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Autore	Good Phillip I
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Nota di contenuto	; Machine generated contents note: ; 1. Very Large Arrays -- ; 1.1. Applications -- ; 1.2. Problems -- ; 1.3. Solutions -- ; 2. Permutation Tests -- ; 2.1. Two-Sample Comparison -- ; 2.1.1. Blocks -- ; 2.2. k-Sample Comparison -- ; 2.3. Computing The p-Value -- ; 2.3.1. Monte Carlo Method -- ; 2.3.2. An R Program -- ; 2.4. Multiple-Variable Comparisons -- ; 2.4.1. Euclidean Distance Matrix Analysis -- ; 2.4.2. Hotelling's T2 -- ; 2.4.3. Mantel's U -- ; 2.4.4. Combining Univariate Tests -- ; 2.4.5. Gene Set Enrichment Analysis -- ; 2.5. Categorical Data -- ; 2.6. Software -- ; 2.7. Summary -- ; 3. Applying the Permutation Test -- ; 3.1. Which Variables Should Be Included? -- ; 3.2. Single-Value Test Statistics -- ; 3.2.1. Categorical Data -- ; 3.2.2. A Multivariate Comparison Based on a Summary Statistic -- ; 3.2.3. A Multivariate Comparison Based on Variants of Hotelling's T2

; 3.2.4. Adjusting for Covariates -- ; 3.2.5. Pre-Post Comparisons -- ; 3.2.6. Choosing a Statistic: Time-Course Microarrays -- ; 3.3. Recommended Approaches -- ; 3.4. To Learn More -- ; 4. Biological Background -- ; 4.1. Medical Imaging -- ; 4.1.1. Ultrasound -- ; 4.1.2. EEG/MEG -- ; 4.1.3. Magnetic Resonance Imaging -- ; 4.1.3.1. MRI -- ; 4.1.3.2. fMRI -- ; 4.1.4. Positron Emission Tomography -- ; 4.2. Microarrays -- ; 4.3. To Learn More -- ; 5. Multiple Tests -- ; 5.1. Reducing the Number of Hypotheses to Be Tested -- ; 5.1.1. Normalization -- ; 5.1.2. Selection Methods -- ; 5.1.2.1. Univariate Statistics -- ; 5.1.2.2. Which Statistic? -- ; 5.1.2.3. Heuristic Methods -- ; 5.1.2.4. Which Method? -- ; 5.2. Controlling the Over All Error Rate -- ; 5.2.1. An Example: Analyzing Data from Microarrays -- ; 5.3. Controlling the False Discovery Rate -- ; 5.3.1. An Example: Analyzing Time-Course Data from Microarrays -- ; 5.4. Gene Set Enrichment Analysis

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