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Template Matching Techniques in Computer Vision

Theory and Practice

Code Companion

Companion Website

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Template Matching Techniques in Computer Vision: Theory and Practice
the code companion

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Contents

Preface

This is the code companion for the book *Template Matching Techniques in Computer Vision: Theory and Practice* (hereafter TM for short), published by Wiley. The book illustrates the R-code in two R packages, AnImAl and TeMa (available at the companion website), providing respectively an interactive image processing environment and a set of algorithms useful in exploring the world of template matching techniques. The structure of the companion matches that of TM: each chapter presents the abstract of the corresponding book chapter and contains code snippets, providing additional examples or insights, as well as an extended bibliography with links to the electronic edition whenever possible.

Due to website constraints, the actual sources of the code companion, including R packages, datasets, and the scripts for the generation of a PDF version of the code companion can be found at `http://tev.fbk.eu/TM`. The site contains:

AnImAl an image processing package for R (`http://tev.fbk.eu/TM/AnImAl.tgz`);

TeMa a template matching package for R (`http://tev.fbk.eu/TM/TeMa.tgz`);

theFaceDbs a set of multiracial face images with feature location (`http://tev.fbk.eu/TM/theFaceDbs.tgz`);

theCodeCompanion source and scripts for the generation of the manual you are reading (`http://tev.fbk.eu/TM/theCodeCompanion.tgz`);

theRenderingWorkshop a modification of PovRay providing partial RenderMan support and some sample scripts (`http://tev.fbk.eu/TM/theRenderingWorkshop.tgz`).

The software is meant to be used in the GNU/Linux operating system: there is currently no support for other operating systems. The most up to date version of this manual will be the one at `http://tev.fbk.eu/TM/html/tmCodeCompanion.html` (and `http://tev.fbk.eu/TM/tmCodeCompanion.pdf`).

Chapter 1

Introduction

Computer vision is a wide research field that aims at creating machines that see, not in the limited acception that they are able to sense the world by optical means, but in the more general acception that they are able to understand its perceivable structure. Template matching techniques, as now available, have proven to be a very useful tool for this intelligent perception process and have led machines to super human performance in recognition tasks such as face recognition. This introductory chapter sets the stage for the rest of the book, where template matching techniques for monochromatic images are discussed and applied to face analysis tasks.

keywords: *computer vision, template matching, face recognition.*

1.1 The software environment

The code used in this handbook is meant to be used in the open source, interactive statistical processing environment commonly known as R, and it is based on two image processing packages: *AnImAl*, an image algebra, and *TeMa*, providing extended template matching support. Both packages require additional ones, all of them freely available from the central repository of CRAN, the Comprehensive R Archive Network (`http://cran.r-project.org`). Detailed information on the functions provided by each package is available within the distributed packages. The following code snippet presents the commands to load the required packages and a couple of supporting functions to generate postscript output to be included in a research report.

```
require(AnImAl)
require(TeMa)
source("R/tm.eps.R")
source("R/tm.pasteImage.R")
```

This handbook makes use of *Sweave* functionalities available within the *R* environment: the textual (latex) source files include special sections of *R*-code that are automatically executed before creating the final text for the document. Most of the images presented in the book are automatically generated in this way: correctness of reported code and alignment of results is therefore ensured. The special `Codelet` sections are automatically formatted from annotated code available in the provided packages or in the set of code snippets used to generate the examples of this book.

1.2 Basic template matching

Template matching is the generic name for a set of techniques that quantify the similarity of two digital images, or portion thereof, in order to establish whether they are the same or not. Digital images are commonly represented with numerical arrays: monochrome images require a single matrix while color images require multiple matrices, one per color component. We will restrict our attention to monochrome images. Digital images can be stored in various formats such as `jpeg`, `tiff`, or `ppm`. A variant of the latter, specific to grey level images, is commonly identified with a `.pgm` suffix. Package *AnImAl* provides convenient functions to read them:

```
sampleimages <- file.path(system.file(package = "AnImAl"), "sampleimages/")
face1        <- as.animage(getChannels(read.pnm(
...                   file.path(sampleimages, "sampleFace_01.pgm"))))
face1
```

```
[1] ai size: 270 x 180 focus: (0, 0), outside: 0, storage: real, document: FALSE
```

Note the darker region: it identifies R output. The coordinate system most often associated to an image is left-handed: the value of the x coordinate increases from left to right while that of the y coordinate increases from top to bottom (see Figure 1.1). This is due to images being stored as arrays and to the fact that the y coordinate is associated to the row number. R provides extensive graphical facilities and function `tm.ploteps` can be used to turn their output to postscript files:

```
# tm.plot.defaultFormat <- "X11"                        1
tm.plot.defaultFormat <- "jpg"                          2
tm.plot(file = "figures/sampleImage", ia.show(face1))   3
```

Setting `tm.plot.defaultFormat <- "X11"` (uncommenting line 1 above) makes subsequent calls to `tm.plot` use the windowing system. We will routinely use `tm.plot` to produce the images inserted in this manual. The existence of an image coordinate system allows us to specify in a compact way rectangular regions: we simply need to provide the coordinates (x_0, y_0) of its upper left corner and the horizontal and vertical dimensions (dx, dy):

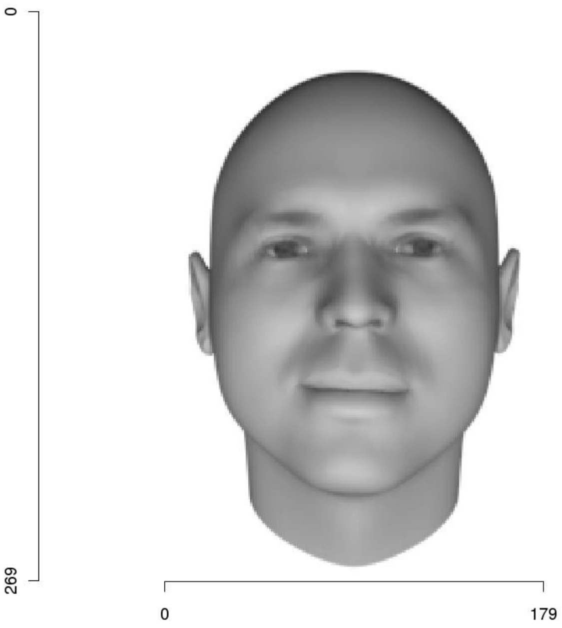

Figure 1.1: A sample monochrome image with its left-handed coordinate system.

```
x0   <- 26
y0   <- 87
dx   <- 58
dy   <- 36
eye1 <- ia.get(face1, animask(x0,y0,dx, dy))
tm.plot("figures/sampleEye", ia.show(eye1))
```

The result, reported in Figure 1.2, is a new, smaller image that carries on the knowledge of its original placement as the axes values show. As clarified in Figure *TM*1.2, the search for a template, such as the one presented in Figure 1.2, within an image, such as the one in Figure 1.1, is performed by scanning the whole image, extracting at each image position a region of interest whose size corresponds to that of the template:

```
for(y in ia.ymin(face1):(ia.ymax(face1)-dy)) {          1
...   for(x in ia.xmin(face1):(ia.xmax(face1)-dx)) {    2
...     w <- ia.get(face1, animask(x, y, dx, dy))       3
...     ia.show(w)                                      4
...   }                                                 5
... }                                                   6
```

Function `ia.show` in line 4 of the above code snippet would show image portion `w` in a window. However, what we need to do is to compare each image `w` to the reference template `eye1` assessing their similarity. We should also store the resulting values in a map so that we can access them freely after the computation is completed.

`Codelet 1` **Basic template matching** (`./R/tm.basicTemplateMatching.R`)

This function illustrates the most basic template matching technique: the template is moved over each image position and the sum of the squared difference of aligned image and template pixels is considered an indicator of template dissimilarity.

```
tm.basicTemplateMatching <- function(image, template) {
```

The first step is to get the linear dimensions of the template

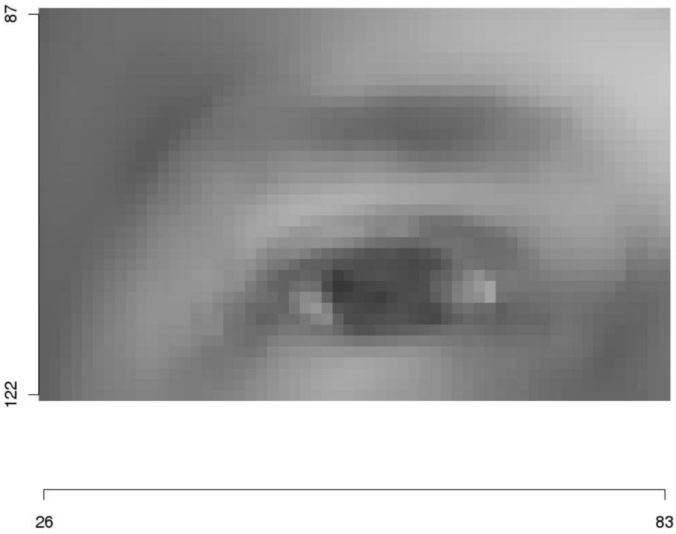

Figure 1.2: A detail of Figure 1.1: let us note that the coordinates in the original image are preserved.

```
  dx <- ia.mask(template)@w
  dy <- ia.mask(template)@h
```

We then determine the extent of the image region of interest over which we need to slide our template

```
  x0 <- ia.xmin(image)
  y0 <- ia.ymin(image)
  x1 <- ia.xmax(image) - dx
  y1 <- ia.ymax(image) - dy
```

This allows us to prepare the storage for the similarity scores

```
  scores <- animage(array(0,dim=c(y1-y0+1,x1-x0+1)),storage="real",focus=image@focus)
```

and to perform the actual computation loop,

```
  for(y in y0:y1) {
    for(x in x0:x1) {
```

sliding along each row and extracting in turn an image portion matching the size of the template

```
      w <- ia.get(image, animask(x, y, dx, dy))
```

We modify the template so that it overlaps the extracted region

```
      template@focus <- w@focus
```

and compute (and store) the matching score

```
      scores[y,x] <- sum(ia.matop(function(x,y) (x-y)**2, w, template)@data)
    }
  }
```

We can finally return the image representing the similarity map

```
  scores
}
```

It is now easy to spot our template in the image:

```
 source("./R/tm.basicTemplateMatching.R")
 distScores <- tm.basicTemplateMatching(ia.subsample(face1,2),
...                                        ia.subsample(eye1,2))
 distScores <- distScores@data / ia.size(eye1)
 # the position of the template is that of minimum distance
 which(distScores == min(distScores), arr.ind = TRUE)
```

```
     row col
[1,]  45  14
```

```
 simScoresA <- 1/(0.001+distScores)
 # the position of the template is that of maximal similarity
 which(simScoresA == max(simScoresA), arr.ind = TRUE)
```

```
     row col
[1,]  45  14
```

Note that the position of the template differs from that of the original `eye1` as we down-sampled the image: the coordinates are halved. We can also have a look at the resulting matrices to get an idea of how extremal the matching value at the correct position is: this is related to the concept of signal to noise ratio that we will consider in depth in later chapters.

```
  tm.plot(file = "figures/distanceMatch",
...           persp(distScores, xlab="y", ylab="x",
...           theta =45, phi = 25, shade = 0.35, expand = 0.75, r = 1,
...           lwd=0.1, ticktype="detailed",zlab="similarity"))
  tm.plot(file = "figures/similarityMatch",
...           persp(simScoresA, xlab="y", ylab="x",
...           theta =45, phi = 25, shade = 0.35, expand = 0.75, r = 1,
...           lwd=0.1, ticktype="detailed",zlab="similarity"))
```

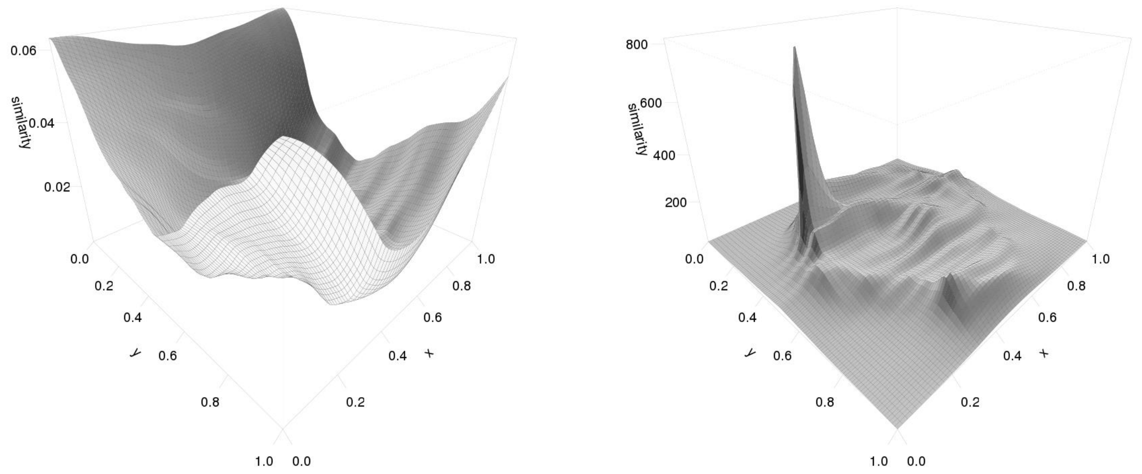

Figure 1.3: The distance map (left) and the similarity map (right) corresponding to the matching of template `eye1` to `face1`.

AnImAl provides `ia.correlation`, a faster and more flexible function to perform the task that will be considered in Chapter 3. Changing the value `0.001` used in the computation of `simScores` significantly affects the distribution of values:

```
simScoresB <- 1/(0.01+distScores)
simScoresC <- 1/(0.1+distScores)
tm.plot(file = "figures/scoresHistA",
...         hist(simScoresA, xlab = "similarity", main="0.001"))
tm.plot(file = "figures/scoresHistB",
...         hist(simScoresB, xlab = "similarity", main="0.01"))
tm.plot(file = "figures/scoresHistC",
...         hist(simScoresC, xlab = "similarity", main="0.1"))
```

The resulting distributions are reported in Figure 1.4.

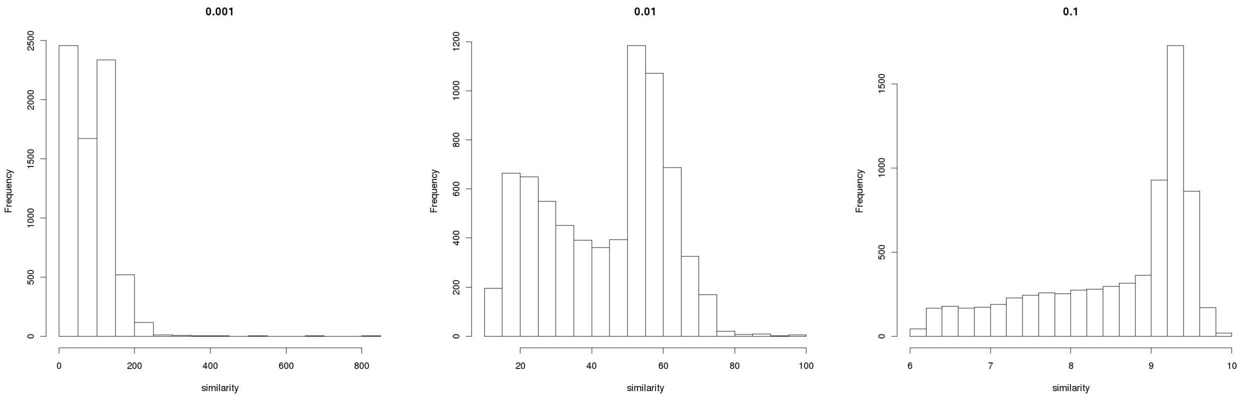

Figure 1.4: The distributions of similarity scores obtained varying the denominator constant, `0.001`, `0.01`, `0.1` respectively from left to right. The highest similarity value determines the x range: the lower the value used in the normalization, the higher the dynamic range exhibited by the scores and the more far apart the value corresponding to the correct position from the remaining ones.

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Chapter 2

The Imaging Process

The chapter discusses some aspects of the imaging process that turn out to be critical in the design of artificial vision systems. The basics of how images are created using electromagnetic stimuli and imaging devices are be considered. Simple concepts from optics will are introduced, including distortion, depth of field, aperture, telecentric lens design. The basic structure of eyes and digital imaging sensors is introduced and some artifacts of digital imaging systems discussed. The sampling theorem is presented and its impact on image representation and common image processing operations such as resizing is investigated.

keywords: *light, optics, noise, diffraction, distortion, telecentric lens design, eye, digital imaging sensor, sampling theorem, log-polar mapping.*

2.1 Image distortions

Real optical systems are usually affected by geometrical distortions whose type and amount varies significantly from barely visible to significant. Furthermore, some characteristics of light propagation in an optical system results in unavoidable effects, such as wide angle lens vignetting. In this section we will look at a few *TeMa* functions that can be used to simulate geometrical distortions and vignetting effects.

The first step is to get some *perfect* images. A simple and cheap way to obtain such images is to generate them using a ray tracing system. Package *TeMa* includes some testing images generated using the Persistence of Vision Ray Tracer (`http://www.povray.org`).

```
tiffdir          <- file.path(system.file(package="TeMa"),
...                             "sampleimages/cameraSimulation")
# normalize pixel value range to [0,255]
i_ortho          <- ia.scale(
...                       ia.readAnimage(
...                          file.path(tiffdir,"ortho_iso12233_large.tif")),
...                             maxValue = 255)
# get the red color channel
i_orthoRed       <- i_ortho[[1]]
# and extract an image portion
i_orthoRedDetail <- ia.get(i_orthoRed, animask(0,0,1201,256))
```

As detailed by Equations TM:2.26-27 geometrical distortions can be considered as image plane effects and can be accurately simulated once the distortion curves are specified. Detailed distortion information is often available for high quality lenses directly from the manufacturer or can be measured using calibration patterns. The following code snippet shows to curves based on the public data for a real wide angle lens: the percent distortion and the vignetting are reported as a function of the distance expressed in millimeters from the optical center of the lens designed for a standard $24 \times 36mm$ frame. The distortion and vignetting curves are obtained using spline interpolation given a set of manually measured points.

```
sampleDistortion<-splinefun(c(0, 5.00,10.00,11.90,15.00,18.30,20.00,21.60),
...                          c(0,-0.41,-1.55,-2.00,-2.45,-2.00,-1.18,-0.11))
sampleVignette  <-splinefun(c(0, 5.00,10.00,15.00,20.00,21.60),
...                          c(1, 0.86, 0.64,0.41,0.23,0.18))
```

Inspection of the distortion curve, reported in Figure 2.1, shows it to be of a complex type, exhibiting both barrel distortion (up to 15mm from the optical center) and pincushion distortion (from 15mm onwards).

```
tm.plot("figures/sampleDistortion",
...        plot(1:21, sampleDistortion(1:21),
...        type="b", xlab="mm", ylab="Distortion"),
...        grid())
```

Generating a vignetted image is a simple task using the functions provided by *TeMa*:

```
vMap   <- tm.computeVignettingMap(width=1201, height = 801,
...                                curve = sampleVignette)
vImage <- tm.vignetteImage(i_orthoRed, vMap)
tm.plot("figures/vImage", ia.show(vImage))
tm.plot("figures/vDeltaProfile",
...        plot(vImage@data[475,]-i_orthoRed@data[475,],
...        type="l",ylab="Delta",xlab="X"))
```

The results are reported in Figure 2.2. A distorted image can be generated in a similar way

```
dMaps  <- tm.computeDistortionMaps(width=1201, height = 801,
...                                 curve = sampleDistortion)
dImage <- tm.distortImage(i_orthoRed, dMaps)
```

A vignetted distorted image can be generated easily

```
vdImage <- tm.vignetteImage(dImage, vMap)
```

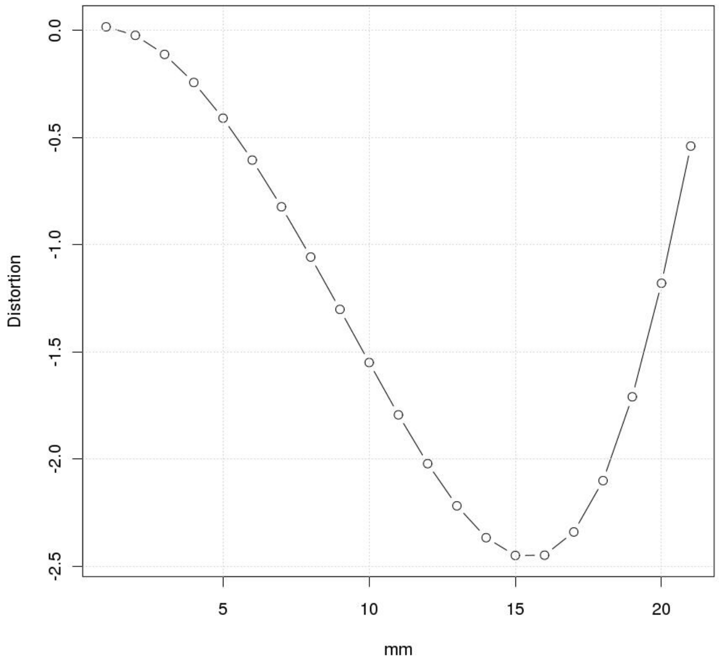


Figure 2.1: A sample distortion curved based on the data for a high quality real lens. The curve tells us that this lens exhibit both barrel and pincushion distortion.

2.2 Diffraction Effects

When light passes through a small aperture, i.e. an aperture whose size if comparable to the wavelength of light, the wave nature of light causes interference effects that result in perceivable image quality loss. Images become more blurred due to the increasing support of the resulting point spread function of the optical system. An immediate consequence is that we cannot indefinitely gain depth of focus by reducing the aperture of the optical system as Equation *tm*:2.22 would suggest.

The following code snippet simulates the effect of diffraction with data corresponding to a high resolution digital compact camera, assuming a default wavelength of $550e-9$m: diffraction is modeled by convolution with an appropriate kernel

```
A  <- ia.get(i_orthoRed, animask(0,0,1201,256))
#
# dK represents the points spread function of the
# optical system (and corresponds to the Aity function)
#
dK <- tm.diffractionKernel(focalLength= 8.9e-3,
...                              fStop=       16,
...                              pixelSize=   (8.8/3264)/1000)
tm.plot("figures/diffractionKernelF16",
...  persp(dK, main = "Airy diffraction kernel at f16"))
#
# In order to better appreciate the shape of the kernel we
# can oversample it: dK3 can then not be used to simulate
# the effect (as it corresponds to 3x oversmoothing)
#
dK3 <- tm.diffractionKernel(focalLength= 8.9e-3,
...                              fStop=       16,
...                              pixelSize=   (8.8/3264)/1000,
...                              superSampling=3)
```

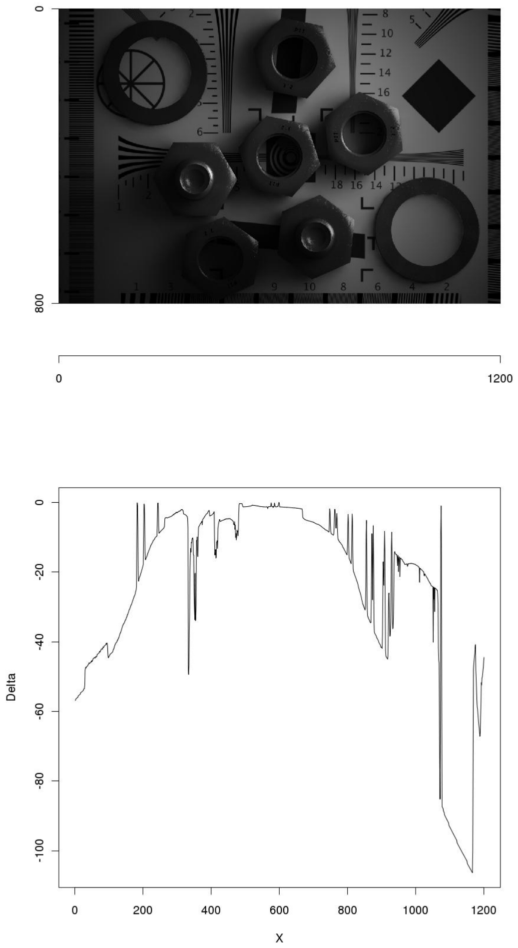


Figure 2.2: Vignetting appears as a (proportional) intensity reduction whose entity increase from the center towards the boundary of the frame. The plot highlights the difference from the *perfect* image along a row in the middle of the image. It is apparent that vignetting can have a significant impact on template matching techniques.

```
tm.plot("figures/diffractionKernelF163x",
...   persp(dK3, main = "Airy diffraction kernel at f16 (3x supersampled)"))
#
# We generate the diffracted image
#
B <- ia.convolution(A, dK)
tm.plot("figures/diffractionEffect",
...            ia.show(B, main="Diffraction at f16"))
#
# and have a detailed look at an intermediate row
#
tm.plot("figures/diffractionDetail",
...          matplot(cbind(A@data[126,],B@data[126,]),
...                  type="l",col=c("black"), pch = 2:3, lty=1:2, xlab="x",
...                  ylab="", main="W(/o) Diffraction"),
...          legend(0,150, c("No diffraction", "Diffraction"),
...                 lty=1:2, col=c("black")),
...          height=3)
```

2.3 Noise

Images are often corrupted by *noise*, random fluctuations that can be characterized by their probability distribution. Two distributions are commonly used to model noise processes: the Gaussian (normal) distribution and the uniform distribution. While several noise processes affecting digital images can be described well by these distributions, quantum nature of light results in a different kind of noise, photon noise, following a Poisson distribution (see Section tm:2.1.4).

`Codelet 2` **Digital camera photon noise** (`../TeMa/R/tm.photonNoise.R`)

Quantum nature of light manifests itself as a Poisson noise affecting digital imaging. In order to simulate this noise process correctly we need to now a few parameters: the maximum number of electrons that fit within a pixel well and the corresponding ISO sensitivity, the ISO sensitivity at which the picture is taken, the maximum intensity value, and the gamma correction factor if any. These data allow us to map an intensity value in the digital image into and absolute number of electrons which is proportional to the number of photons. The latter provides the (single) parameter λ controlling the Poisson process. The default `fullWell` value is typical of a high-end digital reflex camera

```
tm.photonNoise <- function(x,
                           maxValue        =   255,
                           gammaCorrection =   (1.0 / 2.2),
                           fullWell        = 51400,
                           fullWellIso     =   100,
                           iso             =   200)
  {
```

The first step is mapping the intensity value into a number proportional to the number of photons:

```
    lambdaOrig      <- ((x/maxValue)**(1.0/gammaCorrection)
                        * fullWell
                        * (fullWellIso / iso))
```

A new, noisy value is generated according to the corresponding Poisson distribution:

```
    lambdaPerturbed <- rpois(1, lambdaOrig)
```

and it is mapped back the digital image context

```
    return(maxValue
           * ((lambdaPerturbed*(iso/fullWellIso))/fullWell)**gammaCorrection)

  }
```

Photon noise is (proportionally) more significant in the darker areas of images: we choose a new sample image with a dark background and we *apply* to it a plausible amount of photon noise for a high ISO value of 3200 (the `scale` parameter of function `tm.addNoise`).

```
sampleimages <- file.path(system.file(package = "AnImAl"), "sampleimages/")
face2        <- as.animage(getChannels(read.pnm(
...                 file.path(sampleimages, "sampleFace_03.pgm"))))
# add a bit of light so that black is not completely black
sFace        <- ia.add(face2, 0.1)
nFace        <- tm.addNoise(sFace, noiseType="photon", scale=3200)
```

We can visually appreciate the effect of noise with a simple compositing operation:

```
x <- ia.add(ia.get(sFace, animask(0,0, 90,270)),
...             ia.get(nFace, animask(90,0, 90,270)))
tm.plot("figures/photonNoiseComposite", ia.show(x))
```

and having a detailed look at a sample row of the image

```
tm.plot("figures/photonNoiseProfile",
...         plot(x@data[100,], type="l", xlab="x", ylab="intensity"))
```

2.4 Digital imaging artifacts

Digital images are affected by characteristic artifacts that may impact significantly on template matching. We will consider two of them: demosaicing and interlacing.

2.4.1 Demosaicing

High quality color imaging requires the sampling of three spectral bands at the same position and at the same time. While solutions exist the most common setup is based on a trick: a lattice of pixels, whose over number corresponds to the sensor resolution, is split into three different groups. The pixels of each group are covered with a small color filter. The result is that spectral information is not spatially aligned: each pixel only has information on one color. Full color information must then be recovered using interpolation techniques and the result is different from what would be obtained with full resolution color imaging especially in the proximity of color discontinuities.

```
img <- ia.scale(ia.readAnimage(file.path(tiffdir,"ortho_gretag_large.tif")),
...              maxValue = 255)
img <- list(ia.get(img[[1]], animask(0,0,1201,256)),
...          ia.get(img[[2]], animask(0,0,1201,256)),
...          ia.get(img[[3]], animask(0,0,1201,256)))
imgB <- tm.bayerizeImage(img)
imgD <- tm.debayerizeImage(imgB)
imgE <- ia.add(ia.abs(ia.sub(img[[1]], imgD[[1]])),
...             ia.add(ia.abs(ia.sub(img[[2]], imgD[[2]])),
...             ia.abs(ia.sub(img[[3]], imgD[[3]]))))
tm.plot("figures/mosaicImage",ia.show(imgB), height=3)
tm.plot("figures/deltaImage",ia.show(ia.matop(`-`, 1,imgE)), height=3)
tm.plot("figures/errorRow",
...     plot(imgE@data[128,],xlab="X",ylab="error",type="l"),height=3)
```

2.4.2 Interlacing

In some cases, image sensor data do not correspond to the same instant. Image rows are subdivided into two disjoint sets, each of them representing a field: all the rows of a single field share the same time but the two fields correspond to different instants. If the sensor is stationary and the scene is static a single image can be reconstructed by collating the two fields. If the camera is moving, or the scene is not static, the single image resulting from the integration of two fields exhibits noticeable artifacts.

`Codelet 3` **Interlaced image generation** (`../TeMa/R/tm.interlaceImage.R`)

Interlaced images are built by juxtaposition of two fields, each providing a partial image representation. This function simulates the generation of a full resolution image from two different fields with user selectable field *distance* specified by `delta`.

```
tm.interlaceImage <- function(img, delta = 0L) {
```

We get the field composed by the odd lines

```
  oddField  <- tm.imageField(img, odd = TRUE)
```

and the one by the even lines

```
  evenField <- tm.imageField(img, odd = FALSE)
```

We can simulate different time lapse factors by changing the value of `delta` and translating one of the fields accordingly:

```
  if(delta != 0) {
```

The full resolution image is simply obtained by summing the two fields:

```
    img <- ia.get(ia.add(oddField,
                         ia.left(evenField, delta)),
                  ia.mask(img))
  } else {
```

A value `delta=0` corresponds to a static scene and stationary camera and is equivalent to the output of a progressive sensor:

```
    img
  }
}
```

Interlacing impacts on template matching: line offset results in image differences that are not compensated by the matching process. As the following code snippet shows, the effect increases with the time delta of the two image fields and with the amount of local image structure (edges are the major sources of difference).

```
# We select the red image channel
A  <- img[[1]]
# and we compute for different deltas
ds <- c()
for (delta in 0:20) {
...   # the integral (over a 11x11 window) of the pixels differences
...   # between the original and the (progressively more) interlaced one
...   ds <- c(ds, sum(ia.average(ia.abs(ia.sub(A,
...                                   tm.interlaceImage(A, delta))),
...                          11, 11)@data))
... }
ds <- ds / ia.size(A)
tm.plot("figures/interlaceDelta",
...       plot(ds, xlab="delta", ylab="error", type="l"))
# Image regions with high gradient (such as edges or structurally reach
# areas) contributes more
tm.plot("figures/interlaceDeltaImage",
...          ia.show(ia.average(ia.abs(ia.sub(A,
...                                        tm.interlaceImage(A, 10L))),
...                           11, 11)),
...          height=3)
```

2.5 Image resampling

Image processing algorithms, template matching techniques included, often require image scaling and rotation. These operations are a subset of the linear transformations described by Equation *TM*:2.74. As an illustrative example let us consider geometric normalization of a face image: a combined rotation, scaling, and translation operation fixing the origin of the image coordinate system at the midpoint of the segment joining the eyes, at the same time making the eye to eye axis horizontal with eyes at a predefined distance from the new origin.

Image transformations of the type considered usually require image values at positions different from those of the original sampling. The computation of the new values can be performed correctly if the requirements of the sampling theorem are satisfied, sometimes requiring a preliminary smoothing step in order to reduce image frequency content, e.g. when reducing image size. The actual resampling operation can then be performed relying on Lanczos interpolation.

The frequency conditioning step can be performed applying a Gaussian smoothing kernel or a Lanczos kernel. Let us consider halving image resolution. As the Gaussian filter is approximately band limited with critical spacing σ and corresponding bad-limit $\sigma^{-1}/2$, it is appropriate to smooth the image with a $\sigma = 2$ Gaussian kernel (as we want to halve its resolution. If we use a Lanczos kernel we can rely on Equations *TM*:2.77-78 and sample the original kernel (twice) more densely. A function is available for computing the kernel, `tm.lanczosKernel`: the sampling density of the kernel is controlled by parameter `factor`.

```
lk12 <- tm.lanczosKernel(factor = 1, support = 2, trim = 5)
lk22 <- tm.lanczosKernel(factor = 2, support = 2, trim = 5)
tm.plot("figures/lanczosKernels",
...             matplot(-5:5,cbind(t(lk12),t(lk22)),type="b",col=c("black"),
...                     pch = 2:3, lty=1:2, xlab="x", ylab="",
...                     main="Lanczos kernels"),
...             legend(-5,0.9, c("factor=1,support=2", "factor=2,support=2"),
...                    pch=2:3, lty=1:2, col=c("black"))
...             )
```

If `trim` is omitted (or set to `TRUE`) the size of the kernel is appropriately computed to cover its support. Kernel `lk22` is the one to use in preconditioning image frequency content prior to subsampling.

```
sampleimages <- file.path(system.file(package = "AnImAl"), "sampleimages/")
face1        <- as.animage(getChannels(read.pnm(
...                   file.path(sampleimages, "sampleFace_01.pgm"))))
A <- tm.normalizeFaceImage(face1,57,113,122,112,ee=22)
B <- tm.normalizeFaceImage(face1,57,113,122,112,ee=22,smooth = FALSE)
tm.plot("figures/normalized1", ia.show(A, main = "Smoothed"))
tm.plot("figures/normalized2", ia.show(B, main = "Aliased"))
```

2.6 Log-polar imaging

While the representation of image as rectangular arrays is the most widespread, alternative exists. Log-polar mapping, described in Section *TM*:2.4 is an example of space variant representation providing a spatial resolution decreasing from the center towards the boundary.

Log-polar mapping is usually obtained with specific sensors but can also be simulated via software to appreciate some of its characteristics. When we change the image representation from a (standard) rectangular lattice to a log-polar spatio-variant structure we are effectively performing a resampling task which is prone to aliasing if frequency content is not properly tuned. As log-polar sensor resolution is spatio-variant so must be the amount of smoothing applied before resampling. Usually, the two sensing structures are compared for a given maximum spatial resolution. In the case of a rectangular sensor the maximum resolution extends over the whole sensor while in the case of a log-polar sensor it is confined to the central (foveal) region.

```
# We select an image portion
#
A <- ia.get(i_orthoRed, animask(472,272,257,257))
tm.plot("figures/lpOrig", ia.show(A, main="Original"))
#
# and we smooth it, increasingly so towards the perifery,
# preparing it for a log-polar mapping with an angular
# resolution of 72 cells
#
sA <- tm.logPolarSmoothing(A, angularResolution = 72)
tm.plot("figures/lpSmooth", ia.show(sA, main="Smoothed"))
#
# and project/back project to get a feeling of the log-polar mapping with
# 3960 pixels instead of 51471
#
lpeA      <- tm.logPolarMapEquivalent(sA, R = 128, 72)
#
# We now create the 'real' log-polar map where the horizontal
# coordinate corresponds to rings, while the vertical one
# represents the angular 'sector'
#
lpmA      <- tm.logPolarMap(sA, 128, angularResolution = 72)
#
# and we plot it with a gamma correction of 2.2
#
tm.plot("figures/lpMap",
...     plot(pixmapGrey((lpmA)**(1.0/2.2)),
```

```
...     main="Log polar map with k=72"))
#
# comparing it to the cartesian back projection
# (with a gamma correction of 2.2)
#
tm.plot("figures/lpEquiv",
...     plot(pixmapGrey((lpeA@data)**(1.0/2.2)),
...     main="Cartesian equivalent of a log-polar map with k=72"))
```

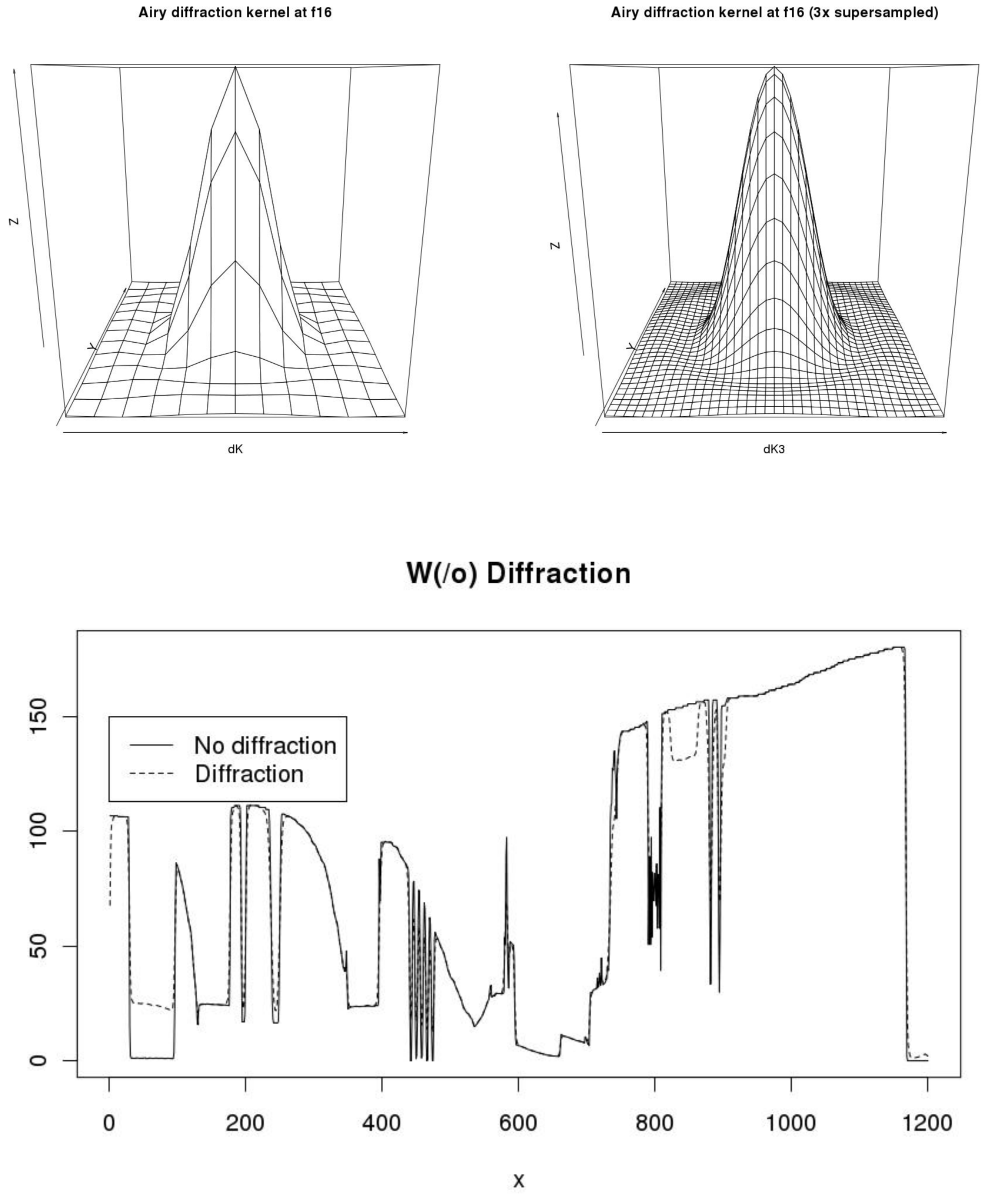


Figure 2.3: Diffraction results in significant contrast loss at commonly encountered operating conditions.

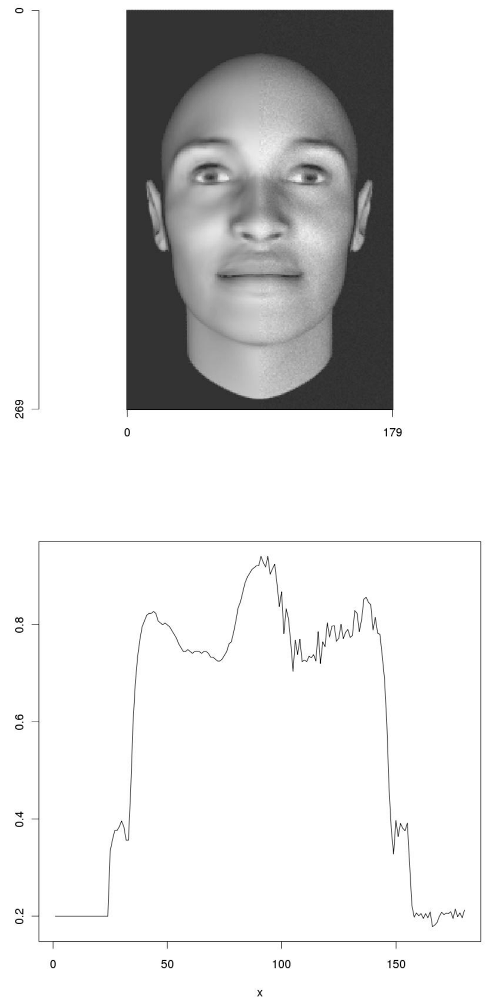


Figure 2.4: Photon noise is due to the quantum nature of light: as its variance is proportional to the square root of the average number of photons, its relative impact can be reduced by increasing the average number of photons, e.g. using large pixels.

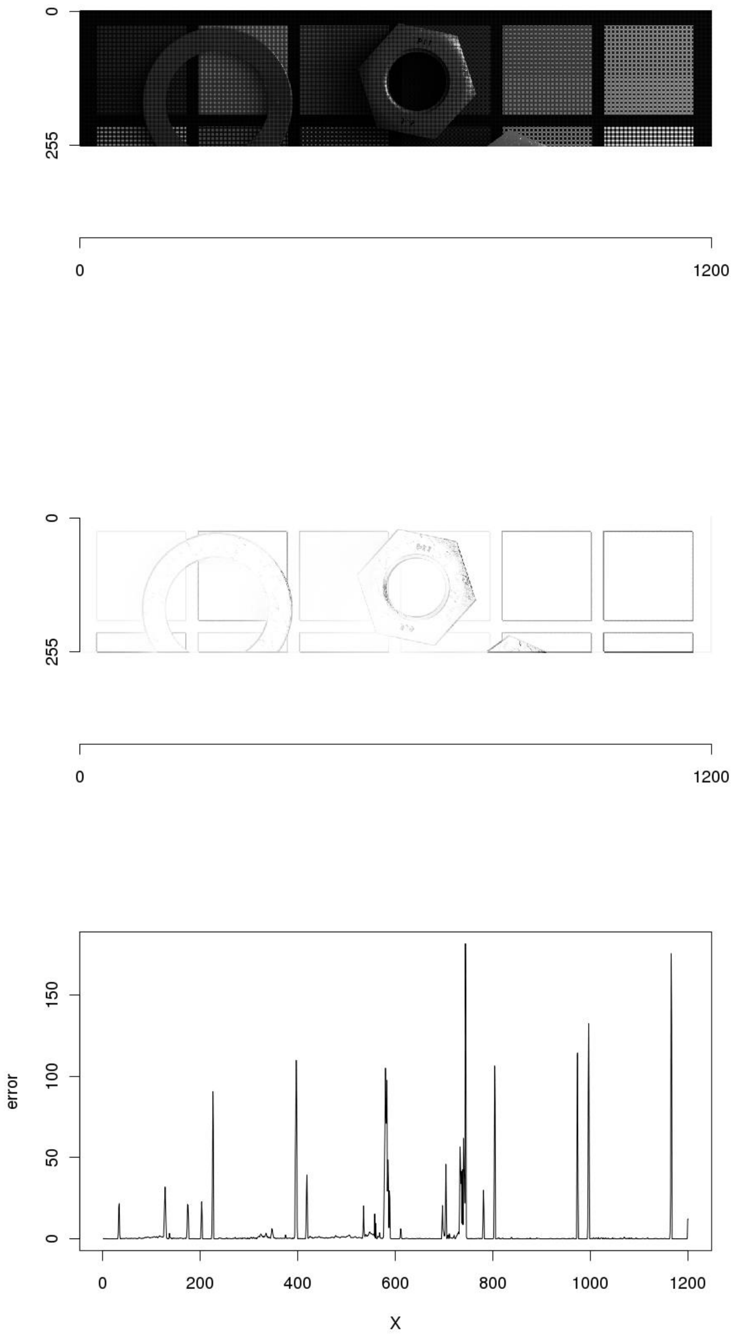
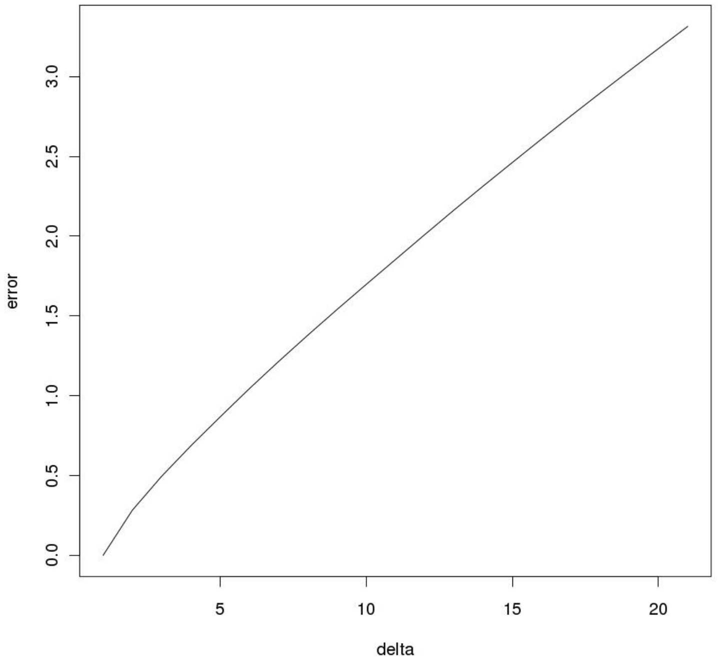


Figure 2.5: Recovering full resolution color information using interpolation techniques is a cheap (but suboptimal) solution that may result in noticeable artifacts.



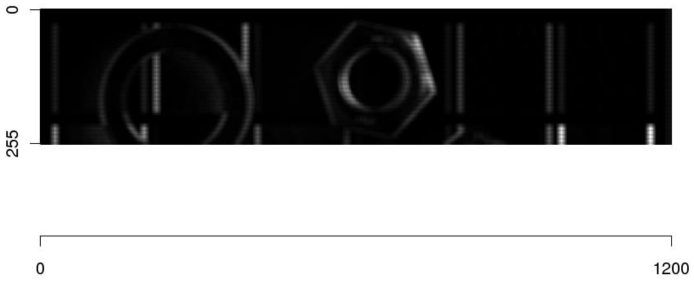


Figure 2.6: Interlacing results in image differences that increase with image field time lapse (top) and with the amount of local image structure (bottom).

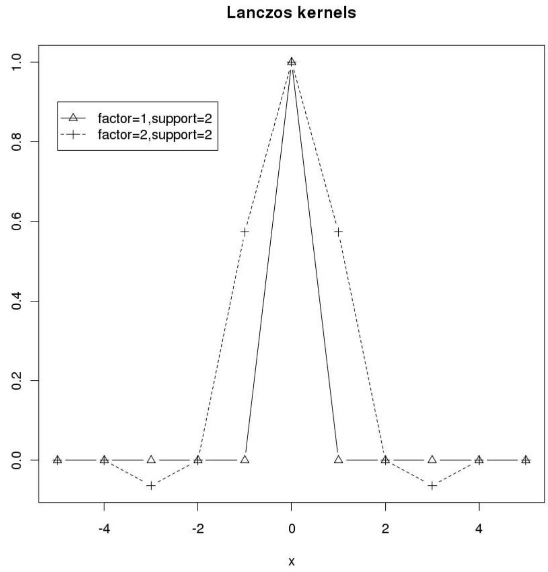


Figure 2.7: A comparison of two Lanczos kernel with different sampling factors: the more dispersed one is the one to use for image smoothing when halving its resolution.

Figure 2.8: An important example of image resampling: a face image is rotated, translated, and scaled so that the (centers of) the eyes of the subject are located at predefined positions. The two images illustrate the difference resulting from proper frequency conditioning via smoothing (left) and the direct use of the affine transform of Equation *TM*:2.76

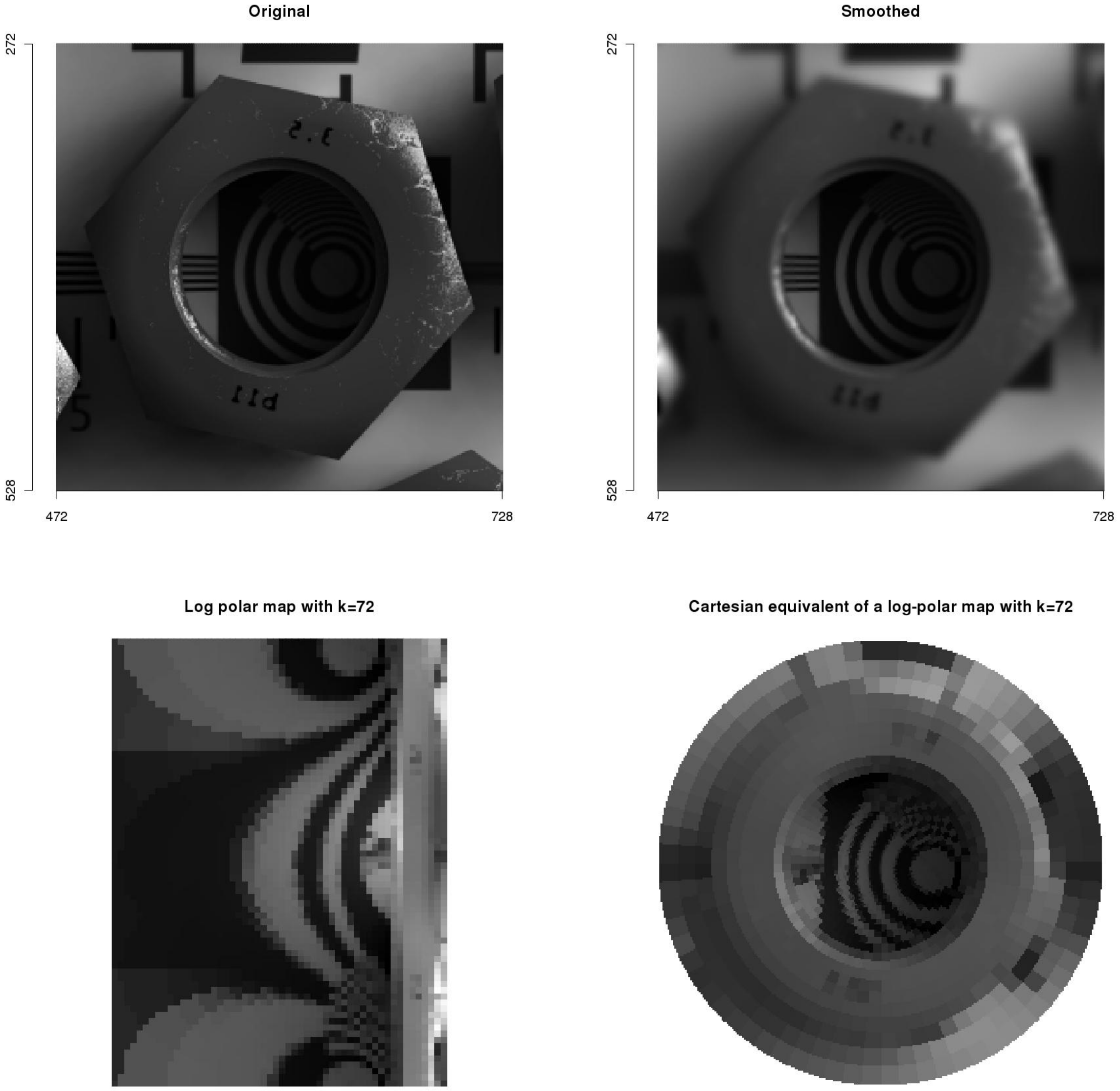


Figure 2.9: Log-polar mapping, providing image representation with spatio-variant resolution, requires a complex smoothing pre-processing. The images in the bottom row present the resulting map (left) and its back-projection in the standard image representation.

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Chapter 3

Template Matching as Testing

The chapter formally introduces template matching as a hypothesis testing problem. The Bayesian and frequentist approaches are considered with particular emphasis on the Neyman-Pearson paradigm. Matched filters are introduced from a signal processing perspective and simple pattern variability is addressed with the normalized Pearson correlation coefficient. Hypothesis test often requires the statistical estimation of the parameters characterizing the associated decision function: some subtleties in the estimation of covariance matrices are discussed.

keywords: *hypothesis testing, classification, Bayes risk criterion, Neyman-Pearson criterion, matched filters, correlation coefficient, maximum likelihood estimation, James-Stein estimator, shrinkage.*

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3.1 The ROC curve

A binary classification task can be considered as a binary hypothesis testin problem where one of the two competing hypotheses H_0 and H_1 must hold. The two basic probabilities characterizing the Neyman-Pearson approach to testing are the *false alarm* error probability P_F and the detection probability P_D. The former is the probability of returning H_1 when the true world state is described by H_0 and is also known as the probability of a type I error (or *false acceptance rate*, FAR). The latter, also known as the test *power*, gives the probability with which H_1 is returned (by the classifier) when the true world state is H_1. Neyman-Pearson classification, which maximizes P_D under a specified bound on P_F, results in a simple thresholding operation on the likelihood ratio value $\Lambda(\vec{x})$ for a pattern $\vec{x}$ under hypothesis H_0:

$$\Lambda(\vec{x}) \underset{H_0}{\overset{H_1}{\gtrless}} \nu \tag{3.1}$$

The relation between the two probabilities, specifically P_D as a function of P_F, is usually represented with a receiver operating characteristic (ROC) curve that is extensively discussed in Appendix *TM*:C:

$$P_D = P_D(P_F) \tag{3.2}$$

The quantity $1 - P_D$ represents the *false negative* error probability and is also known as the *false rejection rate* (FRR). The ROC curve is often reported as

$$\mathrm{FAR} = \mathrm{FAR}(\mathrm{FRR}) \tag{3.3}$$

While the ROC curve provides detailed information on the trade-off between the two types of errors, classification system are often synthetically characterized by means of the *equal error rate* (EER), the intersection of the ROC curve with the diagonal

$$\mathrm{FAR} = \mathrm{FRR} \tag{3.4}$$

When the data distribution under the two competing hypotheses is Gaussian with the same covariance matrix (and different means) the probabilities considered above can be computed in close form (see Section *TM*:3.3) and the multidimensional case does not present significant differences from the one dimensional one. The key parameter, fixing the maximum achieavable performance, is the separation of the distributions mean with respect to distribution standard deviation. With reference to Equations *TM*:3.50-58, we can from parameter ν to

$$z = \frac{\nu}{\sigma_0} + \frac{\sigma_0}{2} \tag{3.5}$$

in order to compute $P_D = P_D(P_F)$ exploint the fact that the Q-function is simply the complement to 1 of the distribution function (`pnorm`)

```
z   <- function(nu, s) (nu/s + s/2)
# generate a sequence of threhsolds
nus <- seq(-10,10,by=0.1)
# transform them to z (with sigma = 3) ...
zs  <- z(nus, 3)
tm.dev("figures/normalRoc")
plot(1-pnorm(zs),  1 - pnorm(zs-3), type="l", lty=1,
...       xlab="False alarm rate", ylab="Detection rate")
zs  <- z(nus, 2)
lines(1-pnorm(zs),  1 - pnorm(zs-2), type="l", lty=2)
zs  <- z(nus, 1)
lines(1-pnorm(zs),  1 - pnorm(zs-1), type="l", lty=3)
grid()
legend(0.6,0.6, c("sigma=3", "sigma=2", "sigma=1"), lty=c(1,2,3))
dev.off()
```

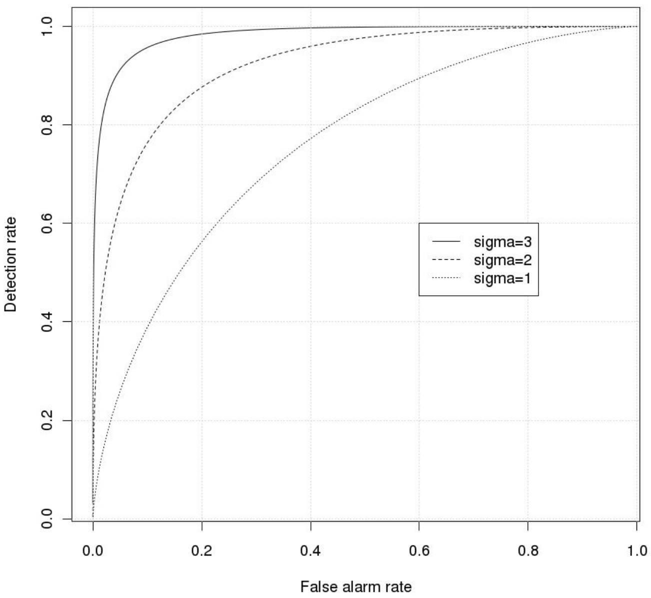

Figure 3.1: When data are normally distributed the maximum achievable performance is determined by the separation of the classes relative to the standard deviation of the distribution σ_0: the higher σ_0, the closer to the upper left corner the curve.

3.2 The normalized correlation coefficient

The basic template matching algorithm described in Chapter 1 is (very) sensitive to some commonly encountered template variations. When taking a digital image of a scene with a digital camera, even if we constrain ourselves to a fixed focal length, position and orientation, we have some remaining degrees of freedom, such as exposure time and focusing distance. We briefly consider the former: if we increase the exposure time (and the scene is relatively static) the result will be a lighter image. More photons are captured by the sensor and the reported intensity value will be proportionally higher. Additionally, sometimes, in order to make better use of the dynamic range available for image representation, the actual intensity values are *streteched* to fill a larger interval. The resulting transformation is of the following type

$$x \rightarrow x' = \alpha x + \beta \tag{3.6}$$

These transformations can be easily simulated:

```
sampleimages <- file.path(system.file(package = "AnImAl"), "sampleimages/")
face1        <- as.animage(getChannels(read.pnm(
...                  file.path(sampleimages, "sampleFace_01.pgm"))))
# generate a low contrast version of the face
lcFace       <- ia.add(ia.div(face1,4),0.25)
lcEye        <- ia.get(lcFace, animask(26,87,58,36))
```

We can modify the basic template matching of the previous chapter computing instead the following similarity measure

$$r_{L_p} = 1 - \frac{1}{d_{\max}} \left(\frac{1}{N} \sum_{\boldsymbol{i}} |A(\boldsymbol{i}) - B(\boldsymbol{i})|^p \right)^{1/p} \tag{3.7}$$

where A, and B are two congruent patterns and $d_{\max}$ is the maximum possible distance between them. This is exactly what `ia.correlation` does when invoked with `type = "Lp"` and `normalize = FALSE`:

```
cpa <- ia.correlation(lcFace, lcEye,
...                  type = "Lp", p=2L, range = 1, normalize = FALSE)[[1]]@data
# get the position of the most similar image region
which(cpa == max(cpa), arr.ind = TRUE)
```

The low contrast eye template is correctly locate in the low contrast face (let us note that `which` acts on array whose indices start from 1 while image indices, in this case, start from 0). However, if we try to locate the eye in the normal contrast image we see that the returned positio is not correct:

```
cpb <- ia.correlation(face1, lcEye, type = "Lp", p = 2L,
...                  range = 1, normalize = FALSE)[[1]]@data
which(cpb == max(cpb), arr.ind = TRUE)
```

The problem can be solved by normalizing each image window to zero average and unit standard deviation before comparing it to the similarly normalized template:

```
cpc <- ia.correlation(face1, lcEye, type = "Lp", p = 2L,
...                  range = 1, normalize = TRUE)[[1]]@data
which(cpc == max(cpc), arr.ind = TRUE)
```

The normalization procedure let us spot the template correctly. The difference between the similarity measure obtained with the normalized/unnormalized L_p similarity measure can be appreciated by inspecting the contour plot of the corresponding maps:

```
  tm.dev("figures/simContours", width=6, height=6)
  par(mfrow = c(2,2))
  persp(cpb, main = "Not normalized")
  persp(cpc, main = "Normalized")
  contour(cpb)
  contour(cpc)
  dev.off()
```

3.3 Stein estimation

As discussed at length in Chapter *TM*:3, an accurate estimate of probability distributions is key to successfull hypotheses testing in general and template matching in particular. Even when coping with the *simple* case of normally distributed patterns, the estimation of the correct probability distribution parameter from experimentally avaialble data poses some challenges. The key quantity to be estimated in this case is the covariance matrix, which, together with the mean, completely characterize the distribution.

Codelet 4 **On covariance estimation errors** (`R/tm.covarianceImpact.R`)

We want to visualize the impact of errors in the estimation of the covariance matrix on P_D, the detection probability, at different operating conditions P_F, as typical in the Neyman-Pearson paradigm. We refer to a single dimensional case, assuming that the distance of class means is 1: the difficulty of the problem is changed by changing the (common) standard deviation σ describing the two distributions. As easily checked from the results of Section *TM*3.3, we have that $\sigma_0 = \sigma^{-1}$. We want to compute the impact on $P_D(\sigma_0)$ given that we set the operating condition using $P_F(\sigma')$, where σ' is our estimate of σ_0 We first need to define a few functions, corresponding to Equation *TM*:3.15,

```
tm.Q <- function(x, sd = 1.0) {
  1 - pnorm(x/sd)
}
```

to Equation *TM*:3.57,

```
tm.Pf <- function(nu, sd0 = 1.0) {
  tm.Q(nu / sd0 + sd0/2)
}
```

and to Equation *TM*:3.58,

```
tm.Pd <- function(nu, sd0 = 1.0) {
  tm.Q(nu / sd0 - sd0/2)
}
```

By choosing $\sigma = 1/3$, from which $\sigma_0 = 3$, we get a reasonable testing case:

```
tm.covarianceImpact <- function(sigma0 = 3,
```

We then consider $P_F \in [0.01, 0.3]$

```
                                pfRange = c(0.01, 0.3, 0.01),
```

and a moderately large range for $\sigma' = \alpha\sigma_0$ $\alpha \in [0.8, 1.2]$:

```
                                pcRange = c(0.8, 1.2, 0.025)) {
```

We generate the sampling sequences:

```
  ats <- seq(-3*sigma0, 3*sigma0, 0.1)
  pfs <- do.call(seq, as.list(pfRange))
  pcs <- do.call(seq, as.list(pcRange)) * sigma0
```

and determine their lengths

```
  npfs <- length(pfs)
  npcs <- length(pcs)
```

from which we appropriately size the map:

```
  ci <- array(0, dim=c(npfs, npcs))
```

We now hypothesize several estimated values σ',

```
  for(c in 1:npcs) {
```

and for each of them, we build the function `nu` $\nu = \nu(x) : P_F(\nu) = x$:

```
    nu  <- splinefun(tm.Pf(ats, sd0=pcs[c]), ats)
    for(f in 1:npfs) {
```

We can now compute for a selected subset of operating conditions $P_F(\sigma')$ based on our estimated standard deviation, the difference in the miss probability with respect to the correct one $P_D(\sigma_0)$:

```
      ci[f,c] <- (1-tm.Pd(nu(pfs[f]), pcs[c])) /(1-tm.Pd(nu(pfs[f]), sigma0))-1
    }
  }
  list(pfs, pcs, ci)
}
```

```
 source("R/tm.covarianceImpact.R")
 sigma0 <- 3
 ci     <- tm.covarianceImpact(sigma0)
 tm.dev("figures/covarianceImpact")
 persp(ci[[1]], ci[[2]]/sigma0, ci[[3]], theta = 150, phi = 10,
...         shade = 0.9, expand = 0.75, r = 3, lwd=0.1,
...         ticktype="detailed",cex=0.5, tcl=-0.5,
...         xlab="false alarm rate", ylab="relative std. dev.",
...         main="Relative change of miss probabilities", zlab="")
 dev.off()
```

```
# load support for shrinkage covariance estimation
#
require(corpcor)
#
source("R/tm.shrinkageAdvantage.R")
# the number of samples
ns <- c(4,8,16,32,64,128,256,512)
# the sample space dimension
ps <- c(4,8,16,32,64,128,256,512)
#
shr <- tm.shrinkageAdvantage(ps, ns, ne = 10, ss = 10)
#
```

```
tm.dev("figures/shrinkageAdvantage")
#
persp(ns, ps, log(shr[[1]]/shr[[2]]),
...       theta = 50,  phi = -10, shade = 0.5,
...       ticktype="detailed", xlab="n", ylab="p",
...       zlab="log(error Frobenius norm)", d=2)
#
dev.off()
```

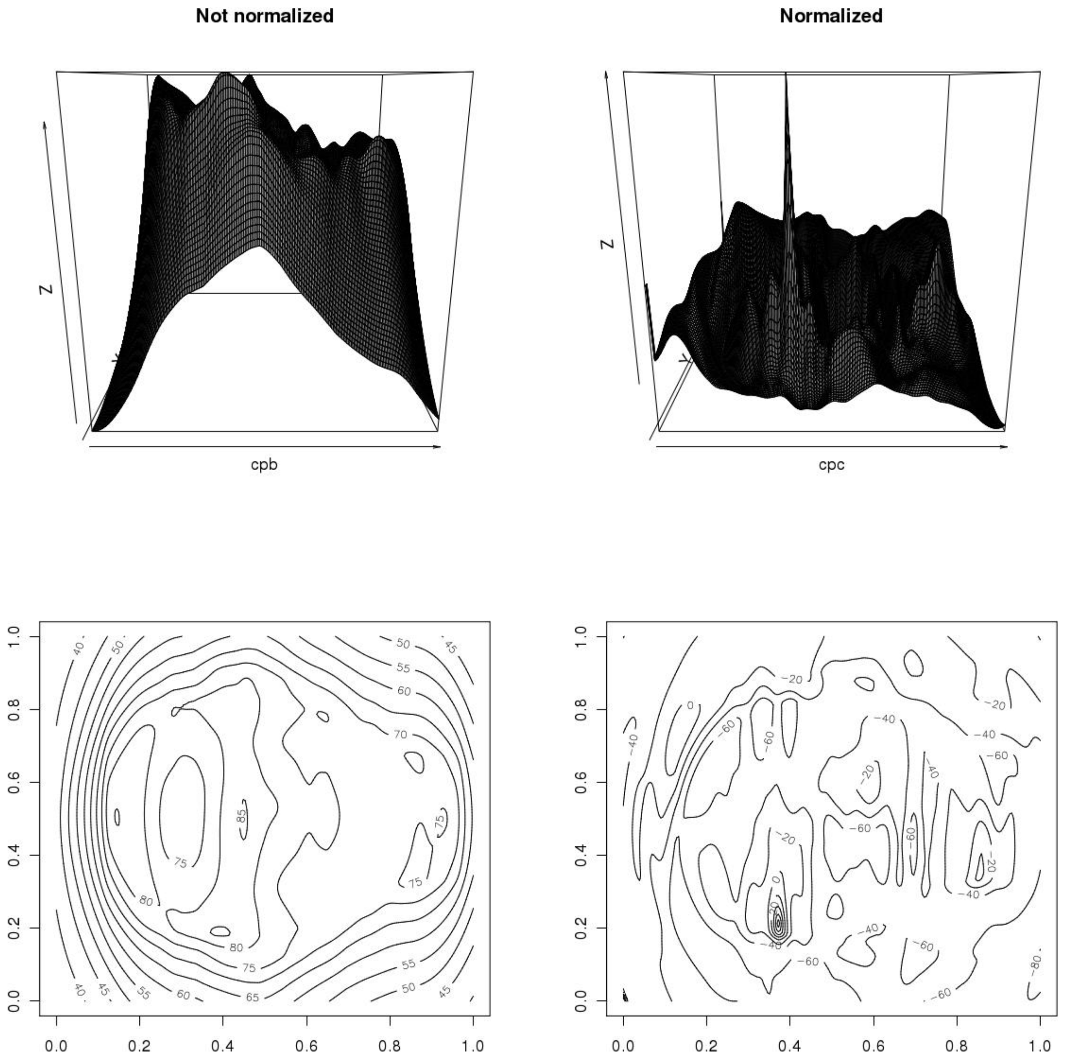

Figure 3.2: When data are normally distributed the maximum achievable performance is determined by the separation of the classes relative to the standard deviation of the distribution σ_0: the higher σ_0, the closer to the upper left corner the curve.

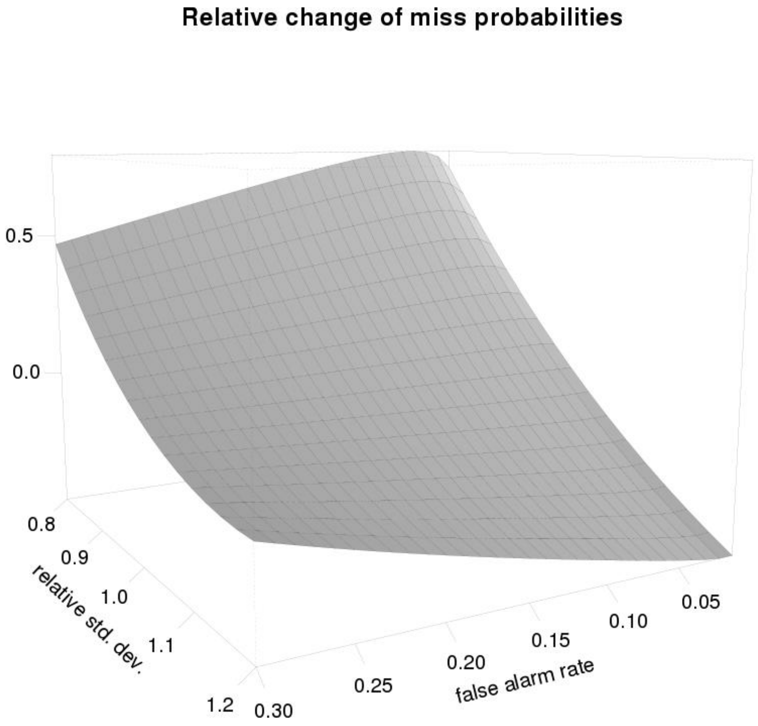

Figure 3.3: Small errors in the estimation of the parameters of the probability ditributions can have a significant impact on classification performance. The plot shows how the error in the estimation of the standard deviation of normally distributed data results in an amplified detection error.

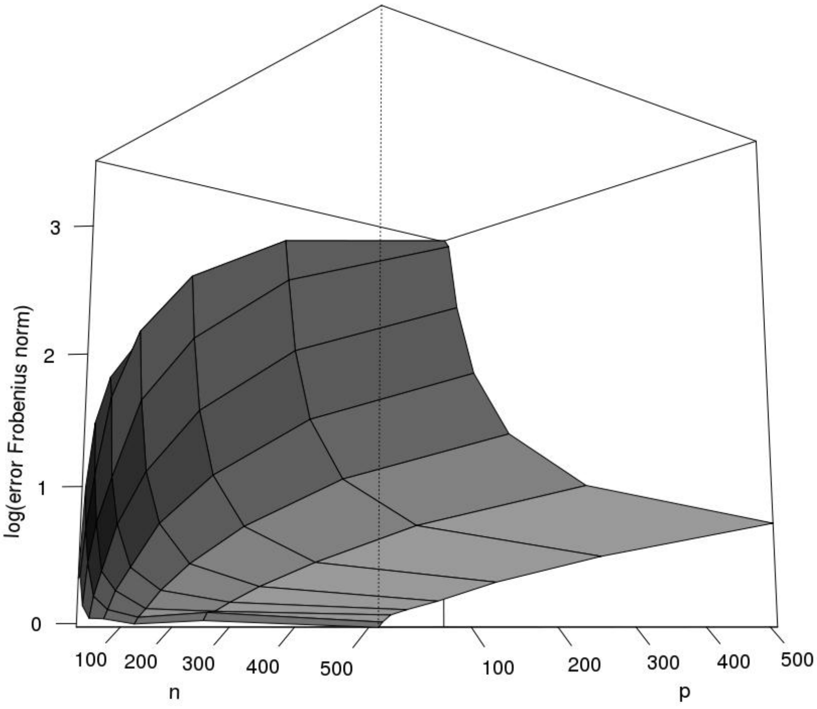

Figure 3.4: Shrinkage covariance estimation, based on the James-Stein insight, significantly outperforms the ordinary maximum likelihood estimator. The advantage increases with pattern space dimensionality p, and inversely to the number of samples.

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Chapter 4

Robust Similarity Estimators

A major issue in template matching is the stability of similarity scores with respect to noise, including unmodeled phenomena. Many commonly used estimators suffer from a lack of robustness: small perturbations in the data can drive them towards uninformative values. This chapter addresses the concept of estimator robustness in a technical way presenting applications of robust statistics to the problem of pattern matching. The approach is mainly based on the concept of influence function. M-estimators are discussed and L_1 based robust correlation measures introduced. A solution to the problem of robust estimation of covariance matrices is discussed.

keywords: *robustness, influence function, M-estimators, breakdown point, robust correlation coefficient.*

4.1 Validity of distributional hypotheses

The discussion of template matching as hypothese testing presented in Chapter *tm*:3 focused on the case of a deterministic signal corrupted by normal noise. The two hypotheses correspond to the case of a deterministic signal corrupted by normal noise and pure normal noise. What happens when we compare slightly displaced versions of the signal? In this case we are not comparing signal (possibly plus noise) with noise, but signal with signal, albeit displaced. What kind of distribution can we expect?

We will experimentally investigate this using two different templates: an eye and a hex nut (see Figure 4.1).

```
sampleimages     <- file.path(system.file(package="TeMa"),
...                            "sampleimages")
#
img1 <- ia.scale(as.animage(getChannels(read.pnm(
...                   file.path(sampleimages, "sampleFace_01.pgm")))),
...                  255)
m1     <- animask(28,89,54,33)
#
img2 <- ia.scale(
...                        ia.readAnimage(
...                           file.path(sampleimages,
...                                     "cameraSimulation",
...                                     "ortho_iso12233_large.tif")),
...                              maxValue = 255)[[1]]
m2   <- animask(485,288,231,225)
#
tm.plot("figures/detail1", ia.show(ia.get(img1,m1)))
tm.plot("figures/detail2", ia.show(ia.get(img2,m2)))
```

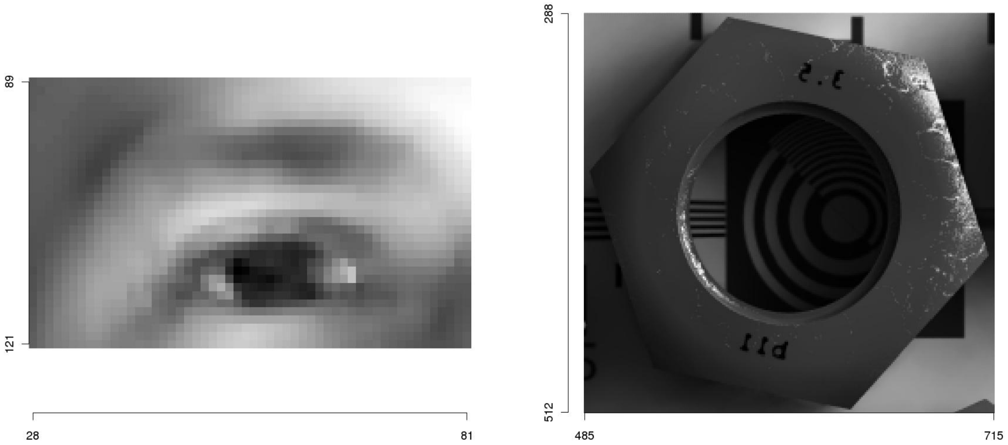


Figure 4.1: The two different templates used to investigate the distribution of pixel differences arising from misalignment and misalignment plus noise.

```
# We first focus on the effect of pattern misalignment:
# we consider the distributions of pixel values arising
# from displacing the patterns by a (Manhattan) distance
# z=1 and z=2
#
#
dtl    <- ia.get(img1, m1)
img    <- img1
m      <- m1
#
```

```
z      <- 1
values <- c()
#
for (i in z*seq(-1,1,by=1)) {
...   for (j in z*seq(-1,1,by=1)) {
...     dimg   <- ia.sub(ia.get(ia.slide(img, z*i, z*j), m),
...                         dtl)
...     values <- c(as.real(dimg@data), values)
...   }
... }
#
tm.dev("figures/dsts_1")
 hist(values,breaks=100,freq=FALSE,xlim=c(-50,50),
...   main="Normal vs. Cauchy (z=1)")
 lines(seq(-50,50),dnorm(seq(-50,50), sd=sqrt(var(values))), lty=1)
 lines(seq(-50,50),dcauchy(seq(-50,50),scale=mad(values,constant=1)),lty=2)
 legend(20,0.15, c("normal", "Cauchy"), lty=1:2)
dev.off()
#
z      <- 2
values <- c()
#
for (i in z*seq(-1,1,by=1)) {
...   for (j in z*seq(-1,1,by=1)) {
...     dimg   <- ia.sub(ia.get(ia.slide(img, z*i, z*j), m),
...                         dtl)
...     values <- c(as.real(dimg@data), values)
...   }
... }
#
tm.dev("figures/dsts_2")
 hist(values,breaks=100,freq=FALSE,xlim=c(-50,50),
...   main="Normal vs. Cauchy (z=2)")
 lines(seq(-50,50),dnorm(seq(-50,50), sd=sqrt(var(values))), lty=1)
 lines(seq(-50,50),dcauchy(seq(-50,50),scale=mad(values,constant=1)),lty=2)
 legend(20,0.04, c("normal", "Cauchy"), lty=1:2)
dev.off()
```

```
# We now consider a slightly different case: we consider
# a single displacement value z=1 (plus z=0) and change the
# amount of normal noise: noise=0 and noise=2
#
#
noise <- 0
img   <- img2
m     <- m2
dtl   <- tm.addNoise(ia.get(img,m),"normal",scale=noise,clipRange=c(0,255))
#
z      <- 1
values <- c()
#
for (i in z*seq(-1,1,by=1)) {
...   for (j in z*seq(-1,1,by=1)) {
...     dimg   <- ia.sub(tm.addNoise(ia.get(ia.slide(img, z*i, z*j), m),
...                             "normal",scale=noise,clipRange=c(0,255)),
...                  dtl)
...     values <- c(as.real(dimg@data), values)
...   }
... }
#
tm.dev("figures/dsts_3")
 hist(values,breaks=100,freq=FALSE,xlim=c(-50,50),
...   main="Normal vs. Cauchy (noise=0)")
 lines(seq(-50,50),dnorm(seq(-50,50), sd=sqrt(var(values))), lty=1)
 lines(seq(-50,50),dcauchy(seq(-50,50),scale=mad(values,constant=1)),lty=2)
 legend(20,0.15, c("normal", "Cauchy"), lty=1:2)
dev.off()
#
noise  <- 2
values <- c()
```

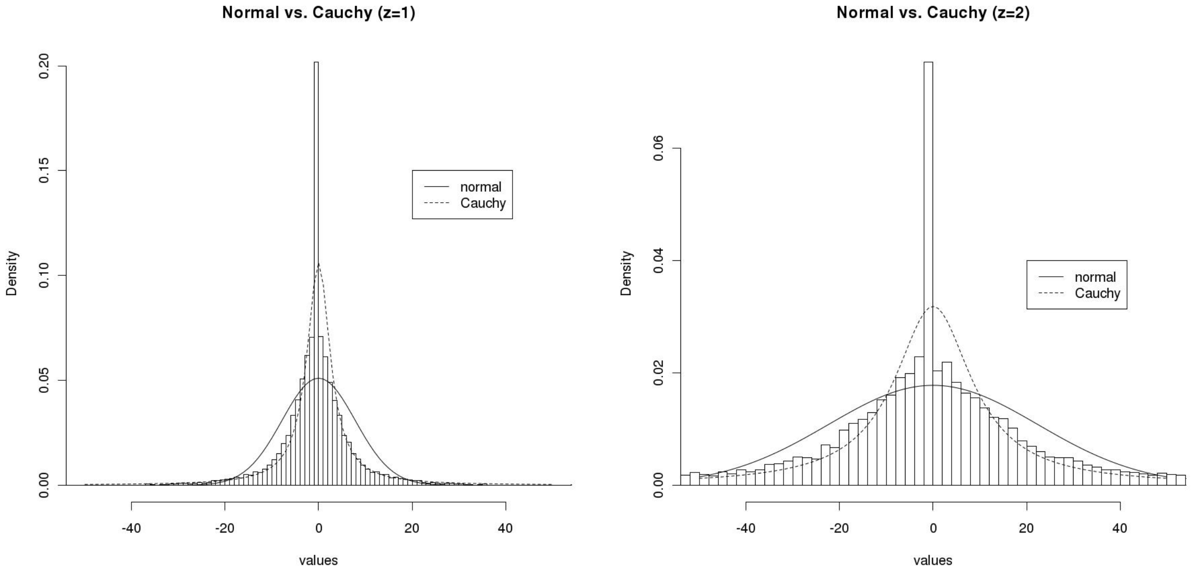


Figure 4.2: Considering slightly translated versions of the template as valid instances to be detected corresponds to the introduction of a template variability whose effect is not dissimilar to the addition of noise. As our lens in the template detection process is the computation of a sum of pixel differences we may get a first appreciation of the resulting variability by looking at the distribution of the differences of aligned pixels. While the detailed distribution depends on the specific template and on the allowed misalignment spacing, many practical cases result in a distribution that is better modeled with a Cauchy distribution than with a normal one. The two plots present the distributions arising from two different misalignments: `z=1` and `z=2`.

```
#
for (i in z*seq(-1,1,by=1)) {
...   for (j in z*seq(-1,1,by=1)) {
...     dimg   <- ia.sub(tm.addNoise(ia.get(ia.slide(img, z*i, z*j), m),
...                             "normal", scale=noise, clipRange=c(0,255)),
...                   dtl)
...     values <- c(as.real(dimg@data), values)
...   }
... }
#
tm.dev("figures/dsts_4")
 hist(values,breaks=100,freq=FALSE,xlim=c(-50,50),
...   main="Normal vs. Cauchy (noise=2)")
 lines(seq(-50,50),dnorm(seq(-50,50), sd=sqrt(var(values))), lty=1)
 lines(seq(-50,50),dcauchy(seq(-50,50),scale=mad(values,constant=1)),lty=2)
 legend(20,0.15, c("normal", "Cauchy"), lty=1:2)
dev.off()
```

4.2 Tanh estimators

Deviations of the actual distribution from the expect (model) one have a profound impact on the resulting parameter estimates. The case we consider in the text, for small values of the contamination location paramter, can be considered as a model for the estimation of image normalization parameters in the context of face recognition. The distribution of face intensity values, while not necessarily Gaussian, could be fruitfully morphed to a normal distribution (we will consider this in the next chapter) and the perturbation considered is somehow similar to

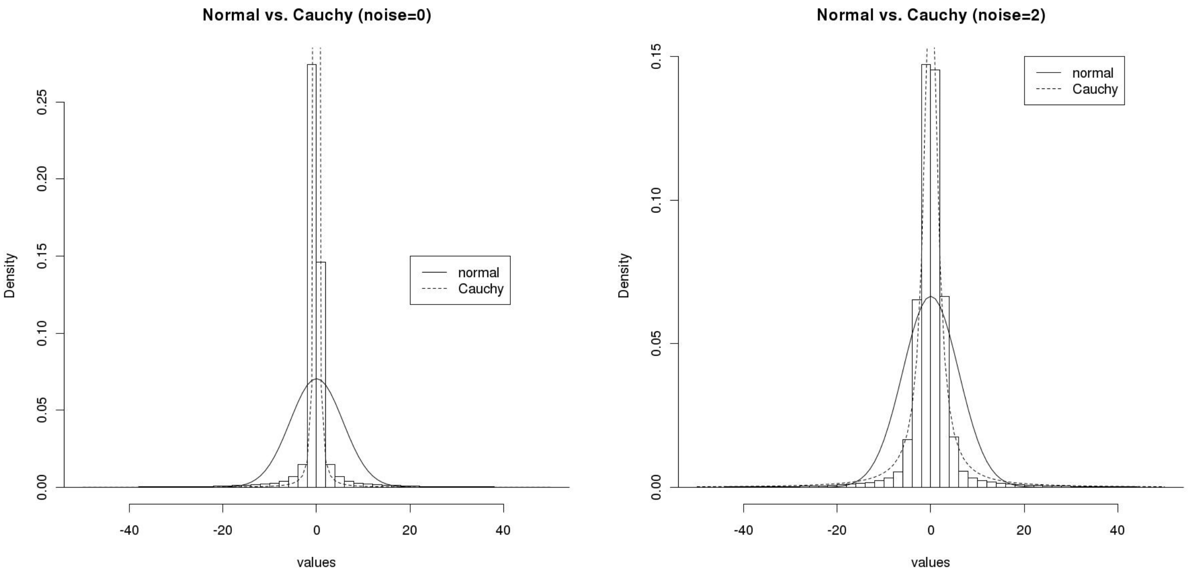


Figure 4.3: The two plots report the distribution of pixel differences in the case of misalignment and no noise (left) and in the case of misalignment plus a small amount of normal noise (right). The Cauchy distribution due to pattern misalignement dominates the normal noise distribution. Of course, increasing the amount of noise would increase the Gaussianity of the final distribution.

the presence of specularities, such as those often appearing at eyes.

```
values <- rnorm(100)
ats    <- seq(1, 20, by=1)
na     <- length(ats)
cs     <- seq(0,  0.2, by=0.01)
nc     <- length(cs)
aveP   <- array(0, dim=c(na,nc))
sdP    <- array(0, dim=c(na,nc))
aveR   <- array(0, dim=c(na,nc))
sdR    <- array(0, dim=c(na,nc))
#
cDist <- function(n=10000, c = 0.01, at=100) {
...  nm      <- as.integer(n*(1-c))
...  array(c(rnorm(nm), rep(at, n-nm)), dim=c(n,1))
... }
#
ic <- 0
for(c in cs) {
...  ic <- ic+1
...  ia <- 0
...  for(a in ats) {
...   ia      <- ia+1
...   values <- cDist(c = c, at = a)
...   estP   <- tm.robustEstimates(values, "p")
...   estR   <- tm.robustEstimates(values, "O")
...   aveP[ia,ic] <- estP[1] ; sdP[ia,ic]  <- estP[2]
...   aveR[ia,ic] <- estR[1] ; sdR[ia,ic]  <- estR[2]
...  }
... }
#
tm.plot("figures/aveP",
...  persp(ats,cs,aveP,theta=45, phi=25,shade=0.35,expand=0.75,r = 1,
...       xlab="contamination", ylab="cont. location",
...       main="Standard sample location estimator",
...       zlim = c(min(min(aveR),min(aveP)),max(max(aveR),max(aveP))),
...       lwd=0.1, ticktype="detailed",zlab="location"))
tm.plot("figures/aveR",
```

```
...  persp(ats,cs,aveR,theta=45, phi=25,shade=0.35,expand=0.75,r = 1,
...        xlab="contamination", ylab="cont. location",
...        main="Location scale estimator",
...        zlim = c(min(min(aveR),min(aveP)),max(max(aveR),max(aveP))),
...        lwd=0.1, ticktype="detailed",zlab="location"))
tm.plot("figures/sdP",
...  persp(ats,cs,sdP,theta=45, phi=25,shade=0.35,expand=0.75,r = 1,
...        xlab="contamination", ylab="cont. location",
...        main="Standard sample scale estimator",
...        zlim = c(min(min(sdR),min(sdP)),max(max(sdR),max(sdP))),
...        lwd=0.1, ticktype="detailed",zlab="scale"))
tm.plot("figures/sdR",
...  persp(ats,cs,sdR,theta=45, phi=25,shade=0.35,expand=0.75,r = 1,
...        xlab="contamination", ylab="cont. location",
...        main="Tanh scale estimator",
...        zlim = c(min(min(sdR),min(sdP)),max(max(sdR),max(sdP))),
...        lwd=0.1, ticktype="detailed",zlab="scale"))
#
tm.plot("figures/avePH",hist(aveP))
tm.plot("figures/aveRH",hist(aveR))
tm.plot("figures/sdPH", hist(sdP))
tm.plot("figures/sdRH", hist(sdR))
```

Tanh estimators can be used to define a robust version of the standard Pearson correlation coefficient as illustrated by function `tm.robustifiedCorrelation`.

Codelet 5 **A simple approach to robustified correlation** (`../TeMa/R/tm.robustifiedCorrelation.R`)

Pearson correlation coefficient is closely related to the computation of the variance of a set of numbers: it is the dot product of two vectors previously normalized to zero average and unitary variance. The sensitivity of the standard sample variance estimator to the presences of outlying values, such as those due to salt and pepper noise, affects the robustness of the Pearson correlation coefficient. Equation *TM*:4.17 shows how we can define a robust correlation coefficient using a robust scale estimator. The function `tm.robustifiedCorrelation` implements Equation *TM*:4.17 using the scale estimates provided by `tm.robustEstimates`.

```
tm.robustifiedCorrelation <- function(X, Y, mode="O") {
```

`X` and `Y` represent two images, usually normalized to zero location and unitary scale using `tm.normalizeImage`. The third parameter, `mode`, can assume three different values: `"p"`, corresponding to the usual (non robust) sample estimator, `"M"`, corresponding to a (non-refined) `tanh` estimator, and `"O"`, corresponding to a one-step version of the `tanh` estimator. In order to exploit Equation *TM*:4.17, we must generate two new random variables that correspond respectively to the sum and to the difference of the two images:

```
  XpY <- ia.add(X, Y)
  XmY <- ia.sub(X, Y)
```

proceeding to the computations required by Equation *TM*:4.17

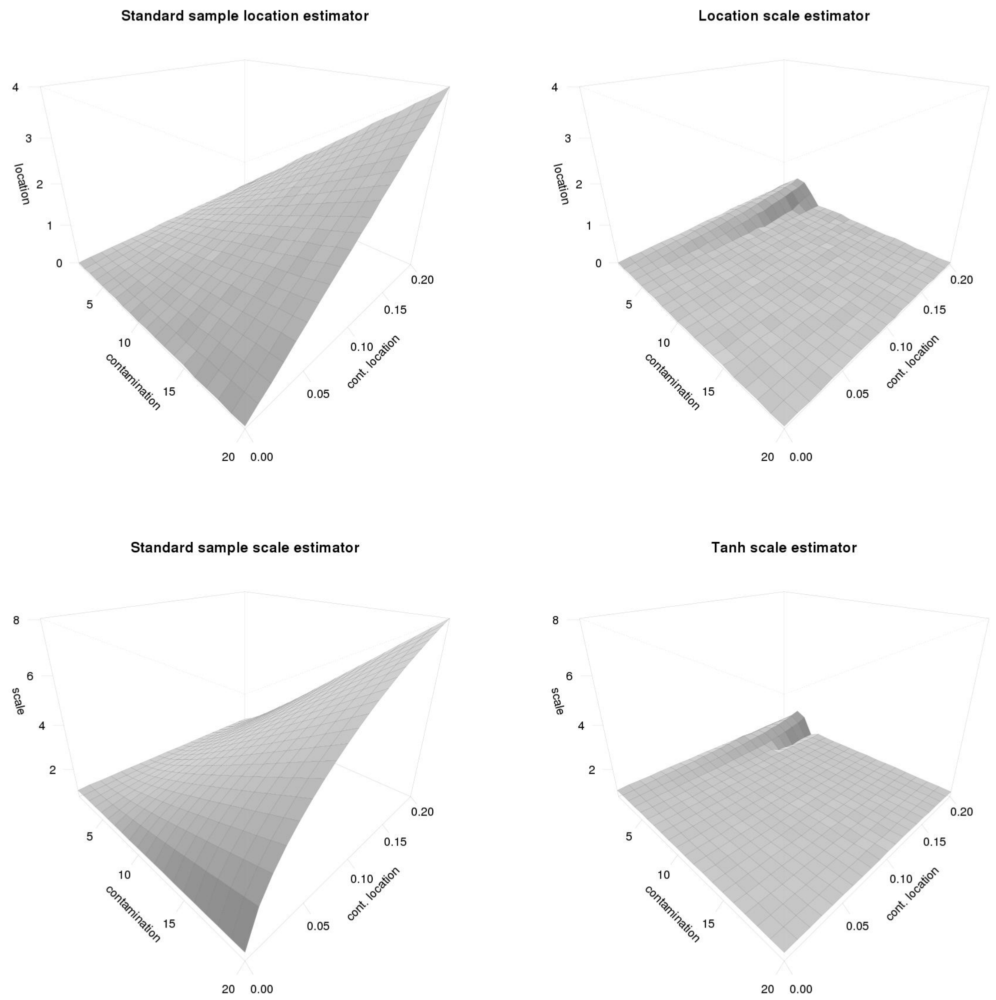
```
  sp  <- tm.robustEstimates(array(XpY@data, dim=c(ia.size(XpY),1)), mode)
  sm  <- tm.robustEstimates(array(XmY@data, dim=c(ia.size(XmY),1)), mode)
```

```
  (sp[2]*sp[2] - sm[2]*sm[2])/ (sp[2]*sp[2] + sm[2]*sm[2])
}
```

4.3 L_1 similarity measures

While the robustness achievable with `tm.robustifiedCorrelation` is remarkable, there are two related problems:

1. it requires a substantial amount of computation;
2. it can be, paradoxically, too robust: it looses discrimination efficiency.


Standard sample location estimator

Location scale estimator

Standard sample scale estimator

Tanh scale estimator

Figure 4.4: The plots make it clear that the *standard* sample estimators suffer significantly from the presence of contamination. The effect is more marked for the estimation of the scale parameter, a value that will turn out to be of paramount importance in many template matching techniques which rely on an accurate estimation of the covariance matrix.

Both problems can be solved using the similarity estimators based on the L_1 norm as described in Section *tm*:4.3.

```
tm.noiseSimilarityImpact <- function(img, cRange=c(0,0.2)) {
...   c0  <- cRange[1]
...   c1  <- cRange[2]
...   cs  <- seq(c0,c1,(c1-c0)/10)
...   n   <- length(cs)
...   #
...   img <- ia.scale(img)
...   res <- array(0, dim=c(n, 5))
...   #
...   i   <- 0
...   X   <- tm.normalizeImage(img)
...   for(c in seq(c0,c1,(c1-c0)/10)) {
...     i <- i + 1
...     res[i,1] <- c
...     #
...     Y <- tm.addNoise(img, noiseType="saltpepper", scale = 1, percent=c)
```

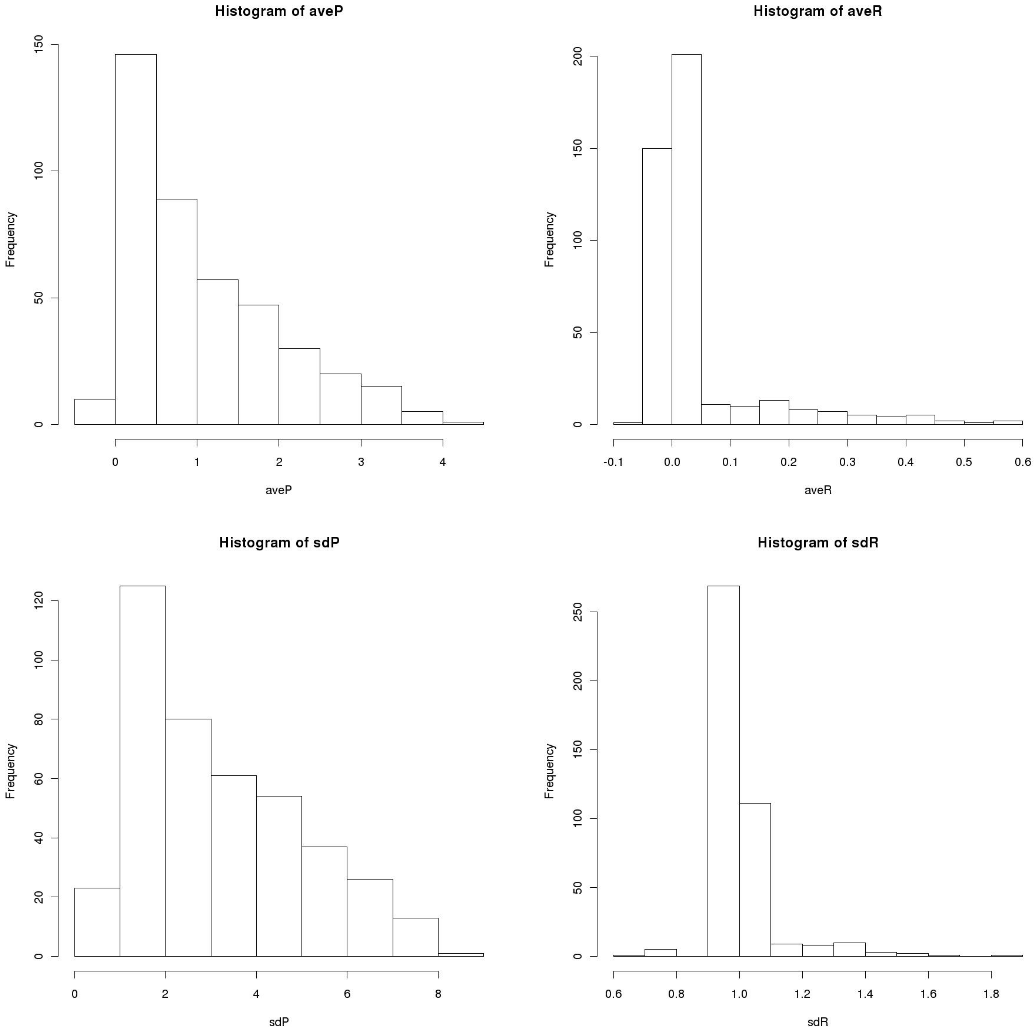


Figure 4.5: This figures presents an alternative view of the data presented in Figure 4.4. We discarde the dependency on contamination value and location and we plot the histogram of the estimates in order to better appreciate the corresponding variability.

```
...     Y <- tm.normalizeImage(Y)
...     #
...     res[i,2] <- tm.robustifiedCorrelation(X, Y, "p")
...     res[i,3] <- tm.robustifiedCorrelation(X, Y, "O")
...     res[i,4] <- max(ia.correlation(X,Y, type="G")[[1]]@data)/100
...     res[i,5] <- max(ia.correlation(X,Y, type="L")[[1]]@data)/100
...   }
...   #
...   res
... }
```

```
f   <- ia.get(img1, animask(32,87,104,104))
nsi <- tm.noiseSimilarityImpact(f)
tm.dev("figures/robustCorrelation")
 matplot(nsi[,1], nsi[,2:5], type="b", pch=2:5, lty=2:5,
...           xlab="Salt&pepper contamination", ylab="Similarity")
 legend(0.1,0.9,c("Pearson", "Tanh", "G", "L"), lty=2:5, pch=2:5)
 grid()
dev.off()
```

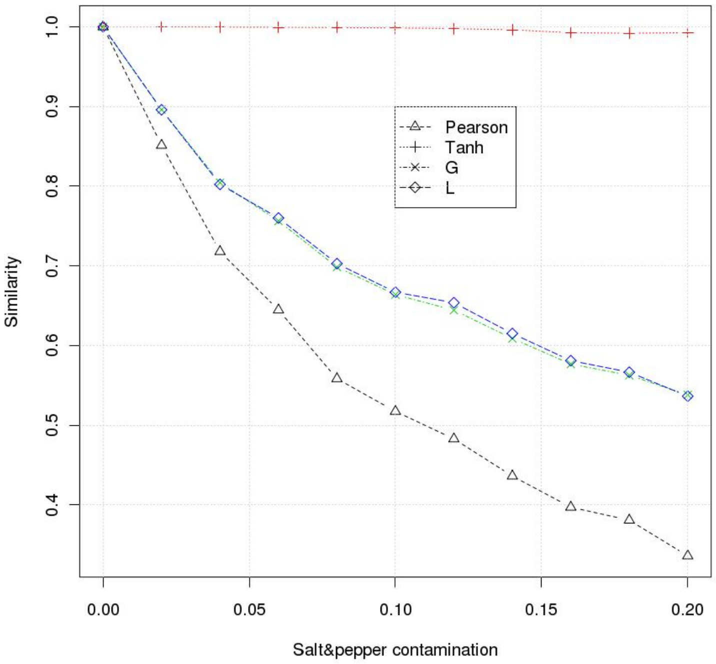


Figure 4.6: The presence of noise adversely affects the correct assessment of pattern similarity. The plot compares the decay of the similarity computed by different estimators at varying degrees of contamination. The superior robustness of the tanh robustified correlation estimator has a downside: it is so robust that its discriminatory ability is reduced.

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Chapter 5

Ordinal Matching Measures

Linear correspondence measures like correlation and the sum of squared differences between intensity distributions are (technically) non robust. Similarity measures based on the relative ordering of intensity values in image regions have demonstrable robustness both to monotonic image mappings and to the presence of outliers. In spite of the amount of information discarded when only ordinal information is used, the associated similarity measures, such as ordinal correlation of rank distances, preserve good pattern discriminability.

keywords: *rank transform, census transform, Spearman correlation coefficient, Kendall correlation coefficient, Bhat-Nayar distance, incremental sign transform.*

5.1 Histogram equalization

The use of the normalized correlation coefficient allows us to cope with global linear intensity remapping of the images being compared.

```
sampleimages     <- file.path(system.file(package="TeMa"),
...                           "sampleimages")
img1 <- ia.scale(as.animage(getChannels(read.pnm(
...                   file.path(sampleimages, "sampleFace_01.pgm")))),
...                  255)
m    <- animask(32,87,104,104)
face <- ia.integerAnimage(ia.scale(ia.get(img1, m), 255))
```

However, in many cases, image intensity undergoes a non linear transformation, a typical case being that of gamma correction, routinely applied by cameras in order to provide images that are more readable from human inspectors. The following code snippet applies a darkening gamma correction:

```
dark   <- ia.matop(function(x) ((x/255)**(4))*255, face)
tm.plot("figures/dark", ia.show(dark))
tm.plot("figures/darkH", hist(dark))
```

If we compute the correlation between `dark` and `face` we do not get 1 but a lower value

```
ia.correlation(ia.realAnimage(dark), ia.realAnimage(face))[[4]]
```

```
[1] 0.957491
```

even if the value is not as low as one would expect by the perceived image difference. Let us consider the following problem: given a set of face images, snapped under different illumination conditions, we want to compare each of them to every other one. This means that for each comparison, the two images may be characterized by two different illumination conditions. A possible solution is to equalize in turn one of the images, the one whose histogram has a lower entropy and hence less information, so that it approximates the histogram of the more informative image. By doing so, we ensure that we do not throw away information. Let us assume that we are working with 8 bits images (256 intensity levels).

```
  tm.entropy <- function(img) {
...      fs <- (hist(img,plot=FALSE,breaks=0:256)$counts)/ia.size(img)
...      fs <- fs[fs > 0]
...      -sum(fs*log2(fs))
...   }
  tm.entropy(dark)
```

```
[1] 6.514707
```

```
  tm.entropy(face)
```

```
[1] 6.642061
```

As `face` has a higher entropy, we equalize `dark` using as target histogra the histogram of `face`:

```
darkEq <- tm.histogramEqualize(dark,
...                                list(type="target",
...                                     histo=tm.histogram(face)))
ia.correlation(ia.realAnimage(darkEq), ia.realAnimage(face))[[4]]
```

```
[1] 0.9999505
```

The histogram of `darkEq` is now very similar to that of `face` and the correlation value of the two images is higher than that of the couple (`dark`, `face`). The major drawback of this strategy is that every time we compare two (different) images we must perform a different equalization. An alternative is to choose a neutral equalization target, and normalize each image towards it.

A *natural* choice is to choose a Gaussian distribution whose location paramters is 128 and whose standard deviation is such that no shadow or highlight clipping occurs when restricting to the interval [0.255]:

```
darkEq <- tm.histogramEqualize(dark,
...                          eqSpecs = list(type="Gaussian",
...                                         gMin=0, gMax=256, mu=128, sd=30))
faceEq <- tm.histogramEqualize(face,
...                          eqSpecs = list(type="Gaussian",
...                                         gMin=0, gMax=256, mu=128, sd=30))
tm.plot("figures/darkEq", ia.show(darkEq))
tm.plot("figures/darkEqH", hist(darkEq))
```

Even in this case we get a better correlation value than the one we got when comparing directly `dark` and `face`:

```
ia.correlation(ia.realAnimage(darkEq), ia.realAnimage(faceEq))[[4]]
```

```
[1] 0.999878
```

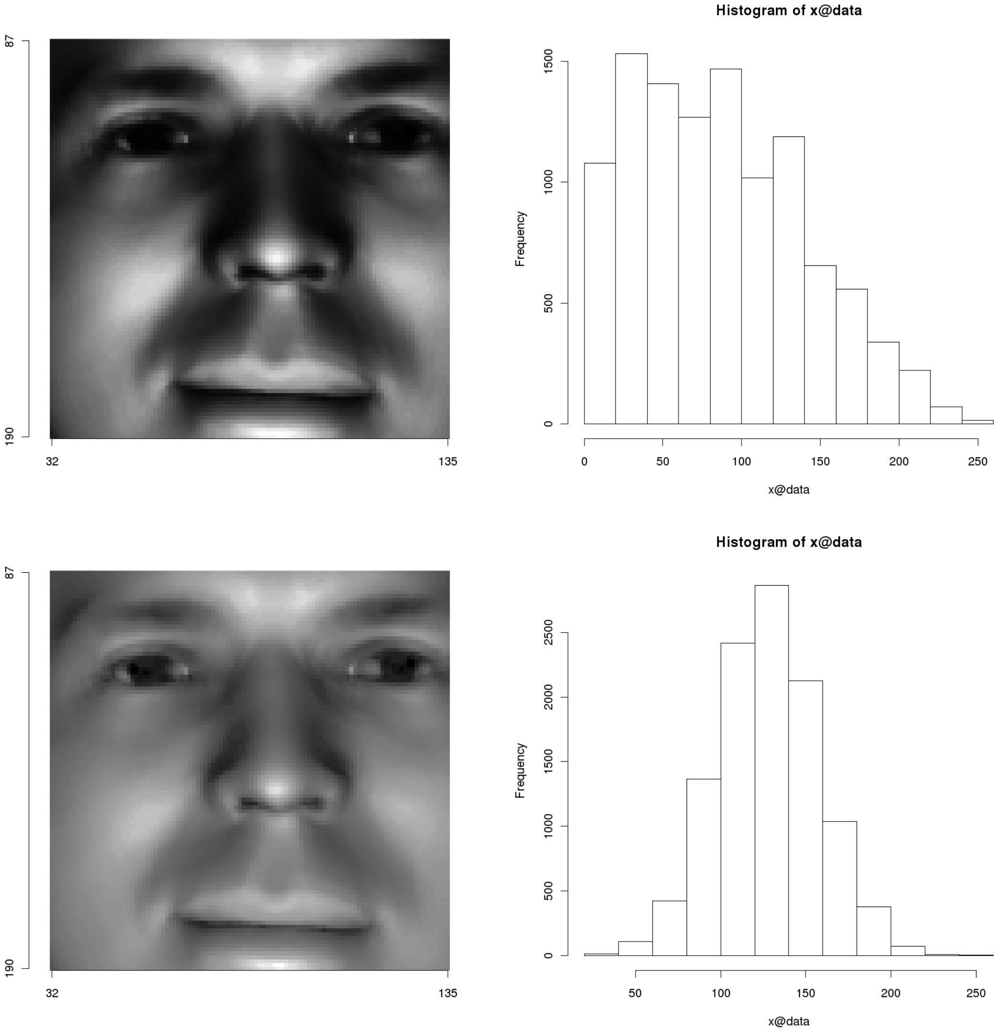

Figure 5.1: Image `dark` (top row) can be equalized so that the distributions of its intensity values approaches a Gaussian distribution (bottom row).

5.2 Ordinal Correlation Measures

An easy way to gain robustness to arbitrary monotone image intensity transformation is to switch from the comparison of absolute intensity values to the comparison of their relative ranking by consideriming ordinal correlation measures. Among them, the Spearman and the Kendall coefficients have been routinely used in statistical analysis. We can use them to compare the two images `dark` and `face`:

```
cor(as.real(dark@data), as.real(face@data), method="spearman")
```

```
[1] 0.9999929
```

```
cor(as.real(dark@data), as.real(face@data), method="kendall")
```

```
[1] 0.9996391
```

```
cor(as.real(dark@data), as.real(face@data), method="pearson")
```

```
[1] 0.957491
```

As expected, the Spearman and Kendall coefficients are insensitive to the applied image transformation while the Pearson coefficient is adversely affected by it. The computation time of the new coefficients is higher and it can be appreciated by timing their computation:

```
system.time(cor(as.real(dark@data), as.real(face@data), method="spearman"))
```

```
   user  system elapsed
  0.009   0.000   0.009
```

```
system.time(cor(as.real(dark@data), as.real(face@data), method="kendall"))
```

```
   user  system elapsed
  3.695   0.000   3.753
```

```
system.time(cor(as.real(dark@data), as.real(face@data), method="pearson"))
```

```
   user  system elapsed
  0.001   0.000   0.001
```

The estimates of correlation based on the Spearman and Kendall coefficient also exhibit a reduced noise sensitivity, a fact that we can check with the following code snippet:

```
  eye     <- ia.get(face, animask(38,89,44,33))
  ns      <- seq(0,0.5,0.025)
  n       <- length(ns)
  cvs     <- array(0, dim = c(n, 4))
  S       <- 5
  for(i in 1:n) {
...     cvs[i,1] <- ns[i]
...     for(s in 1:S) {
...       neye    <- tm.addNoise(eye, "saltpepper", scale=255,
...                              clipRange=c(0L, 255L), percent = ns[i])
...       cvs[i,2] <- cvs[i,2] + cor(as.real(eye@data), as.real(neye@data),
...                                 method="spearman")
...       cvs[i,3] <- cvs[i,3] + cor(as.real(eye@data), as.real(neye@data),
...                                 method="kendall")
...       cvs[i,4] <- cvs[i,4] + cor(as.real(eye@data), as.real(neye@data),
...                                 method="pearson")
...     }
...   }
  cvs[,2] <- cvs[,2]/S
  cvs[,3] <- cvs[,3]/S
  cvs[,4] <- cvs[,4]/S
```

```
tm.dev("figures/ordinalRobustness")
 matplot(cvs[,1], cvs[,2:4], pch=1:3, lty=1:3, type="b",
...           xlab="noise perc.", ylab="correlation")
 legend(0.2,1, c("Spearman", "Kendall", "Pearson"), lty=1:3, pch=1:3)
 grid()
dev.off()
```

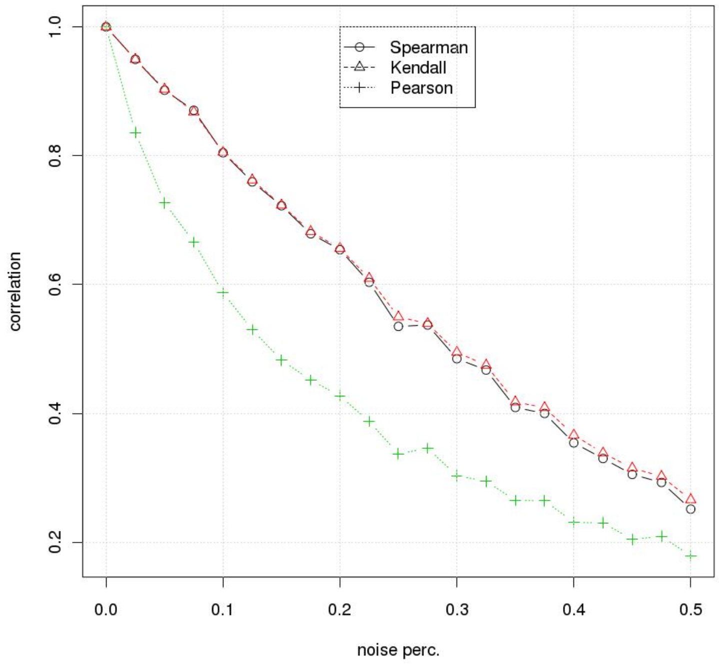

Figure 5.2: The ordinal correlation estimates from the Spearman and Kendall coefficients are less sensitive to noise than the estimate provided by the Pearson coeffcient. The robustness of the Spearman and Kendall estimates, at least in the present case, is very similar suggesting the usage of the Spearman coefficient whose computation is much faster.

5.3 Bhat-Nayar correlation

A simple and useful way to characterize the discriminatory power of a template matcher is to compute its signal to noise ratio SNR: its response at the correct location divided by its average response everywhere else. If the SNR is high, detection is expected to be reliable. We can detect our template simply by thresholding the response of the detector: small amounts of noise are not expected to make the value drop below threshold or making the value of other patterns arise above threshold. If the SNR is low, detection by thresholding might be unreliable or downright impossible. Function `tm.snr` provides a sample implementation of this quality parameter:

```
tm.snr <- function(map, at) {
...   n <- ia.size(map)
...   map[at[2], at[1]]/((sum(map@data) - map[at[2], at[1]])/(n-1))
... }
```

We can apply the concept of SNR to the comparison of the original Bhat-Nayar correlation measure (Equation *TM*:5.24) to the modified version Equation *TM*:5.27. The testbed we consider is that of matching a no-noise version of the eye region of the original face `face` image to a noisy version of the `dark` face. We compute the modified Bhat-Nayar correlation weighting the average part of the contribution with α:

$$r'_{\mathrm{BN}}(\alpha) = 1 - \left[(1-\alpha)\frac{\max_{i=1}^{N} d_m^i}{\lfloor \frac{N}{2} \rfloor} + \alpha \frac{\sum_{i=1}^{N} d_m^i}{\lfloor \frac{N^2}{4} \rfloor}\right]. \tag{5.1}$$

When $\alpha = 0$ we recover the original Bhat-Nayar definition, while $\alpha = 1$ keeps only the average distance. In order to compute the SNR we must identify the reference template position: the image coordinates representing the upper left corner of the eye template, i.e. $(38, 89)$. Besides computing the signal to noise ratio, we want to check the actual correlation value returned at the reference template location.

```
nDark  <- tm.addNoise(dark, "saltpepper", scale=255, clipRange=c(0L, 255L),
...                     percent = 0.01)
alphas <- seq(0,1,0.1)
n      <- length(alphas)
snrs   <- array(0, dim = c(n, 3))
for(a in 1:n) {
...   snrs[a,1] <- alphas[a]
...   bnC       <- tm.bhatNayarCorrelation(nDark, eye, alpha=alphas[a])
...   snrs[a,2] <- tm.snr(bnC[[1]], c(38,89))
...   snrs[a,3] <- bnC[[1]][89,38]
... }
tm.dev("figures/bnSNR")
plot(snrs[,1], snrs[,2], main="Modified Bhat-Nayar correlation SNR",
...      type="b", xlab="alpha", ylab="SNR")
grid()
dev.off()
tm.dev("figures/bnC")
plot(snrs[,1], snrs[,3], main="Modified Bhat-Nayar correlation",
...      type="b", xlab="alpha", ylab="correlation")
grid()
dev.off()
```

As we can appreciate from the corresponding plots reported in Figure 5.3, the averaged version of the Bhat-Nayar distance exhibits a better SNR and a better correlation value. The Bhat-Nayar similarity measure is an excellent example of the kind of robustness that we can achieve using ordinal similarity measures: monotone intensity transformation have no impact on the resulting estimates and noise effects are markedly reduced with respect to standard correlation:

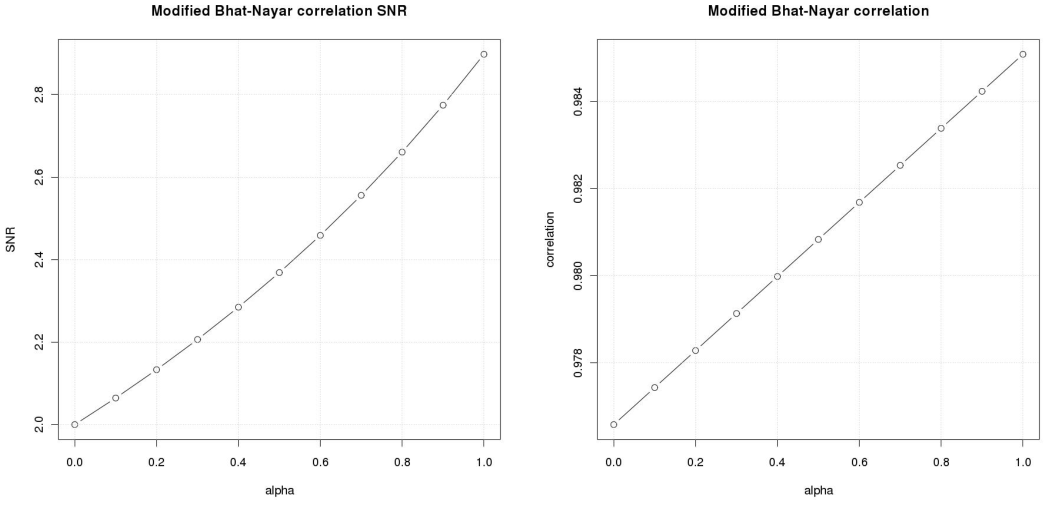

Figure 5.3: The signal to noise ratio and the maximum correlation value for the modified Bhat-Nayar correlation measure discussed in the text.

```
ia.correlation(ia.realAnimage(nDark),ia.realAnimage(eye))[[4]]
```

```
[1] 0.8974402
```

5.4 Non Parametric Local Transforms

Another way to gain robustness to intensity transformations and small amounts of noise is by means of local image operations transforming intensity values into pseudo intensity values based on local rank information. The transformed values are then insensitive to positive monotone image mappings and can accomodate a small amount of noise as long as noise does not change the relative rank of the intensity values. We consider four different non parametric local transforms based on ordinal information:

1. rank,
2. census,
3. modified census, including the central reference pixel,
4. incremental sign transform.

All the above transforms are provided by function `tm.ordinalTransform` with the use of a proper `mode` selector value (see Figure 5.4. Let us note that, as the transform cannot be computed at the boundary of the image, function `tm.ordinalTransform` performs an autoframing operation by default: we can prevent it by using `autoFrame=FALSE`.

```
N8        <- tm.squareNeighborhood(1L)
rankT     <- tm.ordinalTransform(face, N8, mode="rank")
censusmT  <- tm.ordinalTransform(face, N8, mode="census")
censusT   <- tm.ordinalTransform(face, N8, mode="censusm")
istT      <- tm.ordinalTransform(face, N8, mode="ist")
tm.plot("figures/rank",    ia.show(rankT,    main="Rank"))
tm.plot("figures/census", ia.show(censusT, main="Census"))
tm.plot("figures/censusm",ia.show(censusmT,main="Census (modified)"))
tm.plot("figures/ist",     ia.show(istT,     main="Ist"))
```

The neighborhood used for the computation of the local transforms is important for several reasons. The (computational) complexity of the transform depends on the number of points in the neighborhood. In the case of the census transform, the storage requirements for the result scale linearly with the number of points. As the result must be stored as an integer number for efficient use in image comparison tasks, the maximum number of points does not exceed 32 (sometimes 64). The number of points directly affects the dynamic range of the rank transform: the range corresponds to the number of points in the neighborhood, the larger, the more detailed the information provided.

It is possible to keep the number of points in the neighborhood small while increasing their spacing. This operation has a beneficial effect as the relative ordering of the pixel intensity values becomes more stable with increasing spacing: for a given local gradient, the farther apart the pixels, the greater the difference, and the more stable the relative ranking. The phenomenon can be visually appreciated in Figure 5.5

```
rankT1      <- tm.ordinalTransform(face, N8,    mode="rank")
rankT2      <- tm.ordinalTransform(face, N8*2L, mode="rank")
rankT3      <- tm.ordinalTransform(face, N8*3L, mode="rank")
tm.plot("figures/spacing1", ia.show(rankT1, main="Rank (1)"))
tm.plot("figures/spacing2", ia.show(rankT2, main="Rank (2)"))
tm.plot("figures/spacing3", ia.show(rankT3, main="Rank (3)"))
```

A similar effect can be observed for the census transform (see Figure 5.6).

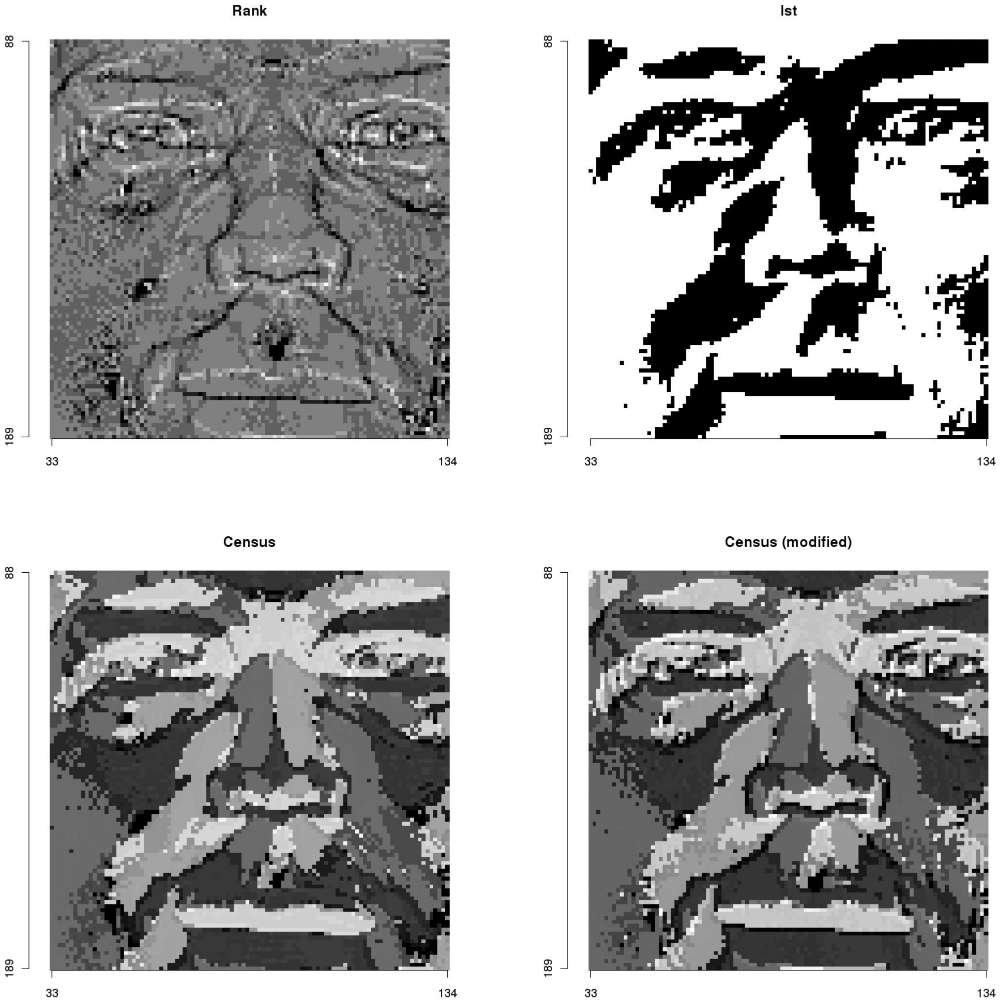

Figure 5.4: The different images present the four non parametric local transforms considered in the text.

```
 #
 cs  <- seq(0,0.4,0.02)
 n   <- length(cs)
 res <- array(0, dim=c(n, 4))
 i   <- 0
 X   <- tm.ordinalTransform(dark, N8, mode="census")
 for(c in cs) {
...     i        <- i + 1
...     res[i,1] <- c
...     #
...     Y <- tm.ordinalTransform(tm.addNoise(dark, noiseType="saltpepper",
...                                          scale = 255, clipRange=c(0L,255L),
...                                          percent=c),
...                                          N8, mode = "census")
...     #
...     res[i,2] <- tm.hamming(X, Y, width=8)
...     res[i,3] <- tm.tanimoto(X, Y)
...     res[i,4] <- tm.dixonKoehler(X, Y, width=8)
...   }
 #
tm.dev("figures/bitDistances")
 matplot(res[,1], res[,2:4], type="b", pch=2:4, lty=2:4,
```

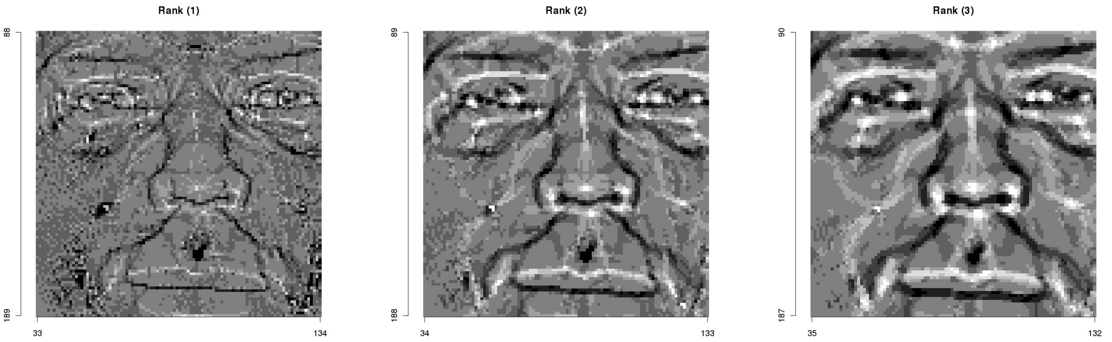

Figure 5.5: Increasing the spacing among the pixels of the neighborhood may increase the stability of the ordinal relations among the pixel intensity values with no impact on computation time or result storage requirements. The above images show what happens for the rank transform.

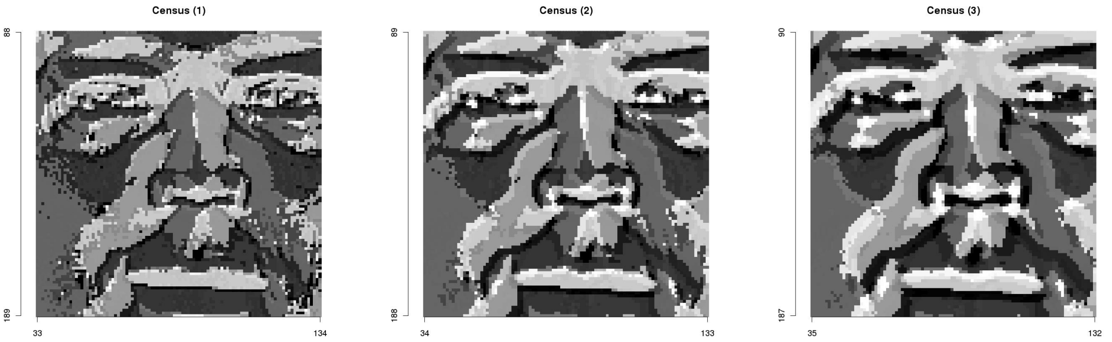

Figure 5.6: The effect of neighborhood spacing on the result of the census transform.

```
...          xlab="Salt&pepper contamination", ylab="Bit distance")
 legend(0.0,0.3,c("Hamming", "Tanimoto", "Dixon-Koehler"), lty=2:4, pch=2:4)
 grid()
dev.off()
```

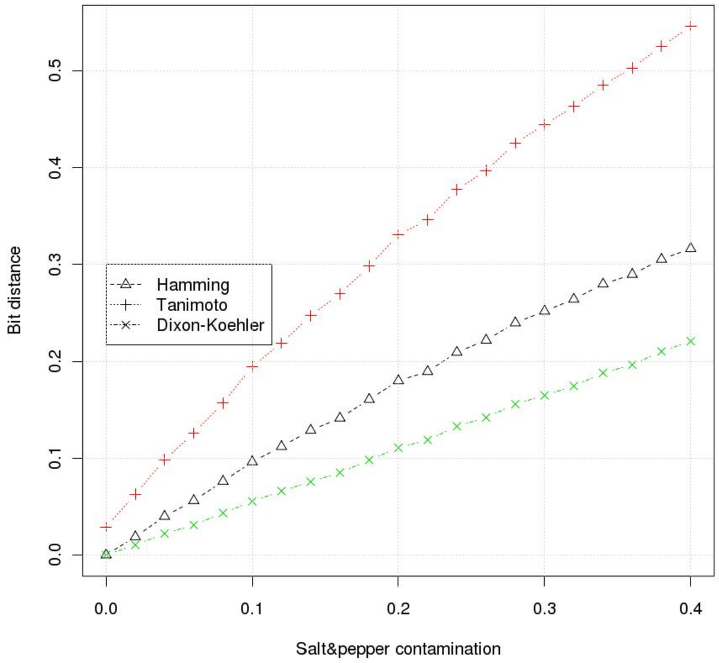

Figure 5.7: The correct way to compare the images resulting from the census transform is to use bit based distances. The plot illustrates the results obtained applying the distances dicussed in the text.

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Chapter 6

Matching Variable Patterns

While finding a single, well defined shape is useful, finding instances of a class of shapes is even more useful. Intraclass variability poses new problems for template matching and several interesting solutions are available. This chapter focuses on the use of projection operators on a one-dimensional space to solve the task: synthetic discriminant functions (SDFs). These projection operators can be optimized to control off peak filter response balancing the requirements of sharp peaks and limited sensitivity to noise while maintaining a constant response over the patterns of a given class.

keywords: *synthetic discriminant function, filter off peak response, non-orthogonal image expansion, least squares synthetic discriminant function.*

6.1 Maximizing SNR over class samples

In this section we start to address the problems arising from intrinsic signal variability. We no longer limit ourselves to the the problem of detecting a single, deterministic signal corrupted by noise, and we move to the problem of detecting a class of signals in the presence of noise. The signals we will consider are images of faces, a class of patterns of significant practical and theoretical interest. The dataset we will be using comprises 800 different faces, equally distributed over four differents races and the two genders.

```
basepath    <- "../theFaceDbs/races"
racesImages <- scan(file.path(basepath, "racesImageNames"), list(""))[[1]]
N           <- length(racesImages)
m           <- animask(5,13,21,25)
d                 <- 21*25
raceSamples       <- c()
raceSamplesMatrix  <- array(0, dim=c(N,d))
for(i in 1:N) {
...   img <- as.animage(getChannels(read.pnm(file.path(basepath,
...                                                 racesImages[[i]]))))
...   img <- ia.get(img, m)
...   raceSamples          <- c(img, raceSamples)
...   raceSamplesMatrix[i,] <- as.real(img@data)
... }
```

It is interesting to note the result of clustering the above data respectivel with 4 clusters, the number of races considered, and with 8 clusters the number of races times the number of genders:

```
kns <- list(2,4,6,8,10,12,14,16,18,20,22,24,26,28,30,32)
kcs <- ia.map(function(n) sort(clara(raceSamplesMatrix,  n)$i.med), kns)
k32 <- raceSamplesMatrix[kcs[[16]],]
```

The default metrics used by function `clara` is the Euclidean norm (L_2) discussed in a previous chapter. Samples are regularly (consecutively) organized in groups of 200 items, 100 males and 100 females. The above clustering procedure, of which we reported the indices identifying each computed cluster within the original data, assigns 1 cluster center to each race (or race and gender) group.

```
tm.dev("figures/fourClusters", width=6, height=2)
par(mfrow = c(1,4))
for(i in kcs[[2]]) {
... ia.show(raceSamples[[i]])
... }
dev.off()
tm.dev("figures/eightClusters", width=6, height=4)
par(mfcol = c(2,4))
for(i in kcs[[4]]) {
... ia.show(raceSamples[[i]])
... }
dev.off()
```

As detailed in Section *tm*:6.1, the optimal matched filter for the whole image set is given by the dominant eigenvector. Let us note that, in this case, the required covariance matrix is the not-centered one:

$$\Sigma = X^T X \tag{6.1}$$

where X is a matrix whose rows correspond to our face images, linearized as vectors:

```
 var <- t(raceSamplesMatrix) %*% raceSamplesMatrix
```

The computation of the eigenvectors is straightforward:

```
 evs <- eigen(var)
 # and we de-linearize the most significant twos
 # into an image
```

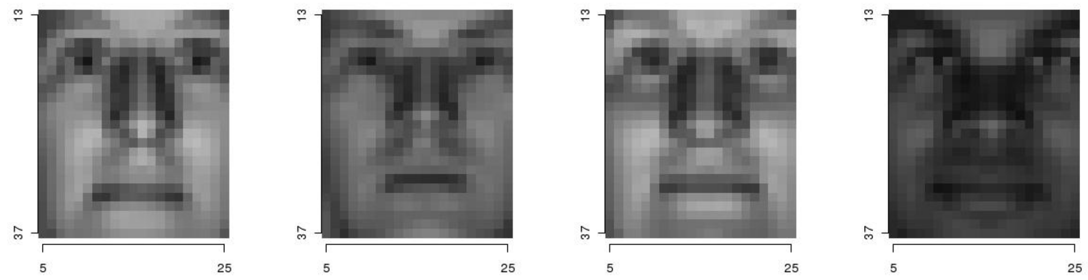

Figure 6.1: The images corresponding to the centers of the four cluster result. They belong to the four different racial groups, suggesting that the task of race discrimination can be effectively solved by template matching techniques using appropriately selected race prototypes.

```
 ev1 <- as.animage(x <- array(evs$vectors[,1], dim=c(25,21)))
 ev2 <- as.animage(x <- array(evs$vectors[,2], dim=c(25,21)))
tm.dev("figures/evs", width=6, height=6)
par(mfcol = c(2,2))
ia.show(ev1)
ia.show(ia.scale(ia.mult(ev1, -1)))
ia.show(ev2)
ia.show(ia.scale(ia.mult(ev2, -1)))
dev.off()
```

6.2 Multi-class Synthetic Discriminant Functions

Synthetic discriminant functions, SDFs for short, are introduced in Chapter *tm*:6.1 as a way to generate a single direction onto which samples from a given set project (more or less) at the same, predefined point. The construction of an SDF relies on the possibility of solving a linear set of equations obtained by enforcing the projection values of a given set of patterns: the solution can be expressed as a linear combination of the available samples. There are two related effects that we want to explore:

1. the distribution of the projection values obtained from patterns of the same class but not explicitly used in building the SDF, and the dependency of its spread on the number of sampels used in the SDF;
2. how does an SDF compares with projection onto the (scaled) mean sample, both visually and interms of the resulting distribution of projection values.

In order to investigate the first issue, we build a sequence of SDFs, using as building samples the centers of an increasing number of clusters computed from the whole set of available faces (using function `clara` from package `cluster`). We build a least squares SDF minimizing the projection error onto the whole face dataset.

```
ks     <- 1:32
breaks <- seq(0.4,1.5,0.05)
map    <- array(0, dim=c(length(breaks)-1, length(ks)))
for(k in 1:length(ks)) {
...   sdf<-tm.sdf(t(clara(raceSamplesMatrix, ks[k])$medoids),
...               t(raceSamplesMatrix))
...   map[,k]<-hist(raceSamplesMatrix %*% sdf,breaks=breaks,main=k)$counts
... }
tm.dev("figures/sdfVsSamples")
```

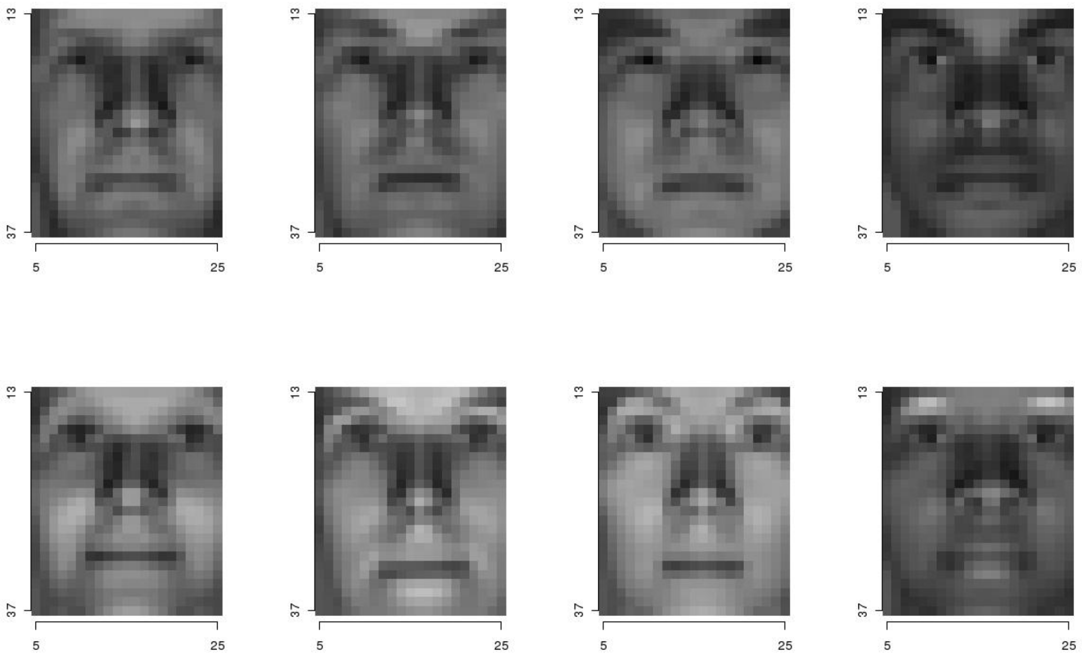

Figure 6.2: The images corresponding to the centers of the eight cluster result. The remark of Figure 6.1 still applies. Interestingly, the upper row presents male samples, the lower row female examples: even the task of automatic gender determination seems to be solvable with template matching techniques. Chapter *tm*:12 addresses the race/gender discrimination problem using a couple of techniques related to template matching: regularization network and support vector machines.

```
persp(seq(0.425, 1.5, 0.05), 1:32, map, theta = 30, phi = 20,
...   shade = 0.7, expand = 0.75, r = 3, lwd=0.1, ylab="Clusters",
...   ticktype="detailed",cex=0.5,tcl=-0.5, xlab="Projection value",zlab="counts")
dev.off()
```

The second issue can be addressed in a straightforward way: we compute the average face, the least squares SDF based on a single cluster description, and the least sqaures SDF based on a 32 cluster description:

```
n    <- dim(raceSamplesMatrix)[1]
mean <- raceSamplesMatrix[1,]
for(i in 2:n)
...     mean <- mean + raceSamplesMatrix[i,]
mean  <-mean / n
sdf.m <-tm.sdf(t(matrix(mean, nrow=1)), t(raceSamplesMatrix))
sdf.1 <-tm.sdf(t(clara(raceSamplesMatrix,1)$medoids),t(raceSamplesMatrix))
sdf.32<-tm.sdf(t(clara(raceSamplesMatrix,32)$medoids),t(raceSamplesMatrix))
#
tm.dev("figures/meanVsSdf", width=6, height=4)
 par(mfrow = c(2,3))
 hist(raceSamplesMatrix %*% sdf.m, breaks=seq(0.4,1.5,0.05),
...         xlab="proj.", main="")
 hist(raceSamplesMatrix %*% sdf.1, breaks=seq(0.4,1.5,0.05),
...        xlab="proj.", main="")
 hist(raceSamplesMatrix %*% sdf.32, breaks=seq(0.4,1.5,0.05),
...        xlab="proj.", main="")
 sdf.m.i  <- as.animage(array(sdf.m,  dim=c(25,21)))
 sdf.1.i  <- as.animage(array(sdf.1,  dim=c(25,21)))
```

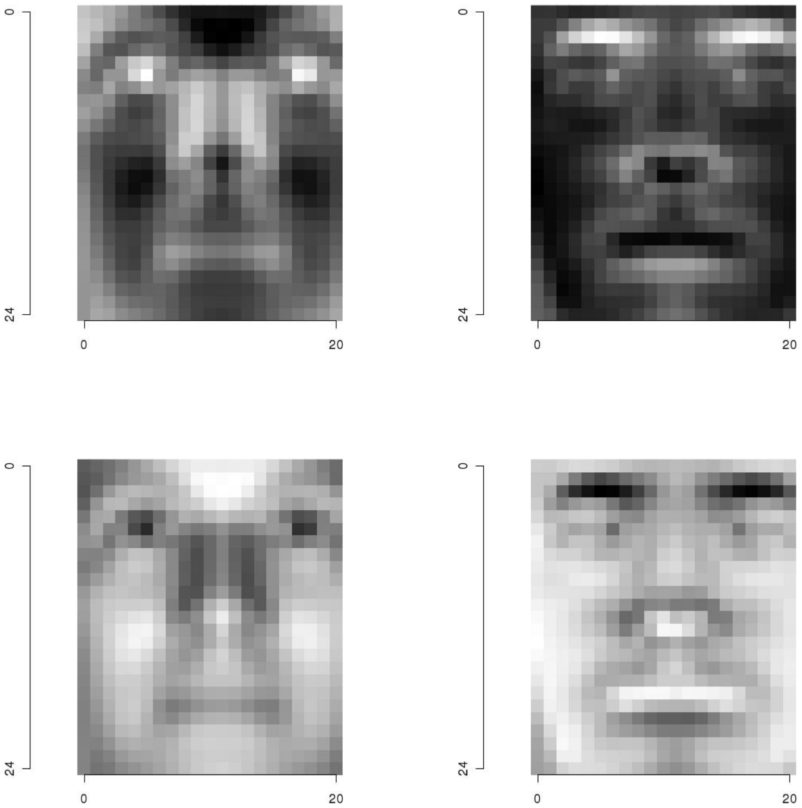

Figure 6.3: The two most significant eigenvectors of the uncentered covariance matrix. The most significant one (first column to the left) resembles the average face. Let us note that there is an ambiguity on sign: the lower row contains the inverted version of the first row (returned as eigenvectors). In this case, we should use the inverted, most significant eigenvector as matched filter.

```
  sdf.32.i <- as.animage(array(sdf.32, dim=c(25,21)))
  ia.show(ia.scale(sdf.m.i),main="sdf (mean)")
  ia.show(ia.scale(sdf.1.i),main="sdf (1)")
  ia.show(ia.scale(sdf.32.i),main="sdf (32)")
dev.off()
```

As we can observe in Figure 6.5, the difference between `sdf.m` and `sdf.1` is minor, but `sdf.32` results in a significantly different filter providing superior performance. The dispersion of the projection values around the required value (i.e. 1) can be easily quantified by computing the variance of the values:

```
var(raceSamplesMatrix %*% sdf.m)
```

```
            [,1]
[1,] 0.03348178
```

```
var(raceSamplesMatrix %*% sdf.1)
```

```
            [,1]
[1,] 0.03331501
```

```
var(raceSamplesMatrix %*% sdf.32)
```

```
              [,1]
[1,] 0.005619665
```

from which we see that there is almost an order of magnitude of difference.

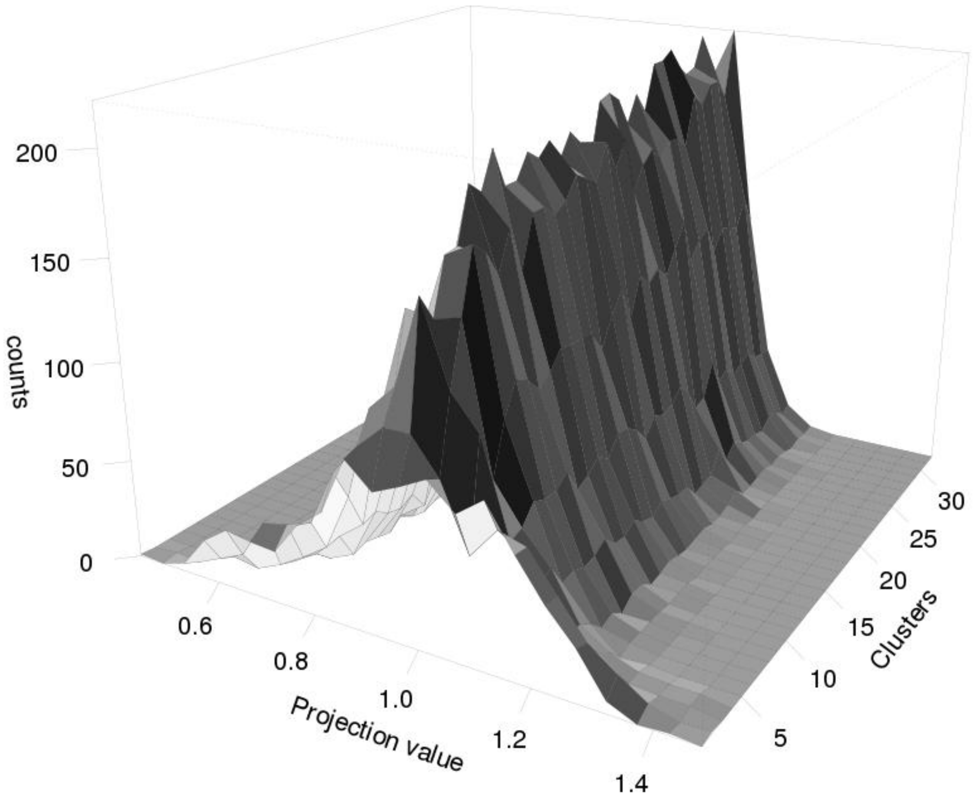

Figure 6.4: By using an increasing number of meaningful samples we are able to build an increasingly better SDF as can be seen from the progressively more peaked projection value distribution. The highly dispersed distribution closer to view, resulting from the SDF built using a single template, means that projecting onto this SDF is not going to be effective: in order to detect a good percentage of faces we need to use a high tolerance threshold, so that many false positives are to be expected. The situation is significantly better when using the SDF built from 32 samples.

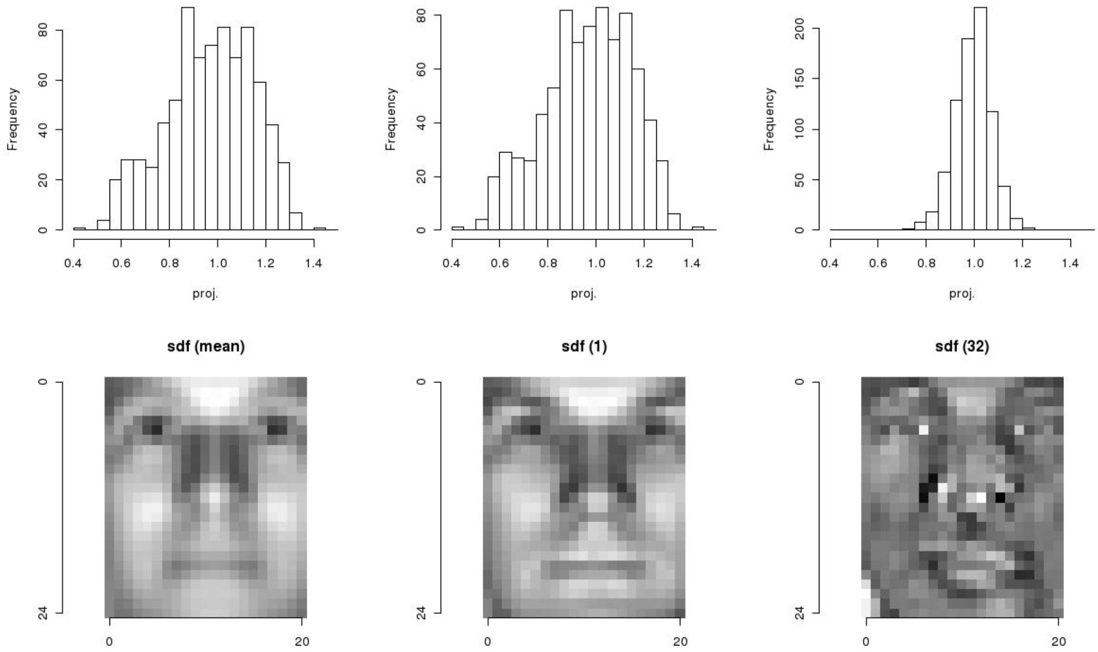

Figure 6.5: SDFs provide an efficient way to compact the information from several samples into a single projection direction. The first image to the left is the average face: even if all images have been previously normalized by fixing eyes location, the remaining facial features appear blurred due to their position variability. The central image is the sample minimizing the Euclidean distance from all the other ones: is is the single cluster center returned by `clara`. The image to the right is the synthetic template generated by a least squares SDF built from the linear combination of 32 cluster centers.

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Chapter 7

Matching Linear Structure: the Hough Transform

Finding simple shapes, such as lines and circles, in images may look like a simple task but computational issues coupled with noise and occlusions require some not so naive solutions. In spite of the apparent diversity of lines and areas, it turns out that common approaches to the detection of linear structures can be seen as a an efficient implementation of matched filters. The chapter describes how to compute salient image discontinuities and how simple shapes embedded in the resulting map can be located with the Radon/Hough transform.

keywords: *edge detection, Radon transform, Hough transform, generalized Hough transform, fixed-band estimator.*

contains material from *Template Matching Techniques in Computer Vision: Theory and Practice*, Roberto Brunelli,

7.1 Edge detection

Many patterns can be profitably represented by means of curves (as opposed to areas). Two new problems arise: how a reliable line based representation of a pattern can be obtained and how such representations can be exploited to efficiently find and compare patterns. In this section we describe a method to derive this kind of representations from a generic image, while the next sections will focus on how such a representation can be exploited to detect patterns in a robust and efficient way.

A basic way to obtain a line drawing from any image is to detect points of significant gradient intensity. The presence of noise makes the task more difficult as noise originates spurious intensity variations. In order to discriminate in a reliable way real gradients from noise originated ones we must have an estimate of the gradient intensity due to noise, and this is related to the amount of noise. In many cases the amount of noise itself is not known and we must estimate it from image data whose structure (distribution) is not necessarily known.

```
sampleimages <- file.path(system.file(package="TeMa"),
...                                 "sampleimages")
face         <- ia.scale(as.animage(getChannels(read.pnm(
...                    file.path(sampleimages, "sampleFace_01.pgm")))),
...                    255)
face@outside <- 255
nface        <- tm.addNoise(face, scale = 2.0, clipRange = c(0,255))
```

This is a good place where robust scale estimators can be profitably used. As Intermezzo *TM*:7.1 points out, we can get an estimate of noise standard deviation by computing the L_2 norm of the convolution with a zero sum, unitary norm high pass filter kernel such as $-1/\sqrt{2}, 1/\sqrt{2}$:

```
sqrt(
...  var(
...   as.real(
...    ia.frame(ia.convolution(nface,
...                            array(c(0, -1/sqrt(2), 1/sqrt(2)),c(1,3))),
...             3)@data)))
```

```
[1] 8.67417
```

but the returned value is way too high. The reason is that the image contains structure: it is not just a uniform value plus noise. However, at least in this specific case, we can consider the amount of image structure as a perturbation of a uniform surface as significant detail is restricted to a small percentage of the whole area. We can then use a robust scale estimator such as the `mad` to automatically get rid of it, obtaining a much more reliable estimate of the noise level:

```
  mad(ia.frame(ia.convolution(nface,       array(c(0,      -1/sqrt(2),
...   1/sqrt(2)),c(1,3))), 3)@data)
```

```
[1] 1.941272
```

that results in a much closer value. Function `tm.estimateNoiseLevel` relies on the above estimator. A simplified version of the method described in Section *TM*:7 is implemented by function `tm.edgeDetection` whose inner workings can be controlled by its several parameters.

While thresholding gradient magnitude to get rid of spurious edges is necessary it is not sufficient as illustrated in Figure 7.1:

```
e1 <- tm.edgeDetection(nface,1,alpha=0.001, onlyFirstThr = TRUE)
e2 <- tm.edgeDetection(nface,1,alpha=0.001, onlyFirstThr = FALSE)
tm.dev("figures/edgeDetection1", width=6, height=2)
par(mfrow = c(1,3))
ia.show(e1)
ia.show(ia.greater(e2, 0))
ia.show(e2)
dev.off()
```

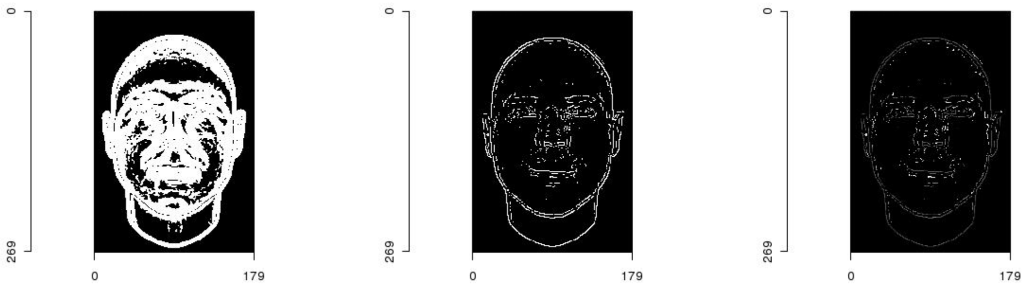


Figure 7.1: Reliable edge detection must take into account non local information to get rid of spurious edges. The image to the left is generated by simple gradient threhsolding: too many pixels get classified as edges. The edge map to the right is computed taking into account the expected response of the second derivative at the pixels that pass the simple gradient intensity test. The analysis of the second derivative provides additional information: the spacing of the extrema is related to the blurring of the detected edges and can be exploited to further filter them, e.g. to create different edge maps representing different image structures. The intensity value of edge pixels is proportional to the second derivative extrema spacing.

```
e3 <- tm.edgeDetection(nface, 2,alpha=0.001, onlyFirstThr = FALSE)
e4 <- tm.edgeDetection(nface, 4,alpha=0.001, onlyFirstThr = FALSE)
e5 <- tm.edgeDetection(nface, 8,alpha=0.001, onlyFirstThr = FALSE)
e6 <- tm.edgeDetection(nface,16,alpha=0.001, onlyFirstThr = FALSE)
tm.dev("figures/edgeDetection2", width=6, height=6)
par(mfrow = c(2,2))
ia.show(ia.greater(e3,0), main="Scale = 2")
ia.show(ia.greater(e4,0), main="Scale = 4")
ia.show(ia.greater(e5,0), main="Scale = 8")
ia.show(ia.greater(e6,0), main="Scale = 16")
dev.off()
```

7.2 The Hough Transform

The Hough transform is an efficient way to perform template matching when the pixel representation of the templates is at the same time sparse (only a fraction of the pixels in the image are representative) and at the same time *continuous* so that local directional information can be used to focus the update of the cells in accumulator space. The *equivalent* template in image space can be obtained by backprojecting a single cell into image space.

The detailed shape of the resulting template is not obvious even in simple cases such as line detection using the normal parametrization (see Figure 7.3).

```
tm.dev("figures/houghImageSpaceLineTemplates", width=6, height=6)
tm.houghImageSpaceClean()
tm.houghLineCell(512, 300,tm.rad(20), 10,tm.rad(10),20)
tm.houghLineCell(512, 300,tm.rad(110),10,tm.rad(5),20)
tm.houghLineCell(512, 300,tm.rad(210),10,tm.rad(0.1),20)
dev.off()
```

```
img       <- animage(matrix(data = 0, nrow=33,ncol=33), storage = "real",
...                        focus = c(-16L,-16L))
noisyImg <- tm.addNoise(ia.mult(img, 0), noiseType="normal", scale=0.4)
#
# compute the standard Hough transform
#
```

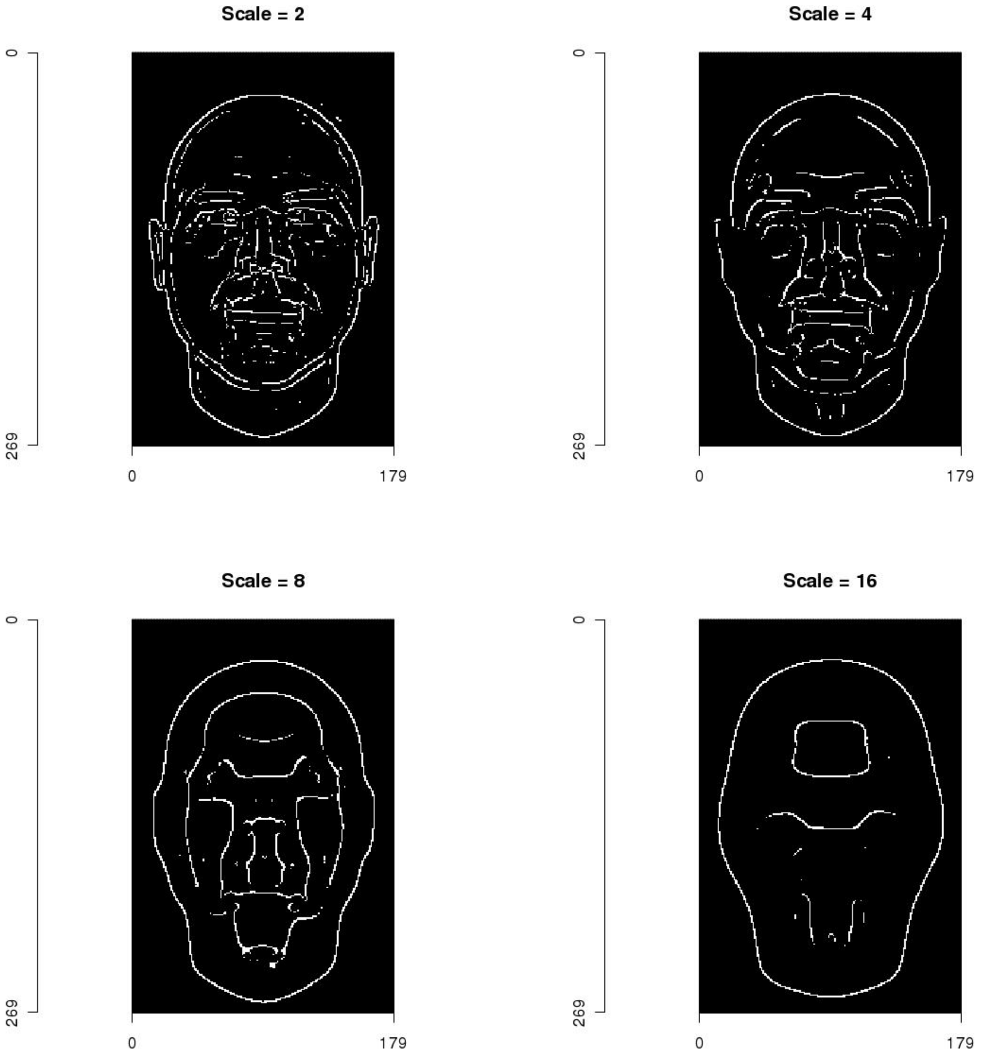


Figure 7.2: The `scale` parameter of `tm.edgeDetection` allows us to investigate the edge structure at different scales, effectively exploring a resolution space.

```
h         <- tm.houghTransform(noisyImg, 33, 16, view = FALSE)
#
# and transform counts into probability
#
hmap       <- tm.mapHoughTransform(noisyImg, 33, 16, 0.4, view = FALSE)
#
tm.dev("figures/houghMap", width=6)
 tm.houghPlot(noisyImg, h, hmap)
dev.off()
```

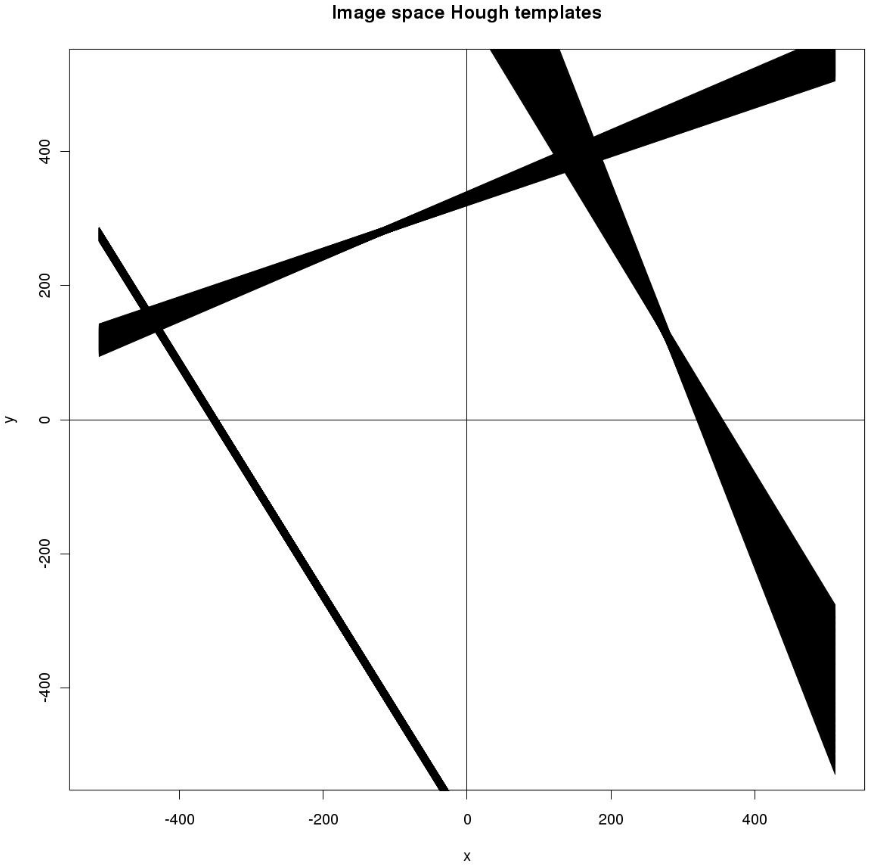
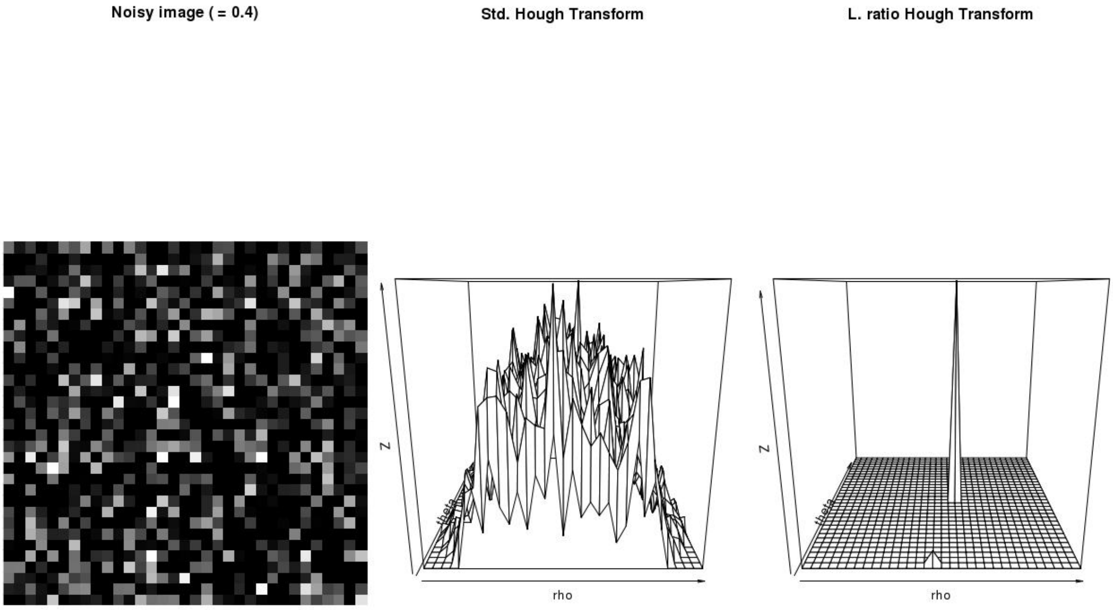


Figure 7.3: The finite extent of a cell in Hough space determines the image space region providing support to the corresponding accumulator. The image shows the image space templates resulting from the normal line representation for increasing angular resolution. The lower the angular resolution the more butterfly like the template.


Noisy image (= 0.4)

Std. Hough Transform

L. ratio Hough Transform

Figure 7.4: The accumulator provided by the Hough transform can be interpreted in a probabilistic way if the distribution of image noise is known. The figure shows the noisy image with a single line (left), the Hough accumulator (middle), and the resulting probability map (right).

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Chapter 8

Low Dimensionality Representations and Matching

This chapter investigates the possibility of alternative ways to represent iconic data so that a large variety of images can be faithfully described using vectors of reduced dimensionality. Besides significant storage savings, these approaches provide significant benefits to template detection and recognition algorithm, improving their efficiency and effectiveness. Three main approaches are considered: principal components analysis (PCA), independent components analysis (ICA), and linear discriminant analysis (LDA). Probabilistic and kernel variants of PCA are described and criteria for choosing the optimal representation dimensionality are discussed. The basics of ICA are provided and Bayesian and classification tuned versions of LDA presented. An application of PCA to the synthesis of facial images and mug-shot database browsing is discussed.

keywords: *principal components analysis, independent components analysis, linear discriminant analysis, kernel PCA, dimensionality reduction, image retrieval.*

8.1 Principal component analysis

One of the drawbacks of template matching is its high computational cost which is related to the resolution of the images being compared. It is then of interest finding a lower dimensionality representation that:

- allows us to represent them faithfully with a reduced set of numbers
- allows us to compare them, at least approximately, using their low dimensionality representation

The most widely used transform satisfying the above constraints is principal component analysis (PCA): a translation and rotation of the original coordinate system, providing a set of directions sorted by decreasing contribution to pattern representation. It is a pattern specific representation that, in many cases of practical interest, allows us to use a limited subset of directions to approximate well the pattern. The better the require approximation, the higher the number of directions required.

We now read a set of 800, geometrically normalized, grey images representing faces from multiple races. We then create two different vectorized sets, extracting the central face region (`raceSample1`) and an extended set with additional 8 congruent images at 1 pixel distance (`raceSample9`).

```
racesImages  <- scan("../theFaceDbs/races/imageNames", list(""))[[1]]
raceSamples1 <- array(0, dim=c(800, 525))
raceSamples9 <- array(0, dim=c(800*9, 525))
#
idx <- 0
for(i in 1:800) {
...   a <- getChannels(read.pnm(paste("../theFaceDbs/races", racesImages[[i]],
...         sep="/")))
...   raceSamples1[i,] <- ia.get(as.animage(a), animask(5,13,21,25))@data
...   for(dy in -1:1)  {
...     for(dx in -1:1) {
...       idx <- idx+1
...       raceSamples9[idx,] <- ia.get(as.animage(a), animask(5+dx,13+dy,21,25))@data
...     }
...   }
... }
```

We can now compute the covariance matrices and, using the singular value decomposition, determine its eigenvalues representing the variance described by each direction

```
mycov1 <- cov(raceSamples1)
mysvd1 <- fast.svd(mycov1)
mycov9 <- cov(raceSamples9)
mysvd9 <- fast.svd(mycov9)
```

generating a comparative plot

```
tm.dev("figures/pca1")
plot(log(mysvd1$d[1:525]), type="l", lty=1, xlab="component", ylab="log(variance)")
lines(log(mysvd9$d[1:525]), type="l", lty=2, xlab="component", ylab="log(variance)")
grid()
legend(200, 0, c("raceSamples1", "raceSamples9"), lty=1:2)
dev.off()
```

The eigenvectors, or eigenfaces in this case, can be obtained directly from the singular value decomposition and de-linearized restoring the spatial layout of the images they derive from

```
  tm.dev("figures/eigenfaces", width=16, height=8)
  par(mfrow=c(2,3),lwd=0.5)
  ia.show(ia.scale(as.animage(array(mysvd1$u[,1], dim=c(25,21)))))
  ia.show(ia.scale(as.animage(array(mysvd1$u[,2], dim=c(25,21)))))
  ia.show(ia.scale(as.animage(array(mysvd1$u[,3], dim=c(25,21)))))
```

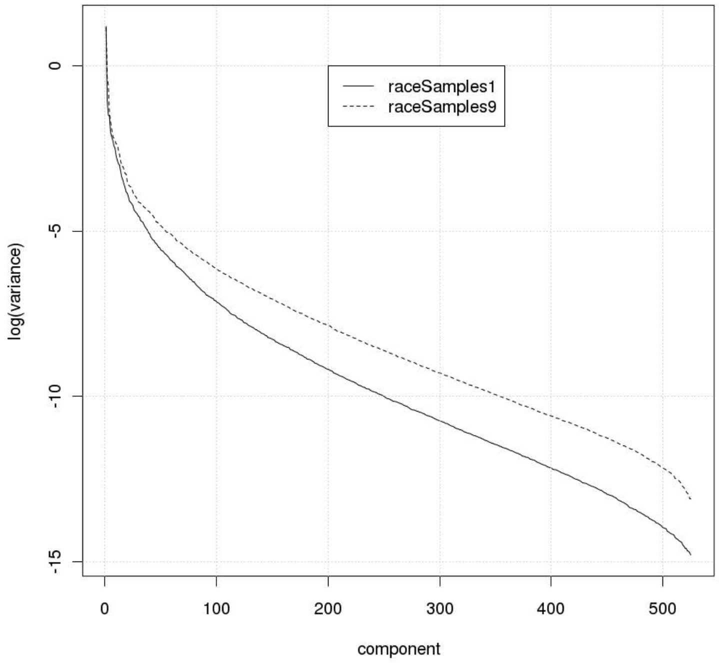

Figure 8.1: The variability of patterns impacts on the number of principal components required to approximate them well. The plot compares the two sets `raceSamples1` and `raceSamples9`: as the variability of the latter is greater than that of the former, the variance captured by the principal directions decreases slowlier.

```
  ia.show(ia.scale(as.animage(array(mysvd9$u[,1], dim=c(25,21)))))
  ia.show(ia.scale(as.animage(array(mysvd9$u[,2], dim=c(25,21)))))
  ia.show(ia.scale(as.animage(array(mysvd9$u[,3], dim=c(25,21)))))
  dev.off()
```

and the first three eigenfaces from `raceSamples1` and `raceSamples9` are shound in Figure 8.2.

The required number of principal components depends on the specific task considered, and on the required performance. In some cases, the appropriate number can be determined by inspection of the values of the variance captured by the different directions. One such a case is that of images corrupted by noise. Usually, in the case of patterns not corrupted by noise, the variance associated to the different directions decreases quickly. When noise is present, i.e. white noise, its contribution may dominate the lowest variance directions. This is particularly evident for white noise, characterized by a constant variance for all directions, due to its spherical distribution. We are then interested in determining the cross point at which the contribution of the signal starts to be dominated by the noise.

We generate a set of pure noise images using two different types of noise: uniform and normal.

```
nu <- array(runif(800*525, min=-0.1,max=0.1), dim=c(800,525))
ng <- array(rnorm(800*525, sd=0.05), dim=c(800,525))
```

We can now perform PCA separately on the set of images corrupted by uniform noise

```
uSamples <- raceSamples1 + nu
mycovU   <- cov(uSamples)
mysvdU   <- fast.svd(mycovU)
```

and on the set of images corrupted by normal noise with a standard deviation of 0.05

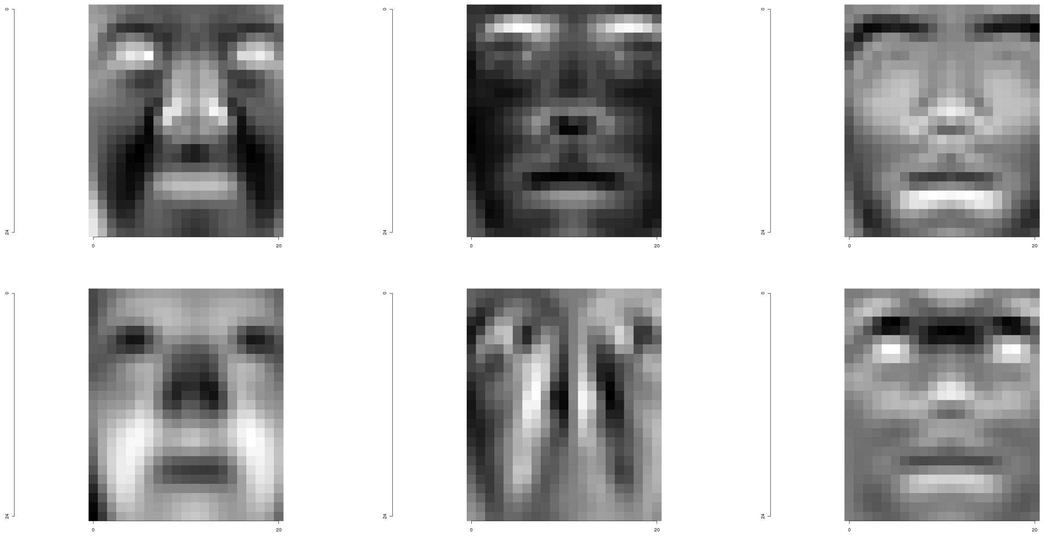

Figure 8.2: A good estimate of the covariance matrix is key to perform meaningful PCA. While the MLE sample estimate is commonly employed, it is far from optimal in the high dimensionality/few samples case.

```
gSamples <- raceSamples1 + ng
mycovG   <- cov(gSamples)
mysvdG   <- fast.svd(mycovG)
```

and with a standard deviation of 0.025

```
gSamples2 <- raceSamples1 + ng/2
mycovG2   <- cov(gSamples2)
mysvdG2   <- fast.svd(mycovG2)
```

```
tm.dev("figures/pca2", height=4.5)
plot(log(mysvd1$d[1:520]), type="l", lty=1, xlab="component", ylab="log(variance)")
lines(log(mysvdU$d[1:520]), lty=2)
lines(log(mysvdG$d[1:520]),    lty=3)
lines(log(mysvdG2$d[1:520]), lty=4)
grid()
legend(0,-10, c("no noise", "uniform [-0.1,0.1]",
...                   "normal (sd=0.05)", "normal (sd=0.025)"),
...         lty=c(1,2,3,4))
dev.off()
```

Let us define a simple indicator function following the description of Section *TM*8.1.2

```
  tm.indf <- function(ls, d, N){
...       vs <- array(0, dim=c(d))
...       for(k in 1:d) {
...         s <- 0
...         for(j in (k+1):d) {
...           s <- s + ls[k]
...         }
...         vs[k] <- sqrt(s/(N*(d-k)))*(1/((d-k)*(d-k)))
...       }
...       vs
... }
```

and apply it to the eigenvalues sets just computed:

```
  tm.dev("figures/pca3",  height=4.5)
  plot(tm.indf(mysvd1$d, 450, 800)[10:200],   type="l", lty=1, xlab="component",
...         ylab="IND")
  lines(tm.indf(mysvdU$d, 450, 800)[10:200],  lty=2)
```

```
  lines(tm.indf(mysvdG$d, 450, 800)[10:200],  lty=3)
  lines(tm.indf(mysvdG2$d, 450, 800)[10:200], lty=4)
  grid()
  legend(25,4e-8, c("no noise", "uniform [-0.1,0.1]",
...                     "normal (sd=0.05)", "normal (sd=0.025)"),
...          lty=c(1,2,3,4))
  dev.off()
```

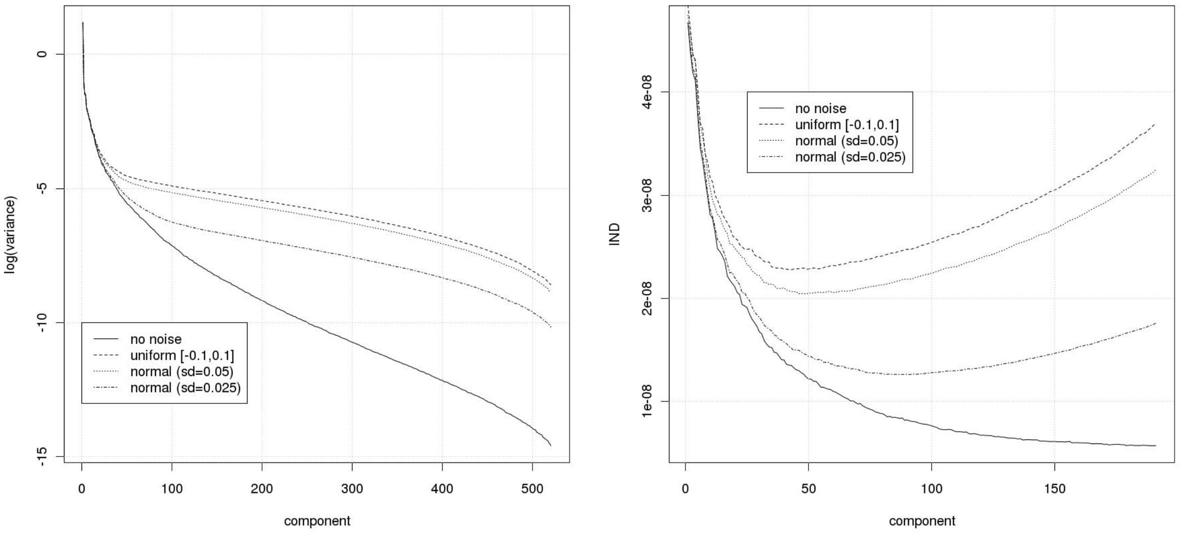

Figure 8.3: Increasing amounts of noise modify the eigenvalue distribution and anticipate the cross over point of the signal to noise ratio: the trend is correctly modeled by the minimum of the indicator function.

8.2 James-Stein estimation

It may be worthwile to perform a simple simulation to check the potential advantage of using non standard estimators for the covariance matrix, the key quantity in PCA, in the case of large dimensionality and small number of samples.

```
# small n, large p
#
p <- 625 ;  n <- 400
#
# generate random pxp covariance matrix
#
sigma <- matrix(rnorm(p*p),ncol=p)
sigma <- crossprod(sigma)+ diag(rep(0.01, p))
#
# simulate multinormal data of sample size n
#
sigsvd <- svd(sigma)
Y      <- t(sigsvd$v %*% (t(sigsvd$u) * sqrt(sigsvd$d)))
X      <- matrix(rnorm(n * ncol(sigma)), nrow = n) %*% Y
```

Having generated our data sample we compute the covoriance matrix using the usual sample estimator and the shrinkage estimator:

```
sSample    <- cov(X)
sShrinkage <- cov.shrink(X)
```

and proceed to the computation of the eigenvalues:

```
eTrue      <- eigen(sigma,      symmetric=TRUE)$values
eSample    <- eigen(sSample,    symmetric=TRUE)$values
eShrinkage <- eigen(sShrinkage, symmetric=TRUE)$values
m          <-max(eTrue, eSample, eShrinkage)
yl         <- c(0, m)
```

As reported in Figure 8.4, the advatange of shrinkage estimators over the standard ones can be dramatic.

```
tm.dev("figures/pca4", width=15)
par(mfcol=c(1,3),lwd=0.5)
plot(eSample[1:200],  main="empirical",ylab="eigenvalue", type="l")
plot(eShrinkage[1:200],  ylim=yl, main="full shrinkage",ylab="", type="l")
plot(eTrue[1:200],  ylim=yl, main="true",ylab="", type="l")
grid(lwd=0.1)
dev.off()
```

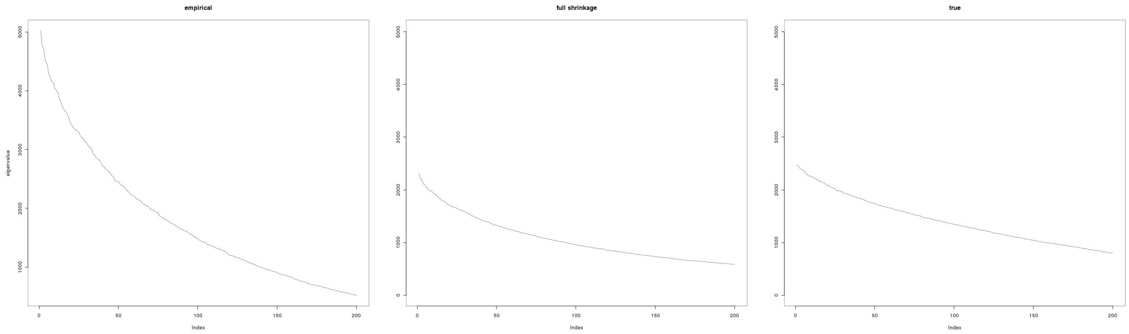

Figure 8.4: A good estimate of the covariance matrix is key to perform meaningful PCA. While the MLE sample estimate is commonly employed, it is far from optimal in the high dimensionality/few samples case.

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Chapter 9

Deformable Templates

There are cases that are not easily reduced to pattern detection and classification. One such a case is the detailed estimation of the parameters of a parametric curve. Another important case is the comparison of anatomical structures, such as brain sections. Instead of modeling the variability of the patterns within a class as a static multidimensional manifold, we may focus on the constrained deformation of a parameterized model and measure similarity by the deformation stress. The chapter analyzes the Hough transform from a dynamical perspective: shapes are attracted from image feature maps acting as physical potential fields. Active shape models, integrating textural and geometrical information, are a natural and efficient extension that benefits from the usage of PCA techniques. The possibility of establishing a dense correspondence field between the pixels of different images opens the way to interesting morphing applications in medical analysis and computer graphics animation.

keywords: *potential field, deformable templates, active shape models, diffeomorphic matching, optical flow.*

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Chapter 10

Computational Aspects of Template Matching

The drawback of template matching is its high computational cost which has two distinct origins. A first source of complexity is the necessity of using multiple templates to accommodate the variability exhibited by the appearance of complex objects. A second source of complexity is related to the representation of the templates: the higher the resolution, i.e. the number of pixels, the heavier the computational requirements. Besides some computational tricks, like early jump-out techniques and the use of integral images, this chapter presents more organized, structural ways to improve the speed at which template matching can be performed: hierarchical matching, metric inequalities, FFT techniques, incremental PCA, and combined approaches. Another important aspect of template matching is the possibility of sub-pixel accuracy: perturbative image expansion and phase correlation techniques are discussed.

keywords: *jump-out, hierarchical matching, FFT correlation, metric inequalities, phase correlation, sub-pixel matching.*

10.1 Hierarchical matching

One of the simplest way to speed up the process of template matching is that of working at different image resolutions, starting from the lowest resolution at which the template can be discriminated, and progressively focusing the computation when increasing image resolution to the most promising candidates.

The basic structure needed to implement a hierarchical matching strategy is that of the resolution pyramid. We can build it starting from the highest available resolution, progressively smoothing and undersampling the current level to avoid aliasing artifacts.

The same procedure must be applied to the template.

In order to spot our template, we start from the lowest resolution level, generating a filter mask containing the most promising locations.

We then iterate the process of zooming the mask, slightly enlarging it, and computing the correlation value only at the corresponding image positions.

As the process relies on a thresholding operation in order to compute the mask constraining the computation, the distribution of the correlation values at the different levels of the pyramid should be considered. The figure reports the distribution of the correlation values (obtained without any filtering mask) at three levels. The plots clearly show that they differ, the distributions from the low resolution levels being suggestive of decreased discrimination capability of the correlation values. The threshold used in the computation of the mask should then be more strict at the first levels. However, as we want to be sure that we are not loosing any valid location and the number of computations is small, it is usually better not to use a (too) high threhsold.

Codelet 6 **Hierachical template matching** (`../TeMa/R/tm.hierarchicalMatching.R`)

This function illustrates how we can achieve a significant speed up in correlation matching by using a multiresolution strategy: we

```
tm.hierarchicalMatching <- function(I, T, levels = 3, thr = 90) {
```

We keep track of the original position of the image region of interest:

```
  ofocus  <- I@focus
```

and consider it (temporarily) as our new coordinate origin

```
  I@focus <- c(0L, 0L)
  T@focus <- c(0L, 0L)
```

The first step is to build the multiresolution representations of the image and of the template by carefully smoothing them at each resolution step before subsampling them:

```
  pyrI    <- tm.gaussianPyramid(I, levels)
  pyrT    <- tm.gaussianPyramid(T, levels)
```

The first element of the resolution list (the pyramid) is the one at the lowest resolution and we create the corresponding computation filter encompassing all pixels:

```
  mask    <- as.animage(array(1, dim(pyrI[[1]]@data)))
```

When we map the mask to the next higher resolution level we want to slightly enlarge it to avoid missing the right template position. Mathematical morphology provides an easy way to implement the growing operation by means of a simple structuring element and using the `ia.mmBitDilation` function:

```
  eltA <- animage(array(1L, c(3,3)), focus=c(-1L,-1L))
```

We start from the lowest resolution level,

```
  for(l in 1:levels) {
```

performing correlation only an selected pixels

```
    cor  <- ia.correlation(pyrI[[l]], pyrT[[l]], filter=mask)[[1]]
```

and compute the mask for the next (higher) resolution level:

```
    mask <- ia.integerAnimage(ia.greater(cor, thr))
    mask <- ia.realAnimage(ia.pzoom(ia.mmBitDilation(mask, eltA), 2L, 2L))
  }
```

finally returning the correlation map, at the correct position in the original coordinate system:

```
  cor@focus <- ofocus
}
```

The following code shows a sample application

```
sampleimages <- file.path(system.file(package="TeMa"),
...                                "sampleimages")
face         <- ia.get(ia.scale(as.animage(getChannels(read.pnm(
...                     file.path(sampleimages, "sampleFace_01.pgm")))),
...                     255), animask(10,60,128,128))
eye          <- ia.get(face, animask(40,92,32,32))
hcor         <- tm.hierarchicalMatching(face, eye)
```

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Chapter 11

Matching Points Sets: the Hausdorff distance

Matching sets of points using techniques targeted at area matching is far from optimal, regarding both efficiency and effectiveness. This chapter shows how to compare sparse templates, composed by points with no textural properties, using the Hausdorff distance. Robustness to noise and template deformation as well as computational efficiency are analyzed. A probabilistic perspective on Hausdorff matching is briefly discussed. Invariant moments, a classical technique for shape matching is also considered.

keywords: *Hausdorff distance, invariant moments, distance transform, metric pattern space, principal components analysis.*

11.1 Hausdorff matching

Binary image templates can be considered as a set of points and their similarity assessed by means of an appropriate point set distance, the Hausdorff distance or its variation, the directed Hausdorff distance. The latter can be computed efficiently using the Euclidean distance transform, a transform that associates to each background image pixel its distance from the closest foreground image pixel. Once the distance transform has been computed, computation of the directed Hausdorff distance can be accomplished by looking at the distance transform value at the pixels representative of the point set.

The resulting set of distance values can be used to compute several variations of the basic definition by taking the maximum, the average, or any specified quantile, improving the robustness of the matching score.

We illustrate it using one of the available sample images and adding noise to it:

```
sampleimages <- file.path(system.file(package="TeMa"),
...                             "sampleimages")
face         <- ia.get(ia.scale(as.animage(getChannels(read.pnm(
...                   file.path(sampleimages, "sampleFace_01.pgm")))),
...                   255), animask(10,60,90,90))
face@outside <- 255
nface        <- tm.addNoise(face, scale = 1.0, clipRange = c(0,255))
eface        <- tm.edgeDetection(nface,2, alpha=0.01, onlyFirstThr = FALSE)
```

As template, we get the eye of the image without noise:

```
eye          <- ia.get(face, animask(32,92,50,30))
eeye         <- tm.edgeDetection(eye,2, alpha=0.01, onlyFirstThr = FALSE)
```

and compute several variations of the partial Hausdorff distance

```
h1 <- tm.hausdorffMatching(eface, eeye, distance="max")
h2 <- tm.hausdorffMatching(eface, eeye, distance="average")
h3 <- tm.hausdorffMatching(eface, eeye, distance="rank", q=0.7)
h4 <- tm.hausdorffMatching(eface, eeye, distance="rank", q=0.95)
```

reporting the results in Figure 11.1.

```
  tm.dev("figures/hausdorffMatching", width=6, height=6)
  par(mfrow = c(2,2))
  ia.show(h1, main = "Max")
  ia.show(h2, main = "Average")
  ia.show(h3, main = "Rank (0.7)")
  ia.show(h4, main = "Rank (0.9)")
  dev.off()
```

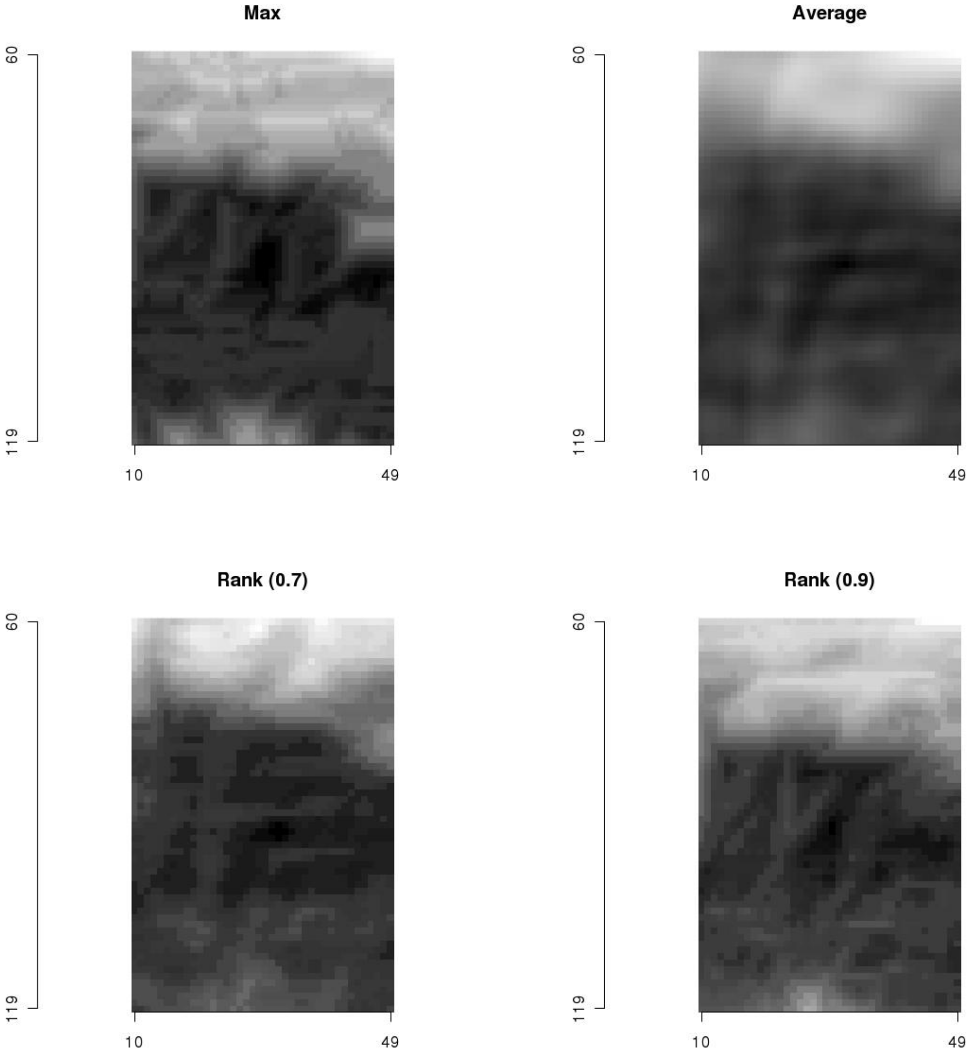

Figure 11.1: The Hausdorff partial distance is a flexible technique to compare templates represented by sets of points. The template would be located at the darkest point, the one with the lowest distance. The figures shows that using the `max` version may not be always the best choice.

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Chapter 12

Support Vector Machines And Friends

When the probability distribution of the templates is unknown, the design of a classifier becomes more complex and many critical estimation issues surfaces. This chapter presents basic results upon which two interrelated, powerful classifier design paradigms stand: regularization networks and support vector machines (SVMs). Several practical hints on how to best use SVM classifiers are described. The techniques are applied to the tasks of gender and race classification based on face images.

keywords: *regularization networks, support vector machines, virtual set method, reproducing kernel Hilbert space.*

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Chapter 13

Feature Templates

Many applications in image processing rely on robust detection of image features and accurate estimation of their parameters. Features may be too numerous to justify the process of deriving a new detector for each one. This chapter exploits principal components analysis to build a single, flexible, and efficient detection mechanism based on the use of composite rejectors. The complementary aspect of detecting templates considered as a set of separate features will also be addressed presenting an efficient architecture: a rejector cascade classifier built by boosting simple, pixel level classifiers applied to a census transformed image.

keywords: *parametric feature manifold, AdaBoost, boosting, census transform, multi-class pattern rejector, constellation matching*

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Chapter 14

Building a Multi-biometric System

Template matching techniques are a key ingredient in many computer vision systems, ranging from quality control to object recognition systems among which biometric identification systems have today a prominent position. Among biometric systems, those based on face recognition have been the subject of extensive research. This popularity is due to many factors, from the non invasiveness of the technique, to the high expectations due to the widely held belief that human face recognition mechanisms perform flawlessly. Building a face recognition system from the ground up is a complex task and this chapter addresses all the required practical steps: preprocessing issues, feature scoring, the integration of multiple features and modalities, and the final classification stage.

keywords: *image normalization, speaker identification, score integration, verification, face recognition, hierarchical matching, robust similarity measures.*

contains material from *Template Matching Techniques in Computer Vision: Theory and Practice*, Roberto Brunelli,

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Appendix A

AnImAl: a Software Environment for Fast Prototyping

The process of developing a computer vision system for a specific task often requires the interactive exploration of several alternative approaches and variants, preliminary parameter tuning, and more. This chapter introduces AnImAl, an image processing package written for the R statistical software system. AnImAl, which relies on an algebraic formalization of the concept of image, supports interactive image processing by adding to images a self documenting capability based on a history mechanism. The documentation facilities of the resulting interactive environment support a practical approach to reproducible research.

keywords: *reproducible research, interactive programming environment, R, image algebra.*

A.1 The AnImAl environment

The requirements of interactive image processing, particularly during the development of algorithms, are the same as those of the larger statistical community and of the even larger community of computational science. A good development environment should rely on a high level programming language with extensive facilities for the manipulation of the most commonly used data structures, the possibility of saving the status of a processing session for later continuation, extensive community support, and means for code verification and high quality documentation. Another important, often neglected, feature is the possibility of accessing the source code of the environment and of its libraries so that the appropriateness of the algorithms underlying the functions provided and the correctness of their implementation can be assessed. R, a language and environment for statistical computing and graphics, based on the system described in [7], fulfills all these requirements and has then been chosen as the programming environment for the implementation the image algebra described in Section *TM*:A.1. Nearly all of the algorithms described in the present book have been implemented in the R environment and are provided as an accompanying set of computer files with extensive documentation and examples.

What we would like to address in the following paragraphs is the extent to which such a development environment can support investigation based on the iteration of hypothesize, test, and refinement cycles, and the accurate reporting of results. The R environment supports selective saving of itself: objects, memory contents, and command history can be saved to be imported at a later date or visually inspected. The history mechanism provided by AnImAl extends these facilities by adding self documenting abilities to a specific data structure (the image) making it even easier to extract the details of every processing step in order to accurately document it. Accurate reporting of results, and of processing work flow, means that enough information should be provided to make the results reproducible: this is the essence of reproducible research. Traditional means of scientific dissemination, such as journal papers, are not up to the task: they merely cite the results supporting the claimed conclusions but do not (easily) lend themselves to independent verification. A viable solution in the case of computational sciences is to adopt more flexible documentation tools that merge as far as possible data acquisition, algorithms description and implementation, and reporting of results and conclusions. A useful concept is that of compendium: a dynamic document that includes both literate algorithms description and their actual implementation. The compendium is a dynamic entity: it can be automatically transformed by executing the algorithms it contains, obtaining the results commented upon by the literate part of the document. This approach has two significant advantages: enough information for the results to be reproducible by the community is provided, and results reported in the description are aligned to the actual processing work flow employed.

The R environment provides extensive support for the creation of compendiums: code such as

```
sampleLuminance <- ia.averageImageChannels(sample,
                                           c(1,2,3),
                                           c(21,72,7))
dens            <- density(sampleLuminance@data)
#
tm.dev("figures/sampleHisto")
#
hist(sampleLuminance@data,
     xlab = "Intensity", ylab = "Probability",
     main = "Luminance histogram and density plot",
     probability = TRUE)
```

```
        lines(dens , lty = 2)
    #
    dev.off()
```

can be freely inserted within the text, with the possibility of hiding it in the final document. The code can be executed, and its results, be they pictorial (see Figures A.1–A.3), or numeric (see Table A.1), automatically inserted at the right places.

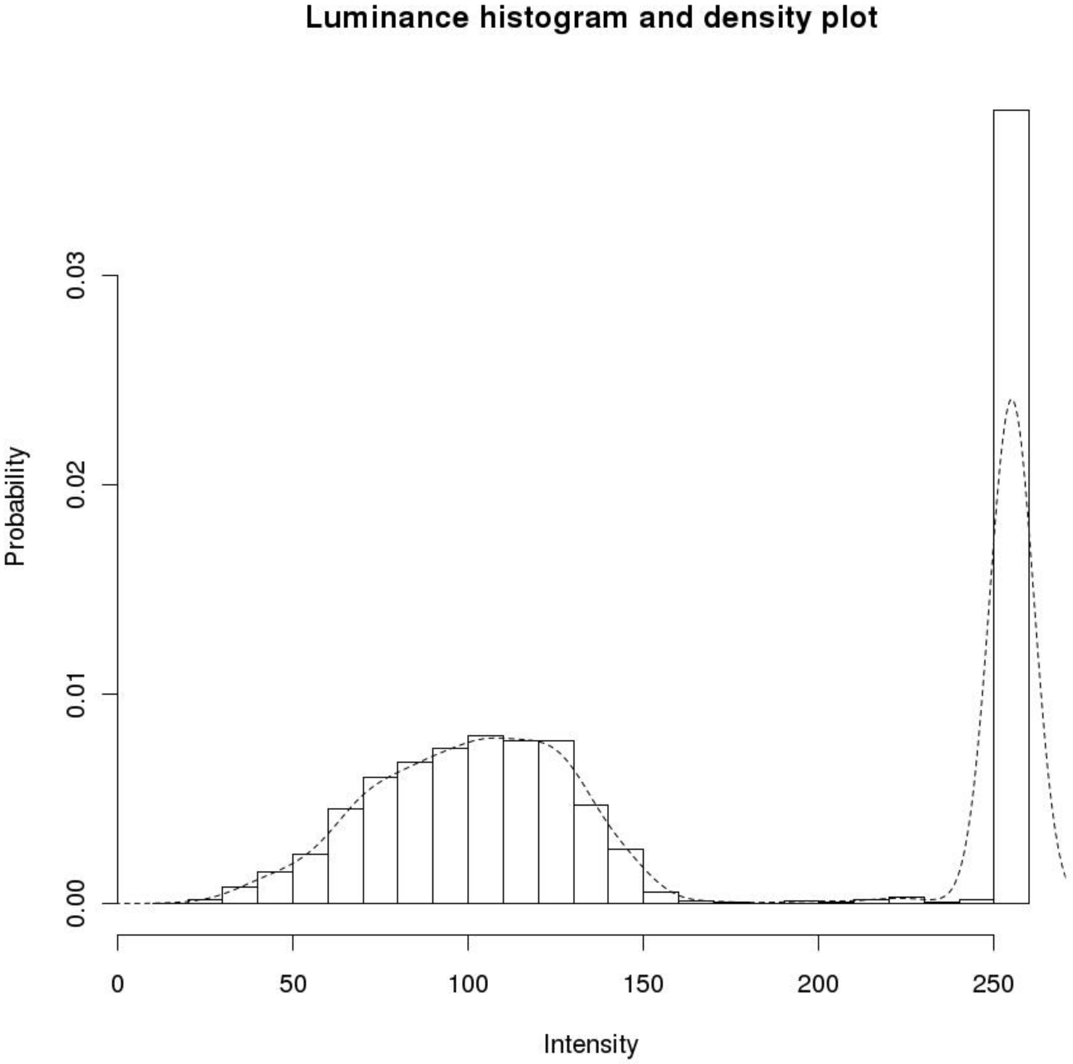

Figure A.1: The histogram of the luminance channel L of a sample image (computed from the R, G, and B color channels as $L = 0.2126\,R + 0.7152\,G + 0.0722\,B$) with overlayed density information.

Literate algorithm descriptions can be inserted as comments in the source code and automatically extracted and formatted to match high quality scientific publication requirements. We report a simple example: the definition of an R function, based on AnImAl, for the computation of the boundaries of shapes in binary images. Insertion in the compendium of the directive

	Dark	Midtone	Highlight
Dark	8 556	1 330	16
Midtone	1 209	31 156	1 808
Highlight	36	1 599	41 045

Table A.1: Cooccurence of dark, midtone, and highlight pixels

```
\inputcode{../AnImAl/R/ia.edge.R}
```

generates the literate description of the function reported in the next paragraphs by suitably formatting code and comments included in the function definition file.

`Codelet 7` **Edge detection for a binary image** (`../AnImAl/R/ia.edge.R`)

This is an example of how the basic bit level logical operators provided by AnImAl can be used to extend its functionalities. In this particular case we define a new function with name `ia_edge` and a single argument `img`:

```
ia.edge <- function (img) {
```

The first step is to check whether image history must be updated in order to produce a coherent image:

```
  document <- img@document
```

We momentarily turn off self documentation as we want to consider the current function as a whole and we do not want its inner workings to be traced by the history mechanism:

```
  img@document <- FALSE
```

In this particular case we fix the region of interest of the resulting image to that of the function argument. As subsequent operations may enlarge we store the initial specification of the region

```
  img_mask <- ia.mask(img)
```

A pixel is considered to be an edge pixel if at least one of the pixels to its left, right, top, or bottom belongs to the image background (value=0):

$$E_{i,j} \leftarrow \overline{(((I_{i,j-1} \wedge I_{i,j+1}) \wedge I_{i+1,j}) \wedge I_{i-1,j})} \wedge I_{i,j}$$

This logical formula can be easily implemented using the bit level logical operations provided by AnImAl:

```
  res <- ia.get(ia.and(img,
                       ia.not(ia.and(ia.up(img),
                                     ia.and(ia.down(img),
                                            ia.and(ia.left(img),
                                                   ia.right(img)
                                                   ))))),
                img_mask)
```

If required by the configuration of the argument image `img` we update the history of the result image `res` to keep it coherent

```
  if(document) {
```

In this case, it is necessary to update the tracing flag:

```
    img@document <- res@document <- document
```

and to get the new root of the history tree which is given by the current function invocation:

```
    resh         <- match.call()
```

We then need to expand the node corresponding to `img` with the corresponding history

```
    resh$img     <- img@history
```

so that complete history information can be stored in the resulting image:

```
    res@history  <- resh
  }
```

before returning the final result:

```
  res }
```

An example of the results provided by this function is reported in Figure A.3.

We did not comment so far on how data acquisition fits within the concept of compendium. Unfortunately this stage is not reproducible unless data result from simulation experiments, a situation for which the reasoning already exposed can be applied without any modification. The approach followed in this book is to leverage on the capability of modern graphical rendering systems to automatically generate high quality imagery on which algorithms are trained and compared, thereby extending the application of reproducible research ideas to the complete data flow. The entire Appendix *TM*:B is devoted to the description of how synthetic, realistic images of complex objects can be generated. Data synthesis can then be regarded as an additional function and merging it with an active document does not require the introduction of any new concept or tool.

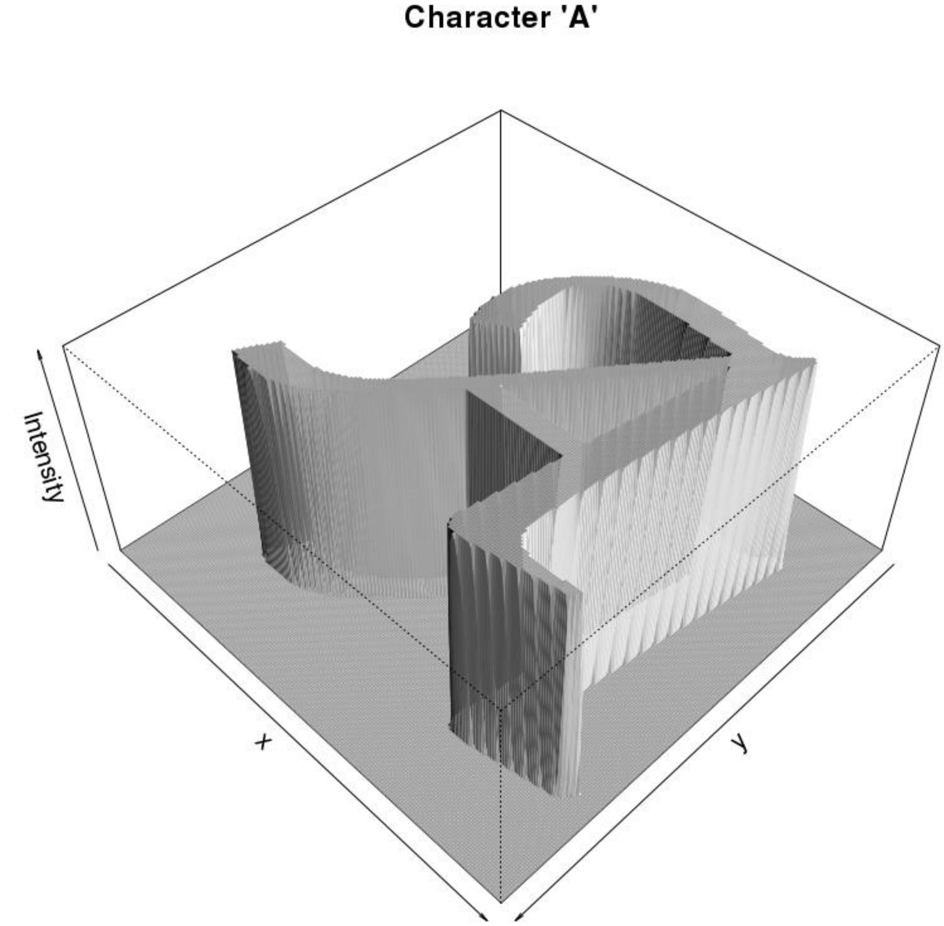

Figure A.2: The R environment provides extensive graphical support that can be applied to the visualization of AnImAl image data. The plot presents a perspective view of character A obtained by mapping intensity information to surface height.

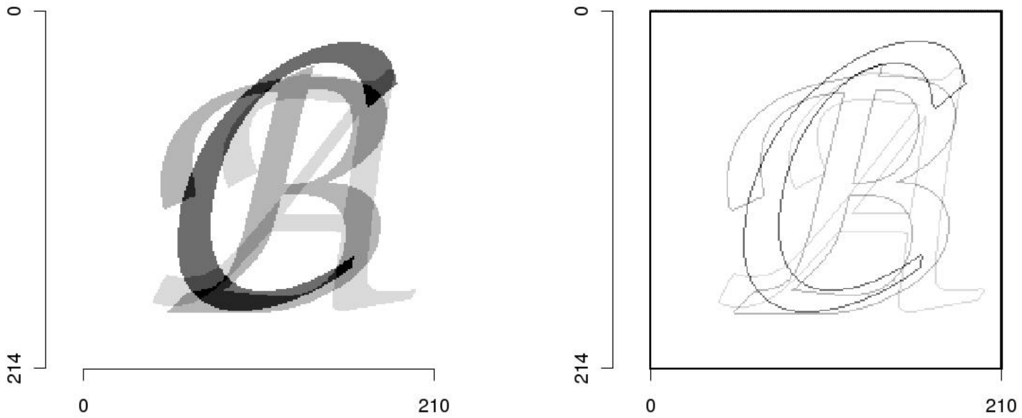

Figure A.3: An example of packed bit images (left) and the result of applying the operator `ia_edge` described in the text (right). Parallel processing occurs at two different levels: simulated, at the PEs which compute the same logical operation on their neighborhood, and real as each PE computes the same logical operation for all the bit planes at the same time. The resulting image can then be unpacked providing three separate images, each one containing the boundary of a single character shape.

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Appendix B

Synthetic Oracles for Algorithm Development

A key need in the development of algorithms in computer vision (as in many other fields) is the availability of large data sets for training and testing them. Ideally, data sets should cover the expected variability range of data and be supported by high quality annotations describing what they represent so that the response of an algorithm can be compared to reality. Gathering large, high quality data sets is however a time consuming effort. An alternative is available for computer vision research: computer graphics systems can be used to generate photo-realistic images of complex environments together with supporting ground truth information. This chapter shows how these systems can be exploited to generate a flexible (and cheap) evaluation environment.

keywords: *computer graphics, ray tracing, shading language, radiosity, photon mapping, camera simulation.*

B.1 Thematic maps

```
tiffdir          <- file.path(system.file(package="TeMa"),
...                                "sampleimages")
```

Modern computer graphics systems allow us to generate photorealistic images that are hardly distinguishable from real world imagery. A significant advantage is that, by using a flexible scene description language we can generate not only *optical* images, but also perfectly aligned descriptive maps, providing us, with pixel level precision, information on the object depicted, its distance from the viewing camera, and also its object centric (UV) coordinates.

This information can be used to implement optical effects on the final rendered image and to gauge the performance of object detection algorithms in a complete automatic way.

The scripts provided allow you to generate a depth map and a label image:

```
  cd theRenderingWorkshop/povray/visual-lab
  ./cameras.sh perspLabel gretag            small daylight      1
```

This result in the generation of two images and which are provided as sample TeMa images (see Figure B.1). Depth information is stored across the color channels and must be recovered usin `tm.getDepth`.

```
  label <- as.animage(read.pnm(file.path(tiffdir,
...                         "perspLabel_gretag_small_daylight.ppm")))
  depth <- tm.getDepth(file.path(tiffdir,
...                           "pp_perspLabel_gretag_small_daylight.ppm"),
...                            depthScale = 40)
  tm.dev("figures/maps", width=6, height=3)
  par(mfrow = c(1,2))
  ia.show(label, main="object map")
  ia.show(depth, main="depth map")
  dev.off()
```

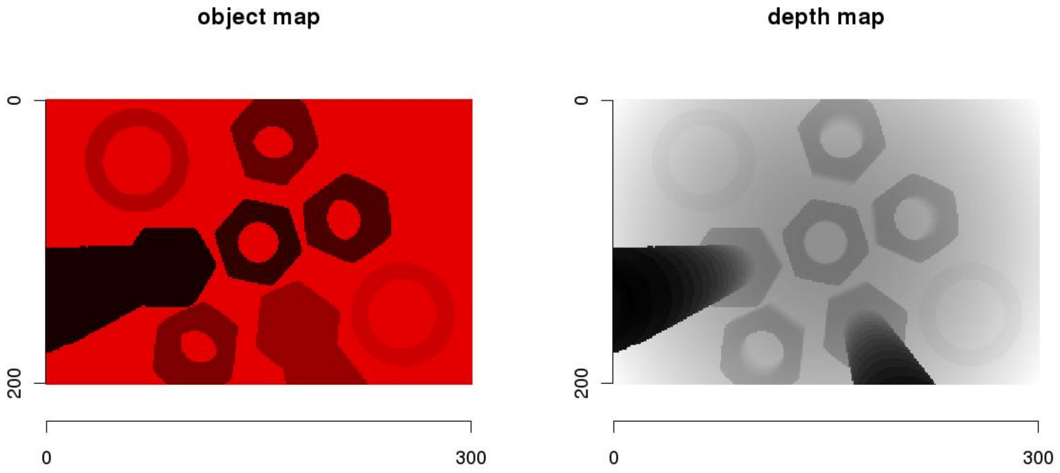

Figure B.1: It is possible to generate an image where all the pixels of an object have a distinct color (left) or the distance of the corresponding object point from the camera.

B.2 Color rendering

The book did not consider specifically the problem of color template matching. However, as briefly pointed out in Chapter *TM*:2, even when monochromatic images are considered, the details of the full imaging process should be considered. It is possible to generate realistic images of the same scene under different illuminations:

```
cd theRenderingWorkshop/povray/visual-lab
./cameras.sh persp gretag           small incandescent 1
./cameras.sh persp gretag           small daylight     1
```

The resulting images are provided as sample images for package TeMa

```
  incandescent <- ia.readAnimage(file.path(tiffdir,
...                                     "persp_gretag_small_incandescent.tif"))
  daylight     <- ia.readAnimage(file.path(tiffdir,
...                                      "persp_gretag_small_daylight.tif"))
  #
  tm.dev("figures/differentLights", width=6, height=3)
  par(mfrow = c(1,2))
  ia.show(incandescent, main="incandescent")
  ia.show(daylight,     main="daylight")
  dev.off()
```

The two color images are shown in Figure B.2. If we generate the corresponding luminance images by averaging the color channels

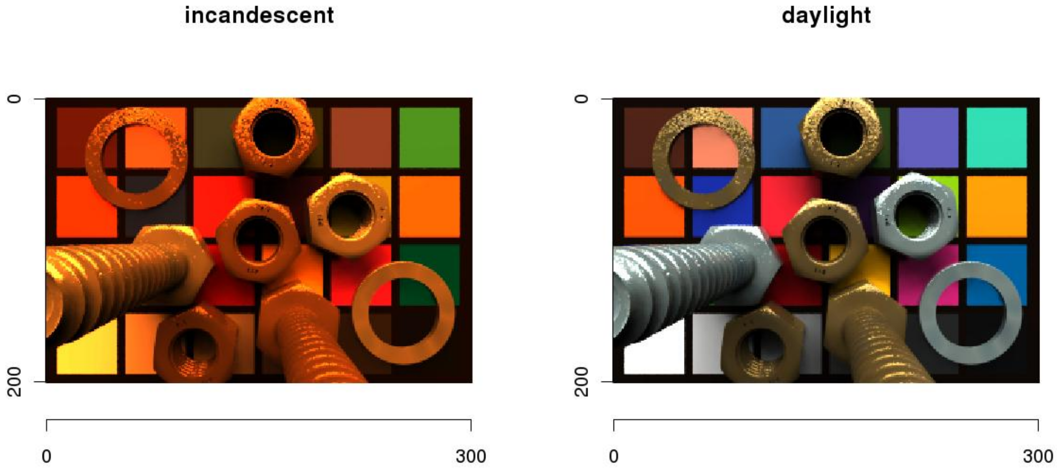

Figure B.2: The same scene lit by different illuminants appears different.

```
  iL <- ia.scale(ia.add(incandescent[[1]],
...                     ia.add(incandescent[[2]],
...                            incandescent[[3]])))
  dL <- ia.scale(ia.add(daylight[[1]],
...                     ia.add(daylight[[2]],
...                            daylight[[3]])))
  #
  tm.dev("figures/differentLightsMono", width=6, height=6)
  par(mfrow = c(2,2))
  ia.show(iL, main="incandescent")
  ia.show(dL,     main="daylight")
  hist(iL, main="incandescent",xlab="")
  hist(dL, ylab="",main="daylight",xlab="")
  dev.off()
```

we obtain different images (see Figure B.3): monochromatic template matching is affected by the illumination conditions of the scene.

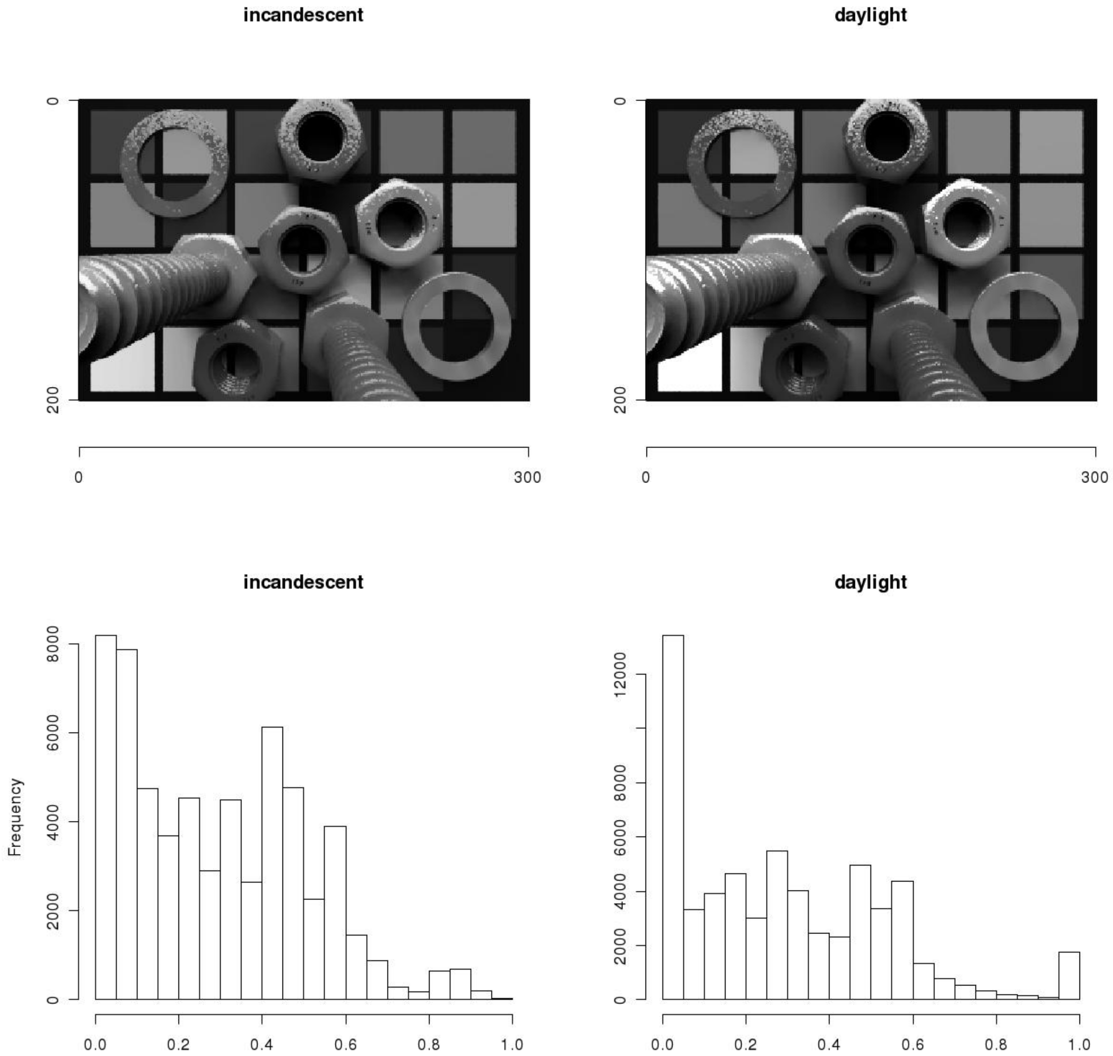

Figure B.3: Monochromatic images of the same scene under different illumination are different.

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Appendix C

On Evaluation

Evaluation of algorithms and systems is a complex task. This chapter addresses four related questions that are important from a practical and methodological point of view: what is a good response of a template matching system, how can we exploit data to train and at the same time evaluate a classification system, how can we describe in a compact but informative way the performance of a classification system, and, finally, how can we compare multiple classification systems for the same task in order to assess the state of the art of a technology.

keywords: *ROC analysis, technology evaluation, classifier training, cross-validation, one-leave-out, bootstrap.*

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Appendix D

Template Matching Literature

The literature on template matching is extremely vast. This chapter includes the papers that have been considered when writing the book. Whenever possible the relevant DOI (digital object identifier) is also reported to easy on line access to bibliographical resources.

keywords: *template matching, classification, PCA, LDA, SVM, RBF.*

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