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function [GTest_pvalue] = GTest(Peptide_Vector,Groups)

% Peptide_Vector is a list of observed and unobserved values for a specific peptide.
% Unobserved values are represented as NaN values

% Groups is a vector of class indices associated with each observation in Peptide_Vector. This vector
% is numeric and sequential, which means that if there are 4 classes, then each position in
% Peptide_Vector will be represented in "Groups" as a 1,2,3 or a 4. If the data are in another format,
% such as a Cell structure it would need to be converted.

% 1) determine how many samples are in each group (nk in paper)
N = length(Groups);
num_g = max(Groups);
nk = zeros(num_g,1);
for i = 1:num_g
    nk(i) = length(find(Groups == i));
end

% 2) Create the Observed Count Matrix (C_Ok and C_Ak in paper)
Count_Matrix = zeros(num_g,2);
% If there is a 0 in the Count_Matrix this will create problems with the log transformation.
% G-test ignores 0's in the sum, they can be replaced with a NaN.
for i = 1:num_g
    Number_Missing = sum(isnan(Peptide_Vector(Groups == i)));
    if Number_Missing == 0
        Count_Matrix(i,1) = NaN;
    else
        Count_Matrix(i,1) = Number_Missing;
    end
    if Number_Missing == nk(i)
        Count_Matrix(i,2) = NaN;
    else
        Count_Matrix(i,2) = nk(i) - Number_Missing;
    end
end

% 3) Create the Expected Count Matrix (E_Ok and E_Ak in paper)
% All summations must be done ignoring the NaN values
M_Values = nansum(Count_Matrix);
Expected_Matrix = (nk * M_Values) ./ N;

% 4) Compute the G statistic and associated significant value (Equation 2 in paper)
G_Value = 2*nansum(nansum(Count_Matrix .* (log(Count_Matrix ./ Expected_Matrix))));
GTest_pvalue = 1 - chi2cdf(G_Value,num_g - 1);

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Figure S4. Generic MatLab® code for computing the G-value in Equation 2 and the associated significance value from a χ^2 distribution.