

Project Based - Toward a Data Mining Portfolio EXTRA CREDIT

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```
#load the mlbench package which has the BreastCancer data set
```

```
library(mlbench)
```

```
# if you don't have any required package, use the install.packages() command
```

```
# load the data set
```

```
data(BreastCancer)
```

```
str(BreastCancer)
```

```
## 'data.frame': 699 obs. of 11 variables:
## $ Id : chr "1000025" "1002945" "1015425" "1016277" ...
## $ Cl.thickness : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<...: 5 5 3 6 4 8 1 2 2 4 ...
## $ Cell.size : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<...: 1 4 1 8 1 10 1 1 1 2 ...
## $ Cell.shape : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<...: 1 4 1 8 1 10 1 2 1 1 ...
## $ Marg.adhesion : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<...: 1 5 1 1 3 8 1 1 1 1 ...
## $ Epith.c.size : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<...: 2 7 2 3 2 7 2 2 2 2 ...
## $ Bare.nuclei : Factor w/ 10 levels "1","2","3","4",...: 1 10 2 4 1 10 10 1 1 1 ...
## $ Bl.cromatin : Factor w/ 10 levels "1","2","3","4",...: 3 3 3 3 3 9 3 3 1 2 ...
## $ Normal.nucleoli: Factor w/ 10 levels "1","2","3","4",...: 1 2 1 7 1 7 1 1 1 1 ...
## $ Mitoses : Factor w/ 9 levels "1","2","3","4",...: 1 1 1 1 1 1 1 1 5 1 ...
## $ Class : Factor w/ 2 levels "benign","malignant": 1 1 1 1 1 2 1 1 1 1 ...
```

```
## Preliminary step. Reviewing the Data Structure. Removing missing values. Remove id column as well si
```

```
dim(BreastCancer)
```

```
## [1] 699 11
```

```
str(BreastCancer)
```

```
## 'data.frame': 699 obs. of 11 variables:
## $ Id : chr "1000025" "1002945" "1015425" "1016277" ...
## $ Cl.thickness : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<...: 5 5 3 6 4 8 1 2 2 4 ...
## $ Cell.size : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<...: 1 4 1 8 1 10 1 1 1 2 ...
## $ Cell.shape : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<...: 1 4 1 8 1 10 1 2 1 1 ...
## $ Marg.adhesion : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<...: 1 5 1 1 3 8 1 1 1 1 ...
## $ Epith.c.size : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<...: 2 7 2 3 2 7 2 2 2 2 ...
## $ Bare.nuclei : Factor w/ 10 levels "1","2","3","4",...: 1 10 2 4 1 10 10 1 1 1 ...
## $ Bl.cromatin : Factor w/ 10 levels "1","2","3","4",...: 3 3 3 3 3 9 3 3 1 2 ...
```

```
## $ Normal.nucleoli: Factor w/ 10 levels "1","2","3","4",...: 1 2 1 7 1 7 1 1 1 1 ...
## $ Mitoses        : Factor w/ 9 levels "1","2","3","4",...: 1 1 1 1 1 1 1 1 5 1 ...
## $ Class          : Factor w/ 2 levels "benign","malignant": 1 1 1 1 1 2 1 1 1 1 ...
```

```
missing_values <- is.na(BreastCancer)

# Count missing values
num_missing <- sum(is.na(BreastCancer))

print(num_missing)
```

```
## [1] 16
```

```
# Remove missing values
BreastCancer <- na.omit(BreastCancer)

print(BreastCancer)
```

```
##      Id Cl.thickness Cell.size Cell.shape Marg.adhesion Epith.c.size
## 1  1000025          5         1         1          1          2
## 2  1002945          5         4         4          5          7
## 3  1015425          3         1         1          1          2
## 4  1016277          6         8         8          1          3
## 5  1017023          4         1         1          3          2
## 6  1017122          8        10        10          8          7
## 7  1018099          1         1         1          1          2
## 8  1018561          2         1         2          1          2
## 9  1033078          2         1         1          1          2
## 10 1033078          4         2         1          1          2
## 11 1035283          1         1         1          1          1
## 12 1036172          2         1         1          1          2
## 13 1041801          5         3         3          3          2
## 14 1043999          1         1         1          1          2
## 15 1044572          8         7         5         10          7
## 16 1047630          7         4         6          4          6
## 17 1048672          4         1         1          1          2
## 18 1049815          4         1         1          1          2
## 19 1050670         10         7         7          6          4
## 20 1050718          6         1         1          1          2
## 21 1054590          7         3         2         10          5
## 22 1054593         10         5         5          3          6
## 23 1056784          3         1         1          1          2
## 25 1059552          1         1         1          1          2
## 26 1065726          5         2         3          4          2
## 27 1066373          3         2         1          1          1
## 28 1066979          5         1         1          1          2
## 29 1067444          2         1         1          1          2
## 30 1070935          1         1         3          1          2
## 31 1070935          3         1         1          1          1
## 32 1071760          2         1         1          1          2
## 33 1072179         10         7         7          3          8
## 34 1074610          2         1         1          2          2
## 35 1075123          3         1         2          1          2
```

## 36	1079304	2	1	1	1	2
## 37	1080185	10	10	10	8	6
## 38	1081791	6	2	1	1	1
## 39	1084584	5	4	4	9	2
## 40	1091262	2	5	3	3	6
## 42	1099510	10	4	3	1	3
## 43	1100524	6	10	10	2	8
## 44	1102573	5	6	5	6	10
## 45	1103608	10	10	10	4	8
## 46	1103722	1	1	1	1	2
## 47	1105257	3	7	7	4	4
## 48	1105524	1	1	1	1	2
## 49	1106095	4	1	1	3	2
## 50	1106829	7	8	7	2	4
## 51	1108370	9	5	8	1	2
## 52	1108449	5	3	3	4	2
## 53	1110102	10	3	6	2	3
## 54	1110503	5	5	5	8	10
## 55	1110524	10	5	5	6	8
## 56	1111249	10	6	6	3	4
## 57	1112209	8	10	10	1	3
## 58	1113038	8	2	4	1	5
## 59	1113483	5	2	3	1	6
## 60	1113906	9	5	5	2	2
## 61	1115282	5	3	5	5	3
## 62	1115293	1	1	1	1	2
## 63	1116116	9	10	10	1	10
## 64	1116132	6	3	4	1	5
## 65	1116192	1	1	1	1	2
## 66	1116998	10	4	2	1	3
## 67	1117152	4	1	1	1	2
## 68	1118039	5	3	4	1	8
## 69	1120559	8	3	8	3	4
## 70	1121732	1	1	1	1	2
## 71	1121919	5	1	3	1	2
## 72	1123061	6	10	2	8	10
## 73	1124651	1	3	3	2	2
## 74	1125035	9	4	5	10	6
## 75	1126417	10	6	4	1	3
## 76	1131294	1	1	2	1	2
## 77	1132347	1	1	4	1	2
## 78	1133041	5	3	1	2	2
## 79	1133136	3	1	1	1	2
## 80	1136142	2	1	1	1	3
## 81	1137156	2	2	2	1	1
## 82	1143978	4	1	1	2	2
## 83	1143978	5	2	1	1	2
## 84	1147044	3	1	1	1	2
## 85	1147699	3	5	7	8	8
## 86	1147748	5	10	6	1	10
## 87	1148278	3	3	6	4	5
## 88	1148873	3	6	6	6	5
## 89	1152331	4	1	1	1	2
## 90	1155546	2	1	1	2	3

## 91	1156272	1	1	1	1	2
## 92	1156948	3	1	1	2	2
## 93	1157734	4	1	1	1	2
## 94	1158247	1	1	1	1	2
## 95	1160476	2	1	1	1	2
## 96	1164066	1	1	1	1	2
## 97	1165297	2	1	1	2	2
## 98	1165790	5	1	1	1	2
## 99	1165926	9	6	9	2	10
## 100	1166630	7	5	6	10	5
## 101	1166654	10	3	5	1	10
## 102	1167439	2	3	4	4	2
## 103	1167471	4	1	2	1	2
## 104	1168359	8	2	3	1	6
## 105	1168736	10	10	10	10	10
## 106	1169049	7	3	4	4	3
## 107	1170419	10	10	10	8	2
## 108	1170420	1	6	8	10	8
## 109	1171710	1	1	1	1	2
## 110	1171710	6	5	4	4	3
## 111	1171795	1	3	1	2	2
## 112	1171845	8	6	4	3	5
## 113	1172152	10	3	3	10	2
## 114	1173216	10	10	10	3	10
## 115	1173235	3	3	2	1	2
## 116	1173347	1	1	1	1	2
## 117	1173347	8	3	3	1	2
## 118	1173509	4	5	5	10	4
## 119	1173514	1	1	1	1	4
## 120	1173681	3	2	1	1	2
## 121	1174057	1	1	2	2	2
## 122	1174057	4	2	1	1	2
## 123	1174131	10	10	10	2	10
## 124	1174428	5	3	5	1	8
## 125	1175937	5	4	6	7	9
## 126	1176406	1	1	1	1	2
## 127	1176881	7	5	3	7	4
## 128	1177027	3	1	1	1	2
## 129	1177399	8	3	5	4	5
## 130	1177512	1	1	1	1	10
## 131	1178580	5	1	3	1	2
## 132	1179818	2	1	1	1	2
## 133	1180194	5	10	8	10	8
## 134	1180523	3	1	1	1	2
## 135	1180831	3	1	1	1	3
## 136	1181356	5	1	1	1	2
## 137	1182404	4	1	1	1	2
## 138	1182410	3	1	1	1	2
## 139	1183240	4	1	2	1	2
## 141	1183516	3	1	1	1	2
## 142	1183911	2	1	1	1	2
## 143	1183983	9	5	5	4	4
## 144	1184184	1	1	1	1	2
## 145	1184241	2	1	1	1	2

## 147	1185609	3	4	5	2	6
## 148	1185610	1	1	1	1	3
## 149	1187457	3	1	1	3	8
## 150	1187805	8	8	7	4	10
## 151	1188472	1	1	1	1	1
## 152	1189266	7	2	4	1	6
## 153	1189286	10	10	8	6	4
## 154	1190394	4	1	1	1	2
## 155	1190485	1	1	1	1	2
## 156	1192325	5	5	5	6	3
## 157	1193091	1	2	2	1	2
## 158	1193210	2	1	1	1	2
## 160	1196295	9	9	10	3	6
## 161	1196915	10	7	7	4	5
## 162	1197080	4	1	1	1	2
## 163	1197270	3	1	1	1	2
## 164	1197440	1	1	1	2	1
## 166	1197979	4	1	1	1	2
## 167	1197993	5	6	7	8	8
## 168	1198128	10	8	10	10	6
## 169	1198641	3	1	1	1	2
## 170	1199219	1	1	1	2	1
## 171	1199731	3	1	1	1	2
## 172	1199983	1	1	1	1	2
## 173	1200772	1	1	1	1	2
## 174	1200847	6	10	10	10	8
## 175	1200892	8	6	5	4	3
## 176	1200952	5	8	7	7	10
## 177	1201834	2	1	1	1	2
## 178	1201936	5	10	10	3	8
## 179	1202125	4	1	1	1	2
## 180	1202812	5	3	3	3	6
## 181	1203096	1	1	1	1	1
## 182	1204242	1	1	1	1	2
## 183	1204898	6	1	1	1	2
## 184	1205138	5	8	8	8	5
## 185	1205579	8	7	6	4	4
## 186	1206089	2	1	1	1	1
## 187	1206695	1	5	8	6	5
## 188	1206841	10	5	6	10	6
## 189	1207986	5	8	4	10	5
## 190	1208301	1	2	3	1	2
## 191	1210963	10	10	10	8	6
## 192	1211202	7	5	10	10	10
## 193	1212232	5	1	1	1	2
## 194	1212251	1	1	1	1	2
## 195	1212422	3	1	1	1	2
## 196	1212422	4	1	1	1	2
## 197	1213375	8	4	4	5	4
## 198	1213383	5	1	1	4	2
## 199	1214092	1	1	1	1	2
## 200	1214556	3	1	1	1	2
## 201	1214966	9	7	7	5	5
## 202	1216694	10	8	8	4	10

## 203	1216947	1	1	1	1	2
## 204	1217051	5	1	1	1	2
## 205	1217264	1	1	1	1	2
## 206	1218105	5	10	10	9	6
## 207	1218741	10	10	9	3	7
## 208	1218860	1	1	1	1	1
## 209	1218860	1	1	1	1	1
## 210	1219406	5	1	1	1	1
## 211	1219525	8	10	10	10	5
## 212	1219859	8	10	8	8	4
## 213	1220330	1	1	1	1	2
## 214	1221863	10	10	10	10	7
## 215	1222047	10	10	10	10	3
## 216	1222936	8	7	8	7	5
## 217	1223282	1	1	1	1	2
## 218	1223426	1	1	1	1	2
## 219	1223793	6	10	7	7	6
## 220	1223967	6	1	3	1	2
## 221	1224329	1	1	1	2	2
## 222	1225799	10	6	4	3	10
## 223	1226012	4	1	1	3	1
## 224	1226612	7	5	6	3	3
## 225	1227210	10	5	5	6	3
## 226	1227244	1	1	1	1	2
## 227	1227481	10	5	7	4	4
## 228	1228152	8	9	9	5	3
## 229	1228311	1	1	1	1	1
## 230	1230175	10	10	10	3	10
## 231	1230688	7	4	7	4	3
## 232	1231387	6	8	7	5	6
## 233	1231706	8	4	6	3	3
## 234	1232225	10	4	5	5	5
## 235	1236043	3	3	2	1	3
## 237	1241559	10	8	8	2	8
## 238	1241679	9	8	8	5	6
## 239	1242364	8	10	10	8	6
## 240	1243256	10	4	3	2	3
## 241	1270479	5	1	3	3	2
## 242	1276091	3	1	1	3	1
## 243	1277018	2	1	1	1	2
## 244	128059	1	1	1	1	2
## 245	1285531	1	1	1	1	2
## 246	1287775	5	1	1	2	2
## 247	144888	8	10	10	8	5
## 248	145447	8	4	4	1	2
## 249	167528	4	1	1	1	2
## 251	183913	1	2	2	1	2
## 252	191250	10	4	4	10	2
## 253	1017023	6	3	3	5	3
## 254	1100524	6	10	10	2	8
## 255	1116116	9	10	10	1	10
## 256	1168736	5	6	6	2	4
## 257	1182404	3	1	1	1	2
## 258	1182404	3	1	1	1	2

## 259	1198641	3	1	1	1	2
## 260	242970	5	7	7	1	5
## 261	255644	10	5	8	10	3
## 262	263538	5	10	10	6	10
## 263	274137	8	8	9	4	5
## 264	303213	10	4	4	10	6
## 265	314428	7	9	4	10	10
## 266	1182404	5	1	4	1	2
## 267	1198641	10	10	6	3	3
## 268	320675	3	3	5	2	3
## 269	324427	10	8	8	2	3
## 270	385103	1	1	1	1	2
## 271	390840	8	4	7	1	3
## 272	411453	5	1	1	1	2
## 273	320675	3	3	5	2	3
## 274	428903	7	2	4	1	3
## 275	431495	3	1	1	1	2
## 277	434518	3	1	1	1	2
## 278	452264	1	1	1	1	2
## 279	456282	1	1	1	1	2
## 280	476903	10	5	7	3	3
## 281	486283	3	1	1	1	2
## 282	486662	2	1	1	2	2
## 283	488173	1	4	3	10	4
## 284	492268	10	4	6	1	2
## 285	508234	7	4	5	10	2
## 286	527363	8	10	10	10	8
## 287	529329	10	10	10	10	10
## 288	535331	3	1	1	1	3
## 289	543558	6	1	3	1	4
## 290	555977	5	6	6	8	6
## 291	560680	1	1	1	1	2
## 292	561477	1	1	1	1	2
## 294	601265	10	4	4	6	2
## 296	606722	5	5	7	8	6
## 297	616240	5	3	4	3	4
## 299	625201	8	2	1	1	5
## 300	63375	9	1	2	6	4
## 301	635844	8	4	10	5	4
## 302	636130	1	1	1	1	2
## 303	640744	10	10	10	7	9
## 304	646904	1	1	1	1	2
## 305	653777	8	3	4	9	3
## 306	659642	10	8	4	4	4
## 307	666090	1	1	1	1	2
## 308	666942	1	1	1	1	2
## 309	667204	7	8	7	6	4
## 310	673637	3	1	1	1	2
## 311	684955	2	1	1	1	3
## 312	688033	1	1	1	1	2
## 313	691628	8	6	4	10	10
## 314	693702	1	1	1	1	2
## 315	704097	1	1	1	1	1
## 317	706426	5	5	5	2	5

## 318	709287	6	8	7	8	6
## 319	718641	1	1	1	1	5
## 320	721482	4	4	4	4	6
## 321	730881	7	6	3	2	5
## 323	733639	3	1	1	1	2
## 324	733823	5	4	6	10	2
## 325	740492	1	1	1	1	2
## 326	743348	3	2	2	1	2
## 327	752904	10	1	1	1	2
## 328	756136	1	1	1	1	2
## 329	760001	8	10	3	2	6
## 330	760239	10	4	6	4	5
## 331	76389	10	4	7	2	2
## 332	764974	5	1	1	1	2
## 333	770066	5	2	2	2	2
## 334	785208	5	4	6	6	4
## 335	785615	8	6	7	3	3
## 336	792744	1	1	1	1	2
## 337	797327	6	5	5	8	4
## 338	798429	1	1	1	1	2
## 339	704097	1	1	1	1	1
## 340	806423	8	5	5	5	2
## 341	809912	10	3	3	1	2
## 342	810104	1	1	1	1	2
## 343	814265	2	1	1	1	2
## 344	814911	1	1	1	1	2
## 345	822829	7	6	4	8	10
## 346	826923	1	1	1	1	2
## 347	830690	5	2	2	2	3
## 348	831268	1	1	1	1	1
## 349	832226	3	4	4	10	5
## 350	832567	4	2	3	5	3
## 351	836433	5	1	1	3	2
## 352	837082	2	1	1	1	2
## 353	846832	3	4	5	3	7
## 354	850831	2	7	10	10	7
## 355	855524	1	1	1	1	2
## 356	857774	4	1	1	1	3
## 357	859164	5	3	3	1	3
## 358	859350	8	10	10	7	10
## 359	866325	8	10	5	3	8
## 360	873549	10	3	5	4	3
## 361	877291	6	10	10	10	10
## 362	877943	3	10	3	10	6
## 363	888169	3	2	2	1	4
## 364	888523	4	4	4	2	2
## 365	896404	2	1	1	1	2
## 366	897172	2	1	1	1	2
## 367	95719	6	10	10	10	8
## 368	160296	5	8	8	10	5
## 369	342245	1	1	3	1	2
## 370	428598	1	1	3	1	1
## 371	492561	4	3	2	1	3
## 372	493452	1	1	3	1	2

## 373	493452	4	1	2	1	2
## 374	521441	5	1	1	2	2
## 375	560680	3	1	2	1	2
## 376	636437	1	1	1	1	2
## 377	640712	1	1	1	1	2
## 378	654244	1	1	1	1	1
## 379	657753	3	1	1	4	3
## 380	685977	5	3	4	1	4
## 381	805448	1	1	1	1	2
## 382	846423	10	6	3	6	4
## 383	1002504	3	2	2	2	2
## 384	1022257	2	1	1	1	2
## 385	1026122	2	1	1	1	2
## 386	1071084	3	3	2	2	3
## 387	1080233	7	6	6	3	2
## 388	1114570	5	3	3	2	3
## 389	1114570	2	1	1	1	2
## 390	1116715	5	1	1	1	3
## 391	1131411	1	1	1	2	2
## 392	1151734	10	8	7	4	3
## 393	1156017	3	1	1	1	2
## 394	1158247	1	1	1	1	1
## 395	1158405	1	2	3	1	2
## 396	1168278	3	1	1	1	2
## 397	1176187	3	1	1	1	2
## 398	1196263	4	1	1	1	2
## 399	1196475	3	2	1	1	2
## 400	1206314	1	2	3	1	2
## 401	1211265	3	10	8	7	6
## 402	1213784	3	1	1	1	2
## 403	1223003	5	3	3	1	2
## 404	1223306	3	1	1	1	2
## 405	1223543	1	2	1	3	2
## 406	1229929	1	1	1	1	2
## 407	1231853	4	2	2	1	2
## 408	1234554	1	1	1	1	2
## 409	1236837	2	3	2	2	2
## 410	1237674	3	1	2	1	2
## 411	1238021	1	1	1	1	2
## 413	1238633	10	10	10	6	8
## 414	1238915	5	1	2	1	2
## 415	1238948	8	5	6	2	3
## 416	1239232	3	3	2	6	3
## 417	1239347	8	7	8	5	10
## 418	1239967	1	1	1	1	2
## 419	1240337	5	2	2	2	2
## 420	1253505	2	3	1	1	5
## 421	1255384	3	2	2	3	2
## 422	1257200	10	10	10	7	10
## 423	1257648	4	3	3	1	2
## 424	1257815	5	1	3	1	2
## 425	1257938	3	1	1	1	2
## 426	1258549	9	10	10	10	10
## 427	1258556	5	3	6	1	2

## 428	1266154	8	7	8	2	4
## 429	1272039	1	1	1	1	2
## 430	1276091	2	1	1	1	2
## 431	1276091	1	3	1	1	2
## 432	1276091	5	1	1	3	4
## 433	1277629	5	1	1	1	2
## 434	1293439	3	2	2	3	2
## 435	1293439	6	9	7	5	5
## 436	1294562	10	8	10	1	3
## 437	1295186	10	10	10	1	6
## 438	527337	4	1	1	1	2
## 439	558538	4	1	3	3	2
## 440	566509	5	1	1	1	2
## 441	608157	10	4	3	10	4
## 442	677910	5	2	2	4	2
## 443	734111	1	1	1	3	2
## 444	734111	1	1	1	1	2
## 445	780555	5	1	1	6	3
## 446	827627	2	1	1	1	2
## 447	1049837	1	1	1	1	2
## 448	1058849	5	1	1	1	2
## 449	1182404	1	1	1	1	1
## 450	1193544	5	7	9	8	6
## 451	1201870	4	1	1	3	1
## 452	1202253	5	1	1	1	2
## 453	1227081	3	1	1	3	2
## 454	1230994	4	5	5	8	6
## 455	1238410	2	3	1	1	3
## 456	1246562	10	2	2	1	2
## 457	1257470	10	6	5	8	5
## 458	1259008	8	8	9	6	6
## 459	1266124	5	1	2	1	2
## 460	1267898	5	1	3	1	2
## 461	1268313	5	1	1	3	2
## 462	1268804	3	1	1	1	2
## 463	1276091	6	1	1	3	2
## 464	1280258	4	1	1	1	2
## 465	1293966	4	1	1	1	2
## 466	1296572	10	9	8	7	6
## 467	1298416	10	6	6	2	4
## 468	1299596	6	6	6	5	4
## 469	1105524	4	1	1	1	2
## 470	1181685	1	1	2	1	2
## 471	1211594	3	1	1	1	1
## 472	1238777	6	1	1	3	2
## 473	1257608	6	1	1	1	1
## 474	1269574	4	1	1	1	2
## 475	1277145	5	1	1	1	2
## 476	1287282	3	1	1	1	2
## 477	1296025	4	1	2	1	2
## 478	1296263	4	1	1	1	2
## 479	1296593	5	2	1	1	2
## 480	1299161	4	8	7	10	4
## 481	1301945	5	1	1	1	1

## 482	1302428	5	3	2	4	2
## 483	1318169	9	10	10	10	10
## 484	474162	8	7	8	5	5
## 485	787451	5	1	2	1	2
## 486	1002025	1	1	1	3	1
## 487	1070522	3	1	1	1	1
## 488	1073960	10	10	10	10	6
## 489	1076352	3	6	4	10	3
## 490	1084139	6	3	2	1	3
## 491	1115293	1	1	1	1	2
## 492	1119189	5	8	9	4	3
## 493	1133991	4	1	1	1	1
## 494	1142706	5	10	10	10	6
## 495	1155967	5	1	2	10	4
## 496	1170945	3	1	1	1	1
## 497	1181567	1	1	1	1	1
## 498	1182404	4	2	1	1	2
## 499	1204558	4	1	1	1	2
## 500	1217952	4	1	1	1	2
## 501	1224565	6	1	1	1	2
## 502	1238186	4	1	1	1	2
## 503	1253917	4	1	1	2	2
## 504	1265899	4	1	1	1	2
## 505	1268766	1	1	1	1	2
## 506	1277268	3	3	1	1	2
## 507	1286943	8	10	10	10	7
## 508	1295508	1	1	1	1	2
## 509	1297327	5	1	1	1	2
## 510	1297522	2	1	1	1	2
## 511	1298360	1	1	1	1	2
## 512	1299924	5	1	1	1	2
## 513	1299994	5	1	1	1	2
## 514	1304595	3	1	1	1	1
## 515	1306282	6	6	7	10	3
## 516	1313325	4	10	4	7	3
## 517	1320077	1	1	1	1	1
## 518	1320077	1	1	1	1	1
## 519	1320304	3	1	2	2	2
## 520	1330439	4	7	8	3	4
## 521	333093	1	1	1	1	3
## 522	369565	4	1	1	1	3
## 523	412300	10	4	5	4	3
## 524	672113	7	5	6	10	4
## 525	749653	3	1	1	1	2
## 526	769612	3	1	1	2	2
## 527	769612	4	1	1	1	2
## 528	798429	4	1	1	1	2
## 529	807657	6	1	3	2	2
## 530	8233704	4	1	1	1	1
## 531	837480	7	4	4	3	4
## 532	867392	4	2	2	1	2
## 533	869828	1	1	1	1	1
## 534	1043068	3	1	1	1	2
## 535	1056171	2	1	1	1	2

## 536	1061990	1	1	3	2	2
## 537	1113061	5	1	1	1	2
## 538	1116192	5	1	2	1	2
## 539	1135090	4	1	1	1	2
## 540	1145420	6	1	1	1	2
## 541	1158157	5	1	1	1	2
## 542	1171578	3	1	1	1	2
## 543	1174841	5	3	1	1	2
## 544	1184586	4	1	1	1	2
## 545	1186936	2	1	3	2	2
## 546	1197527	5	1	1	1	2
## 547	1222464	6	10	10	10	4
## 548	1240603	2	1	1	1	1
## 549	1240603	3	1	1	1	1
## 550	1241035	7	8	3	7	4
## 551	1287971	3	1	1	1	2
## 552	1289391	1	1	1	1	2
## 553	1299924	3	2	2	2	2
## 554	1306339	4	4	2	1	2
## 555	1313658	3	1	1	1	2
## 556	1313982	4	3	1	1	2
## 557	1321264	5	2	2	2	1
## 558	1321321	5	1	1	3	2
## 559	1321348	2	1	1	1	2
## 560	1321931	5	1	1	1	2
## 561	1321942	5	1	1	1	2
## 562	1321942	5	1	1	1	2
## 563	1328331	1	1	1	1	2
## 564	1328755	3	1	1	1	2
## 565	1331405	4	1	1	1	2
## 566	1331412	5	7	10	10	5
## 567	1333104	3	1	2	1	2
## 568	1334071	4	1	1	1	2
## 569	1343068	8	4	4	1	6
## 570	1343374	10	10	8	10	6
## 571	1344121	8	10	4	4	8
## 572	142932	7	6	10	5	3
## 573	183936	3	1	1	1	2
## 574	324382	1	1	1	1	2
## 575	378275	10	9	7	3	4
## 576	385103	5	1	2	1	2
## 577	690557	5	1	1	1	2
## 578	695091	1	1	1	1	2
## 579	695219	1	1	1	1	2
## 580	824249	1	1	1	1	2
## 581	871549	5	1	2	1	2
## 582	878358	5	7	10	6	5
## 583	1107684	6	10	5	5	4
## 584	1115762	3	1	1	1	2
## 585	1217717	5	1	1	6	3
## 586	1239420	1	1	1	1	2
## 587	1254538	8	10	10	10	6
## 588	1261751	5	1	1	1	2
## 589	1268275	9	8	8	9	6

## 590	1272166	5	1	1	1	2
## 591	1294261	4	10	8	5	4
## 592	1295529	2	5	7	6	4
## 593	1298484	10	3	4	5	3
## 594	1311875	5	1	2	1	2
## 595	1315506	4	8	6	3	4
## 596	1320141	5	1	1	1	2
## 597	1325309	4	1	2	1	2
## 598	1333063	5	1	3	1	2
## 599	1333495	3	1	1	1	2
## 600	1334659	5	2	4	1	1
## 601	1336798	3	1	1	1	2
## 602	1344449	1	1	1	1	1
## 603	1350568	4	1	1	1	2
## 604	1352663	5	4	6	8	4
## 605	188336	5	3	2	8	5
## 606	352431	10	5	10	3	5
## 607	353098	4	1	1	2	2
## 608	411453	1	1	1	1	2
## 609	557583	5	10	10	10	10
## 610	636375	5	1	1	1	2
## 611	736150	10	4	3	10	3
## 612	803531	5	10	10	10	5
## 613	822829	8	10	10	10	6
## 614	1016634	2	3	1	1	2
## 615	1031608	2	1	1	1	1
## 616	1041043	4	1	3	1	2
## 617	1042252	3	1	1	1	2
## 619	1061990	4	1	1	1	2
## 620	1073836	5	1	1	1	2
## 621	1083817	3	1	1	1	2
## 622	1096352	6	3	3	3	3
## 623	1140597	7	1	2	3	2
## 624	1149548	1	1	1	1	2
## 625	1174009	5	1	1	2	1
## 626	1183596	3	1	3	1	3
## 627	1190386	4	6	6	5	7
## 628	1190546	2	1	1	1	2
## 629	1213273	2	1	1	1	2
## 630	1218982	4	1	1	1	2
## 631	1225382	6	2	3	1	2
## 632	1235807	5	1	1	1	2
## 633	1238777	1	1	1	1	2
## 634	1253955	8	7	4	4	5
## 635	1257366	3	1	1	1	2
## 636	1260659	3	1	4	1	2
## 637	1268952	10	10	7	8	7
## 638	1275807	4	2	4	3	2
## 639	1277792	4	1	1	1	2
## 640	1277792	5	1	1	3	2
## 641	1285722	4	1	1	3	2
## 642	1288608	3	1	1	1	2
## 643	1290203	3	1	1	1	2
## 644	1294413	1	1	1	1	2

## 645	1299596	2	1	1	1	2
## 646	1303489	3	1	1	1	2
## 647	1311033	1	2	2	1	2
## 648	1311108	1	1	1	3	2
## 649	1315807	5	10	10	10	10
## 650	1318671	3	1	1	1	2
## 651	1319609	3	1	1	2	3
## 652	1323477	1	2	1	3	2
## 653	1324572	5	1	1	1	2
## 654	1324681	4	1	1	1	2
## 655	1325159	3	1	1	1	2
## 656	1326892	3	1	1	1	2
## 657	1330361	5	1	1	1	2
## 658	1333877	5	4	5	1	8
## 659	1334015	7	8	8	7	3
## 660	1334667	1	1	1	1	2
## 661	1339781	1	1	1	1	2
## 662	1339781	4	1	1	1	2
## 663	13454352	1	1	3	1	2
## 664	1345452	1	1	3	1	2
## 665	1345593	3	1	1	3	2
## 666	1347749	1	1	1	1	2
## 667	1347943	5	2	2	2	2
## 668	1348851	3	1	1	1	2
## 669	1350319	5	7	4	1	6
## 670	1350423	5	10	10	8	5
## 671	1352848	3	10	7	8	5
## 672	1353092	3	2	1	2	2
## 673	1354840	2	1	1	1	2
## 674	1354840	5	3	2	1	3
## 675	1355260	1	1	1	1	2
## 676	1365075	4	1	4	1	2
## 677	1365328	1	1	2	1	2
## 678	1368267	5	1	1	1	2
## 679	1368273	1	1	1	1	2
## 680	1368882	2	1	1	1	2
## 681	1369821	10	10	10	10	5
## 682	1371026	5	10	10	10	4
## 683	1371920	5	1	1	1	2
## 684	466906	1	1	1	1	2
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## 686	534555	1	1	1	1	2
## 687	536708	1	1	1	1	2
## 688	566346	3	1	1	1	2
## 689	603148	4	1	1	1	2
## 690	654546	1	1	1	1	2
## 691	654546	1	1	1	3	2
## 692	695091	5	10	10	5	4
## 693	714039	3	1	1	1	2
## 694	763235	3	1	1	1	2
## 695	776715	3	1	1	1	3
## 696	841769	2	1	1	1	2
## 697	888820	5	10	10	3	7
## 698	897471	4	8	6	4	3

## 699	897471	4	8	8	5	4
##	Bare.nuclei	Bl.cromatin	Normal.nucleoli	Mitoses	Class	
## 1	1	3	1	1	benign	
## 2	10	3	2	1	benign	
## 3	2	3	1	1	benign	
## 4	4	3	7	1	benign	
## 5	1	3	1	1	benign	
## 6	10	9	7	1	malignant	
## 7	10	3	1	1	benign	
## 8	1	3	1	1	benign	
## 9	1	1	1	5	benign	
## 10	1	2	1	1	benign	
## 11	1	3	1	1	benign	
## 12	1	2	1	1	benign	
## 13	3	4	4	1	malignant	
## 14	3	3	1	1	benign	
## 15	9	5	5	4	malignant	
## 16	1	4	3	1	malignant	
## 17	1	2	1	1	benign	
## 18	1	3	1	1	benign	
## 19	10	4	1	2	malignant	
## 20	1	3	1	1	benign	
## 21	10	5	4	4	malignant	
## 22	7	7	10	1	malignant	
## 23	1	2	1	1	benign	
## 25	1	3	1	1	benign	
## 26	7	3	6	1	malignant	
## 27	1	2	1	1	benign	
## 28	1	2	1	1	benign	
## 29	1	2	1	1	benign	
## 30	1	1	1	1	benign	
## 31	1	2	1	1	benign	
## 32	1	3	1	1	benign	
## 33	5	7	4	3	malignant	
## 34	1	3	1	1	benign	
## 35	1	2	1	1	benign	
## 36	1	2	1	1	benign	
## 37	1	8	9	1	malignant	
## 38	1	7	1	1	benign	
## 39	10	5	6	1	malignant	
## 40	7	7	5	1	malignant	
## 42	3	6	5	2	malignant	
## 43	10	7	3	3	malignant	
## 44	1	3	1	1	malignant	
## 45	1	8	10	1	malignant	
## 46	1	2	1	2	benign	
## 47	9	4	8	1	malignant	
## 48	1	2	1	1	benign	
## 49	1	3	1	1	benign	
## 50	8	3	8	2	malignant	
## 51	3	2	1	5	malignant	
## 52	4	3	4	1	malignant	
## 53	5	4	10	2	malignant	
## 54	8	7	3	7	malignant	

## 55	8	7	1	1 malignant
## 56	5	3	6	1 malignant
## 57	6	3	9	1 malignant
## 58	1	5	4	4 malignant
## 59	10	5	1	1 malignant
## 60	2	5	1	1 malignant
## 61	3	4	10	1 malignant
## 62	2	2	1	1 benign
## 63	8	3	3	1 malignant
## 64	2	3	9	1 malignant
## 65	1	2	1	1 benign
## 66	2	4	3	10 malignant
## 67	1	3	1	1 benign
## 68	10	4	9	1 malignant
## 69	9	8	9	8 malignant
## 70	1	3	2	1 benign
## 71	1	2	1	1 benign
## 72	2	7	8	10 malignant
## 73	1	7	2	1 benign
## 74	10	4	8	1 malignant
## 75	4	3	2	3 malignant
## 76	2	4	2	1 benign
## 77	1	2	1	1 benign
## 78	1	2	1	1 benign
## 79	3	3	1	1 benign
## 80	1	2	1	1 benign
## 81	1	7	1	1 benign
## 82	1	2	1	1 benign
## 83	1	3	1	1 benign
## 84	2	7	1	1 benign
## 85	9	7	10	7 malignant
## 86	4	4	10	10 malignant
## 87	8	4	4	1 malignant
## 88	10	6	8	3 malignant
## 89	1	3	1	1 benign
## 90	1	2	1	1 benign
## 91	1	3	1	1 benign
## 92	1	1	1	1 benign
## 93	1	3	1	1 benign
## 94	1	2	1	1 benign
## 95	1	3	1	1 benign
## 96	1	3	1	1 benign
## 97	1	1	1	1 benign
## 98	1	3	1	1 benign
## 99	6	2	9	10 malignant
## 100	10	7	9	4 malignant
## 101	5	3	10	2 malignant
## 102	5	2	5	1 malignant
## 103	1	3	1	1 benign
## 104	3	7	1	1 malignant
## 105	1	8	8	8 malignant
## 106	3	3	2	7 malignant
## 107	10	4	1	1 malignant
## 108	10	5	7	1 malignant

## 109	1	2	3	1	benign
## 110	9	7	8	3	malignant
## 111	2	5	3	2	benign
## 112	9	3	1	1	malignant
## 113	10	7	3	3	malignant
## 114	8	8	1	1	malignant
## 115	3	3	1	1	benign
## 116	5	1	1	1	benign
## 117	2	3	2	1	benign
## 118	10	7	5	8	malignant
## 119	3	1	1	1	benign
## 120	2	3	1	1	benign
## 121	1	3	1	1	benign
## 122	2	3	1	1	benign
## 123	10	5	3	3	malignant
## 124	10	5	3	1	malignant
## 125	7	8	10	1	malignant
## 126	1	2	1	1	benign
## 127	10	7	5	5	malignant
## 128	1	3	1	1	benign
## 129	10	1	6	2	malignant
## 130	1	1	1	1	benign
## 131	1	2	1	1	benign
## 132	1	3	1	1	benign
## 133	10	3	6	3	malignant
## 134	1	2	2	1	benign
## 135	1	2	1	1	benign
## 136	2	3	3	1	benign
## 137	1	2	1	1	benign
## 138	1	1	1	1	benign
## 139	1	2	1	1	benign
## 141	1	1	1	1	benign
## 142	1	1	1	1	benign
## 143	5	4	3	3	malignant
## 144	5	1	1	1	benign
## 145	1	2	1	1	benign
## 147	8	4	1	1	malignant
## 148	2	2	1	1	benign
## 149	1	5	8	1	benign
## 150	10	7	8	7	malignant
## 151	1	3	1	1	benign
## 152	10	5	4	3	malignant
## 153	5	8	10	1	malignant
## 154	3	1	1	1	benign
## 155	1	1	1	1	benign
## 156	10	3	1	1	malignant
## 157	1	2	1	1	benign
## 158	1	3	1	1	benign
## 160	10	7	10	6	malignant
## 161	10	5	7	2	malignant
## 162	1	3	2	1	benign
## 163	1	3	1	1	benign
## 164	3	1	1	7	benign
## 166	2	3	2	1	benign

## 167	10	3	10	3 malignant
## 168	1	3	1	10 malignant
## 169	1	3	1	1 benign
## 170	1	1	1	1 benign
## 171	1	1	1	1 benign
## 172	1	3	1	1 benign
## 173	1	2	1	1 benign
## 174	10	10	10	7 malignant
## 175	10	6	1	1 malignant
## 176	10	5	7	1 malignant
## 177	1	3	1	1 benign
## 178	1	5	10	3 malignant
## 179	1	3	1	1 benign
## 180	10	3	1	1 malignant
## 181	1	3	1	1 benign
## 182	1	1	1	1 benign
## 183	1	3	1	1 benign
## 184	10	7	8	1 malignant
## 185	10	5	1	1 malignant
## 186	1	3	1	1 benign
## 187	8	7	10	1 malignant
## 188	10	7	7	10 malignant
## 189	8	9	10	1 malignant
## 190	1	3	1	1 benign
## 191	8	7	10	1 malignant
## 192	10	4	10	3 malignant
## 193	1	2	1	1 benign
## 194	1	3	1	1 benign
## 195	1	3	1	1 benign
## 196	1	3	1	1 benign
## 197	7	7	8	2 benign
## 198	1	3	1	1 benign
## 199	1	1	1	1 benign
## 200	1	2	1	1 benign
## 201	10	7	8	3 malignant
## 202	10	8	1	1 malignant
## 203	1	3	1	1 benign
## 204	1	3	1	1 benign
## 205	1	3	1	1 benign
## 206	10	7	10	5 malignant
## 207	5	3	5	1 malignant
## 208	1	3	1	1 benign
## 209	1	3	1	1 benign
## 210	1	3	1	1 benign
## 211	10	8	10	6 malignant
## 212	8	7	7	1 malignant
## 213	1	3	1	1 benign
## 214	10	7	10	4 malignant
## 215	10	10	6	1 malignant
## 216	5	5	10	2 malignant
## 217	1	2	1	1 benign
## 218	1	3	1	1 benign
## 219	4	8	10	2 malignant
## 220	1	3	1	1 benign

## 221	1	3	1	1	benign
## 222	10	9	10	1	malignant
## 223	5	2	1	1	malignant
## 224	8	7	4	1	malignant
## 225	10	7	9	2	malignant
## 226	1	2	1	1	benign
## 227	10	8	9	1	malignant
## 228	5	7	7	1	malignant
## 229	1	3	1	1	benign
## 230	10	9	10	1	malignant
## 231	7	7	6	1	malignant
## 232	8	8	9	2	malignant
## 233	1	4	3	1	benign
## 234	10	4	1	1	malignant
## 235	1	3	6	1	benign
## 237	10	4	8	10	malignant
## 238	2	4	10	4	malignant
## 239	9	3	10	10	malignant
## 240	10	5	3	2	malignant
## 241	2	2	3	1	benign
## 242	1	3	1	1	benign
## 243	1	3	1	1	benign
## 244	5	5	1	1	benign
## 245	1	3	1	1	benign
## 246	2	3	1	1	benign
## 247	10	7	8	1	malignant
## 248	9	3	3	1	malignant
## 249	1	3	6	1	benign
## 251	1	1	1	1	benign
## 252	10	5	3	3	malignant
## 253	10	3	5	3	benign
## 254	10	7	3	3	malignant
## 255	8	3	3	1	malignant
## 256	10	3	6	1	malignant
## 257	1	1	1	1	benign
## 258	1	2	1	1	benign
## 259	1	3	1	1	benign
## 260	8	3	4	1	benign
## 261	10	5	1	3	malignant
## 262	10	10	6	5	malignant
## 263	10	7	8	1	malignant
## 264	10	5	5	1	malignant
## 265	3	5	3	3	malignant
## 266	1	3	2	1	benign
## 267	10	4	3	2	malignant
## 268	10	7	1	1	malignant
## 269	4	8	7	8	malignant
## 270	1	3	1	1	benign
## 271	10	3	9	2	malignant
## 272	1	3	1	1	benign
## 273	10	7	1	1	malignant
## 274	4	3	3	1	malignant
## 275	1	3	2	1	benign
## 277	1	2	1	1	benign

## 278	1	2	1	1	benign
## 279	1	3	1	1	benign
## 280	7	3	3	8	malignant
## 281	1	3	1	1	benign
## 282	1	3	1	1	benign
## 283	10	5	6	1	malignant
## 284	10	5	3	1	malignant
## 285	10	3	8	2	malignant
## 286	10	10	7	3	malignant
## 287	10	4	10	10	malignant
## 288	1	2	1	1	benign
## 289	5	5	10	1	malignant
## 290	10	4	10	4	malignant
## 291	1	1	1	1	benign
## 292	1	3	1	1	benign
## 294	10	2	3	1	malignant
## 296	10	7	4	1	malignant
## 297	5	4	7	1	benign
## 299	1	1	1	1	benign
## 300	10	7	7	2	malignant
## 301	4	7	10	1	malignant
## 302	1	3	1	1	benign
## 303	10	7	10	10	malignant
## 304	1	3	1	1	benign
## 305	10	3	3	1	malignant
## 306	10	3	10	4	malignant
## 307	1	3	1	1	benign
## 308	1	3	1	1	benign
## 309	3	8	8	4	malignant
## 310	5	5	1	1	benign
## 311	1	2	1	1	benign
## 312	1	1	1	1	benign
## 313	1	3	5	1	malignant
## 314	1	1	1	1	benign
## 315	1	2	1	1	benign
## 317	10	4	3	1	malignant
## 318	8	8	9	1	malignant
## 319	1	3	1	1	benign
## 320	5	7	3	1	benign
## 321	10	7	4	6	malignant
## 323	1	3	1	1	benign
## 324	10	4	1	1	malignant
## 325	1	3	1	1	benign
## 326	1	2	3	1	benign
## 327	10	5	4	1	malignant
## 328	1	2	1	1	benign
## 329	4	3	10	1	malignant
## 330	10	7	1	1	malignant
## 331	8	6	1	1	malignant
## 332	1	3	1	2	benign
## 333	1	2	2	1	benign
## 334	10	4	3	1	malignant
## 335	10	3	4	2	malignant
## 336	1	1	1	1	benign

## 337	10	3	4	1 malignant
## 338	1	3	1	1 benign
## 339	1	2	1	1 benign
## 340	10	4	3	1 malignant
## 341	10	7	6	1 malignant
## 342	1	3	1	1 benign
## 343	1	1	1	1 benign
## 344	1	1	1	1 benign
## 345	10	9	5	3 malignant
## 346	1	1	1	1 benign
## 347	1	1	3	1 benign
## 348	1	1	3	1 benign
## 349	1	3	3	1 malignant
## 350	8	7	6	1 malignant
## 351	1	1	1	1 benign
## 352	1	3	1	1 benign
## 353	3	4	6	1 benign
## 354	10	4	9	4 malignant
## 355	1	2	1	1 benign
## 356	1	2	2	1 benign
## 357	3	3	3	3 malignant
## 358	10	7	3	8 malignant
## 359	4	4	10	3 malignant
## 360	7	3	5	3 malignant
## 361	10	8	10	10 malignant
## 362	10	5	1	4 malignant
## 363	3	2	1	1 benign
## 364	3	2	1	1 benign
## 365	1	3	1	1 benign
## 366	1	2	1	1 benign
## 367	10	7	10	7 malignant
## 368	10	8	10	3 malignant
## 369	1	1	1	1 benign
## 370	1	2	1	1 benign
## 371	1	2	1	1 benign
## 372	1	1	1	1 benign
## 373	1	2	1	1 benign
## 374	1	2	1	1 benign
## 375	1	2	1	1 benign
## 376	1	1	1	1 benign
## 377	1	2	1	1 benign
## 378	1	2	1	1 benign
## 379	1	2	2	1 benign
## 380	1	3	1	1 benign
## 381	1	1	1	1 benign
## 382	10	7	8	4 malignant
## 383	1	3	2	1 benign
## 384	1	1	1	1 benign
## 385	1	1	1	1 benign
## 386	1	1	2	3 benign
## 387	10	7	1	1 malignant
## 388	1	3	1	1 benign
## 389	1	2	2	1 benign
## 390	2	2	2	1 benign

## 391	1	2	1	1	benign
## 392	10	7	9	1	malignant
## 393	1	2	1	1	benign
## 394	1	1	1	1	benign
## 395	1	2	1	1	benign
## 396	1	2	1	1	benign
## 397	1	3	1	1	benign
## 398	1	1	1	1	benign
## 399	1	2	2	1	benign
## 400	1	1	1	1	benign
## 401	9	9	3	8	malignant
## 402	1	1	1	1	benign
## 403	1	2	1	1	benign
## 404	4	1	1	1	benign
## 405	1	1	2	1	benign
## 406	1	2	1	1	benign
## 407	1	2	1	1	benign
## 408	1	2	1	1	benign
## 409	2	3	1	1	benign
## 410	1	2	1	1	benign
## 411	1	2	1	1	benign
## 413	4	8	5	1	malignant
## 414	1	3	1	1	benign
## 415	10	6	6	1	malignant
## 416	3	3	5	1	benign
## 417	10	7	2	1	malignant
## 418	1	2	1	1	benign
## 419	2	3	2	2	benign
## 420	1	1	1	1	benign
## 421	3	3	1	1	benign
## 422	10	8	2	1	malignant
## 423	1	3	3	1	benign
## 424	1	2	1	1	benign
## 425	1	1	1	1	benign
## 426	10	10	10	1	malignant
## 427	1	1	1	1	benign
## 428	2	5	10	1	malignant
## 429	1	2	1	1	benign
## 430	1	2	1	1	benign
## 431	1	2	2	1	benign
## 432	1	3	2	1	benign
## 433	1	2	2	1	benign
## 434	1	1	1	1	benign
## 435	8	4	2	1	benign
## 436	10	5	1	1	malignant
## 437	1	2	8	1	malignant
## 438	1	1	1	1	benign
## 439	1	1	1	1	benign
## 440	1	1	1	1	benign
## 441	10	10	1	1	malignant
## 442	4	1	1	1	benign
## 443	3	1	1	1	benign
## 444	2	1	1	1	benign
## 445	1	2	1	1	benign

## 446	1	1	1	1	benign
## 447	1	1	1	1	benign
## 448	1	1	1	1	benign
## 449	1	1	1	1	benign
## 450	10	8	10	1	malignant
## 451	1	2	1	1	benign
## 452	1	1	1	1	benign
## 453	1	1	1	1	benign
## 454	10	10	7	1	malignant
## 455	1	1	1	1	benign
## 456	6	1	1	2	malignant
## 457	10	8	6	1	malignant
## 458	3	10	10	1	malignant
## 459	1	1	1	1	benign
## 460	1	1	1	1	benign
## 461	1	1	1	1	benign
## 462	5	1	1	1	benign
## 463	1	1	1	1	benign
## 464	1	1	2	1	benign
## 465	1	1	1	1	benign
## 466	4	7	10	3	malignant
## 467	10	9	7	1	malignant
## 468	10	7	6	2	malignant
## 469	1	1	1	1	benign
## 470	1	2	1	1	benign
## 471	1	2	1	1	benign
## 472	1	1	1	1	benign
## 473	1	1	1	1	benign
## 474	1	1	1	1	benign
## 475	1	1	1	1	benign
## 476	1	1	1	1	benign
## 477	1	1	1	1	benign
## 478	1	1	1	1	benign
## 479	1	1	1	1	benign
## 480	10	7	5	1	malignant
## 481	1	1	1	1	benign
## 482	1	1	1	1	benign
## 483	5	10	10	10	malignant
## 484	10	9	10	1	malignant
## 485	1	1	1	1	benign
## 486	3	1	1	1	benign
## 487	1	2	1	1	benign
## 488	10	8	1	5	malignant
## 489	3	3	4	1	malignant
## 490	4	4	1	1	malignant
## 491	1	1	1	1	benign
## 492	10	7	1	1	malignant
## 493	1	2	1	1	benign
## 494	10	6	5	2	malignant
## 495	5	2	1	1	benign
## 496	1	2	1	1	benign
## 497	1	1	1	1	benign
## 498	1	1	1	1	benign
## 499	1	2	1	1	benign

## 500	1	2	1	1	benign
## 501	1	3	1	1	benign
## 502	1	2	1	1	benign
## 503	1	2	1	1	benign
## 504	1	3	1	1	benign
## 505	1	1	1	1	benign
## 506	1	1	1	1	benign
## 507	5	4	8	7	malignant
## 508	4	1	1	1	benign
## 509	1	1	1	1	benign
## 510	1	1	1	1	benign
## 511	1	1	1	1	benign
## 512	1	2	1	1	benign
## 513	1	1	1	1	benign
## 514	1	2	1	1	benign
## 515	10	8	10	2	malignant
## 516	10	9	10	1	malignant
## 517	1	1	1	1	benign
## 518	1	2	1	1	benign
## 519	1	1	1	1	benign
## 520	10	9	1	1	malignant
## 521	1	1	1	1	benign
## 522	1	1	1	1	benign
## 523	5	7	3	1	malignant
## 524	10	5	3	1	malignant
## 525	1	2	1	1	benign
## 526	1	1	1	1	benign
## 527	1	1	1	1	benign
## 528	1	3	1	1	benign
## 529	1	1	1	1	benign
## 530	1	2	1	1	benign
## 531	10	6	9	1	malignant
## 532	1	2	1	1	benign
## 533	1	3	1	1	benign
## 534	1	2	1	1	benign
## 535	1	2	1	1	benign
## 536	1	3	1	1	benign
## 537	1	3	1	1	benign
## 538	1	3	1	1	benign
## 539	1	2	1	1	benign
## 540	1	2	1	1	benign
## 541	2	2	1	1	benign
## 542	1	1	1	1	benign
## 543	1	1	1	1	benign
## 544	1	2	1	1	benign
## 545	1	2	1	1	benign
## 546	1	2	1	1	benign
## 547	10	7	10	1	malignant
## 548	1	1	1	1	benign
## 549	1	1	1	1	benign
## 550	5	7	8	2	malignant
## 551	1	2	1	1	benign
## 552	1	3	1	1	benign
## 553	1	4	2	1	benign

## 554	5	2	1	2	benign
## 555	1	1	1	1	benign
## 556	1	4	8	1	benign
## 557	1	2	1	1	benign
## 558	1	1	1	1	benign
## 559	1	2	1	1	benign
## 560	1	2	1	1	benign
## 561	1	3	1	1	benign
## 562	1	3	1	1	benign
## 563	1	3	1	1	benign
## 564	1	2	1	1	benign
## 565	1	3	2	1	benign
## 566	10	10	10	1	malignant
## 567	1	3	1	1	benign
## 568	3	2	1	1	benign
## 569	10	2	5	2	malignant
## 570	5	10	3	1	malignant
## 571	10	8	2	1	malignant
## 572	10	9	10	2	malignant
## 573	1	2	1	1	benign
## 574	1	2	1	1	benign
## 575	2	7	7	1	malignant
## 576	1	3	1	1	benign
## 577	1	2	1	1	benign
## 578	1	2	1	1	benign
## 579	1	2	1	1	benign
## 580	1	3	1	1	benign
## 581	1	2	1	1	benign
## 582	10	7	5	1	malignant
## 583	10	6	10	1	malignant
## 584	1	1	1	1	benign
## 585	1	1	1	1	benign
## 586	1	1	1	1	benign
## 587	10	10	10	1	malignant
## 588	1	2	2	1	benign
## 589	3	4	1	1	malignant
## 590	1	1	1	1	benign
## 591	1	10	1	1	malignant
## 592	10	7	6	1	malignant
## 593	10	4	1	1	malignant
## 594	1	1	1	1	benign
## 595	10	7	1	1	malignant
## 596	1	2	1	1	benign
## 597	1	2	1	1	benign
## 598	1	3	1	1	benign
## 599	1	2	1	1	benign
## 600	1	1	1	1	benign
## 601	1	2	1	1	benign
## 602	1	2	1	1	benign
## 603	1	2	1	1	benign
## 604	1	8	10	1	malignant
## 605	10	8	1	2	malignant
## 606	8	7	8	3	malignant
## 607	1	1	1	1	benign

## 608	1	1	1	1	benign
## 609	10	10	1	1	malignant
## 610	1	1	1	1	benign
## 611	10	7	1	2	malignant
## 612	2	8	5	1	malignant
## 613	10	10	10	10	malignant
## 614	1	2	1	1	benign
## 615	1	2	1	1	benign
## 616	1	2	1	1	benign
## 617	1	2	1	1	benign
## 619	1	2	1	1	benign
## 620	1	2	1	1	benign
## 621	1	2	1	1	benign
## 622	2	6	1	1	benign
## 623	1	2	1	1	benign
## 624	1	1	1	1	benign
## 625	1	2	1	1	benign
## 626	4	1	1	1	benign
## 627	6	7	7	3	malignant
## 628	5	1	1	1	benign
## 629	1	1	1	1	benign
## 630	1	1	1	1	benign
## 631	1	1	1	1	benign
## 632	1	2	1	1	benign
## 633	1	1	1	1	benign
## 634	3	5	10	1	malignant
## 635	1	1	1	1	benign
## 636	1	1	1	1	benign
## 637	1	10	10	3	malignant
## 638	2	2	1	1	benign
## 639	1	1	1	1	benign
## 640	1	1	1	1	benign
## 641	1	1	1	1	benign
## 642	1	2	1	1	benign
## 643	1	2	1	1	benign
## 644	1	1	1	1	benign
## 645	1	1	1	1	benign
## 646	1	2	1	1	benign
## 647	1	1	1	1	benign
## 648	1	1	1	1	benign
## 649	2	10	10	10	malignant
## 650	1	2	1	1	benign
## 651	4	1	1	1	benign
## 652	1	2	1	1	benign
## 653	1	2	2	1	benign
## 654	1	2	1	1	benign
## 655	1	3	1	1	benign
## 656	1	2	1	1	benign
## 657	1	2	1	1	benign
## 658	1	3	6	1	benign
## 659	10	7	2	3	malignant
## 660	1	1	1	1	benign
## 661	1	2	1	1	benign
## 662	1	3	1	1	benign

```
## 663      1      2      1      1      benign
## 664      1      2      1      1      benign
## 665      1      2      1      1      benign
## 666      1      1      1      1      benign
## 667      1      1      1      2      benign
## 668      1      3      1      1      benign
## 669      1      7     10      3     malignant
## 670      5      7     10      1     malignant
## 671      8      7      4      1     malignant
## 672      1      3      1      1      benign
## 673      1      3      1      1      benign
## 674      1      1      1      1      benign
## 675      1      2      1      1      benign
## 676      1      1      1      1      benign
## 677      1      2      1      1      benign
## 678      1      1      1      1      benign
## 679      1      1      1      1      benign
## 680      1      1      1      1      benign
## 681     10     10     10      7     malignant
## 682     10      5      6      3     malignant
## 683      1      3      2      1      benign
## 684      1      1      1      1      benign
## 685      1      1      1      1      benign
## 686      1      1      1      1      benign
## 687      1      1      1      1      benign
## 688      1      2      3      1      benign
## 689      1      1      1      1      benign
## 690      1      1      1      8      benign
## 691      1      1      1      1      benign
## 692      5      4      4      1     malignant
## 693      1      1      1      1      benign
## 694      1      2      1      2      benign
## 695      2      1      1      1      benign
## 696      1      1      1      1      benign
## 697      3      8     10      2     malignant
## 698      4     10      6      1     malignant
## 699      5     10      4      1     malignant
```

```
# Remove Id column
```

```
BreastCancer <- BreastCancer[, -1]
```

```
# Now, the Class variable is converted into a factor since we need to do this in order to do classifica
```

```
## 1 = Benign and 0 = Malignant
```

```
# Convert "Class" into a factor with levels 1 and 0
```

```
BreastCancer$Class <- factor(BreastCancer$Class, levels = c("benign", "malignant"), labels = c(1, 0))
```

```
str(BreastCancer)
```

```
## 'data.frame': 683 obs. of 10 variables:
```

```
## $ Cl.thickness : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<..: 5 5 3 6 4 8 1 2 2 4 ...
## $ Cell.size : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<..: 1 4 1 8 1 10 1 1 1 2 ...
## $ Cell.shape : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<..: 1 4 1 8 1 10 1 2 1 1 ...
## $ Marg.adhesion : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<..: 1 5 1 1 3 8 1 1 1 1 ...
## $ Epith.c.size : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<..: 2 7 2 3 2 7 2 2 2 2 ...
```

```
## $ Bare.nuclei      : Factor w/ 10 levels "1","2","3","4",...: 1 10 2 4 1 10 10 1 1 1 ...
## $ Bl.cromatin      : Factor w/ 10 levels "1","2","3","4",...: 3 3 3 3 3 9 3 3 1 2 ...
## $ Normal.nucleoli: Factor w/ 10 levels "1","2","3","4",...: 1 2 1 7 1 7 1 1 1 1 ...
## $ Mitoses          : Factor w/ 9 levels "1","2","3","4",...: 1 1 1 1 1 1 1 1 5 1 ...
## $ Class            : Factor w/ 2 levels "1","0": 1 1 1 1 1 2 1 1 1 1 ...
```

After reviewing the data we have determined that Class Variable will be the response variable to ana

We will need to determine if the data is balanced by reviewing the count of the class column.

```
Class_counts <- table(BreastCancer$Class)
print(Class_counts)
```

```
##
##      1      0
## 444 239
```

Since the "class" count is not balanced we will use random sampling method to randomly select from 1

Separate the data into two data frames

```
class_0 <- BreastCancer[BreastCancer$Class == 0, ]
class_1 <- BreastCancer[BreastCancer$Class == 1, ]
```

```
minority_size <- nrow(class_0)
```

Randomly sample rows from the majority class to match the minority class size

```
class_1_sampled <- class_1[sample(nrow(class_1), minority_size), ]
```

Combine the sampled majority class with the minority class

```
balanced_data <- rbind(class_1_sampled, class_0)
```

Shuffle the rows to randomize the order

```
balanced_data <- balanced_data[sample(nrow(balanced_data)), ]
```

Check the class distribution after balancing

```
table(balanced_data$Class)
```

```
##
##      1      0
## 239 239
```

Class is now balanced for a count of 239 each for 0 and 1. Now we will create a training and test da

```
library(caret)
```

```
## Loading required package: ggplot2
```

```
## Loading required package: lattice
```

```

# Create data partition indices
train_index <- createDataPartition(balanced_data$Class, p = 0.7, list = FALSE)

# Create training and test sets
train <- balanced_data[train_index, ]
test <- balanced_data[-train_index, ]

# Convert ordinal factors to numeric
train$Cl.thickness <- as.numeric(train$Cl.thickness)
test$Cl.thickness <- as.numeric(test$Cl.thickness)

# Check dimensions of train and test sets
dim(train)

```

```
## [1] 336 10
```

```
dim(test)
```

```
## [1] 142 10
```

```
str(train)
```

```

## 'data.frame': 336 obs. of 10 variables:
## $ Cl.thickness : num 10 5 1 9 8 1 5 10 3 4 ...
## $ Cell.size : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<...: 5 10 1 9 10 1 3 8 1 1 ...
## $ Cell.shape : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<...: 7 10 3 10 10 1 4 8 1 1 ...
## $ Marg.adhesion : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<...: 3 10 2 3 10 1 1 2 1 1 ...
## $ Epith.c.size : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<...: 3 10 2 6 5 3 8 3 2 1 ...
## $ Bare.nuclei : Factor w/ 10 levels "1","2","3","4",...: 7 2 1 10 10 2 10 4 1 1 ...
## $ Bl.cromatin : Factor w/ 10 levels "1","2","3","4",...: 3 10 3 7 8 2 4 8 1 2 ...
## $ Normal.nucleoli: Factor w/ 10 levels "1","2","3","4",...: 3 10 1 10 10 1 9 7 1 1 ...
## $ Mitoses : Factor w/ 9 levels "1","2","3","4",...: 8 9 1 6 6 1 1 8 1 1 ...
## $ Class : Factor w/ 2 levels "1","0": 2 2 1 2 2 1 2 2 1 1 ...

```

```
str(test)
```

```

## 'data.frame': 142 obs. of 10 variables:
## $ Cl.thickness : num 10 1 9 5 5 3 3 7 5 2 ...
## $ Cell.size : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<...: 10 1 10 3 1 2 4 6 10 1 ...
## $ Cell.shape : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<...: 10 1 10 5 1 2 5 10 10 1 ...
## $ Marg.adhesion : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<...: 8 3 1 5 2 1 2 5 6 1 ...
## $ Epith.c.size : Ord.factor w/ 10 levels "1"<"2"<"3"<"4"<...: 2 1 10 3 2 2 6 3 10 3 ...
## $ Bare.nuclei : Factor w/ 10 levels "1","2","3","4",...: 10 3 8 3 2 1 8 10 10 1 ...
## $ Bl.cromatin : Factor w/ 10 levels "1","2","3","4",...: 4 1 3 4 3 2 4 9 10 2 ...
## $ Normal.nucleoli: Factor w/ 10 levels "1","2","3","4",...: 1 1 3 10 1 3 1 10 6 1 ...
## $ Mitoses : Factor w/ 9 levels "1","2","3","4",...: 1 1 1 1 1 1 1 2 5 1 ...
## $ Class : Factor w/ 2 levels "1","0": 2 1 2 2 1 1 2 2 2 1 ...

```

```
## We will run 4 different types of model. Logistic Regression, Naive Bayes, SVM and Random Forest. Ran
```

```
## Logistic regression did not perform well for this data. Probabaly because there is ordinal data.
```

```

library(caret)

# Fit logistic regression model
model <- glm(Class ~ ., data = train, family = binomial)

## Warning: glm.fit: algorithm did not converge

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

# Predict probabilities for the training data
train_probabilities <- predict(model, newdata = train, type = "response")

# Convert probabilities to class predictions for training data
train_predictions <- ifelse(train_probabilities >= 0.5, 1, 0) # Assuming 0.5 threshold for binary clas

# Predict probabilities for the test data
test_probabilities <- predict(model, newdata = test, type = "response")

# Convert probabilities to class predictions for test data
test_predictions <- ifelse(test_probabilities >= 0.5, 1, 0) # Assuming 0.5 threshold for binary classi

# Function to compute performance measures
compute_performance <- function(predictions, true_labels) {
  # Create confusion matrix
  conf_mat <- confusionMatrix(as.factor(predictions), as.factor(true_labels))

  # Extract performance measures
  accuracy <- conf_mat$overall['Accuracy']
  recall <- conf_mat$byClass['Sensitivity']
  precision <- conf_mat$byClass['Pos Pred Value']
  f1_score <- 2 * (precision * recall) / (precision + recall)

  # Return performance measures
  return(list(conf_mat = conf_mat$table,
             accuracy = accuracy,
             recall = recall,
             precision = precision,
             f1_score = f1_score))
}

# Compute performance measures for training data
train_performance <- compute_performance(train_predictions, train$Class)

## Warning in confusionMatrix.default(as.factor(predictions),
## as.factor(true_labels)): Levels are not in the same order for reference and
## data. Refactoring data to match.

# Compute performance measures for test data
test_performance <- compute_performance(test_predictions, test$Class)

## Warning in confusionMatrix.default(as.factor(predictions),
## as.factor(true_labels)): Levels are not in the same order for reference and
## data. Refactoring data to match.

```

```
# Print performance measures for training data
cat("Performance measures for training data:\n")
```

```
## Performance measures for training data:
```

```
cat("Confusion Matrix:\n")
```

```
## Confusion Matrix:
```

```
print(train_performance$conf_mat)
```

```
##           Reference
## Prediction    1    0
##           1    0 168
##           0 168    0
```

```
cat("\nAccuracy:", train_performance$accuracy)
```

```
##
## Accuracy: 0
```

```
cat("\nRecall (Sensitivity):", train_performance$recall)
```

```
##
## Recall (Sensitivity): 0
```

```
cat("\nPrecision (Positive Predictive Value):", train_performance$precision)
```

```
##
## Precision (Positive Predictive Value): 0
```

```
cat("\nF1-score:", train_performance$f1_score)
```

```
##
## F1-score: NaN
```

```
# Print performance measures for test data
cat("\n\nPerformance measures for test data:\n")
```

```
##
##
## Performance measures for test data:
```

```
cat("Confusion Matrix:\n")
```

```
## Confusion Matrix:
```

```
print(test_performance$conf_mat)
```

```
##           Reference
## Prediction  1   0
##           1   1 62
##           0  70   9
```

```
cat("\nAccuracy:", test_performance$accuracy)
```

```
##
## Accuracy: 0.07042254
```

```
cat("\nRecall (Sensitivity):", test_performance$recall)
```

```
##
## Recall (Sensitivity): 0.01408451
```

```
cat("\nPrecision (Positive Predictive Value):", test_performance$precision)
```

```
##
## Precision (Positive Predictive Value): 0.01587302
```

```
cat("\nF1-score:", test_performance$f1_score)
```

```
##
## F1-score: 0.01492537
```

```
## Naive Bayes: Did well, but concerned about overfitting.
```

```
# Load the required library
library(e1071)
```

```
# Fit Naive Bayes model to the training data
nb_model <- naiveBayes(Class ~ ., data = train)
```

```
# Make predictions on the train and test data
train_predictions <- predict(nb_model, train)
test_predictions <- predict(nb_model, test)
```

```
# Evaluate model performance on train data
train_confusion_matrix <- table(train_predictions, train$Class)
train_accuracy <- sum(diag(train_confusion_matrix)) / sum(train_confusion_matrix)
train_precision <- train_confusion_matrix[2, 2] / sum(train_confusion_matrix[, 2])
train_recall <- train_confusion_matrix[2, 2] / sum(train_confusion_matrix[2, ])
train_f1_score <- 2 * train_precision * train_recall / (train_precision + train_recall)
```

```
# Evaluate model performance on test data
test_confusion_matrix <- table(test_predictions, test$Class)
test_accuracy <- sum(diag(test_confusion_matrix)) / sum(test_confusion_matrix)
```



```
test_precision <- test_confusion_matrix[2, 2] / sum(test_confusion_matrix[, 2])
test_recall <- test_confusion_matrix[2, 2] / sum(test_confusion_matrix[2, ])
test_f1_score <- 2 * test_precision * test_recall / (test_precision + test_recall)
```

```
# Print performance measures for train data
cat("Performance measures for train data:\n")
```

```
## Performance measures for train data:
```

```
cat("Confusion Matrix:\n", train_confusion_matrix, "\n")
```

```
## Confusion Matrix:
## 164 4 2 166
```

```
cat("\nAccuracy:", train_accuracy)
```

```
##
## Accuracy: 0.9821429
```

```
cat("\nPrecision:", train_precision)
```

```
##
## Precision: 0.9880952
```

```
cat("\nRecall (Sensitivity):", train_recall)
```

```
##
## Recall (Sensitivity): 0.9764706
```

```
cat("\nF1-score:", train_f1_score, "\n")
```

```
##
## F1-score: 0.9822485
```

```
# Print performance measures for test data
cat("\nPerformance measures for test data:\n")
```

```
##
## Performance measures for test data:
```

```
cat("Confusion Matrix:\n", test_confusion_matrix, "\n")
```

```
## Confusion Matrix:
## 70 1 1 70
```

```

cat("\nAccuracy:", test_accuracy)

##
## Accuracy: 0.9859155

cat("\nPrecision:", test_precision)

##
## Precision: 0.9859155

cat("\nRecall (Sensitivity):", test_recall)

##
## Recall (Sensitivity): 0.9859155

cat("\nF1-score:", test_f1_score)

##
## F1-score: 0.9859155

# Load the required library
library(randomForest)

## randomForest 4.7-1.1

## Type rfNews() to see new features/changes/bug fixes.

##
## Attaching package: 'randomForest'

## The following object is masked from 'package:ggplot2':
##
##     margin

# Assuming you have a training dataset named 'train' and a test dataset named 'test'

# Fit Random Forest model
rf_model <- randomForest(Class ~ ., data = train)

# Make predictions on the training data
train_predictions <- predict(rf_model, train)

# Evaluate model performance on the training data
train_confusion_matrix <- table(train_predictions, train$Class)
train_accuracy <- sum(diag(train_confusion_matrix)) / sum(train_confusion_matrix)
train_precision <- train_confusion_matrix[2, 2] / sum(train_confusion_matrix[, 2])
train_recall <- train_confusion_matrix[2, 2] / sum(train_confusion_matrix[2, ])
train_f1_score <- 2 * train_precision * train_recall / (train_precision + train_recall)

# Print performance measures for the training data
cat("Performance measures for training data:\n")

```

```
## Performance measures for training data:
```

```
cat("Confusion Matrix:\n", train_confusion_matrix, "\n")
```

```
## Confusion Matrix:
```

```
## 168 0 0 168
```

```
cat("\nAccuracy:", train_accuracy)
```

```
##
```

```
## Accuracy: 1
```

```
cat("\nPrecision:", train_precision)
```

```
##
```

```
## Precision: 1
```

```
cat("\nRecall (Sensitivity):", train_recall)
```

```
##
```

```
## Recall (Sensitivity): 1
```

```
cat("\nF1-score:", train_f1_score)
```

```
##
```

```
## F1-score: 1
```

```
# Make predictions on the test data
```

```
test_predictions <- predict(rf_model, test)
```

```
# Evaluate model performance on the test data
```

```
test_confusion_matrix <- table(test_predictions, test$Class)
```

```
test_accuracy <- sum(diag(test_confusion_matrix)) / sum(test_confusion_matrix)
```

```
test_precision <- test_confusion_matrix[2, 2] / sum(test_confusion_matrix[, 2])
```

```
test_recall <- test_confusion_matrix[2, 2] / sum(test_confusion_matrix[2, ])
```

```
test_f1_score <- 2 * test_precision * test_recall / (test_precision + test_recall)
```

```
# Print performance measures for the test data
```

```
cat("\n\nPerformance measures for test data:\n")
```

```
##
```

```
##
```

```
## Performance measures for test data:
```

```
cat("Confusion Matrix:\n", test_confusion_matrix, "\n")
```

```
## Confusion Matrix:
```

```
## 70 1 2 69
```

```
cat("\nAccuracy:", test_accuracy)
```

```
##  
## Accuracy: 0.9788732
```

```
cat("\nPrecision:", test_precision)
```

```
##  
## Precision: 0.971831
```

```
cat("\nRecall (Sensitivity):", test_recall)
```

```
##  
## Recall (Sensitivity): 0.9857143
```

```
cat("\nF1-score:", test_f1_score)
```

```
##  
## F1-score: 0.9787234
```

SVM Model

```
# Load the required library  
library(e1071)
```

```
# Fit SVM model  
svm_model <- svm(Class ~ ., data = train)
```

```
# Make predictions on the train data  
svm_train_predictions <- predict(svm_model, train)
```

```
# Evaluate model performance on train data  
svm_train_confusion_matrix <- table(svm_train_predictions, train$Class)  
train_accuracy <- sum(diag(svm_train_confusion_matrix)) / sum(svm_train_confusion_matrix)  
train_precision <- svm_train_confusion_matrix[2, 2] / sum(svm_train_confusion_matrix[, 2])  
train_recall <- svm_train_confusion_matrix[2, 2] / sum(svm_train_confusion_matrix[2, ])  
train_f1_score <- 2 * train_precision * train_recall / (train_precision + train_recall)
```

```
# Print performance measures for train data  
cat("Performance measures for train data:\n")
```

```
## Performance measures for train data:
```

```
cat("Confusion Matrix:\n", svm_train_confusion_matrix, "\n")
```

```
## Confusion Matrix:  
## 162 6 1 167
```

```
cat("\nAccuracy:", train_accuracy)
```

```
##  
## Accuracy: 0.9791667
```

```
cat("\nPrecision:", train_precision)
```

```
##  
## Precision: 0.9940476
```

```
cat("\nRecall (Sensitivity):", train_recall)
```

```
##  
## Recall (Sensitivity): 0.9653179
```

```
cat("\nF1-score:", train_f1_score)
```

```
##  
## F1-score: 0.9794721
```

```
# Make predictions on the test data  
svm_test_predictions <- predict(svm_model, test)
```

```
# Evaluate model performance on test data  
svm_test_confusion_matrix <- table(svm_test_predictions, test$Class)  
test_accuracy <- sum(diag(svm_test_confusion_matrix)) / sum(svm_test_confusion_matrix)  
test_precision <- svm_test_confusion_matrix[2, 2] / sum(svm_test_confusion_matrix[, 2])  
test_recall <- svm_test_confusion_matrix[2, 2] / sum(svm_test_confusion_matrix[2, ])  
test_f1_score <- 2 * test_precision * test_recall / (test_precision + test_recall)
```

```
# Print performance measures for test data  
cat("\n\nPerformance measures for test data:\n")
```

```
##  
##  
## Performance measures for test data:
```

```
cat("Confusion Matrix:\n", svm_test_confusion_matrix, "\n")
```

```
## Confusion Matrix:  
## 70 1 1 70
```

```
cat("\nAccuracy:", test_accuracy)
```

```
##  
## Accuracy: 0.9859155
```

```
cat("\nPrecision:", test_precision)
```

```
##  
## Precision: 0.9859155
```

```
cat("\nRecall (Sensitivity):", test_recall)
```

```
##  
## Recall (Sensitivity): 0.9859155
```

```
cat("\nF1-score:", test_f1_score)
```

```
##  
## F1-score: 0.9859155
```

```
## Combine the classifiers in an ensemble
```

```
# Load required libraries
```

```
library(caret)
```

```
library(e1071)
```

```
library(randomForest)
```

```
# Assuming you have your data loaded as train and test datasets
```

```
# Fit models
```

```
logistic_model <- glm(Class ~ ., data = train, family = "binomial")
```

```
## Warning: glm.fit: algorithm did not converge
```

```
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
```

```
nb_model <- naiveBayes(Class ~ ., data = train)
```

```
svm_model <- svm(Class ~ ., data = train)
```

```
rf_model <- randomForest(Class ~ ., data = train)
```

```
# Make predictions for each model
```

```
logistic_predictions_train <- predict(logistic_model, newdata = train, type = "response")
```

```
nb_predictions_train <- predict(nb_model, newdata = train, type = "raw")
```

```
svm_predictions_train <- predict(svm_model, newdata = train, probability = TRUE)
```

```
## Warning in predict.svm(svm_model, newdata = train, probability = TRUE): SVM has  
## not been trained using 'probability = TRUE', probabilities not available for  
## predictions.
```

```
rf_predictions_train <- predict(rf_model, newdata = train, type = "response")
```

```
# Combine predictions into a data frame
```

```
combined_predictions_train <- data.frame(  
  Logistic = logistic_predictions_train,  
  NaiveBayes = nb_predictions_train,  
  RandomForest = rf_predictions_train,  
  SVM = svm_predictions_train,  
  Class = train$Class)
```

```

SVM = svm_predictions_train,
RandomForest = rf_predictions_train
)

# Take a majority vote for each observation
ensemble_predictions_train <- apply(combined_predictions_train, 1, function(row) {
  majority_vote <- ifelse(sum(row == "1") >= sum(row == "0"), "1", "0")
})

# Convert predictions to factors with the same levels as train$Class
ensemble_predictions_train <- factor(ensemble_predictions_train, levels = levels(train$Class))

# Evaluate model performance for training data
ensemble_confusion_matrix_train <- confusionMatrix(ensemble_predictions_train, train$Class)
print("Performance measures for train data:")

```

```
## [1] "Performance measures for train data:"
```

```
print(ensemble_confusion_matrix_train)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   1    0
##           1 168    0
##           0   0 168
##
##           Accuracy : 1
##           95% CI : (0.9891, 1)
##       No Information Rate : 0.5
##       P-Value [Acc > NIR] : < 2.2e-16
##
##           Kappa : 1
##
##  Mcnemar's Test P-Value : NA
##
##           Sensitivity : 1.0
##           Specificity : 1.0
##       Pos Pred Value : 1.0
##       Neg Pred Value : 1.0
##           Prevalence : 0.5
##       Detection Rate : 0.5
##  Detection Prevalence : 0.5
##       Balanced Accuracy : 1.0
##
##       'Positive' Class : 1
##

```

```

# Make predictions for test data
logistic_predictions_test <- predict(logistic_model, newdata = test, type = "response")
nb_predictions_test <- predict(nb_model, newdata = test, type = "raw")
svm_predictions_test <- predict(svm_model, newdata = test, probability = TRUE)

```

```
## Warning in predict.svm(svm_model, newdata = test, probability = TRUE): SVM has
## not been trained using 'probability = TRUE', probabilities not available for
## predictions.
```

```
rf_predictions_test <- predict(rf_model, newdata = test, type = "response")

# Combine predictions into a data frame for test data
combined_predictions_test <- data.frame(
  Logistic = logistic_predictions_test,
  NaiveBayes = nb_predictions_test,
  SVM = svm_predictions_test,
  RandomForest = rf_predictions_test
)

# Take a majority vote for each observation for test data
ensemble_predictions_test <- apply(combined_predictions_test, 1, function(row) {
  majority_vote <- ifelse(sum(row == "1") >= sum(row == "0"), "1", "0")
})

# Convert predictions to factors with the same levels as test$Class
ensemble_predictions_test <- factor(ensemble_predictions_test, levels = levels(test$Class))

# Evaluate model performance for test data
ensemble_confusion_matrix_test <- confusionMatrix(ensemble_predictions_test, test$Class)
print("Performance measures for test data:")
```

```
## [1] "Performance measures for test data:"
```

```
print(ensemble_confusion_matrix_test)
```

```
## Confusion Matrix and Statistics
##
##              Reference
## Prediction  1  0
##           1 70  2
##           0  1 69
##
##              Accuracy : 0.9789
##              95% CI : (0.9395, 0.9956)
##      No Information Rate : 0.5
##      P-Value [Acc > NIR] : <2e-16
##
##              Kappa : 0.9577
##
##  McNemar's Test P-Value : 1
##
##              Sensitivity : 0.9859
##              Specificity : 0.9718
##      Pos Pred Value : 0.9722
##      Neg Pred Value : 0.9857
##              Prevalence : 0.5000
##      Detection Rate : 0.4930
```



```
## Detection Prevalence : 0.5070
## Balanced Accuracy : 0.9789
##
## 'Positive' Class : 1
##
```

```
““
```