simulation_week6

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```r
library(tidyverse)
library(purrr)
library(ggplot2)
library(here)
devtools::load_all()
set.seed(1222)
```

Commonly used kernel functions

In the beta family kernel density, lambda=0,1,2,3 correspond to the uniform, the Epanech- nikov, the biweight, and the triweight kernel functions, respectively.

```r
kernel_beta <- function(x,lambda){(1-x^2)^lambda*(abs(x)<=1)/beta(lambda+1,0.5)}

kernel_comp <- tibble(
  grid = seq(-3,3,by=0.1),
  Normal = dnorm(grid),
  Uniform = kernel_beta(grid,0),
  Epanechnikov = kernel_beta(grid,1),
  Biweight = kernel_beta(grid,2),
  Triweight = kernel_beta(grid,3)
  )

kernel_comp_long <- kernel_comp %>%
  pivot_longer(c(`Normal`, `Uniform`,`Epanechnikov`,
                 `Biweight`,`Triweight`), names_to = "Kernel", values_to = "Density")


ggplot(data=kernel_comp_long) +
  geom_line(aes(x = grid, y = Density, color = Kernel)) +
  labs(title = "Commonly used kernel functions") +
  theme_light()
```

Commonly used kernel functions
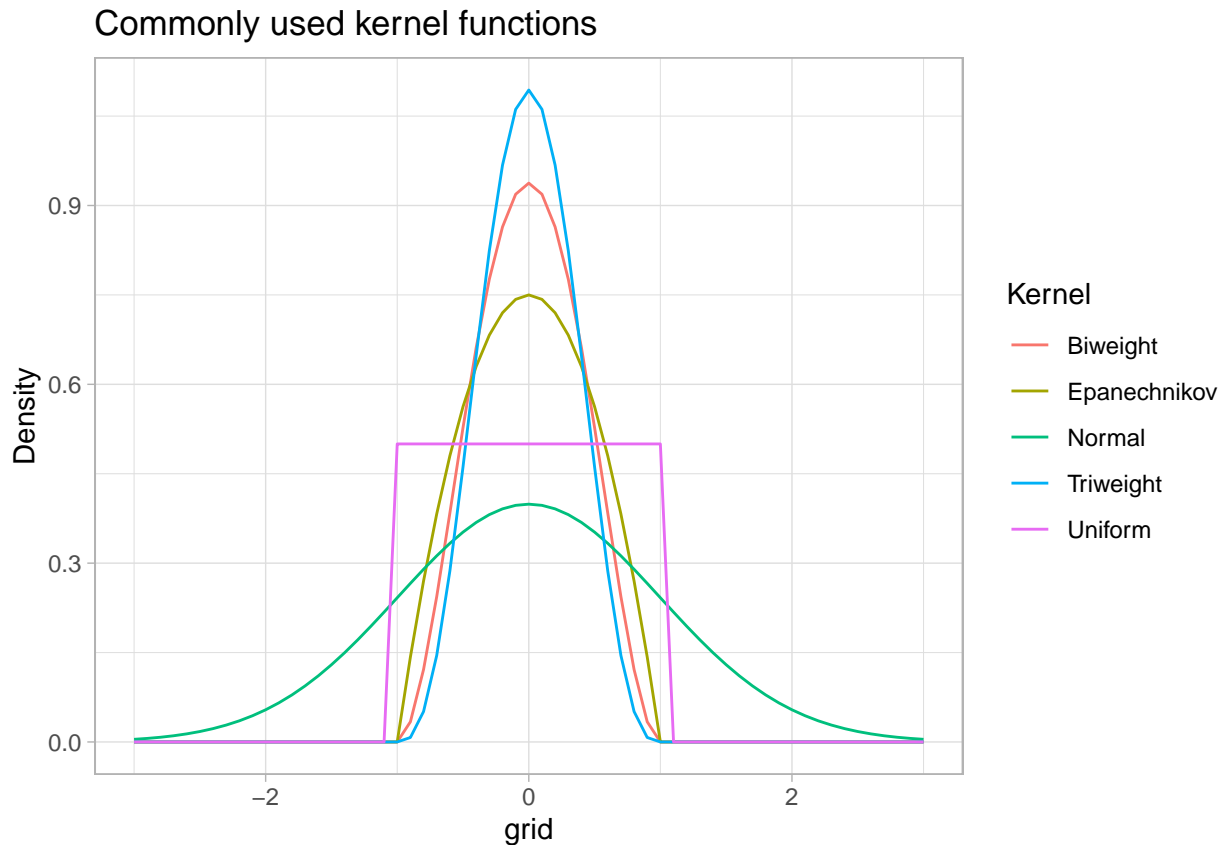
Compute the MADE (Mean Absolute Deviation Errors)

The Mean Absolute Deviation Errors for $\hat{f}(\cdot)$ is defined as

$$MADE = \frac{1}{n}\sum_{k=1}^{n}|(\hat{f}(u_k) - f(u_k))|$$

, where $\hat{f}(u_k)$ is the kernel estimte of $f(u_k)$), and $\{u_k\}$ are the frid points taken to be arbitrary within the range of data.

When the sample is generated from the known distribution like exp,beta, gamma, etc., we can use corresponding built-in functions (dexp(), dgamma, etc.) to calculated the true denstities of the grid points. If the sample is not from the familar distributions, we can use the built-in function "denstiy()" in R to get the value of $f(u_k)$)s.

Simulation

Explore the simulation results with different sample sizes & kernels

Build simulation functions that can save the MADE.

```
# Define some functions for gievn h=bandwidth,
# simulate over different sample size and kernels
```

```r
kde_n_ker_est <- function(x, n, ker, grid){
  # x large population
  # n sample sizes
  # ker name of kernels
  # grid grid points
  map2(.x = n, .y = ker,
       ~KDE_est(sample(x, .x, replace = FALSE),
                grid, h= 1.06*100^(-0.2), ker = .y)$f_est)
}


sim_made <- function(ns, kes, x, grid, true_f){
  # generates every combination of parameters (ns:kers)
  simulation_params_big <- list(
  n = ns,
  kernel_type = kers)
  n_ker_est_big <- cross_df(simulation_params_big)

  n_ker_est_big <- n_ker_est_big %>%
  mutate(
    f_ests = kde_n_ker_est(x, n, kernel_type, grid),
    f_true = map(1:length(n), ~true_f)
  ) %>%
  mutate(
    MADE = map2_dbl(.x = f_ests, .y = f_true, ~made(.x,.y))
  )
  return(n_ker_est_big$MADE)
}
```

Simulation

Generate samples from t(3) distribution. Then, using five types of kernel function and different size of samples that are drawn from the large population.

```r
# population
x <- rt(50000, df=3)

# simulaiton parameters
ns <- c(100, 500, 1000, 1500) # sample sizes
kers  <- c("normal", "uniform", "epanech", "biweight", "triweight") # kernel functions
grid <- seq(-5,15, 0.1)

# true density
true_f <- dt(grid, df=3)

# simulation
n.sim <- 100 # number of replicates
sim_rlt <- map(1:n.sim, ~sim_made(ns, kers, x, grid,true_f))
```

Save result

```r
made_mat <- matrix(unlist(sim_rlt), nrow = length(ns)*length(kers) )

made_comapre <- tibble(
  n =rep(ns, time=length(kers)),
  kernel_type = rep(kers, each=length(ns)),
  made_mean = apply(made_mat, 1, mean),
  made_sd = apply(made_mat, 1, sd)
)
write_rds(made_mat , here("results", "week6-sim.rds"))
write_rds(made_comapre, here("results", "week6-sim-plot.rds"))
```