Single parameter models

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Outline

Probability distributions

Bernoulli Distribution

Bernoulli Distribution: Definition

- Discrete probability distribution for **binary outcomes**
- Random variable X takes values:

$$X = \begin{cases} 1 & \text{with probability } p \\ 0 & \text{with probability } 1 - p \end{cases}$$

- Probability mass function (PMF):

$$P(X = k) = p^k (1 - p)^{1-k} \quad \text{for } k \in \{0, 1\}$$

- Parameters: $p \in [0, 1]$ (probability of success)

Real-World Example

Login Attempt Success

Consider a website login system where:

- Each login attempt succeeds with probability $p = 0.3$
- Fails with probability 0.7

Let:

$$X = \begin{cases} 1 & \text{Successful login} \\ 0 & \text{Failed login} \end{cases}$$

This is a Bernoulli(p $=$ 0.3) random variable.

Simulation and Comparison in R


```r
# Parameters
n <- 1000
p <- 0.3

# Generate random samples
set.seed(123)
samples <- rbinom(n, 1, p)

# Calculate empirical probabilities
emp_probs <- table(samples)/n
```

Theoretical results:

- P(X=0) = 0.7
- P(X=1) = 0.3

Empirical results:

- P(X=0) = emp_probs[1]
- P(X=1) = emp_probs[2]

Visual Comparison

PMF Comparison:

```
# Theoretical PMF
theoretical <- c(0.7, 0.3)

# Plot comparison
barplot(rbind(theoretical, emp_probs),
        beside = TRUE,
        col = c("red", "blue"),
        main = "PMF Comparison")
```

Visual Comparison

CDF Comparison:

```
# Plot theoretical CDF
plot(stepfun(c(0,1), c(0,0.7,1)),
     main = "CDF Comparison",
     xlim = c(-0.5,1.5))

# Add empirical CDF
lines(ecdf(samples),
      col = 'blue', lty = 2)
```

Activity: Simulating Disease Transmission

Scenario: COVID-19 exposure at a school (N = 500 students)

Simulation Steps:

```r
# Set parameters:
set.seed(456)
# Transmission probability
p_infect <- 0.15
n_students <- 500
# Simulate infections:
infected <- rbinom(n_students, 1, p_infect)
# Calculate outcomes:
n_infected <- sum(infected)
attack_rate <- mean(infected)
# Visualize
barplot(c(Theoretical = p_infect,
          Observed = attack_rate),
        ylab = "Probability",
        col = c("red3", "dodgerblue"),
        main = "Infection Risk Comparison")
```

Immediate Tasks:

- Report number infected
- Compare red vs. blue bars
- Compute: $\frac{\text{Infected}}{\text{Total}}$
- Expected vs. observed cases

Activity: Analysis & Public Health Insights (Part 1)

Follow-up from Simulation Results

```
# Confidence interval for attack rate
prop.test(n_infected, n_students)

# Simulate new variant impact
p_new_variant <- 0.30  # 30% infection probability
infected_new <- rbinom(n_students, 1, p_new_variant)
```

Initial Questions:

- How would you interpret the 95% confidence interval?
- What does changing p_new_variant from 0.15 to 0.30 imply about:
  - Hospitalization rates?
  - Healthcare system capacity?

Key concepts introduced: Confidence intervals, parameter sensitivity

Activity: Analysis & Public Health Insights (Part 2)

Vaccine Efficacy (VE)

- Definition: Relative reduction in infection risk for vaccinated vs unvaccinated
- Formula:

$$VE = 1 - \frac{\text{Risk}_{\text{vaccinated}}}{\text{Risk}_{\text{unvaccinated}}}$$

- R implementation:

```
p_control <- 0.25   # Infection rate in control group
p_vax <- 0.05       # Infection rate in vaccinated group
ve <- 1 - (p_vax/p_control)  # Returns 0.8 (80% efficacy)
```

Sample Size Calculation

- Theory: For 95% CI with margin of error e: We would like to know the needed sample if we would a 95% CI mean $\pm$ 2%

$$n = \frac{Z_{\alpha/2}^2 \cdot p(1-p)}{e^2}$$

- R implementation:

```
p <- 0.5    # Conservative estimate
e <- 0.02   # Desired precision
n <- (qnorm(0.975)^2 * p*(1-p)) / e^2
```

Binomial Distribution

Binomial Distribution: Definition

- Discrete distribution for **success counts in n trials**
- $X \sim \text{Bin}(n, p)$ where:
  - n: Number of independent trials
  - p: Success probability per trial
- PMF:

$$P(X = k) = \binom{n}{k} p^k (1 - p)^{n-k} \quad k = 0, 1, \ldots, n$$

- Expectation: $\mathbb{E}[X] = np$
  Variance: $\text{Var}(X) = np(1 - p)$

Epidemiological Example

Vaccine Efficacy Trial

In a COVID-19 vaccine trial with 100 participants:

- Each participant has 5% infection risk (placebo group)
- Let X = number of infections in the group
- $X \sim \text{Bin}(n = 100, p = 0.05)$

Probability questions:

- $P(X \geq 10)$ - Extreme outbreak risk
- $P(5 \leq X \leq 15)$ - Expected range

Simulation and Comparison in R

```
# Parameters
n_trials <- 1000
n <- 100    # Participants
p <- 0.05   # Infection risk

# Simulate outbreaks
set.seed(123)
infections <- rbinom(n_trials, n, p)

# Theoretical PMF
k <- 0:n
pmf <- dbinom(k, n, p)
```

Comparison checks:

- Empirical mean vs np
- Sample variance vs $np(1-p)$
- Histogram shape vs PMF

```
mean(infections)
# Should be ~5
var(infections)
# Should be ~4.75
```

Visual Comparison

- PMF Comparison:

```r
hist(infections, freq=FALSE,
     main = "Infection Distribution",
     xlab = "Number of Cases")
lines(k, pmf, col="red", lwd=2)
```

- CDF Comparison:

```r
plot(ecdf(infections),
     main = "CDF Comparison")
lines(k, pbinom(k, n, p),
      col="red", type="s")
```

Poisson Distribution

Poisson Distribution: Definition

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- Discrete distribution for **event counts in fixed interval/area**
- $X \sim \text{Pois}(\lambda)$ where:
  - λ: Average rate (events per unit)
  - Constant event risk, independent occurrences
- PMF:

$$P(X = k) = \frac{e^{-\lambda}\lambda^k}{k!} \quad k = 0, 1, 2, \ldots$$

- Expectation/Variance: $\mathbb{E}[X] = \text{Var}(X) = \lambda$

Environmental Science Example

Microplastic Pollution Monitoring

Water quality researchers study a river:

- Average of 4 microplastic particles per liter ($\lambda = 4$)
- $X =$ number of particles in 1L sample
- $X \sim \text{Pois}(4)$

Key questions:

- $P(X \geq 8)$ - Extreme pollution probability
- $P(X \leq 2)$ - Compliance with safety standards
- 95% prediction interval for particle counts

Simulation and Comparison in R


```r
# Parameters
lambda <- 4
n_samples <- 1000

# Simulate water samples
set.seed(123)
particles <- rpois(n_samples, lambda)

# Theoretical PMF
k <- 0:15
pmf <- dpois(k, lambda)
```

Validation checks:

- Empirical mean: `mean(particles)`
- Sample variance: `var(particles)`
- Zero-inflation test: `mean(particles==0)`

```r
# Expected
# vs observed zeros
exp(-lambda)
# Theoretical P(X=0)
mean(particles == 0)
```

Visual Comparison

- PMF Comparison:

```
hist(particles, freq=FALSE, breaks=0:15,
     main = "Microplastic Particles/Liter",
     xlab = "Count")
points(k, pmf, col="red", pch=19)
```

- Time Series:

```
plot(particles[1:50], type="b",
     main = "Particle Count Time Series",
     xlab = "Sample ID", ylab = "Count",
     col = "darkgreen")
abline(h = lambda, col="red", lty=2)
```

Activity: Pollution Hotspot Analysis

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Scenario: Comparing two river sites

Simulation Task:

```r
# Downstream (polluted)
lambda_ds <- 8
# Upstream (reference)
lambda_us <- 3

samples <- 500
set.seed(456)
ds_counts <- rpois(samples, lambda_ds)
us_counts <- rpois(samples, lambda_us)
```

Analysis:

- Test $\lambda_{ds} > \lambda_{us}$
- Compute $P(\text{ds} \geq 10)$
- Visualize PMF comparisons
- Estimate pollution ratio
- Check dispersion (var/mean ratio)

Negative Binomial Distribution

Negative Binomial Distribution: Definition (Traditional)

- Discrete distribution for the number of trials needed to achieve r successes.
- Assumes independent Bernoulli trials with success probability p.
- PMF:

$$P(X = k) = \binom{k-1}{r-1} p^r (1-p)^{k-r}, \quad k = r, r+1, r+2, \ldots$$

- Moments:
  - Mean: $\mathbb{E}[X] = \frac{r}{p}$
  - Variance: $\mathrm{Var}(X) = \frac{r(1-p)}{p^2}$

Customer Acquisition Costs

A SaaS company models trial-to-paid conversions:

- Each website visit is a trial with conversion probability $p = \frac{1}{3}$.
- A conversion requires one successful visit ($r = 1$).
- X = number of visits until conversion.
- $X \sim \text{NB}(r = 1, p = \frac{1}{3})$ (geometric distribution).

Key business questions:

- What is the probability of conversion in ≤ 2 visits?
- What is the 95th percentile of required visits?
- How does this inform customer acquisition cost modeling?

Simulation and Comparison in R

```
# Parameters
r <- 1          # Conversion requires 1 success
p <- 1/3        # Conversion probability per visit
n <- 1000

# Simulate number of visits until conversion
set.seed(2023)
failures <- rnbinom(n, size = r, prob = p)
visits <- failures + r  # Total visits (failures + 1 success)

# Theoretical PMF for number of visits
k <- 1:15
pmf <- p * (1 - p)^(k - 1)

# Empirical dispersion check
dispersion <- var(visits) / mean(visits)
dispersion  # Should be > 1 indicating overdispersion
```

Visual Comparison

- PMF Comparison:

```
hist(visits, freq=FALSE, breaks=0:20,
     main = "Visits Until Conversion",
     xlab = "Website Visits")
lines(k, pmf, col="red", type="h")
```

- QQ-Plot:

```
# Compare to Poisson
qqplot(rpois(1000, mu), visits,
       main = "NB vs Poisson QQ-Plot")
abline(0,1, col="red")
```

Normal Distribution

Normal Distribution: Definition

- Continuous distribution for **symmetric, bell-shaped data**
- $X \sim N(\mu, \sigma^2)$ where:
  - μ: Mean (location parameter)
  - σ: Standard deviation (scale parameter)
- Probability density function (PDF):

$$f(x) = \frac{1}{\sigma\sqrt{2\pi}} e^{-\frac{1}{2}\left(\frac{x-\mu}{\sigma}\right)^2}$$

- Properties:
  - Symmetric about μ
  - 68-95-99.7 rule for standard normal

Psychology Example

IQ Score Distribution

Standardized intelligence testing:

- IQ scores follow $N(100, 15^2)$
- Population parameters:
  - Mean $\mu = 100$
  - SD $\sigma = 15$
- Diagnostic thresholds:
  - Gifted: > 130 (top 2.3%)
  - Intellectual disability: < 70 (bottom 2.3%)

Simulation and Comparison in R


```r
# Parameters
mu <- 100
sigma <- 15
n <- 1000

# Generate scores
set.seed(123)
iq_scores <- rnorm(n, mu, sigma)

# Theoretical PDF
x <- seq(55, 145, length=100)
pdf <- dnorm(x, mu, sigma)
```

Validation checks:

- Empirical mean/SD vs parameters
- Shapiro-Wilk normality test
- Check 68-95-99.7 rule

```r
mean(iq_scores)
# Should be ~100
sd(iq_scores)
# Should be ~15
shapiro.test(iq_scores)
```

- Density Comparison:

```
hist(iq_scores, freq=FALSE, breaks=20,
     main = "IQ Score Distribution",
     xlab = "IQ")
lines(x, pdf, col="red", lwd=2)
```

- QQ-Plot:

```
qqnorm(iq_scores, main = "Normal Q-Q Plot")
qqline(iq_scores, col="red")
```

Exponential Distribution

Exponential Distribution: Definition

- Continuous distribution for **time between events in Poisson process**
- $X \sim \text{Exp}(\lambda)$ where:
  - λ: Rate parameter (events per unit time)
  - Mean time between events: $\mu = 1/\lambda$
- PDF:

$$f(x) = \lambda e^{-\lambda x} \quad x \geq 0$$

- Key property: Memoryless

$$P(X > s + t | X > s) = P(X > t)$$

Cybersecurity Example

Network Intrusion Detection

A corporate network experiences:

- Average of 1 intrusion every 10 days ($\mu = 10$)
- $\lambda = 0.1$ intrusions/day
- $X =$ days between intrusions
- $X \sim \text{Exp}(0.1)$

Security questions:

- $P(\text{Next intrusion} < 24\text{hrs}) = ?$
- 90th percentile of safe period
- Probability of > 30 days without intrusion

Simulation and Comparison in R


```r
# Parameters
lambda <- 0.1  # Rate
mu <- 1/lambda # Mean = 10
n <- 1000

# Simulate inter-arrival times
set.seed(123)
durations <- rexp(n, lambda)

# Theoretical PDF
x <- seq(0, 30, length=100)
pdf <- dexp(x, lambda)
```

Validation checks:

- Empirical mean vs $1/\lambda$
- Variance vs $1/\lambda^2$
- Memoryless property test

```r
mean(durations)
# Should be ~10
var(durations)
# Should be ~100
```

Visual Comparison

- Density Comparison:

```
hist(durations, freq=FALSE, breaks=30,
     main = "Time Between Intrusions",
     xlab = "Days")
lines(x, pdf, col="red", lwd=2)
```

- Survival Function:

```
plot(ecdf(durations),
     main = "CDF Comparison")
lines(x, pexp(x, lambda),
      col="red", lwd=2)
```

Gamma Distribution

Gamma Distribution: Definition

- Continuous distribution for **positive-valued, skewed data**
- $X \sim \Gamma(k, \theta)$ where:
  - k: Shape parameter (controls skewness)
  - θ: Scale parameter
- PDF:

$$f(x) = \frac{1}{\Gamma(k)\theta^k} x^{k-1} e^{-x/\theta} \quad x > 0$$

- Properties:
  - $\mathbb{E}[X] = k\theta$, $\mathrm{Var}(X) = k\theta^2$
  - Generalizes Exponential ($k = 1$) and χ^2 distributions

Healthcare Example

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Hospital Length of Stay

Modeling patient stays in a surgical ward:

- Average stay duration: 5 days ($k = 2, \theta = 2.5$)
- X = number of days hospitalized
- $X \sim \Gamma(2, 2.5)$

Clinical applications:

- $P(\text{Stay} > 10 \text{ days})$ - Identify long-stay patients
- 75th percentile for resource planning
- Compare recovery times between procedures
- Model healthcare costs associated with stays

Why Gamma?

Simulation and Comparison in R

```r
# Parameters
shape <- 2
scale <- 2.5
n <- 1000

# Simulate hospital stays
set.seed(123)
stays <- rgamma(n, shape=shape, scale=scale)

# Theoretical PDF
x <- seq(0, 20, length=100)
pdf <- dgamma(x, shape=shape, scale=scale)
```

Validation checks:

- Empirical mean vs $k\theta$
- Variance vs $k\theta^2$
- Skewness assessment

```r
mean(stays)
# Should be ~5
var(stays)
# Should be ~12.5
moments::skewness(stays)
# ~1.41
```

Visual Comparison

- Density Comparison:

```
hist(stays, freq=FALSE, breaks=30,
     main = "Hospital Stay Duration",
     xlab = "Days", col="lightblue")
lines(x, pdf, col="maroon", lwd=2)
legend("topright",
        legend=c("Theory","Empirical"),
       col=c("maroon","lightblue"), lwd=2)
```

- CDF Comparison:

```
plot(ecdf(stays),
    main="Empirical vs Theoretical CDF")
lines(x, pgamma(x, shape=shape, scale=scale),
      col="darkgreen", lwd=2)
```

Beta Distribution

Beta Distribution: Definition

- Continuous distribution for **probabilities/proportions** (0-1)
- $X \sim \text{Beta}(\alpha, \beta)$ where:
  - α: Shape 1 (successes + 1)
  - β: Shape 2 (failures + 1)
- PDF:

$$f(x) = \frac{x^{\alpha-1}(1-x)^{\beta-1}}{B(\alpha, \beta)} \quad 0 \leq x \leq 1$$

- Properties:
  - $\mathbb{E}[X] = \dfrac{\alpha}{\alpha+\beta}$
  - $\text{Var}(X) = \dfrac{\alpha\beta}{(\alpha+\beta)^2(\alpha+\beta+1)}$
  - Generalizes Uniform ($\alpha = \beta = 1$)

Marketing Example

A/B Test Conversion Rates

Comparing website versions:

- Version A: 45 conversions / 1000 visits
- Version B: 65 conversions / 1000 visits
- Model conversion rates as:
  - $r_A \sim \text{Beta}(46, 956)$
  - $r_B \sim \text{Beta}(66, 936)$

Business questions:

- $P(r_B > r_A)$ - Version superiority probability
- 95% credible intervals for rates
- Minimum detectable effect size

Why Beta?

- Natural for bounded probabilities
- Conjugate prior for Binomial
- Flexible uncertainty representation

Simulation and Comparison in R

```r
# Parameters
alpha <- 46
beta <- 956
n <- 10000

# Simulate conversion rates
set.seed(123)
rates <- rbeta(n, alpha, beta)

# Theoretical PDF
x <- seq(0, 0.1, length=100)
pdf <- dbeta(x, alpha, beta)
```

Validation checks:

- Empirical mean vs $\alpha/(\alpha+\beta)$
- Variance comparison
- Uniform check when $\alpha = \beta = 1$

```r
mean(rates)
# Should be ~0.046
quantile(rates, c(0.025,0.975))
```

Visual Comparison

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- Density Comparison:

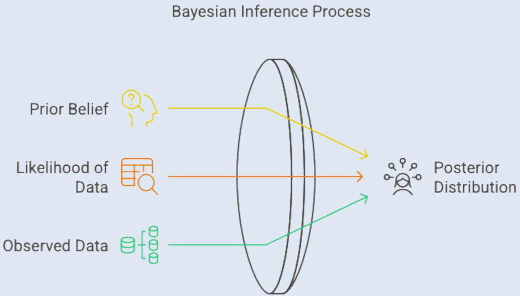
```
hist(rates, freq=FALSE, breaks=50,
     main = "Conversion Rate Distribution",
     xlab = "Conversion Rate", col="skyblue")
lines(x, pdf, col="darkred", lwd=2)
```

- CDF Comparison:

```
plot(ecdf(rates), main="Beta CDF Comparison")
lines(x, pbeta(x, alpha, beta),
      col="darkgreen", lwd=2)
```

Bayesian single parameter Models

Single Parameter Mode



$$\underbrace{p(\theta \mid \text{Data})}_{\text{posterior}} \propto \underbrace{L(\text{Data} \mid \theta)}_{\text{likelihood}} \times \underbrace{p(\theta)}_{\text{prior}}$$

Bernoulli Model

Example: Influence of Prior Beliefs on Bayesian Updating

- Scenario: Estimating the probability of success for a new treatment based on observed trial results.
- Observations: Suppose you observe 10 trials of a new treatment, where 6 trials are successful.
- Prior Beliefs:
  - **Non-Informative Prior**: We start with no prior information, reflecting a neutral stance on the treatment's effectiveness. This prior does not influence the likelihood gained from the observed data.
  - **Weakly Informative Prior**: We have some previous experience or expert opinion suggesting the treatment's success rate is around 50

Choosing the Prior Distribution

- **Prior**: Represents initial beliefs about p (probability of success).
- Common choices:
  - **Conjugate Prior (Beta)**:

$$p \sim \text{Beta}(\alpha, \beta)$$

    - α: Prior successes $+ 1$
    - β: Prior failures $+ 1$
  - **Non-Informative Prior**: $\text{Beta}(1, 1)$ (uniform over $[0, 1]$)
  - **Weakly Informative Prior**: $\text{Beta}(2, 2)$ (gentle nudge toward 0.5)

Posterior Distribution

Given observed data $y = (y_1, y_2, \ldots, y_n)$, the posterior is:

$$p \mid y \sim \text{Beta}(\alpha + \text{successes}, \beta + \text{failures})$$

- **Successes**: $\sum_{i=1}^{n} y_i$
- **Failures**: $n - \sum_{i=1}^{n} y_i$

R Example: Analytical Solution


```r
# Data
successes <- 7
failures <- 3

# Priors
prior_uniform <- c(1, 1)          # Non-informative
prior_weak <- c(2, 2)             # Weakly informative
prior_informative <- c(5, 5)      # Informative

# Posteriors
posterior_uniform <- c(prior_uniform[1] + successes,
                        prior_uniform[2] + failures)
posterior_weak <- c(prior_weak[1] + successes,
                    prior_weak[2] + failures)
posterior_informative <- c(prior_informative[1] + successes,
                    prior_informative[2] + failures)
```

R Example: Analytical Solution

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```
# Plot
curve(dbeta(x, posterior_uniform[1], posterior_uniform[2]),
      xlab="p", ylab="Density", col="blue",
      lwd=2, ylim=c(0, 4))
curve(dbeta(x, posterior_weak[1],
     posterior_weak[2]),
      col="red", lwd=2, add=TRUE)
curve(dbeta(x, posterior_informative[1],
      posterior_informative[2]),
      col="green", lwd=2, add=TRUE)
legend("topright",
       legend=c("Uniform", "Weak", "Informative"),
       col=c("blue", "red", "green"), lwd=2)
```

R Example: Using rstan

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Stan Code (bernoulli_model.stan):

```
data {
  int<lower=0> N;          // Number of trials
  int<lower=0, upper=1> y[N];  // Binary outcomes
}
parameters {
  real<lower=0, upper=1> p;  // Probability of success
}
model {
  p ~ beta(1, 1);          // Uniform prior
  y ~ bernoulli(p);        // Likelihood
}
```

R Example: Using rstan

R Code to Run Stan:

```
library(rstan)
y <- c(1, 0, 1, 1, 0, 1, 1, 1, 0, 1)
stan_data <- list(N = length(y), y = y)
fit <- stan(file = "bernoulli_model.stan",
       data = stan_data,
      iter = 2000, chains = 4)
print(fit)  # Summary of posterior
plot(fit)   # Visualize posterior distribution
```

Activity: Vaccine Efficacy

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Scenario: A new vaccine is tested on 100 individuals. 15 develop side effects.

Task:

- Define a Beta prior for side effect probability p.
- Compute the posterior distribution.
- Compare results for:
  - Non-informative prior ($\text{Beta}(1, 1)$)
  - Weakly informative prior ($\text{Beta}(2, 2)$)
  - Informative prior ($\text{Beta}(5, 95)$)
- Use `rstan` to fit the model and compare results.

Questions:

- What is $P(p > 0.2)$ under each prior?
- How does the choice of prior affect the posterior?
- What sample size would reduce prior influence?

Normal Model

Case 1: Unknown Mean, Known Variance

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- **Model**: $y \sim N(\mu, \sigma^2)$, where σ^2 is known.
- **Conjugate Prior**: Normal distribution for μ:

$$\mu \sim N(\mu_0, \tau_0^2)$$

  - μ_0: Prior mean
  - τ_0^2: Prior variance

- **Posterior**:

$$\mu \mid y \sim N\left(\mu_n, \tau_n^2\right)$$

  where:

$$\mu_n = \frac{\frac{\mu_0}{\tau_0^2} + \frac{n\bar{y}}{\sigma^2}}{\frac{1}{\tau_0^2} + \frac{n}{\sigma^2}}, \quad \tau_n^2 = \left(\frac{1}{\tau_0^2} + \frac{n}{\sigma^2}\right)^{-1}$$

R Example: Unknown Mean, Known Variance


```r
# Data
y <- c(5.1, 5.5, 4.9, 5.3, 5.7)  # Sample data
n <- length(y)
sigma2 <- 0.5  # Known variance

# Prior
mu0 <- 5.0  # Prior mean
tau02 <- 1.0  # Prior variance

# Posterior
mu_n <- (mu0/tau02 + n*mean(y)/sigma2) / (1/tau02 + n/sigma2)
tau_n2 <- 1 / (1/tau02 + n/sigma2)

# Plot
curve(dnorm(x, mu0, sqrt(tau02)), xlim=c(4, 6), ylab="Density",
      col="blue", lwd=2, main="Prior vs Posterior")
curve(dnorm(x, mu_n, sqrt(tau_n2)), col="red", lwd=2, add=TRUE)
legend("topright", legend=c("Prior", "Posterior"),
       col=c("blue", "red"), lwd=2)
```

Case 2: Unknown Mean and Variance

- **Model**: $y \sim N(\mu, \sigma^2)$, both μ and σ^2 unknown.
- **Conjugate Prior**: Normal-Inverse-Gamma (NIG):

$$\mu \mid \sigma^2 \sim N(\mu_0, \sigma^2/\kappa_0), \quad \sigma^2 \sim \text{Inv-Gamma}(\alpha_0, \beta_0)$$

- μ_0: Prior mean
- κ_0: Prior precision scaling
- α_0, β_0: Shape and scale for σ^2

- **Posterior**:

$$\mu \mid \sigma^2, y \sim N(\mu_n, \sigma^2/\kappa_n), \quad \sigma^2 \mid y \sim \text{Inv-Gamma}(\alpha_n, \beta_n)$$

where:

$$\mu_n = \frac{\kappa_0\mu_0 + n\bar{y}}{\kappa_0 + n}, \quad \kappa_n = \kappa_0 + n, \quad \alpha_n = \alpha_0 + \frac{n}{2},$$

$$\beta_n = \beta_0 + \frac{1}{2}\sum_{i=1}^{n}(y_i - \bar{y})^2 + \frac{\kappa_0 n(\bar{y} - \mu_0)^2}{2(\kappa_0 + n)}$$

R Example: Unknown Mean and Variance


```r
# Data
y <- c(5.1, 5.5, 4.9, 5.3, 5.7)  # Sample data
n <- length(y)

# Prior
mu0 <- 5.0  # Prior mean
kappa0 <- 1  # Prior precision scaling
alpha0 <- 2  # Prior shape for sigma^2
beta0 <- 1   # Prior scale for sigma^2

# Posterior
mu_n <- (kappa0 * mu0 + n * mean(y)) / (kappa0 + n)
kappa_n <- kappa0 + n
alpha_n <- alpha0 + n/2
beta_n <- beta0 + 0.5*sum((y - mean(y))^2) +
          (kappa0 *n*(mean(y) - mu0)^2)/(2*(kappa0 + n))
```

R Example: Unknown Mean and Variance

```
# Plot posterior for mu
curve(dnorm(x, mu_n, sqrt(beta_n / (alpha_n * kappa_n))),
      xlim=c(4, 6), ylab="Density", col="red", lwd=2,
      main="Posterior for Mean")
```

Using `rstan` for Unknown Mean and Variance

Stan Code (`normal_model.stan`):

```
data {
  int<lower=0> N;          // Number of observations
  real y[N];               // Data
}
parameters {
  real mu;                 // Mean
  real<lower=0> sigma2; // Variance
}
model {
  mu ~ normal(5.0, sqrt(sigma2));  // Prior for mu
  sigma2 ~ inv_gamma(2, 1);        // Prior for sigma2
  y ~ normal(mu, sqrt(sigma2));    // Likelihood
}
```

Using rstan for Unknown Mean and Variance

R Code to Run Stan:

```
library(rstan)
y <- c(5.1, 5.5, 4.9, 5.3, 5.7)  # Sample data
stan_data <- list(N = length(y), y = y)
fit <- stan(file = "normal_model.stan", data = stan_data, ite
print(fit)  # Summary of posterior
plot(fit)   # Visualize posterior distributions
```

Activity: Climate Change Analysis

Scenario: Analyze annual temperature anomalies (in °C) for a city:

$$y = \{0.9, 1.1, 1.3, 1.0, 1.2, 1.4, 1.1, 1.3, 1.5, 1.2\}$$

Task:

- Assume $\sigma^2 = 0.1$ is known. Use a Normal$(1.0, 0.5)$ prior for μ. Compute the posterior.
- Assume both μ and σ^2 are unknown. Use a NIG$(1.0, 1, 2, 1)$ prior. Compute the posterior.
- Compare results using `rstan`.

Questions:

- What is $P(\mu > 1.2)$ under each model?
- How does prior choice affect results?
- What sample size reduces prior influence?

Poisson Model

Introduction to Poisson Model

- The Poisson distribution is often used to model the number of events occurring within a fixed period of time.
- **Model Assumption**: Events occur independently at a constant rate.
- Common applications: Counting the number of occurrences of events (e.g., arrival of customers, mutation occurrences in a DNA sequence).

Bayesian Poisson Model

- In Bayesian inference, we combine prior beliefs about a parameter with the likelihood of observed data.
- **Likelihood**: Assuming y events observed follows $y \sim \text{Poisson}(\lambda)$.
- **Prior for λ**: Typically a Gamma distribution due to its conjugacy, $\lambda \sim \text{Gamma}(a, b)$.
  - A non-informative prior can be implemented by setting a and b very close to zero (e.g., 0.001). This results in a very flat distribution, indicating high uncertainty and allowing the data to have a stronger influence on the posterior.
  - The flatness ensures that the prior does not overly constrain the likelihood, providing minimal initial information about the parameter.

Poisson Model in RStan

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Stan Code (poisson_model.stan):

```
data {
  int<lower=0> N;         // Number of events observed
  int y[N];               // Observed counts
}
parameters {
  real<lower=0> lambda; // Rate parameter of Poisson
}
model {
  // Non-informative prior: lambda ~ gamma(0.001, 0.001)
  // Informative prior: lambda ~ gamma(9, 0.5)
  lambda ~ gamma(9, 0.5);      // Change as needed
  y ~ poisson(lambda);
}
```

Poisson Model in RStan

R Code to Run Stan:

```
library(rstan)
data_obs <- c(3, 2, 1, 5, 4)  // Example data
stan_data <- list(N = length(data_obs), y = data_obs)
fit <- stan(file = "poisson_model.stan", data = stan_data,
            iter = 2000, chains = 4)
print(fit)  // Summary of posterior
plot(fit)   // Visualize posterior distribution
```