

ANOVA

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Review of ANOVA

Analysis of Variance (ANOVA)

For two-level data, ANOVA provides an additive *decomposition of variance*:

$$\text{total variation} = \text{across-group variation} + \text{within-group variation}$$

A typical ANOVA includes

- an estimate of within-group variance;
- an estimate of between-group variance (variance of subpopulation means);
- estimates and tests of contrasts of subpopulation means.

ANOVA decomposition

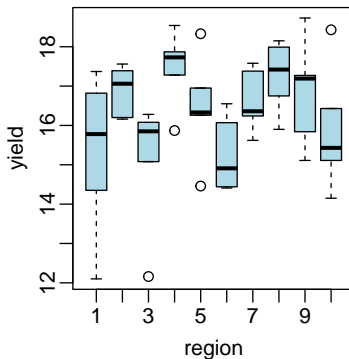
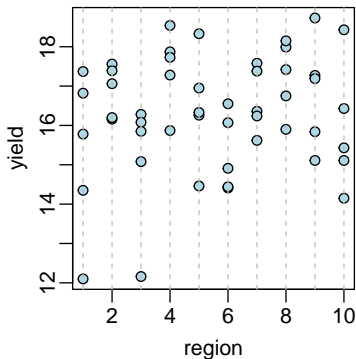
ANOVA estimation

ANOVA inference

One-factor balanced design

Example (wheat yield):

- $m = 10$ regions of land were randomly selected,
- $n = 5$ plots of land were seeded within each region.
- $y_{i,j}$ = the yield of plot i in region j .



ANOVA decomposition

Every observation can be written as equal to

- the grand mean, plus
- the difference between its group mean and the grand mean, plus
- the difference between the observation and the group mean.

$$\begin{aligned} y_{i,j} &= \bar{y}_{..} + (\bar{y}_{.j} - \bar{y}_{..}) + (y_{i,j} - \bar{y}_{.j}) \\ &\equiv \hat{\mu} + \hat{a}_j + \hat{\epsilon}_{i,j}. \end{aligned}$$

ANOVA decomposition

Total		Across		Within
$y_{11} - \bar{y}_{..}$	=	$(\bar{y}_{.1} - \bar{y}_{..})$	+	$(y_{11} - \bar{y}_{.1})$
$y_{21} - \bar{y}_{..}$	=	$(\bar{y}_{.1} - \bar{y}_{..})$	+	$(y_{21} - \bar{y}_{.1})$
.	=	.	+	.
.	=	.	+	.
.	=	.	+	.
$y_{n1} - \bar{y}_{..}$	=	$(\bar{y}_{.1} - \bar{y}_{..})$	+	$(y_{n1} - \bar{y}_{.1})$
$y_{12} - \bar{y}_{..}$	=	$(\bar{y}_{.2} - \bar{y}_{..})$	+	$(y_{12} - \bar{y}_{.2})$
.	=	.	+	.
.	=	.	+	.
.	=	.	+	.
$y_{n2} - \bar{y}_{..}$	=	$(\bar{y}_{.2} - \bar{y}_{..})$	+	$(y_{n2} - \bar{y}_{.2})$
⋮		⋮		⋮
$y_{1m} - \bar{y}_{..}$	=	$(\bar{y}_{.m} - \bar{y}_{..})$	+	$(y_{1m} - \bar{y}_{.m})$
.	=	.	+	.
.	=	.	+	.
.	=	.	+	.
$y_{nm} - \bar{y}_{..}$	=	$(\bar{y}_{.m} - \bar{y}_{..})$	+	$(y_{nm} - \bar{y}_{.m})$
<hr/>				
SST	=	SSA	+	SSW
$mn - 1$	=	$m - 1$	+	$m(n - 1)$

Degrees of freedom

Residual vectors: Each vector $\mathbf{r}_T, \mathbf{r}_A, \mathbf{r}_W$ in the preceding table is of length $N = m \times n$, but lives in a lower-dimensional space:

Total: \mathbf{r}_T lives in an $mn - 1$ dimensional subspace;

Across groups: \mathbf{r}_A has m lives in an $m - 1$ dimensional subspace;

Within groups: \mathbf{r}_W lives in an $mn - m$ dimensional subspace.

These subspace dimensions are known as *degrees of freedom*.

Exercise: Explain the above results.

ANOVA decomposition

$SST = ||\mathbf{r}_T||^2$ = Total sum of squares variation = variation of $y_{i,j}$'s around $\bar{y}_{..}$;

$SSA = ||\mathbf{r}_A||^2$ = Across group variation = variation of \bar{y}_j 's around $\bar{y}_{..}$;

$SSW = ||\mathbf{r}_W||^2$ = Within group variation = variation of $y_{i,j}$'s around \bar{y}_j 's.

Exercise: Show that

- $\mathbf{r}_T = \mathbf{r}_A + \mathbf{r}_W$;
- $\mathbf{r}_T \cdot \mathbf{r}_A = \mathbf{r}_T \cdot \mathbf{r}_W = \mathbf{r}_A \cdot \mathbf{r}_W = 0$.

Sum of squares decomposition: You can show that

$$\begin{array}{rclcl} SST & = & SSA & + & SSW \\ \text{total variation} & = & \text{between group variation} & + & \text{within group variation} \end{array}$$

ANOVA for wheat yield

```
y
## [1] 17.37 15.78 14.35 12.10 16.82 16.16 16.20 17.56 17.39 17.06 16.28 16.08
## [13] 15.08 12.16 15.85 17.87 17.73 15.87 17.28 18.54 18.33 16.26 16.95 16.33
## [25] 14.46 14.41 14.44 14.91 16.55 16.07 16.36 16.24 17.58 17.38 15.62 15.90
## [37] 17.42 17.99 16.75 18.15 17.27 15.84 17.19 15.11 18.73 18.43 15.11 14.15
## [49] 16.43 15.43

g
## [1] 1 1 1 1 1 2 2 2 2 2 3 3 3 3 3 4 4 4 4 4 5 5 5 5 5
## [26] 6 6 6 6 6 7 7 7 7 7 8 8 8 8 8 9 9 9 9 9 10 10 10 10 10

ybGrand<-mean(y)
ybGroup<-tapply(y,g,mean) ; a<-ybGroup-ybGrand

ybGrand
## [1] 16.3064

mean(ybGroup)
## [1] 16.3064

a
## 1 2 3 4 5 6 7 8 9 10
## -1.0224 0.5676 -1.2164 1.1516 0.1596 -1.0304 0.3296 0.9356 0.5216 -0.3964

mean(a)
## [1] -1.776628e-16
```

ANOVA for wheat yield

```
SST<-sum( (y-ybGrand)^2 )
```

```
SST
```

```
## [1] 104.8566
```

```
ybGroup[ g ]
```

```
##      1      1      1      1      1      2      2      2      2      2      3
## 15.284 15.284 15.284 15.284 15.284 16.874 16.874 16.874 16.874 16.874 15.090
##      3      3      3      3      4      4      4      4      4      5      5
## 15.090 15.090 15.090 15.090 17.458 17.458 17.458 17.458 17.458 16.466 16.466
##      5      5      5      6      6      6      6      6      7      7      7
## 16.466 16.466 16.466 15.276 15.276 15.276 15.276 15.276 16.636 16.636 16.636
##      7      7      8      8      8      8      8      9      9      9      9
## 16.636 16.636 17.242 17.242 17.242 17.242 17.242 16.828 16.828 16.828 16.828
##      9     10     10     10     10     10
## 16.828 15.910 15.910 15.910 15.910 15.910
```

```
SSA<-sum( (ybGroup[g]-ybGrand)^2 )
```

```
SSA
```

```
## [1] 33.36831
```

```
n*sum( (ybGroup-ybGrand)^2 )
```

```
## [1] 33.36831
```

```
n*sum(a^2)
```

```
## [1] 33.36831
```

ANOVA for wheat yield

```
SSW<-sum( (y-ybGroup[g])^2 )  
SSW  
  
## [1] 71.48824  
  
SSW+SSA  
  
## [1] 104.8566  
  
SST  
  
## [1] 104.8566
```

ANOVA table

The ANOVA decomposition is usually summarized with an ANOVA table:

<u>source</u>	<u>deg of freedom</u>	<u>SS</u>	<u>MS</u>	<u>F-ratio</u>
across	$m - 1$	SSA	$MSA = SSA / (m - 1)$	MSA / MSW
within	$m(n - 1)$	SSW	$MSW = SSW / m(n - 1)$	
total	$mn - 1$	SST		

```
anova( lm(y~as.factor(g)) )  
  
## Analysis of Variance Table  
##  
## Response: y  
##          Df Sum Sq Mean Sq F value Pr(>F)  
## as.factor(g)  9 33.368   3.7076   2.0745 0.0555 .  
## Residuals    40 71.488   1.7872  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

ANOVA table

```
anova( lm(y~as.factor(g)) )

## Analysis of Variance Table
##
## Response: y
##           Df Sum Sq Mean Sq F value Pr(>F)
## as.factor(g)  9 33.368   3.7076   2.0745 0.0555 .
## Residuals    40 71.488   1.7872
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

SSA

## [1] 33.36831

SSA/(m-1)

## [1] 3.70759

SSW

## [1] 71.48824

SSW/(m*(n-1))

## [1] 1.787206

(SSA/(m-1)) / (SSW/(m*(n-1)))

## [1] 2.074518
```

ANOVA decomposition as a description

The ANOVA decomposition and sums of squares provide

Descriptions of center:

- overall mean: $\bar{y}_{..}$
- group means: $\bar{y}_1, \dots, \bar{y}_m$
- group effects: $\bar{y}_1 - \bar{y}_{..}, \dots, \bar{y}_m - \bar{y}_{..}$

Descriptions of variability:

- across group variability

$$\begin{aligned} \text{SSA} &= \sum_j \sum_i (\bar{y}_j - \bar{y}_{..})^2 \\ &= n \sum_j (\bar{y}_j - \bar{y}_{..})^2 = n \times (m - 1) \times \text{sample variance}(\bar{y}_1, \dots, \bar{y}_m) \end{aligned}$$

- within group variability

$$\text{SSW} = \sum_j \sum_i (y_{i,j} - \bar{y}_j)^2 = \sum_j (n - 1) s_j^2$$

Checking calculations

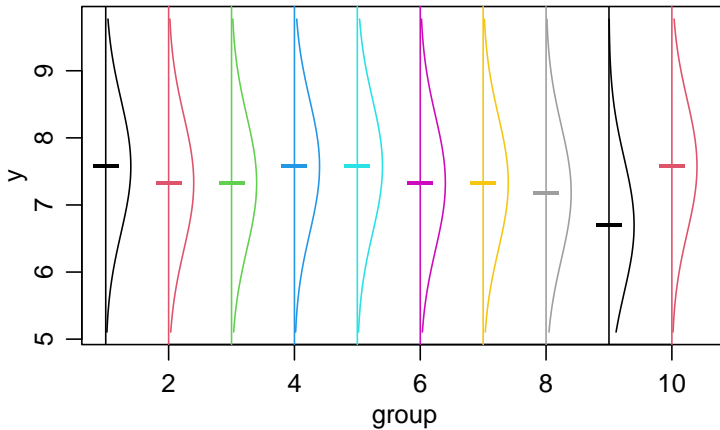
SSA:

```
SSA
## [1] 33.36831
n*(m-1)*var(ybGroup)
## [1] 33.36831
```

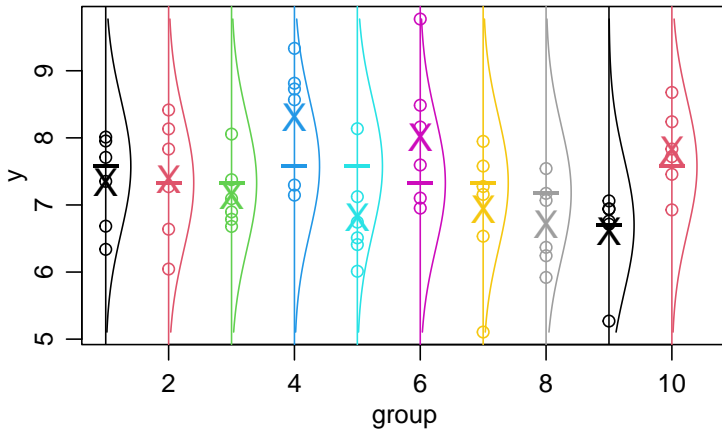
SSW:

```
SSW
## [1] 71.48824
tapply(y,g,var)
##          1          2          3          4          5          6          7          8          9         10
## 4.49173 0.43388 2.88970 0.99197 1.94843 0.95908 0.67748 0.86467 1.96792 2.64720
sum( ( n-1)* tapply(y,g,var) )
## [1] 71.48824
```

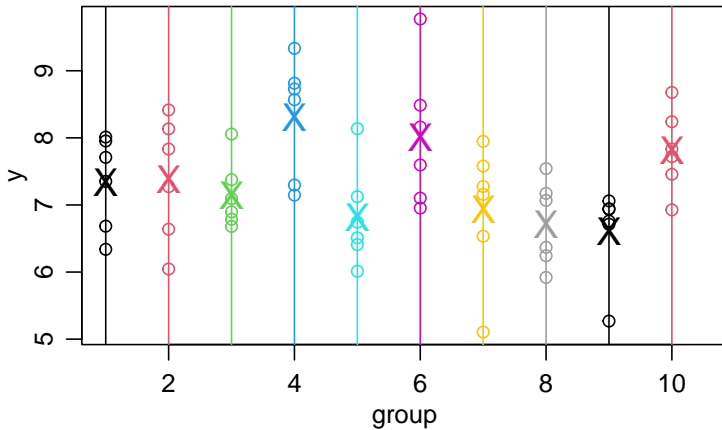
One-way means model



One-way means model



One-way means model



One-way means model

$$y_{i,j} = \mu + a_j + \epsilon_{i,j} \quad (\text{treatment effects model}) , \text{ or}$$

$$y_{i,j} = \theta_j + \epsilon_{i,j} \quad (\text{treatment means model}),$$

where $\theta_j = \mu + a_j$.

- μ is expected yield across all regions;
- θ_j is expected yield from region j ;
- a_j is the deviation of region-specific expected yield from μ ;

$$\theta_j = \mu + a_j \Leftrightarrow a_j = \theta_j - \mu$$

- $\epsilon_{i,j}$ is the deviation of an observed yield from its region-specific expectation.

Identifiability

The standard “ANOVA” model parameterizes things so that

- $\sum_j a_j = 0$ (sum-to-zero side conditions),
- $\{\epsilon_{i,j}\} \sim \text{i.i.d. from some mean-zero distribution.}$

In this case,

$$\begin{aligned} E[y_{i,j} | \mu, a_1, \dots, a_m] &= E[\mu + a_j + \epsilon_{i,j} | \mu, a_1, \dots, a_m] \\ &= E[\mu | \mu, a_1, \dots, a_m] + E[a_j | \mu, a_1, \dots, a_m] + E[\epsilon_{i,j} | \mu, a_1, \dots, a_m] \\ &= \mu + a_j \\ &= \theta_j \end{aligned}$$

If we assume $\{\epsilon_{i,j}\} \sim \text{i.i.d. } N(0, \sigma^2)$, then the model is

$$\begin{aligned} y_{i,j} &\sim N(\mu + a_j, \sigma^2) \text{ or equivalently,} \\ y_{i,j} &\sim N(\theta_j, \sigma^2). \end{aligned}$$

Parameter estimates

Parameters to estimate include

- $\{\theta_1, \dots, \theta_m, \sigma^2\}$, or equivalently
- $\{\mu, a_1, \dots, a_m, \sigma^2\}$

If $\hat{\theta}_j$ is an estimate of θ_j , we say that

- $\hat{y}_{i,j} = \hat{\theta}_j$ is the *fitted value* of $y_{i,j}$;
- $\hat{\epsilon}_{i,j} = y_{i,j} - \hat{y}_{i,j} = y_{i,j} - \hat{\theta}_j$ is the *residual* for $y_{i,j}$.

OLS estimation

The OLS estimates of $\theta_1, \dots, \theta_m$ are the values that minimize SSR :

$$\begin{aligned} SSR(\hat{\theta}_1, \dots, \hat{\theta}_m) &= \sum_{j=1}^m \sum_{i=1}^n (y_{i,j} - \hat{\theta}_j)^2 \\ &= \sum_{i=1}^n (y_{i,1} - \hat{\theta}_1)^2 + \dots + \sum_{i=1}^n (y_{i,m} - \hat{\theta}_m)^2 \end{aligned}$$

Exercise: Show that $\hat{\theta}_j = \bar{y}_j$ is the OLSE/MLE for θ_j .

Note: For $\hat{\theta}_j = \bar{y}_j$, $SSR = SSW$.

OLS estimation

For the “treatment effects” parametrization, we have that

- $\theta_j = \mu + a_j$
- $\sum_j a_j = 0,$

which together imply that

$$\mu = \sum \theta_j / m.$$

So our OLS estimates of $\{\mu, a_1, \dots, a_m\}$ are

$$\hat{\mu} = \sum \hat{\theta}_j / m$$

$$\hat{a}_j = \hat{\theta}_j - \hat{\mu}.$$

Unbiased variance estimation

Recall we assumed that within each group j ,

$$y_{i,j} = \theta_j + \epsilon_{i,j}$$

where the $\epsilon_{i,j}$'s are independent with mean 0 and variance σ^2 .

This implies

- $E[y_{i,j}|\theta_j, \sigma^2] = \theta_j$;
- $\text{Var}[y_{i,j}|\theta_j, \sigma^2] = \sigma^2$;
- $y_{1,j}, \dots, y_{n,j}$ are uncorrelated with each other.

This further implies that the sample variance is an unbiased estimator of σ^2 :

$$s_j^2 = \sum_i (y_{i,j} - \bar{y}_j)^2 / (n - 1)$$

$$E[s_j^2|\theta_j, \sigma^2] = \sigma^2$$

Pooled sample variance

We pool all the sample variances to obtain an unbiased estimate of σ^2 :

$$\begin{aligned}\hat{\sigma}^2 &= (s_1^2 + \cdots + s_m^2)/m \\ E[\sigma^2 | \theta, \sigma^2] &= (E[s_1^2 | \theta, \sigma^2] + \cdots + E[s_m^2 | \theta, \sigma^2])/m \\ &= (\sigma^2 + \cdots + \sigma_m^2)/m = \sigma^2.\end{aligned}$$

Variance estimate via SSW

$$\begin{aligned}SSW &= \sum_{i=1}^n (y_{i,1} - \hat{\theta}_1)^2 + \cdots + \sum_{i=1}^n (y_{i,m} - \hat{\theta}_m)^2 \\ &= \sum_{i=1}^n (y_{i,1} - \bar{y}_1)^2 + \cdots + \sum_{i=1}^n (y_{i,m} - \bar{y}_m)^2 \\ &= (n-1)s_1^2 + \cdots + (n-1)s_m^2\end{aligned}$$

so

$$\hat{\sigma}^2 = SSW/[m(n-1)].$$

The estimate $\hat{\sigma}^2$ is sometimes called the MSW, MSR or MSE.

Wheat yield data

```
## pooled sample variance
```

```
s2groups<-tapply(y,g,var)
```

```
s2groups
```

```
##          1          2          3          4          5          6          7          8          9         10
## 4.49173 0.43388 2.88970 0.99197 1.94843 0.95908 0.67748 0.86467 1.96792 2.64720
```

```
mean(s2groups)
```

```
## [1] 1.787206
```

```
## SSW and MSW
```

```
SSW<-sum( (y-ybGroup[g])^2 ) # was SSW
```

```
SSW
```

```
## [1] 71.48824
```

```
MSW<-SSW/(m*(n-1))
```

```
MSW
```

```
## [1] 1.787206
```

MSW, MSA and the F -statistic

```
anova(lm( y ~ as.factor(g) ))

## Analysis of Variance Table
##
## Response: y
##          Df Sum Sq Mean Sq F value Pr(>F)
## as.factor(g)  9 33.368   3.7076   2.0745 0.0555 .
## Residuals    40 71.488   1.7872
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

MSW<-SSW/(m*(n-1))
MSW

## [1] 1.787206

MSA<-SSA/(m-1)
MSA

## [1] 3.70759

MSA/MSW

## [1] 2.074518
```

Testing for across-group heterogeneity

Model:

$$y_{i,j} = \mu + a_j + \epsilon_{i,j} \quad \{\epsilon_{i,j}\} \sim \text{iid } N(0, \sigma^2)$$

Hypotheses: Consider deciding between the following hypotheses:

$$H_0 : a_j = 0 \text{ for all } j$$

$$H_1 : a_j \neq 0 \text{ for some } j$$

H_0 implies all group means are the same, H_1 implies the opposite.

Statistical inference: How to evaluate H_1 versus H_0 using the observed data?

MSA as a measure of across-group heterogeneity

$$\begin{aligned}SSA &= \sum_{i=1}^n \sum_{j=1}^m (\bar{y}_j - \bar{y})^2 \\&= n \times \sum_{j=1}^m (\bar{y}_j - \bar{y})^2 \\MSA &= SSA / (m - 1) \\&= n \times \sum_{j=1}^m (\bar{y}_j - \bar{y}_{..})^2 / (m - 1) \\&= n \times \text{sample variance}(\bar{y}_1, \dots, \bar{y}_m)\end{aligned}$$

because the average of the \bar{y}_j 's is $\bar{y}_{..}$.

MSA as a measure of across-group heterogeneity

$$\begin{aligned}E[\bar{y}_j] &= \mu + a_j \\ \bar{y}_j &\approx \mu + a_j\end{aligned}$$

$$\begin{aligned}\text{sample variance}(\bar{y}_1, \dots, \bar{y}_m) &\approx \text{sample variance}(\mu + a_1, \dots, \mu + a_m) \\ &= \text{sample variance}(a_1, \dots, a_m) \\ &= \frac{1}{m-1} \sum a_j^2\end{aligned}$$

Intuitively,

$$H_0 \text{ true} \Leftrightarrow \frac{1}{m-1} \sum a_j^2 = 0 \Leftrightarrow \text{small MSA}$$

$$H_1 \text{ true} \Leftrightarrow \frac{1}{m-1} \sum a_j^2 > 0 \Leftrightarrow \text{large MSA}$$

Expected mean squares

$$\begin{aligned}MSA &= n \times \text{sample variance}(\bar{y}_1, \dots, \bar{y}_m) \\&\approx n \times \text{sample variance}(a_1, \dots, a_m) \\&= n \times \frac{1}{m-1} \sum a_j^2\end{aligned}$$

More precisely, one can show that

$$E[MSA] = \sigma^2 + n \times \frac{1}{m-1} \sum a_j^2,$$

where the σ^2 comes from the fact that \bar{y}_j only approximates a_j .

Letting $\tau^2 = \frac{1}{m-1} \sum a_j^2$, we have

$$E[MSG] = \sigma^2 + n \times \tau^2,$$

where τ^2 is the *across-group variability* - the “empirical” variance of a_1, \dots, a_m .

Testing across-group variability

How can we use MSA to evaluate $H_0 : \tau^2 = 0$?

Idea:

$$MSA \approx \sigma^2 \Rightarrow \tau^2 \text{ is small or zero} \Rightarrow \text{accept } H_0$$

$$MSA > \sigma^2 \Rightarrow \tau^2 \text{ is not zero} \Rightarrow \text{accept } H_1$$

Problem: We don't know what σ^2 is.

Solution: Compare MSA to an estimate of σ^2 .

Testing across-group variability

We have shown that

$$\begin{aligned}MSW &= SSW/m(n-1) = \frac{1}{m(n-1)} \sum_j \sum_i (y_{i,j} - \bar{y}_j)^2 \\&= \frac{1}{m} \sum_j s_j^2 \\E[MSW] &= \sigma^2.\end{aligned}$$

Under H_0 and H_1 :

$$\begin{aligned}E[MSA] &= \sigma^2 + n \times \tau^2 \\E[MSW] &= \sigma^2\end{aligned}$$

Under H_0 only:

$$\begin{aligned}E[MSA] &= \sigma^2 \\E[MSW] &= \sigma^2\end{aligned}$$

The F -statistic and distribution

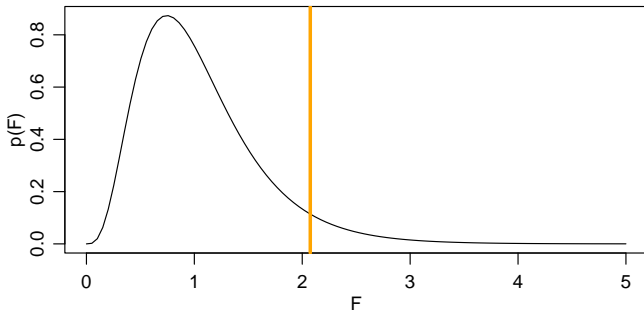
Let $F = MSA/MSW$. Then

under H_0 , MSA/MSW should be around 1,

under H_1 , MSA/MSW should be bigger than 1.

Under the normal model $y_{1,1}, \dots, y_{n,m} \sim \text{i.i.d. } N(\mu, \sigma^2)$,

$$MSA/MSW = F \sim F_{m-1, m(n-1)}.$$



Classical testing for across-group heterogeneity

- We expect an $F_{m-1, m(n-1)}$ -distribution under H_0 .
- We observe $F(\mathbf{y}) = MSA/MSW$.
- Discrepancy between $F_{m-1, m(n-1)}$ and $F(\mathbf{y})$ is evidence against H_0 .

$$p\text{-value} = \Pr(F_{m-1, m(n-1)} \geq F(\mathbf{y}))$$

```
MSA<-SSA/(m-1)
MSW<-SSW/(m*(n-1))
MSA/MSW

## [1] 2.074518

1-pf( MSA/MSW, m-1, m*(n-1))

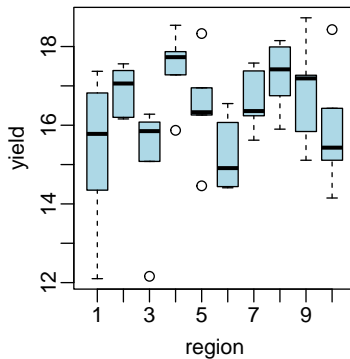
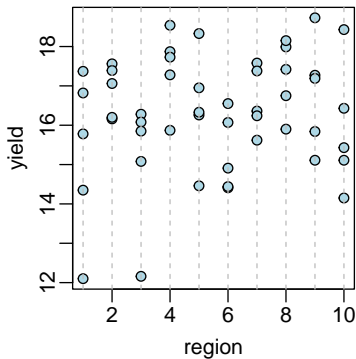
## [1] 0.05550019
```

ANOVA table

```
anova(lm(y~as.factor(g)))  
  
## Analysis of Variance Table  
##  
## Response: y  
##          Df Sum Sq Mean Sq F value Pr(>F)  
## as.factor(g)  9 33.368   3.7076   2.0745 0.0555 .  
## Residuals    40 71.488   1.7872  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Group comparisons

If $H : \tau^2 = 0$ is rejected, which groups are likely different from each other?



Confidence intervals and pairwise comparisons

Under the normal model,

$$\bar{y}_j \sim N(\theta_j, \sigma^2/n)$$

Based on this result,

$$c_j(\mathbf{y}) = \bar{y}_j \pm t_{1-\alpha/2, m(n-1)} \times \sqrt{\hat{\sigma}^2/n}$$

is a $1 - \alpha$ confidence interval for θ_j . This means

$$\Pr(\theta_j \in c_j(\mathbf{y}) | \theta_1, \dots, \theta_m, \sigma^2) = 1 - \alpha,$$

where the probability is over the data \mathbf{y} .

Confidence intervals and pairwise comparisons

Similarly, under the normal model,

$$\bar{y}_j - \bar{y}_k \sim N(\theta_j - \theta_k, 2\sigma^2/n)$$

Confidence interval: A $1 - \alpha$ confidence interval for $\theta_j - \theta_k$ is

$$c_{j,k}(\mathbf{y}) = (\bar{y}_j - \bar{y}_k) \pm t_{1-\alpha/2, m(n-1)} \times \sqrt{2\hat{\sigma}^2/n}$$

Two-sample t -test: The hypothesis $H_{j,k} : \theta_j = \theta_k$ is rejected at level α if

$$t_{j,k} = \frac{|\bar{y}_j - \bar{y}_k|}{\sqrt{2\hat{\sigma}^2/n}} > t_{1-\alpha/2, m(n-1)}.$$

Wheat yield example

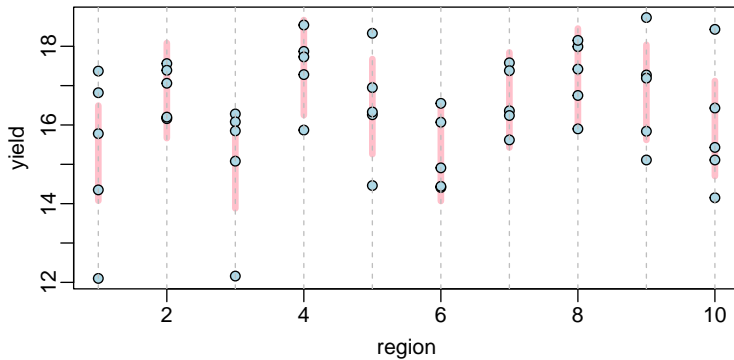
```
## using confint
fit<-lm( y ~ -1+as.factor(g) )
ciTheta<-confint(fit)
ciTheta

##              2.5 %    97.5 %
## as.factor(g)1 14.07567 16.49233
## as.factor(g)2 15.66567 18.08233
## as.factor(g)3 13.88167 16.29833
## as.factor(g)4 16.24967 18.66633
## as.factor(g)5 15.25767 17.67433
## as.factor(g)6 14.06767 16.48433
## as.factor(g)7 15.42767 17.84433
## as.factor(g)8 16.03367 18.45033
## as.factor(g)9 15.61967 18.03633
## as.factor(g)10 14.70167 17.11833

## "by hand"
s2hat<-anova(fit)[2,3]
mean(y[g==3]) + c(-1,1)*qt(.975,m*(n-1))*sqrt(s2hat/n)

## [1] 13.88167 16.29833
```


Wheat yield example



Wheat yield example

```
wheat.compare<-agricolae::LSD.test(aov(y~as.factor(g)),"as.factor(g)")
wheat.compare$means
```

##		y	std	r	se	LCL	UCL	Min	Max	Q25	Q50	Q75
## 1	15.284	2.1193702	5	0.5978639	14.07567	16.49233	12.10	17.37	14.35	15.78	16.82	
## 10	15.910	1.6270218	5	0.5978639	14.70167	17.11833	14.15	18.43	15.11	15.43	16.43	
## 2	16.874	0.6586957	5	0.5978639	15.66567	18.08233	16.16	17.56	16.20	17.06	17.39	
## 3	15.090	1.6999118	5	0.5978639	13.88167	16.29833	12.16	16.28	15.08	15.85	16.08	
## 4	17.458	0.9959769	5	0.5978639	16.24967	18.66633	15.87	18.54	17.28	17.73	17.87	
## 5	16.466	1.3958617	5	0.5978639	15.25767	17.67433	14.46	18.33	16.26	16.33	16.95	
## 6	15.276	0.9793263	5	0.5978639	14.06767	16.48433	14.41	16.55	14.44	14.91	16.07	
## 7	16.636	0.8230917	5	0.5978639	15.42767	17.84433	15.62	17.58	16.24	16.36	17.38	
## 8	17.242	0.9298763	5	0.5978639	16.03367	18.45033	15.90	18.15	16.75	17.42	17.99	
## 9	16.828	1.4028257	5	0.5978639	15.61967	18.03633	15.11	18.73	15.84	17.19	17.27	

```
wheat.compare$groups
```

##		y	groups
## 4	17.458		a
## 8	17.242		a
## 2	16.874		ab
## 9	16.828		ab
## 7	16.636		abc
## 5	16.466		abc
## 10	15.910		abc
## 1	15.284		bc
## 6	15.276		bc
## 3	15.090		c