

README: Bayesian Posterior Analysis

Overview

This project estimates the current weight of a group of people based on a Bayesian framework. The posterior distribution for the population mean (μ) and variance (σ^2) is computed using Monte Carlo sampling, given sample data and prior information.

File Structure

1. **data.txt**:
 - Contains the sample data: sample size, mean, and variance.
 2. **prior.txt**:
 - Contains prior information for a single case. Modify this file to specify the prior parameters for each case.
 3. **normalInvGamma.r**:
 - Implements the posterior computation for μ and σ^2 using the Normal-Inverse-Gamma conjugate prior.
 4. **normalInvGammaRun.r**:
 - Main script that:
 1. Loads sample data and priors.
 2. Calls the posterior computation function.
 3. Outputs posterior mean, 95% credible intervals, and hypothesis test results.
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Instructions

1. Prepare the Input Files

- **data.txt**: Ensure the data is valid and follows the format:

```
sampleSize sampleMean sampleVariance
10 176 9
```

- **prior.txt**: Specify the prior parameters for the case you are analyzing. Update the file before running the script:

```
priorMean priorSampleSize shape rate
176 0.5 2 3 # Case a
```

Example:

- For **Case b**: Replace 176, 0.5, 2, 3 with the values for Case b.
 - For **Case c**: Replace the values for Case c.
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2. Run the Analysis

1. Open R in the directory containing the scripts.
2. Run the main script:

```
source("normalInvGammaRun.r")
```

3. The script will:
 - Read the sample data from `data.txt`.
 - Read the prior parameters from `prior.txt`.
 - Compute posterior mean and 95% credible intervals for μ .
 - Test whether $\mu=200$ lies within the 95% credible interval.
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3. Output

The results will be printed in the console, including:

- Posterior mean,
- 95% credible interval for μ ,
- Hypothesis test result for $\mu=200$.

Example:

```
----- Case a -----  
Posterior Mean: 176.01  
95% Credible Interval for  $\mu$ : [174.20, 177.82]  
Hypothesis  $\mu = 200$  is rejected.
```

Workflow

1. Modify `prior.txt` with the parameters for the desired case (e.g., Case a, Case b, or Case c).
 2. Run the analysis with `source("normalInvGammaRun.r")`.
 3. Review the console output for results.
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Notes

- To analyze multiple cases, update `prior.txt` with parameters for each case sequentially.