

Standard deviation and standard error of the mean

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In most clinical and experimental studies, the standard deviation (SD) and the estimated standard error of the mean (SEM) are used to present the characteristics of sample data and to explain statistical analysis results. However, some authors occasionally muddle the distinctive usage between the SD and SEM in medical literature. Because the process of calculating the SD and SEM includes different statistical inferences, each of them has its own meaning. SD is the dispersion of data in a normal distribution. In other words, SD indicates how accurately the mean represents sample data. However the meaning of SEM includes statistical inference based on the sampling distribution. SEM is the SD of the theoretical distribution of the sample means (the sampling distribution). While either SD or SEM can be applied to describe data and statistical results, one should be aware of reasonable methods with which to use SD and SEM. We aim to elucidate the distinctions between SD and SEM and to provide proper usage guidelines for both, which summarize data and describe statistical results.

Key Words: Standard deviation, Standard error of the mean

A data is said to follow a *normal distribution* when the values of the data are dispersed evenly around one representative value. A *normal distribution* is a prerequisite for a parametric statistical analysis [1]. The *mean* in a normally distributed data represents the central tendency of the values of the data. However, the *mean* alone is not sufficient when attempting to explain the shape of the distribution; therefore, many medical literatures employ the *standard deviation* (SD) and the *standard error of the mean* (SEM) along with the *mean* to report statistical analysis results [2].

The objective of this article is to state the differences with regard to the use of the SD and SEM, which are used in descriptive and statistical analysis of normally distributed data, and to

propose a standard against which statistical analysis results in medial literatures can be evaluated.

Medical studies begin by establishing a hypothesis about a *population* and extracting a sample from the *population* to test the hypothesis. The extracted sample will take a *normal distribution* if the sampling process was conducted via an appropriate *randomization method* with a sufficient *sample size*. As with all normally distributed data, the characteristics of the sample are represented by the *mean*, *variance* or SD. The *variance* or SD includes the differences of the observed values from the *mean* (Fig. 1); thus, these values represent the variation of the data [1-3]. For instance, if the observed values are scattered closely around the *mean* value, the *variance* — as well as the SD — are reduced. However, the *variance* can confuse the interpretation of the data because it is computed by squaring the units of the observed values. Hence, the SD, which uses the same units used with the *mean*, is more appropriate [3] (Equations 1 and 2).

Sample: $x_1, x_2, x_3, \dots, x_n$ (*sample size* = n)

$$\text{Mean } (\bar{x}) = \frac{\sum_{i=1}^n x_i}{n} \dots\dots\dots \text{Equation 1}$$

$$\text{Variance} = \frac{\sum_{i=1}^n (\bar{x} - x_i)^2}{n-1}, \text{ Standard Deviation (SD)} = \sqrt{\frac{\sum_{i=1}^n (\bar{x} - x_i)^2}{n-1}} \dots\dots\dots \text{Equation 2}$$

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Received: April 2, 2015.
 Revised: 1st, April 21, 2015; 2nd, April 24, 2015; 3rd, May 6, 2015.
 Accepted: May 7, 2015.

Korean J Anesthesiol 2015 June 68(3): 220-223
<http://dx.doi.org/10.4097/kjae.2015.68.3.220>

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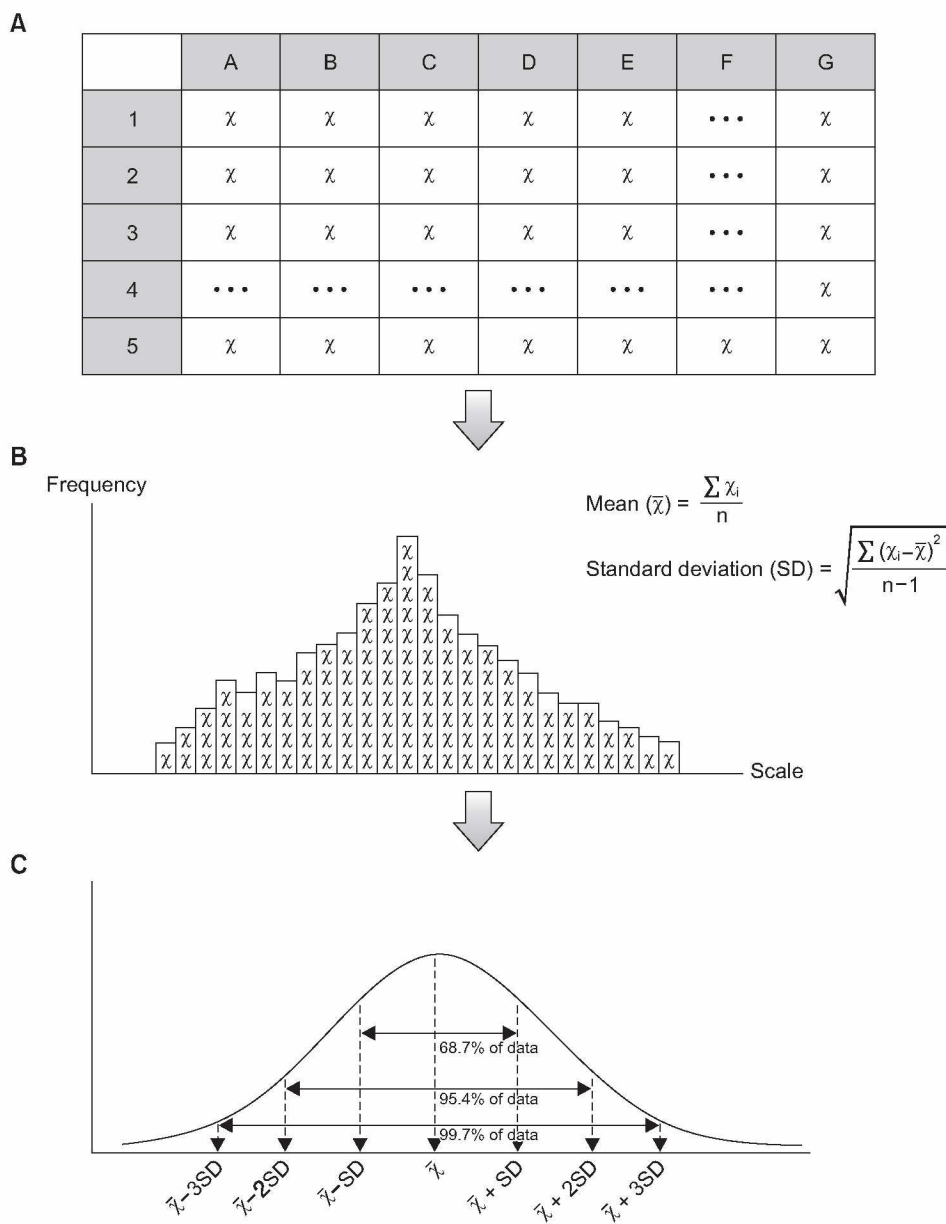


Fig. 1. Process of data description. First, we gather raw data from the population by means of randomization (A). We then arrange the each value according to the scale (frequency distribution); we can presume the shape of the distribution (probability distribution) and can calculate the mean and standard deviation (B). Using these mean and standard deviation, we produce a model of the normal distribution (C). This distribution represents the characteristics of the data we gathered and is the normal distribution, with which statistical inferences can be made (\bar{x} : mean, SD: standard deviation, x_i : observation value, n: sample size).

As mentioned previously, using the SD concurrently with the mean can more accurately estimate the variation in a normally distributed data. In other words, a normally distributed statistical model can be achieved by examining the mean and the SD of the data [1] (Fig. 1, Equations 1 and 2). In such models, approximately 68.7% of the observed values are placed within one SD from the mean, approximately 95.4% of the observed values are arranged within two SDs from the mean, and about 99.7% of the observed values are positioned within three SDs from the mean [1,4]. For this reason, most medical literatures report their samples in the form of the mean and SD [5].

The sample as referred to in medical literature is a set of observed values from a population. An experiment must be

conducted on the entire population to acquire a more accurate confirmation of a hypothesis, but it is essentially impossible to survey an entire population. As a result, an appropriate sampling process — a process of extracting a sample that represents the characteristics of a population — is essential to acquire reliable results. For this purpose, an appropriate sample size is determined during the research planning stage and the sampling is done via a randomization method. Nevertheless, the extracted sample is still a part of the population; thus, the sample mean is an estimated value of the population mean. When the samples of the same sample size are repeatedly and randomly taken from the same population, they are different each other because of sampling variation as well as sample means (Fig. 2, Level B). The

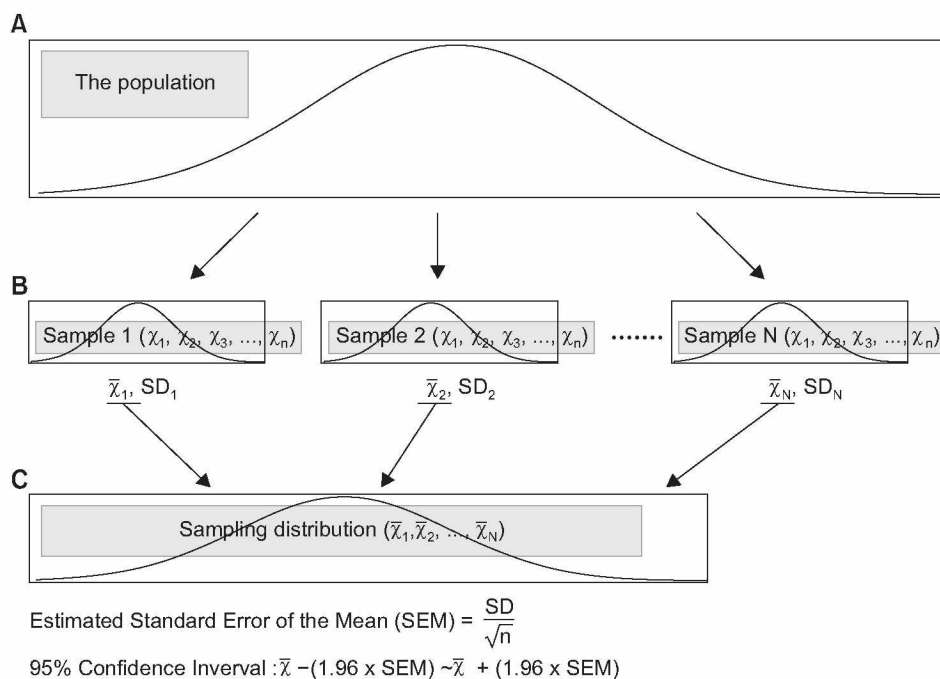


Fig. 2. Process of statistical inference. Level A indicates the population. In most experiments, we only obtain one set of sample data from the population using randomization (Level B); the mean and standard deviation are calculated from sample data we have. For statistical inference purposes, we assume that there are several sample data sets from the population (Level B); the means of each sample data set produce the sampling distribution (Level C). Using this sampling distribution, statistical analysis can be conducted. In this situation, the estimated standard error of the mean or the 95% confidence interval has an important role during the statistical analysis process (\bar{x} : mean, SD: standard deviation, n: sample size, N: number of sample data sets extracted from population).

distribution of different *sample means*, which is achieved via repeated sampling processes, is referred to as the *sampling distribution* and it takes a *normal distribution* pattern (Fig. 2, Level C) [1,6,7]. Therefore, the SD of the *sampling distribution* can be computed; this value is referred to as the SEM [1,6,7]. The SEM is dependent on the variation in the *population* and the number of the extracted samples. A large variation in the *population* causes a large difference in the *sample means*, ultimately resulting in a larger SEM. However, as more samples are extracted from the *population*, the *sample means* move closer to the *population mean*, which results in a smaller SEM. In short, the SEM is an indicator of how close the *sample mean* is to the *population mean* [7]. In reality, however, only one sample is extracted from the *population*. Therefore, the SEM is estimated using the SD and a *sample size* (Estimated SEM). The SEM computed by a statistical program is an estimated value calculated via this process [5] (Equation 3).

$$\text{Estimated Standard Error of the Mean (SEM)} = \frac{SD}{\sqrt{n}} \cdots \text{Equation 3}$$

A *confidence interval* is set to illustrate the *population mean* intuitively. A 95% *confidence interval* is the most common [3,7]. The SEM of a *sampling distribution* is estimated from one sample, and a *confidence interval* is determined from the SEM (Fig. 2, Level C). In the strict sense, the 95% *confidence interval* provides the information about a range within which the 95% *sample means* will fall, it is not a range for the *population mean* with 95% confidence. For example, a 95% *confidence interval* signifies that when 100 *sample means* are calculated from 100 samples

from a *population*, 95 of them are included within the said *confidence interval* and 5 are placed outside of the *confidence interval*. In other words, it does not mean that there is a 95% probability that the *population mean* lies within the 95% *confidence interval*.

When statistically comparing data sets, researchers estimate the *population* of each sample and examine whether they are identical. The SEM — not the SD, which represents the variation in the sample — is used to estimate the *population mean* (Fig. 2) [4,8,9]. Via this process, researchers conclude that the sample used in their studies appropriately represents the *population* within the error range specified by the pre-set significance level [4,6,8].

The SEM is smaller than the SD, as the SEM is estimated usually the SD divided by the square root of the *sample size* (Equations 2 and 3). For this reason, researchers are tempted to use the SEM when describing their samples. It is acceptable to use either the SEM or SD to compare two different groups if the *sample sizes* of the two groups are equal; however, the *sample size* must be stated in order to deliver accurate information. For example, when a *population* has a large amount of variation, the SD of an extracted sample from this *population* must be large. However, the SEM will be small if the *sample size* is deliberately increased. In such cases, it would be easy to misinterpret the *population* from using the SEM in *descriptive statistics*. Such cases are common in medical research, because the *variables* in medical research impose many possible *biases* originated from inter- and intra-individual variations originated from underlying general conditions of the patients and so on. When interpreting the SD

and SEM, however, the exact meaning and purposes of the SD and SEM should be considered to deliver correct information. [3,4,6,7,10].

We examined 36 clinical or experimental studies published in Volume 6, Numbers 1 through 6 of the *Korean Journal of Anesthesiology* and found that a few of the studies inappropriately used the SD and SEM. First, examining the *descriptive statistics*, we found that all of the studies used the *mean* and SD or the observed number and percentage. One study suggested a *95% confidence interval*; this particular study appropriately stated the *sample size* along the *confidence interval*, offering a clearer understanding of the data suggested in the study [11]. Among the 36 studies examined, only one study described the results of a *normality test* [12]. Second, all 36 studies used the SD, the observed number or the percentage to describe their statistical results. One study did not specify what the values in the graphs and tables represent (i.e., the *mean*, SD or *interquartile range*). There was also a study that used the *mean* in the text but showed an *interquartile range* in the graphs. Sixteen studies used either the observed number or the percentage, and most of them reported their results without a *confidence interval*. Only two studies stated *confidence intervals*, but only one of those two studies

appropriately used the *confidence interval* [13]. As shown above, we found that some of the studies have inappropriately used the SD, SEM and *confidence intervals* in reporting their statistical results. Such instances of the inappropriate use of *statistics* must be meticulously screened during manuscript reviews and evaluations because they may hamper an accurate comprehension of a study's data.

In conclusion, the SD reflects the variation in a normally distributed data, and the SEM represents the variation in the *sample means* of a *sampling distribution*. With this in mind, it is pertinent to use the SD (paired with a *normality test*) to describe the characteristics of a sample; however, the SEM or *confidence interval* can be used for the same purpose if the *sample size* is specified. The SEM, paired with the *sample size*, is more useful when reporting statistical results because it allows an intuitive comparison between the estimated populations via graphs or tables.

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