

log_reg.R

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```
##### Logistic Regression #####
#install.packages("cowplot",
#lib="/Library/Frameworks/R.framework/Versions/3.5/Resources/Library")
library(cowplot)

##
## *****

## Note: As of version 1.0.0, cowplot does not change the
## default ggplot2 theme anymore. To recover the previous
## behavior, execute:
## theme_set(theme_cowplot())

## *****

library(dplyr)

##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
## filter, lag

## The following objects are masked from 'package:base':
##
## intersect, setdiff, setequal, union

library(ggplot2)
data <- read.csv("C:/Users/saiprasad/Desktop/Fall 2019/Multi
analysis/MVA/Project/Dataset/HCV-EGY-Data.csv")
attach(data)
Survivorship = data$Survivorship <- if_else( RNA.EOT >= 400000 , 'NC','C')
cbind(data.frame(Survivorship),data)

##      Survivorship Age Gender BMI Fever Nausea.Vomting Headache Diarrhea
## 1                C  56     1  35     2             1         1         1
## 2                C  46     1  29     1             2         2         1
## 3               NC  57     1  33     2             2         2         2
## 4               NC  49     2  33     1             2         1         2
## 5                C  59     1  32     1             1         2         1
## 6                C  58     2  22     2             2         2         1
```

## 7	C	42	2	26	1	1	2	2
## 8	C	48	2	30	1	1	2	2
## 9	C	44	1	23	1	1	2	2
## 10	C	45	1	30	2	1	2	2
## 11	NC	37	2	24	2	1	2	1
## 12	C	36	1	22	2	2	1	1
## 13	C	45	2	25	2	1	1	1
## 14	C	34	1	22	1	2	1	1
## 15	NC	40	2	32	2	2	2	1
## 16	NC	58	1	34	2	1	1	1
## 17	C	61	1	35	1	2	2	2
## 18	C	55	2	24	2	1	2	2
## 19	NC	56	1	27	1	2	2	2
## 20	NC	35	2	23	2	2	1	1
## 21	NC	57	2	23	1	1	2	2
## 22	C	33	1	25	2	1	2	2
## 23	C	41	1	23	1	2	2	2
## 24	C	39	2	29	1	2	1	2
## 25	C	33	2	24	1	2	2	2
## 26	C	43	2	34	2	2	2	1
## 27	NC	51	1	34	2	1	2	2
## 28	NC	39	2	33	2	1	2	1
## 29	C	57	2	26	1	2	2	1
## 30	C	47	2	29	1	1	2	1
## 31	C	55	2	33	1	2	2	1
## 32	C	58	2	35	2	2	2	2
## 33	NC	47	2	25	2	1	2	2
## 34	C	61	1	33	1	2	2	2
## 35	NC	37	1	27	2	2	1	2
## 36	NC	41	1	29	1	2	1	1
## 37	C	60	2	32	2	2	1	2
## 38	C	54	1	29	1	1	1	2
## 39	C	40	2	28	2	1	2	1
## 40	C	32	1	31	1	2	1	1
## 41	NC	58	2	33	1	2	2	2
## 42	C	37	2	23	2	2	1	1
## 43	C	58	1	23	1	1	1	2
## 44	NC	36	1	23	2	2	1	2
## 45	C	47	2	35	1	2	2	1
## 46	C	50	1	33	2	2	1	1
## 47	C	44	1	31	1	1	1	1
## 48	NC	43	1	33	1	1	2	2
## 49	NC	54	1	33	2	1	1	2
## 50	NC	59	2	26	2	1	1	1
## 51	C	33	2	31	1	1	1	2
## 52	C	56	2	23	1	1	1	2
## 53	NC	41	1	33	2	1	1	1
## 54	NC	59	1	32	2	1	1	1
## 55	C	47	1	27	2	2	1	1
## 56	C	50	2	34	1	1	1	2

##	Fatigue...generalized.bone.ache	Jaundice	Epigastric.pain	WBC
## 1	2	2	2	7425
## 2	2	2	1	12101
## 3	1	1	1	4178
## 4	1	2	1	6490
## 5	2	2	2	3661
## 6	2	2	1	11785
## 7	2	2	2	11620
## 8	1	1	2	7335
## 9	2	1	2	10480
## 10	1	1	2	6681
## 11	2	2	1	4437
## 12	1	1	1	6052
## 13	2	1	2	9279
## 14	2	2	1	5638
## 15	2	1	1	11507
## 16	2	1	1	8035
## 17	1	1	2	10843
## 18	2	2	2	8476
## 19	2	2	2	6599
## 20	1	1	2	4845
## 21	1	1	1	5925
## 22	2	2	2	9952
## 23	2	1	2	7961
## 24	1	1	2	7136
## 25	2	1	2	6057
## 26	1	1	1	6648
## 27	1	1	2	11032
## 28	1	1	2	5234
## 29	1	1	2	6038
## 30	2	1	2	5846
## 31	2	1	2	5383
## 32	1	1	1	7378
## 33	2	1	2	7486
## 34	1	1	1	11770
## 35	2	2	2	6441
## 36	2	1	2	10304
## 37	2	2	1	7365
## 38	2	1	1	10704
## 39	1	1	1	3009
## 40	1	1	2	9956
## 41	1	2	2	6627
## 42	2	2	1	10393
## 43	1	1	2	10236
## 44	2	2	2	4387
## 45	2	2	2	11924
## 46	2	1	2	10140
## 47	2	1	2	3470
## 48	2	1	2	5420

## 49		1	2		1	6963
## 50		1	1		2	6249
## 51		1	2		1	5094
## 52		2	2		2	4797
## 53		2	2		2	5041
## 54		1	2		2	6901
## 55		1	1		1	7256
## 56		2	1		1	8219
## 57		1	1		1	4418
## 58		1	1		2	6358
## 59		2	1		2	8669
## 60		1	1		2	9435
## 61		2	2		2	11144
## 62		1	2		2	5060
## 63		1	1		1	7766
## 64		2	1		2	10879
## 65		1	2		2	11490
## 66		1	1		1	4082
## 67		2	2		1	5078
## 68		1	2		2	4580
## 69		2	1		2	7983
## 70		2	2		2	5500

##	RBC	HGB	Plat	AST.1	ALT.1	ALT4	ALT.12	ALT.24	ALT.36	ALT.48
## 1	4248807	14	112132	99	84	52	109	81	5	5
## 2	4429425	10	129367	91	123	95	75	113	57	123
## 3	4621191	12	151522	113	49	95	107	116	5	5
## 4	4794631	10	146457	43	64	109	80	88	48	77
## 5	4606375	11	187684	99	104	67	48	120	94	90
## 6	3882456	15	131228	66	104	121	96	65	73	114
## 7	4747333	12	177261	78	57	113	118	107	84	80
## 8	4405941	11	216176	119	112	80	127	45	96	53
## 9	4608464	12	148889	93	83	55	102	97	122	39
## 10	4455329	12	98200	55	68	72	127	81	125	43
## 11	4265042	12	166027	103	124	111	74	53	123	101
## 12	4130219	13	144266	75	49	93	52	46	46	59
## 13	4116937	13	203003	97	101	66	53	95	55	104
## 14	4321603	14	141110	120	61	64	51	78	90	113
## 15	4165603	14	222874	127	122	106	105	88	111	111
## 16	4896464	11	149506	117	53	50	80	120	66	86
## 17	4165219	10	197640	86	105	70	86	83	87	47
## 18	4466885	14	163276	53	101	50	95	112	97	68
## 19	4448466	15	190642	53	124	62	76	57	46	93
## 20	4436025	10	111819	115	121	63	127	95	124	93
## 21	4031637	15	116558	86	109	118	119	55	103	84
## 22	4994729	10	109023	84	77	67	81	117	68	42
## 23	4595487	14	94733	45	92	103	104	40	115	93
## 24	4625248	10	211363	70	102	76	58	111	95	58
## 25	4300774	11	222135	62	91	116	128	41	70	106
## 26	4529290	15	109871	48	112	99	85	59	87	78
## 27	4052583	15	94503	41	54	128	64	71	89	87

## 28	4906158	12	190314	61	120	113	75	88	114	99
## 29	4763261	13	126721	51	118	98	42	93	53	83
## 30	4753531	15	104729	120	72	117	126	45	95	49
## 31	3999388	15	182262	96	49	59	88	62	58	81
## 32	3998925	10	201114	57	110	128	96	69	105	72
## 33	4599496	11	167354	94	64	54	122	64	64	96
## 34	4581099	13	125642	42	47	82	102	48	76	53

##	ALT.after.24.w	RNA.Base	RNA.4	RNA.12	RNA.EOT	RNA.EF
## 1	5	655330	634536	288194	5	5
## 2	44	40620	538635	637056	336804	31085
## 3	5	571148	661346	5	735945	558829
## 4	33	1041941	449939	585688	744463	582301
## 5	30	660410	738756	3731527	338946	242861
## 6	29	1157452	1086852	5	5	5
## 7	28	325694	1034008	275095	214566	635157
## 8	39	641129	72050	787295	370605	506296
## 9	45	591441	757361	5	371090	203042
## 10	30	1151206	230488	267320	275295	555516
## 11	33	1023123	103190	731929	448466	59998
## 12	45	137712	1122999	561438	63145	806204
## 13	26	936444	536969	5	5	5
## 14	23	392976	884322	586834	182775	782154
## 15	36	1133727	1111871	421304	437544	124609
## 16	34	614951	314296	83690	671490	135145
## 17	33	900099	721460	5	5	5
## 18	27	1145310	230993	457882	318363	256415
## 19	26	506756	359181	743399	405175	162983
## 20	42	1080499	76404	717159	404314	477719
## 21	32	169624	786017	669076	531187	282524
## 22	32	1135200	572747	5	5	5
## 23	33	293380	440576	53098	18292	187341
## 24	25	993940	992652	96482	334897	762760
## 25	43	243433	981370	12504	360015	753383
## 26	35	955296	540654	5	5	5
## 27	34	766355	531269	737603	734863	372837
## 28	43	486467	45990	45578	733292	19572
## 29	45	285374	186657	5	5	5
## 30	38	426136	247777	767015	377123	315150
## 31	41	1194301	928679	29778	124250	244049
## 32	26	557708	287714	623587	66891	35044
## 33	24	604063	416313	323352	716655	678548
## 34	34	1159877	318505	463260	381345	282914
## 35	45	272600	91626	404523	674101	242552
## 36	40	1165166	51508	367178	588014	746328
## 37	35	112401	489112	461641	336006	287261
## 38	43	47190	581000	789780	262941	118971
## 39	31	961292	71146	28241	31034	1417
## 40	39	855099	102520	407306	220006	405497
## 41	33	1047535	320353	349454	546832	643942

## 42	33	271349	206329	151217	307729	174523
## 43	39	272507	1061189	230947	201997	293804
## 44	43	594248	1156859	436512	728279	685286
## 45	26	651671	422729	412086	91529	376394
## 46	35	57911	867787	758773	319688	159764
## 47	32	751073	825583	355919	100948	634168
## 48	28	740502	1197447	180453	524563	291808

##	Baseline.histological.Grading	Baselinehistological.staging
## 1	13	2
## 2	4	2
## 3	4	4
## 4	10	3
## 5	11	1
## 6	4	4
## 7	12	4
## 8	12	3
## 9	5	2
## 10	4	2
## 11	15	2
## 12	16	1
## 13	8	1
## 14	9	2
## 15	8	2
## 16	15	1
## 17	3	4
## 18	4	3
## 19	6	4
## 20	16	4
## 21	6	2
## 22	4	1
## 23	10	3
## 24	15	4
## 25	6	3
## 26	9	4
## 27	5	1
## 28	15	2
## 29	9	3
## 30	9	1
## 31	7	1
## 32	5	2
## 33	8	1
## 34	10	1
## 35	11	3
## 36	16	3
## 37	5	2
## 38	15	1
## 39	9	2
## 40	7	4
## 41	13	1

## 42	6	1
## 43	14	3
## 44	5	4
## 45	12	3
## 46	13	2
## 47	11	4
## 48	15	2
## 49	9	3
## 50	15	1
## 51	8	4
## 52	13	2
## 53	8	1
## 54	5	2
## 55	13	1
## 56	11	2
## 57	14	3
## 58	13	4
## 59	13	1
## 60	3	1
## 61	8	4
## 62	12	3

##	Survivorship
## 1	C
## 2	C
## 3	NC
## 4	NC
## 5	C
## 6	C
## 7	C
## 8	C
## 9	C
## 10	C
## 11	NC
## 12	C
## 13	C
## 14	C
## 15	NC
## 16	NC
## 17	C
## 18	C
## 19	NC
## 20	NC
## 21	NC
## 22	C
## 23	C
## 24	C
## 25	C
## 26	C
## 27	NC

## 28	NC
## 29	C
## 30	C
## 31	C
## 32	C
## 33	NC
## 34	C
## 35	NC
## 36	NC
## 37	C
## 38	C
## 39	C
## 40	C
## 41	NC
## 42	C
## 43	C
## 44	NC
## 45	C
## 46	C
## 47	C
## 48	NC
## 49	NC
## 50	NC
## 51	C
## 52	C
## 53	NC
## 54	NC
## 55	C
## 56	C
## 57	C
## 58	C
## 59	C
## 60	NC
## 61	C
## 62	C
## 63	NC
## 64	NC
## 65	NC
## 66	C
## 67	C
## 68	C
## 69	NC
## 70	NC
## 71	C
## 72	C
## 73	C
## 74	NC
## 75	NC


```

data$Survivorship <- as.factor(data$Survivorship)
#####
##
## Reformat the data so that it is
## 1) Easy to use (add nice column names)
## 2) Interpreted correctly by glm()..
##
#####
head(data) # you see data, but no column names

##   Age Gender BMI Fever Nausea.Vomting Headache Diarrhea
## 1  56      1  35     2           1           1           1
## 2  46      1  29     1           2           2           1
## 3  57      1  33     2           2           2           2
## 4  49      2  33     1           2           1           2
## 5  59      1  32     1           1           2           1
## 6  58      2  22     2           2           2           1
##   Fatigue...generalized.bone.ache Jaundice Epigastric.pain   WBC   RBC
## 1                                2           2           2  7425 4248807
## 2                                2           2           1 12101 4429425
## 3                                1           1           1  4178 4621191
## 4                                1           2           1  6490 4794631
## 5                                2           2           2  3661 4606375
## 6                                2           2           1 11785 3882456
##   HGB   Plat AST.1 ALT.1 ALT4 ALT.12 ALT.24 ALT.36 ALT.48 ALT.after.24.w
## 1  14 112132   99   84   52   109   81     5     5           5
## 2  10 129367   91  123   95   75   113   57   123           44
## 3  12 151522  113   49   95  107  116   5     5           5
## 4  10 146457   43   64  109   80   88   48   77           33
## 5  11 187684   99  104   67   48  120   94   90           30
## 6  15 131228   66  104  121   96   65   73  114           29
##   RNA.Base   RNA.4   RNA.12 RNA.EOT RNA.EF Baseline.histological.Grading
## 1   655330  634536  288194      5      5                               13
## 2    40620  538635  637056 336804 31085                               4
## 3   571148  661346      5  735945 558829                               4
## 4  1041941  449939  585688  744463 582301                               10
## 5   660410  738756 3731527  338946 242861                               11
## 6  1157452 1086852      5      5      5                               4
##   Baselinehistological.staging Survivorship
## 1                                2           C
## 2                                2           C
## 3                                4           NC
## 4                                3           NC
## 5                                1           C
## 6                                4           C

str(data)

## 'data.frame':   1385 obs. of  30 variables:
##  $ Age          : int  56 46 57 49 59 58 42 48 44 45 ...

```

```

## $ Gender : int 1 1 1 2 1 2 2 2 1 1 ...
## $ BMI : int 35 29 33 33 32 22 26 30 23 30 ...
## $ Fever : int 2 1 2 1 1 2 1 1 1 2 ...
## $ Nausea.Vomting : int 1 2 2 2 1 2 1 1 1 1 ...
## $ Headache : int 1 2 2 1 2 2 2 2 2 2 ...
## $ Diarrhea : int 1 1 2 2 1 1 2 2 2 2 ...
## $ Fatigue...generalized.bone.ache: int 2 2 1 1 2 2 2 1 2 1 ...
## $ Jaundice : int 2 2 1 2 2 2 2 1 1 1 ...
## $ Epigastric.pain : int 2 1 1 1 2 1 2 2 2 2 ...
## $ WBC : int 7425 12101 4178 6490 3661 11785
11620 7335 10480 6681 ...
## $ RBC : num 4248807 4429425 4621191 4794631
4606375 ...
## $ HGB : int 14 10 12 10 11 15 12 11 12 12 ...
## $ Plat : num 112132 129367 151522 146457
187684 ...
## $ AST.1 : int 99 91 113 43 99 66 78 119 93 55
...
## $ ALT.1 : int 84 123 49 64 104 104 57 112 83 68
...
## $ ALT4 : num 52 95 95 109 67 121 113 80 55 72
...
## $ ALT.12 : int 109 75 107 80 48 96 118 127 102
127 ...
## $ ALT.24 : int 81 113 116 88 120 65 107 45 97 81
...
## $ ALT.36 : int 5 57 5 48 94 73 84 96 122 125 ...
## $ ALT.48 : int 5 123 5 77 90 114 80 53 39 43 ...
## $ ALT.after.24.w : int 5 44 5 33 30 29 28 39 45 30 ...
## $ RNA.Base : int 655330 40620 571148 1041941
660410 1157452 325694 641129 591441 1151206 ...
## $ RNA.4 : int 634536 538635 661346 449939
738756 1086852 1034008 72050 757361 230488 ...
## $ RNA.12 : int 288194 637056 5 585688 3731527 5
275095 787295 5 267320 ...
## $ RNA.EOT : int 5 336804 735945 744463 338946 5
214566 370605 371090 275295 ...
## $ RNA.EF : int 5 31085 558829 582301 242861 5
635157 506296 203042 555516 ...
## $ Baseline.histological.Grading : int 13 4 4 10 11 4 12 12 5 4 ...
## $ Baselinehistological.staging : int 2 2 4 3 1 4 4 3 2 2 ...
## $ Survivorship : Factor w/ 2 levels "C","NC": 1 1 2 2 1
1 1 1 1 1 ...

```

this shows that we need to tell R which columns contain factors it also shows us that there are some missing values. There are "?"s in the dataset. These are in the "ca" and "thal" columns. First, convert "?"s to NAs...

```
data[data == "?"] <- NA
```

Now add factors for variables that are factors and clean up the factors

that had missing data...

```
data[data$Gender == 1,]$Gender <- "M"
data[data$Gender == 2,]$Gender <- "F"
data$Gender <- as.factor(data$Gender)
data[data$Fever == 1,]$Fever <- "No"
data[data$Fever == 2,]$Fever <- "Yes"
data$Fever <- as.factor(data$Fever)
data[data$Nausea.Vomting == 1,]$Nausea.Vomting <- "No"
data[data$Nausea.Vomting == 2,]$Nausea.Vomting <- "Yes"
data$Nausea.Vomting <- as.factor(data$Nausea.Vomting)
data[data$Headache == 1,]$Headache <- "No"
data[data$Headache == 2,]$Headache <- "Yes"
data$Headache <- as.factor(data$Headache)
data[data$Diarrhea == 1,]$Diarrhea <- "No"
data[data$Diarrhea == 2,]$Diarrhea <- "Yes"
data$Diarrhea <- as.factor(data$Diarrhea)
data[data$Fatigue...generalized.bone.ache ==
1,]$Fatigue...generalized.bone.ache <- "No"
data[data$Fatigue...generalized.bone.ache ==
2,]$Fatigue...generalized.bone.ache <- "Yes"
data$Fatigue...generalized.bone.ache <-
as.factor(data$Fatigue...generalized.bone.ache)
data[data$Jaundice == 1,]$Jaundice <- "No"
data[data$Jaundice == 2,]$Jaundice <- "Yes"
data$Jaundice <- as.factor(data$Jaundice)
data[data$Epigastric.pain == 1,]$Epigastric.pain <- "No"
data[data$Epigastric.pain == 2,]$Epigastric.pain <- "Yes"
data$Epigastric.pain <- as.factor(data$Epigastric.pain)
data[data$Baselinehistological.staging == 1,]$Baselinehistological.staging <-
"Portal Fibrosis"
data[data$Baselinehistological.staging == 2,]$Baselinehistological.staging<-
"Few Septa"
data[data$Baselinehistological.staging == 3,]$Baselinehistological.staging <-
"Many Septa "
data[data$Baselinehistological.staging == 4,]$Baselinehistological.staging <-
"Cirrhosis"
data$Baseline.histological.Grading <-
as.factor(data$Baseline.histological.Grading)
data$Baselinehistological.staging <-
as.factor(data$Baselinehistological.staging)
str(data)

## 'data.frame':    1385 obs. of  30 variables:
##  $ Age                : int   56 46 57 49 59 58 42 48 44 45 ...
##  $ Gender              : Factor w/ 2 levels "F","M": 2 2 2 1 2
1 1 1 2 2 ...
##  $ BMI                 : int   35 29 33 33 32 22 26 30 23 30 ...
##  $ Fever               : Factor w/ 2 levels "No","Yes": 2 1 2 1
1 2 1 1 1 2 ...
##  $ Nausea.Vomting      : Factor w/ 2 levels "No","Yes": 1 2 2 2
```

```

1 2 1 1 1 1 ...
## $ Headache : Factor w/ 2 levels "No","Yes": 1 2 2 1
2 2 2 2 2 2 ...
## $ Diarrhea : Factor w/ 2 levels "No","Yes": 1 1 2 2
1 1 2 2 2 2 ...
## $ Fatigue...generalized.bone.ache: Factor w/ 2 levels "No","Yes": 2 2 1 1
2 2 2 1 2 1 ...
## $ Jaundice : Factor w/ 2 levels "No","Yes": 2 2 1 2
2 2 2 1 1 1 ...
## $ Epigastric.pain : Factor w/ 2 levels "No","Yes": 2 1 1 1
2 1 2 2 2 2 ...
## $ WBC : int 7425 12101 4178 6490 3661 11785
11620 7335 10480 6681 ...
## $ RBC : num 4248807 4429425 4621191 4794631
4606375 ...
## $ HGB : int 14 10 12 10 11 15 12 11 12 12 ...
## $ Plat : num 112132 129367 151522 146457
187684 ...
## $ AST.1 : int 99 91 113 43 99 66 78 119 93 55
...
## $ ALT.1 : int 84 123 49 64 104 104 57 112 83 68
...
## $ ALT4 : num 52 95 95 109 67 121 113 80 55 72
...
## $ ALT.12 : int 109 75 107 80 48 96 118 127 102
127 ...
## $ ALT.24 : int 81 113 116 88 120 65 107 45 97 81
...
## $ ALT.36 : int 5 57 5 48 94 73 84 96 122 125 ...
## $ ALT.48 : int 5 123 5 77 90 114 80 53 39 43 ...
## $ ALT.after.24.w : int 5 44 5 33 30 29 28 39 45 30 ...
## $ RNA.Base : int 655330 40620 571148 1041941
660410 1157452 325694 641129 591441 1151206 ...
## $ RNA.4 : int 634536 538635 661346 449939
738756 1086852 1034008 72050 757361 230488 ...
## $ RNA.12 : int 288194 637056 5 585688 3731527 5
275095 787295 5 267320 ...
## $ RNA.EOT : int 5 336804 735945 744463 338946 5
214566 370605 371090 275295 ...
## $ RNA.EF : int 5 31085 558829 582301 242861 5
635157 506296 203042 555516 ...
## $ Baseline.histological.Grading : Factor w/ 14 levels
"3","4","5","6",...: 11 2 2 8 9 2 10 10 3 2 ...
## $ Baselinehistological.staging : Factor w/ 4 levels "Cirrhosis","Few
Septa",...: 2 2 1 3 4 1 1 3 2 2 ...
## $ Survivorship : Factor w/ 2 levels "C","NC": 1 1 2 2 1
1 1 1 1 1 ...

```

```
#####
```

```
xtabs(~ Survivorship + Gender, data=data)
```

```

##                Gender
## Survivorship   F    M
##                C  425 478
##                NC  253 229

xtabs(~ Survivorship + Fever, data=data)

##                Fever
## Survivorship   No Yes
##                C  440 463
##                NC  231 251

xtabs(~ Survivorship + Nausea.Vomting, data=data)

##                Nausea.Vomting
## Survivorship   No Yes
##                C  451 452
##                NC  238 244

xtabs(~ Survivorship + Headache, data=data)

##                Headache
## Survivorship   No Yes
##                C  450 453
##                NC  248 234

xtabs(~ Survivorship + Diarrhea, data=data)

##                Diarrhea
## Survivorship   No Yes
##                C  452 451
##                NC  237 245

xtabs(~ Survivorship + Fatigue...generalized.bone.ache, data=data)

##                Fatigue...generalized.bone.ache
## Survivorship   No Yes
##                C  463 440
##                NC  231 251

xtabs(~ Survivorship + Jaundice, data=data)

##                Jaundice
## Survivorship   No Yes
##                C  462 441
##                NC  229 253

xtabs(~ Survivorship + Epigastric.pain, data=data)

##                Epigastric.pain
## Survivorship   No Yes
##                C  458 445
##                NC  229 253

```

```

xtabs(~ Survivorship + Baselinehistological.staging, data=data)

##              Baselinehistological.staging
## Survivorship Cirrhosis Few Septa Many Septa Portal Fibrosis
##           C      235      221      234      213
##           NC      127      111      121      123

## Now we are ready for some Logistic regression. First we'll create a very
## simple model that uses sex to predict heart disease
##
xtabs(~ Survivorship + Gender, data=data)

##              Gender
## Survivorship  F    M
##           C  425  478
##           NC  253  229

## Most of the females are healthy and most of the males are unhealthy.
## Being female is likely to decrease the odds in being unhealthy.
## In other words, if a sample is female, the odds are against it that it
## will be unhealthy
## Being male is likely to increase the odds in being unhealthy...
## In other words, if a sample is male, the odds are for it being
unhealthy
logistic_simple <- glm(Survivorship ~ Gender, data=data, family="binomial")
summary(logistic_simple)

##
## Call:
## glm(formula = Survivorship ~ Gender, family = "binomial", data = data)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -0.9665  -0.9665  -0.8848   1.4041   1.5015
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.51870    0.07941  -6.532 6.48e-11 ***
## GenderM      -0.21719    0.11298  -1.922  0.0546 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 1790.0  on 1384  degrees of freedom
## Residual deviance: 1786.3  on 1383  degrees of freedom
## AIC: 1790.3
##
## Number of Fisher Scoring iterations: 4

```

```

## The intercept is the log(odds) a female will be unhealthy. This is because
## female is the first factor in "sex" (the factors are ordered,
## alphabetically by default, "female", "male")
## Now let's look at the second coefficient...
## sexM          1.2737      0.2725    4.674 2.95e-06 ***
##
## sexM is the log(odds ratio) that tells us that if a sample has sex=M, the
## odds of being unhealthy are, on a log scale, 1.27 times greater than if
## a sample has sex=F.
female.log.odds <- log(253 / 425)
female.log.odds

## [1] -0.5186997

# Now you know how these are calculated
male.log.odds.ratio <- log((229 / 478) / (253/425))
male.log.odds.ratio

## [1] -0.217189

## Now calculate the overall "Pseudo R-squared" and its p-value
## NOTE: Since we are doing logistic regression...
## Null deviance = 2*(0 - LogLikelihood(null model))
##              = -2*LogLikelihood(null model)
## Residual deviance = 2*(0 - LogLikelihood(proposed model))
##              = -2*LogLikelihood(proposed model)
ll.null <- logistic_simple$null.deviance/-2
ll.proposed <- logistic_simple$deviance/-2
ll.null

## [1] -894.9992

ll.proposed

## [1] -893.1488

## McFadden's Pseudo R^2 = [ LL(Null) - LL(Proposed) ] / LL(Null)
(ll.null - ll.proposed) / ll.null

## [1] 0.002067477

## chi-square value = 2*(LL(Proposed) - LL(Null))
## p-value = 1 - pchisq(chi-square value, df = 2-1)
1 - pchisq(2*(ll.proposed - ll.null), df=1)

## [1] 0.05438701

1 - pchisq((logistic_simple$null.deviance - logistic_simple$deviance), df=1)

## [1] 0.05438701

## Lastly, let's see what this logistic regression predicts, given
## that a patient is either female or male (and no other data about them).

```

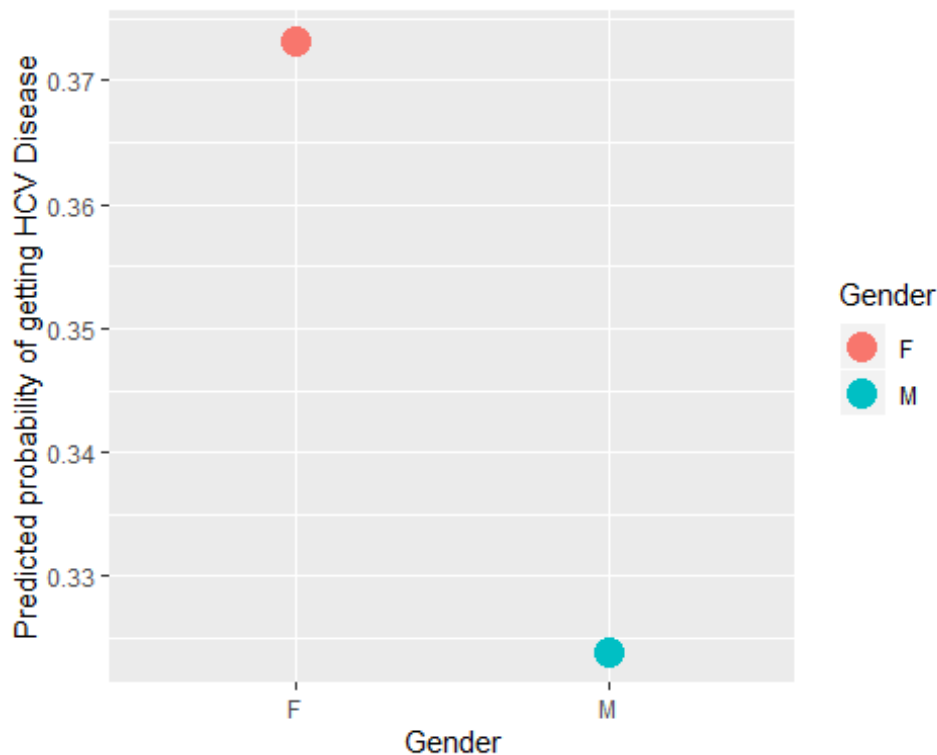
```
predicted.data <-  
data.frame(probability.of.Survivorship=logistic_simple$fitted.values,Gender=d  
ata$Gender)  
predicted.data
```

##	probability.of.Survivorship	Gender
## 1	0.3239038	M
## 2	0.3239038	M
## 3	0.3239038	M
## 4	0.3731563	F
## 5	0.3239038	M
## 6	0.3731563	F
## 7	0.3731563	F
## 8	0.3731563	F
## 9	0.3239038	M
## 10	0.3239038	M
## 11	0.3731563	F
## 12	0.3239038	M
## 13	0.3731563	F
## 14	0.3239038	M
## 15	0.3731563	F
## 16	0.3239038	M
## 17	0.3239038	M
## 18	0.3731563	F
## 19	0.3239038	M
## 20	0.3731563	F
## 21	0.3731563	F
## 22	0.3239038	M
## 23	0.3239038	M
## 24	0.3731563	F
## 25	0.3731563	F
## 26	0.3731563	F
## 27	0.3239038	M
## 28	0.3731563	F
## 29	0.3731563	F
## 30	0.3731563	F
## 31	0.3731563	F
## 32	0.3731563	F
## 33	0.3731563	F
## 34	0.3239038	M
## 35	0.3239038	M
## 36	0.3239038	M
## 37	0.3731563	F
## 38	0.3239038	M
## 39	0.3731563	F
## 40	0.3239038	M
## 41	0.3731563	F
## 42	0.3731563	F
## 43	0.3239038	M
## 44	0.3239038	M

## 45	0.3731563	F
## 46	0.3239038	M
## 47	0.3239038	M
## 48	0.3239038	M
## 49	0.3239038	M
## 50	0.3731563	F
## 51	0.3731563	F
## 52	0.3731563	F
## 53	0.3239038	M
## 54	0.3239038	M
## 55	0.3239038	M
## 56	0.3731563	F
## 57	0.3731563	F
## 58	0.3239038	M
## 59	0.3731563	F
## 60	0.3731563	F
## 61	0.3731563	F
## 62	0.3731563	F
## 63	0.3731563	F
## 64	0.3731563	F
## 65	0.3239038	M
## 66	0.3239038	M
## 67	0.3731563	F
## 68	0.3731563	F
## 69	0.3731563	F
## 70	0.3239038	M
## 71	0.3239038	M
## 72	0.3731563	F
## 73	0.3731563	F
## 74	0.3239038	M
## 75	0.3731563	F
## 76	0.3239038	M
## 77	0.3731563	F
## 78	0.3239038	M
## 79	0.3239038	M
## 80	0.3239038	M
## 81	0.3239038	M
## 82	0.3239038	M
## 83	0.3239038	M
## 84	0.3239038	M
## 85	0.3731563	F
## 86	0.3239038	M
## 87	0.3731563	F
## 88	0.3731563	F
## 89	0.3239038	M
## 90	0.3239038	M
## 91	0.3731563	F
## 92	0.3731563	F
## 93	0.3731563	F
## 94	0.3239038	M

```
## We can plot the data...
```

```
ggplot(data=predicted.data, aes(x=Gender, y=probability.of.Survivorship)) +  
  geom_point(aes(color=Gender), size=5) +  
  xlab("Gender") +  
  ylab("Predicted probability of getting HCV Disease")
```



```
## Since there are only two probabilities (one for females and one for  
## males),
```

```
## we can use a table to summarize the predicted probabilities.
```

```
xtabs(~ probability.of.Survivorship + Gender, data=predicted.data)
```

```
##  
##           probability.of.Survivorship  Gender  
##           0.323903818953405      F      M  
##           0.373156342182894     678    707
```

```
#####
```

```
##
```

```
## Now we will use all of the data available to predict heart disease. This  
## is not the best way to do this
```

```
##
```

```
#####
```

```
logistic <- glm(Survivorship ~ ., data=data, family="binomial")
```

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

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

```
summary(logistic)
```

```
##
## Call:
## glm(formula = Survivorship ~ ., family = "binomial", data = data)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -2.001e-04 -2.100e-08 -2.100e-08  2.100e-08  2.034e-04
##
## Coefficients:
##              Estimate Std. Error z value
## (Intercept)    -6.147e+02  6.931e+04  -0.009
## Age             -4.518e-01  4.139e+02  -0.001
## GenderM         -3.424e+00  1.281e+04   0.000
## BMI             -2.747e-01  6.578e+02   0.000
## FeverYes        8.441e+00  7.660e+03   0.001
## Nausea.VomtingYes -1.017e+01  7.678e+03  -0.001
## HeadacheYes     -2.229e+00  6.399e+03   0.000
## DiarrheaYes      2.269e+00  6.636e+03   0.000
## Fatigue...generalized.bone.acheYes 4.740e+00  9.352e+03   0.001
## JaundiceYes      1.829e+01  5.086e+03   0.004
## Epigastric.painYes -4.547e+00  1.172e+04   0.000
## WBC              7.295e-04  1.239e+00   0.001
## RBC              8.384e-06  1.097e-02   0.001
## HGB              5.689e+00  1.694e+03   0.003
## Plat            3.605e-05  7.103e-02   0.001
## AST.1            1.728e-02  9.804e+01   0.000
## ALT.1            -1.263e-01  2.944e+02   0.000
## ALT4             2.783e-01  1.365e+02   0.002
## ALT.12           5.809e-02  9.432e+01   0.001
## ALT.24           1.513e-01  1.629e+02   0.001
## ALT.36           1.265e-01  1.200e+02   0.001
## ALT.48           1.336e-01  1.011e+02   0.001
## ALT.after.24.w   -1.292e+00  8.390e+02  -0.002
## RNA.Base         2.232e-05  1.296e-02   0.002
## RNA.4            -7.059e-06  6.352e-03  -0.001
## RNA.12           1.689e-06  1.613e-02   0.000
## RNA.EOT          1.236e-03  7.123e-02   0.017
## RNA.EF          -2.340e-05  1.077e-02  -0.002
## Baseline.histological.Grading4     1.320e+01  1.614e+04   0.001
## Baseline.histological.Grading5     -3.246e+00  1.755e+04   0.000
## Baseline.histological.Grading6      3.274e+01  3.118e+04   0.001
## Baseline.histological.Grading7      4.915e+00  1.318e+05   0.000
## Baseline.histological.Grading8     -5.185e-01  1.415e+04   0.000
## Baseline.histological.Grading9      1.295e+01  6.432e+04   0.000
## Baseline.histological.Grading10     1.530e+01  1.485e+04   0.001
## Baseline.histological.Grading11     1.852e+01  2.826e+04   0.001
## Baseline.histological.Grading12     2.538e+01  1.779e+04   0.001
## Baseline.histological.Grading13    -1.473e+01  2.040e+04  -0.001
```

## Baseline.histological.Grading14	1.434e+01	1.784e+04	0.001
## Baseline.histological.Grading15	1.279e+01	1.579e+04	0.001
## Baseline.histological.Grading16	4.808e+01	2.328e+04	0.002
## Baselinehistological.stagingFew Septa	-1.186e+01	9.410e+03	-0.001
## Baselinehistological.stagingMany Septa	-5.362e+00	7.264e+03	-0.001
## Baselinehistological.stagingPortal Fibrosis	-9.128e+00	1.078e+04	-0.001
##	Pr(> z)		
## (Intercept)	0.993		
## Age	0.999		
## GenderM	1.000		
## BMI	1.000		
## FeverYes	0.999		
## Nausea.VomtingYes	0.999		
## HeadacheYes	1.000		
## DiarrheaYes	1.000		
## Fatigue...generalized.bone.acheYes	1.000		
## JaundiceYes	0.997		
## Epigastric.painYes	1.000		
## WBC	1.000		
## RBC	0.999		
## HGB	0.997		
## Plat	1.000		
## AST.1	1.000		
## ALT.1	1.000		
## ALT4	0.998		
## ALT.12	1.000		
## ALT.24	0.999		
## ALT.36	0.999		
## ALT.48	0.999		
## ALT.after.24.w	0.999		
## RNA.Base	0.999		
## RNA.4	0.999		
## RNA.12	1.000		
## RNA.EOT	0.986		
## RNA.EF	0.998		
## Baseline.histological.Grading4	0.999		
## Baseline.histological.Grading5	1.000		
## Baseline.histological.Grading6	0.999		
## Baseline.histological.Grading7	1.000		
## Baseline.histological.Grading8	1.000		
## Baseline.histological.Grading9	1.000		
## Baseline.histological.Grading10	0.999		
## Baseline.histological.Grading11	0.999		
## Baseline.histological.Grading12	0.999		
## Baseline.histological.Grading13	0.999		
## Baseline.histological.Grading14	0.999		
## Baseline.histological.Grading15	0.999		
## Baseline.histological.Grading16	0.998		
## Baselinehistological.stagingFew Septa	0.999		
## Baselinehistological.stagingMany Septa	0.999		

```

## Baselinehistological.stagingPortal Fibrosis    0.999
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 1.790e+03  on 1384  degrees of freedom
## Residual deviance: 6.632e-07  on 1341  degrees of freedom
## AIC: 88
##
## Number of Fisher Scoring iterations: 25

## Now calculate the overall "Pseudo R-squared" and its p-value
ll.null <- logistic$null.deviance/-2
ll.proposed <- logistic$deviance/-2
## McFadden's Pseudo R^2 = [ LL(Null) - LL(Proposed) ] / LL(Null)
(ll.null - ll.proposed) / ll.null

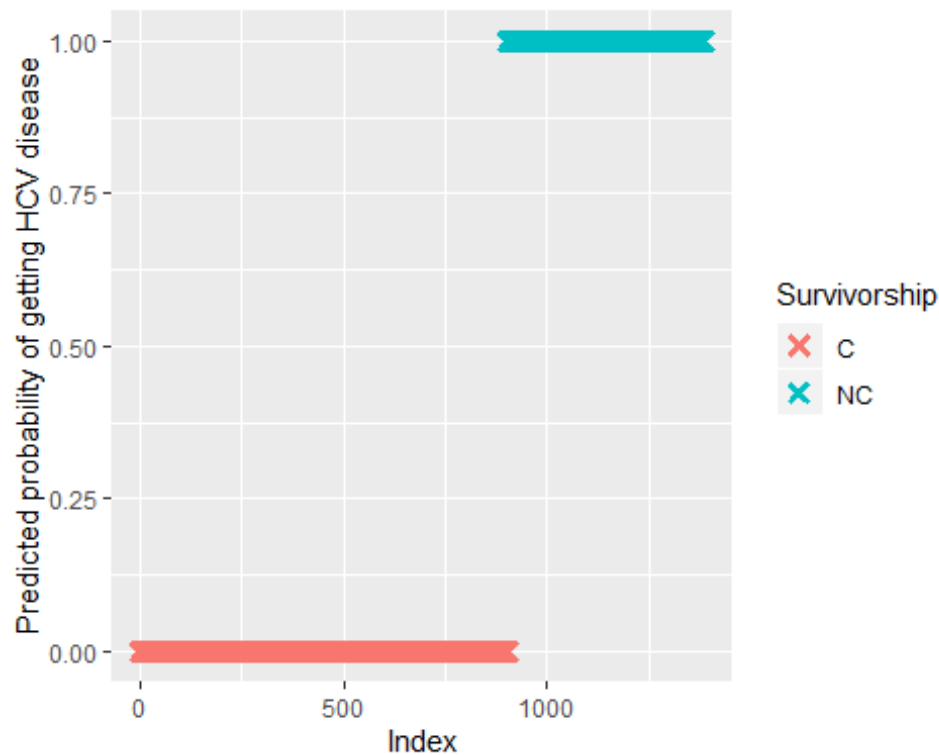
## [1] 1

## The p-value for the R^2
1 - pchisq(2*(ll.proposed - ll.null), df=(length(logistic$coefficients)-1))

## [1] 0

## now we can plot the data
predicted.data <-
data.frame(probability.of.Survivorship=logistic$fitted.values, Survivorship=da
ta$Survivorship)
predicted.data <-
predicted.data[order(predicted.data$probability.of.Survivorship,
decreasing=FALSE),]
predicted.data$rank <- 1:nrow(predicted.data)
## Lastly, we can plot the predicted probabilities for each sample having
## heart disease and color by whether or not they actually had heart disease
ggplot(data=predicted.data, aes(x=rank, y=probability.of.Survivorship)) +
  geom_point(aes(color=Survivorship), alpha=1, shape=4, stroke=2) +
  xlab("Index") +
  ylab("Predicted probability of getting HCV disease")

```



```
# Few packages for confusion matrix. Lets look at them one by one
#install.packages("regclass",
  lib="/Library/Frameworks/R.framework/Versions/3.5/Resources/Library")
library(regclass)

## Loading required package: bestglm
## Loading required package: leaps
## Loading required package: VGAM
## Loading required package: stats4
## Loading required package: splines
## Loading required package: rpart
## Loading required package: randomForest
## randomForest 4.6-14
## Type rfNews() to see new features/changes/bug fixes.
##
## Attaching package: 'randomForest'
##
## The following object is masked from 'package:ggplot2':
##
##     margin
```

```

## The following object is masked from 'package:dplyr':
##
##      combine

## Important regclass change from 1.3:
## All functions that had a . in the name now have an _
## all.correlations -> all_correlations, cor.demo -> cor_demo, etc.

confusion_matrix(logistic)

##           Predicted C Predicted NC Total
## Actual C           903           0   903
## Actual NC           0           482   482
## Total             903           482  1385

#install.packages("caret",
#lib="/Library/Frameworks/R.framework/Versions/3.5/Resources/Library")
library(caret)

## Loading required package: lattice

##
## Attaching package: 'lattice'

## The following object is masked from 'package:regclass':
##
##      qq

##
## Attaching package: 'caret'

## The following object is masked from 'package:VGAM':
##
##      predictors

pdata <- predict(logistic,newdata=data,type="response" )
pdata

##           1           2           3           4           5
## 2.220446e-16 2.220446e-16 1.000000e+00 1.000000e+00 2.220446e-16
##           6           7           8           9          10
## 2.220446e-16 2.220446e-16 2.220446e-16 2.220446e-16 2.220446e-16
##          11          12          13          14          15
## 1.000000e+00 2.220446e-16 2.220446e-16 2.220446e-16 1.000000e+00
##          16          17          18          19          20
## 1.000000e+00 2.220446e-16 2.220446e-16 1.000000e+00 1.000000e+00
##          21          22          23          24          25
## 1.000000e+00 2.220446e-16 2.220446e-16 2.220446e-16 2.220446e-16
##          26          27          28          29          30
## 2.220446e-16 1.000000e+00 1.000000e+00 2.220446e-16 2.220446e-16
##          31          32          33          34          35
## 2.220446e-16 2.220446e-16 1.000000e+00 2.220446e-16 1.000000e+00

```

##	36	37	38	39	40
##	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	41	42	43	44	45
##	1.000000e+00	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16
##	46	47	48	49	50
##	2.220446e-16	2.220446e-16	1.000000e+00	1.000000e+00	1.000000e+00
##	51	52	53	54	55
##	2.220446e-16	2.220446e-16	1.000000e+00	1.000000e+00	2.220446e-16
##	56	57	58	59	60
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00
##	61	62	63	64	65
##	2.220446e-16	2.220446e-16	1.000000e+00	1.000000e+00	1.000000e+00
##	66	67	68	69	70
##	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00	1.000000e+00
##	71	72	73	74	75
##	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00	1.000000e+00
##	76	77	78	79	80
##	2.220446e-16	2.220446e-16	1.000000e+00	1.000000e+00	2.220446e-16
##	81	82	83	84	85
##	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16	1.000000e+00
##	86	87	88	89	90
##	2.220446e-16	1.000000e+00	1.000000e+00	1.000000e+00	2.220446e-16
##	91	92	93	94	95
##	2.220446e-16	1.000000e+00	2.220446e-16	1.000000e+00	1.000000e+00
##	96	97	98	99	100
##	2.220446e-16	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16
##	101	102	103	104	105
##	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	106	107	108	109	110
##	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16
##	111	112	113	114	115
##	2.220446e-16	1.000000e+00	1.000000e+00	1.000000e+00	1.000000e+00
##	116	117	118	119	120
##	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16	2.220446e-16
##	121	122	123	124	125
##	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16	2.220446e-16
##	126	127	128	129	130
##	2.220446e-16	1.000000e+00	2.220446e-16	1.000000e+00	2.220446e-16
##	131	132	133	134	135
##	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	136	137	138	139	140
##	1.000000e+00	1.000000e+00	1.000000e+00	1.000000e+00	2.220446e-16
##	141	142	143	144	145
##	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16	2.220446e-16
##	146	147	148	149	150
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	151	152	153	154	155
##	2.220446e-16	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16
##	156	157	158	159	160
##	1.000000e+00	1.000000e+00	2.220446e-16	1.000000e+00	2.220446e-16

##	161	162	163	164	165
##	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16
##	166	167	168	169	170
##	1.000000e+00	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16
##	171	172	173	174	175
##	2.220446e-16	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16
##	176	177	178	179	180
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	181	182	183	184	185
##	2.220446e-16	2.220446e-16	1.000000e+00	1.000000e+00	2.220446e-16
##	186	187	188	189	190
##	2.220446e-16	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16
##	191	192	193	194	195
##	2.220446e-16	1.000000e+00	2.220446e-16	1.000000e+00	2.220446e-16
##	196	197	198	199	200
##	1.000000e+00	4.624073e-09	2.220446e-16	2.220446e-16	1.000000e+00
##	201	202	203	204	205
##	1.000000e+00	2.220446e-16	1.000000e+00	2.220446e-16	2.220446e-16
##	206	207	208	209	210
##	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00	1.000000e+00
##	211	212	213	214	215
##	2.220446e-16	1.000000e+00	1.000000e+00	2.220446e-16	2.220446e-16
##	216	217	218	219	220
##	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16
##	221	222	223	224	225
##	2.220446e-16	2.220446e-16	1.000000e+00	1.000000e+00	2.220446e-16
##	226	227	228	229	230
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00
##	231	232	233	234	235
##	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16
##	236	237	238	239	240
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	241	242	243	244	245
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	246	247	248	249	250
##	2.220446e-16	1.000000e+00	2.220446e-16	1.000000e+00	2.220446e-16
##	251	252	253	254	255
##	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	256	257	258	259	260
##	2.220446e-16	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16
##	261	262	263	264	265
##	1.000000e+00	1.000000e+00	1.000000e+00	2.220446e-16	2.220446e-16
##	266	267	268	269	270
##	2.220446e-16	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16
##	271	272	273	274	275
##	1.000000e+00	1.000000e+00	1.000000e+00	2.220446e-16	1.000000e+00
##	276	277	278	279	280
##	1.000000e+00	1.000000e+00	2.220446e-16	2.220446e-16	1.000000e+00
##	281	282	283	284	285
##	1.226682e-12	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16

##	286	287	288	289	290
##	2.220446e-16	2.220446e-16	1.000000e+00	1.000000e+00	1.000000e+00
##	291	292	293	294	295
##	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00	1.000000e+00
##	296	297	298	299	300
##	1.400537e-08	1.000000e+00	2.220446e-16	2.220446e-16	1.000000e+00
##	301	302	303	304	305
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	306	307	308	309	310
##	1.000000e+00	1.000000e+00	2.220446e-16	1.000000e+00	1.000000e+00
##	311	312	313	314	315
##	1.000000e+00	1.000000e+00	1.000000e+00	2.220446e-16	1.000000e+00
##	316	317	318	319	320
##	2.220446e-16	1.000000e+00	2.220446e-16	2.220446e-16	1.000000e+00
##	321	322	323	324	325
##	1.000000e+00	2.220446e-16	2.220446e-16	1.062546e-13	2.220446e-16
##	326	327	328	329	330
##	1.000000e+00	1.000000e+00	1.000000e+00	2.220446e-16	1.000000e+00
##	331	332	333	334	335
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	336	337	338	339	340
##	1.000000e+00	1.000000e+00	2.144440e-11	1.000000e+00	2.220446e-16
##	341	342	343	344	345
##	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16	2.220446e-16
##	346	347	348	349	350
##	1.096984e-10	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00
##	351	352	353	354	355
##	1.000000e+00	1.000000e+00	2.220446e-16	1.000000e+00	2.220446e-16
##	356	357	358	359	360
##	2.220446e-16	1.000000e+00	1.000000e+00	2.220446e-16	2.220446e-16
##	361	362	363	364	365
##	2.220446e-16	1.000000e+00	2.220446e-16	1.000000e+00	1.000000e+00
##	366	367	368	369	370
##	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16
##	371	372	373	374	375
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	376	377	378	379	380
##	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16
##	381	382	383	384	385
##	2.220446e-16	2.220446e-16	1.000000e+00	1.000000e+00	2.220446e-16
##	386	387	388	389	390
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	391	392	393	394	395
##	1.000000e+00	1.000000e+00	1.000000e+00	2.220446e-16	2.220446e-16
##	396	397	398	399	400
##	2.220446e-16	1.000000e+00	1.000000e+00	2.220446e-16	2.220446e-16
##	401	402	403	404	405
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	406	407	408	409	410
##	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00	1.000000e+00

##	411	412	413	414	415
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	416	417	418	419	420
##	1.000000e+00	1.000000e+00	1.000000e+00	2.220446e-16	1.000000e+00
##	421	422	423	424	425
##	1.000000e+00	1.000000e+00	2.220446e-16	1.000000e+00	1.000000e+00
##	426	427	428	429	430
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	431	432	433	434	435
##	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	436	437	438	439	440
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00
##	441	442	443	444	445
##	2.220446e-16	1.000000e+00	2.220446e-16	1.000000e+00	2.220446e-16
##	446	447	448	449	450
##	2.220446e-16	1.000000e+00	1.000000e+00	1.000000e+00	1.000000e+00
##	451	452	453	454	455
##	1.000000e+00	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16
##	456	457	458	459	460
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	461	462	463	464	465
##	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00	1.000000e+00
##	466	467	468	469	470
##	2.220446e-16	1.000000e+00	1.000000e+00	2.220446e-16	1.000000e+00
##	471	472	473	474	475
##	2.220446e-16	2.553865e-10	1.000000e+00	1.000000e+00	2.220446e-16
##	476	477	478	479	480
##	1.000000e+00	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16
##	481	482	483	484	485
##	2.220446e-16	1.000000e+00	1.000000e+00	2.220446e-16	1.000000e+00
##	486	487	488	489	490
##	1.000000e+00	1.000000e+00	1.000000e+00	1.000000e+00	2.220446e-16
##	491	492	493	494	495
##	2.220446e-16	1.000000e+00	2.220446e-16	6.696274e-09	2.220446e-16
##	496	497	498	499	500
##	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16	1.000000e+00
##	501	502	503	504	505
##	1.000000e+00	1.000000e+00	1.422738e-08	2.220446e-16	1.000000e+00
##	506	507	508	509	510
##	1.000000e+00	2.220446e-16	1.000000e+00	1.000000e+00	1.000000e+00
##	511	512	513	514	515
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00
##	516	517	518	519	520
##	1.000000e+00	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16
##	521	522	523	524	525
##	2.858549e-09	1.000000e+00	1.000000e+00	1.000000e+00	2.220446e-16
##	526	527	528	529	530
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	531	532	533	534	535
##	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16

##	536	537	538	539	540
##	2.220446e-16	1.000000e+00	2.220446e-16	1.000000e+00	1.000000e+00
##	541	542	543	544	545
##	1.000000e+00	1.000000e+00	2.220446e-16	1.000000e+00	2.220446e-16
##	546	547	548	549	550
##	2.220446e-16	1.000000e+00	1.000000e+00	2.220446e-16	2.220446e-16
##	551	552	553	554	555
##	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16
##	556	557	558	559	560
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	561	562	563	564	565
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	566	567	568	569	570
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	571	572	573	574	575
##	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16
##	576	577	578	579	580
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00
##	581	582	583	584	585
##	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00
##	586	587	588	589	590
##	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16
##	591	592	593	594	595
##	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16
##	596	597	598	599	600
##	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16	2.220446e-16
##	601	602	603	604	605
##	2.220446e-16	1.000000e+00	2.220446e-16	1.000000e+00	2.220446e-16
##	606	607	608	609	610
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	611	612	613	614	615
##	2.220446e-16	1.000000e+00	2.220446e-16	2.220446e-16	1.000000e+00
##	616	617	618	619	620
##	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00
##	621	622	623	624	625
##	2.220446e-16	1.000000e+00	1.000000e+00	2.220446e-16	5.933679e-09
##	626	627	628	629	630
##	1.000000e+00	2.220446e-16	2.220446e-16	1.000000e+00	1.000000e+00
##	631	632	633	634	635
##	3.887578e-09	2.220446e-16	2.220446e-16	1.000000e+00	1.000000e+00
##	636	637	638	639	640
##	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	641	642	643	644	645
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	646	647	648	649	650
##	2.220446e-16	1.000000e+00	1.000000e+00	2.220446e-16	1.000000e+00
##	651	652	653	654	655
##	1.000000e+00	1.000000e+00	1.000000e+00	2.220446e-16	2.220446e-16
##	656	657	658	659	660
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00

##	661	662	663	664	665
##	1.000000e+00	1.000000e+00	1.000000e+00	2.220446e-16	2.220446e-16
##	666	667	668	669	670
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00
##	671	672	673	674	675
##	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16	2.220446e-16
##	676	677	678	679	680
##	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16	1.000000e+00
##	681	682	683	684	685
##	1.000000e+00	1.000000e+00	2.220446e-16	1.000000e+00	2.220446e-16
##	686	687	688	689	690
##	1.000000e+00	2.220446e-16	1.000000e+00	1.000000e+00	1.000000e+00
##	691	692	693	694	695
##	2.220446e-16	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16
##	696	697	698	699	700
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	701	702	703	704	705
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00
##	706	707	708	709	710
##	1.000000e+00	1.000000e+00	2.220446e-16	1.000000e+00	2.220446e-16
##	711	712	713	714	715
##	2.220446e-16	1.000000e+00	2.220446e-16	1.000000e+00	2.220446e-16
##	716	717	718	719	720
##	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	721	722	723	724	725
##	2.220446e-16	2.220446e-16	1.000000e+00	1.350791e-08	1.000000e+00
##	726	727	728	729	730
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00
##	731	732	733	734	735
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	736	737	738	739	740
##	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16	2.220446e-16
##	741	742	743	744	745
##	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16	1.000000e+00
##	746	747	748	749	750
##	2.220446e-16	1.124887e-08	2.220446e-16	2.220446e-16	2.220446e-16
##	751	752	753	754	755
##	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16	1.000000e+00
##	756	757	758	759	760
##	1.000000e+00	3.704052e-09	1.000000e+00	2.220446e-16	1.000000e+00
##	761	762	763	764	765
##	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	766	767	768	769	770
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	771	772	773	774	775
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	776	777	778	779	780
##	5.595202e-10	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16
##	781	782	783	784	785
##	2.220446e-16	1.000000e+00	1.000000e+00	1.000000e+00	1.000000e+00

##	786	787	788	789	790
##	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00
##	791	792	793	794	795
##	1.000000e+00	1.000000e+00	2.220446e-16	2.220446e-16	1.000000e+00
##	796	797	798	799	800
##	2.220446e-16	1.000000e+00	1.034868e-10	1.000000e+00	1.000000e+00
##	801	802	803	804	805
##	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	806	807	808	809	810
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	811	812	813	814	815
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	816	817	818	819	820
##	1.000000e+00	7.154129e-09	1.000000e+00	2.220446e-16	2.220446e-16
##	821	822	823	824	825
##	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00
##	826	827	828	829	830
##	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16	2.220446e-16
##	831	832	833	834	835
##	2.220446e-16	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16
##	836	837	838	839	840
##	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00	2.001750e-08
##	841	842	843	844	845
##	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16	1.000000e+00
##	846	847	848	849	850
##	2.220446e-16	1.000000e+00	2.220446e-16	1.000000e+00	2.220446e-16
##	851	852	853	854	855
##	2.220446e-16	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16
##	856	857	858	859	860
##	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	861	862	863	864	865
##	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16	2.220446e-16
##	866	867	868	869	870
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00
##	871	872	873	874	875
##	2.220446e-16	1.000000e+00	1.000000e+00	1.000000e+00	2.220446e-16
##	876	877	878	879	880
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	881	882	883	884	885
##	2.220446e-16	2.220446e-16	1.000000e+00	1.000000e+00	2.220446e-16
##	886	887	888	889	890
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00
##	891	892	893	894	895
##	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00	1.000000e+00
##	896	897	898	899	900
##	1.000000e+00	2.220446e-16	1.000000e+00	2.220446e-16	2.220446e-16
##	901	902	903	904	905
##	1.000000e+00	1.000000e+00	2.220446e-16	2.220446e-16	1.000000e+00
##	906	907	908	909	910
##	1.000000e+00	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16

##	911	912	913	914	915
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	916	917	918	919	920
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	921	922	923	924	925
##	1.000000e+00	1.239056e-08	1.000000e+00	1.466301e-09	2.220446e-16
##	926	927	928	929	930
##	1.000000e+00	2.220446e-16	1.000000e+00	1.000000e+00	1.000000e+00
##	931	932	933	934	935
##	2.220446e-16	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16
##	936	937	938	939	940
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00
##	941	942	943	944	945
##	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	946	947	948	949	950
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	951	952	953	954	955
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	956	957	958	959	960
##	2.220446e-16	2.220446e-16	2.220446e-16	8.654866e-09	1.000000e+00
##	961	962	963	964	965
##	1.000000e+00	1.000000e+00	2.220446e-16	2.220446e-16	1.000000e+00
##	966	967	968	969	970
##	1.000000e+00	2.220446e-16	1.000000e+00	1.000000e+00	1.000000e+00
##	971	972	973	974	975
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00
##	976	977	978	979	980
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00
##	981	982	983	984	985
##	2.220446e-16	1.000000e+00	2.220446e-16	1.000000e+00	1.000000e+00
##	986	987	988	989	990
##	1.000000e+00	2.220446e-16	1.000000e+00	1.000000e+00	2.220446e-16
##	991	992	993	994	995
##	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16
##	996	997	998	999	1000
##	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00	1.000000e+00
##	1001	1002	1003	1004	1005
##	1.000000e+00	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16
##	1006	1007	1008	1009	1010
##	2.220446e-16	1.000000e+00	2.220446e-16	2.220446e-16	1.000000e+00
##	1011	1012	1013	1014	1015
##	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16	1.000000e+00
##	1016	1017	1018	1019	1020
##	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00	1.000000e+00
##	1021	1022	1023	1024	1025
##	1.000000e+00	2.220446e-16	1.000000e+00	2.220446e-16	2.220446e-16
##	1026	1027	1028	1029	1030
##	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00
##	1031	1032	1033	1034	1035
##	2.220446e-16	1.000000e+00	2.220446e-16	1.000000e+00	2.220446e-16

##	1036	1037	1038	1039	1040
##	2.220446e-16	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16
##	1041	1042	1043	1044	1045
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	1046	1047	1048	1049	1050
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00
##	1051	1052	1053	1054	1055
##	1.000000e+00	2.220446e-16	1.000000e+00	1.000000e+00	2.220446e-16
##	1056	1057	1058	1059	1060
##	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	1061	1062	1063	1064	1065
##	2.220446e-16	1.000000e+00	1.000000e+00	1.000000e+00	2.220446e-16
##	1066	1067	1068	1069	1070
##	1.000000e+00	2.220446e-16	1.000000e+00	2.220446e-16	2.220446e-16
##	1071	1072	1073	1074	1075
##	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16	3.639874e-09
##	1076	1077	1078	1079	1080
##	2.220446e-16	1.000000e+00	2.220446e-16	1.000000e+00	1.000000e+00
##	1081	1082	1083	1084	1085
##	1.000000e+00	2.220446e-16	1.000000e+00	2.220446e-16	1.000000e+00
##	1086	1087	1088	1089	1090
##	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	1091	1092	1093	1094	1095
##	2.220446e-16	1.000000e+00	1.000000e+00	1.000000e+00	1.000000e+00
##	1096	1097	1098	1099	1100
##	2.220446e-16	2.220446e-16	1.000000e+00	1.000000e+00	2.220446e-16
##	1101	1102	1103	1104	1105
##	2.220446e-16	1.000000e+00	2.220446e-16	1.000000e+00	1.000000e+00
##	1106	1107	1108	1109	1110
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16
##	1111	1112	1113	1114	1115
##	1.000000e+00	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16
##	1116	1117	1118	1119	1120
##	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16
##	1121	1122	1123	1124	1125
##	1.000000e+00	1.000000e+00	1.000000e+00	1.000000e+00	1.000000e+00
##	1126	1127	1128	1129	1130
##	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16	2.220446e-16
##	1131	1132	1133	1134	1135
##	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16	1.000000e+00
##	1136	1137	1138	1139	1140
##	1.000000e+00	1.000000e+00	1.000000e+00	2.220446e-16	1.000000e+00
##	1141	1142	1143	1144	1145
##	2.220446e-16	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16
##	1146	1147	1148	1149	1150
##	2.220446e-16	2.220446e-16	1.000000e+00	1.237843e-08	1.000000e+00
##	1151	1152	1153	1154	1155
##	2.220446e-16	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16
##	1156	1157	1158	1159	1160
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00

##	1161	1162	1163	1164	1165
##	1.000000e+00	2.220446e-16	2.220446e-16	1.000000e+00	1.000000e+00
##	1166	1167	1168	1169	1170
##	1.000000e+00	1.000000e+00	2.220446e-16	1.000000e+00	2.220446e-16
##	1171	1172	1173	1174	1175
##	2.220446e-16	2.220446e-16	1.000000e+00	1.000000e+00	2.220446e-16
##	1176	1177	1178	1179	1180
##	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00	1.000000e+00
##	1181	1182	1183	1184	1185
##	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00	1.000000e+00
##	1186	1187	1188	1189	1190
##	1.000000e+00	1.000000e+00	1.000000e+00	1.000000e+00	1.000000e+00
##	1191	1192	1193	1194	1195
##	1.000000e+00	2.220446e-16	2.220446e-16	2.356545e-13	2.220446e-16
##	1196	1197	1198	1199	1200
##	2.220446e-16	1.000000e+00	2.220446e-16	4.090227e-10	2.220446e-16
##	1201	1202	1203	1204	1205
##	2.220446e-16	1.000000e+00	1.000000e+00	1.000000e+00	1.000000e+00
##	1206	1207	1208	1209	1210
##	2.220446e-16	1.000000e+00	1.000000e+00	2.220446e-16	2.220446e-16
##	1211	1212	1213	1214	1215
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	3.378042e-13
##	1216	1217	1218	1219	1220
##	2.220446e-16	2.220446e-16	1.000000e+00	1.000000e+00	1.000000e+00
##	1221	1222	1223	1224	1225
##	2.220446e-16	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16
##	1226	1227	1228	1229	1230
##	1.000000e+00	1.000000e+00	1.000000e+00	9.498026e-09	2.220446e-16
##	1231	1232	1233	1234	1235
##	1.000000e+00	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16
##	1236	1237	1238	1239	1240
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00
##	1241	1242	1243	1244	1245
##	2.220446e-16	1.000000e+00	1.000000e+00	2.220446e-16	2.220446e-16
##	1246	1247	1248	1249	1250
##	2.220446e-16	2.220446e-16	2.220446e-16	2.220446e-16	1.000000e+00
##	1251	1252	1253	1254	1255
##	2.220446e-16	1.000000e+00	2.220446e-16	1.000000e+00	2.220446e-16
##	1256	1257	1258	1259	1260
##	1.000000e+00	1.000000e+00	2.220446e-16	2.220446e-16	2.220446e-16
##	1261	1262	1263	1264	1265
##	2.220446e-16	1.000000e+00	1.000000e+00	2.220446e-16	2.220446e-16
##	1266	1267	1268	1269	1270
##	2.220446e-16	2.220446e-16	1.000000e+00	2.220446e-16	1.000000e+00
##	1271	1272	1273	1274	1275
##	2.220446e-16	2.220446e-16	1.000000e+00	1.000000e+00	2.220446e-16
##	1276	1277	1278	1279	1280
##	1.000000e+00	1.000000e+00	1.000000e+00	2.220446e-16	2.220446e-16
##	1281	1282	1283	1284	1285
##	1.000000e+00	1.000000e+00	1.000000e+00	1.000000e+00	1.000000e+00

```
##          1286          1287          1288          1289          1290
## 2.220446e-16 1.000000e+00 2.220446e-16 2.220446e-16 1.000000e+00
##          1291          1292          1293          1294          1295
## 2.220446e-16 2.220446e-16 2.220446e-16 2.220446e-16 2.220446e-16
##          1296          1297          1298          1299          1300
## 2.220446e-16 2.220446e-16 2.220446e-16 2.220446e-16 1.000000e+00
##          1301          1302          1303          1304          1305
## 1.000000e+00 2.220446e-16 2.220446e-16 1.000000e+00 2.220446e-16
##          1306          1307          1308          1309          1310
## 1.000000e+00 2.220446e-16 2.220446e-16 1.000000e+00 2.220446e-16
##          1311          1312          1313          1314          1315
## 1.000000e+00 2.220446e-16 2.220446e-16 2.220446e-16 2.220446e-16
##          1316          1317          1318          1319          1320
## 2.220446e-16 2.220446e-16 2.220446e-16 1.000000e+00 2.220446e-16
##          1321          1322          1323          1324          1325
## 1.000000e+00 2.220446e-16 1.000000e+00 2.220446e-16 2.220446e-16
##          1326          1327          1328          1329          1330
## 1.000000e+00 2.220446e-16 1.000000e+00 1.000000e+00 2.220446e-16
##          1331          1332          1333          1334          1335
## 2.220446e-16 2.220446e-16 2.220446e-16 5.198558e-12 2.220446e-16
##          1336          1337          1338          1339          1340
## 2.220446e-16 1.135848e-08 2.220446e-16 1.000000e+00 2.220446e-16
##          1341          1342          1343          1344          1345
## 1.000000e+00 2.220446e-16 2.220446e-16 1.000000e+00 1.000000e+00
##          1346          1347          1348          1349          1350
## 2.220446e-16 2.220446e-16 2.220446e-16 2.220446e-16 2.220446e-16
##          1351          1352          1353          1354          1355
## 2.220446e-16 2.220446e-16 1.000000e+00 1.000000e+00 2.220446e-16
##          1356          1357          1358          1359          1360
## 2.220446e-16 2.220446e-16 2.220446e-16 1.000000e+00 2.220446e-16
##          1361          1362          1363          1364          1365
## 2.220446e-16 1.000000e+00 2.220446e-16 1.000000e+00 1.000000e+00
##          1366          1367          1368          1369          1370
## 2.220446e-16 2.220446e-16 2.220446e-16 2.220446e-16 2.220446e-16
##          1371          1372          1373          1374          1375
## 2.220446e-16 2.220446e-16 2.220446e-16 2.220446e-16 2.220446e-16
##          1376          1377          1378          1379          1380
## 2.220446e-16 2.220446e-16 1.000000e+00 1.000000e+00 1.000000e+00
##          1381          1382          1383          1384          1385
## 2.220446e-16 2.220446e-16 1.932294e-10 2.220446e-16 2.220446e-16
```

```
data$Survivorship
```

```
##      [1] C  C  NC NC C  C  C  C  C  C  NC C  C  C  NC NC C  C  NC NC NC C  C
##      [24] C  C  C  NC NC C  C  C  C  NC C  NC NC C  C  C  C  NC C  C  NC C  C
##      [47] C  NC NC NC C  C  NC NC C  C  C  C  C  NC C  C  NC NC NC C  C  C
##      [70] NC C  C  C  NC NC C  C  NC NC C  C  C  NC C  NC C  NC NC NC C  C
##      [93] C  NC NC C  NC C  C  C  NC C  C  C  C  C  C  C  NC C  C  NC NC NC
```

NC																								
##	[116]	C	C	NC	C	C	C	C	NC	C	C	C	NC	C	NC	C	NC	C	C	C	C	NC	NC	
NC																								
##	[139]	NC	C	C	C	NC	C	C	C	C	C	C	C	C	NC	C	C	C	NC	NC	C	NC	C	C
##	[162]	C	C	NC	C	NC	NC	C	C	C	C	NC	C	C	C	C	C	C	C	C	C	C	NC	
NC																								
##	[185]	C	C	NC	C	C	C	C	NC	C	NC	C	NC	C	C	C	NC	NC	C	NC	C	C	C	C
##	[208]	C	NC	NC	C	NC	NC	C	C	C	C	C	NC	C	C	C	NC	NC	C	C	C	C	C	
NC																								
##	[231]	C	C	C	NC	C	C	C	C	C	C	C	C	C	C	C	C	NC	C	NC	C	NC	C	C
##	[254]	C	C	C	NC	C	C	C	NC	NC	NC	C	C	C	NC	C	C	C	NC	NC	NC	C	NC	
NC																								
##	[277]	NC	C	C	NC	C	C	C	NC	C	C	C	NC	NC	NC	C	C	C	NC	NC	C	NC	C	C
##	[300]	NC	C	C	C	C	C	NC	NC	C	NC	NC	NC	NC	NC	C	NC	C	NC	C	C	NC	NC	C
##	[323]	C	C	C	NC	NC	NC	C	NC	C	C	C	C	C	NC	NC	C	NC	C	C	C	NC	C	C
##	[346]	C	C	C	C	NC	NC	NC	C	NC	C	C	NC	NC	C	C	C	NC	C	NC	NC	C	C	C
##	[369]	NC	C	C	C	C	C	C	C	C	C	NC	C	C	C	NC	NC	C	C	C	C	C	C	
NC																								
##	[392]	NC	NC	C	C	C	NC	NC	C	C	C	C	C	C	C	C	C	C	NC	NC	C	C	C	C
##	[415]	C	NC	NC	NC	C	NC	NC	NC	C	NC	NC	C	C	C	C	C	NC	C	C	C	C	C	C
##	[438]	C	C	NC	C	NC	C	NC	C	C	NC	NC	NC	NC	NC	NC	C	C	C	C	C	C	C	C
##	[461]	C	C	C	NC	NC	C	NC	NC	C	NC	C	C	NC	NC	C	NC	C	C	NC	C	C	NC	
NC																								
##	[484]	C	NC	NC	NC	NC	NC	C	C	NC	C	C	C	C	C	NC	C	NC	NC	NC	C	C	NC	
NC																								
##	[507]	C	NC	NC	NC	C	C	C	C	NC	NC	NC	C	C	C	C	NC	NC	NC	C	C	C	C	C
##	[530]	C	C	C	C	NC	C	C	NC	C	NC	NC	NC	NC	C	NC	C	C	NC	NC	C	C	C	C
##	[553]	C	NC	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	NC	C
##	[576]	C	C	C	C	NC	NC	C	C	C	NC	C	C	C	NC	C	C	C	C	NC	C	C	C	
NC																								
##	[599]	C	C	C	NC	C	NC	C	C	C	C	C	C	C	NC	C	C	NC	NC	C	C	C	NC	C
##	[622]	NC	NC	C	C	NC	C	C	NC															

```

NC
## [967] C NC NC NC C C C C NC C C C C NC C NC C NC NC NC C NC
NC
## [990] C C C C NC C C C C NC NC NC NC C C C C NC C C NC C C
## [1013] NC C NC C C C C NC NC NC C NC C C C NC C C C NC C NC C NC C
## [1036] C NC C C C C C C C C C C C C NC NC C NC NC C NC C C
## [1059] C C C NC NC NC C NC C NC C C NC C C C C C NC C NC NC
NC
## [1082] C NC C NC NC C C C C C NC NC NC NC C C NC NC C C NC C
NC
## [1105] NC C C C C C NC C C NC C C C C NC C NC NC NC NC NC C C
## [1128] NC C C C C NC C NC NC NC NC C NC C NC C C C C NC C
NC
## [1151] C NC C C C C C C C NC NC C C NC NC NC NC C NC C C C
NC
## [1174] NC C C C C NC NC C C C NC NC NC NC NC NC NC NC C C C C C
## [1197] NC C C C C NC NC NC NC C NC NC C C C C C C C C C NC
NC
## [1220] NC C NC C C C NC NC NC C C NC NC C C C C C C C NC C
NC
## [1243] NC C C C C C C NC C NC C NC C NC NC C C C C NC NC C C
## [1266] C C NC C NC C C NC NC C NC NC NC C C NC NC NC NC NC C NC C
## [1289] C NC C C C C C C C C C NC NC C C NC C NC C C NC C
NC
## [1312] C C C C C C C NC C NC C NC C C NC C NC NC C C C C C
## [1335] C C C C NC C NC C C NC NC C C C C C C C C NC NC C C C
## [1358] C NC C C NC C NC NC C C C C C C C C C C C C C NC NC
NC
## [1381] C C C C C
## Levels: C NC

```

```

#pdataF <- as.factor(ifelse(test=as.numeric(pdata>0.5) == 0, yes="Healthy",
no="Unhealthy"))

```

```

#install.packages("e1071",
lib="/Library/Frameworks/R.framework/Versions/3.5/Resources/Library")

```

```

library(e1071)

```

```

#confusionMatrix(pdataF, data$Survivorship)

```

```

#install.packages("pROC",

```

```

lib="/Library/Frameworks/R.framework/Versions/3.5/Resources/Library")

```

```

library(pROC)

```

```

## Type 'citation("pROC")' for a citation.

```

```

##

```

```

## Attaching package: 'pROC'

```

```

## The following objects are masked from 'package:stats':

```

```

##

```

```

## cov, smooth, var

```

```

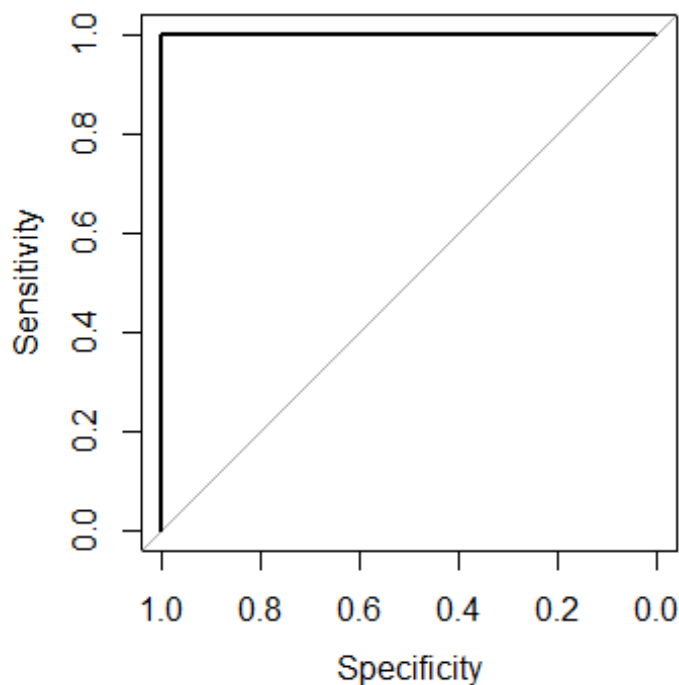
roc(data$Survivorship,logistic$fitted.values,plot=TRUE)

```

```
## Setting levels: control = C, case = NC
## Setting direction: controls < cases
##
## Call:
## roc.default(response = data$Survivorship, predictor =
logistic$fitted.values, plot = TRUE)
##
## Data: logistic$fitted.values in 903 controls (data$Survivorship C) < 482
cases (data$Survivorship NC).
## Area under the curve: 1

par(pty = "s")
roc(data$Survivorship, logistic$fitted.values, plot=TRUE)

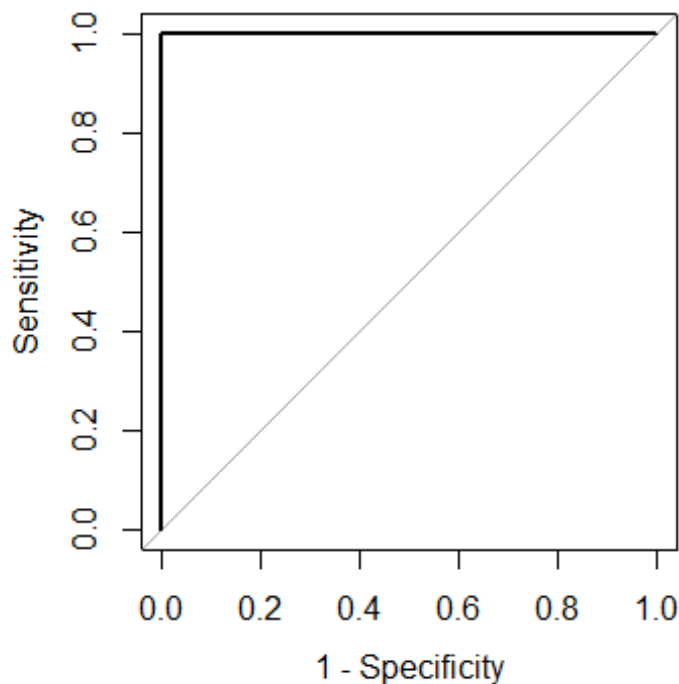
## Setting levels: control = C, case = NC
## Setting direction: controls < cases
```



```
##
## Call:
## roc.default(response = data$Survivorship, predictor =
logistic$fitted.values, plot = TRUE)
##
## Data: logistic$fitted.values in 903 controls (data$Survivorship C) < 482
cases (data$Survivorship NC).
## Area under the curve: 1
```

```
## NOTE: By default, roc() uses specificity on the x-axis and the values
range
## from 1 to 0. This makes the graph look like what we would expect, but the
## x-axis itself might induce a headache. To use 1-specificity (i.e. the
## False Positive Rate) on the x-axis, set "legacy.axes" to TRUE.
roc(data$Survivorship, logistic$fitted.values, plot=TRUE, legacy.axes=TRUE)

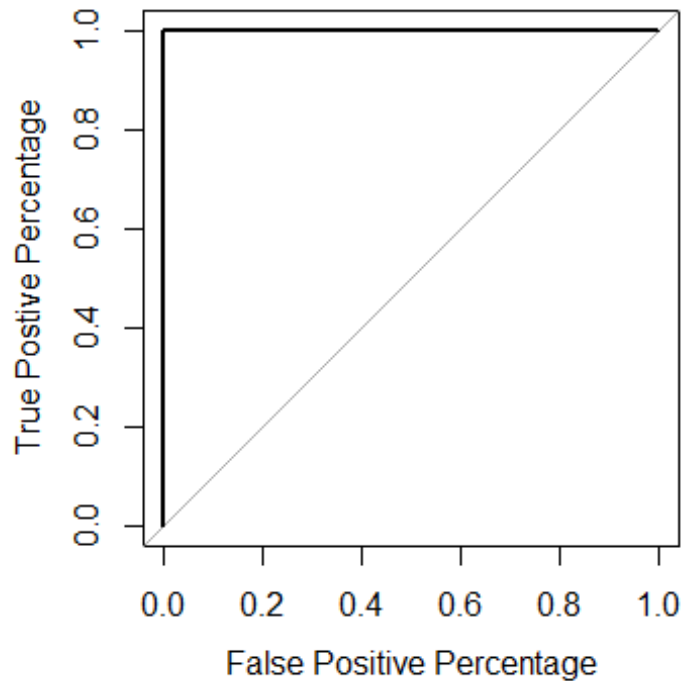
## Setting levels: control = C, case = NC
## Setting direction: controls < cases
```



```
##
## Call:
## roc.default(response = data$Survivorship, predictor =
logistic$fitted.values, plot = TRUE, legacy.axes = TRUE)
##
## Data: logistic$fitted.values in 903 controls (data$Survivorship C) < 482
cases (data$Survivorship NC).
## Area under the curve: 1

roc(data$Survivorship, logistic$fitted.values, plot=TRUE, legacy.axes=TRUE,
xlab="False Positive Percentage", ylab="True Positive Percentage")

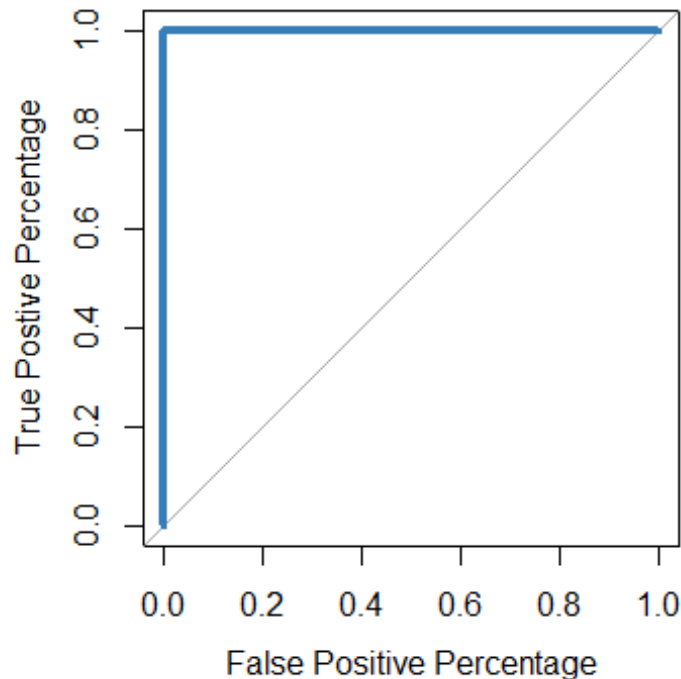
## Setting levels: control = C, case = NC
## Setting direction: controls < cases
```



```
##
## Call:
## roc.default(response = data$Survivorship, predictor =
logistic$fitted.values,      plot = TRUE, legacy.axes = TRUE, xlab = "False
Positive Percentage",      ylab = "True Postive Percentage")
##
## Data: logistic$fitted.values in 903 controls (data$Survivorship C) < 482
cases (data$Survivorship NC).
## Area under the curve: 1

roc(data$Survivorship,logistic$fitted.values,plot=TRUE, legacy.axes=TRUE,
xlab="False Positive Percentage", ylab="True Postive Percentage",
col="#377eb8", lwd=4)

## Setting levels: control = C, case = NC
## Setting direction: controls < cases
```



```
##
## Call:
## roc.default(response = data$Survivorship, predictor =
logistic$fitted.values,      plot = TRUE, legacy.axes = TRUE, xlab = "False
Positive Percentage",      ylab = "True Postive Percentage", col = "#377eb8",
lwd = 4)
##
## Data: logistic$fitted.values in 903 controls (data$Survivorship C) < 482
cases (data$Survivorship NC).
## Area under the curve: 1

roc(data$Survivorship,logistic$fitted.values,plot=TRUE, legacy.axes=TRUE,
xlab="False Positive Percentage", ylab="True Postive Percentage",
col="#377eb8", lwd=4)

## Setting levels: control = C, case = NC
## Setting direction: controls < cases

##
## Call:
## roc.default(response = data$Survivorship, predictor =
logistic$fitted.values,      plot = TRUE, legacy.axes = TRUE, xlab = "False
Positive Percentage",      ylab = "True Postive Percentage", col = "#377eb8",
lwd = 4)
##
## Data: logistic$fitted.values in 903 controls (data$Survivorship C) < 482
```



```

cases (data$Survivorship NC).
## Area under the curve: 1

## If we want to find out the optimal threshold we can store the
## data used to make the ROC graph in a variable...
roc.info <- roc(data$Survivorship, logistic$fitted.values, legacy.axes=TRUE)

## Setting levels: control = C, case = NC
## Setting direction: controls < cases

str(roc.info)

## List of 15
## $ percent          : logi FALSE
## $ sensitivities     : num [1:71] 1 1 1 1 1 1 1 1 1 1 ...
## $ specificities     : num [1:71] 0 0.966 0.967 0.968 0.969 ...
## $ thresholds        : num [1:71] -Inf 5.32e-14 1.71e-13 2.87e-13 7.82e-13
...
## $ direction         : chr "<"
## $ cases              : Named num [1:482] 1 1 1 1 1 ...
## .. attr(*, "names")= chr [1:482] "3" "4" "11" "15" ...
## $ controls           : Named num [1:903] 2.22e-16 2.22e-16 2.22e-16 2.22e-16
2.22e-16 ...
## .. attr(*, "names")= chr [1:903] "1" "2" "5" "6" ...
## $ fun.sesp           :function (thresholds, controls, cases, direction)
## $ auc                : 'auc' num 1
## .. attr(*, "partial.auc")= logi FALSE
## .. attr(*, "percent")= logi FALSE
## .. attr(*, "roc")=List of 15
## .. ..$ percent          : logi FALSE
## .. ..$ sensitivities     : num [1:71] 1 1 1 1 1 1 1 1 1 1 ...
## .. ..$ specificities     : num [1:71] 0 0.966 0.967 0.968 0.969 ...
## .. ..$ thresholds        : num [1:71] -Inf 5.32e-14 1.71e-13 2.87e-13
7.82e-13 ...
## .. ..$ direction         : chr "<"
## .. ..$ cases              : Named num [1:482] 1 1 1 1 1 ...
## .. .. .. attr(*, "names")= chr [1:482] "3" "4" "11" "15" ...
## .. ..$ controls           : Named num [1:903] 2.22e-16 2.22e-16 2.22e-16
2.22e-16 2.22e-16 ...
## .. .. .. attr(*, "names")= chr [1:903] "1" "2" "5" "6" ...
## .. ..$ fun.sesp           :function (thresholds, controls, cases,
direction)
## .. ..$ auc                : 'auc' num 1
## .. .. .. attr(*, "partial.auc")= logi FALSE
## .. .. .. attr(*, "percent")= logi FALSE
## .. .. .. attr(*, "roc")=List of 8
## .. .. .. ..$ percent          : logi FALSE
## .. .. .. ..$ sensitivities: num [1:71] 1 1 1 1 1 1 1 1 1 1 ...
## .. .. .. ..$ specificities: num [1:71] 0 0.966 0.967 0.968 0.969 ...
## .. .. .. ..$ thresholds    : num [1:71] -Inf 5.32e-14 1.71e-13 2.87e-13
7.82e-13 ...

```

```

## .. ..$ direction      : chr "<"
## .. ..$ cases          : Named num [1:482] 1 1 1 1 1 ...
## .. ..$ attr(*, "names")= chr [1:482] "3" "4" "11" "15" ...
## .. ..$ controls       : Named num [1:903] 2.22e-16 2.22e-16 2.22e-16
2.22e-16 2.22e-16 ...
## .. ..$ attr(*, "names")= chr [1:903] "1" "2" "5" "6" ...
## .. ..$ fun.sesp       :function (thresholds, controls, cases,
direction)
## .. ..$ attr(*, "class")= chr "roc"
## .. ..$ call           : language roc.default(response =
data$Survivorship, predictor = logistic$fitted.values,      legacy.axes =
TRUE)
## .. ..$ original.predictor: Named num [1:1385] 2.22e-16 2.22e-16 1.00
1.00 2.22e-16 ...
## .. ..$ attr(*, "names")= chr [1:1385] "1" "2" "3" "4" ...
## .. ..$ original.response : Factor w/ 2 levels "C","NC": 1 1 2 2 1 1 1 1
1 1 ...
## .. ..$ predictor       : Named num [1:1385] 2.22e-16 2.22e-16 1.00
1.00 2.22e-16 ...
## .. ..$ attr(*, "names")= chr [1:1385] "1" "2" "3" "4" ...
## .. ..$ response        : Factor w/ 2 levels "C","NC": 1 1 2 2 1 1 1 1
1 1 ...
## .. ..$ levels          : chr [1:2] "C" "NC"
## .. ..$ attr(*, "class")= chr "roc"
## $ call                 : language roc.default(response = data$Survivorship,
predictor = logistic$fitted.values,      legacy.axes = TRUE)
## $ original.predictor: Named num [1:1385] 2.22e-16 2.22e-16 1.00 1.00
2.22e-16 ...
## ..$ attr(*, "names")= chr [1:1385] "1" "2" "3" "4" ...
## $ original.response : Factor w/ 2 levels "C","NC": 1 1 2 2 1 1 1 1 1 1
...
## $ predictor           : Named num [1:1385] 2.22e-16 2.22e-16 1.00 1.00
2.22e-16 ...
## ..$ attr(*, "names")= chr [1:1385] "1" "2" "3" "4" ...
## $ response            : Factor w/ 2 levels "C","NC": 1 1 2 2 1 1 1 1 1 1
...
## $ levels              : chr [1:2] "C" "NC"
## - attr(*, "class")= chr "roc"

roc.df <- data.frame(tpp=roc.info$sensitivities*100, ## tpp = true positive
percentage
                    fpp=(1 - roc.info$specificities)*100, ## fpp = false
positive precentage
                    thresholds=roc.info$thresholds)
roc.df

##          tpp          fpp  thresholds
## 1  100.00000 100.0000000      -Inf
## 2  100.00000   3.4330011 5.323833e-14
## 3  100.00000   3.3222591 1.709546e-13

```

## 4	100.00000	3.2115172	2.867293e-13
## 5	100.00000	3.1007752	7.822429e-13
## 6	100.00000	2.9900332	3.212620e-12
## 7	100.00000	2.8792913	1.332148e-11
## 8	100.00000	2.7685493	6.246558e-11
## 9	100.00000	2.6578073	1.065926e-10
## 10	100.00000	2.5470653	1.514639e-10
## 11	100.00000	2.4363234	2.243080e-10
## 12	100.00000	2.3255814	3.322046e-10
## 13	100.00000	2.2148394	4.842714e-10
## 14	100.00000	2.1040975	1.012910e-09
## 15	100.00000	1.9933555	2.162425e-09
## 16	100.00000	1.8826135	3.249212e-09
## 17	100.00000	1.7718715	3.671963e-09
## 18	100.00000	1.6611296	3.795815e-09
## 19	100.00000	1.5503876	4.255825e-09
## 20	100.00000	1.4396456	5.278876e-09
## 21	100.00000	1.3289037	6.314976e-09
## 22	100.00000	1.2181617	6.925201e-09
## 23	100.00000	1.1074197	7.904498e-09
## 24	100.00000	0.9966777	9.076446e-09
## 25	100.00000	0.8859358	1.037345e-08
## 26	100.00000	0.7751938	1.130368e-08
## 27	100.00000	0.6644518	1.186846e-08
## 28	100.00000	0.5537099	1.238450e-08
## 29	100.00000	0.4429679	1.294924e-08
## 30	100.00000	0.3322259	1.375664e-08
## 31	100.00000	0.2214839	1.411637e-08
## 32	100.00000	0.1107420	1.712244e-08
## 33	100.00000	0.0000000	5.000000e-01
## 34	99.79253	0.0000000	1.000000e+00
## 35	99.58506	0.0000000	1.000000e+00
## 36	99.37759	0.0000000	1.000000e+00
## 37	99.17012	0.0000000	1.000000e+00
## 38	98.96266	0.0000000	1.000000e+00
## 39	98.75519	0.0000000	1.000000e+00
## 40	98.54772	0.0000000	1.000000e+00
## 41	98.34025	0.0000000	1.000000e+00
## 42	98.13278	0.0000000	1.000000e+00
## 43	97.92531	0.0000000	1.000000e+00
## 44	97.71784	0.0000000	1.000000e+00
## 45	97.51037	0.0000000	1.000000e+00
## 46	97.30290	0.0000000	1.000000e+00
## 47	97.09544	0.0000000	1.000000e+00
## 48	96.88797	0.0000000	1.000000e+00
## 49	96.68050	0.0000000	1.000000e+00
## 50	96.47303	0.0000000	1.000000e+00
## 51	96.26556	0.0000000	1.000000e+00
## 52	96.05809	0.0000000	1.000000e+00
## 53	95.85062	0.0000000	1.000000e+00

```
## 54 95.64315 0.000000 1.000000e+00
## 55 95.43568 0.000000 1.000000e+00
## 56 95.22822 0.000000 1.000000e+00
## 57 95.02075 0.000000 1.000000e+00
## 58 94.81328 0.000000 1.000000e+00
## 59 94.60581 0.000000 1.000000e+00
## 60 94.39834 0.000000 1.000000e+00
## 61 94.19087 0.000000 1.000000e+00
## 62 93.98340 0.000000 1.000000e+00
## 63 93.77593 0.000000 1.000000e+00
## 64 93.56846 0.000000 1.000000e+00
## 65 93.36100 0.000000 1.000000e+00
## 66 93.15353 0.000000 1.000000e+00
## 67 92.94606 0.000000 1.000000e+00
## 68 92.73859 0.000000 1.000000e+00
## 69 92.53112 0.000000 1.000000e+00
## 70 92.32365 0.000000 1.000000e+00
## 71 0.00000 0.000000 Inf
```

`head(roc.df)` *## head() will show us the values for the upper right-hand corner of the ROC graph, when the threshold is so low*

```
## tpp fpp thresholds
## 1 100 100.000000 -Inf
## 2 100 3.433001 5.323833e-14
## 3 100 3.322259 1.709546e-13
## 4 100 3.211517 2.867293e-13
## 5 100 3.100775 7.822429e-13
## 6 100 2.990033 3.212620e-12
```

(negative infinity) that every single sample is called "obese".

Thus TPP = 100% and FPP = 100%

`tail(roc.df)` *## tail() will show us the values for the lower left-hand corner*

```
## tpp fpp thresholds
## 66 93.15353 0 1
## 67 92.94606 0 1
## 68 92.73859 0 1
## 69 92.53112 0 1
## 70 92.32365 0 1
## 71 0.00000 0 Inf
```

of the ROC graph, when the threshold is so high (infinity)

that every single sample is called "not obese".

Thus, TPP = 0% and FPP = 0%

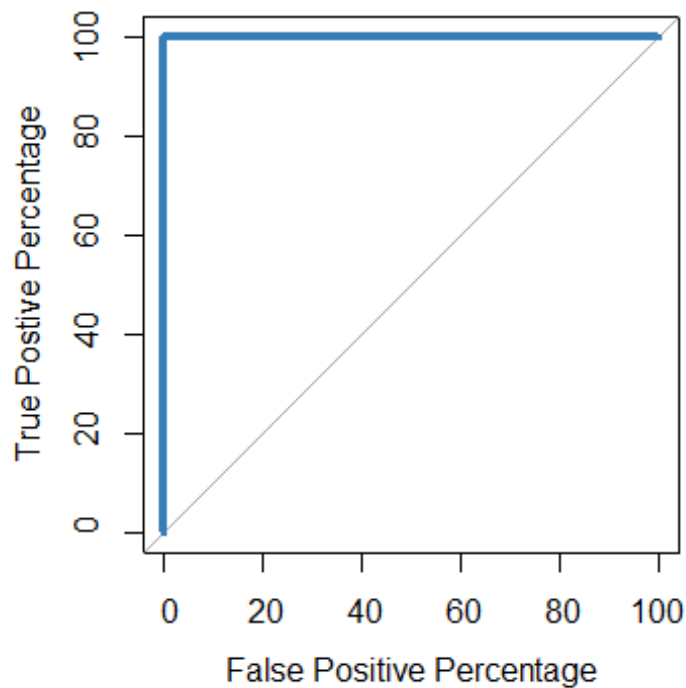
now Let's Look at the thresholds between TPP 60% and 80%

```
roc.df[roc.df$tpp > 60 & roc.df$tpp < 80,]
```

```
## [1] tpp fpp thresholds
## <0 rows> (or 0-length row.names)
```

```
roc(data$Survivorship,logistic$fitted.values,plot=TRUE, legacy.axes=TRUE,
xlab="False Positive Percentage", ylab="True Postive Percentage",
col="#377eb8", lwd=4, percent=TRUE)
```

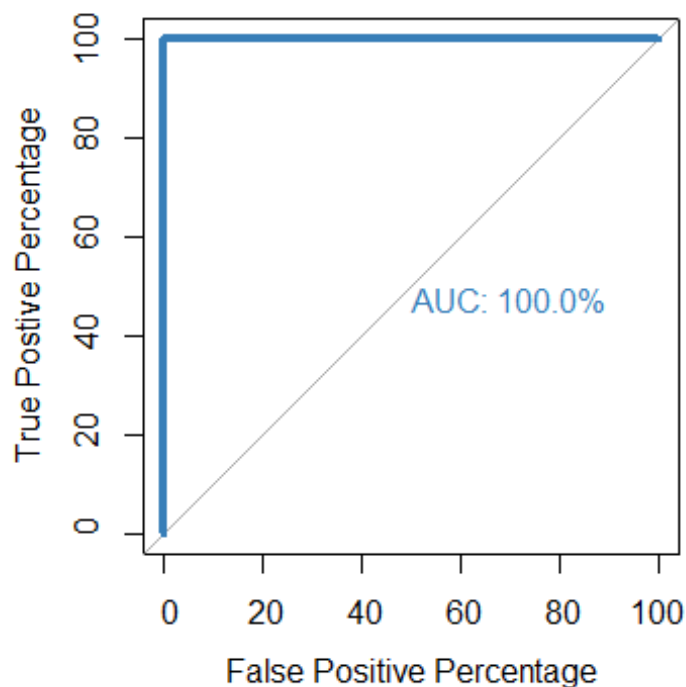
```
## Setting levels: control = C, case = NC
## Setting direction: controls < cases
```



```
##
## Call:
## roc.default(response = data$Survivorship, predictor =
logistic$fitted.values, percent = TRUE, plot = TRUE, legacy.axes = TRUE,
xlab = "False Positive Percentage", ylab = "True Postive Percentage", col
= "#377eb8", lwd = 4)
##
## Data: logistic$fitted.values in 903 controls (data$Survivorship C) < 482
cases (data$Survivorship NC).
## Area under the curve: 100%
```

```
roc(data$Survivorship,logistic$fitted.values,plot=TRUE, legacy.axes=TRUE,
xlab="False Positive Percentage", ylab="True Postive Percentage",
col="#377eb8", lwd=4, percent=TRUE, print.auc=TRUE)
```

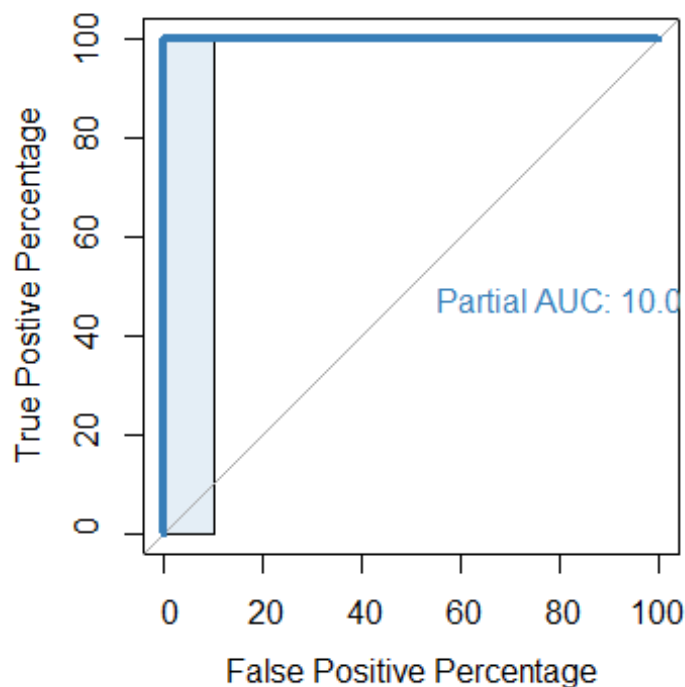
```
## Setting levels: control = C, case = NC
## Setting direction: controls < cases
```



```
##
## Call:
## roc.default(response = data$Survivorship, predictor =
logistic$fitted.values, percent = TRUE, plot = TRUE, legacy.axes = TRUE,
xlab = "False Positive Percentage", ylab = "True Postive Percentage", col
= "#377eb8", lwd = 4, print.auc = TRUE)
##
## Data: logistic$fitted.values in 903 controls (data$Survivorship C) < 482
cases (data$Survivorship NC).
## Area under the curve: 100%

roc(data$Survivorship,logistic$fitted.values,plot=TRUE, legacy.axes=TRUE,
xlab="False Positive Percentage", ylab="True Postive Percentage",
col="#377eb8", lwd=4, percent=TRUE, print.auc=TRUE, partial.auc=c(100, 90),
auc.polygon = TRUE, auc.polygon.col = "#377eb822", print.auc.x=45)

## Setting levels: control = C, case = NC
## Setting direction: controls < cases
```



```
##
## Call:
## roc.default(response = data$Survivorship, predictor =
logistic$fitted.values, percent = TRUE, plot = TRUE, legacy.axes = TRUE,
xlab = "False Positive Percentage", ylab = "True Postive Percentage", col
= "#377eb8", lwd = 4, print.auc = TRUE, partial.auc = c(100, 90),
auc.polygon = TRUE, auc.polygon.col = "#377eb822", print.auc.x = 45)
##
## Data: logistic$fitted.values in 903 controls (data$Survivorship C) < 482
cases (data$Survivorship NC).
## Partial area under the curve (specificity 100%-90%): 10%

# Lets do two roc plots to understand which model is better
roc(data$Survivorship, logistic_simple$fitted.values, plot=TRUE,
legacy.axes=TRUE, percent=TRUE, xlab="False Positive Percentage", ylab="True
Postive Percentage", col="#377eb8", lwd=4, print.auc=TRUE)

## Setting levels: control = C, case = NC
## Setting direction: controls < cases

##
## Call:
## roc.default(response = data$Survivorship, predictor =
logistic_simple$fitted.values, percent = TRUE, plot = TRUE, legacy.axes =
TRUE, xlab = "False Positive Percentage", ylab = "True Postive
Percentage", col = "#377eb8", lwd = 4, print.auc = TRUE)
##
```

```
## Data: logistic_simple$fitted.values in 903 controls (data$Survivorship C)
< 482 cases (data$Survivorship NC).
## Area under the curve: 52.71%

# Lets add the other graph
plot.roc(data$Survivorship, logistic$fitted.values, percent=TRUE,
col="#4daf4a", lwd=4, print.auc=TRUE, add=TRUE, print.auc.y=40)

## Setting levels: control = C, case = NC
## Setting direction: controls < cases

legend("bottomright", legend=c("Simple", "Non Simple"), col=c("#377eb8",
"#4daf4a"), lwd=4) # Make it user friendly
```

