Preface

Power is the probability that a study will reject the null hypothesis. The estimated probability is a function of sample size, variability, level of significance, and the difference between the null and alternative hypotheses. Similarly, the sample size required to ensure a pre-specified power for a hypothesis test depends on variability, level of significance, and the null vs. alternative difference. In order to understand our terms, we will review these key components of hypothesis testing before embarking on a numeric example of power and sample size estimation for the one-sample case.

Overview of Power Analysis and Sample Size Estimation

A hypothesis is a claim or statement about one or more population parameters, e.g. a mean or a proportion. A hypothesis test is a statistical method of using data to quantify evidence in order to reach a decision about a hypothesis. We begin by stating a null hypothesis, H₀, a claim about a population parameter (for example, the mean). We initially assume the null hypothesis to be true. H₀ is where we place the burden of proof for the data. The investigator usually hopes that the evidence in the data will disprove the null hypothesis. For a one-sample test of the mean, the null hypothesis H₀ is a simple statement about the expected value of the mean if the sample is representative of a given reference population. (Should this sentence be about the paired sample t-Test, and not the one-sample test?)

As an example, let us say that a Phase II one-arm pre vs. post trial design will be used to examine changes in Ki67 (a measure of cell proliferation, % of cells staining for Ki-67) after administration of resveratrol, an antioxidant found in the skins of grapes and other fruits, in persons at high risk of head and neck cancer. Ki-67 is measured in a tissue biopsy before the administration of resveratrol, and again 6 months after. The goal is to compare mean Ki-67 before resveratrol, $\mu_{Ki-67, pre}$, to mean Ki-67 after resveratrol, $\mu_{Ki-67, post}$. The null hypothesis is that there is no change in Ki-67, i.e. $H_0: \mu_{\Delta Ki-67} = \mu_{Ki-67, pre} - \mu_{Ki-67, post} = 0\%$. An opposing, or alternative hypothesis $H_1$ is then stated, contradicting $H_0$, e.g. $H_1: \mu_{\Delta Ki-67} = \mu_{Ki-67, pre} - \mu_{Ki-67, post} \neq 0\%$, $H_1: \mu_{\Delta Ki-67} = \mu_{Ki-67, pre} - \mu_{Ki-67, post} < 0\%$, or $H_1: \mu_{\Delta Ki-67} = \mu_{Ki-67, pre} - \mu_{Ki-67, post} > 0\%$. If the mean change from the sample is sufficiently different from 0% a decision is made to reject the null hypothesis. If the sample mean is close to zero, the null hypothesis cannot be rejected, but neither can a claim be made that the hypothesis is unequivocally true.
Because of sampling there is inherent uncertainty in the conclusion drawn from a hypothesis test. Either a correct or an incorrect decision will be made, and the goal is to minimize the chances of making an incorrect one. The probability of rejecting a true null hypothesis, called Type I Error, is denoted by $\alpha$. The probability of failing to rejecting a false null hypothesis, called Type II Error, is denoted by $\beta$. The possible outcomes of a hypothesis test are summarized in the table below along with the conditional probabilities of their occurrence.

<table>
<thead>
<tr>
<th>State of Nature</th>
<th>$H_0$ True</th>
<th>$H_1$ True</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Hypothesis Testing</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Decision</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>$\text{Fail to reject } H_0$</td>
<td>True negative</td>
<td>False negative</td>
</tr>
<tr>
<td></td>
<td>A correct decision</td>
<td>A Type II Error</td>
</tr>
<tr>
<td></td>
<td>Prob(True negative) = $1-\alpha$</td>
<td>Prob(False negative) = $\beta$</td>
</tr>
<tr>
<td>$\text{Reject } H_0$</td>
<td>False positive</td>
<td>True Positive</td>
</tr>
<tr>
<td></td>
<td>A Type I Error</td>
<td>A correct decision</td>
</tr>
<tr>
<td></td>
<td>Prob(False positive) = $\alpha$</td>
<td>Prob(True positive) = $1-\beta$</td>
</tr>
</tbody>
</table>

A Type I error occurs when $H_0$ is incorrectly rejected in favor of the alternative (i.e. $H_0$ is true). A Type II error occurs when $H_0$ is not rejected but should have been (i.e. $H_1$ is true). To keep the chances of making a correct decision high, the probability of a Type I error ($\alpha$, the level of significance of a hypothesis test) is kept low, usually 0.05 or less, and the power of the test (1-$\beta$, the probability of rejecting $H_0$ when $H_1$ is true) is kept high, usually 0.8 or more. When $H_0$ is true, the power of the test is equal to the level of significance. For a fixed sample size, the probability of making a Type II error is inversely related to the probability of making a Type I error. Thus, in order to achieve a desirable power for a fixed level of significance, the sample size will generally need to increase.

Other factors that impact power and sample size determinations include variability as summarized by $\sigma_\Delta^2$, where $\sigma_\Delta$ is the standard deviation of change in the population;
and the difference between the mean change under the null hypothesis and the mean change under a specific alternative, e.g. $\mu_{\Delta Ki-67} = 0\%$ vs. $\mu_{\Delta Ki-67} = 20\%$. In practice, $\sigma_\Delta$ can be difficult to specify. Previous work reported in the literature is a good source of information about variability of the change, but sometimes a pilot study needs to be carried out in order to obtain a reasonable estimate. Specifying the magnitude of the difference you wish to detect between the null and alternative hypothesis means varies by consideration of subject matter. The importance of a difference varies by discipline and context.

The following summarizes the interrelationships of power, sample size, level of significance, variability and detectable difference:

To increase power, $1-\beta$:

- Increase: Required Sample Size, $n$; Detectable Difference, between the mean under $H_0$ and $H_1$, $|\mu_0 - \mu_1|$; Level of significance, $\alpha$;
- Decrease: Variability, $\sigma_1^2$ and $\sigma_2^2$

To reduce required sample size, $n = n_1 + n_2$ -

- Increase: Detectable Difference, between the mean under $H_0$ and $H_1$, $|\mu_0 - \mu_1|$; Level of significance, $\alpha$
- Decrease: Variability, $\sigma_1^2$ and $\sigma_2^2$; power, $1-\beta$

The applet available through the link below illustrates these relationships:

http://wise.cgu.edu/power_applet/power.asp
An additional consideration for power analysis and sample size estimation is the direction of the alternative hypothesis. A one-sided alternative hypothesis, e.g. $H_1: \mu_{\Delta Ki} > 20\%$, leads to greater achievable power than a two-sided alternative for a fixed sample size, or a lower required sample size for a fixed power. The use of one-sided tests is controversial and should be well justified based on subject matter and context.

**Uncertainty in specifications of mean difference, variability**

For a discussion of the role of uncertainty regarding inputs to power analysis and sample size estimation, refer to the tutorial in this series on *Uncertainty in Power and Sample Size Estimation*. 
Content A: Features and Assumptions
Study design description: Ki-67 and resveratrol example

In the Ki-67 example, the inference relates to the mean change in Ki-67 in a single population. The outcome variable is continuous (change in % staining) with an unknown but finite variance of the change, $\sigma^2$. Since we base the % staining on a large number of tumor cells, we may reasonably assume a normal distribution value for that Ki-67 value. As linear functions of normally distributed quantities are also normally distributed, the change in Ki-67 from before treatment to after treatment is normally distributed. The $a\ priori$ stated hypothesis regards the mean change of Ki-67 and whether the mean is 0%. These are the features that make the example suitable for a paired-sample t-test.

In carrying out a paired-sample t-test we make the assumption that the individual change values are randomly sampled from a well-characterized population and are independent of each other, i.e. that there is no clustering between subjects or units of observation. In most cases, we can easily verify this assumption. In addition, we assume an approximately normal underlying distribution of change in Ki-67 with resveratrol. This assumption is harder to verify. For large samples the t-distribution will be a good approximation to the t-statistic for the data, but in small to moderate sized samples the approximation will not be as good.

Paired-sample t-test: inference about the mean change $\mu_\Delta$ when the variance of the change $\sigma^2_\Delta$ is unknown

To test the hypothesis about the mean change in Ki-67, the standardized value of the sample mean change, $\bar{X}_{Ki-67}$, becomes the test statistic, $t$. We assumed the $t$ value to follow a t distribution with $n-1$ degrees of freedom, i.e. the sample size minus 1:

$$t = \frac{\bar{X}_{Ki-67} - \mu_{\Delta_0}}{s_{\Delta Ki-67}/\sqrt{n}} \sim t_{n-1}$$

where $\mu_{\Delta_0}$ is the mean change under $H_0$, and $s_{\Delta Ki-67}$ is the sample standard deviation of the mean change in Ki-67. To test the hypothesis $H_0: \mu_{\Delta Ki-67} = 0\%$ vs. $H_1: \mu_{\Delta Ki-67} \neq 0\%$, we reject $H_0$ if:

$$\bar{X}_{Ki-67} > 0\% + t_{n-1,\frac{\alpha}{2}} s_{\Delta Ki-67}/\sqrt{n} \quad \text{or} \quad \bar{X}_{Ki-67} < 0\% - t_{n-1,1-\frac{\alpha}{2}} s_{\Delta Ki-67}/\sqrt{n},$$
where \( t_{n-1, 1-\alpha/2} \) is the \((1-\alpha/2) \times 100th \) percentile of the \( t \) distribution with \( n-1 \) degrees of freedom.

**The paired t-test as a General Linear Model (GLM)**

**Univariate test**

A more general characterization of the paired t-test can be made using the general linear model (GLM), \( Y = X \beta + \varepsilon \). For the test of the mean change in Ki-67, \( Y \) is an \( n \times 1 \) matrix of Ki-67 change values, \( X \) is an \( n \times 1 \) matrix of 1s, \( \beta \) is a \( 1 \times 1 \) matrix of the unknown regression coefficient (in this case the estimated mean change in Ki-67), and \( \varepsilon \) is an \( n \times 1 \) matrix that represents the random deviation of a single Ki-67 change value from the mean change. The \( Y \) and \( X \) matrices are shown below:

<table>
<thead>
<tr>
<th>( Y_\Delta )</th>
<th>( X )</th>
</tr>
</thead>
<tbody>
<tr>
<td>( Y_{1\text{Pre}} - Y_{1\text{Post}} )</td>
<td>1</td>
</tr>
<tr>
<td>( Y_{2\text{Pre}} - Y_{2\text{Post}} )</td>
<td>1</td>
</tr>
<tr>
<td>( \vdots )</td>
<td>( \vdots )</td>
</tr>
<tr>
<td>( Y_{n\text{Pre}} - Y_{n\text{Post}} )</td>
<td>1</td>
</tr>
</tbody>
</table>

The assumptions of the GLM are:

- **Existence**: For any fixed value of the variable \( X \), \( Y \) is a random variable with a certain probability distribution having finite mean and variance.
- **Independence**: The \( Y \)-values are statistically independent of one another.
- **Linearity**: The mean value of \( Y \) is a straight-line function of \( X \).
- **Homoscedasticity (equal variances)**: The variance of \( Y \) is the same for any value of \( X \). That is,
  \[
  \sigma^2_{Y|X} = \sigma^2_{Y|X=1} = \sigma^2_{Y|X=2} = \ldots = \sigma^2_{Y|X=x}
  \]

- **Normal Distribution**: For any fixed value of \( X \), \( Y \) has a normal distribution. Note this assumption does **not** claim normal distribution for \( Y \).

We obtain the estimate of \( \beta \), \( \hat{\beta} \), using the method of least squares. To test the hypothesis \( H_0: \mu_{\Delta \text{Ki-67}} = 0\% \), we use the standardized value of \( \hat{\beta} \), which is distributed
as a t with n-1 degrees of freedom: \( t = \frac{\hat{\beta} - 0\%}{\sqrt{\frac{s_{y|x}}{\sqrt{n}}}} - t_{n-1} \), where \( s_{y|x} \) is the square root of the residual variance from the GLM.

**Test based on repeated measures**

Alternatively, still using the GLM, the hypothesis can be tested using a repeated measures design. In this design Y is an n x 2 matrix, where the first column contains the pre-treatment and the second column contains the post-treatment measures. X is an n x 1 matrix of 1s, \( \beta \) is a 1 x 2 matrix of the unknown regression coefficients, in this case the estimated pre- (\( \hat{\beta}_1 \)) and post-treatment (\( \hat{\beta}_2 \)) Ki-67 means, and \( \varepsilon \) is an n x 2 matrix that represents the random deviations of single Ki-67 observations from the pre-treatment mean (column 1) and from the post-treatment mean (column 2). The Y and X matrices are shown below:

\[
\begin{array}{ccc}
Y_{pre} & Y_{post} & X \\
Y_{1Pre} & Y_{1Post} & 1 \\
Y_{2Pre} & Y_{2Post} & 1 \\
\vdots & \vdots & \vdots \\
Y_{nPre} & Y_{nPost} & 1 \\
\end{array}
\]

The hypothesis, e.g. \( H_0: \mu_{\Delta Ki-67} = \mu_{Ki-67, pre} - \mu_{Ki-67, post} = 0\% \), is tested by contrasting the elements of \( \beta \): \( t = \frac{(\hat{\beta}_1 - \hat{\beta}_2)}{\sqrt{\frac{s^2_{\hat{\beta}_1} + s^2_{\hat{\beta}_2} - 2 \text{cov}(\hat{\beta}_1, \hat{\beta}_2)}}} \sim t_{n-1} \), where \( s^2_{\hat{\beta}_1} \) and \( s^2_{\hat{\beta}_2} \) are the estimated variances of \( \hat{\beta}_1 \) and \( \hat{\beta}_2 \), respectively, and \( \text{cov}(\hat{\beta}_1, \hat{\beta}_2) \) is the covariance between them.

For a more general presentation on power and sample size analysis for repeated measures, refer to the tutorial on Repeated Measures.
Content B: How to obtain inputs for power analysis and sample size estimation

B.1 Inputs for Power analysis

A power analysis for mean change consists of determining the achievable power for a specified difference between the mean change under the stated $H_0$ and under the stated $H_1$, sample size, standard deviation of the change, and $\alpha$-level. By varying these four quantities a set of power curves can be obtained that show the tradeoffs.

Information about mean change values and variability of change can be obtained from the published literature. Sample size can be varied over a feasible range of values, and various values of $\alpha$ can be selected to illustrate the sensitivity of the results to conservative vs. liberal choices for the Type I error rate.

For the change in Ki-67 expected with resveratrol, we look to a study examining change in Ki-67 which reports a standard deviation of 14% for change in Ki-67. It should be noted that in some publications, standard error values are reported. Standard errors refer to the precision of a mean, not to the variability in a single sample. To convert a standard error to a standard deviation, multiply the standard error by the square root of the sample size. Often separate standard deviations of the pre- and post- measures are reported instead of the standard deviation of the change. In this case, assumptions must be made about the correlation, $\rho$, between the pre- and post- measures in order to obtain an estimate for the standard deviation of change. A value of 0 for $\rho$ means the pre- and post- measures are uncorrelated while a value of 1 means they are perfectly correlated. Low values of $\rho$ would lead to conservative power and sample size estimates while large values of $\rho$ would lead to liberal ones. For a specific $\rho$ value, we obtain the standard deviation of change as:

$$s_\Delta = \sqrt{s_{\text{pre}}^2 + s_{\text{post}}^2 - 2\rho s_{\text{pre}} s_{\text{post}}}$$

where $s^2$ and $s$ are the sample variance and standard deviation, respectively. Rarely is the variance reported in a publication. If reported, the researchers usually obtain the standard deviation as the square root of the variance.

Even when using information from large studies in the literature, we cannot assume that the means and standard deviations are known quantities. These values are estimates, and as such lead to uncertainty in estimated power. For further discussion about uncertainty refer to the Tutorial 0: Uncertainty in Power and Sample Size Estimation.
Specification of the difference between means for change, $\mu_{A0} - \mu_{A1}$

As noted above, subject matter considerations dictate the choice of a value for the difference between the null and alternative mean change. The goal is to specify the smallest difference that would be considered scientifically important. For the paired-sample Ki-67 example, we consider a difference of 20% biologically important.

B.2 Inputs for sample size estimation

Sample size estimation for a single mean from paired observations consists of determining the required sample size to achieve a specified level of power for a given difference between the mean change under the stated $H_0$ and under the stated $H_1$, standard deviation of the change, and $\alpha$-level. By varying these four quantities we can obtain a set of sample size curves that show the tradeoffs.

As with power analysis, information about mean values and variability can be obtained from the published literature. Uncertainty in these estimates should be incorporated into the sample size estimation by either allowing those values to vary over a reasonable range, e.g. from 0.5 times up to twice the standard deviation, or by using sampling variability to obtain confidence intervals for power or sample size. Power can be varied over a desired range of values, and various values of $\alpha$ can be selected to illustrate the sensitivity of the results to conservative vs. liberal choices for the Type I and Type II error rates.
Content C: How to use the software
How to perform the analysis in GLIMMPSE

To start GLIMMPSE 2.0 beta, type [http://samplesizeshop.com/calculate-power-and-sample-size-now/](http://samplesizeshop.com/calculate-power-and-sample-size-now/) in your browser window or visit [www.SampleSizeShop.com](http://www.SampleSizeShop.com) and click on the GLIMMPSE tab, then on GLIMMPSE 2.0.0 Beta is Here! Google Chrome is the suggested browser for this application.

C.1 Power analysis using Guided Study Design mode

Guided Study Design mode is suggested for most users.

![Guided Study Design](image)

Selecting *Guided Study Design* takes you to the *Introduction* page:
Throughout your use of the GLIMMPSE website, use the blue arrows at the bottom of the screen to move forward and backwards. The pencil symbols beside the screen names on the left indicate required information that has not yet been entered. In the above picture, the pencils appear next to the **Solving For** and the **Type I Error** screen names.

Once the required information is entered, the pencils become green check marks. A red circle with a slash through it indicates that a previous screen needs to be filled out before the screen with the red circle can be accessed. Search for a pencil beside a screen name in the previous tabs to find the screen with missing entries.

Once you have read the information on the **Introduction** screen, click the forward arrow to move to the next screen.

The **Solving For** screen allows you to select Power or Sample Size for your study design. For the purposes of this tutorial, click **Power**. Click the forward arrow to move to the next screen.
The *Type I Error* screen allows you to specify the fixed levels of significance for the hypothesis to be tested. Once you have entered your values, click the forward arrow to move to the next screen.
Read the information on the Sampling Unit: Introduction screen and click next to move to the next screen.

For a one-sample test, there is one fixed predictor with one level. On the Study Groups screen, select One group and click the forward arrow to move to the next screen.

Since no covariate and no clustering will be used, skip the Covariate and the Clustering screens.

Use the Sample Size screen to specify the size of the smallest group for your sample size(s). Although only one sample is being used for this example, entering multiple values for the smallest group size allows you to consider a range of total sample sizes.
Read the *Responses Introduction* screen, and click the forward arrow when you have finished.

The *Response Variable* screen allows you to enter the response variable(s) of interest. In this example, the response variable is Ki-67. Click the forward arrow when you have finished entering your value(s).
The *Repeated Measures* screen should be skipped, as there are no repeated measures for this example.

Read the *Hypothesis: Introduction* screen, then click the forward arrow to move to the *Hypothesis* screen.

The *Hypotheses* screen allows you to enter the known mean values for your primary hypothesis. For this example, enter 0.
Read the information on the *Means: Introduction* screen, then click the forward arrow. The *Mean Differences* screen allows you to specify the difference between the null and alternative hypothesis means. For this example, enter 20%, or 20, in the screen below, then click the forward arrow to continue.

The *Beta Scale Factors* screen allows you to see how power varies with the assumed difference, so that you can allow it to vary over a reasonable range. GLIMMPSE allows this to be from 0.5x to 2x the stated difference, e.g. from 10% to 20% to 40%. Click *Yes*, then click on the forward arrow to continue.
Read the information on the *Variability: Introduction* screen, then click the forward arrow to continue.

The *Within Participant Variability* screen allows you to specify the expected variability in terms of standard deviation of the outcome variable. For this example, the standard deviation of the change in Ki-67 was estimated to be 14%. Enter 14 and click Next to continue.

The true variability in change in Ki-67 is also uncertain. To see how power varies with the assumed s.d., you can allow the s.d. to vary over a reasonable range. GLIMMPSE allows this to be from 0.5x to 2x the stated s.d., e.g. from 7% to 14% to 28%. Click on Yes, then click the forward arrow to continue.
Read the information on the Options screen, then click the forward arrow to continue.

For the paired-sample test of mean change, the available tests in GLIMMPPSE yield equivalent results. Click on any one of the tests and then click the forward arrow to continue.

Leave the box checked in the Confidence Interval Options screen, and click forward to continue to the next screen.

Power analysis results are best displayed on a graph. To obtain a plot, first uncheck No thanks on the Power Curve Options screen.
From the pull down menu that appears once you have unchecked the box, select the variable to be used as the horizontal axis (e.g. *Total sample size* or *Variability Scale Factor*). GLIMMPSE will produce one power plot based on specific levels of the input variables that you specify on this page. If you specified more than one value for an input variable, choose the specific level you want GLIMMPSE to use to plot the power curve.

After you have made your inputs, click Add to populate the screen, then click the forward arrow to see your results.

The power curve and table results for these inputs are shown in Section D below.
C.2 Sample size estimation with GLIMMPSE

To start, click on Total Sample Size in the Solving For screen. Click on the forward arrow to move to the next screen.

Enter the values for desired power, then click the forward arrow to move to the next screen.

The remaining screens are filled in as above for power.
Content D: Interpret the results

Power analysis interpretation

For the power analysis inputs in Guided Study Design Mode (Section C.1), GLIMMPSE produces a curve showing the relationship between achievable power, mean difference (beta scale), standard deviation (variability scale), and fixed values of total sample size and level of significance. A complete downloadable table of results in Excel.csv format is also produced. The plot below shows achievable power over a range of differences in mean change in Ki-67 and standard deviations of change in Ki-67 with an $\alpha$-level of 0.05 (two-sided) and a sample size of 30.

It can be observed in the graph below that above a certain level of variability, power is much less sensitive to changes in specified values. The sensitivity of power to assumptions within a certain range of values has been called the slippery slope of power. In order to avoid the slippery slope, it is best to assume a large amount of variability and/or a large difference between null and alternative means.
Sample size estimation interpretation

For the sample size estimation inputs in Guided Study Design mode above, GLIMMPSE produces a downloadable table showing the relationship between required sample size, desired power, level of significance, variability, and difference between null and alternative hypothesis means. This can be saved in Excel.csv format and plotted.
List of matrices used in calculation:

\[
E_0(X) = \begin{bmatrix} 1.0000 \end{bmatrix}
\]

\[
B = \begin{bmatrix} 20.0000 \end{bmatrix}
\]

\[
C = \begin{bmatrix} 1.0000 \end{bmatrix}
\]

\[
U = \begin{bmatrix} 1.0000 \end{bmatrix}
\]

\[
\Theta_0 = \begin{bmatrix} 0.0000 \end{bmatrix}
\]

\[
\Sigma_\beta = \begin{bmatrix} 196.0000 \end{bmatrix}
\]

For the paired-sample t-test, GLIMMPSE works with the matrices listed above in making the computations. Since only a single mean is being tested the matrices are all of dimension 1 x 1. The \( \Theta_0 \) matrix represents the mean under \( H_0 \) and the \( \Sigma_\epsilon \) matrix represents the between-subject variance. The remaining matrices \( E_0(X) \), \( C \) and \( U \) are scalars with a value of 1.

References


Ki-67 staining

Figure 2
Immunohistochemical detection in primary pretreatment biopsies of: (A) a low percentage (17%) of Ki-67-positive nuclear staining; (B) a high percentage (93%) of Ki-67-positive nuclear staining.

From: Br J Cancer. 2008 October 7; 99(7): 1121–1128. Published online 2008 September 2. doi: 10.1038/sj.bjc.6604633

Copyright/License Request permission to reuse

Normal curves for power analysis and sample size estimation

Consider the distribution of $\bar{X}$ if $\mu = \mu_0$ and if $\mu = \mu_1$

$\bar{X} \sim N\left(\mu_1, \frac{\sigma^2}{n}\right)$  \hspace{1cm} $\bar{X} \sim N\left(\mu_0, \frac{\sigma^2}{n}\right)$

Area = $\alpha/2$  \hspace{1cm} Area = $\alpha/2$

1-\(\beta\)  \hspace{1cm} $\frac{\sigma}{\sqrt{n}}$

Lower Rejection Region  \hspace{1cm} Acceptance Region  \hspace{1cm} Upper Rejection Region