# **SVMRtext**

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```
library(tm)
## Loading required package: NLP
library(stringr)
library(wordcloud)
## Loading required package: RColorBrewer
library(SnowballC)
library(arules)
## Loading required package: Matrix
##
## Attaching package: 'arules'
## The following object is masked from 'package:tm':
##
##
       inspect
## The following objects are masked from 'package:base':
##
##
       abbreviate, write
library(cluster)
library(stringi)
library(Matrix)
library(tidytext)
library(plyr)
library(factoextra)
## Loading required package: ggplot2
## Attaching package: 'ggplot2'
```

```
## The following object is masked from 'package:NLP':
##
##
      annotate
## Welcome! Want to learn more? See two factoextra-related books at https://goo.gl/ve3WBa
library(mclust)
## Package 'mclust' version 5.4.7
## Type 'citation("mclust")' for citing this R package in publications.
library(naivebayes)
## naivebayes 0.9.7 loaded
library(tidyverse)
## -- Attaching packages ------ tidyverse 1.3.0 --
## v tidyr 1.1.3 v dplyr 1.0.5
## v readr 1.4.0 v forcats 0.5.1
## -- Conflicts ----- tidyverse_conflicts() --
## x ggplot2::annotate() masks NLP::annotate()
## x dplyr::arrange() masks plyr::arrange()
## x purrr::compact() masks plyr::compact()
                    masks plyr::count()
masks Matrix::expan
## x dplyr::count()
## x tidyr::expand()
                       masks Matrix::expand()
## x dplyr::failwith() masks plyr::failwith()
## x dplyr::filter()
                       masks stats::filter()
## x dplyr::id()
                       masks plyr::id()
## x dplyr::lag()
                       masks stats::lag()
## x purrr::map()
                       masks mclust::map()
## x dplyr::mutate()
                       masks plyr::mutate()
                       masks Matrix::pack()
## x tidyr::pack()
## x dplyr::recode()
                       masks arules::recode()
## x dplyr::rename()
                       masks plyr::rename()
## x dplyr::summarise() masks plyr::summarise()
## x dplyr::summarize() masks plyr::summarize()
## x tidyr::unpack()
                       masks Matrix::unpack()
library(ggplot2)
library(caret)
## Loading required package: lattice
##
## Attaching package: 'caret'
```

```
## The following object is masked from 'package:purrr':
##
##
       lift
library(caretEnsemble)
##
## Attaching package: 'caretEnsemble'
## The following object is masked from 'package:ggplot2':
##
##
       autoplot
library(psych)
##
## Attaching package: 'psych'
## The following object is masked from 'package:mclust':
##
##
       sim
## The following objects are masked from 'package:ggplot2':
##
##
       %+%, alpha
library(Amelia)
## Loading required package: Rcpp
## ##
## ## Amelia II: Multiple Imputation
## ## (Version 1.8.0, built: 2021-05-26)
## ## Copyright (C) 2005-2021 James Honaker, Gary King and Matthew Blackwell
## ## Refer to http://gking.harvard.edu/amelia/ for more information
## ##
library(mice)
## Attaching package: 'mice'
## The following object is masked from 'package:stats':
##
##
       filter
## The following objects are masked from 'package:base':
##
##
       cbind, rbind
```

```
library(GGally)
## Registered S3 method overwritten by 'GGally':
    method from
##
    +.gg
           ggplot2
library(e1071)
library(ggthemes)
library(Cairo)
library(network)
## 'network' 1.17.1 (2021-06-12), part of the Statnet Project
## * 'news(package="network")' for changes since last version
## * 'citation("network")' for citation information
## * 'https://statnet.org' for help, support, and other information
##
## Attaching package: 'network'
## The following object is masked from 'package:plyr':
##
##
       is.discrete
library(ggtext)
library(readxl)
library(RColorBrewer)
library(slam)
library(proxy)
##
## Attaching package: 'proxy'
## The following object is masked from 'package:Matrix':
##
##
       as.matrix
## The following objects are masked from 'package:stats':
##
##
       as.dist, dist
## The following object is masked from 'package:base':
##
##
       as.matrix
library(stringr)
library(textmineR)
## Attaching package: 'textmineR'
```

```
## The following object is masked from 'package:Matrix':
##
       update
##
## The following object is masked from 'package:stats':
##
##
       update
library(igraph)
##
## Attaching package: 'igraph'
## The following objects are masked from 'package:network':
##
##
       %c%, %s%, add.edges, add.vertices, delete.edges, delete.vertices,
##
       get.edge.attribute, get.edges, get.vertex.attribute, is.bipartite,
##
       is.directed, list.edge.attributes, list.vertex.attributes,
       set.edge.attribute, set.vertex.attribute
##
## The following objects are masked from 'package:dplyr':
##
       as_data_frame, groups, union
##
## The following objects are masked from 'package:purrr':
##
##
       compose, simplify
## The following object is masked from 'package:tidyr':
##
##
       crossing
##
  The following object is masked from 'package:tibble':
##
##
       as_data_frame
## The following object is masked from 'package:arules':
##
##
       union
## The following objects are masked from 'package:stats':
##
##
       decompose, spectrum
## The following object is masked from 'package:base':
##
##
       union
library(klaR)
```

## Loading required package: MASS

```
##
## Attaching package: 'MASS'
## The following object is masked from 'package:dplyr':
##
## select
head(CropDF<-read.csv("/Users/raezh1/Documents/Georgetown/ANLY501/assignment_5new/files/Crop_recommenda</pre>
```

```
N P K temperature humidity humidity_level
                                                    ph rainfall label
##
## 1 90 42 43
               20.87974 82.00274
                                          High 6.502985 202.9355 rice
## 2 85 58 41
               21.77046 80.31964
                                          High 7.038096 226.6555 rice
## 3 60 55 44 23.00446 82.32076
                                          High 7.840207 263.9642 rice
## 4 74 35 40 26.49110 80.15836
                                          High 6.980401 242.8640 rice
## 5 78 42 42 20.13017 81.60487
                                          High 7.628473 262.7173 rice
## 6 69 37 42
               23.05805 83.37012
                                          High 7.073454 251.0550 rice
```

### Make test and train data

## Testing data

### Change data type

```
str(CropDF)
## 'data.frame':
                   2200 obs. of 9 variables:
## $ N
                   : int 90 85 60 74 78 69 69 94 89 68 ...
## $ P
                   : int 42 58 55 35 42 37 55 53 54 58 ...
## $ K
                   : int 43 41 44 40 42 42 38 40 38 38 ...
                  : num 20.9 21.8 23 26.5 20.1 ...
## $ temperature
## $ humidity
                 : num 82 80.3 82.3 80.2 81.6 ...
## $ humidity_level: chr
                          "High" "High" "High" "High" ...
## $ ph
                   : num 6.5 7.04 7.84 6.98 7.63 ...
## $ rainfall
                   : num 203 227 264 243 263 ...
## $ label
                   : chr "rice" "rice" "rice" "rice" ...
CropDF$N <- as.numeric(CropDF$N)</pre>
CropDF$P <- as.numeric(CropDF$P)</pre>
CropDF$K <- as.numeric(CropDF$K)</pre>
CropDF$label <- as.factor(CropDF$label)</pre>
str(CropDF)
## 'data.frame':
                   2200 obs. of 9 variables:
                   : num 90 85 60 74 78 69 69 94 89 68 ...
## $ N
## $ P
                   : num 42 58 55 35 42 37 55 53 54 58 ...
## $ K
                   : num 43 41 44 40 42 42 38 40 38 38 ...
## $ temperature : num 20.9 21.8 23 26.5 20.1 ...
## $ humidity : num 82 80.3 82.3 80.2 81.6 ...
```

### Remove the labels and store them

```
DF_Test_Crop_Labels <- DF_Test_Crop$label
```

### Remove the labels

```
DF_Test_Crop_NL<-DF_Test_Crop[ , -which(names(DF_Test_Crop) %in% c("label"))]
```

### Check size

```
(nrow(DF_Test_Crop_NL))
```

## [1] 550

# Training data

### Copy the Labels

```
DF_Train_Crop_Labels <- DF_Train_Crop$label
```

### Remove the labels

```
DF_Train_Crop_NL<-DF_Train_Crop[ , -which(names(DF_Train_Crop) %in% c("label"))]
head(DF_Train_Crop_NL)</pre>
```

#### Check size

```
(nrow(DF_Train_Crop_NL))
## [1] 1650
```

## "tune" the SVM by altering the cost

```
## Parameter tuning of 'svm':
## - sampling method: 10-fold cross validation
##
## - best parameters:
##
  cost
##
##
## - best performance: 0.01333333
## - Detailed performance results:
##
      cost
                error dispersion
## 1 1e-02 0.20666667 0.04877439
## 2 1e-01 0.02363636 0.01523881
## 3 1e+00 0.01393939 0.01279284
## 4 1e+01 0.01333333 0.01333945
## 5 1e+02 0.01454545 0.01076599
## 6 1e+03 0.01454545 0.01184879
```

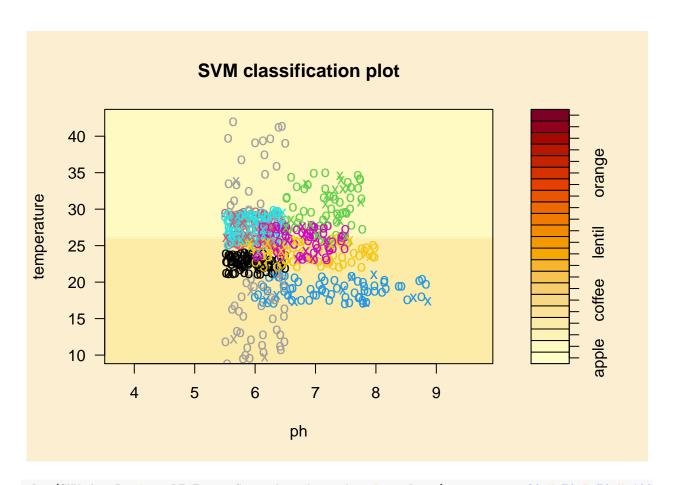
# Set up the SVM

### Polynomial Kernel

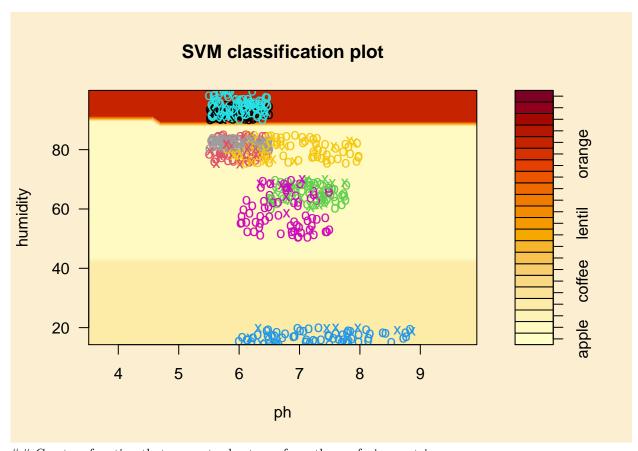
```
str(DF_Train_Crop)
                   1650 obs. of 8 variables:
## 'data.frame':
## $ N
                : num 90 85 60 78 69 94 89 68 90 78 ...
## $ P
                 : num 42 58 55 42 55 53 54 58 46 58 ...
## $ K
                 : num 43 41 44 42 38 40 38 38 42 44 ...
## $ temperature: num 20.9 21.8 23 20.1 22.7 ...
                 : num 82 80.3 82.3 81.6 82.6 ...
## $ humidity
## $ ph
                 : num 6.5 7.04 7.84 7.63 5.7 ...
## $ rainfall
                 : num 203 227 264 263 271 ...
## $ label
                 : Factor w/ 22 levels "apple", "banana",...: 21 21 21 21 21 21 21 21 21 21 21 ...
SVM_fit_P <- svm(label~., data=DF_Train_Crop,</pre>
               kernel="polynomial", cost=100,
               scale=FALSE)
print(SVM_fit_P)
##
## Call:
## svm(formula = label ~ ., data = DF_Train_Crop, kernel = "polynomial",
       cost = 100, scale = FALSE)
##
##
## Parameters:
##
      SVM-Type: C-classification
##
   SVM-Kernel: polynomial
##
         cost: 100
        degree: 3
##
##
        coef.0: 0
##
## Number of Support Vectors: 340
```

### Prediction

```
pred_P <- predict(SVM_fit_P, DF_Test_Crop_NL, type="class")
par(bg = "#fbeed1")
plot(SVM_fit_P, data=DF_Train_Crop, temperature~ph, slice=list(humidity=42,N=70,P=70,K=100,rainfall=150)</pre>
```



plot(SVM\_fit\_P, data=DF\_Train\_Crop, humidity~ph, slice=list(temperature=20,N=70,P=70,K=100,rainfall=150



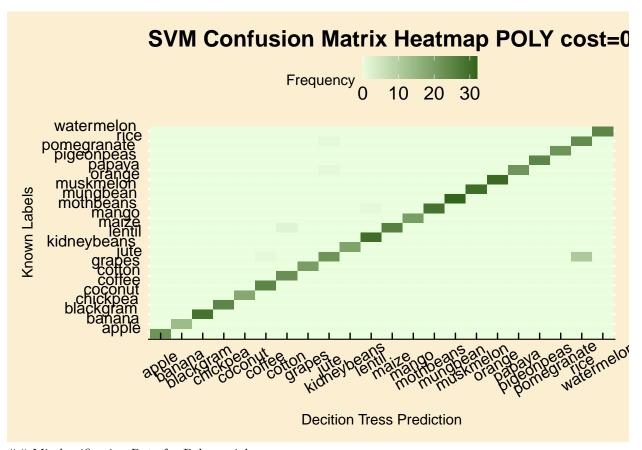
## Create a function that generates heatmap from the confusion matrix

#### Confusion Matrix

	_							_		_	•	•
##	apple	22	0		0	0		0	0	0	0	0
##	banana	0	14		0	0		0	0	0	0	0
##	blackgram	0	0		29	0		0	0	0	0	0
##	chickpea	0	0		0	25		0	0	0	0	0
##	coconut	0	0		0	0		18	0	0	0	0
##	coffee	0	0		0	0		0	25	0	0	1
##	cotton	0	0		0	0		0	0	23	0	0
##	grapes	0	0		0	0		0	0	0	20	0
##	jute	0	0		0	0		0	0	0	0	22
##	kidneybeans	0	0		0	0		0	0	0	0	0
##	lentil	0	0		0	0		0	0	0	0	0
##	maize	0	0		0	0		0	0	0	0	0
##	mango	0	0		0	0		0	0	0	0	0
##	mothbeans	0	0		0	0		0	0	0	0	0
##	mungbean	0	0		0	0		0	0	0	0	0
##	muskmelon	0	0		0	0		0	0	0	0	0
##	orange	0	0		0	0		0	0	0	0	0
##	papaya	0	0		0	0		0	0	0	0	0
##	pigeonpeas	0	0		0	0		0	0	0	0	0
##	pomegranate	0	0		0	0		0	0	0	0	0
##	rice	0	0		0	0		0	0	0	0	11
## ##	watermelon	0	0	. h . 7 .	0	0		0	0	0	0	0
		F_Test_					4 1 1 .			1		
## ##	pred_P	ктапеу	oeans re	0	maize 0	mango n	iio cii be	eans i	nungbean 0	musk	0	
##	apple banana		0	0	0	0		0	0		0	
##	blackgram		0	0	0	0		0	0		0	
##	chickpea		0	0	0	0		0	0		0	
##	coconut		0	0	0	0		0	0		0	
##	coffee		0	0	0	0		0	0		0	
##	cotton		0	0	2	0		0	0		0	
##	grapes		0	0	0	0		0	0		0	
##	jute		0	0	0	0		0	0		0	
##	kidneybeans		19	0	0	0		0	0		0	
##	lentil		0	30	0	0		1	0		0	
##	maize		0	0	26	0		0	0		0	
##	mango		0	0	0			•	·		•	
##	_				U	20		0	0		0	
	mothbeans					20 0		0 29	0		0	
##			0	0	0	0		29	0		0	
## ##	mungbean		0	0	0	0		29	0 32		0	
##	mungbean muskmelon		0	0 0	0 0	0		29 0 0	0 32 0		0 0 30	
## ##	mungbean muskmelon orange		0 0	0 0 0	0 0 0	0 0		29 0 0 0	0 32 0 0		0 0 30 0	
## ## ##	mungbean muskmelon orange papaya		0 0 0	0 0 0 0	0 0 0 0	0 0 0		29 0 0 0 0	0 32 0 0		0 0 30 0	
## ##	mungbean muskmelon orange papaya pigeonpeas		0 0 0 0	0 0 0	0 0 0 0 0 0	0 0 0 0		29 0 0 0	0 32 0 0		0 0 30 0 0	
## ## ## ##	mungbean muskmelon orange papaya pigeonpeas pomegranate		0 0 0 0 0 0	0 0 0 0 0	0 0 0 0 0 0 0	0 0 0 0 0		29 0 0 0 0	0 32 0 0 0		0 0 30 0 0 0	
## ## ## ##	mungbean muskmelon orange papaya pigeonpeas pomegranate rice		0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0	0 0 0 0 0 0	0 0 0 0 0		29 0 0 0 0 0	0 32 0 0 0		0 0 30 0 0	
## ## ## ## ##	mungbean muskmelon orange papaya pigeonpeas pomegranate rice watermelon	)F Test	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0	0 0 0 0 0 0		29 0 0 0 0 0 0	0 32 0 0 0 0		0 0 30 0 0 0	
## ## ## ## ##	mungbean muskmelon orange papaya pigeonpeas pomegranate rice watermelon	F_Test orange	0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0	anate	29 0 0 0 0 0 0 0	0 32 0 0 0 0 0	on	0 0 30 0 0 0	
## ## ## ## ##	mungbean muskmelon orange papaya pigeonpeas pomegranate rice watermelon  I pred_P		0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0	anate 0	29 0 0 0 0 0 0 0	0 32 0 0 0 0	.on 0	0 0 30 0 0 0	
## ## ## ## ## ##	mungbean muskmelon orange papaya pigeonpeas pomegranate rice watermelon	orange	0 0 0 0 0 0 0 0 0 Crop_La	0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0		29 0 0 0 0 0 0 0 0	0 32 0 0 0 0 0		0 0 30 0 0 0	
## ## ## ## ## ##	mungbean muskmelon orange papaya pigeonpeas pomegranate rice watermelon  pred_P apple banana	orange 0	0 0 0 0 0 0 0 0 Crop_Lapaya	0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0	0	29 0 0 0 0 0 0 0 0 0	0 32 0 0 0 0 0	0	0 0 30 0 0 0	
## ## ## ## ## ##	mungbean muskmelon orange papaya pigeonpeas pomegranate rice watermelon  pred_P apple	orange 0 0	0 0 0 0 0 0 0 0 _Crop_L: papaya 0	0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0	0	29 0 0 0 0 0 0 0 0 0 0	0 32 0 0 0 0 0	0	0 0 30 0 0 0	
######################################	mungbean muskmelon orange papaya pigeonpeas pomegranate rice watermelon  pred_P apple banana blackgram	orange 0 0 0	0 0 0 0 0 0 0 0 Crop_Lapaya 0 0	0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0	0 0 0	29 0 0 0 0 0 0 0 0 0 0 0	0 32 0 0 0 0 0	0 0 0	0 0 30 0 0 0	

##	cotton	0	0	0	0	0	0
##	grapes	0	0	0	0	0	0
##	jute	0	1	0	0	1	0
##	kidneybeans	0	0	0	0	0	0
##	lentil	0	0	0	0	0	0
##	maize	0	0	0	0	0	0
##	mango	0	0	0	0	0	0
##	mothbeans	0	0	0	0	0	0
##	mungbean	0	0	0	0	0	0
##	muskmelon	0	0	0	0	0	0
##	orange	31	0	0	0	0	0
##	papaya	0	22	0	0	0	0
##	pigeonpeas	0	0	25	0	0	0
##	pomegranate	0	0	0	22	0	0
##	rice	0	0	0	0	24	0
##	watermelon	0	0	0	0	0	25

get\_heatmap("SVM Confusion Matrix Heatmap POLY cost=0.1", pred\_P)



## Misclassification Rate for Polynomial

(MR\_P <- 1 - sum(diag(Ptable))/sum(Ptable))</pre>

## [1] 0.03090909

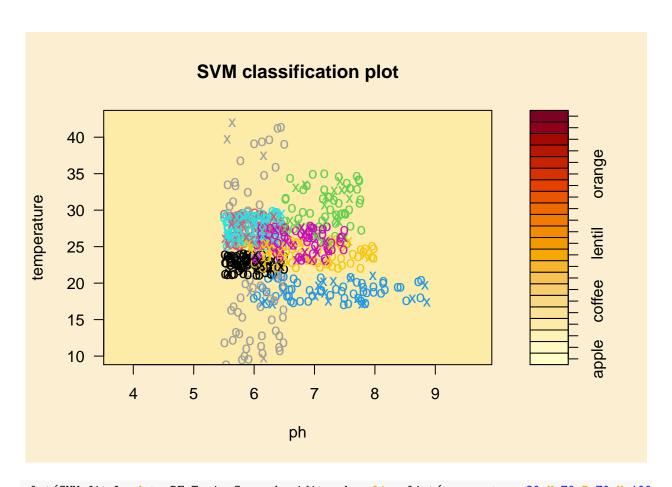
## Linear Kernel...

```
SVM_fit_L <- svm(label~., data=DF_Train_Crop,</pre>
                 kernel="linear", cost=10,
                 scale=FALSE)
print(SVM_fit_L)
##
## Call:
## svm(formula = label ~ ., data = DF_Train_Crop, kernel = "linear",
       cost = 10, scale = FALSE)
##
##
## Parameters:
      SVM-Type: C-classification
##
## SVM-Kernel: linear
         cost: 10
##
##
## Number of Support Vectors: 382
```

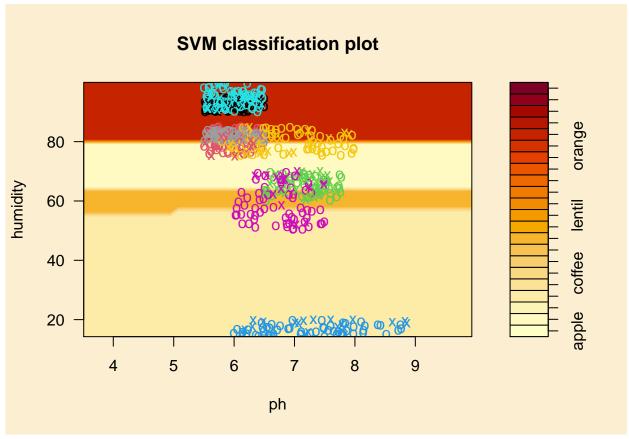
## Prediction

```
pred_L <- predict(SVM_fit_L, DF_Test_Crop_NL, type="class")

par(bg = "#fbeed1")
plot(SVM_fit_L, data=DF_Train_Crop, temperature~ph, slice=list(humidity=42,N=70,P=70,K=100,rainfall=150)</pre>
```



plot(SVM\_fit\_L, data=DF\_Train\_Crop, humidity~ph, slice=list(temperature=20,N=70,P=70,K=100,rainfall=150



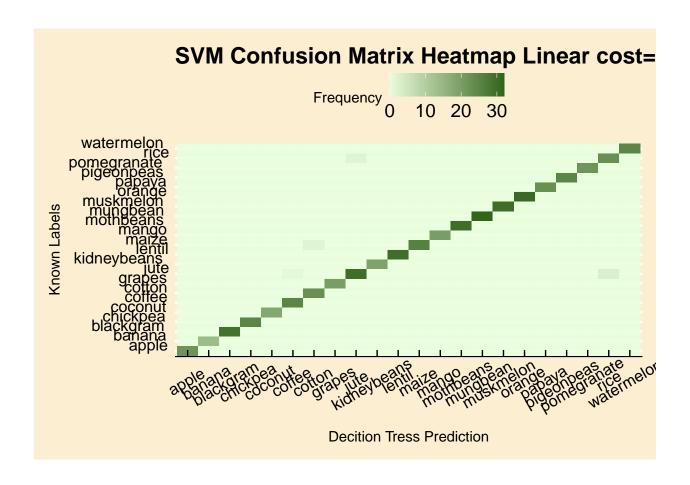
## Confusion Matrix

(Ltable <- table(pred\_L, DF\_Test\_Crop\_Labels))</pre>

##	## DF_Test_Crop_Labels										
##	pred_L	apple	${\tt banana}$	blackgram	${\tt chickpea}$	${\tt coconut}$	coffee	${\tt cotton}$	grapes	jute	
##	apple	22	0	0	0	0	0	0	0	0	
##	banana	0	14	0	0	0	0	0	0	0	
##	blackgram	0	0	29	0	0	0	0	0	0	
##	chickpea	0	0	0	25	0	0	0	0	0	
##	coconut	0	0	0	0	18	0	0	0	0	
##	coffee	0	0	0	0	0	25	0	0	1	
##	cotton	0	0	0	0	0	0	23	0	0	
##	grapes	0	0	0	0	0	0	0	20	0	
##	jute	0	0	0	0	0	0	0	0	30	
##	kidneybeans	0	0	0	0	0	0	0	0	0	
##	lentil	0	0	0	0	0	0	0	0	0	
##	maize	0	0	0	0	0	0	0	0	0	
##	mango	0	0	0	0	0	0	0	0	0	
##	mothbeans	0	0	0	0	0	0	0	0	0	
##	mungbean	0	0	0	0	0	0	0	0	0	
##	muskmelon	0	0	0	0	0	0	0	0	0	
##	orange	0	0	0	0	0	0	0	0	0	
##	papaya	0	0	0	0	0	0	0	0	0	
##	pigeonpeas	0	0	0	0	0	0	0	0	0	
##	pomegranate	0	0	0	0	0	0	0	0	0	
##	rice	0	0	0	0	0	0	0	0	3	

##	watermelon	0 DF_Test	O Crop I	ahale	0	(	)	0	0	0	0	0
	pred_L		_		maize	mango	mothbe	aang	mungbean	musk	melon	
##	apple	Ridicy	0	0	0	0	mound	0		muon	0	
##	banana		0	0	0	0		0	0		0	
##	blackgram		0	0	0	0		0	0		0	
##	chickpea		0	0	0	0		0	0		0	
##	coconut		0	0	0	0		0	0		0	
##	coffee		0	0	0	0		0	0		0	
##	cotton		0	0	2	0		0	0		0	
##	grapes		0	0	0	0		0	0		0	
##	jute		0	0	0	0		0	0		0	
##	kidneybeans		19	0	0	0		0	0		0	
##	lentil		0	30	0	0		0	0		0	
##	maize		0	0	26	0		0	0		0	
##	mango		0	0	0	20		0	0		0	
##	mothbeans		0	0	0	0		30	0		0	
##	mungbean		0	0	0	0		0	32		0	
##	muskmelon		0	0	0	0		0	0		30	
##	orange		0	0	0	0		0	0		0	
##	papaya		0	0	0	0		0	0		0	
##	pigeonpeas		0	0	0	0		0	0		0	
##	pomegranate		0	0	0	0		0	0		0	
##	rice		0	0	0	0		0	0		0	
##	watermelon		0	0	0	0		0	0		0	
##		DF_Test_										
	pred_L					pomeg			waterme.			
##	apple	0	0		0		0	0		0		
##	banana	0	0		0		0	0		0		
##	blackgram	0	0		0		0	0		0		
##	chickpea	0	0		0		0	0		0		
##	coconut	0	0		0		0	0		0		
## ##	coffee	0	0		0		0	0		0		
##	cotton	0	0		0		0	0		0		
##	grapes jute	0	0		0		0	2		0		
##	kidneybeans	0	0		0		0	0		0		
##	lentil	0	0		0		0	0		0		
##	maize	0	0		0		0	0		0		
##	mango	0	0		0		0	0		0		
##	mothbeans	0	0		0		0	0		0		
##	mungbean	0	0		0		0	0		0		
##	muskmelon	0	0		0		0	0		0		
##	orange	31	0		0		0	0		0		
##	papaya	0	23		0		0	0		0		
##	pigeonpeas	0	0		25		0	0		0		
##	pomegranate	0	0		0		22			0		
##	rice	0	0		0		0	23		0		
##	watermelon	0	0		0		0	0		25		

get\_heatmap("SVM Confusion Matrix Heatmap Linear cost=0.1", pred\_L)



### Misclassification Rate for Linear

```
(MR_L <- 1 - sum(diag(Ltable))/sum(Ltable))
```

## [1] 0.01454545

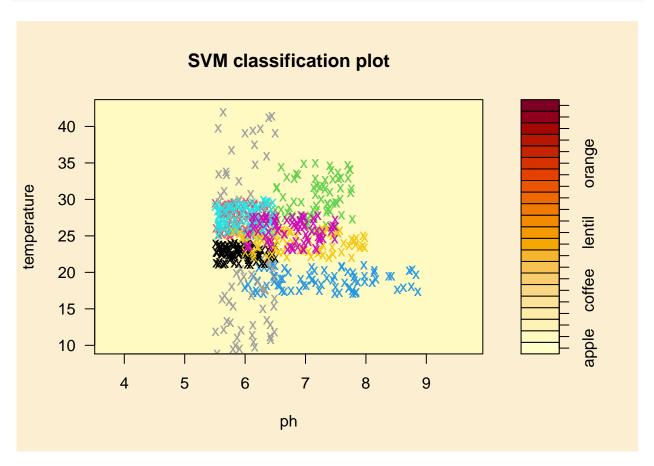
# Radial Kernel

```
## SVM-Type: C-classification
## SVM-Kernel: radial
## cost: 0.1
##
## Number of Support Vectors: 1650
```

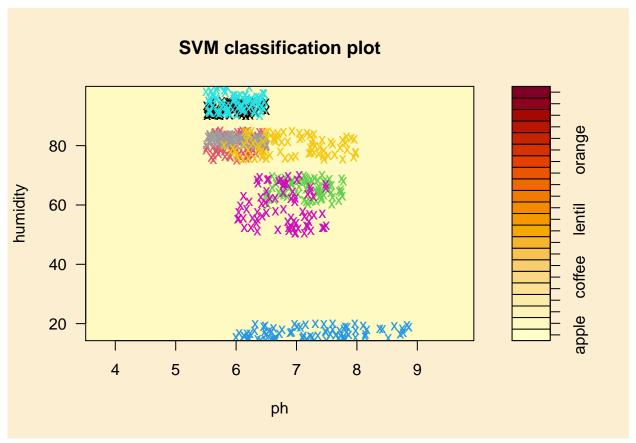
## Prediction

```
pred_R <- predict(SVM_fit_R, DF_Test_Crop_NL, type="class")

par(bg = "#fbeed1")
plot(SVM_fit_R, data=DF_Train_Crop, temperature~ph, slice=list(humidity=42,N=70,P=70,K=100,rainfall=150)</pre>
```



plot(SVM\_fit\_R, data=DF\_Train\_Crop, humidity~ph, slice=list(temperature=20,N=70,P=70,K=100,rainfall=150



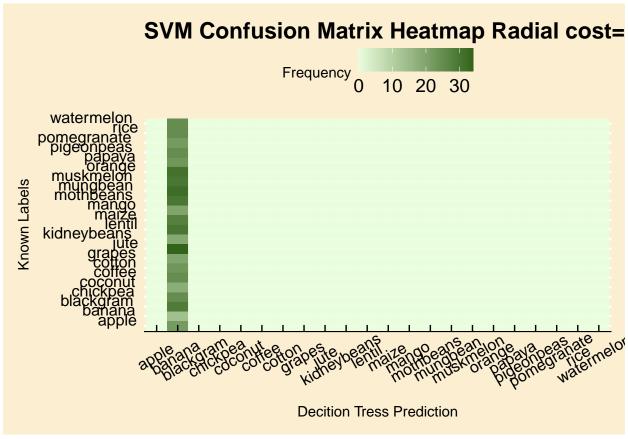
## Confusion Matrix

(Rtable <- table(pred\_R, DF\_Test\_Crop\_Labels))

##	## DF_Test_Crop_Labels										
##	pred_R	apple	banana	blackgram	chickpea	coconut	${\tt coffee}$	${\tt cotton}$	grapes	jute	
##	apple	0	0	0	0	0	0	0	0	0	
##	banana	22	14	29	25	18	25	23	20	34	
##	blackgram	0	0	0	0	0	0	0	0	0	
##	chickpea	0	0	0	0	0	0	0	0	0	
##	coconut	0	0	0	0	0	0	0	0	0	
##	coffee	0	0	0	0	0	0	0	0	0	
##	cotton	0	0	0	0	0	0	0	0	0	
##	grapes	0	0	0	0	0	0	0	0	0	
##	jute	0	0	0	0	0	0	0	0	0	
##	kidneybeans	0	0	0	0	0	0	0	0	0	
##	lentil	0	0	0	0	0	0	0	0	0	
##	maize	0	0	0	0	0	0	0	0	0	
##	mango	0	0	0	0	0	0	0	0	0	
##	mothbeans	0	0	0	0	0	0	0	0	0	
##	mungbean	0	0	0	0	0	0	0	0	0	
##	muskmelon	0	0	0	0	0	0	0	0	0	
##	orange	0	0	0	0	0	0	0	0	0	
##	papaya	0	0	0	0	0	0	0	0	0	
##	pigeonpeas	0	0	0	0	0	0	0	0	0	
##	pomegranate	0	0	0	0	0	0	0	0	0	
##	rice	0	0	0	0	0	0	0	0	0	

##	watermelon	0	0		0	(	)	0	0	0	0	0
##	I	DF_Test_	_Crop_L	abels								
##	pred_R	kidneyb	peans 1	entil	${\tt maize}$	mango	mothbe	eans	mungbean	musk	melon	
##	apple		0	0	0	0		0	0		0	
##	banana		19	30	28	20		30	32		30	
##	blackgram		0	0	0	0		0	0		0	
##	chickpea		0	0	0	0		0	0		0	
##	coconut		0	0	0	0		0	0		0	
##	coffee		0	0	0	0		0	0		0	
##	cotton		0	0	0	0		0	0		0	
##	grapes		0	0	0	0		0	0		0	
##	jute		0	0	0	0		0	0		0	
##	kidneybeans		0	0	0	0		0	0		0	
##	lentil		0	0	0	0		0	0		0	
##	maize		0	0	0	0		0	0		0	
##	mango		0	0	0	0		0	0		0	
##	mothbeans		0	0	0	0		0	0		0	
##	mungbean		0	0	0	0		0	0		0	
##	muskmelon		0	0	0	0		0	0		0	
##	orange		0	0	0	0		0	0		0	
##	papaya		0	0	0	0		0	0		0	
##	pigeonpeas		0	0	0	0		0	0		0	
##	pomegranate		0	0	0	0		0	0		0	
##	rice		0	0	0	0		0	0		0	
##	watermelon		0	0	0	0		0	0		0	
##		OF_Test_	_			n . m . m		mi	+	lan		
##	pred_R	orange 0	papaya O		onpeas 0	pomeg.	o lanate	0	waterme	0		
##	apple banana	31	23		25		22	25		25		
##	blackgram	0	0		0		0	0		0		
##	chickpea	0	0		0		0	0		0		
##	coconut	0	O		0		0	0		0		
##	coffee	0	O		0		0	0		0		
##	cotton	0	O		0		0	0		0		
##	grapes	0	O		0		0	0		0		
##	jute	0	0		0		0	0		0		
##	kidneybeans	0	0	)	0		0	0		0		
##	lentil	0	0	)	0		0	0		0		
##	maize	0	0		0		0	0		0		
##	mango	0	0	)	0		0	0		0		
##	mothbeans	0	0	)	0		0	0		0		
##	mungbean	0	0	)	0		0	0		0		
##	muskmelon	0	O	)	0		0	0		0		
##	orange	0	0	)	0		0	0		0		
##	papaya	0	0	)	0		0	0		0		
##	pigeonpeas	0	C	)	0		0	0		0		
##	pomegranate	0	C	)	0		0	0		0		
##	rice	0	0		0		0	0		0		
##	watermelon	0	0	)	0		0	0		0		

get\_heatmap("SVM Confusion Matrix Heatmap Radial cost=0.1", pred\_R)



## Misclassification Rate for Radial

(MR\_R <- 1 - sum(diag(Rtable))/sum(Rtable))

## [1] 0.9745455