University of Wisconsin - Madison

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Analyses for
Test-Retest fMRI Studies

Documentation

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Contents

1 Connectivity Matrices

Most of the computation time in functional MRI (fMRI) reliability analysis comes from the creation of the connectivity matrices. An m x m connectivity matrix is generated for each fMRI scan by correlating each of the m fMRI signals of interest with every fMRI signal of interest and converting the resulting Pearson's r into a z_r via the Fisher transform (equation 1) [7]. It saves time to only compute the $m(m-1)/2$ unique correlations (i.e., upper right triangle of matrix).

$$z_r = \frac{1}{2}\ln\left(\frac{1+r}{1-r}\right) \iff \frac{e^{2z_r}-1}{e^{2z_r}+1} = r \qquad (1)$$

The m fMRI signals of interest may be selected in different ways, such as averaging the signal within m a *priori* regions of interest (ROIs) [4] or deriving m signals from the fMRI data itself via independent components analysis [14]. Depending on the selection method, other correction/processing techniques may be desired. This includes but is not limited to physiological noise correction [8] and the removal of signals from the white matter (WM), cerebral spinal fluid (CSF), soft tissues, and entire brain (i.e., global signal) [9] [3] [2] [19]. In addition, it is common to include the six rigid body motion registration parameters in the nuisance variable regression [10].

All of these correction/processing techniques involve regressing out signals of no interest (i.e., non-neuronal fluctuations) from the fMRI data and carrying the residuals from this regression into the next stage of analysis. One degree of freedom will be lost for each of these regressors; however, most programs will not automatically keep track of this change in the degrees of freedom. Furthermore, when time points corrupted by motion are censored out [15], the degrees of freedom may be different for each fMRI scan. Keeping track of the degrees of freedom allows for determination of significance by transforming the Pearson's r (with known degrees of freedom) into a t-statistic (equation 2) and using the cumulative distribution function (cdf) to obtain a p-value [7].

$$t = \frac{r\sqrt{df}}{\sqrt{1-r^2}} \iff \frac{t}{\sqrt{df+t^2}} = r \qquad (2)$$

Conversely, a significant z_r threshold can found by determining the t-statistic (with known degrees of freedom) into a p-value via the inverse cdf, transforming the t-statistic into an r (equation 2) and substituting the r into the Fisher transform (equation 1). Finally, when determining the significance, correct the p-value for multiple comparisons. For example, a Bonferroni-corrected p-value is the p-value divided by the total number of comparisons, which in this case is the $m(m-1)/2$ unique connections [20].

2 Intraclass Correlation Coefficient

The Intraclass Correlation Coefficient (ICC) is a measure of the reliability with which k judges independently rate a sample of n targets [18]. In fMRI, it has been used to measure the reliability with which fMRI scans (judges) estimate a functional connection in individuals' connectivity matrices (targets). Specifically, there will exist an n x k matrix for each functional connection, where n is the number of subjects and k is the number of fMRI scans [17].

2.1 Definition

ICCs are divided into three models. In the first model, a different group of k judges, who have been selected from a larger population of judges, rate each target (random effects). In the second model, the same group of k judges, who have been selected from a larger population of judges, rate each target (mixed effects). In the third model, the same group of k judges, who are the only judges of interest, rate each target (fixed

effects). Each model has a unique formulation for individual ratings (1) and the mean of several ratings (k) [18]. As there is nothing intrinsic about the label "scan one" for each of the subjects' scans (all scans have occurred at different times), it is appropriate use a random effects model [17].

Let $\mathbf{X}$ be an n x k matrix, where n is the number of targets and k the number of judges. Then let BMS denote the between targets (row) mean square, WMS denote the within target (row) mean square, JMS denote the between judges (column) mean square, and EMS denote the residual mean square (see Appendix A). Then define

$$ICC(1,1) = \frac{BMS - WMS}{BMS + (k-1)WMS} \qquad ICC(1,k) = \frac{BMS - WMS}{BMS} \tag{3}$$

$$ICC(2,1) = \frac{BMS - EMS}{BMS + (k-1)EMS + k(JMS)/n} \qquad ICC(2,k) = \frac{BMS - EMS}{BMS + (JMS - EMS)/n} \tag{4}$$

$$ICC(3,1) = \frac{BMS - EMS}{BMS + (k-1)EMS} \qquad ICC(3,k) = \frac{BMS - EMS}{BMS} \tag{5}$$

2.2   Example

Let $\mathbf{X}$ be the 6 x 4 matrix [18]

$$\mathbf{X} = \begin{pmatrix} 9 & 2 & 5 & 8 \\ 6 & 1 & 3 & 2 \\ 8 & 4 & 6 & 8 \\ 7 & 1 & 2 & 6 \\ 10 & 5 & 6 & 9 \\ 6 & 2 & 4 & 7 \end{pmatrix}$$

Then (see Table 2, Appendix A)

$$BMS = MS_{br} = 11.24 \qquad\qquad WMS = MS_{wr} = 6.26$$

$$JMS = MS_{bc} = 32.49 \qquad\qquad EMS = MS_e = 1.02$$

and by definition

$$ICC(1,1) = \frac{11.24 - 6.26}{11.24 + (4-1)6.26} = 0.17 \qquad ICC(1,k) = \frac{11.24 - 6.26}{11.24} = 0.44$$

$$ICC(2,1) = \frac{11.24 - 1.02}{11.24 + (4-1)1.02 + 4(32.49)/6} = 0.29 \quad ICC(2,k) = \frac{11.24 - 1.02}{11.24 + (32.49 - 1.02)/6} = 0.62$$

$$ICC(3,1) = \frac{11.24 - 1.02}{11.24 + (4-1)1.02} = 0.71 \qquad ICC(3,k) = \frac{11.24 - 1.02}{11.24} = 0.91$$

3

2.3 MATLAB Code

```matlab
1  function [ICC] = ICC(X, model, rating)
2  % ————————————————————————————————————————————————
3  % Intraclass Correlation Coefficient
4  %
5  % [ICC] = ICC(X, model, rating)
6  %         returns the Intraclass Correlation Coefficient of X
7  %
8  % The input X is an n x k matrix, where n is the number of tar−
9  % gets and k the number of judges. ICCs are divided into three
10 % models for two types of ratings.
11 %
12 % Model Types:
13 % '1' = random effects model => a different group of k judges,
14 %       who have been selected from a larger population of jud−
15 %       ges, rate each target
16 % '2' = mixed effects model => the same group of k judges, who
17 %       have been selected from a larger population of judges,
18 %       rate each target
19 % '3' = fixed effects model => the same group of k judges, who
20 %       are the only judges of interest, rate each targets.
21 %
22 % Rating Types:
23 % '1' = individual rating
24 % 'k' = mean of several ratings
25 % ————————————————————————————————————————————————
26 % Script:
27     [n,k] = size(X);
28     table = ANOVA_for_ICC(X, 'off');
29
30     BMS = table{6,4}; WMS = table{7,4};
31     JMS = table{3,4}; EMS = table{8,4};
32
33     if isequal(rating,'1')
34         if isequal(model,'1')
35             ICC = (BMS − WMS) / ...
36                   (BMS + (k−1)*WMS);
37         elseif isequal(model,'2')
38             ICC = (BMS − EMS) / ...
39                   (BMS + (k−1)*EMS + k*(JMS−EMS)/n);
40         elseif isequal(model,'3')
41             ICC = (BMS − EMS) / ...
42                   (BMS + (k−1)*EMS);
43         else
44             error('Model type does not exist.');
45         end
46     elseif isequal(rating,'k')
47         if isequal(model,'1')
48             ICC = (BMS − WMS) /
49                   BMS;
50         elseif isequal(model,'2')
51             ICC = (BMS − EMS) / ...
52                   (BMS + (JMS−EMS)/n);
53         elseif isequal(model,'3')
54             ICC = (BMS − EMS) /
55                   BMS;
56         else
57             error('Model type does not exist.');
58         end
59     else
60         error('Rating type does not exist.');
61     end
62 % ————————————————————————————————————————————————
```

3 Kendall's Coefficient of Concordance

Kendall's Coefficient of Concordance (W) is a measure of the consistency with which p judges rank n objects. It ranges from 0 to 1, where 0 indicates no agreement among judges and 1 indicates perfect agreement of the judges [11] [13]. In fMRI, it has been used to measure the agreement of ranking subjects (objects) across multiple fMRI scans (judges) based on the strength of one specific connection (i.e., there exists one matrix per connection). It has also been used to show the agreement of ranking an individual's connections (objects) across multiple functional MRI scans (judges) based on the strength of each connection (i.e., there exists one matrix per subject). In the former use, multiple analyses with random permutations of the scan order would be appropriate as there is nothing intrinsic about the label "scan one" for each of the subjects; all scans have occurred at different times [17].

3.1 Definition

Let $\mathbf{X}$ be $p \times n$ matrix, where p is the number of judges and n is the number of objects. Let K_i be the total number of unique elements in row i, and let each unique element in row i be denoted by k_i, where $i \in \{1, ..., K_i\}$. Then the tie correction factor for each row is defined as

$$T_i = \sum_{k_i=1}^{K_i} (t_{k_i}^3 - t_{k_i}), \text{ where } t_{k_i} \text{ is the total number instances of } k_i \text{ in row } i \tag{6}$$

Let $\mathbf{X}^{\text{ranked}}$ be matrix $\mathbf{X}$ where the elements of each row have been ranked from 1 to n. If there exists a tie between two or more elements, average the possible rankings for the elements in the tie and assign this averaged rank. Then

$$\mathbf{R} = \left(\sum_{i=1}^{p} X_{i,1}^{\text{ranked}} \quad \sum_{i=1}^{p} X_{i,2}^{\text{ranked}} \quad \cdots \quad \sum_{i=1}^{p} X_{i,n}^{\text{ranked}} \right) \tag{7}$$

$$\bar{R} = \frac{\sum_{j=1}^{n} R_j}{n} = \frac{1}{2} \times p \times (n+1) \tag{8}$$

$$S = \sum_{j=1}^{n} (R_j - \bar{R})^2 \tag{9}$$

and by definition

$$W = \frac{12 \times S}{\left(p^2 \times (n^3 - n) \right) - \left(p \times \sum_{i=1}^{p} T_i \right)} \tag{10}$$

$$\chi^2 = p \times (n-1) \times W, \quad df = n-1 \tag{11}$$

3.2 Example

Let $\mathbf{X}$ be the 3 x 5 matrix

$$\mathbf{X} = \begin{pmatrix} 14 & 13 & 13 & 14 & 13 \\ 11 & 12 & 13 & 16 & 15 \\ 12 & 10 & 13 & 16 & 15 \end{pmatrix}$$

As row one has 2 ties (there are 2 instances of element 14 and 3 instances of element 13), and both row two and row three have 0 ties (there is exactly 1 instance of each element), the tie correction matrix is

$$\mathbf{T} = \begin{pmatrix} (2^3 - 2) + (3^3 - 3) \\ (1^3 - 1) + (1^3 - 1) + (1^3 - 1) + (1^3 - 1) + (1^3 - 1) \\ (1^3 - 1) + (1^3 - 1) + (1^3 - 1) + (1^3 - 1) + (1^3 - 1) \end{pmatrix} = \begin{pmatrix} 30 \\ 0 \\ 0 \end{pmatrix}$$

In row one, element 14 could be ranked either fourth or fifth, and element 13 could be either ranked first, second, or third. Rank all instances of 13 and 14 with the average of their respective potential ranks to create

$$\mathbf{X}^{\text{ranked}} = \begin{pmatrix} 4.5 & 2 & 2 & 4.5 & 2 \\ 1 & 2 & 3 & 5 & 4 \\ 2 & 1 & 3 & 5 & 4 \end{pmatrix}$$

Then

$$\mathbf{R} = \begin{pmatrix} 7.5 & 5 & 8 & 14.5 & 10 \end{pmatrix}$$

$$\bar{R} = \frac{1}{2} \times 3 \times (5+1) = 9.0$$

$$S = (7.5 - 9)^2 + (5 - 9)^2 + (8 - 9)^2 + (14.5 - 9)^2 + (10 - 9)^2 = 50.5$$

Thus Kendall's W is

$$\frac{12 \times 50.5}{(3^2 \times (5^3 - 5)) - (3 \times (30 + 0 + 0))} = 0.6121$$

$$\chi^2 = 3 \times (5 - 1) \times 0.6121 = 7.3455, \quad df = 5 - 1 = 4 \quad \rightarrow \quad p = 0.1187$$

3.3 MATLAB Code

Please note that $\mathbf{X}$ from above should be transposed (i.e., the input is an n x p matrix, where n is the number of objects and p is the number of judges).

```matlab
function [W, Chi2, df, pval] = KendallsW(X)
% ───────────────────────────────────────────────
% Kendall's Correlation of Concordance (W)
%
% [W] = KendallsW(X)
%         returns the Kendall's W of X
% [W, Chi2, df, pval] = KendallsW(X)
%                       returns the Kendall's W of X with
%                       Friedman's Chi-Squared, degrees of
%                       freedom, and p-value
%
% The input X is an n x p matrix, where n is the number of
% objects and p is the number of judges (i.e., ranking occurs
% within columns).
% ───────────────────────────────────────────────
% Script:
    [n,p] = size(X);

    % Tie Correction Factors
    for i = 1:p
        [V,iv,ix] = unique(X(:,i)); ixs = sort(ix);
        t = hist(ixs, ixs(end));
        T(i) = sum(t.^3 - t);
    end

    % Kendall's W
    R = sum(tiedrank(X), 2); R_mean = mean(R);
    S = sum((R - R_mean).^2);
    W = (12*S) / ((p^2*(n^3-n)) - p*sum(T));

    % Friedman's Chi-Squared, degrees of freedom, and p-value
    Chi2 = p*(n-1)*W; df = n-1;
    pval = gammainc(Chi2/2, df/2, 'upper');
% ───────────────────────────────────────────────
```

4 Root-Mean-Square Deviation

The Root-Mean-Standard Deviation is typically used to describe the difference between predicted values from a model and experimentally observed values [16]; however, in functional MRI, it has been used examine the "reproducibility" with which functional MRI can estimate an individual's connectivity matrix [1]. This is easily generalizable to 3-dimensions for use on Statistical Parametric Maps (SPMs). While this metric is not biased by thresholding (see Dice Coefficient), it is extremely important to be working with normalized connectivity matrices. In addition, this metric would be biased by head motion or anything that would systematically alter the correlations.

4.1 Definition

Let $\mathbf{A}$ and $\mathbf{B}$ be m x n matrices. Then the root-mean-square deviation is defined as

$$\sqrt{\frac{\sum\limits_{i=1}^{m}\sum\limits_{j=1}^{n}\left(\mathrm{A}_{ij}-\mathrm{B}_{ij}\right)^2}{m \times n}} = \sqrt{\frac{\sum\limits_{i=1}^{m}\sum\limits_{j=1}^{n}\left(\mathbf{A}-\mathbf{B}\right)^2}{m \times n}} \tag{12}$$

4.2 Example

Let $\mathbf{A}$ and $\mathbf{B}$ be the 3 x 5 matrices

$$\mathbf{A} = \begin{pmatrix} 14 & 13 & 13 & 14 & 13 \\ 11 & 12 & 13 & 16 & 15 \\ 12 & 10 & 13 & 16 & 15 \end{pmatrix} \qquad \mathbf{B} = \begin{pmatrix} 12 & 18 & 19 & 14 & 16 \\ 13 & 17 & 12 & 12 & 15 \\ 10 & 16 & 18 & 11 & 11 \end{pmatrix}$$

Then

$$(\mathbf{A}-\mathbf{B})^2 = \begin{pmatrix} 2 & -5 & -6 & 0 & -3 \\ -2 & -5 & 1 & 4 & 0 \\ 2 & -6 & -5 & 5 & 4 \end{pmatrix}^2 = \begin{pmatrix} 4 & 25 & 36 & 0 & 9 \\ 4 & 25 & 1 & 16 & 0 \\ 4 & 36 & 25 & 25 & 16 \end{pmatrix}$$

Thus the Root-Mean-Square Deviation is

$$\sqrt{\frac{4+25+36+0+9+4+25+1+16+0+4+36+25+25+16}{3 \times 5}} = \sqrt{\frac{226}{15}} = 3.88$$

functional MRI literature [1]:
I originally found the root-mean-square deviation as the "mean difference in correlation" used by Anderson et al. 2011; however, the formula given on page 549 does not square the difference. I assumed this was an error, since this definition could result in a negative under the radical. Furthermore, in the case below the "mean difference in correlation" would be 0 when it is clearly 1. Let $\mathbf{A}$ and $\mathbf{B}$ be the 1 x 4 matrices

$$\mathbf{A} = \begin{pmatrix} 1 & 3 & 5 & 7 \end{pmatrix} \qquad\qquad \mathbf{B} = \begin{pmatrix} 2 & 2 & 6 & 6 \end{pmatrix}$$

Then

$$\left(\mathbf{A}-\mathbf{B}\right)^2 = \begin{pmatrix} -1 & 1 & -1 & 1 \end{pmatrix}^2 = \begin{pmatrix} 1 & 1 & 1 & 1 \end{pmatrix}$$

$$\sqrt{\frac{\sum\limits_{i=1}^{m}\sum\limits_{j=1}^{n}\left(\mathbf{A}-\mathbf{B}\right)^2}{m \times n}} = \sqrt{\frac{1+1+1+1}{1 \times 4}} = 1 \neq 0 = \sqrt{\frac{-1+1-1+1}{1 \times 4}} = \sqrt{\frac{\sum\limits_{i=1}^{m}\sum\limits_{j=1}^{n}\left(\mathbf{A}-\mathbf{B}\right)}{m \times n}}$$

4.3 MATLAB Code

```matlab
function [RMSD] = RMSD(A, B)
% ────────────────────────────────────────────
% Root-Mean-Square Deviation
%
% RMSD = RMSD(A, B)
%          returns the RMSD of A and B
%
% The inputs A and B are both n dimensional matrices.
% ────────────────────────────────────────────
% Script:
    if ~isequal(size(A), size(B))
        error('Matrices dimensions do not match.');
    end

    sqdifs = (A - B).^2;
    RMSD = sqrt(sum(sqdifs(:)) / prod(size(A)));
% ────────────────────────────────────────────
```

5   Dice Coefficient

The Dice Coefficient is a measure of the similarity between sets ranging from 0 to 1, where 0 indicates the sets are disjoint and 1 indicates the sets are identical [6]. In functional MRI, it has been used to assess the similarity between those connections which survive a particular threshold in two different connectivity matrices (e.g., two matrices from the same individual). This method is dependent on the choice of threshold, so it is preferable to use a "meaningful" threshold. For example, consider connections that survive thresholding by a significant p-value (Bonferroni-corrected) to be "connected" (i.e., exist in the set) and connections that do not survive to be "un-connected" (i.e., do not exist in the set). This is easily generalizable to 3-dimensions for use on Statistical Parametric Maps (SPMs).

Note that the Dice Coefficient is applied to sets; however, each connection could be considered an edge in graph. Consider the set of nodes $\{a, b, c, d, e, f\}$ and graphs $\mathcal{G}_1$ and $\mathcal{G}_2$ with edges $\{(a, c), (b, c), (c, d), (d, e), (d, f)\}$ and $\{(a, c), (b, c), (d, e), (d, f)\}$, respectively. The Dice Coefficient between these sets of edges is 0.89 (very high); however, (c, d) is an "edge cut" making graph $\mathcal{G}_2$ disconnected. The Dice Coefficient does not account for how differences between sets of edges affect the fundamental properties of their graphs.

5.1   Definition

Let A and B be sets. Then the Dice Coefficient of A and B is defined as simply

$$\frac{2 \times |A \cap B|}{|A| + |B|} \tag{13}$$

functional MRI literature [5]:
Let $\mathbf{X}$ be a m x n matrix and given a value t define the function

$$f(X_{ij}, t) = \begin{cases} 1 & \text{if } X_{ij} > t \\ 0 & \text{if } X_{ij} \leq t \end{cases} \text{ , where } i \in \{1, ..., m\} \text{ and } j \in \{1, ..., n\} \tag{14}$$

If $f(X_{ij}) = 1$, then we say the element with indices $ij \in f(\mathbf{X})$. Similarly, if $f(X_{ij}) = 0$, then we say the element with indices $ij \notin f(\mathbf{X})$. Therefore, we can define Dice Coefficient of m x n matrices $\mathbf{A}$ and $\mathbf{B}$ with

respective thresholds t_A and t_B as

$$\frac{2 \times \sum\limits_{i=1}^{m} \sum\limits_{j=1}^{n} f(\mathrm{A}_{ij}, t_A) f(\mathrm{B}_{ij}, t_B)}{\sum\limits_{i=1}^{m} \sum\limits_{j=1}^{n} f(\mathrm{A}_{ij}, t_A) + \sum\limits_{i=1}^{m} \sum\limits_{j=1}^{n} f(\mathrm{B}_{ij}, t_B)} = \frac{2 \times \sum\limits_{i=1}^{m} \sum\limits_{j=1}^{n} (f(\mathbf{A}, t_A) \circ f(\mathbf{B}, t_B))_{ij}}{\sum\limits_{i=1}^{m} \sum\limits_{j=1}^{n} (f(\mathbf{A}, t_A))_{ij} + \sum\limits_{i=1}^{m} \sum\limits_{j=1}^{n} (f(\mathbf{B}, t_B))_{ij}} \tag{15}$$

5.2 Example

Let $t_A = t_B = 13$, and let $\mathbf{A}$ and $\mathbf{B}$ be the 3 x 5 matrices

$$\mathbf{A} = \begin{pmatrix} 14 & 13 & 13 & 14 & 13 \\ 11 & 12 & 13 & 16 & 15 \\ 12 & 10 & 13 & 16 & 15 \end{pmatrix} \qquad \mathbf{B} = \begin{pmatrix} 12 & 18 & 19 & 14 & 16 \\ 13 & 17 & 12 & 12 & 15 \\ 10 & 16 & 18 & 11 & 11 \end{pmatrix}$$

Then

$$f(\mathbf{A}, t_A) = \begin{pmatrix} 1 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 & 1 \\ 0 & 0 & 0 & 1 & 1 \end{pmatrix} \qquad f(\mathbf{B}, t_B) = \begin{pmatrix} 0 & 1 & 1 & 1 & 1 \\ 0 & 1 & 0 & 0 & 1 \\ 0 & 1 & 1 & 0 & 0 \end{pmatrix}$$

and

$$f(\mathbf{A}, t_A) \circ f(\mathbf{B}, t_B) = \begin{pmatrix} 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix}$$

Thus the Dice Coefficient is

$$\frac{2 \times 2}{6 + 8} = \frac{4}{14} = 0.29$$

5.3 MATLAB Code

```matlab
function [DC] = DC(A, B, tA, tB, absolute)
% ────────────────────────────────────────────
% Dice Coefficient (i.e., Similarity Index for Sets)
%
% [DC] = DC(A, B, tA, tB, absolute)
%          returns the Dice Coefficient of A and B
%
% The inputs A and B are both n dimensional matrices; tA and tB
% are the thresholds for A and B, respectively. Absolute is a
% logical, which determines how the threshold is applied (true/1
% = absolute value greater than threshold, false/0 = value great−
% er than threshold).
% ────────────────────────────────────────────
% Script:
    if ~isequal(size(A), size(B))
        error('Matrix dimensions do not match.');
    end

    % Threshold Matrices
    if isequal(absolute, 1)
        fA = abs(A)>tA; fB = abs(B)>tB;
    else
        fA = A>tA; fB = B>tB;
    end
    fAfB = fA.*fB;

    % Dice Coefficient
    DC = (2*sum(fAfB(:))) / (sum(fA(:)) + sum(fB(:)));
% ────────────────────────────────────────────
```

A Analysis of Variance for Intraclass Correlations

A.1 Definition

Let $\mathbf{X}$ be the m x n matrix. Then define the following quantities [7]

$$SS_{bc} = \frac{\sum_{i=1}^{m}\left(\sum_{j=1}^{n}X_j\right)^2}{m} - \frac{\left(\sum_{i=1}^{m}\sum_{j=1}^{n}X_{ij}\right)^2}{(m-1)\times(n-1)} \qquad SS_{br} = \frac{\sum_{j=1}^{n}\left(\sum_{i=1}^{m}X_i\right)^2}{n} - \frac{\left(\sum_{i=1}^{m}\sum_{j=1}^{n}X_{ij}\right)^2}{(m-1)\times(n-1)}$$

$$MS_{bc} = \frac{SS_{bc}}{n-1} \qquad\qquad MS_{br} = \frac{SS_{br}}{m-1}$$

$$SS_{wc} = \sum_{i=1}^{m}\sum_{j=1}^{n}X_{ij}^2 - \frac{1}{m}\sum_{i=1}^{m}\left(\sum_{j=1}^{n}X_j\right)^2 \qquad SS_{wr} = \sum_{i=1}^{m}\sum_{j=1}^{n}X_{ij}^2 - \frac{1}{n}\sum_{j=1}^{n}\left(\sum_{i=1}^{m}X_i\right)^2$$

$$MS_{wc} = \frac{SS_{wc}}{n(m-1)} \qquad\qquad MS_{wr} = \frac{SS_{wr}}{m(n-1)}$$

$$SS_e = \sum_{i=1}^{m}\sum_{j=1}^{n}X_{ij}^2 - \frac{1}{n}\sum_{j=1}^{n}\left(\sum_{i=1}^{m}X_i\right)^2 - \frac{1}{m}\sum_{i=1}^{m}\left(\sum_{j=1}^{n}X_j\right)^2 + \frac{\left(\sum_{i=1}^{m}\sum_{j=1}^{n}X_{ij}\right)^2}{(m-1)\times(n-1)}$$

$$MS_e = \frac{SS_e}{(m-1)(n-1)}$$

$$F_{bc} = \frac{SS_{bc}}{MS_e}, \text{ where } df_1 = n-1 \text{ and } df_2 = (m-1)(n-1)$$

$$F_{br} = \frac{SS_{br}}{MS_e}, \text{ where } df_1 = m-1 \text{ and } df_2 = (m-1)(n-1)$$

Table 1: ANOVA Summary Table

Source	SS	df	MS	F	p
Columns					
between	SS_{bc}	$(n-1)$	MS_{bc}	F_{bc}	p_{bc}
within	SS_{wc}	$m(n-1)$	MS_{wc}		
Rows					
between	SS_{br}	$(m-1)$	MS_{br}	F_{br}	p_{br}
within	SS_{wr}	$n(m-1)$	MS_{wr}		
Residual	SS_e	$(m-1)(n-1)$	MS_e		

Note that all quantities can be calculated from the same four terms:

$$A = \sum_{i=1}^{m} \sum_{j=1}^{n} X_{ij}^2$$

$$B_c = \frac{\sum_{i=1}^{m} \left(\sum_{j=1}^{n} X_j \right)^2}{m} \qquad\qquad B_r = \frac{\sum_{j=1}^{n} \left(\sum_{i=1}^{m} X_i \right)^2}{n}$$

$$D = \frac{\left(\sum_{i=1}^{m} \sum_{j=1}^{n} X_{ij} \right)^2}{(m-1) \times (n-1)}$$

A.2   Example

Let **X** be the 6 x 4 matrix [18]

$$\mathbf{X} = \begin{pmatrix} 9 & 2 & 5 & 8 \\ 6 & 1 & 3 & 2 \\ 8 & 4 & 6 & 8 \\ 7 & 1 & 2 & 6 \\ 10 & 5 & 6 & 9 \\ 6 & 2 & 4 & 7 \end{pmatrix} \qquad\qquad \mathbf{X}^2 = \begin{pmatrix} 81 & 4 & 25 & 64 \\ 36 & 1 & 9 & 4 \\ 64 & 16 & 36 & 64 \\ 49 & 1 & 4 & 36 \\ 100 & 25 & 36 & 81 \\ 36 & 4 & 16 & 49 \end{pmatrix}$$

Then

$$\sum_{i=1}^{m} X_i = \begin{pmatrix} 46 & 15 & 26 & 40 \end{pmatrix} \qquad\qquad \left(\sum_{i=1}^{m} X_i \right)^2 = \begin{pmatrix} 2116 & 225 & 676 & 1600 \end{pmatrix}$$

$$\sum_{j=1}^{n} X_j = \begin{pmatrix} 24 \\ 12 \\ 26 \\ 16 \\ 30 \\ 19 \end{pmatrix} \qquad\qquad \left(\sum_{j=1}^{n} X_j \right)^2 = \begin{pmatrix} 576 \\ 144 \\ 676 \\ 256 \\ 900 \\ 361 \end{pmatrix}$$

and thus by definition

$$A = \sum_{i=1}^{m} \sum_{j=1}^{n} X_{ij}^2 = 81 + 4 + 25 + ... + 4 + 16 + 49 = 841$$

$$B_c = \frac{\sum_{i=1}^{m} \left(\sum_{j=1}^{n} X_j \right)^2}{m} = \frac{2116 + 225 + 676 + 1600}{6} = \frac{4617}{6} = 769.5$$

$$B_r = \frac{\sum_{j=1}^{n} \left(\sum_{i=1}^{m} X_i \right)^2}{n} = \frac{576 + 144 + 676 + 256 + 900 + 36}{4} = \frac{2913}{4} = 728.25$$

$$D = \frac{\left(\sum\limits_{i=1}^{m}\sum\limits_{j=1}^{n} X_{ij}\right)^2}{(m-1)\times(n-1)} = \frac{(9+2+5+...+2+4+7)^2}{(m-1)\times(n-1)} = \frac{127^2}{5\times 3} = \frac{16129}{24} = 672.04$$

$$SS_{bc} = B_c - A = 769.5 - 672.04 = 97.46 \qquad\qquad SS_{wc} = D - S_c = 841 - 769.5 = 71.5$$

$$MS_{bc} = \frac{97.46}{4-1} = 32.49 \qquad\qquad MS_{wc} = \frac{71.5}{4\times(6-1)} = 3.58$$

$$SS_{br} = B_r - A = 728.25 - 672.04 = 56.21 \qquad\qquad SS_{wr} = D - B_r = 841 - 728.25 = 112.75$$

$$MS_{br} = \frac{56.21}{6-1} = 11.24 \qquad\qquad MS_{wr} = \frac{112.75}{6\times(4-1)} = 6.26$$

$$SS_e = 841 - 769.5 - 728.25 + 672.04 = 15.29$$

$$MS_e = \frac{15.29}{(6-1)\times(4-1)} = 1.02$$

$$F_{bc} = \frac{32.49}{1.02} = 31.87, \text{ where } df_1 = 3 \text{ and } df_2 = 15 \quad \rightarrow \quad p_{bc} = 9.45e-07$$

$$F_{br} = \frac{11.24}{1.02} = 11.02, \text{ where } df_1 = 5 \text{ and } df_2 = 15 \quad \rightarrow \quad p_{br} = 1.35e-04$$

Table 2: ANOVA Summary Table

Source	SS	df	MS	F	p
Columns					
between	97.46	3	32.49	31.87	9.45e-7
within	71.5	20	3.58		
Rows					
between	56.21	5	11.24	11.02	1.35e-4
within	112.75	18	6.26		
Residual	15.29	15	1.02		

A.3 MATLAB Code

```matlab
function [table] = ANOVA_for_ICC(X, displayopt)
% ─────────────────────────────────────────────────
% Analysis of Variance for Ratings (for Intraclass Correlations)
%
% [table] = ANOVA_for_ICC(X, displayopt)
%           returns the ANOVA summary table as a cell array
%
% The input X is an n x k matrix, where n is the number of tar-
% gets and k is he number of judges. The option of displaying
% an ANOVA summary table is handled by displayopt, which can be
% set to 'on' (default) or 'off.'
% ─────────────────────────────────────────────────
% Script:
    [m,n] = size(X);
    total = m*n;

    A  = sum(sum(X.^2));
    Bc = sum(sum(X,1).^2)/m;
    Br = sum(sum(X,2).^2)/n;
    D  = sum(sum(X))^2/total;

    SSbc = Bc-D;
    SSwc = A-Bc;
    SSbr = Br-D;
    SSwr = A-Br;
    SSe  = A-Br-Bc+D;

    DFbc = n-1;
    DFwc = n*(m-1);
    DFbr = m-1;
    DFwr = m*(n-1);
    DFe  = DFbc*DFbr;

    MSbc = SSbc/DFbc;
    MSwc = SSwc/DFwc;
    MSbr = SSbr/DFbr;
    MSwr = SSwr/DFwr;
    MSe  = SSe/DFe;

    Fbc = MSbc/MSe; Pbc = 1-fcdf(Fbc, DFbc, DFe);
    Fbr = MSbr/MSe; Pbr = 1-fcdf(Fbr, DFbr, DFe);

    table = { 'Source of Variance' 'SS' 'df' 'MS' 'F' 'Prob>F'
              'Columns'                []    []    []    []   []
              '    betweeen'          SSbc DFbc MSbc Fbc  Pbc
              '    within'            SSwc DFwc MSwc []   []
              'Rows'                   []    []    []    []   []
              '    between'           SSbr DFbr MSbr Fbr  Pbr
              '    within'            SSwr DFwr MSwr []   []
              'Residual'             SSe  DFe  MSe  []   []  };

    if isequal(nargin, 1) || isequal(displayopt, 'on')
        statdisptable(table, 'ANOVA for ICC', ...
                      'ANOVA Summary Table', '');
    end
% ─────────────────────────────────────────────────
```

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