Predicting Breast Cancer

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In this project, we will use machine learning algorithms to predict a binary outcome, in this case whether a woman either has a benign or malignant tumor. We will get a dataset from the UC Irvine Machine Learning database. The rows are different woman and the rows are different features of intrest.

```
uciwd ="https://archive.ics.uci.edu/ml/machine-learning-databases/"
mldata = paste(uciwd, "breast-cancer-wisconsin/breast-cancer-wisconsin.data", sep="")
bcancer = read.csv(mldata)  # Treat the first row as variable names
bcancer
```

##		X1000025	Х5	X1	X1.1	X1.2	Х2	X1.3	ХЗ	X1.4	X1.5	X2.1
##	1	1002945	5	4	4	5	7	10	3	2	1	2
##	2	1002345	3	1	1	1	2	2	3	1	1	2
##	3	1016277	6	8	8	1	3	4	3	7	1	2
##	4	1010277	4	1	1	3	2	1	3	1	1	2
##	5	1017023	8	10	10	8	7	10	9	7	1	4
##	6	1017122	1	1	1	1	2	10	3	1	1	2
##	7	1018561	2	1	2	1	2	1	3	1	1	2
##	8	1033078	2	1	1	1	2	1	1	1	5	2
##	9	1033078	4	2	1	1	2	1	2	1	1	2
##	10	1035283	1	1	1	1	1	1	3	1	1	2
##	11	1036172	2	1	1	1	2	1	2	1	1	2
##	12	1041801	5	3	3	3	2	3	4	4	1	4
##	13	1043999	1	1	1	1	2	3	3	1	1	2
##	14	1044572	8	7	5	10	7	9	5	5	4	4
##	15	1047630	7	4	6	4	6	1	4	3	1	4
##	16	1048672	4	1	1	1	2	1	2	1	1	2
##	17	1049815	4	1	1	1	2	1	3	1	1	2
##	18	1050670	10	7	7	6	4	10	4	1	2	4
##	19	1050718	6	1	1	1	2	1	3	1	1	2
##	20	1054590	7	3	2	10	5	10	5	4	4	4
##	21	1054593	10	5	5	3	6	7	7	10	1	4
##	22	1056784	3	1	1	1	2	1	2	1	1	2
##	23	1057013	8	4	5	1	2	?	7	3	1	4
##	24	1059552	1	1	1	1	2	1	3	1	1	2
##	25	1065726	5	2	3	4	2	7	3	6	1	4
##	26	1066373	3	2	1	1	1	1	2	1	1	2
##	27	1066979	5	1	1	1	2	1	2	1	1	2
##	28	1067444	2	1	1	1	2	1	2	1	1	2
##	29	1070935	1	1	3	1	2	1	1	1	1	2
##	30	1070935	3	1	1	1	1	1	2	1	1	2
##	31	1071760	2	1	1	1	2	1	3	1	1	2
##	32	1072179	10	7	7	3	8	5	7	4	3	4
##	33	1074610	2	1	1	2	2	1	3	1	1	2
##	34	1075123	3	1	2	1	2	1	2	1	1	2
##	35	1079304	2	1	1	1	2	1	2	1	1	2
##	36 37	1080185	10	10	10	8	6	1 1	8	9	1 1	4
##		1081791	6	2 4	1	1	1 2	_	7	1 6	_	2
##	38	1084584	5	4	4	9	2	10	5	6	1	4

##	39	1091262	2	5	3	3	6	7	7	5	1	4
##	40	1096800	6	6	6	9	6	?	7	8	1	2
##	41	1099510	10	4	3	1	3	3	6	5	2	4
##	42	1100524	6	10	10	2	8	10	7	3	3	4
##	43	1102573	5	6	5	6	10	1	3	1	1	4
##	44	1103608	10	10	10	4	8	1	8	10	1	4
##	45	1103722	1	1	1	1	2	1	2	1	2	2
##	46	1105257	3	7	7	4	4	9	4	8	1	4
##	47	1105524	1	1	1	1	2	1	2	1	1	2
##	48	1106095	4	1	1	3	2	1	3	1	1	2
##	49	1106829	7	8	7	2	4	8	3	8	2	4
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##	54	1110524	10	5	5	6	8	8	7	1	1	4
##	55	1111249	10	6	6	3	4	5	3	6	1	4
##	56	1112209	8	10	10	1	3	6	3	9	1	4
##	57	1113038	8	2	4	1	5	1	5	4	4	4
##	58	1113483	5	2	3	1	6	10	5	1	1	4
##	59	1113906	9	5	5	2	2	2	5	1	1	4
##	60	1115282	5	3	5	5	3	3	4	10	1	4
##	61	1115293	1	1	1	1	2	2	2	1	1	2
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##	65	1116998	10	4	2	1	3	2	4	3	10	4
##	66	1117152	4	1	1	1	2	1	3	1	1	2
##	67	1117132	5	3	4	1	8	10	4	9	1	4
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##	72	1124651	1	3	3	2	2	1	7	2	1	2
##	73	1125035	9	4	5	10	6	10	4	8	1	4
##	74	1126417	10	6	4	1	3	4	3	2	3	4
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	80	1137156	2	2	2	1	1	1	7	1	1	2
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	83	1147044	3	1	1	1	2	2	7	1	1	2
	84	1147699	3	5	7	8	8	9	7	10	7	4
	85	1147748	5	10	6	1	10	4	4	10		4
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##	101	1167439	2	3	4	4	2	5	2	5	1	4
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##	104	1168736	10	10	10	10	10	1	8	8	8	4
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##	106	1170419	10	10	10	8	2	10	4	1	1	4
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##	111	1171845	8	6	4	3	5	9	3	1	1	4
##	112	1172152	10	3	3	10	2	10	7	3	3	4
##	113	1173216	10	10	10	3	10	8	8	1	1	4
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##	117	1173509	4	5	5	10	4	10	7	5	8	4
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##	123	1174428	5	3 4	5	1	8	10	5	3	1	4
##	124 125	1175937 1176406	5 1	4	6 1	7 1	9 2	7 1	8 2	10 1	1 1	4
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	130	1178580	5	1	3	1	2	1	2	1	1	2
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##	139	1183246	1	1	1	1	1	?	2	1	1	2
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##	145	1184840	1	1	3	1	2	?	2	1	1	2
##	146	1185609	3	4	5	2	6	8	4	1	1	4

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##	148	1187457	3	1	1	3	8	1	5	8	1	2
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##	149	1187805	8	8		4	10	10		8	7	
##	150	1188472	1	1	1	1	1	1	3	1	1	2
##	151	1189266	7	2	4	1	6	10	5	4	3	4
##	152	1189286	10	10	8	6	4	5	8	10	1	4
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##	156	1193091	1	2	2	1	2	1	2	1	1	2
##	157	1193210	2	1	1	1	2	1	3	1	1	2
##	158	1193683	1	1	2	1	3	?	1	1	1	2
##	159	1196295	9	9	10	3	6	10	7	10	6	4
##	160	1196915	10	7	7	4	5	10	5	7	2	4
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##	164	1197510	5	1	1	1	2	?	3	1	1	2
##	165	1197979	4	1	1	1	2	2	3	2	1	2
##	166	1197993	5	6	7	8	8	10	3	10	3	4
##	167	1198128	10	8	10	10	6	1	3	1	10	4
##	168	1198641	3	1	1	1	2	1	3	1	1	2
##	169	1199219	1	1	1	2	1	1	1	1	1	2
##	170	1199731	3	1	1	1	2	1	1	1	1	2
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##	174	1200892	8	6	5	4	3	10	6	1	1	4
##	175	1200952	5	8	7	7	10	10	5	7	1	4
##	176	1201834	2	1	1	1	2	1	3	1	1	2
##	177	1201936	5	10	10	3	8	1	5	10	3	4
##	178	1202125	4	1	1	1	2	1	3	1	1	2
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##	187	1206841	10	5	6	10	6	10	7	7	10	4
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##	191	1211202	7	5	10	10	10	10	4	10	3	4
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##	193	1212251	1	1	1	1	2	1	3	1	1	2
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##	194	1212422	4	1	1		2	1	3	1	1	2
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##	197	1213383	5	1	1	4	2	1	3	1	1	2
##	198	1214092	1	1	1	1	2	1	1	1	1	2
##	199	1214556	3	1	1	1	2	1	2	1	1	2
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##	204	1217264	1	1	1	1	2	1	3	1	1	2
##	205	1218105	5	10	10	9	6	10	7	10	5	4
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	214	1222936	8	7	8	7	5	5	5	10	2	4
##	216			1								
##		1223282	1		1	1	2	1	2	1	1	2
##	217	1223426	1	1	1	1	2	1	3	1	1	2
##	218	1223793	6	10	7	7	6	4	8	10	2	4
##	219	1223967	6	1	3	1	2	1	3	1	1	2
##	220	1224329	1	1	1	2	2	1	3	1	1	2
##	221	1225799	10	6	4	3	10	10	9	10	1	4
##	222	1226012	4	1	1	3	1	5	2	1	1	4
##	223	1226612	7	5	6	3	3	8	7	4	1	4
##	224	1227210	10	5	5	6	3	10	7	9	2	4
##	225	1227244	1	1	1	1	2	1	2	1	1	2
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##	229	1230175	10	10	10	3	10	10	9	10	1	4
##	230	1230688	7	4	7	4	3	7	7	6	1	4
##	231	1231387	6	8	7	5	6	8	8	9	2	4
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##	235	1241232	3	1	4	1	2	?	3	1	1	2
##	236	1241559	10	8	8	2	8	10	4	8	10	4
##	237	1241679	9	8	8	5	6	2	4	10	4	4
##	238	1242364	8	10	10	8	6	9	3	10	10	4
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	242	1277018	2	1	1	1	2	1	3	1	1	2
	243	128059	1	1	1	1	2	5	5	1	1	2
	244	1285531	1	1	1	1	2	1	3	1	1	2
	245	1287775	5	1	1	2	2	2	3	1	1	2
	246	144888	8	10	10	8	5	10	7	8	1	4
	247	145447	8	4	4	1	2	9	3	3	1	4
	248	167528	4	1	1	1	2	1	3	6	1	2
	249	169356	3	1	1	1	2	?	3	1	1	2
	250	183913	1	2	2	1	2	: 1	1	1	1	2
	250 251	191250	10	4	4		2	10	5	3	3	4
	251	191250	6	3	3	10 5	3		3	5 5	3 3	2
								10				
	253	1100524	6	10	10	2	8	10	7	3	3	4
##	254	1116116	9	10	10	1	10	8	3	3	1	4

			_	_	_	_	_		_	_		_
##	255	1168736	5	6	6	2	4	10	3	6	1	4
##	256	1182404	3	1	1	1	2	1	1	1	1	2
##	257	1182404	3	1	1	1	2	1	2	1	1	2
##	258	1198641	3	1	1	1	2	1	3	1	1	2
##	259	242970	5	7	7	1	5	8	3	4	1	2
##	260	255644	10	5	8	10	3	10	5	1	3	4
##	261	263538	5	10	10	6	10	10	10	6	5	4
##	262	274137	8	8	9	4	5	10	7	8	1	4
##	263	303213	10	4	4	10	6	10	5	5	1	4
##	264	314428	7	9	4	10	10	3	5	3	3	4
##	265	1182404	5	1	4	1	2	1	3	2	1	2
##	266	1198641	10	10	6	3	3	10	4	3	2	4
##	267	320675	3	3	5	2	3	10	7	1	1	4
##	268	324427	10	8	8	2	3	4	8	7	8	4
##	269	385103	1	1	1	1	2	1	3	1	1	2
##	270	390840	8	4	7	1	3	10	3	9	2	4
##	271	411453	5	1	1	1	2	1	3	1	1	2
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##	273	428903	7	2	4	1	3	4	3	3	1	4
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##	280	486283	3	1	1	1	2	1	3	1	1	2
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##	283	492268	10	4	6	1	2	10	5	3	1	4
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##	285	527363	8	10	10	10	8	10	10	7	3	4
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##	289	555977	5	6	6	8	6	10	4	10	4	4
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##	299	63375	9	1	2	6	4	10	7	7	2	4
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##	301	636130	1	1	1	1	2	1	3	1	1	2
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##	553	1306339	4	4	2	1	2	5	2	1	2	2
##	554	1313658	3	1	1	1	2	1	1	1	1	2
##	555	1313982	4	3	1	1	2	1	4	8	1	2
##	556	1321264	5	2	2	2	1	1	2	1	1	2
##	557	1321321	5	1	1	3	2	1	1	1	1	2
##	558	1321348	2	1	1	1	2	1	2	1	1	2
##	559	1321931	5	1	1	1	2	1	2	1	1	2
##	560	1321942	5	1	1	1	2	1	3	1	1	2
##	561	1321942	5	1	1	1	2	1	3	1	1	2
##	562	1328331	1	1	1	1	2	1	3	1	1	2
##	563	1328755	3	1	1	1	2	1	2	1	1	2
##	564	1331405	4	1	1	1	2	1	3	2	1	2
##	565	1331412	5	7	10	10	5	10	10	10	1	4
##	566	1333104	3	1	2	1	2	1	3	1	1	2
##	567	1334071	4	1	1	1	2	3	2	1	1	2
##	568	1343068	8	4	4	1	6	10	2	5	2	4
##	569	1343374	10	10	8	10	6	5	10	3	1	4
##	570	1344121	8	10	4	4		10		2	1	4
##	570		7	6		5	8	10	8 9	10		
		142932			10						2	4
##	572	183936	3	1	1	1	2	1	2	1	1	2
##	573	324382	1	1	1	1	2	1	2	1	1	2
##	574	378275	10	9	7	3	4	2	7	7	1	4
##	575	385103	5	1	2	1	2	1	3	1	1	2
##	576	690557	5	1	1	1	2	1	2	1	1	2
##	577	695091	1	1	1	1	2	1	2	1	1	2
##	578	695219	1	1	1	1	2	1	2	1	1	2

##	579	824249	1	1	1	1	2	1 3	3 1	1	2
##	580	871549	5	1	2	1	2	1 2		1	2
##	581	878358	5	7	10	6	5	10 7		1	4
##	582	1107684	6	10	5	5	4	10 6		1	4
##	583	1115762	3	1	1	1	2	1 1		1	2
##	584	1217717	5	1	1	6	3	1 1		1	2
##	585	1239420	1	1	1	1	2	1 1		1	2
##	586	1254538	8	10	10	10	6	10 10		1	4
##	587	1261751	5	1	1	1	2	1 2		1	2
##	588	1268275	9	8	8	9	6	3 4	: 1	1	4
##	589	1272166	5	1	1	1	2	1 1	. 1	1	2
##	590	1294261	4	10	8	5	4	1 10) 1	1	4
##	591	1295529	2	5	7	6	4	10 7	6	1	4
##	592	1298484	10	3	4	5	3	10 4	: 1	1	4
##	593	1311875	5	1	2	1	2	1 1	. 1	1	2
##	594	1315506	4	8	6	3	4	10 7	1	1	4
##	595	1320141	5	1	1	1	2	1 2	2 1	1	2
##	596	1325309	4	1	2	1	2	1 2	2 1	1	2
##	597	1333063	5	1	3	1	2	1 3	3 1	1	2
##	598	1333495	3	1	1	1	2	1 2	2 1	1	2
##	599	1334659	5	2	4	1	1	1 1	. 1	1	2
##	600	1336798	3	1	1	1	2	1 2	2 1	1	2
##	601	1344449	1	1	1	1	1	1 2	2 1	1	2
##	602	1350568	4	1	1	1	2	1 2	2 1	1	2
##	603	1352663	5	4	6	8	4	1 8	10	1	4
##	604	188336	5	3	2	8	5	10 8	3 1	2	4
##	605	352431	10	5	10	3	5	8 7	8	3	4
##	606	353098	4	1	1	2	2	1 1	. 1	1	2
##	607	411453	1	1	1	1	2	1 1	. 1	1	2
##	608	557583	5	10	10	10	10	10 10	1	1	4
##	609	636375	5	1	1	1	2	1 1	. 1	1	2
##	610	736150	10	4	3	10	3	10 7	1	2	4
##	611	803531	5	10	10	10	5	2 8	5	1	4
##	612	822829	8	10	10	10	6	10 10	10	10	4
##	613	1016634	2	3	1	1	2	1 2	. 1	1	2
##	614	1031608	2	1	1	1	1	1 2	2 1	1	2
##	615	1041043	4	1	3	1	2	1 2		1	2
##	616	1042252	3	1	1	1	2	1 2	2 1	1	2
##	617	1057067	1	1	1	1	1	? 1		1	2
##	618	1061990	4	1	1	1	2	1 2		1	2
##	619	1073836	5	1	1	1	2	1 2		1	2
##	620	1083817	3	1	1	1	2	1 2		1	2
##	621	1096352	6	3	3	3	3	2 6		1	2
##	622	1140597	7	1	2	3	2	1 2		1	2
##	623	1149548	1	1	1	1	2	1 1		1	2
##	624	1174009	5	1	1	2	1	1 2		1	2
##	625	1183596	3	1	3	1	3	4 1		1	2
##	626	1190386	4	6	6	5	7	6 7		3	4
##	627	1190546	2	1	1	1	2	5 1		1	2
##	628	1213273	2	1	1	1	2	1 1		1	2
##	629	1218982	4	1	1	1	2	1 1		1	2
##	630	1216362	6	2	3	1	2	1 1		1	2
##	631	1235807	5	1	1	1	2	1 2		1	2
##	632	1238777	1	1	1	1	2	1 1		1	2
##	032	1230111	1	T	T	T	2	1 1	. 1	T	2

##	633	1253955	8	7	4	4	5	3	5	10	1	4
##	634	1257366	3	1	1	1	2	1	1	1	1	2
##	635	1260659	3	1	4	1	2	1	1	1	1	2
##	636	1268952	10	10	7	8	7	1	10	10	3	4
##	637	1275807	4	2	4	3	2	2	2	10	1	2
##	638	1277792	4	1	1	1	2	1	1	1	1	2
##	639	1277792	5	1	1	3	2	1	1	1	1	2
	640		4	1		3	2					
##		1285722	_	1	1		2	1	1 2	1	1	2
##	641	1288608	3	_	1	1		1	2	1	1	2
##	642	1290203	3	1	1	1	2	1		1	1	2
##	643	1294413	1	1	1	1	2	1	1	1	1	2
##	644	1299596	2	1	1	1	2	1	1	1	1	2
##	645	1303489	3	1	1	1	2	1	2	1	1	2
##	646	1311033	1	2	2	1	2	1	1	1	1	2
##	647	1311108	1	1	1	3	2	1	1	1	1	2
##	648	1315807	5	10	10	10	10	2	10	10	10	4
##	649	1318671	3	1	1	1	2	1	2	1	1	2
##	650	1319609	3	1	1	2	3	4	1	1	1	2
##	651	1323477	1	2	1	3	2	1	2	1	1	2
##	652	1324572	5	1	1	1	2	1	2	2	1	2
##	653	1324681	4	1	1	1	2	1	2	1	1	2
##	654	1325159	3	1	1	1	2	1	3	1	1	2
##	655	1326892	3	1	1	1	2	1	2	1	1	2
##	656	1330361	5	1	1	1	2	1	2	1	1	2
##	657	1333877	5	4	5	1	8	1	3	6	1	2
##	658	1334015	7	8	8	7	3	10	7	2	3	4
##	659	1334667	1	1	1	1	2	1	1	1	1	2
##	660	1339781	1	1	1	1	2	1	2	1	1	2
##	661	1339781	4	1	1	1	2	1	3	1	1	2
##	662	13454352	1	1	3	1	2	1	2	1	1	2
##	663	1345452	1	1	3	1	2	1	2	1	1	2
##	664	1345593	3	1	1	3	2	1	2	1	1	2
##	665	1347749	1	1	1	1	2	1	1	1	1	2
##	666	1347943	5	2	2	2	2	1	1	1	2	2
##	667	1348851	3	1	1	1	2	1	3	1	1	2
##	668	1350319	5	7	4	1	6	1	7	10	3	4
##	669	1350423	5	10	10	8	5	5	7	10	1	4
##	670	1352848	3	10	7	8	5	8	7	4	1	4
##	671	1353092	3	2	1	2	2	1	3	1	1	2
##	672	1354840	2	1	1	1	2	1	3	1	1	2
##	673	1354840	5	3	2	1	3	1	1	1	1	2
##	674	1355260	1	1	1	1	2	1	2	1	1	2
##	675	1365075	4	1	4	1	2	1	1	1	1	2
##	676	1365328	1	1	2	1	2	1	2	1	1	2
##	677	1368267	5	1	1	1	2	1	1	1	1	2
##	678	1368273	1	1	1	1	2	1	1	1	1	2
##	679	1368882	2	1	1	1	2	1	1	1	1	2
##	680	1369821	10	10	10	10	5	10	10	10	7	4
##	681	1371026	5	10	10	10	4	10	5	6	3	4
##	682	1371920	5	1	1	1	2	1	3	2	1	2
##	683	466906	1	1	1	1	2	1	1	1	1	2
##	684	466906	1	1	1	1	2	1	1	1	1	2
##	685	534555	1	1	1	1	2	1	1	1	1	2
##	686	536708	1	1	1	1	2	1	1	1	1	2
		200,00	-	-	-	-	_	-	-	-	-	-

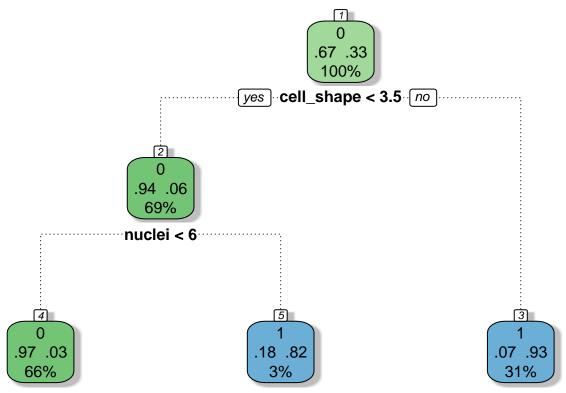
```
## 687
        566346 3 1
                             1
                                    1 2
                        1
## 688
        603148 4 1
                             1
                               2
                                    1
                                                 1
                                                      2
                        1
                                       1
                                            1
## 689
                             1 2
        654546 1 1
                                    1
                                                      2
## 690
        654546 1 1
                             3
                               2
                        1
                                    1
                                       1
                                            1
                                                 1
## 691
        695091 5 10
                       10
                             5
                               4
                                    5
                                       4
                                            4
                                                      4
## 692
        714039 3 1
                             1
                               2
                                                      2
                        1
                                    1
                                       1
                                            1
                                                 1
## 693
        763235 3 1
                             1
                               2
                        1
                                    1
                                            1
## 694
        776715 3 1
                        1
                             1
                               3
                                    2
                                       1
                                            1
                                                 1
                                                      2
## 695
        841769 2 1
                        1
                             1
                               2
                                    1
                                       1
                                            1
                                                 1
                                                      2
## 696
        888820 5 10
                             3 7
                                                 2
                                                      4
                       10
                                    3 8
                                           10
## 697
        897471 4 8
                        6
                             4 3
                                    4 10
                                            6
                                                 1
## 698
        897471 4 8
                             5 4
                                                      4
                        8
                                    5 10
                                            4
                                                 1
bcancer = read.csv(mldata, header=F) # Treat the data begins from the first row
colnames(bcancer)=c("ID","clump_thick","cell_size","cell_shape", "marginal","epithelial","nuclei",
                   "chromatin", "nucleoli", "mitoses", "class")
str(bcancer)
## 'data.frame':
                   699 obs. of 11 variables:
                : int 1000025 1002945 1015425 1016277 1017023 1017122 1018099 1018561 1033078 1033078
   $ clump_thick: int
                      5 5 3 6 4 8 1 2 2 4 ...
                      1 4 1 8 1 10 1 1 1 2 ...
##
   $ cell_size : int
##
   $ cell_shape : int
                      1 4 1 8 1 10 1 2 1 1 ...
## $ marginal
                : int
                      1511381111...
## $ epithelial : int 2 7 2 3 2 7 2 2 2 2 ...
                : Factor w/ 11 levels "?","1","10","2",...: 2 3 4 6 2 3 3 2 2 2 ...
## $ nuclei
## $ chromatin : int 3 3 3 3 3 9 3 3 1 2 ...
## $ nucleoli : int 1 2 1 7 1 7 1 1 1 1 ...
## $ mitoses
                : int 1 1 1 1 1 1 1 5 1 ...
   $ class
                : int 2 2 2 2 2 4 2 2 2 2 ...
summary(bcancer)
##
         ID
                       clump_thick
                                        cell_size
                                                         cell_shape
## Min.
         :
                      Min. : 1.000
                                      Min. : 1.000
                                                      Min. : 1.000
              61634
                      1st Qu.: 2.000
                                                      1st Qu.: 1.000
   1st Qu.: 870688
                                      1st Qu.: 1.000
## Median : 1171710
                     Median : 4.000
                                      Median : 1.000
                                                      Median : 1.000
## Mean : 1071704
                     Mean : 4.418
                                      Mean : 3.134
                                                      Mean : 3.207
   3rd Qu.: 1238298 3rd Qu.: 6.000
                                      3rd Qu.: 5.000
                                                       3rd Qu.: 5.000
##
  Max. :13454352
                    Max. :10.000
                                      Max. :10.000
                                                      Max. :10.000
##
##
      marginal
                      epithelial
                                        nuclei
                                                    chromatin
   Min. : 1.000
##
                    Min. : 1.000
                                           :402
                                                  Min. : 1.000
                                    1
##
   1st Qu.: 1.000
                    1st Qu.: 2.000
                                    10
                                           :132
                                                  1st Qu.: 2.000
   Median : 1.000
                    Median : 2.000
                                    2
                                           : 30
                                                  Median : 3.000
##
   Mean : 2.807
                    Mean : 3.216
                                    5
                                           : 30
                                                  Mean : 3.438
##
   3rd Qu.: 4.000
                    3rd Qu.: 4.000
                                    3
                                           : 28
                                                  3rd Qu.: 5.000
##
   Max. :10.000
                    Max. :10.000
                                           : 21
                                                  Max. :10.000
##
                                    (Other): 56
##
      nucleoli
                      mitoses
                                        class
## Min. : 1.000
                    Min. : 1.000
                                           :2.00
                                    Min.
   1st Qu.: 1.000
                    1st Qu.: 1.000
                                    1st Qu.:2.00
## Median : 1.000
                    Median : 1.000
                                    Median:2.00
## Mean : 2.867
                    Mean : 1.589
                                    Mean :2.69
```

```
## 3rd Qu.: 4.000 3rd Qu.: 1.000 3rd Qu.:4.00
## Max. :10.000 Max. :10.000 Max.
                                           :4.00
##
table(bcancer$nuclei)
##
##
        1 10
                2
                    3
                        4
                            5
## 16 402 132 30 28 19 30
                                4 8 21
bcancer$nuclei=as.numeric(gsub("\\?","NA",bcancer$nuclei))
## Warning: NAs introduced by coercion
library(Hmisc)
## Loading required package: lattice
## Loading required package: survival
## Loading required package: Formula
## Loading required package: ggplot2
## Attaching package: 'Hmisc'
## The following objects are masked from 'package:base':
##
##
      format.pval, units
bcancer$nuclei <- impute(bcancer$nuclei, mean)</pre>
anyNA(bcancer$nuclei)
## [1] FALSE
attach(bcancer)
bcancer$class <- as.numeric(gsub(2, 0, bcancer$class))</pre>
bcancer$class <- as.numeric(gsub(4, 1, bcancer$class))</pre>
bcancer$nuclei <- as.integer(bcancer$nuclei)</pre>
str(bcancer)
## 'data.frame':
                   699 obs. of 11 variables:
           : int 1000025 1002945 1015425 1016277 1017023 1017122 1018099 1018561 1033078 1033078
## $ clump_thick: int 5 5 3 6 4 8 1 2 2 4 ...
## $ cell_size : int 1 4 1 8 1 10 1 1 1 2 ...
## $ cell_shape : int 1 4 1 8 1 10 1 2 1 1 ...
## $ marginal
                : int 1511381111...
## $ epithelial : int 2 7 2 3 2 7 2 2 2 2 ...
## $ nuclei
              : int 1 10 2 4 1 10 10 1 1 1 1 ...
## $ chromatin : int 3 3 3 3 3 9 3 3 1 2 ...
## $ nucleoli : int 1 2 1 7 1 7 1 1 1 1 ...
## $ mitoses : int 1 1 1 1 1 1 1 5 1 ...
                : num 0000010000...
## $ class
Now we will divide the data into the training and testing set.
library(caret)
```

Attaching package: 'caret'

```
## The following object is masked from 'package:survival':
##
##
       cluster
set.seed(99)
cancer_set <- bcancer[, -1]</pre>
total_set <- createDataPartition(cancer_set$class, p = 0.60, list = FALSE)
training_set <- cancer_set[total_set,]</pre>
testing_set <- cancer_set[-total_set,]</pre>
Now we will run a tree model. A tree model breaks down all obervations from the training set by the key
predictors which in this case are cell size and nuceli.
library(rattle)
## Rattle: A free graphical interface for data science with R.
## Version 5.2.0 Copyright (c) 2006-2018 Togaware Pty Ltd.
## Type 'rattle()' to shake, rattle, and roll your data.
attach(training_set)
## The following objects are masked from bcancer:
##
##
       cell_shape, cell_size, chromatin, class, clump_thick,
##
       epithelial, marginal, mitoses, nuclei, nucleoli
training_set$class <- as.factor(training_set$class)</pre>
tree_model <- train(class~., data=training_set, method="rpart")</pre>
tree_model
## CART
##
## 420 samples
##
     9 predictor
##
     2 classes: '0', '1'
##
## No pre-processing
## Resampling: Bootstrapped (25 reps)
## Summary of sample sizes: 420, 420, 420, 420, 420, 420, ...
## Resampling results across tuning parameters:
##
##
                 Accuracy
                             Kappa
     ср
##
     0.00000000 0.9366472 0.8572399
     0.05072464 0.9320596 0.8477359
     0.81884058 0.8393058 0.5552945
##
## Accuracy was used to select the optimal model using the largest value.
## The final value used for the model was cp = 0.
```

fancyRpartPlot(tree_model\$finalModel)



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Now we will run a LDA Model using 10-Fold Cross Validation. The LDA algorithm uses a linear combinition of features, in this case the features of breast cancer like skin type, that characterizes the predictor variable.

```
control <- trainControl(method="cv", number=10)</pre>
metric <- "Accuracy"
set.seed(99)
lda_fit <- train(class~., data=training_set, method="lda", metric=metric, trControl=control)</pre>
## Linear Discriminant Analysis
##
## 420 samples
##
     9 predictor
     2 classes: '0', '1'
##
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 378, 377, 378, 379, 378, 378, ...
##
  Resampling results:
##
##
     Accuracy
                Kappa
     0.9545823
                0.895795
##
```

We will now use a KNN Machine Learning Algorithm. We attempt to predict the type of tumor by looking at the neighbors of the observation we are working on at that moment. In this context of the problem, this may not be the best model.

```
set.seed(99)
knn_fit <- train(class~., data=training_set, method="knn", metric=metric, trControl=control)
knn_fit
## k-Nearest Neighbors
##
## 420 samples
    9 predictor
##
     2 classes: '0', '1'
##
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 378, 377, 378, 379, 378, 378, ...
## Resampling results across tuning parameters:
##
##
    k Accuracy
                   Kappa
##
    5 0.9689261 0.9296265
##
    7 0.9665451 0.9239771
##
    9 0.9713070 0.9348862
##
## Accuracy was used to select the optimal model using the largest value.
## The final value used for the model was k = 9.
We will now use a Bayesian Generalized Linear Model
set.seed(99)
bayes_fit <- train(class~., data=training_set, method="bayesglm", metric=metric, trControl=control)
bayes_fit
## Bayesian Generalized Linear Model
##
## 420 samples
##
    9 predictor
##
    2 classes: '0', '1'
##
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 378, 377, 378, 379, 378, 378, ...
## Resampling results:
##
##
     Accuracy Kappa
##
     0.968868
               0.928889
We will now use an SVM Machine Learning Model. This model creates a boundary called a hyperplane and
examines the observations closest to the boundary to classify.
set.seed(99)
svm_fit <- train(class~., data=training_set, method="svmRadial", metric=metric, trControl=control)</pre>
svm\_fit
## Support Vector Machines with Radial Basis Function Kernel
##
## 420 samples
##
    9 predictor
##
     2 classes: '0', '1'
```

##

```
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 378, 377, 378, 379, 378, 378, ...
## Resampling results across tuning parameters:
##
     C
##
           Accuracy
                      Kappa
    0.25 0.9306593 0.8530663
##
##
     0.50
          0.9355347 0.8617385
##
     1.00 0.9546404 0.9011021
##
## Tuning parameter 'sigma' was held constant at a value of 0.793333
## Accuracy was used to select the optimal model using the largest value.
## The final values used for the model were sigma = 0.793333 and C = 1.
```

We will now use a Random Forest Model. We take a random number of predictors and create models with them. After several times of using random predictors and creating several models, we average them out to create one powerful model using elements from each of the weaker submodels.

```
set.seed(99)
random_forest_fit <- train(class~., data=training_set, method="rf", metric=metric, trControl=control)
random_forest_fit
## Random Forest
##
## 420 samples
##
     9 predictor
##
     2 classes: '0', '1'
##
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 378, 377, 378, 379, 378, 378, ...
## Resampling results across tuning parameters:
##
##
     mtry Accuracy
                      Kappa
           0.9761270 0.9460765
##
     2
##
     5
           0.9664870 0.9241409
           0.9592861 0.9077390
##
##
## Accuracy was used to select the optimal model using the largest value.
## The final value used for the model was mtry = 2.
```

Finally, we will use a XGB Linear Boosting Model. This model is based on the concept of Boosting. This is a method for reducing our variance. We obtain new datasets by drawing existing observations from our existing dataset with replacement. This way we can train our model further and average out all predictions. In addition, we grow our models sequentially and fit a model to the residuals of the previous model for further accuracy.

```
set.seed(99)
boosting_fit <- train(class~ ., data=training_set, method="xgbLinear", metric=metric, trControl=control
boosting_fit

## eXtreme Gradient Boosting
##
## 420 samples
## 9 predictor</pre>
```

2 classes: '0', '1'

##

```
##
## No pre-processing
   Resampling: Cross-Validated (10 fold)
   Summary of sample sizes: 378, 377, 378, 379, 378, 378, ...
##
   Resampling results across tuning parameters:
##
##
     lambda
              alpha
                     nrounds
                               Accuracy
                                           Kappa
##
     0e+00
              0e+00
                      50
                               0.9616671
                                           0.9139308
##
     0e+00
              0e+00
                     100
                               0.9616671
                                           0.9139308
##
     0e+00
              0e+00
                     150
                               0.9616671
                                           0.9139308
##
     0e+00
              1e-04
                      50
                               0.9616671
                                           0.9139308
##
     0e+00
              1e-04
                     100
                               0.9616671
                                           0.9139308
##
     0e+00
              1e-04
                     150
                               0.9592280
                                           0.9079579
     0e+00
##
              1e-01
                      50
                               0.9592280
                                           0.9079579
##
     0e+00
                                           0.9079579
              1e-01
                     100
                               0.9592280
##
     0e+00
              1e-01
                      150
                               0.9592280
                                           0.9079579
##
     1e-04
              0e+00
                      50
                                           0.9139308
                               0.9616671
##
     1e-04
              0e+00
                     100
                               0.9616671
                                           0.9139308
##
     1e-04
              0e+00
                     150
                               0.9616671
                                           0.9139308
##
     1e-04
              1e-04
                      50
                               0.9616671
                                           0.9139308
##
     1e-04
              1e-04
                     100
                               0.9616671
                                           0.9139308
     1e-04
                               0.9592280
                                           0.9079579
##
              1e-04
                     150
##
     1e-04
              1e-01
                               0.9592280
                                           0.9079579
                      50
##
     1e-04
              1e-01
                     100
                               0.9592280
                                           0.9079579
##
     1e-04
              1e-01
                     150
                               0.9592280
                                           0.9079579
##
     1e-01
              0e+00
                      50
                               0.9640480
                                           0.9193854
##
                               0.9640480
     1e-01
              0e+00
                     100
                                           0.9193854
##
     1e-01
              0e+00
                     150
                               0.9640480
                                           0.9193854
##
     1e-01
              1e-04
                      50
                               0.9640480
                                           0.9193854
                     100
##
     1e-01
              1e-04
                               0.9640480
                                           0.9193854
##
     1e-01
              1e-04
                      150
                               0.9640480
                                           0.9193854
##
     1e-01
              1e-01
                      50
                               0.9616671
                                           0.9139308
##
     1e-01
              1e-01
                     100
                               0.9616671
                                           0.9139308
##
     1e-01
              1e-01
                     150
                               0.9616671
                                           0.9139308
##
  Tuning parameter 'eta' was held constant at a value of 0.3
  Accuracy was used to select the optimal model using the largest value.
   The final values used for the model were nrounds = 50, lambda = 0.1,
    alpha = 0 and eta = 0.3.
```

The best model is the one with the highest kappa value. Recall that kappa represents the accuracy of the model, which is based on the Observed Accuracy and the Expected Accuracy. The Observed Accuracy is defined to be all instances where the machine learning model was in agreement with the ground truth. In the context of this problem, the Observed Accuracy is all instances where the model's prediction of weather the person has a benign or malignant tumor was in agreement of what type of tumor the patient had in real life. It is the number of times the model was correct. The Expected Accuracy is based on the number of times we classify the type of cancer according to ground truth multiplied by the number of times we classify the type of cancer according to ground truth. Then kappa is equal to $\kappa = \frac{O-E}{1-E}$, where O is Oberved Accuracy and E is Expected Accuracy. The kappa values for each model are as follows:

- The kappa value for the XGB Linear Boosting Model is .912
- The kappa value for the Random Forest Model is .923
- $\bullet\,$ The kappa value for the SVM Model is .873

- $\bullet\,$ The kappa value for the Bayes Model is .895
- $\bullet~$ The kappa value for the KNN Model is .159
- $\bullet\,$ The kappa value for the LDA Model is .905

Judging by these values, it seems that the Random Forest Model is the best model followed closely by the XGB Linear Boosting Model and the LDA Model.