Projektaufgaben Block 2

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1 Nichtparametrisches Testen

1.1 Zwillingsstudie

Um zu testen, ob der Kindergartenbesuch einen signifikanten Einfluss auf die sozialen Fähigkeiten eines Kindes hat, führen wir einen zweiseitigen t-Test und einen zweiseitigen Wilcoxon-Vorzeichen-Test, jeweils zum Signifikanzniveau $\alpha = 0.05$, durch:

```
# Enter data
x <- c(82,69,73,43,58,56,76,65)
y <- c(63,42,74,37,51,43,80,62)

# Two-sided t-test
t.test(x, y, alternative = "two.sided", mu = 0, conf.level = 0.95, paired = TRUE)
```

```
##
##  Paired t-test
##
## data:  x and y
## t = 2.3791, df = 7, p-value = 0.04895
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##   0.05320077 17.44679923
## sample estimates:
## mean of the differences
##                    8.75
```

```
# t.test(x-y, alternative = "two.sided", mu = 0, conf.level = 0.95)  # alternative

# Two-sided Wilcoxon signed rank test
wilcox.test(x, y, alternative = "two.sided", mu = 0, conf.level = 0.95,
            paired = TRUE, conf.int = TRUE)
```

```
##
##  Wilcoxon signed rank test
##
## data:  x and y
## V = 32, p-value = 0.05469
## alternative hypothesis: true location shift is not equal to 0
## 95 percent confidence interval:
##  -0.5 19.0
## sample estimates:
## (pseudo)median
##           7.75
```

```
# wilcox.test(x-y, alternative = "two.sided", mu = 0, conf.level = 0.95,
#             conf.int = TRUE)  # alternative
```

Wir können sehen, dass der t-Test die Nullhypothese ablehnt ($p = 0.04895 < 0.05 = \alpha$) und somit einen signifikanten Einfluss feststellt. Der Wilcoxon-Vorzeichen-Test verwirft die Nullhypothese dagegen nicht ($p = 0.05469 > 0.05 = \alpha$). Durch die Normalverteilungsannahme $X_i - Y_i \sim N(0, \sigma^2)$, die für gegebenes Sample in Frage gestellt werden kann, besitzt der t-Test eine größere Power. Der nichtparametrische Wilcoxon-Vorzeichen-Test benötigt hingegen keine Verteilungsannahme, besitzt jedoch eine kleinere Power.

1.2 t-Test vs. Wilcoxon-Vorzeichen-Test

```
fnTestPowerMC <- function(fnError, n = 30, theta = 0, alpha = 0.05, nSim = 10^4,
                          ...) {
  # This function estimates the probability of rejecting the null hypothesis of a
  # t-test and a Wilcoxon signed rank test using Monte Carlo simulations of iid
  # random variables X_i = \theta + \epsilon_i.
  #
  # Args:
  #   fnError:  Function which generates random samples from a symmetric error
  #             distribution \epsilon
  #   n:        Number of random samples used in tests
  #   theta:    True parameter
  #   alpha:    Significance level used in tests
  #   nSim:     Number of MC simulations of size n
  #   ...:      Further arguments to be passed to fnError
  #
  # Returns:
  #   A list containing the following elements:
  #     $TProb:       MC estimation of rejection probability for the t-test
  #     $WilcoxProb:  MC estimation of rejection probability for the Wilcoxon
  #                   signed rank test

  # Perform MC simulation
  matX <- matrix(theta + fnError(n*nSim, ...), ncol = n)

  # Define sub-functions which only return p-values from the two tests
  fnPvalT <- function(x, theta) {
    return(t.test(x, mu = theta)$p.value)
  }
  fnPvalWilcox <- function(x, theta) {
    return(wilcox.test(x, mu = theta)$p.value)
  }

  # Perform nSim number of tests with sample size n for each of the two tests
  vecPvalT <- apply(matX, 1, fnPvalT, theta = theta)
  vecPvalWilcox <- apply(matX, 1, fnPvalWilcox, theta = theta)

  # Compute and return estimations of rejection probabilities
  result <- list()
  result$TProb <- mean(vecPvalT < alpha)
  result$WilcoxProb <- mean(vecPvalWilcox < alpha)
```

```
  return(result)
}
```

```
# Set seed
set.seed(42)

# Normal errors
fnTestPowerMC(fnError = rnorm, nSim = 10^5, theta = 0)
```

```
## $TProb
## [1] 0.04999
##
## $WilcoxProb
## [1] 0.04981
```

```
# Cauchy errors (t-distribution with df = 1)
fnTestPowerMC(fnError = rt, nSim = 10^5, df = 1)
```

```
## $TProb
## [1] 0.02034
##
## $WilcoxProb
## [1] 0.04947
```

```
# Uniform errors
fnTestPowerMC(fnError = runif, nSim = 10^5, min = -1, max = 1)
```

```
## $TProb
## [1] 0.05177
##
## $WilcoxProb
## [1] 0.05073
```

2 Dichteschätzung

2.1 Kerndichteschätzer

```
fnKernelDensityEst <- function(x, X, K, h) {
  # This function computes the kernel density estimates for a given sample X and
  # kernel K with bandwidth h at points x.
  #
  # Args:
  #   x: Points for which the kernel density estimates are computed
  #   X: Data sample on which the kernel density estimation is fitted
  #   K: Kernel function to be used for smoothing
  #   h: Smoothing Bandwidth
  #
  # Returns:
```

```
  #   A vector of the kernel density estimates at the points x

  # Get number of points and sample size
  nPts <- length(x)
  n <- length(X)

  # Compute the estimated kernel density values for every bandwidth
  kernels <- list()
  for(i in 1:length(h)) {
    matKernel <- K((matrix(rep(X, nPts), ncol = n, byrow = TRUE) - x) / h[i])
    kernels <- append(kernels, list((1/(n*h[i])) * apply(matKernel, 1, sum)))
  }

  # If h is scalar return just a matrix with the kernels
  # If h is a vector return a list with multiple kernels, their x and h values
  if(length(h) == 1) {
    return(kernels[[1]])
  } else {
    return(list(x = x, h = h, kernels = kernels))
  }
}
```

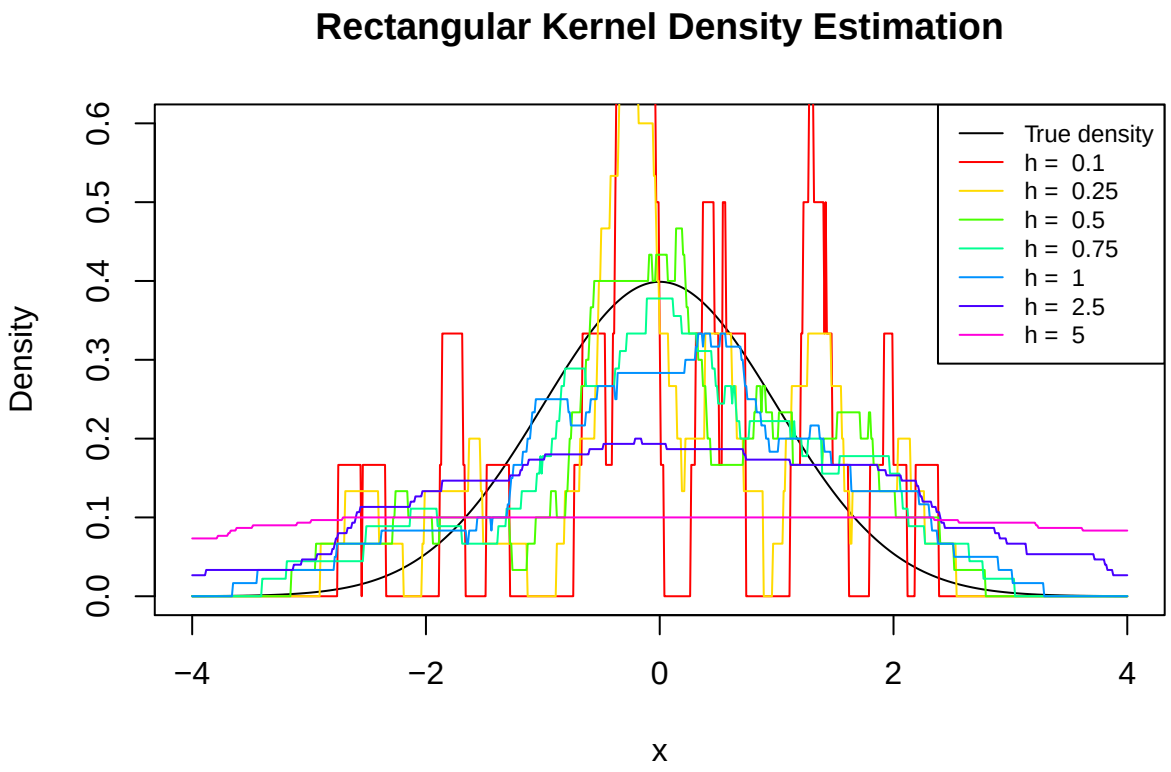
```
fnKernelPlot <- function(listKernels, title = NULL, data = NULL) {
  # This function plots the kernel density estimates for a given kernel list
  #
  # Args:
  #   listKernels: list of kernels calculated with fnKernelDensityEst
  #   title: main title of plot
  #
  # Returns:
  #   -

  # Save number of kernels (each with a different bandwidth)
  nKernels <- length(listKernels$kernels)

  # Create palette depending on size of list
  cols <- rainbow(nKernels, alpha = 1)

  # Plot theoretical density of histogram (if data is available)
  if(is.null(data)) {
    plot(listKernels$x, dnorm(listKernels$x), type = "l",
         main = title, xlab = "x", ylab = "Density", ylim = c(0,0.6))
  } else {
    plot(density(data), main = title, xlab = "x",
         ylab = "Density", ylim = c(0,0.6))
  }

  # Print kernels
  for(i in 1:nKernels) {
    lines(listKernels$x, listKernels$kernels[[i]], col = cols[i])
  }

  # Create and add legend
```

```
  dlegend <- ifelse(is.null(data), "True density", "R density()")
  hlegend <- sapply(listKernels$h, function(x) {x <- paste("h = ", x)})
  legend("topright", legend = c(dlegend, hlegend),
         col = c("black", cols), lty = 1, cex = 0.75)
}
```

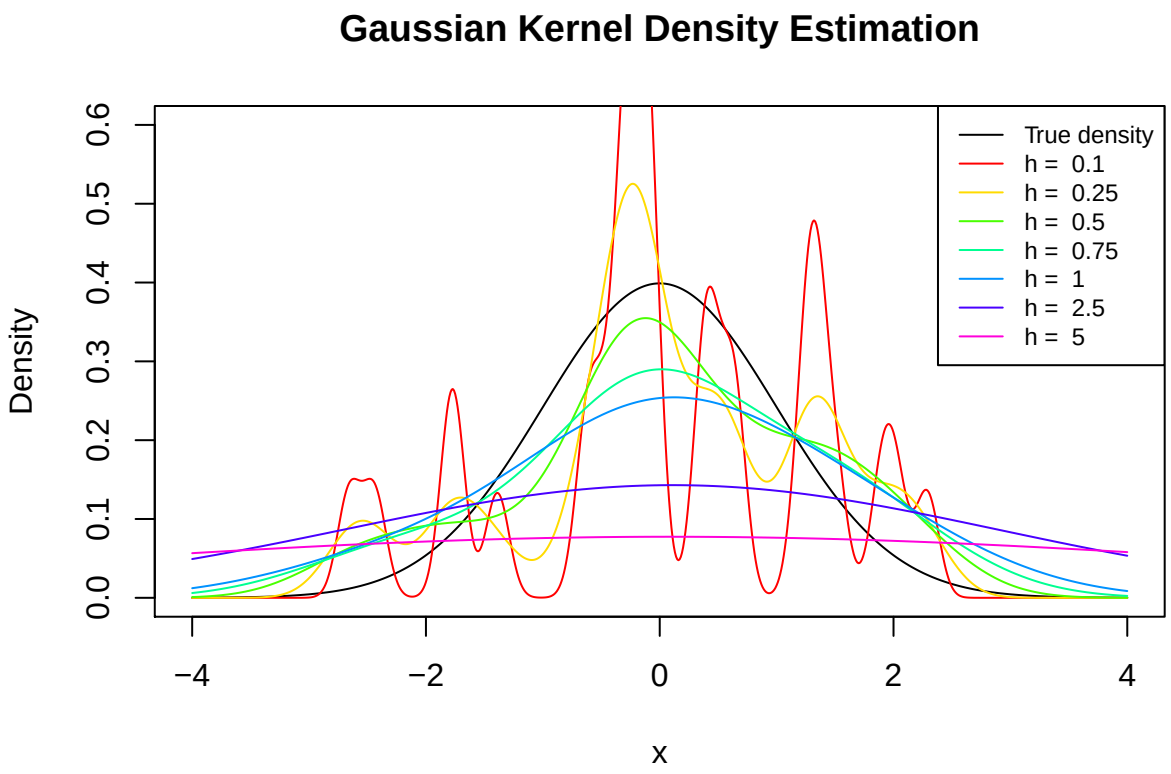
```
# Define different smoothing kernels

fnRectangularKernel <- function(x) {
  return(0.5 * (abs(x) <= 1))
}

fnGaussianKernel <- function(x) {
  return((1/sqrt(2*pi)) * exp((-0.5) * x^2))
}

fnEpanechnikovKernel <- function(x) {
  return(0.75 * (1 - x^2) * (abs(x) <= 1))
}
```

2.1.1 Anwendung auf standardnormalverteilte Daten

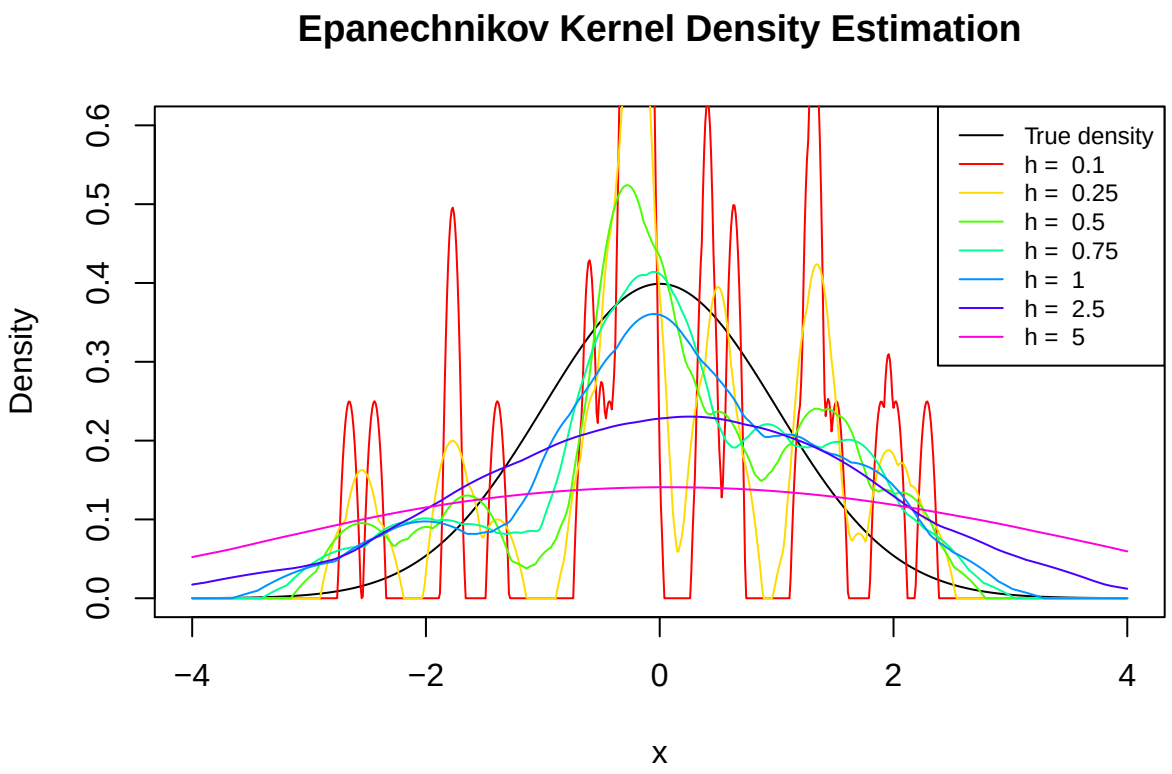
```
# Sample size and generate sample
set.seed(42)
n <- 30
X <- rnorm(n)

# Define points to estimate kernel density on
x <- seq(-4, 4, 0.01)

# Set different bandwidths
#h <- c(0.1, 1, 10)
h <- c(0.1, 0.25, 0.5, 0.75, 1, 2.5, 5)

# Rectangular kernel density estimation
fnKernelPlot(fnKernelDensityEst(x, X, K = fnRectangularKernel, h),
             title = "Rectangular Kernel Density Estimation")
```




```r
# Gaussian kernel density estimation
fnKernelPlot(fnKernelDensityEst(x, X, K = fnGaussianKernel, h),
             title = "Gaussian Kernel Density Estimation")
```

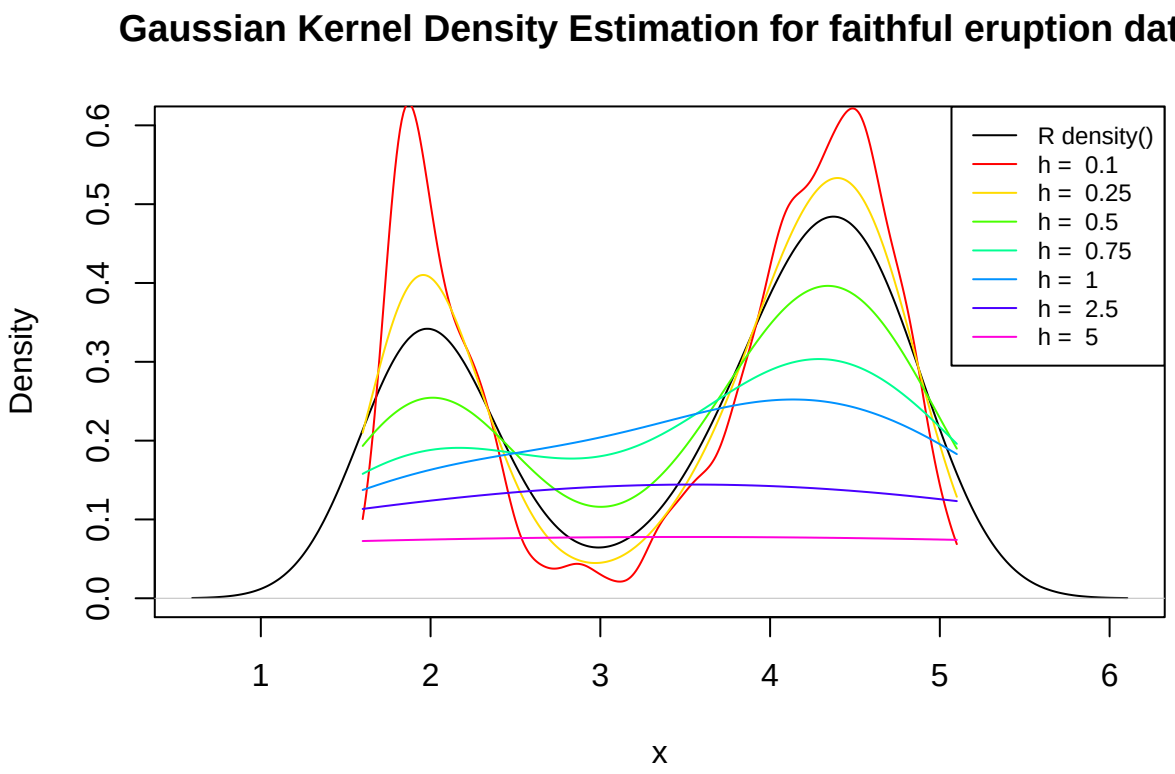


```r
# Epanechnikov kernel density estimation
fnKernelPlot(fnKernelDensityEst(x, X, K = fnEpanechnikovKernel, h),
             title = "Epanechnikov Kernel Density Estimation")
```



2.1.2 Anwendung auf faitful Datensatz

```r
# Faithful kernel density estimation
data <- faithful$eruptions
x <- seq(min(data), max(data), 0.01)

fnKernelPlot(fnKernelDensityEst(x, data, K = fnGaussianKernel, h),
             title = "Gaussian Kernel Density Estimation for faithful eruption data",
             data = data)
```



2.2 Kreuzvalidierung zur Bandweitenwahl

```
fnG <- function(x, X, K, h) {
  # This function computes the function G for given bandwidth
  #
  # Args:
  #   x: Points for which the kernel density estimates are computed
  #   X: Data sample on which the kernel density estimation is fitted
  #   K: Kernel function to be used for smoothing
  #   h: Smoothing Bandwidth
  #
  # Returns:
  #   Result of function G

  # Get number of points and sample size
  nPts <- length(x)
  n <- length(X)

  G <- 0
  for(j in 1:n) {
    fj <- 0
    for(k in 1:n) {
      if(k != j) {
        fj <- fj + K((X[k] - X[j]) / h)
      }
    }
    G <- G + fj/((n-1)*h)
```

```
  }
  return(G/n)
}

fnJ <- function(x, X, h) {
  # Calculates J for given bandwidth
  G <- fnG(x, X, fnGaussianKernel, h)
  f <- fnKernelDensityEst(x, X, fnGaussianKernel, h)
  return(sum(f^2) - (2*G))
}

X <- rnorm(30)
x <- seq(-4, 4, 0.01)
vech <- c(seq(0.1,0.9,0.1), seq(1,10,1))

vecJ <- NULL
for(h in vech) {
  vecJ <- c(vecJ, fnJ(x, X, h))
}
vech[which.min(vecJ)]
```

```
## [1] 10
```

3 Bildentrauschen

```
# Load image
imgColor = readImage("Block2/lena.png")

# Display colored image
par(mfrow = c(1,2))
display(imgColor, method="raster")

# Change image to grayscale
img<- channel(imgColor, "gray")

# Display grayscaled image
display(img, method="raster")

# Add noise to image
sigma <- 0.25
imgNoise <- img + rnorm(512*512, 0, sigma)

# Adjust values below 0 and above 1
imgNoise[imgNoise < 0] = 0
imgNoise[imgNoise > 1] = 1

# Display image with noise
par(mfrow = c(1,1))
display(imgNoise, method="raster")
```