For SVM and TUNING

library('e1071')

## Warning: package 'e1071' was built under R version 3.3.3

setwd('D:\\packages\\sem5\\AI')

Reading the data

orgdata<-read.csv("wdbc.csv",header=T)  
n=nrow(orgdata)  
c=ncol(orgdata)  
n

## [1] 569

c

## [1] 32

(class(orgdata))

## [1] "data.frame"

Normalisation and separation

orgdata[, -c(1,2)] <- scale(orgdata[, -c(1,2)])  
  
BenignData=orgdata[which(orgdata$diagnosis=='B'),-c(1,2)]  
MalignantData=orgdata[which(orgdata$diagnosis=='M'),-c(1,2)]  
data=orgdata[,-c(1,2)]

To calculate Optimum K centroids for B, We calculate davg which is the average distance of each node from its cluster representative. Then we calculate dmin which is the min distance between any pair of centroids We intend to calculate the validity ratio as davg/dmin, this means that we want to reduce the distance between the nodes and their centroids and maximise the distance between centroids.Then we find the optimum k as the number that corresponds to the minimum validity ratio

We do for Benign data first, We set seed to generate the same random number for the same value

BenignValRatio=c()  
  
set.seed(100);  
for(k in 2:30)  
{  
   
 davg=0  
 #KMEANS returns centroids centres ($centers) and which cluster a node belongs to($cluster)   
 BenignCluster <- kmeans(BenignData, k, nstart = 20)  
   
 #Finding dAvg  
 for(i in 1:nrow(BenignData))  
 {  
 davg=davg+dist(rbind(BenignData[i,],BenignCluster$centers[BenignCluster$cluster[i],]))   
 }  
 davg=davg/nrow(BenignData)  
 dmin=Inf  
 for(i in 1:(k-1))  
 {  
 y=BenignCluster$centers[i,]  
 x=BenignCluster$centers[(i+1):k,]  
 if(i==(k-1))  
 {  
 dis=dist(rbind(x,y))  
 }  
 else  
 {  
 dis=min(apply(x,1,function(x,y)dist(rbind(x,y)),y)) #Getting the minimum distance  
 }  
 if(dmin>dis)  
 {  
 dmin=dis  
 }  
 }  
 ValRatio=davg/dmin  
 BenignValRatio=c(BenignValRatio,ValRatio)   
}  
BenignValRatio

## [1] 0.6368107 1.0653281 0.9890476 0.9295580 1.0543914 0.9883099 1.1291082  
## [8] 1.0249236 1.0341845 1.1337941 1.0387253 1.1437275 1.0685933 1.1235532  
## [15] 1.1910931 1.1137276 1.1051545 1.2266194 1.0370036 1.0683409 1.2649455  
## [22] 1.2094550 1.2074616 1.1845665 1.0545818 1.1779263 1.1819344 1.2453094  
## [29] 1.1403826

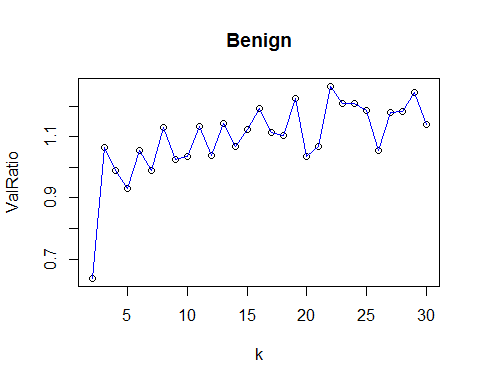
Now we do for malignant

MalignantValRatio=c()  
for(k in 2:30)  
{  
   
 #KMEANS returns centroids centres ($centers) and the which cluster a node belongs to($cluster)   
 MalignantCluster <- kmeans(MalignantData, k, nstart = 20)  
 davg=0  
 #Finding dAvg  
 for(i in 1:nrow(MalignantData))  
 {  
   
 davg=davg+dist(rbind(MalignantData[i,],MalignantCluster$centers[MalignantCluster$cluster[i],]))   
   
 }  
 davg=davg/nrow(MalignantData)  
 dmin=Inf  
 for(i in 1:(k-1))  
 {  
 y=MalignantCluster$centers[i,]  
 x=MalignantCluster$centers[(i+1):k,]  
   
 if(i==(k-1))  
 {  
 dis=dist(rbind(x,y))  
 }  
 else  
 {  
 dis=min(apply(x,1,function(x,y)dist(rbind(x,y)),y)) #Getting the minimum distance  
 }  
 if(dmin>dis)  
 {  
 dmin=dis  
 }  
 }  
 ValRatio=davg/dmin  
 MalignantValRatio=c(MalignantValRatio,ValRatio)   
}  
MalignantValRatio

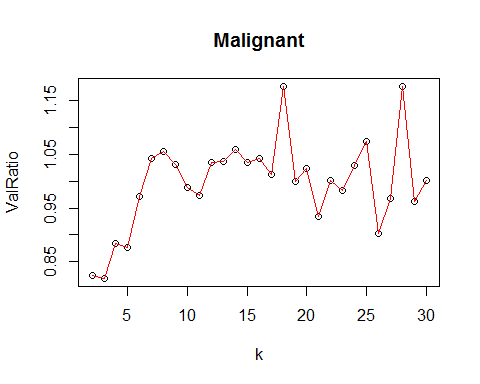
## [1] 0.8242617 0.8189348 0.8842880 0.8764074 0.9710980 1.0432042 1.0558108  
## [8] 1.0318712 0.9894545 0.9733857 1.0344501 1.0372808 1.0586698 1.0353476  
## [15] 1.0419239 1.0132496 1.1762568 1.0006116 1.0234885 0.9352517 1.0009392  
## [22] 0.9823969 1.0299260 1.0751698 0.9030916 0.9675665 1.1771739 0.9616807  
## [29] 1.0019330

Now We plot the k vs validity ratio graphs

krange=(2:30)  
plot(krange, BenignValRatio, xlim=range((2:30)), ylim=range(BenignValRatio), xlab="k", ylab="ValRatio", main = "Benign")  
lines(krange[order(krange)], BenignValRatio[order(krange)], xlim=range(krange), ylim=range(BenignValRatio),col="blue")



plot(krange, MalignantValRatio, xlim=range((2:30)), ylim=range(MalignantValRatio), xlab="k", ylab="ValRatio", main ="Malignant")  
lines(krange[order(krange)], MalignantValRatio[order(krange)], xlim=range(krange), ylim=range(MalignantValRatio),col="red")



Taking K=3 we proceed as per the research paper

BenignCluster <- kmeans(BenignData, 3, nstart = 20)  
MalignantCluster <- kmeans(MalignantData, 3, nstart = 20)

Now we define new features for all the nodes. We define 6 new features that reduces the feature space to 6 from 32. The similarity between the untested and the symbolic tumors plays an important role. To measure the similarity we use a membership function as per the research paper.

Finding Min and Max for each type and each cluster of each feature Example: Among all 1st feature that belongs to first cluster find minimum Do similarly for all others too!

#Finding MIN and MAX of each type  
minBenign=aggregate(BenignData, by=list(BenignCluster$cluster), FUN=min)  
  
maxBenign=aggregate(BenignData, by=list(BenignCluster$cluster), FUN=max)  
  
minMalignant=aggregate(MalignantData, by=list(MalignantCluster$cluster), FUN=min)  
  
maxMalignant=aggregate(MalignantData, by=list(MalignantCluster$cluster), FUN=max)  
  
minBenign=minBenign[2:31]  
maxBenign=maxBenign[2:31]  
minMalignant=minMalignant[2:31]  
maxMalignant=maxMalignant[2:31]  
  
#For removing the cluster numbers as a column  
#Example of one  
minBenign

## radius\_mean texture\_mean perimeter\_mean area\_mean smoothness\_mean  
## 1 -1.806811 -2.227289 -1.812793 -1.346604 -3.109349  
## 2 -1.826391 -1.492582 -1.795509 -1.376725 -1.279161  
## 3 -2.027864 -1.969211 -1.982759 -1.453164 -2.149460  
## compactness\_mean concavity\_mean concave.points\_mean symmetry\_mean  
## 1 -1.6087208 -1.1138927 -1.2607103 -2.741705  
## 2 0.1336612 -0.0343618 -0.9091897 -1.848010  
## 3 -1.2018116 -1.1138927 -1.2607103 -1.687510  
## fractal\_dimension\_mean radius\_se texture\_se perimeter\_se area\_se  
## 1 -1.55057327 -1.045289 -1.552898 -1.0431310 -0.7371804  
## 2 -0.06623029 -1.058992 -1.407878 -0.8027577 -0.7278159  
## 3 -0.72766938 -1.048535 -1.504135 -0.9615722 -0.7272444  
## smoothness\_se compactness\_se concavity\_se concave.points\_se symmetry\_se  
## 1 -1.7745036 -1.2969570 -1.05657101 -1.9117653 -1.331092  
## 2 -0.7034026 1.1135616 0.09727283 -0.2554399 -1.010395  
## 3 -1.1810017 -0.9725801 -1.05657101 -1.9117653 -1.063623  
## fractal\_dimension\_se radius\_worst texture\_worst perimeter\_worst  
## 1 -1.0960038 -1.449791 -2.222039 -1.455283  
## 2 0.6825577 -1.570621 -1.628182 -1.570453  
## 3 -0.9742384 -1.725382 -2.145570 -1.691872  
## area\_worst smoothness\_worst compactness\_worst concavity\_worst  
## 1 -1.091377 -2.680337 -1.4426091 -1.3046827  
## 2 -1.153904 -1.877969 -0.4446842 -0.6173226  
## 3 -1.221348 -1.655478 -1.1224036 -1.3046827  
## concave.points\_worst symmetry\_worst fractal\_dimension\_worst  
## 1 -1.743529 -2.157444 -1.5910189  
## 2 -1.158429 -2.018437 -0.7671564  
## 3 -1.743529 -1.614347 -1.3075393

Benigncenters=BenignCluster$centers  
Malignantcenters=MalignantCluster$centers  
BenignDen=c()  
MalignantDen=c()  
for(i in 1:3)  
{  
 #For each we find the maximum of (centroid value minus min value or max value of the same feature)  
 #Either of these must give the maximum  
 temp1=apply(rbind(abs(Benigncenters[i,]-minBenign[i,]),abs(maxBenign[i,]-Benigncenters[i,])),2,max)  
   
 BenignDen=rbind(BenignDen,temp1)  
   
 temp2=apply(rbind(abs(Malignantcenters[i,]-minMalignant[i,]),abs(maxMalignant[i,]-Malignantcenters[i,])),2,max)  
   
   
 MalignantDen=rbind(MalignantDen,temp2)  
}  
#Can also use when 3 rows are already present,Initially throws error  
#MalignantDen[1:3,]=apply(rbind(abs(Malignantcenters[1:3,]-minMalignant[1:3,]),abs(maxMalignant[1:3,]-M#alignantcenters[1:3,])),2,max)

We create new features for each row and this is the training data!!

F=ncol(data)  
for(i in 1:n)  
{  
 newfeature=c()  
 for(c in 1:3)  
 {  
 val=0  
 for(f in 1:F)  
 {  
 if(data[i,f]>=minBenign[c,f] & data[i,f]<=maxBenign[c,f])  
 {  
 val=val+1-(abs(Benigncenters[c,f]-data[i,f])/BenignDen[c,f])  
 }  
 }  
 val=val/F  
 newfeature=c(newfeature,val)  
 }  
 for(c in 1:3)  
 {  
 val=0  
 for(f in 1:F)  
 {  
 if(data[i,f]>=minMalignant[c,f] & data[i,f]<=maxMalignant[c,f])  
 {  
 val=val+1-(abs(Malignantcenters[c,f]-data[i,f])/MalignantDen[c,f])  
 }  
 }  
 val=val/F  
 newfeature=c(newfeature,val)  
 }  
   
 if(i==1)  
 {  
 finaldata=newfeature  
 }  
 else  
 {  
 finaldata=rbind(finaldata,newfeature)  
 }  
}  
  
finaldata

## [,1] [,2] [,3] [,4] [,5] [,6]  
## finaldata 0.14250253 0.3163871 0.2182445 0.4405285 0.3469429 0.6845277  
## newfeature 0.51790345 0.3601564 0.5253968 0.3154070 0.7509622 0.5436376  
## newfeature 0.26247880 0.3945743 0.3862383 0.5341817 0.6458650 0.8244616  
## newfeature 0.34077747 0.4688993 0.3687807 0.4541980 0.3182084 0.3474854  
## newfeature 0.32712467 0.3735843 0.4344066 0.3703772 0.7318673 0.6737428  
## newfeature 0.48299797 0.5312002 0.5215218 0.7856588 0.5016422 0.4268817  
## newfeature 0.44889200 0.3500170 0.5026627 0.4887327 0.8792209 0.5428931  
## newfeature 0.40184239 0.4867039 0.5026024 0.7685987 0.6388665 0.4669653  
## newfeature 0.47067806 0.4470015 0.4884405 0.8000748 0.4950764 0.4984043  
## newfeature 0.40698576 0.4641941 0.3944750 0.5962932 0.3813120 0.3764410  
## newfeature 0.67818539 0.2997051 0.5576348 0.4343458 0.6977176 0.2937208  
## newfeature 0.39203449 0.4077806 0.4846886 0.7360839 0.7925346 0.5237401  
## newfeature 0.13600422 0.3404809 0.1631548 0.3778486 0.4663090 0.5861163  
## newfeature 0.55830066 0.4727696 0.5448743 0.5601028 0.7235315 0.3829263  
## newfeature 0.41301950 0.4572696 0.4343586 0.7706930 0.4834493 0.4877670  
## newfeature 0.34721257 0.3838989 0.3767478 0.8581210 0.5461164 0.4313269  
## newfeature 0.58799953 0.3561063 0.5917958 0.5576548 0.7831874 0.3659179  
## newfeature 0.28949707 0.3789442 0.3536467 0.7798233 0.6734516 0.5975065  
## newfeature 0.36948754 0.2929966 0.4063890 0.4148420 0.6852443 0.7297546  
## newfeature 0.74408642 0.4541950 0.7513884 0.4699814 0.6684476 0.3417568  
## newfeature 0.73093409 0.4546171 0.7770833 0.4330199 0.5524542 0.3511226  
## newfeature 0.69136982 0.4485088 0.7460057 0.2880984 0.4610500 0.2968620  
## newfeature 0.27104046 0.4009408 0.3477250 0.7237693 0.4816930 0.5139462  
## newfeature 0.41937024 0.2697334 0.4217748 0.3564150 0.7065900 0.6370625  
## newfeature 0.30110095 0.3205197 0.3832983 0.6265177 0.6485712 0.7173847  
## newfeature 0.17892509 0.3913957 0.3059020 0.5208813 0.5205376 0.6978744  
## newfeature 0.41214284 0.3316765 0.4572996 0.8081694 0.5531184 0.4774778  
## newfeature 0.36820126 0.3696300 0.4457596 0.4157214 0.8411938 0.6154510  
## newfeature 0.34281411 0.3638780 0.4007628 0.8046226 0.6474935 0.5540549  
## newfeature 0.44049340 0.3795220 0.5262666 0.5169930 0.8731465 0.5180473  
## newfeature 0.23066548 0.3305651 0.3535540 0.5698355 0.6132703 0.8138985  
## newfeature 0.40548181 0.5436472 0.4886715 0.7576250 0.5376051 0.4151061  
## newfeature 0.27428746 0.3792338 0.4051604 0.6829357 0.7015172 0.6858170  
## newfeature 0.30745690 0.3290077 0.3719074 0.5919827 0.6909273 0.6708245  
## newfeature 0.40561762 0.3682443 0.4682185 0.7646748 0.6858176 0.5135197  
## newfeature 0.38406766 0.4447658 0.4439829 0.7158877 0.7987999 0.5306695  
## newfeature 0.52634762 0.4747273 0.5895457 0.7819841 0.7082664 0.4988448  
## newfeature 0.78788833 0.3767642 0.6142017 0.2208227 0.3515895 0.1828053  
## newfeature 0.57141244 0.1971416 0.4038763 0.2442098 0.4476561 0.2787117  
## newfeature 0.58574144 0.4592787 0.6298241 0.6924575 0.6254967 0.4730130  
## newfeature 0.81788285 0.3299161 0.6259155 0.3483846 0.6025308 0.2379384  
## newfeature 0.54814090 0.5850319 0.7323624 0.5822629 0.5527329 0.4084131  
## newfeature 0.16488505 0.2985505 0.2017894 0.3726237 0.4101743 0.6869191  
## newfeature 0.50939542 0.4815405 0.6053729 0.7649843 0.6639475 0.4470378  
## newfeature 0.59183786 0.3436953 0.5637197 0.4713975 0.6508271 0.3639590  
## newfeature 0.26364310 0.3940657 0.3661308 0.6096020 0.6486539 0.7436450  
## newfeature 0.64023922 0.3757837 0.6439667 0.2374779 0.4151169 0.2874865  
## newfeature 0.52316057 0.4608298 0.5842441 0.7775374 0.5808860 0.4573343  
## newfeature 0.79860444 0.4643540 0.8291477 0.3684470 0.5829639 0.3434347  
## newfeature 0.81126947 0.3829418 0.7032716 0.4085674 0.6505437 0.3054844  
## newfeature 0.82717523 0.4391235 0.7160409 0.3054508 0.4616895 0.2062403  
## newfeature 0.85982734 0.2871080 0.6826442 0.2995502 0.4578751 0.2291576  
## newfeature 0.86627645 0.4482218 0.7788065 0.3323988 0.4393744 0.2494374  
## newfeature 0.36869479 0.3688103 0.4900275 0.4913362 0.7428092 0.6308838  
## newfeature 0.68004903 0.2940304 0.5809044 0.4553761 0.7271501 0.2698797  
## newfeature 0.81038132 0.5108552 0.8104357 0.3366258 0.5056156 0.2824501  
## newfeature 0.32862044 0.3563368 0.4486003 0.5225662 0.7502050 0.7365486  
## newfeature 0.41927080 0.4166898 0.5106704 0.8715181 0.6980407 0.4901450  
## newfeature 0.77603329 0.4079195 0.5906881 0.3840053 0.4392889 0.2272447  
## newfeature 0.58779116 0.3245222 0.6123907 0.2133657 0.3322836 0.2305814  
## newfeature 0.54550983 0.4528883 0.6336870 0.3086547 0.3776649 0.2764836  
## newfeature 0.55873395 0.3952017 0.6798910 0.3877770 0.4722449 0.3545588  
## newfeature 0.29803582 0.4526114 0.3406744 0.7636368 0.5809254 0.5726715  
## newfeature 0.52766176 0.4627201 0.6550177 0.3736612 0.3886360 0.3361994  
## newfeature 0.46186033 0.4655179 0.5613732 0.7982472 0.6523104 0.4554975  
## newfeature 0.46781736 0.4196407 0.5506626 0.8298121 0.6923289 0.4708080  
## newfeature 0.63960693 0.4439312 0.7445919 0.3756941 0.4550726 0.3724407  
## newfeature 0.82858332 0.5100165 0.7752706 0.2638661 0.4797414 0.2345577  
## newfeature 0.29824050 0.6388960 0.4600923 0.4391225 0.3301261 0.3654197  
## newfeature 0.84351507 0.4298192 0.7124071 0.2829113 0.4856265 0.2451499  
## newfeature 0.45659189 0.2493087 0.4308974 0.3118958 0.7608569 0.5497104  
## newfeature 0.44098365 0.6381137 0.5413986 0.3124066 0.4140088 0.3180406  
## newfeature 0.25571559 0.3802415 0.3380941 0.6826602 0.6727753 0.6523921  
## newfeature 0.63305130 0.4342603 0.6831704 0.5545305 0.6378327 0.3603361  
## newfeature 0.91324148 0.4407864 0.8096193 0.3361518 0.5804768 0.2828156  
## newfeature 0.43355894 0.3676722 0.4846885 0.4589339 0.8024940 0.4702356  
## newfeature 0.62754135 0.3995400 0.6857726 0.4392083 0.5081417 0.2853108  
## newfeature 0.16155840 0.4127424 0.3216501 0.5557885 0.5600295 0.7425475  
## newfeature 0.08459667 0.2852722 0.1472069 0.3151178 0.3148436 0.6084170  
## newfeature 0.88544850 0.4634330 0.8429227 0.4329602 0.6340639 0.3299254  
## newfeature 0.70430051 0.4970482 0.8602628 0.4613067 0.5067577 0.3726053  
## newfeature 0.50100491 0.5604185 0.6263834 0.7517731 0.5732888 0.4966928  
## newfeature 0.18052046 0.3272327 0.2816507 0.4156173 0.3429502 0.7150012  
## newfeature 0.23942049 0.3781722 0.3323566 0.4639343 0.6140390 0.6614919  
## newfeature 0.82017378 0.4825404 0.8332345 0.4090927 0.5774218 0.3406570  
## newfeature 0.37770984 0.3505500 0.4959873 0.5165311 0.8245083 0.6662858  
## newfeature 0.55384723 0.4838179 0.5758636 0.6053026 0.7448129 0.4323188  
## newfeature 0.37254495 0.3707735 0.3999415 0.5703694 0.7857744 0.6041011  
## newfeature 0.72295645 0.5475398 0.8386985 0.5214441 0.6363258 0.4240873  
## newfeature 0.46132602 0.4743515 0.5626570 0.6744220 0.6897833 0.4473669  
## newfeature 0.82144431 0.2922157 0.6625055 0.4726824 0.6580562 0.2913566  
## newfeature 0.60399757 0.4353487 0.6033001 0.5807170 0.7571734 0.3935363  
## newfeature 0.75095849 0.3143622 0.5645517 0.3733666 0.5122381 0.1649800  
## newfeature 0.86118040 0.4034850 0.7686437 0.3855729 0.6252526 0.3250381  
## newfeature 0.40415198 0.4695940 0.4801716 0.7849708 0.7239194 0.5389893  
## newfeature 0.31504398 0.3921266 0.3842065 0.4861817 0.7499759 0.6983408  
## newfeature 0.79095936 0.5373229 0.8151240 0.3788065 0.4933146 0.3260951  
## newfeature 0.61795979 0.4699207 0.6788207 0.2914005 0.3729180 0.2990260  
## newfeature 0.78348430 0.4705218 0.8467738 0.3002172 0.4737016 0.2496153  
## newfeature 0.55268927 0.4618153 0.6631099 0.7076086 0.7357058 0.4594710  
## newfeature 0.69631007 0.4026419 0.6248339 0.4764564 0.7316613 0.3532545  
## newfeature 0.44091572 0.3472722 0.5284039 0.3084944 0.3052347 0.2846337  
## newfeature 0.84772315 0.3796176 0.6607736 0.2314016 0.3838554 0.2221305  
## newfeature 0.63867174 0.5532841 0.8202601 0.3765819 0.5556358 0.4165118  
## newfeature 0.73024832 0.5382373 0.8131301 0.3870718 0.4937506 0.3565678  
## newfeature 0.45038844 0.5260301 0.4580358 0.7644090 0.5162494 0.4428563  
## newfeature 0.64215976 0.5727722 0.8609496 0.5403754 0.5763792 0.4273031  
## newfeature 0.83896973 0.3951801 0.7034527 0.2298059 0.4778860 0.2397058  
## newfeature 0.14331375 0.2847705 0.2321895 0.3634446 0.2576902 0.6313776  
## newfeature 0.74771248 0.4837113 0.8226441 0.4140162 0.5111912 0.3273363  
## newfeature 0.63038870 0.5470931 0.7966986 0.3537107 0.4871437 0.3659129  
## newfeature 0.59149222 0.6712130 0.7438759 0.5068875 0.6002166 0.4167047  
## newfeature 0.45170178 0.5873390 0.3934294 0.5802962 0.4617115 0.3631817  
## newfeature 0.57208958 0.6827271 0.7628812 0.4119691 0.4897921 0.4096995  
## newfeature 0.56401547 0.4885881 0.6860131 0.3276622 0.4363198 0.3338203  
## newfeature 0.80010344 0.4677693 0.8493007 0.4532159 0.5761668 0.3506668  
## newfeature 0.48173774 0.5774513 0.5517662 0.2839032 0.4315613 0.2913000  
## newfeature 0.37419634 0.4262791 0.4520489 0.8673877 0.6218583 0.4940389  
## newfeature 0.25326307 0.4128055 0.3184799 0.7932183 0.6202701 0.6057595  
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## newfeature 0.32107763 0.3639432 0.3549389 0.7018569 0.5028242 0.4801439  
## newfeature 0.19130513 0.3616640 0.3218749 0.4685490 0.4484148 0.8676537  
## newfeature 0.31527962 0.3198850 0.3759692 0.3622189 0.5823656 0.8016373  
## newfeature 0.39648292 0.2807829 0.3729008 0.3298071 0.7347205 0.6131543  
## newfeature 0.46824175 0.3789331 0.4455167 0.5178594 0.8019980 0.4028388  
## newfeature 0.11721481 0.3015066 0.2013364 0.4050771 0.3840657 0.6889855  
## newfeature 0.56611886 0.3133914 0.4647259 0.2642791 0.3502768 0.2553693

class=data[,2]  
svm\_tune <- tune(svm, train.x=finaldata, train.y=class, kernel="radial", ranges=list(cost=10^(-1:2), gamma=c(.5,1,2)))

## Warning in data.row.names(row.names, rowsi, i): some row.names duplicated:  
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## Warning in data.row.names(row.names, rowsi, i): some row.names duplicated:  
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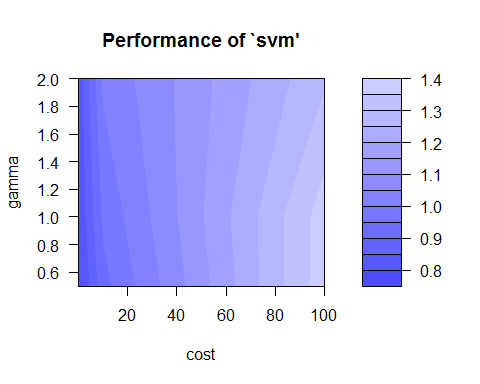
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## --> row.names NOT used  
  
## Warning in data.row.names(row.names, rowsi, i): some row.names duplicated:  
## 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95,96,98,99,100,101,102,103,104,105,106,107,108,109,110,111,112,113,114,115,116,117,118,119,120,121,122,123,124,125,126,127,128,129,130,131,132,133,134,135,136,137,138,139,140,141,142,143,144,145,146,147,148,149,150,151,152,153,154,155,156,157,158,159,160,161,162,163,164,165,166,167,168,169,170,171,172,173,174,175,176,177,178,179,180,181,182,183,184,185,186,187,188,189,190,191,192,193,194,195,196,197,198,199,200,201,202,203,204,205,206,207,208,209,210,211,212,213,214,215,216,217,218,219,220,221,222,223,224,225,226,227,228,229,230,231,232,233,234,235,236,237,238,239,240,241,242,243,244,245,246,247,248,249,250,251,252,253,254,255,256,257,258,259,260,261,262,263,264,265,266,267,268,269,270,271,272,273,274,275,276,277,278,279,280,281,282,283,284,285,286,287,288,289,290,291,292,293,294,295,296,297,298,299,300,301,302,303,304,305,306,307,308,309,310,311,312,313,314,315,316,317,318,319,320,321,322,323,324,325,326,327,328,329,330,331,332,333,334,335,336,337,338,339,340,341,342,343,344,345,346,347,348,349,350,351,352,353,354,355,356,357,358,359,360,361,362,363,364,365,366,367,368,369,370,371,372,373,374,375,376,377,378,379,380,381,382,383,384,385,386,387,388,389,390,391,392,393,394,395,396,397,398,399,400,401,402,403,404,405,406,407,408,409,410,411,412,413,414,415,416,417,418,419,420,421,422,423,424,425,426,427,428,429,430,431,432,433,434,435,436,437,438,439,440,441,442,443,444,445,446,447,448,449,450,451,452,453,454,455,456,457,458,459,460,461,462,463,464,465,466,467,468,469,470,471,472,473,474,475,476,477,478,479,480,481,482,483,484,485,486,487,488,489,490,491,492,493,494,495,496,497,498,499,500,501,502,503,504,505,506,507,508,509,510,511,512  
## --> row.names NOT used

## Warning in data.row.names(row.names, rowsi, i): some row.names duplicated:  
## 3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98,99,100,101,102,103,104,105,106,107,108,109,110,111,112,113,114,115,116,117,118,119,120,121,122,123,124,125,126,127,128,129,130,131,132,133,134,135,136,137,138,139,140,141,142,143,144,145,146,147,148,149,150,151,152,153,154,155,156,157,158,159,160,161,162,163,164,165,166,167,168,169,170,171,172,173,174,175,176,177,178,179,180,181,182,183,184,185,186,187,188,189,190,191,192,193,194,195,196,197,198,199,200,201,202,203,204,205,206,207,208,209,210,211,212,213,214,215,216,217,218,219,220,221,222,223,224,225,226,227,228,229,230,231,232,233,234,235,236,237,238,239,240,241,242,243,244,245,246,247,248,249,250,251,252,253,254,255,256,257,258,259,260,261,262,263,264,265,266,267,268,269,270,271,272,273,274,275,276,277,278,279,280,281,282,283,284,285,286,287,288,289,290,291,292,293,294,295,296,297,298,299,300,301,302,303,304,305,306,307,308,309,310,311,312,313,314,315,316,317,318,319,320,321,322,323,324,325,326,327,328,329,330,331,332,333,334,335,336,337,338,339,340,341,342,343,344,345,346,347,348,349,350,351,352,353,354,355,356,357,358,359,360,361,362,363,364,365,366,367,368,369,370,371,372,373,374,375,376,377,378,379,380,381,382,383,384,385,386,387,388,389,390,391,392,393,394,395,396,397,398,399,400,401,402,403,404,405,406,407,408,409,410,411,412,413,414,415,416,417,418,419,420,421,422,423,424,425,426,427,428,429,430,431,432,433,434,435,436,437,438,439,440,441,442,443,444,445,446,447,448,449,450,451,452,453,454,455,456,457,458,459,460,461,462,463,464,465,466,467,468,469,470,471,472,473,474,475,476,477,478,479,480,481,482,483,484,485,486,487,488,489,490,491,492,493,494,495,496,497,498,499,500,501,502,503,504,505,506,507,508,509,510,511,512,513,514,515,516,517,518,519,520,521,522,523,524,525,526,527,528,529,530,531,532,533,534,535,536,537,538,539,540,541,542,543,544,545,546,547,548,549,550,551,552,553,554,555,556,557,558,559,560,561,562,563,564,565,566,567,568,569  
## --> row.names NOT used

plot(svm\_tune)



print(svm\_tune)

##   
## Parameter tuning of 'svm':  
##   
## - sampling method: 10-fold cross validation   
##   
## - best parameters:  
## cost gamma  
## 1 0.5  
##   
## - best performance: 0.7983003

model <- svm(finaldata, class,kernel = 'radial', gamma = 0.5, cost = 1, cross=10)

## Warning in data.row.names(row.names, rowsi, i): some row.names duplicated:  
## 3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98,99,100,101,102,103,104,105,106,107,108,109,110,111,112,113,114,115,116,117,118,119,120,121,122,123,124,125,126,127,128,129,130,131,132,133,134,135,136,137,138,139,140,141,142,143,144,145,146,147,148,149,150,151,152,153,154,155,156,157,158,159,160,161,162,163,164,165,166,167,168,169,170,171,172,173,174,175,176,177,178,179,180,181,182,183,184,185,186,187,188,189,190,191,192,193,194,195,196,197,198,199,200,201,202,203,204,205,206,207,208,209,210,211,212,213,214,215,216,217,218,219,220,221,222,223,224,225,226,227,228,229,230,231,232,233,234,235,236,237,238,239,240,241,242,243,244,245,246,247,248,249,250,251,252,253,254,255,256,257,258,259,260,261,262,263,264,265,266,267,268,269,270,271,272,273,274,275,276,277,278,279,280,281,282,283,284,285,286,287,288,289,290,291,292,293,294,295,296,297,298,299,300,301,302,303,304,305,306,307,308,309,310,311,312,313,314,315,316,317,318,319,320,321,322,323,324,325,326,327,328,329,330,331,332,333,334,335,336,337,338,339,340,341,342,343,344,345,346,347,348,349,350,351,352,353,354,355,356,357,358,359,360,361,362,363,364,365,366,367,368,369,370,371,372,373,374,375,376,377,378,379,380,381,382,383,384,385,386,387,388,389,390,391,392,393,394,395,396,397,398,399,400,401,402,403,404,405,406,407,408,409,410,411,412,413,414,415,416,417,418,419,420,421,422,423,424,425,426,427,428,429,430,431,432,433,434,435,436,437,438,439,440,441,442,443,444,445,446,447,448,449,450,451,452,453,454,455,456,457,458,459,460,461,462,463,464,465,466,467,468,469,470,471,472,473,474,475,476,477,478,479,480,481,482,483,484,485,486,487,488,489,490,491,492,493,494,495,496,497,498,499,500,501,502,503,504,505,506,507,508,509,510,511,512,513,514,515,516,517,518,519,520,521,522,523,524,525,526,527,528,529,530,531,532,533,534,535,536,537,538,539,540,541,542,543,544,545,546,547,548,549,550,551,552,553,554,555,556,557,558,559,560,561,562,563,564,565,566,567,568,569  
## --> row.names NOT used

summary(model)

##   
## Call:  
## svm.default(x = finaldata, y = class, kernel = "radial", gamma = 0.5,   
## cost = 1, cross = 10)  
##   
##   
## Parameters:  
## SVM-Type: eps-regression   
## SVM-Kernel: radial   
## cost: 1   
## gamma: 0.5   
## epsilon: 0.1   
##   
##   
## Number of Support Vectors: 500  
##   
##   
##   
## 10-fold cross-validation on training data:  
##   
## Total Mean Squared Error: 0.7886095   
## Squared Correlation Coefficient: 0.2278762   
## Mean Squared Errors:  
## 0.5730806 0.6487815 0.6626185 0.9163434 0.5718871 1.268323 0.7415933 0.8478971 0.7037026 0.948087