NAME : EDWARD
NIM : 2201741971
CLASS : LB-08

Buatlah **DRAFT PUBLIKASI** dalam bentuk **PAPER REVIEW** untuk area bidang **ILMU KOMPUTER** dengan mengikuti instruksi sebagai berikut:

a. **Ada bagian** dari tugas ini yang dikerjakan secara **individu** dan juga **berkelompok (Sesuai dengan kesepakatan yang telah dibuat di kelas)**.
b. Topik yang dipakai adalah **topik yang diajukan sebagai final project kelas**. Pastikan topic dalam area bidang **ILMU KOMPUTER** (artificial intelligence, software engineering, databases, games and multimedia dan bidang ilmu komputer lainnya)
c. **[60%]** Bagian yang dilakukan secara **INDIVIDU** :
    i. Tuliskan draft **STATE OF THE ART** dari topik yang akan dipelajari berdasarkan minimal 9 makalah dari jurnal / konferensi internasional terbaru (5 tahun terakhir).
    ii. Pastikan 9 makalah dari jurnal / konferensi international yang dipakai tersebut **harus berbeda** dengan anggota kelompok yang lainnya.
    iii. Guna memfasilitasi penulisan draft **STATE OF THE ART**, kamu sebagai individu dapat mempersiapkan tabel daftar referensi, Tabel 1, yang dapat membantu penulisan.
d. **[40%]** Bagian yang dilakukan secara **BERKELOMPOK**:
    I. Kemudian susun semua publikasi yang dirujuk dalam sebuah daftar pustaka menggunakan format **APA STYLE** (atau sesuai template yang dipilih)
    II. Draft publikasi (menggunakan format A4) dapat mengikuti template IEEE yang dapat diunduh pada link sebagai berikut:
    https://www.ieee.org/conferences/publishing/templates.html
    atau template Procedia Computer Science pada link sebagai berikut:
    https://www.elsevier.com/wps/find/journaldescription.cws_home/719435?generatepdf=true

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INDIVIDU (60%)

Jawaban :

STATE OF THE ART :

1. **Tahun Publikasi** : 2016

   Penulis: Harshada, Ms & Snehal, & Shitole, Sanjay & Pranaya, Mhatre & Suchita, Kadam & Shweta, Ghanate & Kurle, Darshana

   Judul: Python Based Image Processing

   Metodologi :

   a. **Metode :** Algoritma Python
   b. **Algoritma / Arsitektur/ Model, dll :** Python Image Library
   c. **Dataset :** File format .jpg

   Kelebihan Metode : Library sudah banyak disediakan oleh Python

   Kelemahan Metode : Bisa jadi membuat Algoritma yang sama

2. **Tahun Publikasi** : 2015

   Penulis: Mendoza, Fernando & Lu, Renfu

   Judul: Basics of Image Analysis

   Metodologi :

   a. **Metode :** Penjelasan Ilmiah
   b. **Algoritma / Arsitektur/ Model, dll :** Model Ilmiah
   c. **Dataset :** tidak memakai dataset

   Kelebihan Metode : Lebih Valid karena didukung dengan Ilmiah

   Kelemahan Metode : Bisa terjadi kesalahan saat penjelasan konsep

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3. **Tahun Publikasi** : 2017

   Penulis: Poningsih, Poningsih.

   Judul: Design of the expert system to analyze disease in Plant Teak using Forward Chaining

   Metodologi :

   a. **Metode :** Forward Chaining
   b. **Algoritma / Arsitektur/ Model, dll :** Computer Vision
   c. **Dataset :** Beberapa Gambar Testing

   Kelebihan Metode : Lebih Valid karena sudah ada Ilmunya di computer vision

   Kelemahan Metode : Ketika tidak teliti, maka hasil bisa keliru

4. **Tahun Publikasi** : 2015

   Penulis: Szegedy, Christian, Wei Liu, Yangqing Jia, Pierre Sermanet, Scott Reed, Dragomir Anguelov, Dumitru Erhan, Vincent Vanhoucke, and Andrew Rabinovich

   Judul: Going deeper with convolutions

   Metodologi :

   a. **Metode :** Reverse order (top-down)
   b. **Algoritma / Arsitektur/ Model, dll :** Inception Module
   c. **Dataset :** Beberapa tes gambar

   Kelebihan Metode : Konsistensi yang bagus untuk beberapa metriks.

   Kelemahan Metode : Bisa tidak konsisten di metriks tertentu.

5. **Tahun Publikasi** : 2017

   Penulis: Su, Hang, Shaogang Gong, Xiatian Zhu, Adrian Popescu, Alexandru Ginsca, Herve Le Borgne, Yuen Peng Loh

   Judul: WebLogo-2M: Scalable Logo Detection by Deep Learning From the Web

   Metodologi :

   a. **Metode :** Bayesian methods to restore 3D scene structures
   b. **Algoritma / Arsitektur/ Model, dll :** Bayesian Rules
   c. **Dataset :** 3D scene

   Kelebihan Metode : Kinerja unggul setelah minimalisasi kesalahan kedalaman piksel-bijaksana dengan set data pelatihan.

   Kelemahan Metode : Kinerja lebih rendah untuk objek citra alami.

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6. **Tahun Publikasi** : 2016

   Penulis: Forder L, Taylor O, Mankin H, Scott RB, Franklin A

   Judul: Colour Terms Affect Detection of Colour and Colour Associated Objects Suppressed from Visual Awareness

   Metodologi :

   a. **Metode :** Psychophysical experiments in dynamic display . Dynamic device design (HDR)
   b. **Algoritma / Arsitektur/ Model, dll :** Dynamic Display
   c. **Dataset :** Objek gambar

   Kelebihan Metode : Kinerja perbedaan piksel dalam kisaran 3,7 unit log di bawah kondisi pengamatan tertentu.

   Kelemahan Metode : Bisa terjadi perbedaan piksel yang besar di gambar tertentu.

7. **Tahun Publikasi** : 2015

   Penulis: Joulan K, Brémond R, Hautière N.

   Judul: Towards an Analytical Age-Dependent Model of Contrast Sensitivity Functions for an Ageing Society

   Metodologi :

   a. **Metode :** Sensitivity technique based on the Contrast Function (CSF)
   b. **Algoritma / Arsitektur/ Model, dll :** psychophysical Model
   c. **Dataset :** Driver Data

   Kelebihan Metode : Mengembangkan deskriptor visibilitas pengemudi yang canggih.

   Kelemahan Metode :Jika tidak ada yang mendaftar.

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8. **Tahun Publikasi** : 2015

   Penulis: Nasrollahi, Kamal, Sergio Escalera, Pejman Rasti, Gholamreza Anbarjafari, Xavier Baro, Hugo Jair Escalante, and Thomas B. Moeslund

   Judul: Deep learning based super-resolution for improved action recognition

   Metodologi :

   a. **Metode :** Image illumination enhancement on color pixel correction
   b. **Algoritma / Arsitektur/ Model, dll :** Pixel Correction
   c. **Dataset :** Standard Histogram & Local Histogram

   Kelebihan Metode : Membandingkan dengan distribusi histogram standar umum (GHE) dan pemerataan histogram lokal (LHE).

   Kelemahan Metode : Bisa terjadi perbedaan yang besar di antara dua data.

9. **Tahun Publikasi** : 2015

   Penulis: Savioja, Lauri, Akio Ando, Ramani Duraiswami, Emanuel AP Habets, and Sascha Spors

   Judul: Introduction to the issue on spatial audio

   Metodologi :

   a. **Metode :** Gaussian and non-Gaussian noise
   b. **Algoritma / Arsitektur/ Model, dll :** various algorithms
   c. **Dataset :** Different set of audio file

   Kelebihan Metode : Sudah menggunakan Algoritma yang telah disediakan

   Kelemahan Metode : Ketika File Audio yang digunakan tidak baik.

Image Analysis With R Programming

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Abstract— The R programming language excels at facilitated assignments. It is broadly utilized as a high level, free and open source language which is re-mark ably unique, deciphered, scripting and multi-world view. It additionally underpins object situated programming highlights and can be utilized as a general purpose programming language. R is simpler to learn and has more straight forward linguistic structure when contrasted with C, C++ and Java. R is similarly popular for work area based applications. The fields where R truly sparkles in are information science and machine learning, numeric, representative computations. Also, it is utilized in different fields like Image processing, Games, Web improvements and Big Data Analytics. Picture preparing with R is an exceptionally efficient and viable procedure for doing tasks such as dissecting the digitization of the pictures to extract the required data. A few activities such as improving the quality, upgrading, zooming, blurring, inverting the picture, composing content on the images, greyscale, performing picture rebuilding, recovering, etc. is conceivable with R. Here's the challenge; given two images, determine if one image is a subset of the other image. This will be valuable for solving this present reality undertakings and procedures in a very effective way.

Keywords—image, analysis, subset, R Programming, processing

I. INTRODUCTION

In our daily life, people use picture as a tool for many things such as memory recovery, new discovery of people and places, certain disease study, crime investigation, map making, and else. Due to how important this picture as a tool in our life, this concept has become a necessity for developers to create a program that can differentiate a lot of images to a certain degree to help human life. As human technology becomes more progressive, there will be one time when an algorithm will be created to differentiate image from one another despite their complexity and structure. This fore-mentioned algorithm is what people called as image analysis and it becomes the fundamental basis of recognizing and differentiating images. Nowadays, image analysis is used for many of daily aspects such as Comparison of image quality with different retargeting methods quickly and reliably [4], Estimation of solid depth map of a single monocular natural image [5], Presentation of a series of psychophysical experiments to determine the simultaneous dynamic series of human visual systems under the full adaptation of background lighting [6], Development of mentoring system that notifies the driver if the speed is insufficient according to the visibility conditions [7], Image-based Illumination Inspired by Using Decomposition of Local Singular Value and Discrete Wavelet Transformation [8], and image processing applied in digital sound system [9]. For example, a face recognition application is installed within our phones to recognize our faces and store them in the storage. [2]

A. Why to learn and use R?

R is an elevated level programming language. R translators are accessible for some working frameworks that permit the execution of R code on a wide assortment of frameworks. R bolsters various programming standards, which incorporates object arranged, practical programming and procedural style. It oversees memory consequently and has an enormous and complete. In 1993 Ross Ihaka and Robert Gentleman created the R language. R is gotten from numerous other programming dialects, for example, C, C++, Unix shell and so on. [1]

B. Why Image Analysis?

An image is merely a visual portrait of something. This means that it can represent a person, an animal, or any living or non-living thing. A picture is basically a rectangular grid of pixels with a definite height and width. Each pixel possesses its own value. Thus, image quality depends on the values of this pixel, and pixel is the information unit present in an image. Image Processing is image enhancement utilizing mathematical operations for which the input is an image, such as an image or video clip and the image processing result can be either an image or a collection of image-related characteristics or parameters.

Need of image processing :

- Humans are not satisfied with the quality of images and therefore they make use of image processing.
- Humans rely upon their visual system (eyes and brain) to collect visual information about their surroundings. Visual information refers to images and videos. In the past, we needed visual information mainly for survival. Nowadays, visual information is required for survival as

well as for communication and entertainment purpose
- To enhance an image
- To extract some useful information from an image that can be utilized for heath sciences, public safety, etc.

[3] So, in short, following steps are involved in image processing:

a. Input image
b. Segmented map before integration
c. Edge map before integration
d. Segmented map and edge map after Integration
e. Pixel clustering

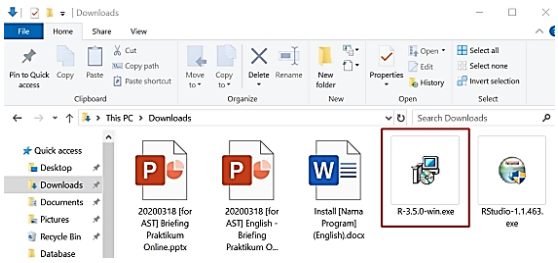
C. Why to make use of R for Image Analysis?

R has multiple packages for multiple purposes like web development, scientific and numeric computing, image analysis. To work on images, R has a packages i.e. R Imaging Library (RIL) for image analysis operations. The R Imaging Library provides many functions for image analysis. We performed some basic operations using RIL modules.

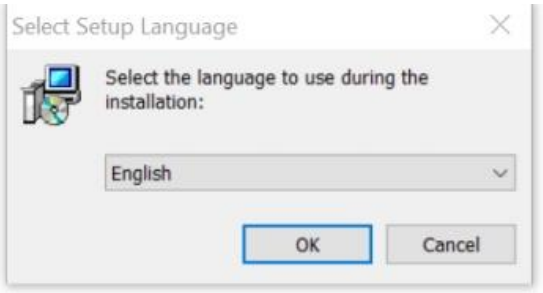
II. METHODOLOGY

A. Installing R Language 3.5.0 on Windows

a. Click on R-3.5.0-win.exe to start the installer

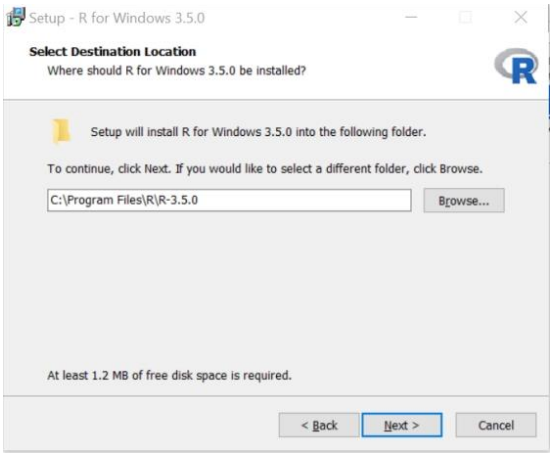


b. Select your preferred language (default english) then click OK

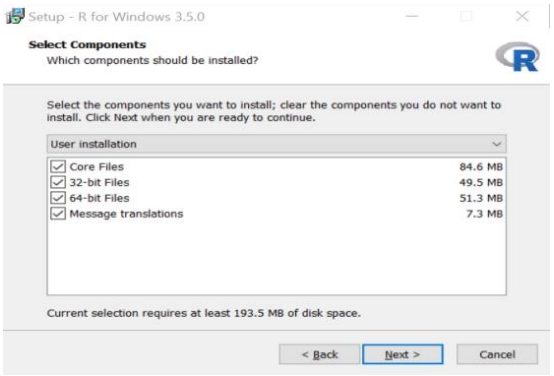


c. Click Next on terms & agreement

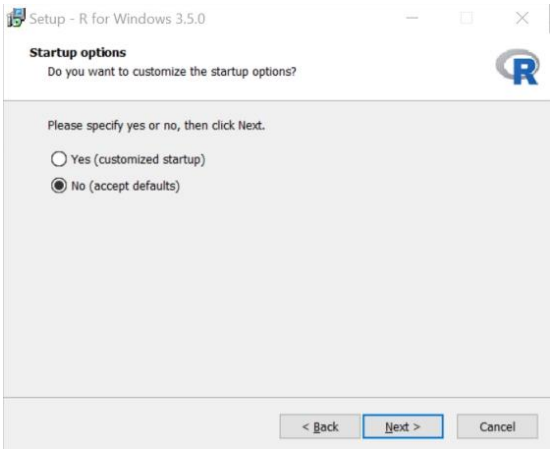
d. Select your preferred installation location then click Next



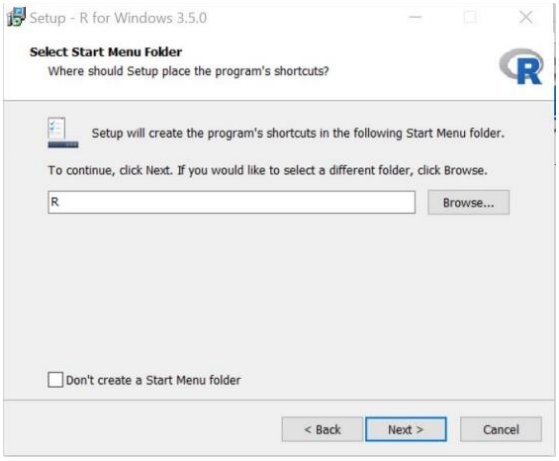
e. Click Next on select file to install



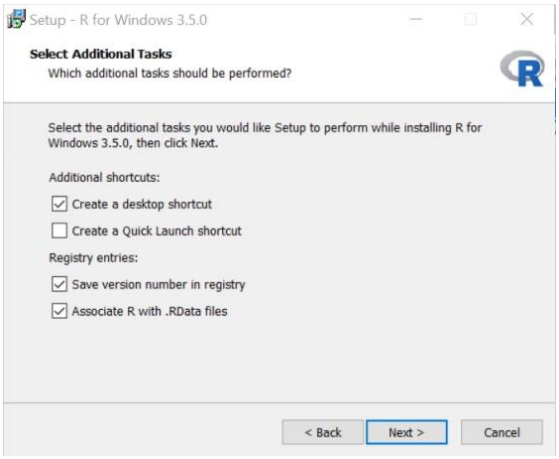
f. Select No to accept the default configuration then click Next



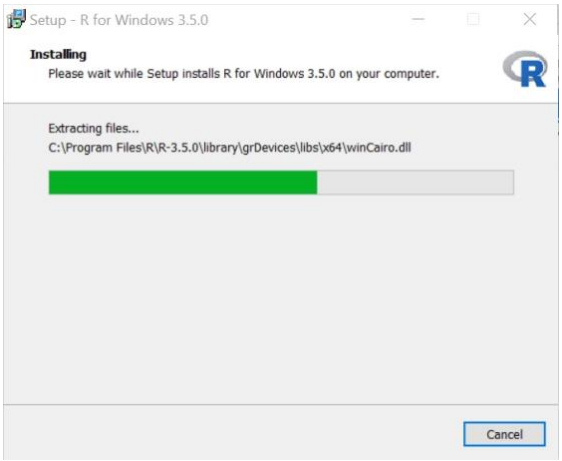
g. Click Next



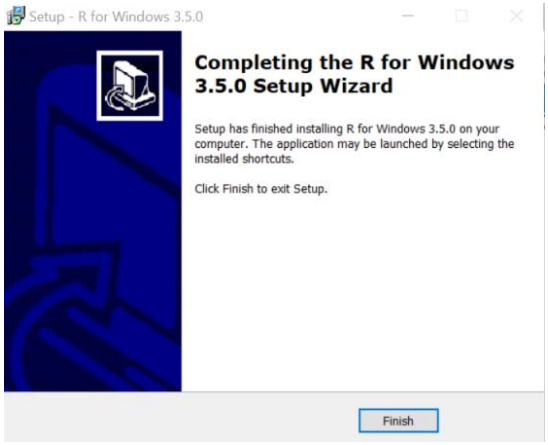
h. Select additional task that you want then click Next



i. Wait the process until completed



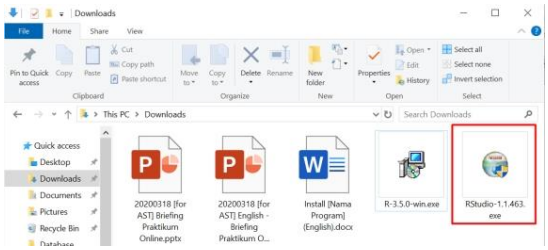
j. Click Finish



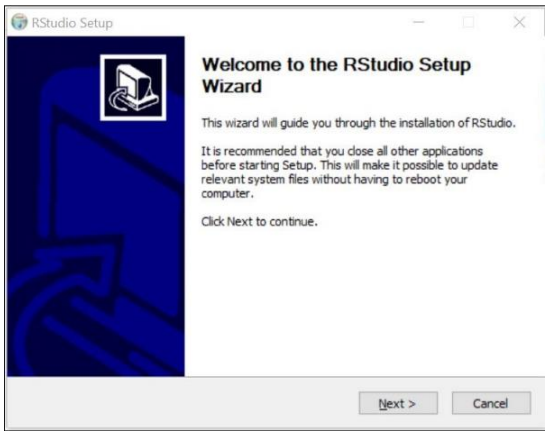
k. Installation process is finished

B. Installing Rstudio 1.1.463 on Windows

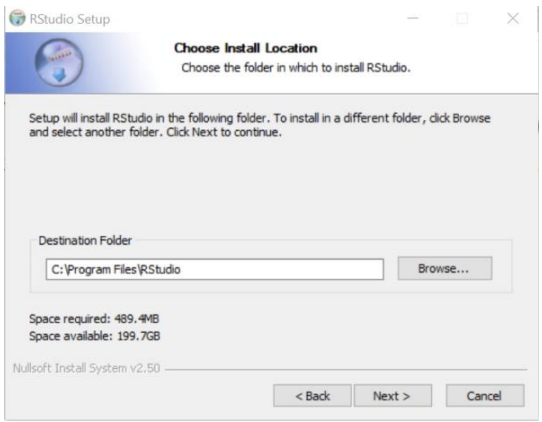
a. Click on RStudio-1.1.463.exe to start the installer



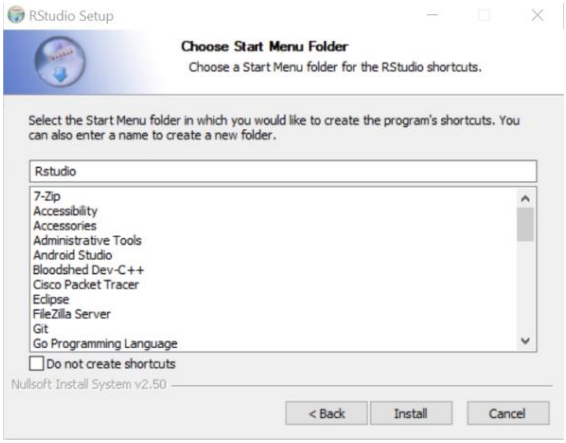
b. Click Next



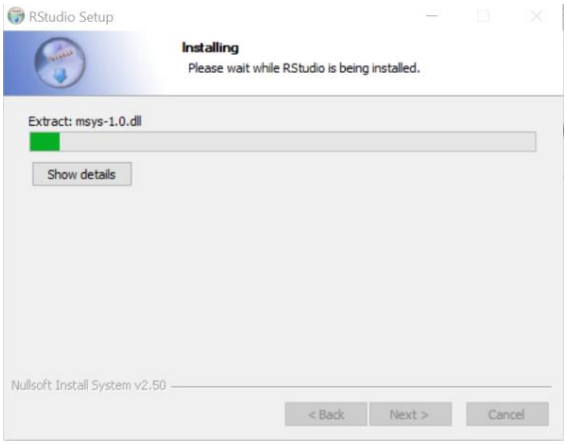
c. Select your preferred installation location then click OK



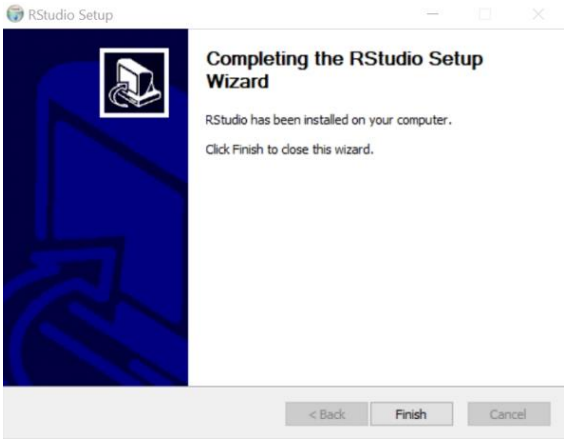
d. Click Next



e. Wait for the process to complete



f. Click Finish to complete the installation

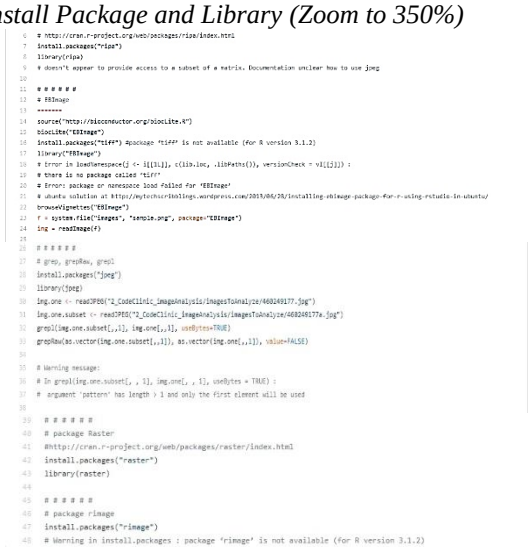


g. Installation process is completed

C. *Code Implementation*

1) *DataSet that will be used*

2) *Install Package and Library (Zoom to 350%)*



```
# http://cran.r-project.org/web/packages/ripa/index.html
install.packages("rtiff")
library(rtiff)
# doesn't appear to provide access to a subset of a matrix. Documentation unclear how to use jpeg

# # # # # #
# EBImage
# # # # # #
source("http://bioconductor.org/biocLite.R")
biocLite("EBImage")
install.packages("tiff") #package 'tiff' is not available (for R version 3.1.2)
library("EBImage")
# Error in loadNamespace(j <- i[[1L]], c(lib.loc, .libPaths()), versionCheck = vI[[j]]) :
# there is no package called 'tiff'
# Error: package or namespace load failed for 'EBImage'
# ubuntu solution at https://mytechnicalblogs.wordpress.com/2015/06/28/installing-ebimage-package-for-r-using-rstudio-in-ubuntu/
browseVignettes("EBImage")
f = system.file("images", "sample.png", package="EBImage")
img = readImage(f)
```

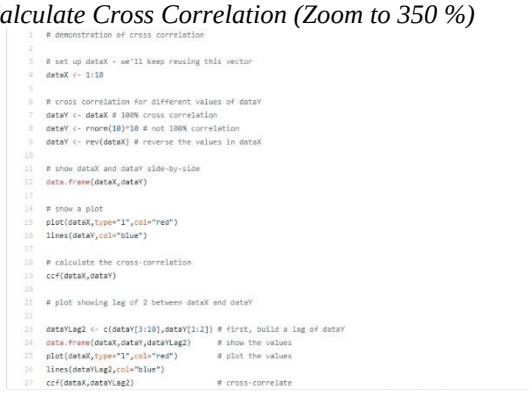


```
# # # # # #
# grep, grepRaw, grepl
install.packages("jpeg")
library(jpeg)
img.one <- readJPEG("2_CodeClinic_ImageAnalysis/ImagesToAnalyze/460249177.jpg")
img.one.subset <- readJPEG("2_CodeClinic_ImageAnalysis/ImagesToAnalyze/460249177a.jpg")
grepl(img.one.subset[,,1], img.one[,,1], useBytes=TRUE)
grepRaw(as.vector(img.one.subset[,,1]), as.vector(img.one[,,1]), value=FALSE)

# Warning message:
# In grepl(img.one.subset[, , 1], img.one[, , 1], useBytes = TRUE) :
#  argument 'pattern' has length > 1 and only the first element will be used

# # # # # #
# package Raster
#http://cran.r-project.org/web/packages/raster/index.html
install.packages("raster")
library(raster)

# # # # # #
# package rimage
install.packages("rimage")
# Warning in install.packages : package 'rimage' is not available (for R version 3.1.2)
```

3) *Plotting The Rasters (Zoom to 350% to clear view)*

```
# testing plotting functions

plotThisJpeg <- myjpeg
ptj.width <- ncol(plotThisJpeg)
ptj.height <- nrow(plotThisJpeg)
plotThisClip <- myjpegclip
ptjc.width <- ncol(plotThisClip)
ptjc.height <- nrow(plotThisClip)

plot(c(0, ptj.width), c(0, ptj.height), type = "n")
# plot(plotThisJpeg,useRaster=TRUE)
# plot(plotThisClip,add=TRUE,useRaster=TRUE)
rasterImage(plotThisJpeg, 0, 0, ptj.width, ptj.height)

rasterImage(plotThisJpeg[1:1500,1:2500,1], 0, 0, ptj.width, ptj.height)

rasterImage(plotThisClip, 500, 500, ptjc.width, ptjc.height)

this <- arrayInd(points.of.interest[1000],dim(haystack.raster))
xleft <- this[2]
ybottom <- this[1]
rect(xleft,ybottom,(ptjc.width+xleft),(ptjc.height+ybottom))

corltMayToNeedle <- function (aPOI) {
  needle.height.offset <- needle.quarter.height + aPOI
  needle.width.offset <- needle.quarter.width + aPOI
  cc=(haystack.raster[aPOI:needle.height.offset,1:needle.width.offset,1],needle.brick)
}

applyResults <- lapply(points.of.interest,corltMayToNeedle)
```

4) *Calculate Cross Correlation (Zoom to 350 %)*



```
# demonstration of cross correlation

# set up dataX - we'll keep reusing this vector
dataX <- 1:10

# cross correlation for different values of dataY
dataY <- dataX # 100% cross correlation
dataY <- rnorm(10)*10 # not 100% correlation
dataY <- rev(dataX) # reverse the values in dataX

# show dataX and dataY side-by-side
data.frame(dataX,dataY)

# show a plot
plot(dataX,type="l",col="red")
lines(dataY,col="blue")

# calculate the cross-correlation
ccf(dataX,dataY)

# plot showing lag of 2 between dateX and dataY

dataYLag2 <- c(dataY[3:10],dataY[1:2]) # first, build a lag of dataY
data.frame(dataX,dataY,dataYLag2)      # show the values
plot(dataX,type="l",col="red")         # plot the values
lines(dataYLag2,col="blue")
ccf(dataX,dataYLag2)                   # cross-correlate
```

5) Function to check if a Image is subset of another Image (Zoom to 350% to clear view)

```
# function to test if one image is a cropped version of another
# needle - image that might be a cropped version
# haystack - image that might be a parent version
# returns TRUE or FALSE

isthisacroppedversionofthat <- function(needle,haystack) {

  #   needle <- paste("imagesToAnalyze/","460249177a.jpg",sep="")
  #   haystack <- paste("imagesToAnalyze/","460249177.jpg",sep="")

  # assumes needle and haystack are jpeg images
  needle.raster <- readJPEG(needle)
  needle.width <- ncol(needle.raster) # width and height are used a lot
  needle.height <- nrow(needle.raster)
  haystack.raster <- readJPEG(haystack)
  haystack.width <- ncol(haystack.raster)
  haystack.height <- nrow(haystack.raster)
  red.layer <- 1 # We're only interested in one layer

  # if needle is larger than or same size as haystack,
  # then needle can't be a cropped version.
  if ((needle.height >= haystack.height)
      && (needle.width >= haystack.width)) return(c(0,0))

  # I'm going to assume that a match in one (of RGB) layers between
  # needle and haystack is a match between all layers. This reduces the
  # amount of data we need to correlate by 2/3
  # This requires versions of needle and haystack with just one layer
  needle.red <- needle.raster[,,red.layer]
  haystack.red <- haystack.raster[,,red.layer]

  # points.of.interest is an array of x,y coordinates that are possible
  # starting points for a subset image. Any points outside of this range
  # are either too narrow or too shallow to fit needle.
  # remember that we are talking about rows and columns of the IMAGE...
  # ...NOT the graph. Images start with 0,0 at upper left.
  # Graphs start with 0,0 in lower left
  diff.haystack.needle.height <- haystack.height-needle.height
  poi.rows <- (1:diff.haystack.needle.height)

  diff.haystack.needle.width <- haystack.width-needle.width
  poi.columns <- (1:diff.haystack.needle.width)

  xpos <<- numeric()
  ypos <<- numeric()
  ccf.max <<- numeric()

  stepSize <- 100
  for (rowIndex in seq(from=poi.rows[1],
                       to=poi.rows[length(poi.rows)],
                       by=stepSize)) {
    for (columnIndex in seq(from=poi.columns[1],
                            to=poi.columns[length(poi.columns)],
                            by=stepSize)) {
      #       if (rowIndex+needle.height < haystack.height &
      #           columnIndex+needle.width < haystack.width) {
      haystack.subset.to.be.correlated <- haystack.red[
        (rowIndex):(rowIndex+needle.height)),
        (columnIndex):(columnIndex+needle.width))
        ]

      ccf.object <- ccf(as.vector(haystack.subset.to.be.correlated),
                        as.vector(needle.red),
                        plot=FALSE)
      max.ccf <- max(ccf.object$acf)
      ccf.max <<- append(ccf.max,max.ccf)
      xpos <<- append(xpos,columnIndex)
      ypos <<- append(ypos,rowIndex)

      ###########
      # creates pretty graphics - and slows things down
      maintitle <- paste("ccf=",round(max.ccf,2),"xpos=",columnIndex,"ypos=",rowIndex)
      maintitle2 <- paste("ccf=",round(max.ccf,2))
      saveHere <- paste0("Plot",sprintf("%04d",rowIndex),sprintf("%04d",columnIndex),"_x",columnIndex,"_y",rowIndex,".
      png(filename=saveHere)
      nf <- layout(matrix(c(1,2),1,2,byrow=T),c(1,1),c(1,1),T)
      #layout.show(nf)
      #boxplot(ccf.object$acf,ylim=c(0,1),main=maintitle2)
      plot(c(0, haystack.width), c(0, haystack.height), main=maintitle,type = "n")

      #       rasterImage(haystack.subset.to.be.correlated,
      #                   xleft=0,
      #                   xright=ncol(haystack.subset.to.be.correlated),
      #                   ytop=nrow(haystack.subset.to.be.correlated),
      #                   ybottom=0)
      rasterImage(haystack.raster,
                  xleft=0,
                  xright=haystack.width,
                  ytop=haystack.height,
                  ybottom=0)

      rasterImage(needle.red,
                  xleft=columnIndex,
                  xright=(needle.width+columnIndex),
                  ytop=(haystack.height-(rowIndex+needle.height)),
                  ybottom=(haystack.height-rowIndex))
      dev.off()
      ###########

      cat("rowIndex=",rowIndex,"columnIndex=",columnIndex,"              \n")
      #       }
    }
  }

  ccf.results <- matrix(c(xpos,ypos,ccf.max),ncol=3)
  colnames(ccf.results) <- c("xpos","ypos","ccf.max")

}
```

6) Testing Cod e if Worked or Not Worked (Zoom to 350%)

```
# set up for test

install.packages("jpeg")
library(jpeg)

setwd("2_CodeClinic_ImageAnalysis")
source("isthisacroppedversionofthat.R")

funcWrapper <- function(anImagePair) {
  needle <- paste("imagesToAnalyze/",anImagePair[1],sep="")
  haystack <- paste("imagesToAnalyze/",anImagePair[2],sep="")
  is.it.a.match <- isthisacroppedversionofthat(needle,haystack)
  if (is.it.a.match[1] > 0) {
    print(paste(anImagePair[1],"is a subset of",anImagePair[2],"with correlation of",is.it.a.match[1],"and at point",is.it.a.match[2]))
  } else {
    print(paste(anImagePair[1],"is not a subset of",anImagePair[2]))
  }
}

# test the function
list.of.images <- list.files("imagesToAnalyze")
image.pairs <- expand.grid(list.of.images,list.of.images)
apply(image.pairs,1,funcWrapper)


# test known subsets
funcWrapper(c("460249177a.jpg","460249177.jpg")) #this is a subset
funcWrapper(c("478946583a.jpg","478946583.jpg")) #this is a subset
funcWrapper(c("78771293a.jpg","78771293.jpg")) #this is a subset
funcWrapper(c("103992931.jpg","78771293.jpg")) #this is not a subset
funcWrapper(c("168680522.jpg","103992931.jpg")) #this is not a subset
```

7) Main Code (zoom to 350%)

```
install.packages("jpeg")
library(jpeg)

setwd("2_CodeClinic_ImageAnalysis")

needle.raster <- readJPEG("imagesToAnalyze/460249177a.jpg")
needle.width <- ncol(needle.raster) # width and height are used a lot
needle.height <- nrow(needle.raster)
needle.brick <- needle.raster[,,1]

haystack.raster <- readJPEG("imagesToAnalyze/460249177.jpg")
haystack.width <- ncol(haystack.raster)
haystack.height <- nrow(haystack.raster)

# discovering the row/column location where these two images match
# places needle on top of haystack
needle.x <- 1450
needle.y <- 1690

plot(c(0, haystack.width), c(0, haystack.height),
     type = "n",main=paste("x=",needle.x,"y=",needle.y))

rasterImage(haystack.raster,
            xleft=0, xright=haystack.width,
            ytop=haystack.height,ybottom=0)

rasterImage(needle.brick,
            xleft=needle.x,
            xright=needle.x+needle.width,
            ytop=needle.y+needle.height,
            ybottom=needle.y)


# creating and confirming a subset of haystack that matches needle
# produces a graph of images side-by-side

red.layer <- 1 # We're only interested in one layer
haystack.topImage <- haystack.height-needle.y-needle.height
haystack.brick <- haystack.raster[haystack.topImage:(needle.height+haystack.topImage),needle.x:(needle.width+needle.x),red.layer]

plot(c(0, haystack.width), c(0, haystack.height), main=date(),type = "n")

rasterImage(haystack.brick,
            xleft=0,
            xright=ncol(haystack.brick),
            ytop=nrow(haystack.brick),
            ybottom=0)

rasterImage(needle.brick,
            xleft=2000,
            xright=(needle.width+2000),
            ytop=nrow(haystack.brick),
            ybottom=0)


# This shows a 100% correlation between two identical images
ccf(as.vector(needle.brick),as.vector(needle.brick),main=date())

# This shows the difference between two similar images
cor1 <- ccf(as.vector(haystack.brick),as.vector(needle.brick),main=date())
max(cor1$acf) # 0.7273756

# This shows the difference between two dissimilar images
ccf(as.vector(haystack.raster),as.vector(needle.brick),main=date())
```

III. Conclusion

In this technologically advanced world, it has become necessary for the beginners in R and image analysis to learn and understand the things very clearly, so that they could be applied and used in the future. Hence, we have performed the Image analysis tasks in R programming language, so that it becomes easy to all to understand the concepts related to it. This paper also provides the use of R Image Library (RIL), using which we can prominently develop the R based image processing software and can be useful for number of applications like remote sensing, agriculture, space center, satellites, medical and health sciences, etc. Thus, it can be concluded that R and Image analysis proves to be the better combination for learning, developing and understanding the capabilities provided in it.

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