I09 - Comparing means

STAT 401 (Engineering) - Iowa State University

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One mean

Consider the model $Y_i \stackrel{ind}{\sim} N(\mu, \sigma^2)$. We have discussed a number of statistical procedures to draw inferences about μ:

- Frequentist: based on distribution of $\frac{\overline{Y} - \mu}{s/\sqrt{n}}$
  - pvalue for a hypothesis test, e.g. $H_0 : \mu = \mu_0$,
  - confidence interval for μ,
- Bayesian: based on posterior for μ
  - credible interval for μ,
  - posterior model probability, e.g. $p(H_0|y)$, and
  - posterior probabilities, e.g. $P(\mu < \mu_0|y)$.

Now, we will consider what happens when you have multiple μs.

Two means

Consider the model

$$Y_{g,i} \overset{ind}{\sim} N(\mu_g, \sigma_g^2)$$

for $g = 1, 2$ and $i = 1, \ldots, n_g$. and you are interested in the relationship between μ_1 and μ_2. We can perform the following statistical procedures:

- Frequentist: based on distribution of

$$\frac{\overline{Y}_1 - \overline{Y}_2 - (\mu_1 - \mu 2)}{\sqrt{\frac{S_1^2}{n_1} + \frac{S_2^2}{n_2}}}$$

  where S_g^2 is the (random) sample variance of group g.
    - pvalue for a hypothesis test, e.g. $H_0 : \mu_1 = \mu_2$,
    - confidence interval for $\mu_1 - \mu_2$,
- Bayesian: based on posterior for μ_1, μ_2, i.e. $p(\mu_1, \mu_2|y)$
    - credible interval for $\mu_1 - \mu_2$,
    - posterior model probability, e.g. $p(H_0|y)$, and
    - probability statements, e.g. $P(\mu_1 < \mu_2|y)$.

where $y = (y_{1,1}, \ldots, y_{1,n_1}, y_{2,1}, \ldots, y_{2,n_2})$.

Simulating data

We will simulate the following data

$$Y_{g,i} \stackrel{ind}{\sim} N(\mu_g, \sigma_g^2)$$

for $g = 1, 2, 3$ and $i = 1, \ldots, n_g$. For the moment we will only use the first two groups, but later we will use all 3 groups.

```
set.seed(20170301)

# Using the unknown population means and standard deviations
d <- bind_rows(
  data_frame(process = "P1", sensitivity = rnorm(22,  7.8, 2.3)),
  data_frame(process = "P2", sensitivity = rnorm(34,  9.3, 2.3)),
  data_frame(process = "P3", sensitivity = rnorm( 7, 10.0, 2.3)))

# readr::write_csv(d, path="sensitivity.csv")
```

Data example

Suppose you have two manufacturing processes to produce sensors and you are interested in the average sensitivity of the sensors.

So you run the two processes and record the sensitivity of each sensor in units of mV/V/mm Hg (http://www.ni.com/white-paper/14860/en/). And you have the following summary statistics:

```
# d <- readr::read_csv("sensitivity.csv")
d2 <- d %>% filter(process %in% c("P1","P2"))
```

```
sm <- d2 %>%
  group_by(process) %>%
  summarize(
    n    = n(),
    mean = mean(sensitivity),
    sd   = sd(sensitivity)
  )
sm
```

```
# A tibble: 2 x 4
  process     n  mean    sd
  <chr>   <int> <dbl> <dbl>
1 P1         22  7.74  1.87
2 P2         34  9.24  2.26
```

Frequentist analysis

Analyses are based on the distribution of

$$\frac{\overline{Y}_1 - \overline{Y}_2 - (\mu_1 - \mu2)}{\sqrt{\frac{S_1^2}{n_1} + \frac{S_2^2}{n_2}}} \sim t_{df}(0, 1).$$

Unfortunately, this distribution is unknown. The standard (although somewhat controversial) approach is to assume this has a t distribution but with an unknown degrees of freedom. The degrees of freedom is often computed using the Satterthwaite approximation:

$$df \approx \frac{\left(\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}\right)^2}{\frac{s_1^4}{n_1^2(n_1-1)} + \frac{s_2^4}{n_2^2(n_2-1)}}.$$

Pvalues and confidence intervals

Because there is no indication that you have any expectation regarding the
sensitivities of process 1 compared to process 2, we will conduct a
two-sided two-sample t-test assuming the variances are not equal, i.e.

$$Y_{g,i} \overset{ind}{\sim} N(\mu_g, \sigma_g^2)$$

and

$$H_0 : \mu_1 = \mu_2 \quad \text{and} \quad H_A : \mu_1 \neq \mu_2$$

```
t.test(sensitivity ~ process, data = d2)


Welch Two Sample t-test

data:  sensitivity by process
t = -2.6932, df = 50.649, p-value = 0.009571
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -2.610398 -0.380530
sample estimates:
mean in group P1 mean in group P2
        7.743761         9.239224
```

Posterior for μ_1, μ_2

Assume

$$Y_{g,i} \overset{ind}{\sim} N(\mu_g, \sigma_g^2) \quad \text{and} \quad p(\mu_1, \mu_2, \sigma_1^2, \sigma_2^2) \propto \frac{1}{\sigma_1^2} \frac{1}{\sigma_2^2}.$$

Then

$$\mu_g | y \overset{ind}{\sim} t_{n_g-1}(\overline{y}_g, s_g^2/n_g)$$

and a draw for μ_g can be obtained by taking

$$\overline{y}_g + T_{n_g-1} s_g / \sqrt{n_g}, \quad T_{n_g-1} \overset{ind}{\sim} t_{n_g-1}(0,1).$$

Simulations:

```
nr = 1e5
sims <- bind_rows(
  data_frame(
    rep = 1:nr,
    process = "P1",
    mu = sm$mean[1] + rt(nr, df = sm$n[1]-1) * sm$sd[1] / sqrt(sm$n[1])),
  data_frame(
    rep = 1:nr,
    process = "P2",
    mu = sm$mean[2] + rt(nr, df = sm$n[2]-1) * sm$sd[2] / sqrt(sm$n[2]))
)
```

We can use these draws to compare the posteriors

Compare posterior histograms for μ_1 and μ_2.

```
ggplot(sims, aes(x=mu, y=..density.., fill=process, group=process)) +
  geom_histogram(position = "identity", alpha=0.5, binwidth=0.1) +
  theme_bw()
```
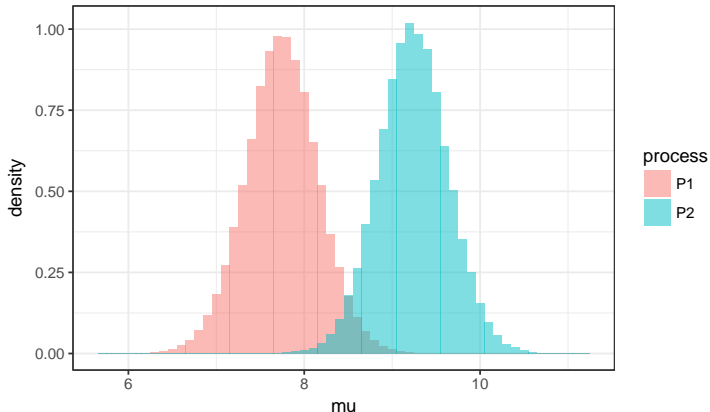
Credible interval for the difference

To obtain statistical inference on the difference, we use the samples and take the difference

```
d3 <- sims %>%
  spread(process, mu) %>%
  mutate(diff = P1-P2)

# Bayes estimate for the difference
mean(d3$diff)

[1] -1.493267


# Estimated 95% equal-tail credible interval
quantile(d3$diff, c(.025,.975))


     2.5%      97.5%
-2.6339752 -0.3483025


# Estimate of the probability that mu1 is larger than mu2
mean(d3$diff > 0)

[1] 0.00591
```

Three or more means

Now, let's consider the more general problem of

$$Y_{g,i} \overset{ind}{\sim} N(\mu_g, \sigma_g^2)$$

for $g = 1, 2, \ldots, G$ and $i = 1, \ldots, n_g$ and you are interested in the relationship amongst the μ_g.

We can perform the following statistical procedures:

- Frequentist:
    - pvalue for a hypothesis test, e.g. $H_0 : \mu_g = \mu$ for all g,
    - confidence interval for $\mu_k - \mu_{k'}$ for a specified k and k',
- Bayesian: based on posterior for $\mu_1, \ldots, \mu_G$
    - credible interval for $\mu_k - \mu_{k'}$ for a specified k and k',
    - posterior model probability, e.g. $p(H_0|y)$, and
    - probability statements, e.g. $P(\mu_k < \mu_{k'}|y)$ for a specified k and k'.

Data example

Suppose you have three manufacturing processes to produce sensors and you are interested in the average sensitivity of the sensors.

So you run the three processes and record the sensitivity of each sensor in units of mV/V/mm Hg (http://www.ni.com/white-paper/14860/en/). And you have the following summary statistics:

```
sm <- d %>%
  group_by(process) %>%
  summarize(
    n    = n(),
    mean = mean(sensitivity),
    sd   = sd(sensitivity)
  )
sm

# A tibble: 3 x 4
  process     n  mean    sd
  <chr>   <int> <dbl> <dbl>
1 P1         22  7.74  1.87
2 P2         34  9.24  2.26
3 P3          7 10.8   1.96
```

Pvalues

When there are lots of means, the first null hypothesis is typically

$$H_0 : \mu_g = \mu \,\forall\, g$$

```
oneway.test(sensitivity ~ process, data = d)

One-way analysis of means (not assuming equal variances)

data:  sensitivity and process
F = 7.6287, num df = 2.000, denom df = 17.418, p-value = 0.004174
```

Then we typically look at pairwise differences:

```
pairwise.t.test(d$sensitivity,
                d$process,
                pool.sd = FALSE,
                p.adjust.method = "none")

Pairwise comparisons using t tests with non-pooled SD

data:  d$sensitivity and d$process

   P1     P2
P2 0.0096 -
P3 0.0045 0.0870

P value adjustment method: none
```

Posteriors for μ

When

$$Y_{g,i} \overset{ind}{\sim} N(\mu_g, \sigma_g^2),$$

we have

$$\mu_g | y \overset{ind}{\sim} t_{n_g-1}(\overline{y}_g, s_g^2/n_g)$$

and that a draw for μ_g can be obtained by taking

$$\overline{y}_g + T_{n_g-1} s_g / \sqrt{n_g}, \quad T_{n_g-1} \overset{ind}{\sim} t_{n_g-1}(0, 1).$$

```
sims <- bind_rows(
  sims, # groups 1 and 2
  data_frame(
    rep = 1:nr,
    process = "P3",
    mu = sm$mean[3] + rt(nr, df = sm$n[3]-1) * sm$sd[3] / sqrt(sm$n[3]))
)
```

We can use these draws to compare the posteriors

We can obtain posteriors for μ and plot histograms (or smoothed histograms) to compare the posteriors.

```
ggplot(sims, aes(x=mu, y=..density.., fill=process, group=process)) +
  geom_histogram(position = "identity", alpha=0.5, binwidth=0.1) +
  theme_bw()
```
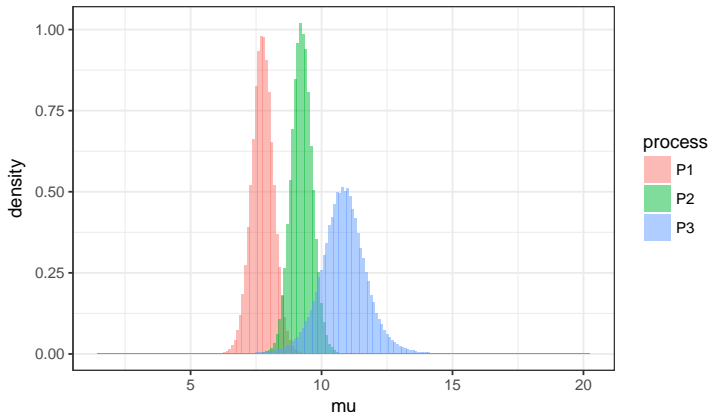
Credible intervals for differences

Use the simulations to calculate posterior probabilities and credible
intervals for differences.

```
# Estimate of the probability that one mean is larger than another
sims %>%
  spread(process, mu) %>%
  mutate(`mu1-mu2` = P1-P2,
         `mu1-mu3` = P1-P3,
         `mu2-mu3` = P2-P3) %>%
  select(`mu1-mu2`,`mu1-mu3`,`mu2-mu3`) %>%
  gather(comparison, diff) %>%
  group_by(comparison) %>%
  summarize(probability = mean(diff>0) %>% round(4),
            lower = quantile(diff, .025) %>% round(2),
            upper = quantile(diff, .975) %>% round(2)) %>%
  mutate(credible_interval = paste("(",lower,",",upper,")", sep="")) %>%
  select(comparison, probability, credible_interval)


# A tibble: 3 x 3
  comparison probability credible_interval
  <chr>            <dbl> <chr>
1 mu1-mu2        0.00590 (-2.63,-0.35)
2 mu1-mu3        0.00370 (-5.06,-1.11)
3 mu2-mu3        0.0493  (-3.56,0.37)
```

Common variance model

In the model

$$Y_{g,i} \overset{ind}{\sim} N(\mu_g, \sigma^2)$$

we can calculate a pvalue for the following null hypothesis:

$$H_0 : \sigma_g = \sigma \, \forall i$$

```
bartlett.test(sensitivity ~ process, data = d)

Bartlett test of homogeneity of variances

data:  sensitivity by process
Bartlett's K-squared = 0.90949, df = 2, p-value = 0.6346
```

This may give us reason to proceed as if the variances is the same in all groups, i.e.

$$Y_{g,i} \overset{ind}{\sim} N(\mu_g, \sigma^2).$$

This assumption is common when the number of observations in the groups is small.

Comparing means when the variances are equal

Assuming $Y_{g,i} \overset{ind}{\sim} N(\mu_g, \sigma^2)$, we can test

$$H_0 : \mu_g = \mu \,\forall\, g$$

```
oneway.test(sensitivity ~ process, data = d, var.equal = TRUE)

One-way analysis of means

data:  sensitivity and process
F = 6.7543, num df = 2, denom df = 60, p-value = 0.002261
```

Then we typically look at pairwise differences, i.e. $H_0 : \mu_k = \mu_{k'}$.

```
pairwise.t.test(d$sensitivity, d$process, p.adjust.method = "none")

Pairwise comparisons using t tests with pooled SD

data:  d$sensitivity and d$process

   P1      P2
P2 0.0116  -
P3 0.0012  0.0720

P value adjustment method: none
```

Posteriors for μ

If $Y_{g,i} \overset{ind}{\sim} N(\mu_g, \sigma^2)$ and we use the prior $p(\mu_1, \ldots, \mu_G, \sigma^2) \propto 1/\sigma^2$, then

$$\mu_g | y, \sigma^2 \overset{ind}{\sim} N(\overline{y}_g, \sigma^2/n_g) \quad \sigma^2 | y \sim IG\left(\frac{n-G}{2}, \frac{1}{2} \sum_{g=1}^{G} \sum_{i=1}^{n_g} (y_{g,i} - \overline{y}_g)^2 \right)$$

where $n = \sum_{g=1}^{G} n_g$. and thus, we obtain joint samples for μ by performing the following

1. $\sigma^{2(m)} \sim p(\sigma^2 | y)$
2. For $g = 1, \ldots, G$, $\mu_g \sim p(\mu_g | y, \sigma^{2(m)})$.

```
nr = 1e5
sims <- data.frame(rep = 1:nr,
  sigma = 1/sqrt( rgamma(nr,
                        shape = sum(sm$n-1)/2,
                        rate = sum((sm$n-1)*sm$sd^2))/2 )) %>%
  mutate(
    mu1 = rnorm(nr, mean = sm$mean[1], sd = sigma / sqrt(sm$n[1])),
    mu2 = rnorm(nr, mean = sm$mean[2], sd = sigma / sqrt(sm$n[2])),
    mu3 = rnorm(nr, mean = sm$mean[3], sd = sigma / sqrt(sm$n[3])))
```

We can use these draws to compare the posteriors

We can obtain posteriors for μ and plot histograms (or smoothed histograms) to compare the posteriors.
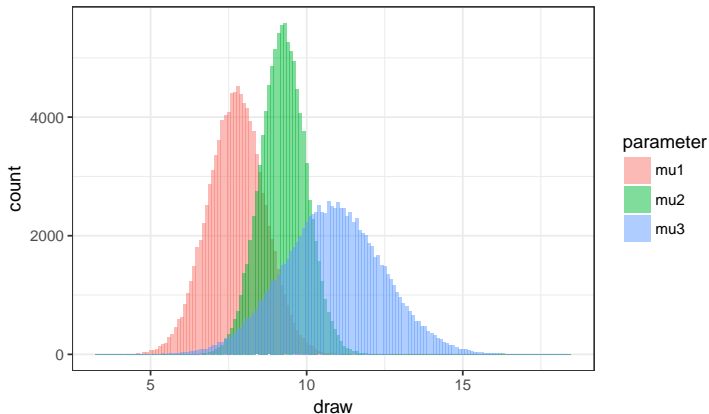
Credible interval for the differences

To compare the means, we compare the samples drawn from the posterior.

```
sims %>%
  mutate(`mu1-mu2` = mu1-mu2,
         `mu1-mu3` = mu1-mu3,
         `mu2-mu3` = mu2-mu3) %>%
  select(`mu1-mu2`,`mu1-mu3`,`mu2-mu3`) %>%
  gather(comparison, diff) %>%
  group_by(comparison) %>%
  summarize(probability = mean(diff>0) %>% round(4),
            lower = quantile(diff, .025) %>% round(2),
            upper = quantile(diff, .975) %>% round(2)) %>%
  mutate(credible_interval = paste("(",lower,",",upper,")", sep="")) %>%
  select(comparison, probability, credible_interval)


# A tibble: 3 x 3
  comparison probability credible_interval
  <chr>            <dbl> <chr>
1 mu1-mu2         0.0986 (-3.8,0.8)
2 mu1-mu3         0.0477 (-6.75,0.57)
3 mu2-mu3         0.181  (-5.09,1.9)
```