A simple correction for non-independent tests

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Complete reproduction files for this tutorial (including data, analyses, and results/formatting) are available at osf.io/re5w2/.

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Abstract

Psychologists wrestle with how to best handle multiple comparisons, while maintaining a balance between false positives and false negatives. Undercorrection, such as ignoring the presence of multiple comparisons altogether, is known to yield an unacceptably high rate of false positives. Overcorrection, such as treating all tests as independent when they are not, results in overly conservative evaluations of statistical significance. This tutorial demonstrates M_{eff} correction, a method for adjusting statistical significance thresholds for multiple comparisons, without the assumption of independence of tests. This method, in which the effective number of tests (M_{eff}) is estimated from the correlations among the variables being tested, was developed and validated in the field of genetics, but is based on statistical concepts (eigenvalues) that are very familiar to psychologists. M_{eff} correction can be applied in psychological research to balance the necessity of correction for multiple comparisons with the concerns that arise from complex, correlated tests.

Keywords: multiple comparisons, null hypothesis significance testing, spectral decomposition, tutorial

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There is ample evidence that unreported multiple comparisons are a common occurrence in psychology (Simonsohn, Nelson, & Simmons, 2014). Failure to acknowledge and correct for the presence of such multiple comparisons is one place where problems often arise (Simmons, Nelson, & Simonsohn, 2011). One barrier to consistent and transparent handling of multiple comparisons in psychology is that most widely known approaches to adjusting for multiple comparisons (e.g. Bonferroni correction, Dunn (1961)) are overly conservative when applied to non-independent (i.e. correlated) tests. This tutorial presents M_{eff} correction, an approach that takes into account multiple comparisons among correlated variables. The particular method described here was developed and validated in genetics (Cheverud, 2001; Nyholt, 2004); however, its statistical derivation may be applied just as well in psychological science. M_{eff} correction is a simple, efficient, and accurate approach to adjusting thresholds for statistical significance, taking into account the number and interrelation of tested hypotheses.

Researchers have proposed reducing the standard threshold for null hypothesis significance testing (NHST) in psychology from $\alpha \leq 0.05$ to $\alpha \leq 0.005$ (Benjamin et al., 2018).¹ Discussions surrounding such proposals often cite genetics, which uses a threshold of $p \leq 5 \times 10^{-8}$ for declaring statistical significance, as an example of a field that has successfully navigated a similar transition. Like psychology, the genetics literature has been rife with false positives and poor replicability, and a sudden explosion in available data (i.e., the advent of genome-wide association studies, GWAS, where many millions of genetic variants are tested for correlation with a given outcome) lead to field-wide adoption of a standard approach to acknowledging and addressing multiple comparisons. The approach taken in genetics has been to embrace these multiple comparisons wholeheartedly, with the

¹Effectiveness of such policies is hotly debated, and alternatives to “fixing” NHST have been proposed, including avoiding categorical decisions of statistical significance versus non-significance altogether, instead focusing on alternative evaluations, such as effect sizes (McShane, Gal, Gelman, Robert, & Tackett, 2017).

field acknowledging that large-scale exploratory analysis is a necessary starting point to fully evaluating effects in the available data. The oft-cited threshold for declaring statistical significance in genetics of $p \leq 5 \times 10^{-8}$ (Dudbridge & Gusnanto, 2008), which applies to GWAS as a *per-test* threshold for evaluating statistical significance. It is not, in fact, the result of a change in the total acceptable Type I or family-wise error rate (FWER), which remains set overall (across all tests) at $\alpha \leq 0.05$.

The per-test threshold of $p \leq 5 \times 10^{-8}$ for declaring statistical significance in GWAS was obtained by correcting the typical total $\alpha \leq 0.05$ threshold applied to a single, standalone test to take into account the equivalent of one million tests being performed (that is, $p \leq 5 \times 10^{-8} = \frac{\alpha \leq 0.05}{1,000,000}$). This threshold remains consistent in GWAS regardless of how many millions of tests have actually been conducted, because the “one million” estimate represents the *effective* number of tests (M_{eff}), taking into account the fact that the tests are not independent of one another (in genetics, this is due to linkage disequilibrium, or LD, the tendency of genetic variants that are physically close to one another to co-occur more than chance). In studies where less than the whole genome is interrogated (for example, testing multiple variants within a single gene of interest), different corrections (similarly derived) are applied to estimate a bespoke per-test threshold for statistical significance, correcting for M_{eff} given the correlations among the tests, while maintaining a consistent total family-wise error rate of $\alpha = 0.05$.

Cheverud (2001) and Nyholt (2004) developed a simple, efficient, and accurate correction for multiple comparisons among correlated variables.² The derivation and application of M_{eff} as a correction factor for multiple testing among non-independent variables is not specific to the field of genetics. For example, the ENIGMA consortium

²Additional estimation methods have been developed, including those that apply permutation-based approaches (Hirschhorn & Daly, 2005) - which was how the GWAS adjustment of $p \leq 5 \times 10^{-8}$ was estimated (Dudbridge & Gusnanto, 2008). The frequentist approach presented here was selected as a balance among efficiency, accuracy, and portability across data forms and software packages likely to be employed by psychologists.

applied M_{eff} correction to testing 70 non-independent cortical measures from brain MRI scans for association with genetic variants (Grasby et al., 2018). M_{eff} correction can be applied to both small and large sets of variables, across varying degrees of intercorrelation. In the genetics literature, this and similar approaches are typically described as relying on spectral decomposition (SpD). Spectral decomposition is already quite familiar to most psychologists, although they may not know that they know it: it is an alternative term for eigendecomposition (or the process of estimating the eigenvalues and eigenvectors to represent a matrix). The application of eigenvalues to estimating M_{eff} and correcting the per-test threshold for statistical significance as a function of the correlations among the tested variables is described in detail below.

Correcting per-test α using M_{eff}

Nyholt (2004) defined the effective number of tests, M_{eff} , among k correlated variables as described below. Given λ as a vector of eigenvalues of length k for the variables of interest:

$$M_{eff} = 1 + [(k - 1) \times (1 - \frac{var(\lambda)}{k})]$$

As the correlations among the variables approach 0, M_{eff} approaches k . Conversely, as the correlations among the variables approach 1, M_{eff} approaches 1.

Given M_{eff} and a specified total α threshold,³ then the per-test corrected α level ($\alpha_{M_{eff}}$) is set at:

$$\alpha_{M_{eff}} = \frac{\alpha}{M_{eff}}$$

Further, in the case where there are two dimensions of multiple comparisons, such as separate sets of predictors and outcomes (as in Example 3 below), where M_{eff_1} is the effective number of tests among the first set of variables and M_{eff_2} is the effective number of tests among the second set of variables, then the per-test corrected α level for all $k_1 \times k_2$

³As the described approach is a form of NHST, the specific α level used must still be thoughtfully selected (Lakens et al., 2018).

comparisons is:

$$\alpha_{M_{eff}} = \frac{\alpha}{M_{eff1} \times M_{eff2}}$$

The following tutorial uses R (R Core Team, 2017) to demonstrate how M_{eff} correction can be applied. However, the above equations for M_{eff} correction can be used with any software that estimates eigenvalues.

Tutorial

Presented here are three instances of applying M_{eff} correction in non-independent multiple comparison scenarios that occur across a wide range of sub-fields of psychology: multiple ANOVAs of group differences in correlated continuous variables (Example 1), multiple multiple regressions for different correlated dependent variables (Example 2), and a correlation matrix exploring relationships between two sets of correlated variables (Example 3). Complete reproduction files for this tutorial (including data, analyses, and output formatting) in R are available at osf.io/re5w2/. All three examples use the same open-source data set.⁴ Analyses presented in this tutorial require the Matrix (Bates & Maechler, 2017), psych (Revelle, 2018), and lsr (Navarro, 2015) packages, and this manuscript was prepared using rmarkdown (Allaire et al., 2018) and papaja (Aust & Barth, 2018).

The meff function

The R function `meff` takes x , which is a dataframe (the default), a correlation matrix (`correl = TRUE`), or a vector of eigenvalues (`eigen = TRUE`). It returns M_{eff} , or the effective number of tests among all k variables included in x , estimated using the method described by Cheverud (2001) and Nyholt (2004). The ability of the `meff` function defined here to accept either raw data or pre-processed correlations or eigenvalues allows easy use of

⁴If we were actually interested in drawing inferences from the results of these tests, we should correct for all tests performed across all three examples within this single “study”. For the purpose of clarity of presentation, however, we correct only for multiple comparisons within each example, effectively evaluating them as standalone studies.

this function with complex or summary data, rather than relying on a specific format or structure of raw data.

The full function code is available in the Appendix. `meff` can be loaded directly into R using: `source('https://osf.io/ws6xc/download')`.

Example data

The examples presented in this tutorial used an open-source Internet survey data set, which included the 26-item Nerdy Personality Attributes Scale (NPAS; Open Source Psychometrics Project (2015)) and the Ten Item Personality Inventory (TIPI; Gosling, Rentfrow, and Swann Jr (2003)), originally obtained from openpsychometrics.org/_rawdata/ in March 2018.⁵ The sample ($N = 1418$) had an average age of 26.60 years (range = 14 – 90; excluding 1 participant who reported an age of 38822) and self-identified their genders as 58% female, 37% male, and 5% other.

M_{eff} was estimated using the `meff()` function for each set of variables (TIPI and NPAS). In this case, we read data directly into the function, which then estimates the correlations among variables to use for estimating M_{eff} . If complex data are being analyzed, where a matrix of standard Pearson correlation coefficients would be inappropriate, the `meff()` function also allows the user to input a pre-specified correlation matrix (using the `correl = TRUE` option) or a vector of eigenvalues (`eigen = TRUE`).

M_{eff} for the TIPI was 9.70 (versus $k = 10$ items), and M_{eff} for the NPAS was 24.81 (versus $k = 26$ items). This may not seem like much of a reduction in tests to be corrected for compared to alternative approaches, such as Bonferroni correction, but consider that this method scales substantially with larger variable sets, or with variables that may only be subtly different (e.g. in scaling or phrasing or response options) and strongly intercorrelated.

⁵Due to complex formatting – commas within a string in a comma-separated-values file – the *major* variable was removed from the original data set.

Table 1

Gender differences for each item from the Ten Item Personality Inventory (TIPI). Table shows the mean (and standard deviation) for each gender group and results of one-way ANOVA tests, evaluated as statistically significant where $p \leq \frac{\alpha}{M_{eff}}$.

	Male	Female	Other	Test	η^2	p-value	sig.
extraverted	3.5 (1.9)	3.5 (1.9)	3.1 (2.0)	$F(2,1409) = 0.98$	0.00	3.7e-01	
critical	4.5 (1.8)	4.0 (1.8)	4.3 (1.8)	$F(2,1408) = 8.2$	0.01	2.8e-04	*
dependable	5.1 (1.7)	5.0 (1.6)	4.5 (1.7)	$F(2,1405) = 3.2$	0.00	3.9e-02	
anxious	3.8 (1.9)	4.8 (1.9)	5.4 (1.8)	$F(2,1409) = 60.2$	0.08	8.0e-26	*
open	5.5 (1.4)	5.6 (1.4)	5.7 (1.4)	$F(2,1407) = 0.64$	0.00	5.3e-01	
reserved	5.2 (1.6)	5.2 (1.7)	5.6 (1.6)	$F(2,1407) = 2.4$	0.00	9.5e-02	
sympathetic	4.6 (1.7)	5.3 (1.5)	5.1 (1.9)	$F(2,1406) = 30.7$	0.04	9.0e-14	*
disorganized	4.0 (2.0)	4.0 (1.9)	4.4 (1.9)	$F(2,1406) = 1.4$	0.00	2.5e-01	
calm	4.9 (1.7)	4.2 (1.8)	3.4 (1.9)	$F(2,1406) = 40.1$	0.05	1.2e-17	*
conventional	2.7 (1.7)	2.5 (1.6)	2.1 (1.4)	$F(2,1406) = 5.4$	0.01	4.7e-03	*

Example 1. Correction for multiple ANOVAs

In the first example, each of the 10 TIPI items were tested for average differences across self-reported gender categories (“male”, “female”, and “other”) using one-way ANOVAs.

The per-test corrected $\alpha_{M_{eff}}$ was calculated as the overall α level divided by M_{eff} . Table 1 shows the results of all 10 tests, with statistical significance (compared to $\alpha_{M_{eff}} = \frac{\alpha}{M_{eff}} = 0.0052$) indicated in the last column.

Example 2. Correction for multiple regression models of multiple outcomes

In the second example, the TIPI items were tested for association with (a) a single Nerdy self-identity item (presented with the same 7-point response options as items in the

Table 2

Result of regressions of (a) Nerdy self-identity, (b) educational attainment, and (c) Autism Spectrum Disorder status on individual Ten Item Personality Inventory (TIPI) items, evaluated as statistically significant where $p \leq \frac{\alpha}{M_{eff\ outcomes} \times k_{TIPI}}$.

	Nerdy	p-value	sig.	Edu	p-value	sig.	ASD	p-value	sig.
extraverted	-0.10	3.2e-05	*	-0.02	2.8e-01		0.00	7.6e-01	
critical	0.05	4.0e-02		-0.05	1.7e-04	*	0.00	9.5e-01	
dependable	0.03	1.8e-01		0.04	2.6e-02		-0.01	1.7e-01	
anxious	0.03	2.2e-01		-0.03	4.1e-02		0.01	2.6e-02	
open	0.06	3.5e-02		0.01	5.9e-01		-0.01	5.1e-02	
reserved	0.01	7.3e-01		-0.06	9.4e-04	*	0.00	2.9e-01	
sympathetic	0.09	5.7e-04	*	0.02	2.3e-01		-0.02	8.6e-05	*
disorganized	0.02	3.3e-01		-0.03	4.3e-02		0.00	8.2e-01	
calm	-0.03	2.2e-01		0.07	1.3e-04	*	-0.01	2.3e-01	
conventional	-0.07	5.2e-03		0.00	8.9e-01		-0.01	1.4e-02	

TIPI), (b) educational attainment (a 4-category ordinal scale), and (c) self-reported lifetime autism spectrum disorder diagnostic status (coded as 0 = no, 1 = yes). A multiple regression was estimated for each outcome predicted by all 10 TIPI items.

Here, we must correct along two dimensions of multiple testing: M_{eff} among the three correlated dependent variables, as well as Bonferroni correction to account for the multiple independent variables. Estimates of independent variable effects within a multiple regression model are independent of one another, even if the original variables were correlated, and so a Bonferroni correction of $\alpha_{per-test} \leq \frac{\alpha}{k}$ is appropriate for addressing multiple testing on the “right” side of the regression equation (Perrett, Schaffer, Piccone, Roozeboom, & others, 2006). Therefore, each result is compared against a corrected per-test $\alpha_{M_{eff}} \leq \frac{\alpha}{k_{IV} \times M_{eff\ DV}}$.

Table 2 shows the results of all 30 tests, with statistical significance of each of 30 tests (compared to $\alpha_{M_{eff}} = \frac{\alpha}{M_{eff\text{outcomes}} \times k_{TIPI}} = 0.0017$) indicated in the last column.

Example 3. Correction for multiple predictors of multiple outcomes

The third example demonstrates the application of M_{eff} correction to a case where we have two fairly large sets of variables, and wish to explore correlations among all possible combinations; in this case 10 TIPI items correlated with 26 NPAS items.

Because multiple comparisons need to be accounted for along two different dimensions of non-independent variable sets, $\alpha_{M_{eff}}$ takes into account both the effective number of predictors (TIPI items, $M_{eff1} = 9.70$) and the effective number of outcomes (NPAS items, $M_{eff2} = 24.81$). Therefore, $\alpha_{M_{eff}} = \frac{\alpha}{M_{eff1} \times M_{eff2}} = 0.00021$.

Here, there were a lot of tests (10 TIPI items $\times$ 26 NPAS items = 260 comparisons), so for brevity only every 20th row from the full table is shown in Table 3. Full results can be generated from the tutorial R script at osf.io/re5w2/.

Summary

As data accumulates and software advances, large-scale exploratory, data-driven, bottom-up research is becoming more prevalent in psychology. Even in smaller-scale research endeavors, there is strong evidence that psychologists are already engaging in such multiple comparisons, even if they are not explicitly reported as such (Simmons et al., 2011; Simonsohn et al., 2014). M_{eff} correction is appropriate in any case where the goal is to control the Type I error rate in an application of null hypothesis significance testing. M_{eff} correction is particularly useful in cases where a large number of available variables makes simultaneous inclusion within a single model impractical or impossible (for example, many highly correlated variables within a regression). Compared to permutation approaches (Sherman & Funder, 2009), M_{eff} correction scales efficiently to large numbers of variables and relies solely on a statistical construct (eigenvalues) that is already familiar to many psychology researchers.

Table 3

Correlations between individual Ten Item Personality Inventory (TIPI) items and individual Nerdy Personality Attributes Scale (NPAS) items, evaluated as statistically significant where $p \leq \frac{\alpha}{M_{eff1} \times M_{eff2}}$.

	TIPI item	NPAS item	N	ρ	p-value	sig.
20	extraverted	odd child	1404	-0.09	1.2e-03	
40	critical	read tech news	1407	-0.12	4.1e-06	*
60	dependable	recreational research	1406	-0.05	5.3e-02	
80	anxious	advanced classes	1403	-0.07	1.3e-02	
100	anxious	enjoy learning	1403	-0.09	4.5e-04	
120	open	introspective	1404	-0.06	1.5e-02	
140	reserved	rather read	1406	-0.03	3.1e-01	
160	sympathetic	appearance < intellect	1409	0.03	1.9e-01	
180	sympathetic	strange person	1404	0.01	5.7e-01	
200	disorganized	read challenging material	1407	-0.02	5.0e-01	
220	calm	time at library	1407	-0.03	3.2e-01	
260	conventional	socially awkward	1404	-0.13	4.2e-07	*

Note. Due to the large size of the full results table (260 rows, representing all pairwise comparisons), only every 20th row is shown here. The first column provides the row number for each printed test; full results can be generated from the tutorial R script available at osf.io/re5w2/.

Compared to the family-wise error rate (FWER) control approaches of M_{eff} correction or Bonferroni correction, false discovery rate (FDR) approaches deal with multiple testing by first ranking already-conducted tests in order of ascending p-values, then determine statistical significance by evaluating each test against a sliding criterion, based on the rank ordering of the test being evaluated. Although commonly used FDR methods (such as Benjamini and Hochberg (1995)) assume independence of tests, alternative approaches are available that account for non-independent testing (Benjamini & Yekutieli, 2001). In well-powered studies, results of FWER and FDR approaches to multiple testing correction are expected to be the same. However, the threshold for statistical significance in FDR is based on the observed distribution of the test results; therefore, the threshold for declaring statistical significance cannot be established *a priori*. With FWER approaches, it is possible to establish *a priori* what the threshold for declaring statistical significance will be (for example, for the purpose of planning data collection). As long as a correlation matrix can be estimated among variables (whether all at once from a single study, or piecemeal from a variety of sources), the appropriate M_{eff} correction can be estimated to plan for multiple testing correction within a new sample.

M_{eff} correction uses eigenvalues to estimate the effective number of tests among non-independent variables (M_{eff}), making it flexible across a wide range of sub-fields and readily accessible to psychologists. Correcting the per-test α -level by M_{eff} allows researchers to transparently and flexibly account for the number of hypotheses explored. M_{eff} correction provides a simple, efficient, and standardized approach to controlling Type I or family-wise error in the presence of multiple non-independent comparisons.

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References

- Allaire, J., Xie, Y., McPherson, J., Luraschi, J., Ushey, K., Atkins, A., . . . Chang, W. (2018). *Rmarkdown: Dynamic documents for r*. Retrieved from <https://CRAN.R-project.org/package=rmarkdown>
- Aust, F., & Barth, M. (2018). *papaja: Create APA manuscripts with R Markdown*. Retrieved from <https://github.com/crsh/papaja>
- Bates, D., & Maechler, M. (2017). *Matrix: Sparse and dense matrix classes and methods*. Retrieved from <https://CRAN.R-project.org/package=Matrix>
- Benjamin, D. J., Berger, J. O., Johannesson, M., Nosek, B. A., Wagenmakers, E.-J., Berk, R., . . . others. (2018). Redefine statistical significance. *Nature Human Behaviour*, 2(1), 6–10.
- Benjamini, Y., & Hochberg, Y. (1995). Controlling the false discovery rate: A practical and powerful approach to multiple testing. *Journal of the Royal Statistical Society. Series B (Methodological)*, 289–300.
- Benjamini, Y., & Yekutieli, D. (2001). The control of the false discovery rate in multiple testing under dependency. *Annals of Statistics*, 1165–1188.
- Cheverud, J. M. (2001). A simple correction for multiple comparisons in interval mapping genome scans. *Heredity*, 87(1), 52–58.
- Cinar, O., & Viechtbauer, W. (2016). *PoolR: Package for pooling the results from (dependent) tests*.
- Dudbridge, F., & Gusnanto, A. (2008). Estimation of significance thresholds for genomewide association scans. *Genetic Epidemiology*, 32(3), 227–234.
- Dunn, O. J. (1961). Multiple comparisons among means. *Journal of the American Statistical Association*, 56(293), 52–64.
- Gosling, S. D., Rentfrow, P. J., & Swann Jr, W. B. (2003). A very brief measure of the big-five personality domains. *Journal of Research in Personality*, 37(6), 504–528.
- Grasby, K. L., Jahanshad, N., Painter, J. N., Colodro-Conde, L., Bralten, J., Hibar, D. P., . . .

- Medland, S. E. (2018). The genetic architecture of the human cerebral cortex. *bioRxiv*. doi:[10.1101/399402](https://doi.org/10.1101/399402)
- Hirschhorn, J. N., & Daly, M. J. (2005). Genome-wide association studies for common diseases and complex traits. *Nature Reviews Genetics*, 6(2), 95–108.
- Lakens, D., Adolphi, F. G., Albers, C. J., Anvari, F., Apps, M. A., Argamon, S. E., ... others. (2018). Justify your alpha. *Nature Human Behaviour*, 2(3), 168–171.
- McShane, B. B., Gal, D., Gelman, A., Robert, C., & Tackett, J. L. (2017). Abandon statistical significance. *arXiv Preprint arXiv:1709.07588*.
- Navarro, D. (2015). *Learning statistics with r: A tutorial for psychology students and other beginners. (version 0.5)*. Adelaide, Australia: University of Adelaide. Retrieved from <http://ua.edu.au/ccs/teaching/lr>
- Nyholt, D. R. (2004). A simple correction for multiple testing for single-nucleotide polymorphisms in linkage disequilibrium with each other. *The American Journal of Human Genetics*, 74(4), 765–769.
- Open Source Psychometrics Project. (2015). *Development of the nerdy personality attributes scale*. Retrieved March 22, 2018, from <https://openpsychometrics.org/tests/NPAS/development/>
- Perrett, D., Schaffer, J., Piccone, A., Roozeboom, M., & others. (2006). Bonferroni adjustments in tests for regression coefficients. *Multiple Linear Regression Viewpoints*, 32, 1–6.
- R Core Team. (2017). *R: A language and environment for statistical computing*. Vienna, Austria: R Foundation for Statistical Computing. Retrieved from <https://www.R-project.org/>
- Revelle, W. (2018). *Psych: Procedures for psychological, psychometric, and personality research*. Evanston, Illinois: Northwestern University. Retrieved from <https://CRAN.R-project.org/package=psych>
- Sherman, R. A., & Funder, D. C. (2009). Evaluating correlations in studies of personality

and behavior: Beyond the number of significant findings to be expected by chance.

Journal of Research in Personality, 43(6), 1053–1063.

Simmons, J. P., Nelson, L. D., & Simonsohn, U. (2011). False-positive psychology:

Undisclosed flexibility in data collection and analysis allows presenting anything as significant. *Psychological Science*, 22(11), 1359–1366.

Simonsohn, U., Nelson, L. D., & Simmons, J. P. (2014). P-curve: A key to the file-drawer.

Journal of Experimental Psychology: General, 143(2), 534.

Appendix. The meff function code

The function defined here is modified from poolR::meff.r (Cinar & Viechtbauer, 2016), licensed under the [GNU General Public License Version 2.0](#). meff can be loaded directly into R using: `source('https://osf.io/ws6xc/download')`.

```
meff = function(x, eigen = FALSE, correl = FALSE) {  
  # if the input x is eigenvalues  
  if(eigen) {  
    if(!class(x) %in% c("numeric", "integer")) {  
      stop("Eigenvalues are not numeric or integer.")  
    }  
    k = length(x)  
    evs = x  
  
    # if the input x is a correlation matrix  
  } else if(correl) {  
    # number of variables  
    k = ncol(x)  
  
    # dimension checks  
    if(!isSymmetric(x)) {  
      stop("Correlation matrix is not symmetric.")  
    }  
  
    # convert the correlation matrix to positive-definite  
    require(Matrix)  
    x = as.matrix(nearPD(x)$mat)  
  
    # get eigenvalues and absolute eigenvalues of correlation matrix  
    evs = eigen(x)$values  
  
    # otherwise the input x is assumed to be a dataframe
```

```
# with variables in columns and observations in rows
} else {

  # number of variables

  k = ncol(x)

  # get correlation matrix

  x = cor(x, use = "pairwise.complete.obs")

  # convert the correlation matrix to positive-definite.

  require(Matrix)

  x = as.matrix(nearPD(x)$mat)

  # get eigenvalues and absolute eigenvalues of R matrix

  evs = eigen(x)$values

}

# effective number of tests (Nyholt, 2004)

eff = 1 + (k - 1) * (1 - var(evs) / k)

return(eff)
}
```