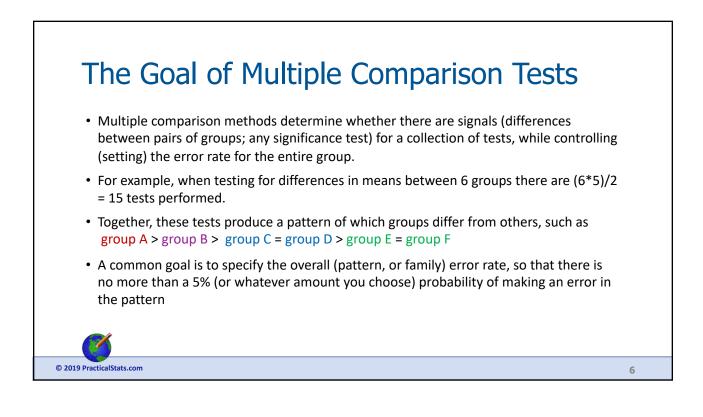


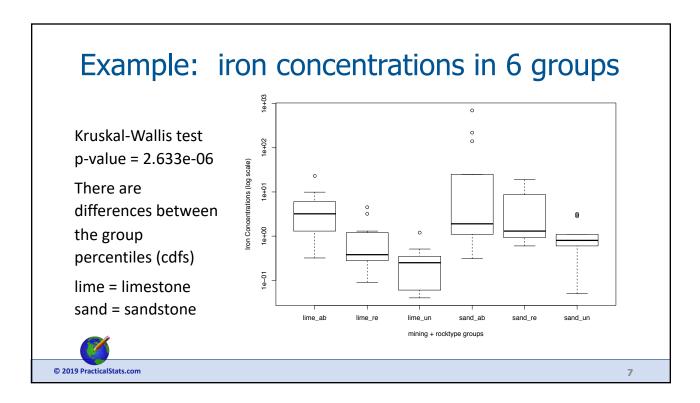
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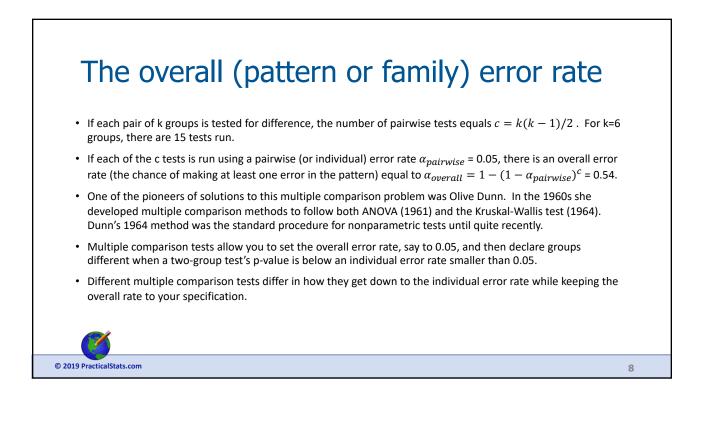
Why Multiple Comparison Tests? When are They Used?

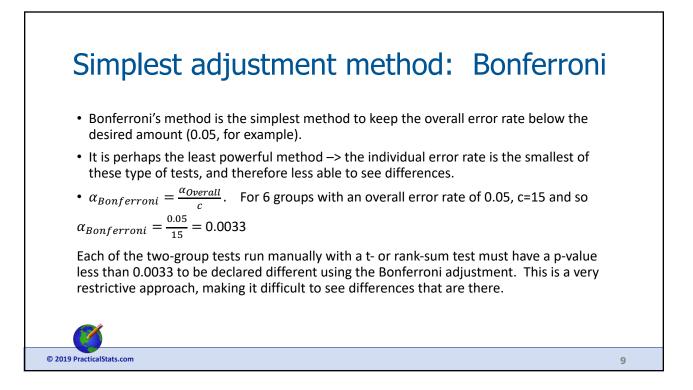
- After Analysis of Variance (ANOVA) and the Kruskal-Wallis (K-W) tests. These two tests do not determine which groups differ from others. Multiple comparison tests come along afterwards to determine which groups differ from others, with the goal of setting the probability of making an error in the pattern of group orderings equal to the alpha level used in the ANOVA or K-W test.
- To control the site-wide false positive rate. At a ground water monitoring site, perhaps 10 different chemicals at 8 wells are tested over time to see if concentrations remain below the legal standard. This requires performing 10*8=80 tests. If each test were run at an alpha = 0.05, there would be a 98% probability that at least 1 test was a false positive, so falsely requiring remediation. Multiple comparison procedures are adopted to set the probability of false positives across the entire site.
- Trend analysis at many sites in a region or any situation where there are multiple tests being run as a group, if each is run with a specific alpha false positive rate such as 5%, the overall error rate for the entire group is much higher. Using the adjustments from multiple comparison tests allow the scientist to set the overall false positive rate for the entire group (entire region / collection of sites / all seasons, etc.)

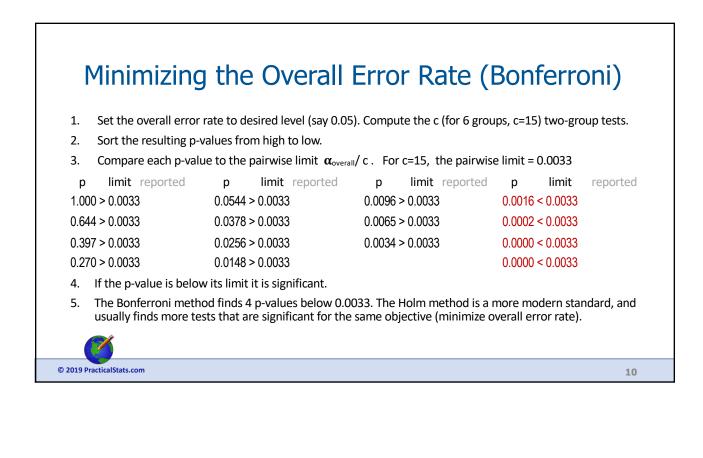


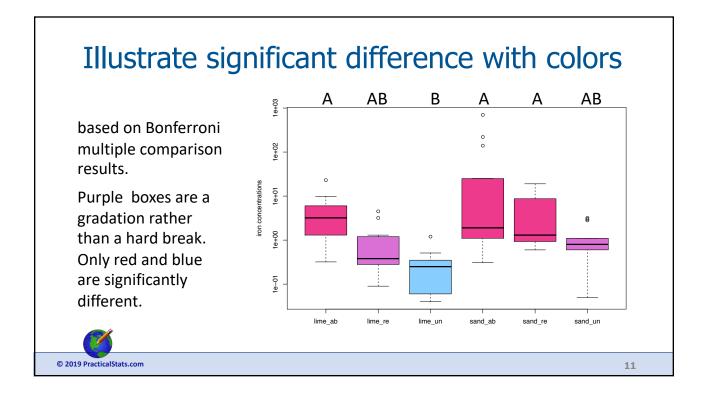


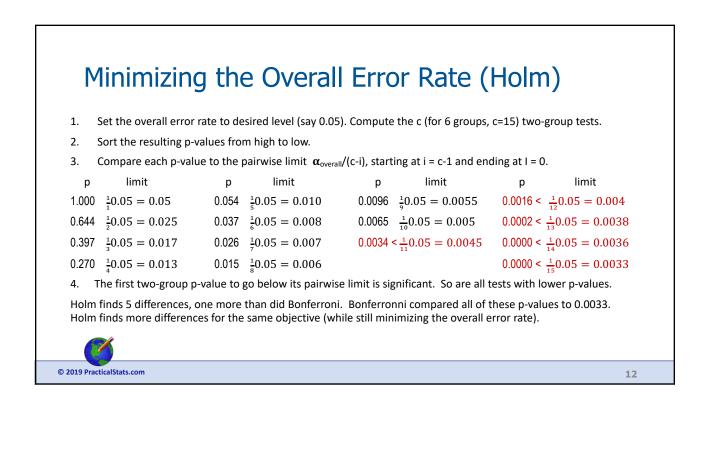












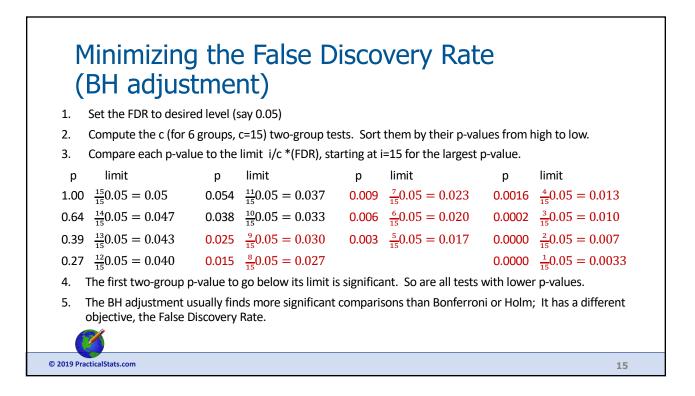
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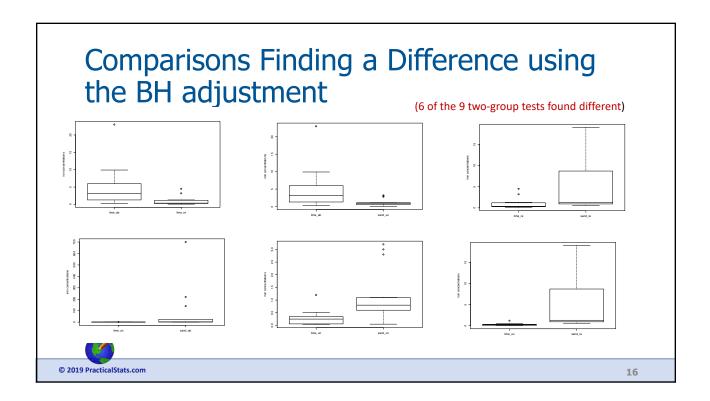
Issues with Multiple Comparison Tests

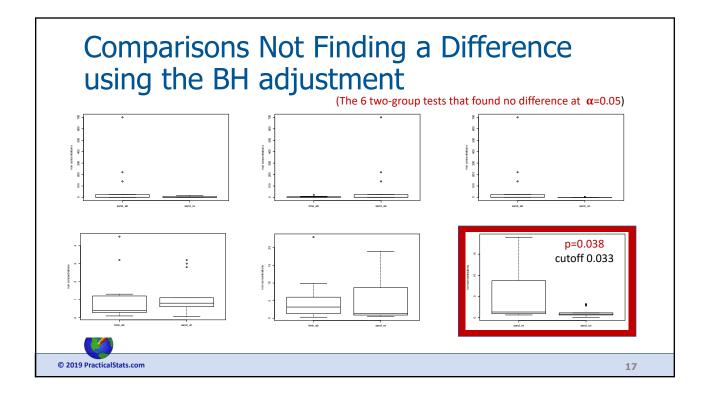
- Earliest tests in the 1950s and 1960s (Duncan's, Least Significant Range tests) set individual error rates, and did not control (set) the overall error rate, which could get quite high.
- Some common tests assume normality for each of the groups (Tukey's, Dunn's following ANOVA). This is rarely true. Non-normality results in lower ability (power) to see the differences with parametric tests.
- Controlling the overall error rate (probability of making at least one error in the pattern) costs power if the adjustment (especially Bonferroni) is not efficient at getting down to the individual error rate, so differences may not be seen. These adjustments (particularly Holm's) have been the standard tests until recently but their loss of power has led to some people recommending not to use them.
- For example, in analysis of microarray gene expression data researchers sometimes perform as many as hundreds to thousands of comparison tests. A Bonferroni adjustment would require pairwise error rates of 0.00001 or smaller, making it extremely unlikely that any significant differences present would be seen.

What's new? Is the Overall Error Rate the best objective?

- Often the overall error rate is not the main issue. The primary interest is often whether an erroneous rejection, a false statement of difference or "false discovery", is made.
- This is a subset of the overall error rate, which was the probability of "making at least one error in the pattern".
- Minimizing only false positives is called the False Discovery Rate (FDR), measured using the Benjamini-Hochberg (BH) adjustment from their paper in 1995.
- The FDR provides a large gain in the power of seeing differences, as compared to the overall error rate used by Bonferroni or Holm adjustments.
- The increase in power by setting the FDR instead of the overall error rate usually results in a larger number of significant differences. It does not control the number of false no-differences. As there are usually fewer observed no-differences using the FDR, this often seems unimportant in comparison to obtaining more power to see differences.



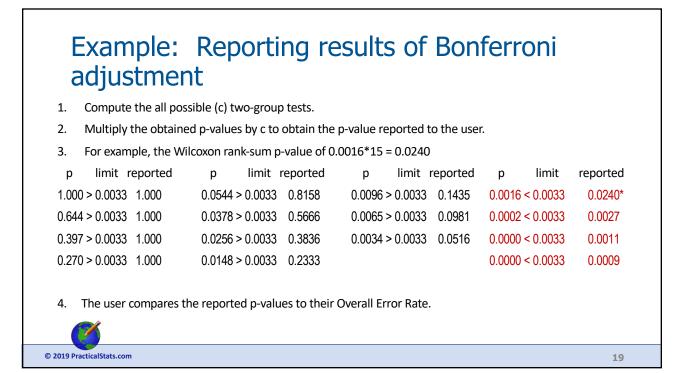


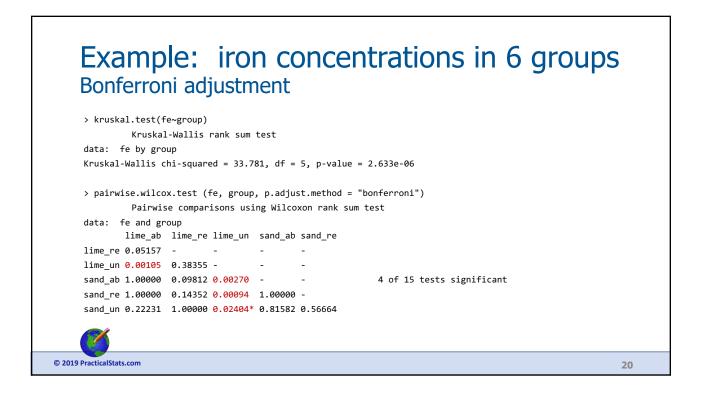


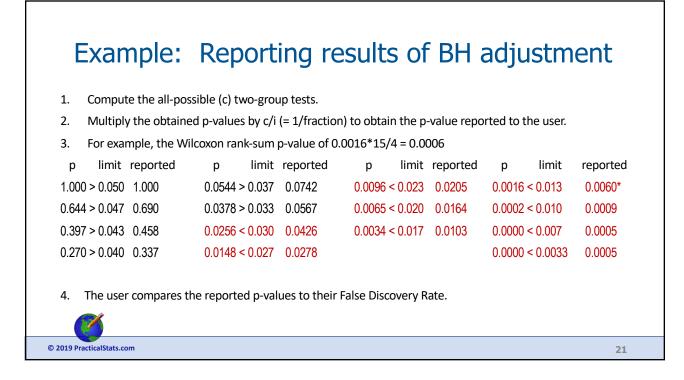
Reporting results of multiple comparison tests

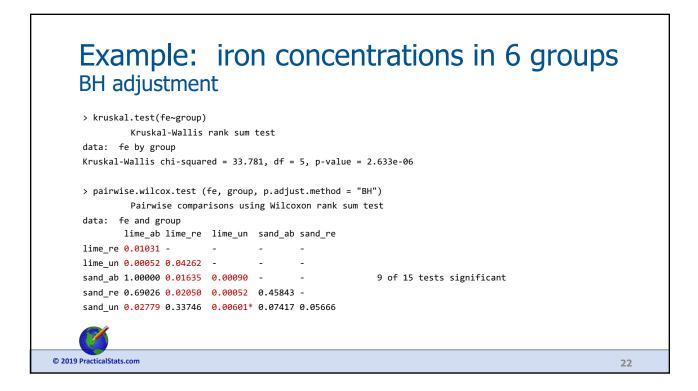
- 1. Each two-group test's p-value is re-scaled by software before reporting it to the user, so that the user can compare its value to their overall error or false discovery rate (say of 0.05).
- 2. For example, individual p-values for c=15 tests were all compared to Bonferroni's 0.05/15 = 0.0033 are multiplied by 15 before reporting them back to the user. A p-value just under 0.0033 would therefore be reported as just under 0.05. The user then compares the reported p-values to their overall error rate. So the highest significant p-value of 0.0016 would be reported in the output as p = 0.0016*15, or 0.024, to compare to the overall error rate.
- 3. BH p-values are multiplied by the 1/fraction used to adjust the FDR. In our example for the first significant p-value, the fractional multiplier of 9/15 becomes a multiplier of 15/9 = 1.667. The obtained p-value of 0.0256 is then reported as 0.0256*1.667 = 0.0426 to the user, who compares it to their false discovery rate of 0.05.
- 4. These re-adjusted p-values are often reported to the user in a triangular matrix.

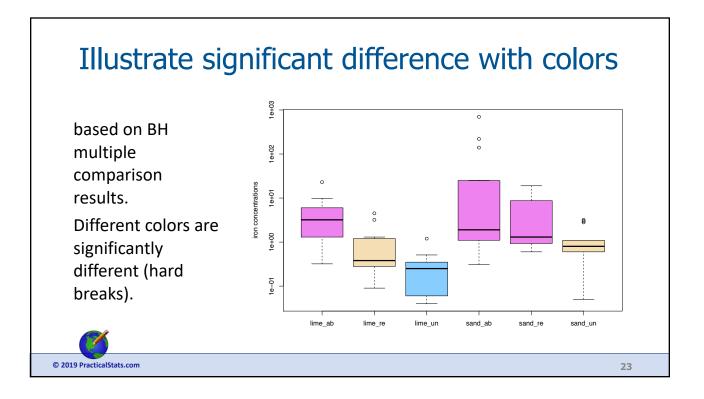












Example: iron concentrations in 6 groups Holm adjustment > kruskal.test(fe~group) Kruskal-Wallis rank sum test data: fe by group Kruskal-Wallis chi-squared = 33.781, df = 5, p-value = 2.633e-06 > pairwise.wilcox.test (fe, group, p.adjust.method = "holm") Pairwise comparisons using Wilcoxon rank sum test data: fe and group lime_ab lime_re lime_un sand_ab sand_re lime_re 0.03782 -lime_un 0.00098 0.17899 -. sand_ab 1.00000 0.06541 0.00234 -5 of 15 tests significant sand re 1.00000 0.08611 0.00094 1.00000 sand un 0.11857 1.00000 0.01923 0.27194 0.22666 © 2019 PracticalStats.com 24

