



Department of  
Primary Industries and  
Regional Development

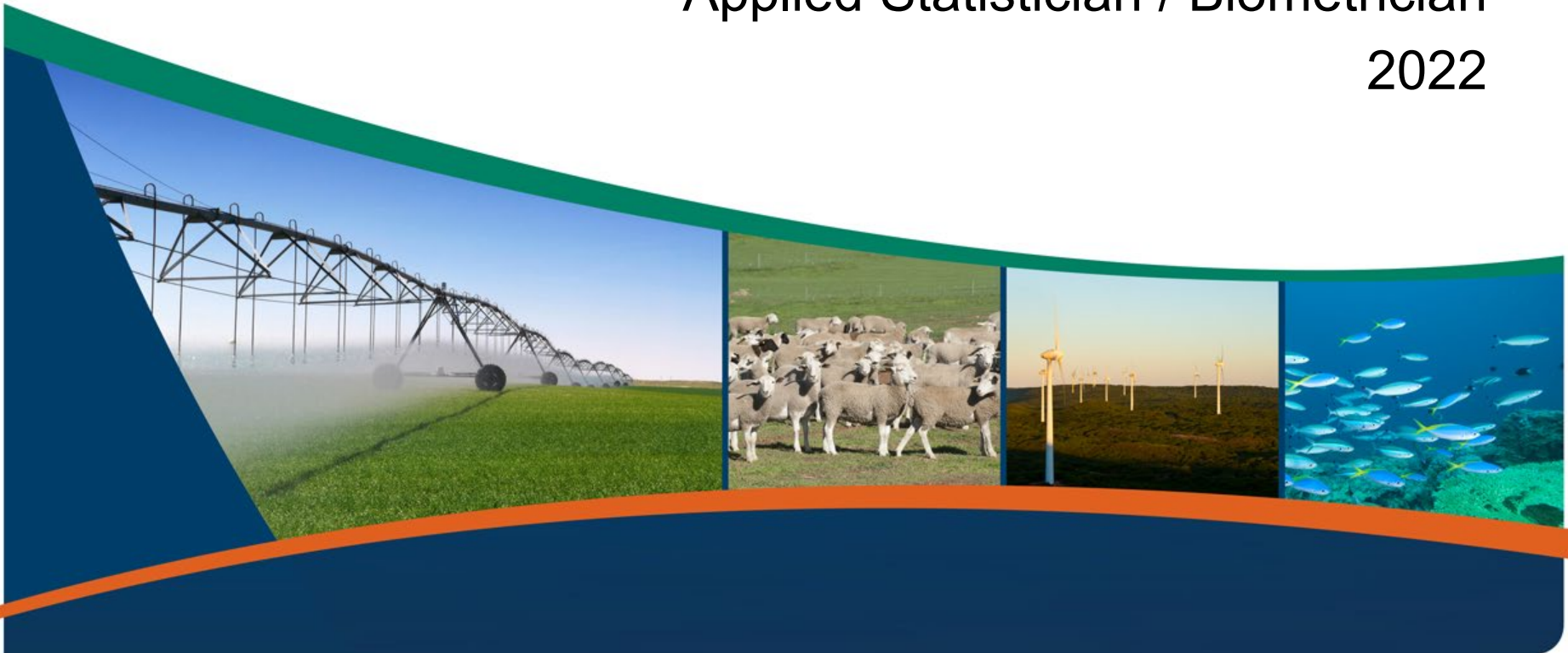


# Analysing Trial Results

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# Example dataset

- **Treatments: Deep rip (DR), Shallow rip (SR), Nil Control (Nil)**



# Analysis

- **ANOVA – Analysis of Variance**
  - Objective tool for assessing treatment differences
  - Gives a p-value – probability value related to treatments:
    - $p < 0.05$  indicating >95% confidence that treatment effects are real
- **Software options:**
  - Genstat – best tool, but there is an annual licence (maybe about \$1000)
  - R – free, but not so easy to use
  - Excel – unable to do what is required

# Analysis in Genstat

- Demonstration...
- Output:

## Analysis of variance (adjusted for covariate)

Variate: Yield  
Covariate: Plot

Source of variation	<u>df</u>	<u>s.s.</u>	<u>m.s.</u>	<u>v.r.</u>	<u>cov.ef</u>	F pr.
Treatment	2	0.32667	0.16333	4.75	1.00	0.070
Covariate	1	0.54150	0.54150	15.76		0.011
Residual	5	0.17183	0.03437		3.46	
Total	8	1.04000				

## Tables of means (adjusted for covariate)

Treatment	Control	Deep Rip	Shallow Rip
	2.067	2.533	2.300

## Least significant differences of means (5% level)

l.s.d.                      0.3891

# Analysis in Genstat

- Treatment comparison summaries:

## Fisher's unprotected least significant difference test

Comparison	Difference	Lower 95%	Upper 95%	t	Probability	Significant
Control vs Shallow Rip	-0.2333	-0.6224	0.1558	-1.542	0.1838	no
Control vs Deep Rip	-0.4667	-0.8558	-0.0776	-3.083	0.0274	yes
Shallow Rip vs Deep Rip	-0.2333	-0.6224	0.1558	-1.542	0.1838	no

	Mean	
Control	2.067	a
Shallow Rip	2.300	ab
Deep Rip	2.533	b

# Analysis in R

## Code:

```
install.packages("agricolae")
library("agricolae")
setwd('C:/FolderwithCsvFile')
Data<-read.csv('Example.csv')
model<-aov(Yield~Treatment+Plot,data=Data)
summary(model)
LSD.test(model,"Treatment",console=T)
```

## Output:

```
> model<-aov(Yield~Treatment+Plot,data=Data)
> summary(model)
              Df Sum Sq Mean Sq F value Pr(>F)
Treatment     2  0.3267   0.1633   4.753 0.0698 .
Plot           1  0.5415   0.5415  15.757 0.0106 *
Residuals     5  0.1718   0.0344
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> LSD.test(model,"Treatment",console=T)

Study: model ~ "Treatment"

LSD t Test for Yield

Mean Square Error:  0.03436667

Treatment, means and individual ( 95 %) CI

      Yield      std r      LCL      UCL Min Max
Control  2.066667  0.1154701  3  1.791536  2.341798  2.0  2.2
Deep Rip  2.533333  0.5507571  3  2.258202  2.808464  1.9  2.9
Shallow Rip 2.300000  0.2000000  3  2.024869  2.575131  2.1  2.5

Alpha: 0.05 ; DF Error: 5
Critical value of t: 2.570582

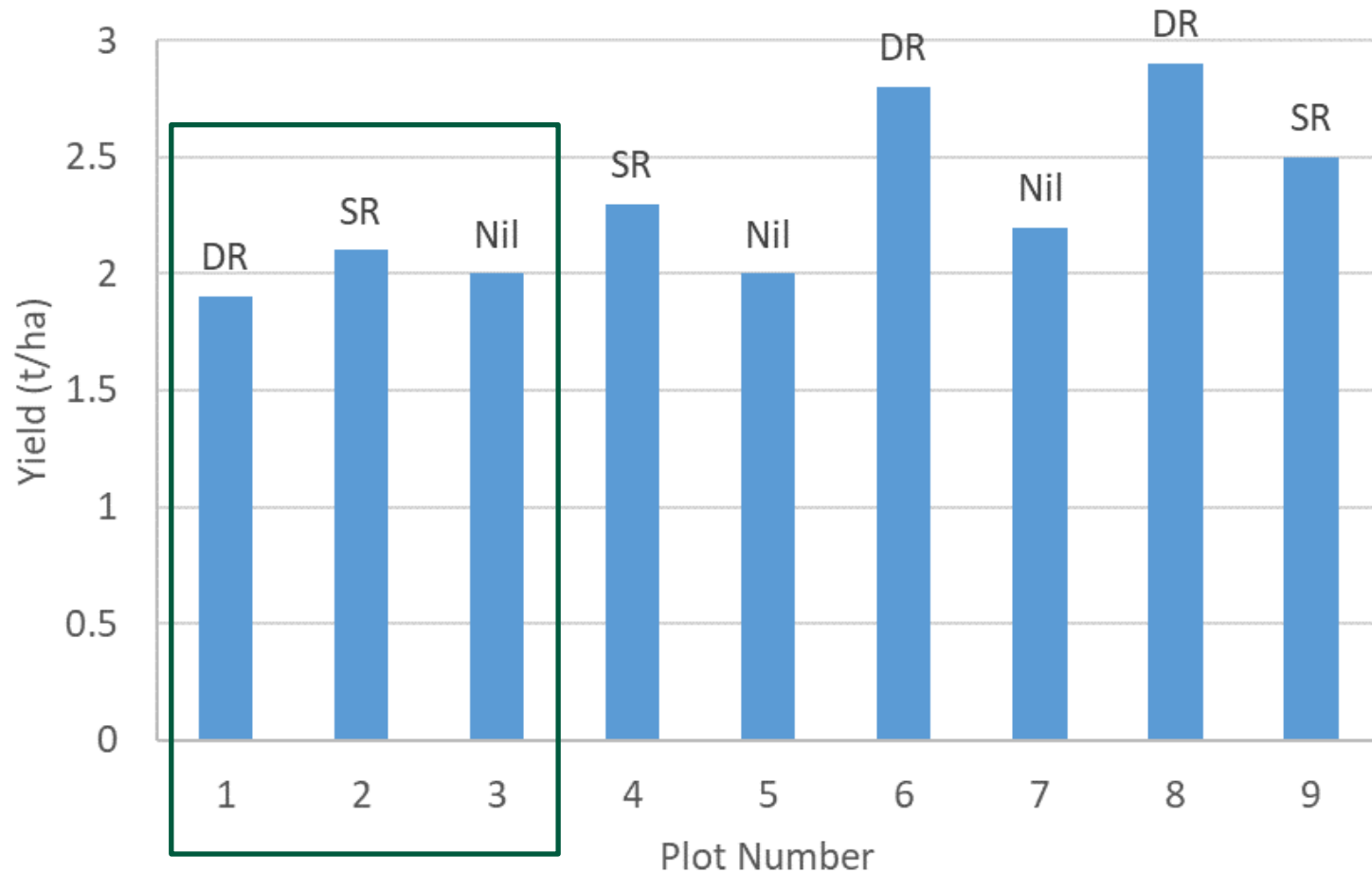
Least significant Difference: 0.389094

Treatments with the same letter are not significantly different.

      Yield groups
Deep Rip  2.533333  a
Shallow Rip 2.300000  ab
Control  2.066667  b
```

# Importance of replication

- What might we have concluded if we only did Rep 1?



# Analysis Support

- **recommend getting maximum value by consulting a biometrician**
  - DPIRD contact: Andrew van Burgel
  - SAGI (“Statistics for the Australian Grains Industry”)
- **Questions?**



# Thank you

Visit [dpird.wa.gov.au](http://dpird.wa.gov.au)

## **Important disclaimer**

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