Friedman rank sum test

-- for multiple correlated samples in a two-way balanced complete block design
-- columns are the "groups" or "treatments"
-- rows are the "blocks" -- Friedman test null Hypothesis H0: there is no significant effect of "groups" or "treatments"

Input Data (scroll as required):

	T_A	T_B	T_C	T_D	T_E	T_F	T_
P_1	3	4	5	5	6	7	4
P_2	6	6	7	7	7	7	8
P_3	6	8	8	7	5	7	8
P_4	3	2	3	3	9	8	7
P_5	7	7	7	8	7	8	9
P_6	5	5	7	5	7	9	9

Results:

Friedman rank sum test for multiple correlated samples in a two-way balanced complete block design

Friedman chi-squared statistic: 22.687928

degrees of freedom df : 11
This is the number of correlated samples (or groups), minus 1

p-value: 0.019554
This p-value is for rejection of the omnibus null hypothesis, that all samples (groups) are from the same distribution, i.e. there is no effect of groups. The alternate hypothesis that one or more of the correlated samples (groups) is different, i.e. there is a group effect.

The omnibus p-value is at or below the respectable critical threshold of 0.05, so post-hoc pairwise multiple comparison tests are conducted to discern which of the pairs have significantly differences. Three of many possible post-hoc tests are conducted: the methods of (1) Conover and (2) Nemenyi. For the (1) Conover method, the p-value is adjusted in two ways, first according to the family-wide error rate (FWER) procedure of Holm, and next by the false discovery rate (FDR) procedure of Benjaminyi-Hochberg.

Post-hoc p-values of all possible pairs (of samples/ groups) are compactly represented as a lower triangular matrix. Each numerical entry is the p-value of row/column pair, i.e. the null hypotheses that the group represented by a particular column name is different from the group represented by a particular row name.

Conover p-values, further adjusted by the Holm FWER method

	T_A	T_B	T_C	T_D	T_E	T_F	T_E.1	T_G	T_H	T_I	T_J
T_B	1.000000										
T_C	1.000000	1.000000									
T_D	1.000000	1.000000	1.0								
T_E	1.000000	1.000000	1.0	1.0							
T_F	0.181791	0.362384	1.0	1.0	1.0						
T_E.1	0.057133	0.125584	1.0	1.0	1.0	1.0					
T_G	1.000000	1.000000	1.0	1.0	1.0	1.0	1.0				
T_H	0.464686	0.867785	1.0	1.0	1.0	1.0	1.0	1.0			

	T_A	T_B	T_C	T_D	T_E	T_F	T_E.1	T_G	T_H	T_I	T_J
T_I	0.307558	0.581888	1.0	1.0	1.0	1.0	1.0	1.0	1.0		
T_J	1.000000	1.000000	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	
T_K	0.285278	0.543381	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0

Conover p-values, further adjusted by the Benjaminyi-Hochberg FDR method

	T_A	T_B	T_C	T_D	T_E	T_F	T_E.1	T_G	T_H
T_B	0.917107								
T_C	0.263583	0.374420							
T_D	0.374420	0.517601	0.917107						
T_E	0.145070	0.211064	0.859001	0.816076					
T_F	0.062491	0.065348	0.560254	0.426649	0.768708				
T_E.1	0.057133	0.062491	0.374420	0.261130	0.568070	0.870891			
T_G	0.124789	0.181959	0.822790	0.816076	0.940847	0.816076	0.614706		
T_H	0.073022	0.100480	0.747811	0.605983	0.822790	0.882662	0.816076	0.859001	
T_I	0.065348	0.073572	0.633346	0.524371	0.816076	0.919771	0.822790	0.822790	0.919771
T_J	0.107386	0.156520	0.822790	0.768708	0.919771	0.816076	0.643199	0.940847	0.894299
T_K	0.065348	0.073572	0.623838	0.517601	0.816076	0.919771	0.822790	0.822790	0.919771

Caution: The Conover method tends to show all or most pairs to be significantly different, i.e. its tends to be very liberal, and hence the p-value adjustment. The Nemenyi method seems to be conservative and its p-value is not adjusted. Further, the Holm and all other FWER methods of p-value adjustment applied as a secondary step are considered to be liberal relative to the rigorous Benjamnyi-Hochberg FDR method.

Nemenyi p-values, with no further adjustment

	T_A	T_B	T_C	T_D	T_E	T_F	T_E.1	T_G	T_H	T_I
T_B	1.000000									
T_C	0.881941	0.954871								
T_D	0.954871	0.987748	1.000000							
T_E	0.667113	0.812027	1.000000	0.999986						
T_F	0.178734	0.293330	0.993280	0.971032	0.999820					
T_E.1	0.072874	0.135201	0.948248	0.869451	0.994586	1.000000				
T_G	0.606080	0.761734	0.999999	0.999944	1.000000	0.999944	0.997315			
T_H	0.345408	0.502213	0.999640	0.996576	0.999999	1.000000	0.999964	1.000000		
T_I	0.261253	0.401677	0.998398	0.989894	0.999986	1.000000	0.999997	0.999997	1.0	
T_J	0.543734	0.706298	0.999995	0.999820	1.000000	0.999986	0.998782	1.000000	1.0	1.0

	T_A	T_B	T_C	T_D	T_E	T_F	T_E.1	T_G	T_H	T_I
T_K	0.246055	0.382505	0.997915	0.987748	0.999977	1.000000	0.999998	0.999995	1.0	1.0

R code to reproduce these results:

```
# Lines that begin with the # character are taken as comment lines by R. # The Friedman test is built-into the
base R.
# The post-hoc tests require one-time installation of the R package PMCMR
# Start R under "Run as Administrator" in Windows or sudo in Linux.
# select a download mirror at the install.packages command
install.packages("PMCMR")
library("PMCMR")
mat1 <-
structure(c(3L, 6L, 6L, 3L, 7L, 5L, 4L, 7L, 5L, 4L, 3L, 3L, 4L,
6L, 8L, 2L, 7L, 5L, 3L, 6L, 4L, 4L, 5L, 5L, 5L, 7L, 8L, 3L, 7L,
7L, 7L, 6L, 5L, 4L, 6L, 5L, 5L, 7L, 7L, 3L, 8L, 5L, 6L, 5L, 5L,
5L, 7L, 5L, 6L, 7L, 5L, 9L, 7L, 7L, 5L, 7L, 6L, 6L, 5L, 5L, 7L,
7L, 7L, 8L, 8L, 9L, 8L, 5L, 7L, 5L, 3L, 7L, 4L, 8L, 8L, 7L, 9L,
9L, 6L, 8L, 5L, 3L, 8L, 8L, 4L, 8L, 6L, 9L, 9L, 3L, 5L, 7L, 4L,
7L, 9L, 5L, 8L, 9L, 8L, 9L, 6L, 5L, 3L, 4L, 7L, 8L, 4L, 6L, 6L,
8L, 9L, 6L, 8L, 5L, 2L, 6L, 7L, 5L, 7L, 7L, 6L, 9L, 6L, 9L, 5L,
3L, 6L, 7L, 5L, 7L, 8L, 5L, 8L, 6L, 8L, 7L, 6L, 7L, 7L, 3L, 7L,
8L, 6L, 7L), .Dim = c(12L, 12L), .Dimnames = list(c("P_1", "P_2",
"P_3", "P_4", "P_5", "P_6", "P_7", "P_8", "P_9", "P_10", "P_11",
"P_12"), c("T_A", "T_B", "T_C", "T_D", "T_E", "T_F", "T_E.1",
"T_G", "T_H", "T_I", "T_J", "T_K")))
f1 <- friedman.test(mat1)
print (f1)
# Post-hoc tests are conducted only if omnimus Kruskal-Wallis test p-value is 0.05 or less.
if ( f1$p.value < 0.05 )
{
c1 <- posthoc.friedman.conover.test(mat1, p.adjust.method="holm")
c2 <- posthoc.friedman.conover.test(mat1, p.adjust.method="fdr")
n1 <- posthoc.friedman.nemenyi.test(mat1)
}
c1; c2; n1;
# alternate representation of post-hoc test results
summary(c1); summary(c2); summary(n1);
```