Consider the scaled uniform distribution, with probability density function (pdf) indexed by parameter $\theta > 0$ given below:

$$f(x;\theta) = \frac{1}{\theta}, \quad 0 < x < \theta < \infty.$$

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$$\pi(\theta) = \frac{ab^a}{\theta^{a+1}}, \quad 0 < b < \theta < \infty, \quad a > 0.$$

- (a) Show that the posterior distribution for θ is Pareto(a', b'), where a' = a + n and $b' = \max(b, X_{(n)}).$ (Note: recall that $X_{(n)} = \max_{i=1,...,n} X_{i}.$)
- (b) Find δ(X₁,...X_n), the Bayes estimator for θ with respect to
 - squared error loss: L(θ, δ) = (δ − θ)².
 - ii. absolute error loss: $L(\theta, \delta) = |\delta \theta|$.
- (c) Suppose we test the hypotheses H₀: θ ≥ θ₀ vs. H_A: θ < θ₀ for some θ₀ > 0.
 - i. Consider the test that rejects the null hypothesis when the posterior probability of H_0 is less than $\alpha \in (0,1)$. Show that the rejection region is given by $\mathcal{R} = \left\{ b' < \theta_0 \alpha_{s'}^{\frac{1}{s'}} \right\}.$
 - ii. Calculate the power function of the test in part (i) above; that is, calculate $\beta(\theta) = \mathbb{P}(\mathcal{R}|\theta).$
 - iii. Calculate $\beta_{UMP}(\theta)$, the power function of the uniformly most powerful (UMP) level α test of H_0 vs H_A .
 - iv. Let $a \to 0$ and $b \to 0$.
 - A. Show that β(θ) → β_{UMP}(θ) pointwise.
 - B. Briefly explain, in qualitative terms, why the performance of the Bayesian test is approaching the performance of a frequentist test (the UMP test is a frequentist test in the sense that it can be defined without reference to a prior distribution). Your answer will be scored based on the soundness of your explanation. Hint: think about what is happening to the prior distribution as a and b go to zero.

 Let X₁, X₂,..., X_n be independent identically distributed random variables having the following probability density function:

$$f_{a,b,c,\theta_1,\theta_2}(x) = \begin{cases} ae^{-\frac{x}{\theta_1}+1}, & x > \theta_1; \\ b, & -\theta_2 < x \le \theta_1; \\ ce^{\frac{x}{\theta_2}+1}, & x \le -\theta_2 \end{cases}$$
(1)

where $a \geq 0$, $b \geq 0$, $c \geq 0$, $\theta_1 > 0$ and $\theta_2 > 0$ are unknown.

- (a) Identify a general formula satisfied by a, b, c, θ₁, and θ₂ such that (1) is a density function. Hint: You may use the values (1/2, 1/2, 1/2, 1/2, 1/2) and (1/2, 1/2, 1/2, 1/3, 2/3) for (a, b, c, θ₁, θ₂) to verify your formula.
- (b) Explicitly express the first two moments μ₁ = E(X₁) and μ₂ = E(X₁²) as a function of a, b, c, θ₁, and θ₂. For μ₃ = E(X₁³) and μ₄ = E(X₁⁴), the following formulas can be used in later parts if needed.

$$\begin{split} E(X_1^3) &= -\left(16c + \frac{b}{4}\right)\theta_2^4 + \left(16a + \frac{b}{4}\right)\theta_1^4, \\ E(X_1^4) &= \left(65c + \frac{b}{5}\right)\theta_2^5 + \left(65a + \frac{b}{5}\right)\theta_1^5. \end{split}$$

- (c) Suppose θ_1 and θ_2 are now fixed, but a > 0, b > 0, and c > 0 are unknown.
 - i) Find a condition on a, b, and c such that $E(X_1)$ is positive.
 - ii) Assuming θ₁ = θ₂ = 1. Prove that there does not exist a set of a, b, and c such that Var(X₁) is minimized.
- (d) Suppose now a = b = c.
 - i) Obtain estimators $\hat{\theta}_1$ of θ_1 , $\hat{\theta}_2$ of θ_2 respectively using the method of moments.
 - ii) Suppose $\theta = \theta_1 = \theta_2$. Obtain a method of moment estimator $\widehat{\theta}$ of θ . Obtain the asymptotic distribution of $\widehat{\theta}$.

Consider the linear regression model

$$Y_{ij} = \alpha_0 + \alpha_i + \varepsilon_{ij}$$
, for $j = 1, 2, ..., n_i$, and $i = 1, ..., m$, (2)

where α_i 's are unknown parameters, $\varepsilon_{ij} \sim N(0, \sigma_i^2)$ are independent Gaussian noise with unknown variance σ_i^2 , n_i is the sample size for group i, and m is the number of groups.

- For this part, assume σ₁² = σ₂² = · · · = σ_m² = σ².
 - (a) Let φ = ∑_{i=0}^m ℓ_iα_i be a linear combination of parameter α_i's with given coefficients ℓ_i's. Prove that φ is estimable if and only if ℓ₀ = ∑_{i=1}^m ℓ_i. Hint: φ is called estimable if it can be represented as the expectation of a linear combination of Y_{ij}.
 - (b) Let μ_i = α₀ + α_i denote the group mean for i = 1,...,m. Write down the least-squares estimates for μ_i's, the MLE σ²_{MLE}, and the unbiased estimator σ²_{usual} for σ².
 - (c) Suppose the data Yij are generated from the ground truth model

$$Y_{ij} = \alpha_0 + \varepsilon_{ij}$$
, with $\varepsilon_{ij} \sim_{i.i.d} N(0, \sigma^2)$. (3)

However, the experimenter uses the overfitted model (2) to fit the data, and reports $\widehat{\sigma}_{usual}^2$ from question (b) as the analysis result. Show that the $\widehat{\sigma}_{usual}^2$ from overfitted model is still an unbiased estimate of σ^2 in model (3), despite the model misspecification.

- (d) Let \(\hat{\sigma}_{red}^2\) be the estimate of \(\sigma^2\) based on reduced (and true) model (3). Consider the 95%-confidence intervals (CI) for \(\sigma^2\) based on the \(\chi^2\) procedure. Show that the expected length of CI from reduced model (i.e., based on \(\hat{\sigma}_{red}^2\)) is smaller than the overfitted model (i.e., based on \(\hat{\sigma}_{usual}^2\)).
- (ii) For this part, suppose there is an additional known variable, denoted η_i, associated with each of the group. We return to the original setting, where both data and fitted model are based on (2),
 - (a) Suppose σ_i² = σ²η_i² for all i = 1,..., m. Find the best linear unbiased estimator for μ_i's. Could you use a standard R function routine to find the results, or would you need to develop a general regression package? Explain.
 - (b) Now suppose η_i values are used to model the mean with the assumption µ_i = β₀+β₁η_i, but we return to assuming that σ²₁ = ··· = σ²_m = σ² as in part (i). The experimenter is interested in testing whether the group means change linearly in η_i, or in an arbitrarily unstructured way over i. Formulate the question into a hypothesis testing problem. State the test statistic, null distribution, and rejection procedure. You could write your answers in matrix or algebraic forms; no need to simply the expressions.

4. Scientists want to study the effect of an anti-bacterial drug in fish lungs. The drug is administered at 5 dose-levels (0, 2, 4, 8, and 16 mg/L) as summarized in the below table to large controlled tanks with 100 fish in each through the filtration system. There are 20 tanks and each dose is randomly assigned to 4 tanks. At the end of the experiment, the fish are sacrificed, and the amount of bacteria in each fish is measured to yield total amount of bacteria per tank.

Let y_{ij} denote the total amount of bacteria from the jth tank with the ith dose, $i = 1, \dots, 5$ and $j = 1, 2, \dots, 4$. Furthermore, suppose

$$y_{ij} = \mu_i + \epsilon_{ij}$$
, (4)

where $\mu_1, \dots, \mu_5 \in \mathbb{R}$ are unknown parameters and ϵ_{ij} are independent and identically distributed $\mathcal{N}(0, \sigma^2)$ random variables for some unknown $\sigma^2 \in \mathbb{R}^+$. Use the R code and partial output provided below to answer the following questions.

- (a) Provide the best linear unbiased estimator of μ₁.
- (b) Provide the best linear unbiased estimator of μ₂.
- (c) Determine the standard error of your esimate of μ₂ from part (b).
- (d) Conduct a test of H₀: μ₁ = μ₂. Provide a test statistics, the distribution of the test statistic (both under the null and the alternative), a p-value, and a conclusion.
- (e) Provide an F-statistic for testing H₀: μ₃ = μ₄.
- (f) Scientists would like to consider a simple linear regression model with total amont of bacteria as a response and anti-bacterial drug dose as a quantitative variable to fit these data. Does such a model provide a better fit compared to the model in (4)? Provide a test statistic, its null distribution, a p-value, and a conclusion. You may find the upper 5th percentiles of various F distributions in the R output useful for drawing your conclusion.
- (g) Provide a matrix A and a vector c such that the null hypothesis of the test in part (f) can be written as $H_0: \overline{\mathbf{A}\mu = c}$, where $\mu = (\mu_1, \dots, \mu_5)^T$.

R code and partial output for question # 4:

d <- rep(c(0, 2, 4, 8, 16), each = 4)
$$= langth(d) = 4.5 = 20$$

y is the data vector representing total amount of bacteria per tank.
Its entries are ordered to appropriately match the vector d.