 'stage_p - Pathological',
331          'metastases_mark_M0',

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```

332         'metastases_mark_M1',
333         'metastases_mark_M1b',
334         'metastases_mark_MX', 'metastases_mark_Not yet Established',
335         'margin_type_לא', 'margin_type_נגועים', 'margin_type_נקיים',
336         'side_צדדי', 'side_ימין', 'side_שמאל', 'stage_LA',
337         'stage_Stage0', 'stage_Stage0is',
338         'stage_Stage1', 'stage_Stage1b', 'stage_Stage1c',
339         'stage_Stage2', 'stage_Stage2a', 'stage_Stage2b', 'stage_Stage3',
340         'stage_Stage3a', 'stage_Stage3b', 'stage_Stage3c', 'stage_Stage4',
341         'form_name_סימפטומים ודיווח סיעודי',
342         'form_name_אנמנזה סיעודית',
343         'form_name_קצרה אנמנזה סיעודית', 'form_name_רפואית אנמנזה',
344         'form_name_ביקור במרפאה',
345         'form_name_אונקולוגית-ביקור במרפאה המטו',
346         'form_name_קרינה במרפאה קרינה', 'form_name_דיווח סיעודי', '',
347         'בלוטות בית שח.הוצ-שד-כיר', 'שנוי מי/הוצ טבעת-לאפ-כיר',
348         'בלוטות+למפקטומי-שד-כירו',
349         'intrabeam') קרינה תוך ניתוחית +בלוטות+למפקטומי-שד-כירו',
350         'הוצאת בלוטות לימפה-כירור', 'בלוטות+מסטקטומי-שד-כירו',
351         'שד מסטקטומי-כירורגיה', 'שד למפקטומי-כירורגיה',
352         'בלוטות+כריתה בגישה זעירה-שד', 'כריתה בגישה זעירה דרך העטרה-שד']]
353     return df_to_parse
354
355
356 def return_dfs(train_feat_file_name, train_labels_file_name,
357               test_feats_file_name):
358     train_feats_df = pd.read_csv(train_feat_file_name, encoding="UTF-8")
359     train_labels_df = pd.read_csv(train_labels_file_name, encoding="UTF-8")
360     test_feats_df = pd.read_csv(test_feats_file_name, encoding="UTF-8")
361     train_df = pd.concat([train_feats_df, train_labels_df], axis=1)
362     return train_df, test_feats_df
363
364
365 if __name__ == "__main__":
366     # Train model
367     train_df, test_feats_df = return_dfs("train.feats.csv",
368                                         "train.labels.1.csv",
369                                         "test.feats.csv") # require
370     parsed_train_df = parse_data(train_df)
371     parsed_train_df.drop(parsed_train_df[parsed_train_df['אבחנה-Tumor size']
372                                         == '.'].index, inplace=True)
373     parsed_test_feats_df = parse_data(test_feats_df, False)
374     train_y = parsed_train_df['אבחנה-Tumor size']
375     rf = RandomForestRegressor(n_estimators=100, ccp_alpha=0.01).fit(
376         parsed_train_df.drop(columns='אבחנה-Tumor size'), train_y)
377
378     # Predict and save
379     predict_y = rf.predict(parsed_test_feats_df)
380     data = {'אבחנה-Tumor size': predict_y}
381     df_predict_y = pd.DataFrame(data)
382     df_predict_y.to_csv("predictions.csv", index=False)

```

9 task2/part2/requirements.txt

```
1 altgraph==0.17
2 anyio==3.5.0
3 argon2-cffi==21.3.0
4 argon2-cffi-bindings==21.2.0
5 asttokens==2.0.5
6 attrs==21.4.0
7 Babel==2.9.1
8 backcall==0.2.0
9 beautifulsoup4==4.10.0
10 bleach==4.1.0
11 certifi==2021.10.8
12 cffi==1.15.0
13 charset-normalizer==2.0.12
14 colorama==0.4.4
15 cycler==0.10.0
16 debugpy==1.5.1
17 decorator==5.1.1
18 defusedxml==0.7.1
19 entrypoints==0.4
20 executing==0.8.3
21 future==0.18.2
22 idna==3.3
23 ipykernel==6.9.1
24 ipython==8.1.1
25 ipython-genutils==0.2.0
26 jedi==0.18.1
27 Jinja2==3.0.3
28 json5==0.9.6
29 jsonschema==4.4.0
30 jupyter-client==7.1.2
31 jupyter-core==4.9.2
32 jupyter-server==1.13.5
33 jupyterlab==3.3.1
34 jupyterlab-pygments==0.1.2
35 jupyterlab-server==2.10.3
36 kiwisolver==1.3.1
37 MarkupSafe==2.1.0
38 matplotlib==3.4.2
39 matplotlib-inline==0.1.3
40 mistune==0.8.4
41 nbclassic==0.3.6
42 nbclient==0.5.13
43 nbconvert==6.4.4
44 nbformat==5.2.0
45 nest-asyncio==1.5.4
46 notebook==6.4.8
47 notebook-shim==0.1.0
48 numpy==1.20.3
49 packaging==21.3
50 pandocfilters==1.5.0
51 parso==0.8.3
52 pefile==2019.4.18
53 pickleshare==0.7.5
54 Pillow==8.2.0
55 prometheus-client==0.13.1
56 prompt-toolkit==3.0.28
57 pure-eval==0.2.2
58 pycparser==2.21
59 Pygments==2.11.2
```

```
60 pyinstaller==4.2
61 pyinstaller-hooks-contrib==2021.1
62 pyparsing==2.4.7
63 pyrsistent==0.18.1
64 python-dateutil==2.8.1
65 pytz==2021.3
66 pywin32==303
67 pywin32-ctypes==0.2.0
68 pywinpty==1.1.6
69 pyzmq==22.3.0
70 requests==2.27.1
71 Send2Trash==1.8.0
72 six==1.16.0
73 sniffio==1.2.0
74 soupsieve==2.3.1
75 stack-data==0.2.0
76 terminado==0.13.3
77 testpath==0.6.0
78 tornado==6.1
79 traitlets==5.1.1
80 urllib3==1.26.8
81 wcwidth==0.2.5
82 webencodings==0.5.1
83 websocket-client==1.3.1
84 scikit-multilearn==0.2.0
85 scikit-learn==1.1.1
86 scikit-multilearn==0.2.0
87 scipy==1.8.1
88 pandas==1.4.2
```