DTSA_5510_final_exam

August 21, 2023

0.0.1 1. Project Topic

1. For my final project I've decided to use genetic data from cancer patients with gliomas. Gliomas is the type of brain cancer and for clinicians it's really important to distinguish between two main types of this tumor - LGG (Lower-Grade Glioma) and GBM (Glioblastoma Multiforme). Dataset has information about 20 genes (mutated or not, binary value) and 3 clinical features. And the main point of this project is to find optimal subset of mutation genes and clinical features for the glioma types.
2. This problem can be considered as specific subset of supervised learning where we would need to find best set of predictors that will give us the best results or we can use unsupervised approach here, for example PCA in order to find the best components (with highest eighenvalue) that are describing the most of variance
3. So the main goal would be to try to use unsupervices approach in order to find best subset of parameters that predict cancer type

0.0.2 2. Data source

1. I got dataset from the study in International Journal of Molecular Sciences [1]

And here is a link to download the data - https://archive.ics.uci.edu/static/public/759/glioma+grading+clinical+a

2. Dataset is in csv format and has data about 839 patients (rows) and 23 attributes (columns). Clinical attributes are: Race (Categorical), Gender (Categorical) and Age_at_diagnosis (Continious). Also data has information about mutations in 20 genes, all these variables are Categorical with only 2 values: NOT_MUTATED and MUTATED. All data is within the single table

[1]. Tasci, E., Zhuge, Y., Kaur, H., Camphausen, K., & Krauze, A. V. (2022). Hierarchical Voting-Based Feature Selection and Ensemble Learning Model Scheme for Glioma Grading with Clinical and Molecular Characteristics. International Journal of Molecular Sciences, 23(22), 14155.

[1]:
```
import re
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
```

0.0.3 3. Data cleaning

[2]:
```
dataset = pd.read_csv("/Users/alexey/Downloads/
 ↪glioma+grading+clinical+and+mutation+features+dataset/
 ↪TCGA_GBM_LGG_Mutations_all.csv")
```

[3]:
```
dataset.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 862 entries, 0 to 861
Data columns (total 27 columns):
 #   Column             Non-Null Count  Dtype
---  ------             --------------  -----
 0   Grade              862 non-null    object
 1   Project            862 non-null    object
 2   Case_ID            862 non-null    object
 3   Gender             862 non-null    object
 4   Age_at_diagnosis   862 non-null    object
 5   Primary_Diagnosis  862 non-null    object
 6   Race               862 non-null    object
 7   IDH1               862 non-null    object
 8   TP53               862 non-null    object
 9   ATRX               862 non-null    object
 10  PTEN               862 non-null    object
 11  EGFR               862 non-null    object
 12  CIC                862 non-null    object
 13  MUC16              862 non-null    object
 14  PIK3CA             862 non-null    object
 15  NF1                862 non-null    object
 16  PIK3R1             862 non-null    object
 17  FUBP1              862 non-null    object
 18  RB1                862 non-null    object
 19  NOTCH1             862 non-null    object
 20  BCOR               862 non-null    object
 21  CSMD3              862 non-null    object
 22  SMARCA4            862 non-null    object
 23  GRIN2A             862 non-null    object
 24  IDH2               862 non-null    object
 25  FAT4               862 non-null    object
 26  PDGFRA             862 non-null    object
dtypes: object(27)
memory usage: 182.0+ KB
```

0.0.4 3.1 First let's explore how many nas we have in the dataset and then decide what we can do with these values

[4]:
```
dataset.isna().any()
```

[4]:
```
Grade                False
Project              False
Case_ID              False
Gender               False
Age_at_diagnosis     False
Primary_Diagnosis    False
Race                 False
IDH1                 False
TP53                 False
ATRX                 False
PTEN                 False
EGFR                 False
CIC                  False
MUC16                False
PIK3CA               False
NF1                  False
PIK3R1               False
FUBP1                False
RB1                  False
NOTCH1               False
BCOR                 False
CSMD3                False
SMARCA4              False
GRIN2A               False
IDH2                 False
FAT4                 False
PDGFRA               False
dtype: bool
```

standard approach doesn't show any missing values, but these values might just be encoded differently; let's print out all unique values for every columns excluding Project and Case_ID, as these columns won't be used in the learning

[5]:
```
for column_name in dataset.columns:
    if column_name not in ['Project', 'Case_ID']:
        print(f"{column_name}\t{','.join(dataset[column_name].unique())}")
```

```
Grade   LGG,GBM
Gender  Male,Female,--
Age_at_diagnosis        51 years 108 days,38 years 261 days,35 years 62 days,32
years 283 days,31 years 187 days,33 years 78 days,35 years 68 days,44 years 239
days,33 years 350 days,87 years,51 years 328 days,54 years 95 days,52 years 214
days,47 years 123 days,34 years 132 days,40 years 192 days,53 years 352 days,41
years 70 days,43 years 161 days,37 years 159 days,47 years 173 days,31 years 8
days,25 years 191 days,66 years 305 days,56 years 250 days,35 years 362 days,51
years 363 days,37 years 32 days,54 years 183 days,32 years 76 days,65 years 28
days,43 years 131 days,51 years 59 days,43 years 221 days,25 years 214 days,45
years 24 days,50 years 153 days,27 years 166 days,53 years 252 days,46 years 144
days,24 years 239 days,--,34 years 70 days,29 years 198 days,45 years 124
```

days,62 years 90 days,46 years 224 days,36 years 247 days,62 years 202 days,70 years 159 days,53 years 41 days,48 years 124 days,40 years 69 days,40 years 7 days,20 years 359 days,57 years 200 days,38 years 322 days,52 years 192 days,56 years 104 days,59 years 275 days,67 years 107 days,48 years 346 days,59 years 254 days,58 years 147 days,27 years 247 days,51 years 230 days,74 years 11 days,52 years 230 days,61 years 62 days,66 years 146 days,42 years 32 days,31 years 344 days,48 years 268 days,33 years 340 days,34 years 213 days,24 years 54 days,55 years 48 days,27 years 323 days,29 years 32 days,39 years 131 days,70 years 3 days,30 years 338 days,39 years 178 days,25 years 41 days,48 years 160 days,57 years 17 days,34 years 307 days,58 years 137 days,55 years 208 days,60 years 49 days,38 years 13 days,56 years 113 days,54 years 180 days,31 years 152 days,54 years 146 days,52 years 241 days,33 years 54 days,42 years 173 days,20 years 75 days,64 years 106 days,29 years 232 days,36 years 222 days,31 years 362 days,36 years 67 days,32 years 173 days,38 years 292 days,29 years 298 days,41 years 76 days,35 years 189 days,33 years 39 days,32 years 50 days,49 years 276 days,69 years 217 days,14 years 154 days,33 years 349 days,47 years 92 days,33 years 58 days,63 years 364 days,62 years 205 days,37 years 83 days,53 years 183 days,53 years 74 days,45 years 76 days,33 years 331 days,53 years 359 days,52 years 156 days,64 years 304 days,71 years 70 days,40 years 300 days,36 years 354 days,25 years 249 days,63 years 170 days,40 years 310 days,47 years 215 days,73 years 241 days,24 years 51 days,48 years 342 days,41 years 325 days,36 years 189 days,45 years 334 days,44 years 204 days,27 years 6 days,50 years 181 days,42 years 141 days,40 years 248 days,62 years 192 days,33 years 195 days,46 years 42 days,41 years 117 days,47 years 333 days,56 years 159 days,38 years 64 days,60 years 64 days,29 years 150 days,59 years 196 days,44 years 66 days,69 years 60 days,63 years 253 days,43 years 142 days,61 years 316 days,39 years 66 days,31 years 315 days,51 years 164 days,41 years 203 days,60 years 360 days,74 years 158 days,63 years 81 days,66 years 170 days,51 years 312 days,39 years 62 days,38 years 111 days,37 years 92 days,30 years 32 days,54 years 143 days,36 years 357 days,48 years 197 days,29 years 81 days,32 years 135 days,44 years 35 days,30 years 329 days,57 years 287 days,19 years 55 days,70 years 242 days,63 years 67 days,41 years 255 days,29 years 291 days,42 years 318 days,51 years 172 days,38 years 25 days,28 years 344 days,32 years 166 days,26 years 43 days,67 years 329 days,40 years 326 days,59 years 295 days,58 years 16 days,56 years 171 days,20 years 276 days,49 years 296 days,37 years 31 days,48 years 243 days,71 years 227 days,43 years 316 days,27 years 309 days,25 years 78 days,30 years 126 days,47 years 335 days,31 years 262 days,30 years 295 days,30 years 276 days,24 years 146 days,41 years 66 days,34 years 189 days,56 years 155 days,39 years 348 days,23 years 3 days,31 years 273 days,17 years 271 days,64 years 110 days,27 years 221 days,69 years 64 days,37 years 51 days,44 years 92 days,25 years 97 days,29 years 235 days,26 years 209 days,47 years 294 days,39 years 252 days,35 years 26 days,33 years 287 days,74 years 204 days,50 years 167 days,65 years 314 days,60 years 116 days,34 years 346 days,44 years 229 days,21 years 243 days,55 years 87 days,43 years 361 days,36 years 49 days,70 years 100 days,23 years 352 days,43 years 195 days,30 years 264 days,38 years 140 days,34 years 188 days,55 years 92 days,30 years 238 days,61 years 68 days,44 years 344 days,35 years 238 days,68 years 129 days,44 years 206 days,38 years 89 days,36 years 304 days,52 years 32 days,36 years 183 days,33 years 176 days,60 years 119 days,44 years 90

days,58 years 157 days,33 years 364 days,62 years 235 days,44 years 226 days,36 years 311 days,29 years 132 days,25 years 282 days,20 years 307 days,61 years 305 days,41 years 222 days,47 years 224 days,59 years 212 days,48 years 311 days,38 years 24 days,27 years 58 days,58 years 15 days,26 years 118 days,44 years 209 days,32 years 196 days,22 years 305 days,25 years 316 days,34 years 27 days,24 years 278 days,30 years 348 days,39 years 280 days,22 years 236 days,53 years 286 days,30 years 355 days,37 years 239 days,36 years 73 days,41 years 314 days,57 years 201 days,52 years 243 days,31 years 346 days,32 years 167 days,44 years 131 days,40 years 106 days,44 years 263 days,39 years 5 days,62 years 93 days,45 years 296 days,48 years 131 days,49 years 187 days,38 years 194 days,28 years 115 days,38 years 273 days,37 years 81 days,41 years 179 days,60 years 15 days,50 years 232 days,75 years 292 days,43 years 143 days,52 years 63 days,38 years 333 days,66 years 344 days,30 years 57 days,59 years 262 days,35 years 37 days,38 years 203 days,42 years 310 days,59 years 166 days,26 years 94 days,58 years 266 days,31 years 10 days,30 years 161 days,45 years 231 days,37 years 166 days,34 years 162 days,34 years 339 days,32 years 53 days,66 years 176 days,46 years 89 days,38 years 326 days,33 years 213 days,40 years 61 days,52 years 145 days,59 years 359 days,58 years 55 days,43 years 281 days,33 years 192 days,55 years 40 days,43 years 226 days,60 years 123 days,33 years 332 days,48 years 80 days,70 years 205 days,53 years 197 days,66 years 136 days,36 years 275 days,40 years 49 days,73 years 103 days,36 years 165 days,74 years 56 days,43 years 145 days,40 years 323 days,38 years 128 days,54 years 291 days,63 years 54 days,62 years 303 days,35 years 53 days,39 years 174 days,29 years 341 days,46 years 333 days,46 years 110 days,51 years 329 days,54 years 221 days,42 years 91 days,64 years 108 days,29 years 220 days,65 years 195 days,41 years 91 days,31 years 206 days,58 years 5 days,54 years 318 days,28 years 26 days,20 years 116 days,34 years 160 days,54 years 198 days,45 years 259 days,48 years 325 days,29 years 86 days,22 years 8 days,32 years 161 days,40 years 50 days,61 years 47 days,57 years 276 days,54 years 100 days,56 years 317 days,34 years 139 days,27 years 289 days,37 years 149 days,43 years 332 days,41 years 10 days,33 years 104 days,39 years 35 days,31 years 300 days,67 years 219 days,30 years 140 days,48 years 212 days,50 years 302 days,45 years 34 days,47 years 299 days,32 years 158 days,26 years 171 days,29 years 213 days,28 years 79 days,66 years 16 days,39 years 304 days,33 years 238 days,60 years 75 days,35 years 65 days,35 years 45 days,58 years 168 days,26 years 50 days,30 years 113 days,38 years 82 days,35 years 325 days,39 years 291 days,55 years 306 days,49 years 337 days,50 years 59 days,52 years 163 days,51 years 121 days,61 years 285 days,52 years 149 days,35 years 66 days,47 years 266 days,35 years 70 days,31 years 105 days,31 years 35 days,37 years 50 days,37 years 97 days,42 years 249 days,32 years 116 days,61 years 22 days,48 years 78 days,34 years 42 days,30 years 252 days,30 years 86 days,28 years 195 days,47 years 226 days,35 years 91 days,23 years 171 days,49 years 264 days,36 years 78 days,54 years 268 days,22 years 300 days,42 years 5 days,28 years 213 days,25 years 232 days,66 years 3 days,46 years 181 days,57 years 310 days,43 years 22 days,49 years 309 days,33 years 99 days,27 years 306 days,62 years 166 days,55 years 153 days,37 years 285 days,37 years 107 days,32 years 122 days,38 years 143 days,42 years 289 days,47 years 165 days,54 years 227 days,29 years 49 days,39 years 359 days,28 years 249 days,23 years 108 days,21 years 276 days,38 years 229 days,49 years 302 days,38 years 308 days,22

years 205 days,67 years 215 days,73 years 329 days,62 years 100 days,57 years 314 days,30 years 334 days,24 years 181 days,20 years 84 days,41 years 116 days,53 years 258 days,34 years 237 days,51 years 350 days,57 years 364 days,31 years 176 days,57 years 141 days,49 years 263 days,60 years 106 days,73 years 250 days,64 years 298 days,73 years 164 days,33 years 239 days,67 years 151 days,72 years 74 days,69 years 124 days,79 years 39 days,68 years 7 days,76 years 5 days,82 years 14 days,58 years 9 days,52 years 251 days,81 years 217 days,74 years 172 days,76 years 87 days,57 years 110 days,67 years 121 days,63 years 313 days,64 years 143 days,69 years 50 days,66 years 28 days,54 years 347 days,60 years 114 days,45 years 230 days,36 years 219 days,49 years 174 days,69 years 219 days,54 years 340 days,58 years 327 days,61 years 183 days,64 years 191 days,65 years 309 days,60 years 298 days,53 years 309 days,39 years 193 days,58 years 227 days,56 years 172 days,65 years 344 days,36 years 59 days,72 years 192 days,48 years 348 days,39 years 157 days,54 years 176 days,63 years 333 days,66 years 159 days,52 years 97 days,89 years 105 days,54 years 242 days,60 years 262 days,77 years 116 days,60 years 264 days,80 years 61 days,51 years 264 days,53 years 145 days,43 years 313 days,74 years 144 days,76 years 118 days,49 years 228 days,48 years 333 days,68 years 334 days,74 years 359 days,69 years 211 days,64 years 192 days,58 years 144 days,47 years 88 days,61 years 282 days,75 years 194 days,52 years 246 days,47 years 199 days,21 years 288 days,72 years 169 days,68 years 108 days,67 years,52 years 238 days,59 years 11 days,59 years 149 days,48 years 362 days,76 years 58 days,72 years 193 days,51 years 113 days,67 years 187 days,82 years 115 days,64 years 209 days,75 years 265 days,85 years 221 days,73 years 105 days,78 years 273 days,45 years 136 days,42 years 225 days,53 years 299 days,68 years 290 days,43 years 245 days,59 years 289 days,52 years 137 days,61 years 244 days,40 years 207 days,63 years 263 days,63 years 307 days,70 years 98 days,59 years 362 days,56 years 101 days,62 years 190 days,24 years 83 days,72 years 345 days,67 years 161 days,54 years 200 days,86 years 155 days,62 years 222 days,63 years 97 days,58 years 200 days,60 years 5 days,67 years 17 days,23 years 310 days,58 years 59 days,64 years 18 days,65 years 37 days,61 years 32 days,52 years 161 days,77 years 139 days,58 years 280 days,78 years 264 days,63 years 122 days,63 years 86 days,23 years 133 days,65 years 94 days,50 years 79 days,55 years 209 days,60 years 258 days,62 years 220 days,69 years 95 days,56 years 187 days,76 years 72 days,76 years 252 days,86 years 8 days,69 years 80 days,59 years 219 days,75 years 337 days,57 years 202 days,69 years 257 days,45 years 226 days,47 years 130 days,74 years 57 days,78 years 93 days,59 years 64 days,21 years 266 days,81 years 34 days,70 years 60 days,62 years 153 days,75 years 191 days,60 years 136 days,63 years 53 days,61 years 52 days,47 years 71 days,76 years 150 days,84 years 287 days,77 years 153 days,48 years 182 days,69 years 223 days,56 years 12 days,76 years 171 days,70 years 117 days,34 years 267 days,68 years 341 days,54 years 216 days,74 years 313 days,73 years 193 days,57 years 112 days,44 years 230 days,83 years 265 days,74 years 291 days,51 years 275 days,52 years 60 days,73 years 102 days,81 years 307 days,78 years 94 days,57 years 312 days,53 years 147 days,50 years 330 days,78 years 56 days,76 years 236 days,57 years 118 days,36 years 108 days,72 years 284 days,31 years 11 days,65 years 66 days,63 years 201 days,49 years 351 days,59 years 311 days,69 years 232 days,62 years 304 days,52 years 270 days,56 years 294 days,81 years 168 days,40 years 293 days,81 years

319 days,50 years 171 days,38 years 8 days,48 years 183 days,51 years 86 days,66 years 341 days,71 years 315 days,24 years 156 days,63 years 195 days,69 years 116 days,78 years 7 days,30 years 155 days,52 years 288 days,65 years 57 days,78 years 271 days,61 years 37 days,50 years 173 days,39 years 57 days,66 years 81 days,49 years 6 days,54 years 78 days,58 years 48 days,73 years 4 days,53 years 303 days,63 years 292 days,66 years 191 days,49 years 322 days,59 years 335 days,54 years 327 days,57 years 274 days,59 years 157 days,44 years 55 days,58 years 14 days,65 years 18 days,67 years 34 days,75 years 172 days,88 years 209 days,53 years 85 days,75 years 126 days,66 years 269 days,51 years 51 days,40 years 360 days,58 years 6 days,57 years 29 days,55 years 144 days,40 years 268 days,40 years 206 days,54 years 89 days,53 years 136 days,56 years 9 days,59 years 306 days,75 years 118 days,59 years 10 days,44 years 135 days,46 years 236 days,68 years 248 days,30 years 340 days,36 years 302 days,78 years 270 days,83 years 235 days,51 years 201 days,63 years 118 days,59 years 227 days,53 years 233 days,74 years 83 days,60 years 246 days,54 years 295 days,63 years 9 days,58 years 308 days,60 years 274 days,71 years 257 days,75 years 78 days,50 years 309 days,67 years 6 days,60 years 358 days,65 years 143 days,51 years 90 days,45 years 301 days,39 years 316 days,70 years 245 days,73 years 133 days,65 years 360 days,72 years 251 days,61 years 177 days,65 years 22 days,30 years 327 days,64 years 50 days,55 years 267 days,79 years 123 days,74 years 294 days,63 years 24 days,81 years 21 days,53 years 86 days,69 years 343 days,60 years 342 days,55 years 214 days,75 years 342 days,47 years 349 days,71 years 148 days,25 years 82 days,61 years 247 days,47 years 302 days,50 years 129 days,72 years 97 days,31 years 7 days,86 years 216 days,38 years 214 days,72 years 302 days,55 years 46 days,66 years 320 days,55 years 361 days,72 years 57 days,33 years 7 days,83 years 114 days,43 years 259 days,68 years 224 days,79 years 183 days,67 years 326 days,49 years 298 days,66 years 256 days,68 years 221 days,47 years 52 days,61 years 218 days,49 years 157 days,67 years 120 days,32 years 268 days,65 years 41 days,66 years 213 days,62 years 281 days,50 years 16 days,34 years 111 days,61 years 11 days,77 years 353 days,54 years 101 days,51 years 32 days,53 years 8 days,78 years 253 days,46 years 337 days,52 years 244 days,48 years 249 days,51 years 205 days,62 years 41 days,58 years 20 days,61 years 112 days,66 years 111 days,64 years 43 days,56 years 114 days,77 years 325 days,85 years 65 days,77 years 178 days,63 years 121 days,76 years 221 days

Primary_Diagnosis Oligodendroglioma, NOS,Mixed glioma,Astrocytoma, NOS,Astrocytoma, anaplastic,Oligodendroglioma, anaplastic,--,Glioblastoma

Race white,asian,black or african american,--,not reported,american indian or alaska native

IDH1 MUTATED,NOT_MUTATED

TP53 NOT_MUTATED,MUTATED

ATRX NOT_MUTATED,MUTATED

PTEN NOT_MUTATED,MUTATED

EGFR NOT_MUTATED,MUTATED

CIC NOT_MUTATED,MUTATED

MUC16 NOT_MUTATED,MUTATED

PIK3CA MUTATED,NOT_MUTATED

NF1 NOT_MUTATED,MUTATED

PIK3R1 NOT_MUTATED,MUTATED

```
FUBP1    MUTATED,NOT_MUTATED
RB1      NOT_MUTATED,MUTATED
NOTCH1   NOT_MUTATED,MUTATED
BCOR     NOT_MUTATED,MUTATED
CSMD3    NOT_MUTATED,MUTATED
SMARCA4  NOT_MUTATED,MUTATED
GRIN2A   NOT_MUTATED,MUTATED
IDH2     NOT_MUTATED,MUTATED
FAT4     NOT_MUTATED,MUTATED
PDGFRA   NOT_MUTATED,MUTATED
```

from the cell above I can see that:

1. missing values are encoded as '–' and as 'not reported'.
2. Age is in string format, so we would need to convert it to some continious form. I would suggest to convert years to days and add these value to the remaining number of days. I won't take into accout leap years as I woulnd't expect this precision to add any value to our model
3. Other categorical variables should be converted to 0s or 1s

so first let's cound how many rows with missing values we have. For this I will need to explore just three columns: Gender, Age_at_diagnosis and Race. I don't need to explore Primary_Diagnosis column as Grade will be used instead for classification

[6]:
```
# Find indices of missing values for Gender column
gender_missing_indices = dataset.index[dataset.Gender.isin(['--', 'not␣
 ↪reported'])].tolist()
```

[7]:
```
# Find indices of missing values for Age_at_diagnosis column
age_missing_indices = dataset.index[dataset.Age_at_diagnosis.isin(['--', 'not␣
 ↪reported'])].tolist()
```

[8]:
```
# Find indices of missing values for Race column
race_missing_indices = dataset.index[dataset.Race.isin(['--', 'not reported'])].
 ↪tolist()
```

[9]:
```
# Merge all indices into one list
missing_values_indices = list()
missing_values_indices.extend(gender_missing_indices)
missing_values_indices.extend(age_missing_indices)
missing_values_indices.extend(race_missing_indices)
```

[10]:
```
# Use set to remove non-unique indices
print(f"Number of missing values: {len(set(missing_values_indices))}")
print(f"Missing values indices: {set(missing_values_indices)}")
```

```
Number of missing values: 23
Missing values indices: {256, 268, 396, 525, 794, 671, 163, 41, 437, 706, 71,
455, 583, 846, 208, 341, 608, 231, 490, 747, 622, 623, 504}
```

As we can see there are only 23 rows with missing values so I think it will be easier to just remove these rows as it won't affect anyhow our future learning model. Also let's remove 'Primary_Diagnosis', 'Project' and 'Case_ID' columns as we won't use them in the analysis

[11]:
```
# let's remove 'Primary_Diagnosis', 'Project' and 'Case_ID' columns from the␣
↪dataset
dataset = dataset.drop(['Primary_Diagnosis', 'Project', 'Case_ID'], axis=1)
dataset.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 862 entries, 0 to 861
Data columns (total 24 columns):
 #   Column            Non-Null Count  Dtype
---  ------            --------------  -----
 0   Grade             862 non-null    object
 1   Gender            862 non-null    object
 2   Age_at_diagnosis  862 non-null    object
 3   Race              862 non-null    object
 4   IDH1              862 non-null    object
 5   TP53              862 non-null    object
 6   ATRX              862 non-null    object
 7   PTEN              862 non-null    object
 8   EGFR              862 non-null    object
 9   CIC               862 non-null    object
 10  MUC16             862 non-null    object
 11  PIK3CA            862 non-null    object
 12  NF1               862 non-null    object
 13  PIK3R1            862 non-null    object
 14  FUBP1             862 non-null    object
 15  RB1               862 non-null    object
 16  NOTCH1            862 non-null    object
 17  BCOR              862 non-null    object
 18  CSMD3             862 non-null    object
 19  SMARCA4           862 non-null    object
 20  GRIN2A            862 non-null    object
 21  IDH2              862 non-null    object
 22  FAT4              862 non-null    object
 23  PDGFRA            862 non-null    object
dtypes: object(24)
memory usage: 161.8+ KB
```

[12]:
```
# let's remove rows with missing values
dataset = dataset.drop(set(missing_values_indices), axis=0)
dataset.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 839 entries, 0 to 861
Data columns (total 24 columns):
```

```
 #   Column            Non-Null Count  Dtype
---  ------            --------------  -----
 0   Grade             839 non-null    object
 1   Gender            839 non-null    object
 2   Age_at_diagnosis  839 non-null    object
 3   Race              839 non-null    object
 4   IDH1              839 non-null    object
 5   TP53              839 non-null    object
 6   ATRX              839 non-null    object
 7   PTEN              839 non-null    object
 8   EGFR              839 non-null    object
 9   CIC               839 non-null    object
 10  MUC16             839 non-null    object
 11  PIK3CA            839 non-null    object
 12  NF1               839 non-null    object
 13  PIK3R1            839 non-null    object
 14  FUBP1             839 non-null    object
 15  RB1               839 non-null    object
 16  NOTCH1            839 non-null    object
 17  BCOR              839 non-null    object
 18  CSMD3             839 non-null    object
 19  SMARCA4           839 non-null    object
 20  GRIN2A            839 non-null    object
 21  IDH2              839 non-null    object
 22  FAT4              839 non-null    object
 23  PDGFRA            839 non-null    object
dtypes: object(24)
memory usage: 163.9+ KB
```

[13]:
```python
# Convert years to days
for row in dataset.iterrows():
    numbers = re.findall(r'\d+', row[1]['Age_at_diagnosis'])
    age = 0
    years_to_day = int(numbers[0]) * 365
    if len(numbers) > 1:
        age = years_to_day + int(numbers[1])
    else:
        age = years_to_day
    row[1]['Age_at_diagnosis'] = years_to_day
```

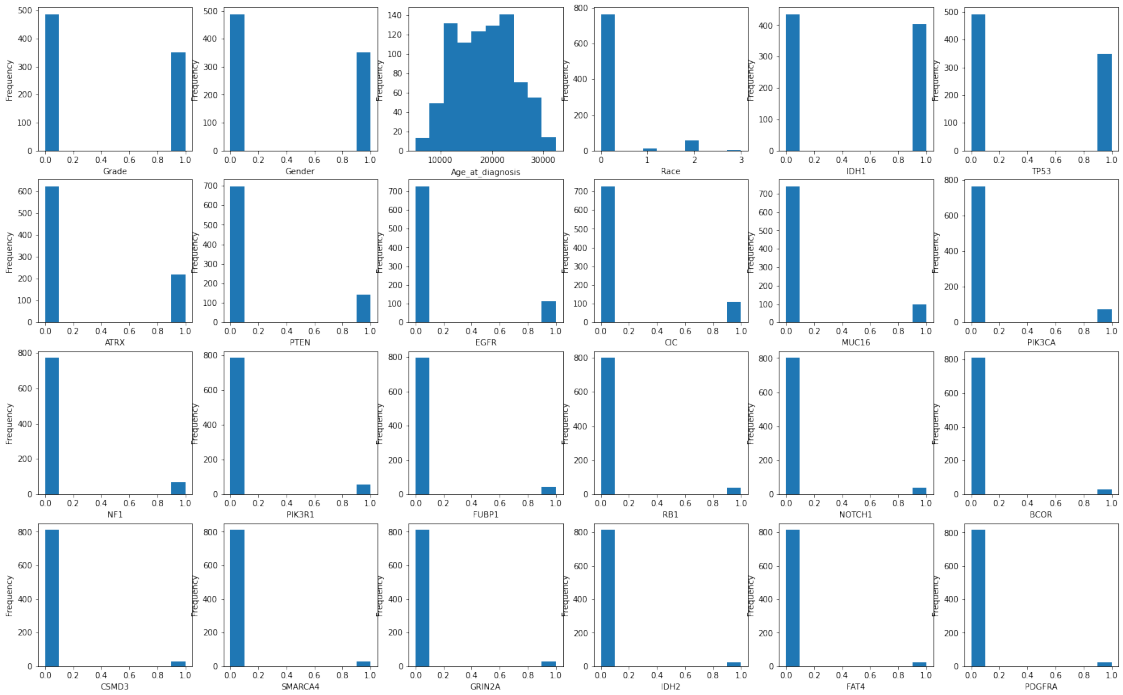
[14]:
```python
# Convert Gender to number, Male = 0, Female = 1
for row in dataset.iterrows():
    if row[1]['Gender'] == 'Male':
        row[1]['Gender'] = 0
    else:
        row[1]['Gender'] = 1
```

[15]:
```
# Convert Grade to number, LGG = 0, GBM = 1
for row in dataset.iterrows():
    if row[1]['Grade'] == 'LGG':
        row[1]['Grade'] = 0
    else:
        row[1]['Grade'] = 1
```

[16]:
```
# Convert Race to humber, white = 0, asian = 1, black or african american = 2,␣
 ↪american indian or alaska native = 3
for row in dataset.iterrows():
    if row[1]['Race'] == 'white':
        row[1]['Race'] = 0
    elif row[1]['Race'] == 'asian':
        row[1]['Race'] = 1
    elif row[1]['Race'] == 'black or african american':
        row[1]['Race'] = 2
    else:
        row[1]['Race'] = 3
```

[17]:
```
# Convert genes mutation status to number, MUTATED = 1, NOT_MUTATED = 0
gene_names = [gene_name for gene_name in dataset.columns if gene_name not in␣
 ↪['Grade', 'Gender', 'Age_at_diagnosis', 'Race']]
for row in dataset.iterrows():
    for gene_name in gene_names:
        if row[1][gene_name] == 'NOT_MUTATED':
            row[1][gene_name] = 0
        else:
            row[1][gene_name] = 1
```

[18]:
```
# let's plot histogram of existin values just to check that cleaning was OK
fig = plt.figure(figsize=(24, 15))
i = 0
for column in dataset:
    sub = fig.add_subplot(4, 6, i+1)
    sub.set_xlabel(column)
    dataset[column].plot(kind='hist')
    i += 1
```



0.0.5 3.2 Cleaning stage conclusion:

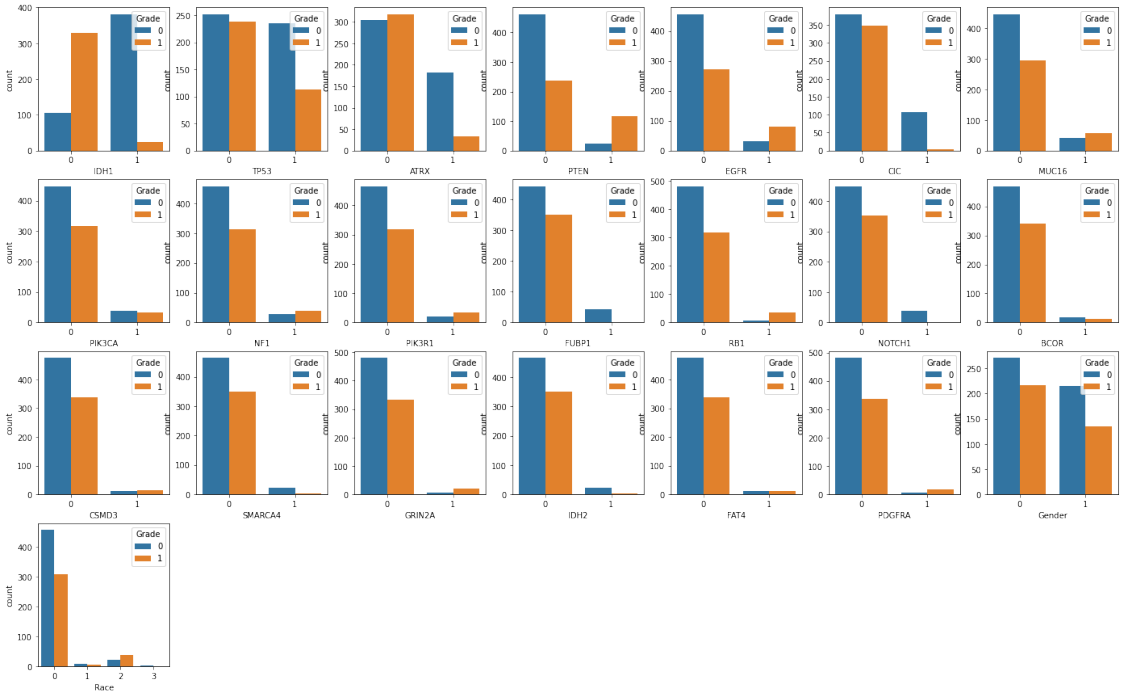
1. We've removed all missing values
2. We've converted Age to the number of days
3. We've convert all other categorical variables to 0s, 1s, etc...

As I can see from the plot above, Grade, Gender and IDH1 variables looks balanced. Age column more or less similar to normal distribution as it should be and other variables, including Race and most of the genes are quite unbalanced (there are more values of one type than another)

0.0.6 4. Exploratory Data Analysis

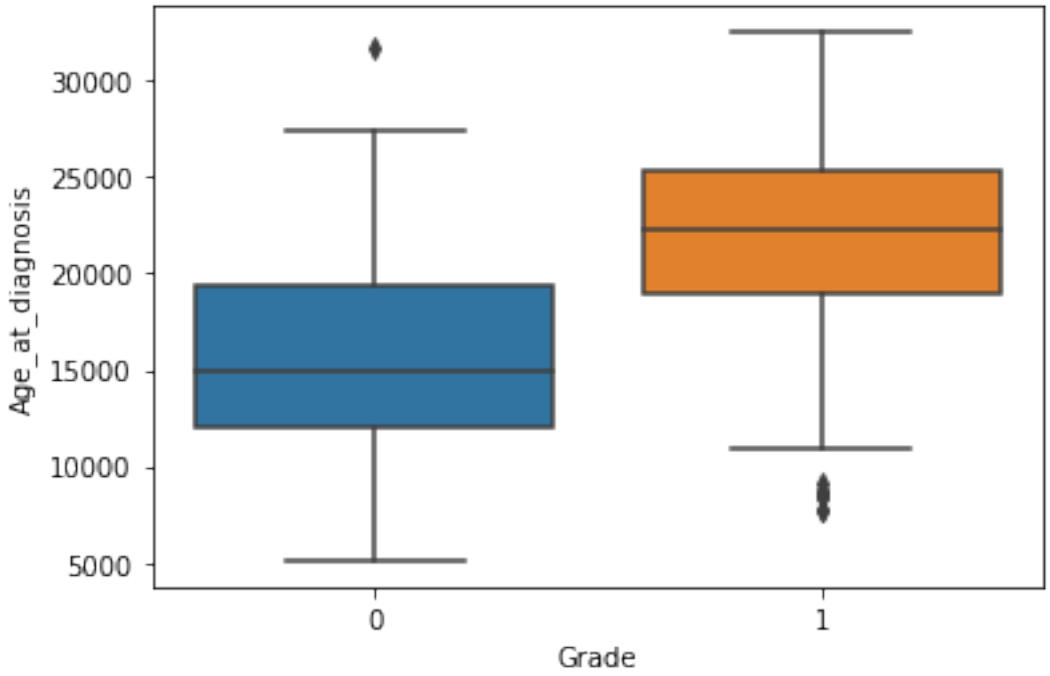
[19]:
```
# I've already built histogram of features above and now it would be great to␣
↪check feature vs target distribution
list_of_columns = gene_names + ['Gender', 'Race']
fig = plt.figure(figsize=(24, 15))

for i in range(len(list_of_columns)):
    column = list_of_columns[i]
    sub = fig.add_subplot(4, 7, i+1)
    chart = sns.countplot(data=dataset, x=column, hue='Grade')
```



[20]:
```
# And finally I would like to build similar plot but for Age_at_diagnosis column
sns.boxplot(x='Grade', y='Age_at_diagnosis', data=dataset)
```

[20]: <Axes: xlabel='Grade', ylabel='Age_at_diagnosis'>



0.0.7 4.1 EDA summary:

1. Many genes represent unbalanced features - it mean that probably they won't give any advantage for a future model
2. For other variables it's possible to see that Grade target is correlated with state of the predictor, it means these feature will be useful for future model
3. Looks like Age_at_diagnosis in generate is linked with GBM

0.0.8 5. Models

there are many usupervised algorithms that we can use here but I would suggest to start with PCA in order to find the best components from the dataset [1]

[78]:
```
from sklearn.decomposition import PCA
from sklearn.model_selection import train_test_split

from sklearn.linear_model import LogisticRegression
from sklearn.naive_bayes import GaussianNB
from sklearn.svm import SVC
from sklearn.neighbors import KNeighborsClassifier
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier, GradientBoostingClassifier

from sklearn import metrics
from sklearn.metrics import classification_report, confusion_matrix
```

[33]:
```
# remove Grade from dataset
data = dataset.drop(['Grade'], axis=1)
# and save it to y varibale
labels = dataset['Grade']
```

[63]:
```
X_reduced = PCA(n_components=2)
X_reduced.fit_transform(data)
```

[63]:
```
array([[ 2.03164470e+02,  1.42837799e-01],
       [-4.54183553e+03,  4.42465398e-01],
       [-5.63683558e+03, -6.94774840e-01],
       …,
       [ 9.69316448e+03, -6.55441796e-01],
       [ 4.58316449e+03, -3.74670840e-01],
       [ 9.32816450e+03,  7.70669453e-01]])
```

[66]:
```
tmp = pd.DataFrame(X_reduced.components_, columns=data.columns, index =␣
↪['PC-1','PC-2'])
print(tmp)
```

```
        Gender  Age_at_diagnosis      Race      IDH1      TP53      ATRX  \
PC-1 -0.000001          1.000000  0.000004 -0.000050 -0.000027 -0.000032
PC-2 -0.079903         -0.000057  0.417245 -0.393159 -0.619215 -0.466266

          PTEN      EGFR       CIC     MUC16  …     FUBP1       RB1  \
PC-1  0.000017  0.000013 -0.000007  0.000005  … -0.000002  0.000004
PC-2  0.128173  0.152162  0.113785 -0.004185  …  0.032832 -0.006332

        NOTCH1          BCOR         CSMD3   SMARCA4        GRIN2A      IDH2  \
PC-1 -0.000002  4.786217e-07  1.195647e-07 -0.000002  8.214369e-07 -0.000004
PC-2 -0.001187 -1.605723e-02 -1.037730e-02 -0.025727  1.754444e-02  0.050358

          FAT4    PDGFRA
PC-1  0.000001  0.000002
PC-2 -0.004877 -0.001755

[2 rows x 23 columns]
```

[67]:
```
tmp.max(axis=1)
```

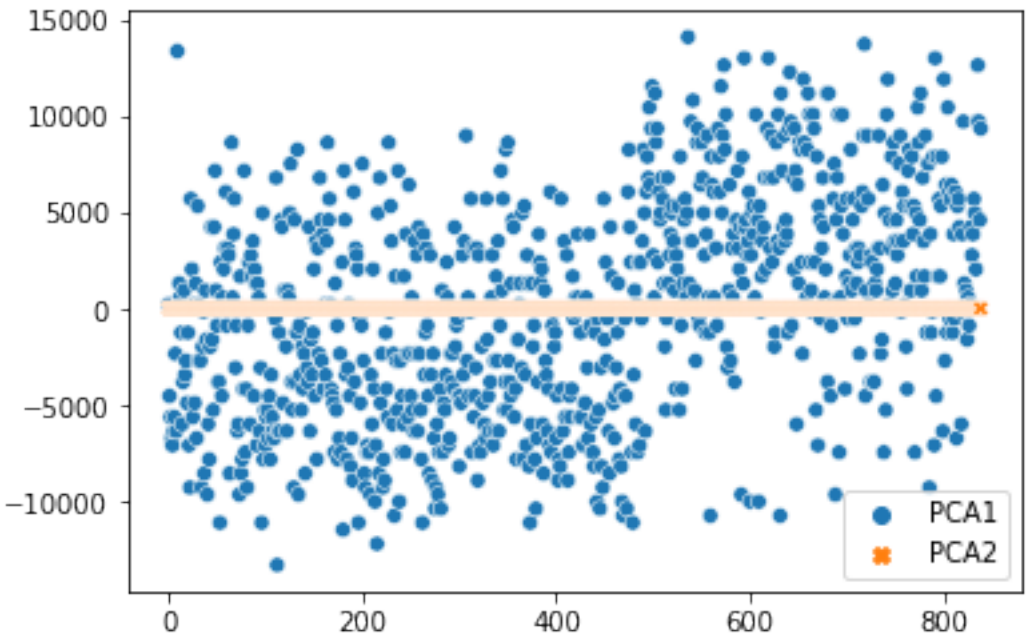
[67]:
```
PC-1    1.000000
PC-2    0.417245
dtype: float64
```

[68]:
```
tmp.min(axis=1)
```

[68]:
```
PC-1   -0.000050
PC-2   -0.619215
dtype: float64
```

[70]:
```
pca = X_reduced.fit_transform(data)
df = pd.DataFrame(data={'PCA1': pca[:, 0], 'PCA2': pca[:, 1]})
sns.scatterplot(df)
```

[70]:
```
<Axes: >
```



[72]:
```
X_reduced.explained_variance_ratio_
```

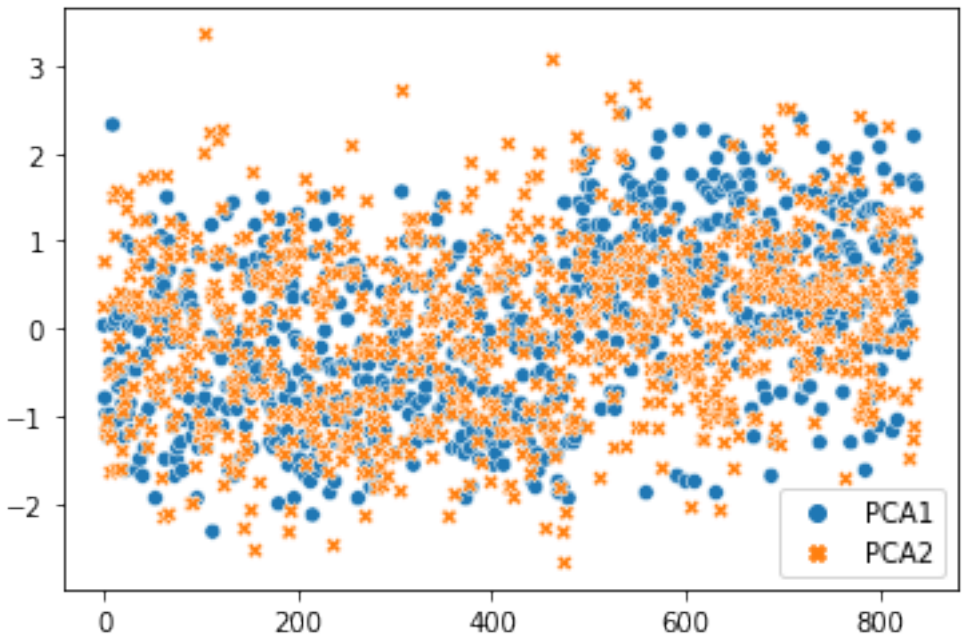
[72]:
```
array([9.99999937e-01, 1.03286230e-08])
```

0.0.9 Let's try to change some hyperparameters and see if we can get better picture

[73]:
```
X_reduced = PCA(n_components=2, whiten=True)
X_reduced.fit_transform(data)

pca = X_reduced.fit_transform(data)
df = pd.DataFrame(data={'PCA1': pca[:, 0], 'PCA2': pca[:, 1]})
sns.scatterplot(df)
```

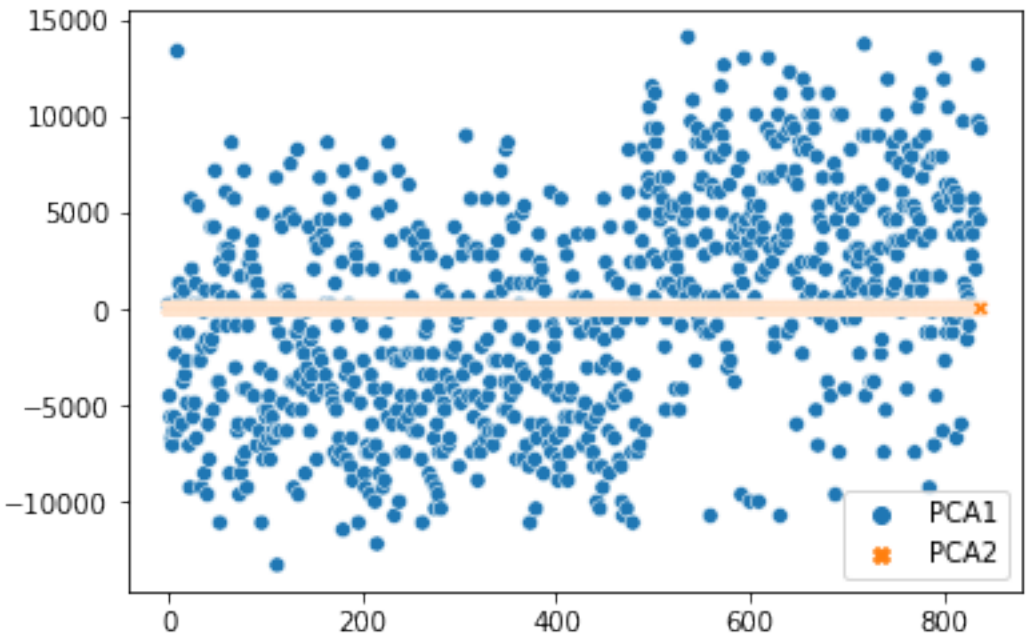
[73]:
```
<Axes: >
```



[75]:
```
X_reduced = PCA(n_components=2, svd_solver='full')
X_reduced.fit_transform(data)

pca = X_reduced.fit_transform(data)
df = pd.DataFrame(data={'PCA1': pca[:, 0], 'PCA2': pca[:, 1]})
sns.scatterplot(df)
```

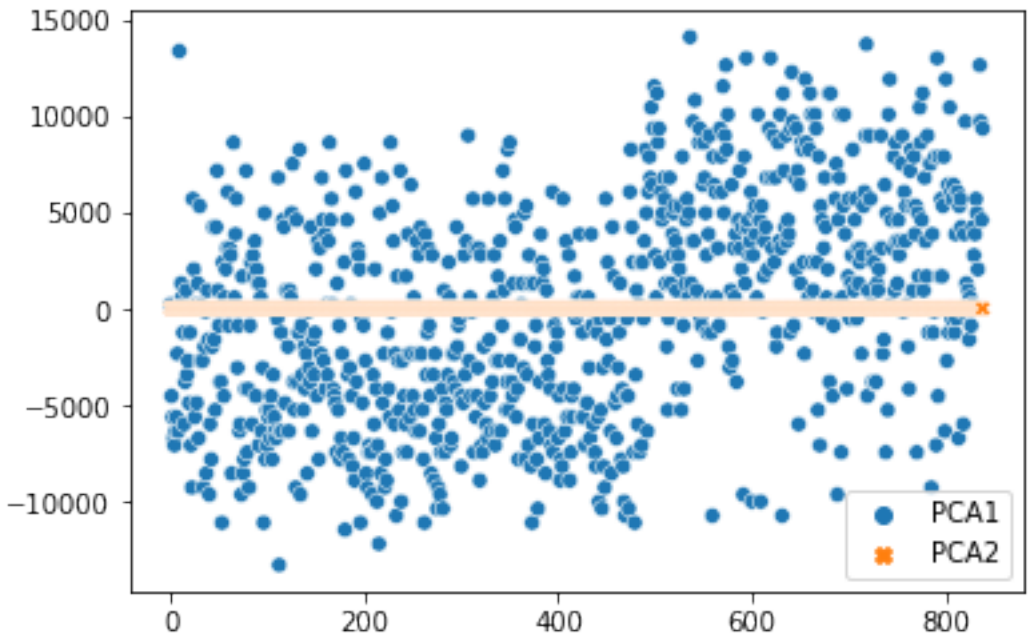
[75]: <Axes: >



[77]:
```
X_reduced = PCA(n_components=2, svd_solver='arpack')
X_reduced.fit_transform(data)

pca = X_reduced.fit_transform(data)
df = pd.DataFrame(data={'PCA1': pca[:, 0], 'PCA2': pca[:, 1]})
sns.scatterplot(df)
```

[77]: <Axes: >



0.0.10 I don't see any substantial improvement so now we can try to compare our results with supervised approach

[79]:
```
# split dataset into train and test with 70% to 30% ratio
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3)
y_train_transformed = y_train.astype('int')
y_test_transformed = y_test.astype('int')

pipeline = list()
pipeline.append(LogisticRegression(solver='liblinear'))
pipeline.append(GaussianNB())
pipeline.append(SVC())

pipeline.append(DecisionTreeClassifier())
pipeline.append(RandomForestClassifier())
pipeline.append(GradientBoostingClassifier())

accuracy_list = list()
auc_list = list()
cm_list = list()
for model in pipeline:
    print(model)
    model.fit(X_train, y_train_transformed)
    y_pred = model.predict(X_test)
    accuracy_list.append(metrics.accuracy_score(y_test_transformed, y_pred))
```

```
    fpr, tpr, _tresholds = metrics.roc_curve(y_test_transformed, y_pred)
    auc_list.append(round(metrics.auc(fpr, tpr), 2))
    cm_list.append(confusion_matrix(y_test_transformed, y_pred))

models = ['LogisticRegression', 'GaussianNB', 'SVC', 'DecisionTreeClassifier',␣
 ↪'RandomForestClassifier', 'GradientBoostingClassifier']

results = pd.DataFrame({'Model': models, 'Accuracy': accuracy_list, 'AUC':␣
 ↪auc_list})
results
```

```
LogisticRegression(solver='liblinear')
GaussianNB()
SVC()
DecisionTreeClassifier()
RandomForestClassifier()
GradientBoostingClassifier()
```

[79]:

	Model	Accuracy	AUC
0	LogisticRegression	0.853175	0.86
1	GaussianNB	0.849206	0.86
2	SVC	0.706349	0.69
3	DecisionTreeClassifier	0.757937	0.75
4	RandomForestClassifier	0.817460	0.81
5	GradientBoostingClassifier	0.857143	0.86

[80]:
```
# To explore logistic regression in more details I would use statsmodel library␣
 ↪instead
import statsmodels.api as sm


tmp = {'Age_at_diagnosis': list(X_train['Age_at_diagnosis']),
                   'Gender': list(X_train['Gender']),
                   'Race': list(X_train['Race']),
                   'grade': list(y_train)}



for gene_name in gene_names:
    tmp[gene_name] = list(X_train[gene_name])

df = pd.DataFrame(tmp)


#define response variable
y = df['grade']
```

```python
#define predictor variables
x = df[['Age_at_diagnosis', 'Gender', 'Race'] + gene_names]

#add constant to predictor variables
x = sm.add_constant(x)

#fit regression model
model = sm.OLS(y, x).fit()

#view summary of model fit
print(model.summary())
```

```
                            OLS Regression Results
==============================================================================
Dep. Variable:                   grade   R-squared:                       0.618
Model:                             OLS   Adj. R-squared:                  0.603
Method:                  Least Squares   F-statistic:                     39.68
Date:                 Mon, 21 Aug 2023   Prob (F-statistic):          5.57e-102
Time:                         13:15:49   Log-Likelihood:                -136.99
No. Observations:                  587   AIC:                             322.0
Df Residuals:                      563   BIC:                             427.0
Df Model:                           23
Covariance Type:            nonrobust
==============================================================================
                 coef    std err          t      P>|t|      [0.025      0.975]
------------------------------------------------------------------------------
const          0.4923      0.074      6.679      0.000       0.348       0.637
Age_at_diagnosis  1.162e-05   3.02e-06      3.846      0.000    5.69e-06    1.76e-05
Gender        -0.0240      0.027     -0.904      0.366      -0.076       0.028
Race           0.0525      0.024      2.233      0.026       0.006       0.099
IDH1          -0.6521      0.047    -13.982      0.000      -0.744      -0.560
TP53           0.1080      0.035      3.050      0.002       0.038       0.177
ATRX          -0.0248      0.040     -0.621      0.535      -0.103       0.054
PTEN           0.0931      0.039      2.403      0.017       0.017       0.169
EGFR          -0.1296      0.042     -3.085      0.002      -0.212      -0.047
CIC           -0.0370      0.050     -0.733      0.464      -0.136
```

```
0.062
MUC16                0.0672      0.041      1.656      0.098      -0.012
0.147
PIK3CA              -0.0104      0.049     -0.213      0.831      -0.106
0.085
NF1                 -0.1207      0.052     -2.300      0.022      -0.224
-0.018
PIK3R1               0.1227      0.053      2.329      0.020       0.019
0.226
FUBP1                0.0095      0.065      0.147      0.883      -0.118
0.137
RB1                  0.0714      0.067      1.070      0.285      -0.060
0.202
NOTCH1              -0.0736      0.064     -1.147      0.252      -0.200
0.052
BCOR                 0.0008      0.072      0.012      0.991      -0.141
0.142
CSMD3                0.0560      0.075      0.750      0.454      -0.091
0.203
SMARCA4             -0.0778      0.082     -0.950      0.342      -0.239
0.083
GRIN2A               0.2057      0.073      2.815      0.005       0.062
0.349
IDH2                -0.5814      0.093     -6.280      0.000      -0.763
-0.400
FAT4                -0.0112      0.078     -0.143      0.886      -0.165
0.143
PDGFRA               0.1680      0.087      1.920      0.055      -0.004
0.340
==============================================================================
Omnibus:                       53.377   Durbin-Watson:                   2.036
Prob(Omnibus):                  0.000   Jarque-Bera (JB):              138.809
Skew:                          -0.461   Prob(JB):                     7.21e-31
Kurtosis:                       5.196   Cond. No.                     1.60e+05
==============================================================================

Notes:
[1] Standard Errors assume that the covariance matrix of the errors is correctly
specified.
[2] The condition number is large, 1.6e+05. This might indicate that there are
strong multicollinearity or other numerical problems.
```

These results are pretty much consistent with what logistic regression tells us, on top of results described above logistic regression also reports that other genes might be linked with grade of the cancer, for example IDH1 and PTEN

0.0.11 6. Discussion and Conclusion

As we can see from the PCA results, first component actually describes almost all available variation and this component corresponds to the Age_at_diagnosis

GitHub Repo for this project can be found here:

https://github.com/also9275/dtsa_5510_final_project

0.0.12 7. References

[1] https://scikit-learn.org/stable/auto_examples/datasets/plot_iris_dataset.html#sphx-glr-auto-examples-datasets-plot-iris-dataset-py

[ ]: