Assignment 4

Exercise 1: Screening of disease in blood Exercise 2: Bayesian Inference with Normal Distribution and Step Function Prior Exercise 3:

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Assignment 4
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#----- Useful functions -----
mean_pdf <- function(f, lower, upper){integrate(function(x) <math>x*f(x), lower, upper)$value}
std_pdf <- function(f, lower, upper) {</pre>
 mu <- mean_pdf(f, lower, upper)</pre>
 sqrt(integrate(function(x) (x - mu)^2 * f(x), lower, upper)$value / integrate(f, lower, upper)$value
cumulative <- function(f, lower, X){integrate(f, lower, X,stop.on.error = FALSE)$value}</pre>
inverse_cumulative <- function(f, p, lower, upper)\{uniroot(function(x) cumulative(f, lower, x)-p, c(lower, upper)\}\}
#inference functions
binom_likelihood <- function(prob, ...) sapply(prob, function(P) prod(dbinom(prob=P, ...)))</pre>
pois_likelihood <- function(mu, ...) sapply(mu, function(MU) prod(dpois (lambda = MU, ...)))</pre>
norm_likelihood <- function(mu, ...) sapply(mu, function(MU) prod(dnorm (mean = MU, ...)))
posterior <- function(parameter, prior, likelihood, lower, upper, ...) {</pre>
 unnormalized <- function(x) likelihood(x, ...)*prior(x)
 norm_factor <- integrate(unnormalized, lower = lower, upper = upper)$value</pre>
 unnormalized(parameter)/norm_factor
}
```

Scenario

Exercise 1: Screening of disease in blood

A young UniPD startUp has developed an innovative method of screening. During the qualification phase, a random sample of n = 75 patients known to have the disease is screened using the new method.

A well established and diffused method for detecting a disease in blood fails to detect the presence of disease in 15% of the patients that actually have the disease.

1. what is the probability distribution of y, the number of times the new method fails to detect the disease? 2. on the n = 75 patients sample, the new method fails to detect the disease in y = 6 cases. What is the frequentist

- estimator of the failure probability of the new method? 3. setup a bayesian computation of the posterior probability, assuming a beta distribution with mean value 0.15 and
- standard deviation 0.14. Plot the posterior distribution for y, and mark on the plot the mean value and variance 4. Perform a test of hypothesis assuming that if the probability of failing to the detect the desease in ill patients is greater or equal than 15%, the new test is no better that the traditional method. Test the sample at a 5% level of significance in the Bayesian way.
- 5. Perform the same hypothesis test in the classical frequentist way. Answers
- 1. y follows a binomial distribution $P_n(y)$ with n being the number of patients and p the probability of failing the detection.

2. Since $\mathbb{E}[y] = p*n$, the frequentist estimator is $p = \frac{6}{75} = 0.08$.

- 3. The parameters for the beta prior are $\alpha \approx 0.83$ and $\beta \approx 4.68$. Since the beta distribution is the conjugate prior for the binomial likelihood, the parameters of the beta posterior are: lpha'=lpha+y=6.83 and $\beta' = \beta + n - y = 73.68.$
- 4. Looking at the plot we can accept at a 5% level of significance that the new method is better than the old one.

fails <- 6 # number of failures

#Conditions for the beta prior

mean = 0.15std = 0.14

12

10

 ∞

9

writeLines(sprintf(

> - The mean of the posterior is: %.3f - The standard deviation is: %.3f

- The margin of the 95% credibility interval is: %.3f

binom.test(fails, N, p = 0.15, alternative = "less")

Exact binomial test

sample estimates:

Tasks:

}

})

probability of success

', mean_beta_posterior, std_beta_posterior, beta_95_interval[2]

Posterior

- #----- SETTING THE INPUT HYPOTESIS -----<- 75 # number of patients
- # ----- INFERENCE CALCULATION -----#calculating the parameters of the prior alpha <- $mean*(mean*(1-mean)/(std^2)-1)$ beta <- (1-mean) * $(mean*(1-mean)/(std^2)$ -1) beta_prior <- function(x) { ifelse(x > 0 & x < 1, dbeta(x, shape1 = alpha, shape2 = beta), 0)} beta_posterior <- function(p) posterior(p, beta_prior, binom_likelihood, lower=0, upper=1, size=N</pre> mean_beta_posterior <- mean_pdf(beta_posterior, lower = 0, upper = 1)</pre> std_beta_posterior <- std_pdf (beta_posterior, lower = 0, upper = 1)</pre> beta_95_interval <- sapply(c(0., 0.95), **function**(P) inverse_cumulative(beta_posterior, p = P, lower = #----- PLOTTING -----
- curve(beta_posterior, from = 0, to = 1, xlab = TeX('\$p_{fail}\$'), ylab = 'Posterior', col=color_vector x_plot <- seq(from=beta_95_interval[1], to=beta_95_interval[2], length.out=500)</pre> y_plot <- c(0, beta_posterior(x_plot), 0)</pre> x_plot <- c(beta_95_interval[1], x_plot, beta_95_interval[2])</pre> polygon(x_plot, y_plot, col = adjustcolor(color_vector[5], alpha.f = 0.25), border = NA) grid() abline(v=mean_beta_posterior, col = color_vector[7], lwd=2, lty='longdash') abline(v=mean_beta_posterior - std_beta_posterior, col = color_vector[6], lwd=2, lty='dashed')
- abline(v=mean_beta_posterior + std_beta_posterior, col = color_vector[6], lwd=2, lty='dashed') legend("topright", legend = c("Beta Posterior", "Mean", "±std"), col = c(color_vector[1], color_vector legend("right", legend="95%% credibility interval", fill=color_vector[5]) Inference on the probability of failing

Beta Posterior

Mean

---- ±std

95%% credibility interval

- 4 7 0.00 0.05 0.10 0.20 0.30 0.15 0.25 p_{fail} ----- WRITE OUTPUT ------
- ## - The mean of the posterior is: 0.085 - The standard deviation is: 0.031 - The margin of the 95% credibility interval is: 0.141 5. In the frequentist approach, we can use a binomial test. Looking at the results, with this approach it is not possible to reject the hypothesis that the new method is worse than the previous one at a 5% level of significance, since the 95% confidence interval includes p = 15%.
- ## ## data: fails and N ## number of successes = 6, number of trials = 75, p-value = 0.05435 ## alternative hypothesis: true probability of success is less than 0.15 ## 95 percent confidence interval: ## 0.0000000 0.1517971

```
0.08
Exercise 2: Bayesian Inference with Normal
Distribution and Step Function Prior
Scenario
A researcher collects 16 observations (n=16) that are supposed to come from a normal distribution with known
variance \sigma^2 = 4. The observations are:
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The prior distribution for the mean (μ) is a step function defined as: $g(\mu) = \left\{ egin{array}{ll} 1, & 0 < \mu \leq 3 \\ 3, & 3 < \mu \leq 5 \\ 8 - \mu, & 5 < \mu \leq 8 \\ 0, & \mu > 8 \end{array} \right.$

4.09, 4.68, 1.87, 2.62, 5.58, 8.68, 4.07, 4.78, 4.79, 4.49, 5.85, 5.09, 2.40, 6.27, 6.30, 4.47

2. Find the 95% credibility interval for μ . 3. Plot the posterior distribution, indicating the mean value, standard deviation, and 95% credibility interval. 4. Plot the prior, likelihood, and posterior distribution on the same graph.

normalized_likelihood <- Vectorize(function(mu) {</pre>

norm_likelihood(mu, x=data, sd=sigma_prior)/norm_const

----- WRITE OUTPUT -----

writeLines(sprintf(

0.5

Posterior

Normalized Likelihood

Normalized Prior

normalized_prior <- function(mu) {</pre>

prior_values(mu)/norm_const

1. Find the posterior distribution, posterior mean, and standard deviation.

Answers n <- 16 # number of observations sigma_prior <- 4 # assumed to be known</pre> data <- c(4.09, 4.68, 1.87, 2.62, 5.58, 8.68, 4.07, 4.78, 4.79, 4.49, 5.85, 5.09, 2.40, 6.27, 6.30, 4.

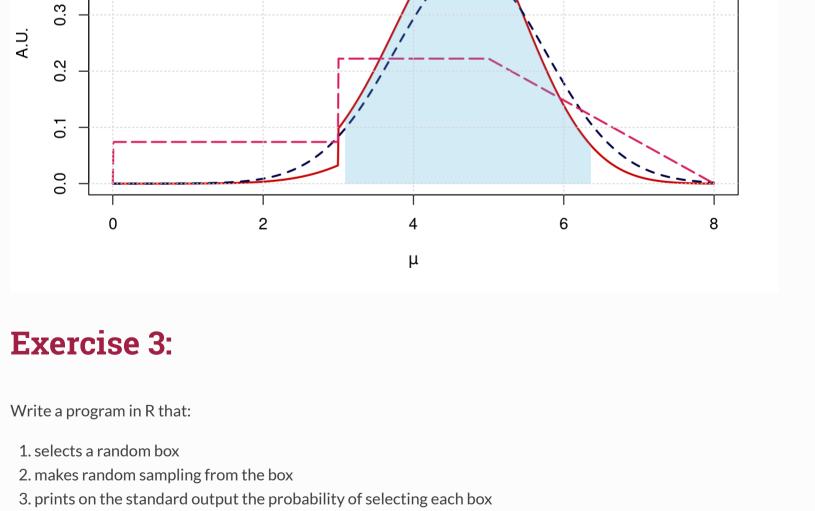
norm_const <- integrate(prior_values, lower = 0, upper = 8)\$value</pre>

prior values <- function(mu) sapply(mu, function(x) ifelse(x>0 && x <= 3, 1., ifelse(x>3&&x<=5, 3., if posterior_values <- function(mu) posterior(mu, prior_values, norm_likelihood, lower = 0, upper = 8, x=

norm_const <- integrate(function(X) norm_likelihood(mu=X, x=data, sd=sigma_prior), lower = -Inf, upp</pre>

```
mean_posterior <- mean_pdf(posterior_values, lower = 0, upper = 8)</pre>
 std_posterior <- std_pdf (posterior_values, lower = 0, upper = 8)</pre>
 cred_95_interval <- sapply(c(0.025, 0.975), function(P) inverse_cumulative(posterior_values, p = P, 1d)
 #----- PLOTTING -----
 curve(posterior_values, from = 0, to = 8, xlab = expression(mu), ylab = 'Posterior', col=color_vector[
 x_plot <- seq(from=cred_95_interval[1], to=cred_95_interval[2], length.out=500)</pre>
 y_plot <- c(0, posterior_values(x_plot), 0)</pre>
 x_plot <- c(cred_95_interval[1], x_plot, cred_95_interval[2])</pre>
 polygon(x_plot, y_plot, col = adjustcolor(color_vector[5], alpha.f = 0.25), border = NA)
 grid()
 abline(v=mean_posterior, col = color_vector[7], lwd=2, lty='longdash')
 abline(v=mean_posterior - std_posterior, col = color_vector[6], lwd=2, lty='dashed')
 abline(v=mean_posterior + std_posterior, col = color_vector[6], lwd=2, lty='dashed')
 legend("topright", legend = c("Posterior", "Mean", "±std"), col = c(color_vector[1], color_vector[7],
 legend("topleft", legend="95% credibility interval", fill=color_vector[5])
                                Inference on the Gaussian Mean
           95%% credibility interval
                                                                                    Posterior
                                                                                   Mean
                                                                              ---- ±std
    0.3
Posterior
    0.2
    0.1
    0.0
                               2
```

```
- The mean of the posterior is: %.3f
  - The standard deviation is: %.3f
  - The 95% credibility interval is: [ %.3f , %.3f ]
', mean_posterior, std_posterior, cred_95_interval[1], cred_95_interval[2]
    - The mean of the posterior is: 4.665
    - The standard deviation is: 0.855
    - The 95% credibility interval is: [ 3.093 , 6.358 ]
#----- PLOTTING -----
curve(posterior_values, from = 0, to = 8, xlab = expression(mu), ylab = 'A.U.', col=color_vector[1], m
curve(normalized_likelihood(x), from = \frac{0}{2}, to = \frac{8}{2}, col=color_vector[\frac{6}{2}], lwd = \frac{2}{2}, lty = \frac{2}{2}, n = \frac{1000}{2}, add
curve(normalized_prior, from = 0, to = 8, col=color_vector[7], lwd = 2, lty = 5, n = 1000, add = TRUE
x_plot <- seq(from=cred_95_interval[1], to=cred_95_interval[2], length.out=500)</pre>
y_plot <- c(0, posterior_values(x_plot), 0)</pre>
x_plot <- c(cred_95_interval[1], x_plot, cred_95_interval[2])</pre>
polygon(x_plot, y_plot, col = adjustcolor(color_vector[5], alpha.f = 0.25), border = NA)
grid()
legend("topleft", legend = c("Posterior", "Normalized Likelihood", "Normalized Prior"), col = c(color_
legend("topright", legend="95% credibility interval", fill=color_vector[5])
```



Prior Likelihood and Posterior

■ 95%% credibility interval

4. plots the probability for each box as a function of the number of trial # building the boxes, s.t. the box i contains i white balls (=1)

P_white <- sapply(0:(N_box-1), function(ibox) ibox/(N_box-1))</pre>

N_extracted_box <- 1 # How many times do we select a new box N_ball <- 50 # How many times do we select a ball from each box

ball_seq <- 1:N_ball</pre>

Emanuele Coradin

likelihood_list <- lapply(1:N_box,</pre>

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box_seq <- 1:N_extracted_box</pre>
# Select the boxes
box_sampling <- sample(1:7, N_extracted_box, replace=TRUE)</pre>
# Coding the process of selecting some balls
ball_sampling <- lapply(box_sampling, function(i) sample(box[[i]], N_ball, replace=TRUE))</pre>
# Calculate the partial sum over the white sampling for each step
N_white <- lapply(box_seq, function(ibox) sapply(ball_seq, function(jball) sum(ball_sampling[[ibox]][1
```

function (ibox) mapply(

function(n_white, n_samples)

, N_white[[1]], ball_seq)

dbinom(x=n_white, size = n_samples, prob = P_white[ibox])

box <- lapply(1:N_box, function(i) sapply(1:N_box-1, function(j) ifelse(j < i, 1, 0)))</pre>

sum_over_boxes <- function(jball) sum(sapply(1:N_box, function(ibox) likelihood_list[[ibox]][jball]))</pre> normalize_over_boxes <function(jball)

posterior_matrix <- sapply(ball_seq, normalize_over_boxes)</pre> colors <- rainbow(N_box)</pre> line_types <- 1:N_box</pre> plot(posterior_matrix[1,], type = 'o', pch = 20, col = colors[1], ylim = range(posterior_matrix), xlab = "Number of sampled balls", ylab = "Posterior Probability",

sapply(1:N_box, function(ibox) likelihood_list[[ibox]][jball]/sum_over_boxes(jball))

grid() legend("topright", legend = paste("Box", 0:(N_box-1)), col = colors, lty = line_types, pch = 20, lwd=2 **Evolution of the posterior along the samples**

void <- sapply(2:N_box, function(ibox) lines(posterior_matrix[ibox,], type = 'o', pch = 20, col = col</pre>