

Analysis of rating scale data using Aligned Rank Transform ANOVA

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Background

The severity of injuries caused by diseases and pests on crops is often assessed using an ordinal rating scale with each class representing a defined range of values or description of symptoms. Scores increase with severity but the magnitude of differences between classes are uneven and cannot be usually quantified especially when descriptions are used. The underlying assumptions of normality and homogeneous variances are often violated when data based on rating scale are analyzed. For scores that correspond to a range of values, it is usually recommended to convert each score to the midpoint of the range prior to data analysis using parametric tests (Madden et al., 2007). Mann-Whitney U test and Kruskal-Wallis test or Friedman test are used for comparing two and more than two treatments respectively, but these tests cannot handle multiple factors. Several rank-based tests have been used and recommended for multiple factors (Shah and Madden, 2004; Madden et al., 2007b) but these are rarely used due to complexity. Aligned Rank Transform (ART) ANOVA was introduced as a relatively simple, nonparametric test for designed experiments involving multiple factors (Higgins et al., 1990). We illustrate its use by analyzing the scores for the rating of root galling caused by *Meloidogyne graminicola*, the rice root-knot nematode, where 0 = no root galls, 1 = trace infection with a few small galls, 2 = < 25%, 3 = 25–50%, 4 = 51–75%, and 5 = > 75% of roots galled (Hussey and Janssen, 2002).

Methodology

The general procedure for conducting ART ANOVA for a two-factor experimental design is shown in the figure below. The analysis involves a preprocessing step called align rank transform procedure. Aligning the response variable is done by taking the means of all values and effects (factors A and B and their interaction) and then removing all effects except the effect to be tested. The next step is taking the rank average of aligned values by ranking the data where the same values get an average rank. This process can be performed using the ARTool program (Wobbrock et al., 2011) or The Real Statistics Resource Pack (Zaiontz, 2023). The generated aligned ranked values are then analyzed using the classic parametric ANOVA appropriate for the experimental design. ART ANOVA is recommended for rating scale data with more than five classes and randomized complete block designs (RCBD). For a two-factor experiment, the results of the three ANOVAs are combined. Only the results for the effect of interest and the associated error term from each ANOVA are considered in the combined ANOVA to individually test the effects.

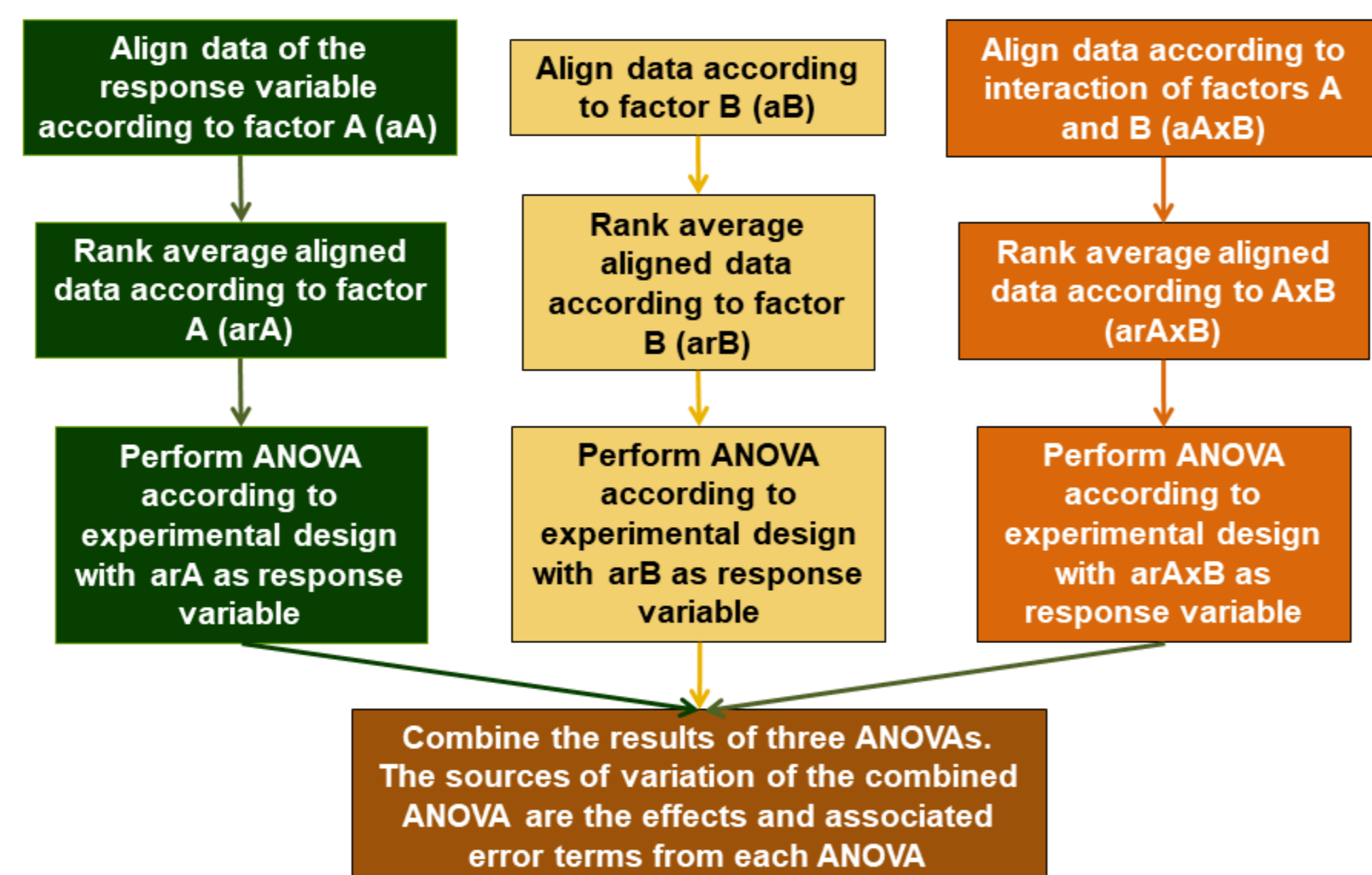


Figure. General procedure for conducting ART ANOVA for two-factor experiments.

Results

Table 1 shows the results of an experiment conducted at IRRI with genotype and initial population of the second infective stage (J2) of *M. graminicola* as factors. The experiment was arranged in a factorial RCBD design with six replications. Root galling was assessed at harvest using the rating scale as described. Actual score, the midpoint and the arcsine transformed values strongly deviate from normal distribution (Kolmogorov-Smirnov test statistic = 0.970, 1.00, and 0.713, respectively; p -value < 2.2e-16) indicating the suitability of using ART ANOVA. Classic parametric ANOVA shows significant effect of genotype on root galling, whereas ART ANOVA shows the significant effects of genotype and initial J2 population.

Table 1. Results of classic RCBD based on non-transformed and transformed values and ART ANOVA.

Source of variation	df	Actual score		Range midpoint		Arcsine-transformed range midpoint		Aligned and ranked score	
		F value	p -value	F value	p -value	F value	p -value	F value	p -value
J2 popn	2	0.96	0.384	1.09	0.599	1.08	0.579	6.01	0.003
Genotype	14	41.24	1e-53	38.06	1e-09	49.23	2e-09	14.59	2e-24
J2 popn x Genotype	28	0.67	0.899	0.68	0.933	0.69	0.933	0.76	0.802

Table 2 shows the results of analyzing a fictitious data from a split plot in RCBD design with water regime as main plot and genotype as subplot. The data were intentionally created in such a way that root galling scores of genotypes differed between water regimes. ART ANOVA shows a significant interaction between water regime and genotype which is not shown with the use of classic split plot ANOVA. The latter results in a misleading conclusion that root galling in all genotypes is the same in all water regimes and vice versa.

Table 2. Results of classic and ART ANOVAs for a split-plot design.

Source of variation	df	Actual score		Aligned and ranked score	
		F value	p -value	F value	p -value
Water regime (WR)	2	40.83	6e-05	68.57	9e-06
Variety (Var)	5	12.17	4e-08	17.14	2e-10
WR x Var	10	1.85	0.072	2.27	0.025

Discussion and conclusion

ART ANOVA should be considered in the analysis of rating scale data. It appears to be more powerful than classic ANOVA in detecting main and interaction effects and reducing type II error (falsely accepting that there are no treatment effects).

Literature cited

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