Parametric measures of variation around the sample mean

For a dataset of \( N \) observations sampled at random from a normally distributed population of interest, the sample mean is the average value per observation given by the sum of the data divided by \( N \). Always accompany the sample mean with a description of the sample variation (v or SD) or an inference about the population based on the sample variation (SE or CI).

The sample variance \((v)\) is a measure of the spread of data around the sample mean, given by the mean square deviation of the data (the average squared deviation from the mean per degree of freedom\(^1\)). In an Analysis of Variance on two or more samples, the variance equals the MS[Error], which is used to calibrate MS[Test] in calculating the statistic \( F \).

The sample standard deviation (SD) equals the square root of \( v \). About 68\% of normally distributed data lies within 1 SD either side of the mean, and 95\% of values lie within 1.96 SD of the mean. Sample means are often described with their SD, or plotted ± 1SD.

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The standard error of the mean (SE) is the SD of sample means around the population mean, and so a measure of the variability amongst the means of samples taken from the same population. It equals the square root of the contribution per observation to the sample variance: \( \sqrt{v/N} \) = SD/\( \sqrt{N} \). An analysis of variance is often illustrated by means ± 1SE.

The confidence interval (CI) hosts the range of plausible values of the population mean \( \mu \) for a population that yields the sample mean and variance. A smaller CI indicates more precision in estimating \( \mu \). The Central Limit Theorem dictates that the CI applies even to non-normally distributed populations, given a large enough sample from the population.

The plot below shows a sample mean and 95% CI. Suppose the sample comprises \( N = 24 \) chicks from a population of interest, and the response \( y \) is their change in body mass (g) over the first 12 hours since hatching. The sample mean = 2.60 g shows that these chicks gained weight on average. The CI reveals, however, that a population with normally distributed growth around a mean of \( \mu = 0 \) would yield sample means at least as deviant as the observed one in more than 5\% of samples comprising 24 randomly selected chicks. Likewise, a population with \( \mu = 5 \) g would yield sample means at least as deviant in > 5\% of samples. The CI encompasses the range of plausible values of \( \mu \) given only the sample data and the assumption of normality. Thus we fail to reject a null hypothesis \( H_0 = 0 \) or 5 or anywhere within the CI. In this scenario, we cannot be confident that the conditions experienced by the sample will favour chick growth in the population.

![Confidence Interval Example](image)

**Fig. 1.** Sample from a population with unknown \( \mu \).

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\(^1\) For a sample of \( N \) data points, the variance has degrees of freedom \( = N - 1 \). This is because by definition of the sample mean \( \bar{y} \), the sum \( \sum_i (y_i - \bar{y}) = 0 \); thus if we know \( N - 1 \) of the deviations, we can calculate the last one, meaning that there are only \( N - 1 \) freely varying deviations.
Formulae for parametric measures of variation

Sample mean: \( \bar{y} = \frac{\sum_{i=1}^{N} y_i}{N} \)

Sample variance: \( v = \frac{\sum_{i=1}^{N} (y_i - \bar{y})^2}{N-1} \)

Standard deviation: \( SD = \sqrt{v} \)

Standard error of the mean: \( SE = \frac{SD}{\sqrt{N}} \)

Confidence interval: \( CI = \bar{y} \pm t_{\alpha\frac{N}{2}} \cdot SE \)

One-sample test of \( H_0 = \mu \): Student’s \( t = (\bar{y} - \mu)/SE \)

The confidence interval, CI, for a threshold Type-I error \( \alpha \), lies either side of the sample mean between limits \( \bar{y} \pm t_{\alpha\frac{N}{2}} \cdot SE \), where the quantile \( t_{\alpha\frac{N}{2}} \) is the critical value of the Student’s \( t \) distribution at two-tailed \( \alpha \) for \( N-1 \) degrees of freedom [given by the R command: \( qt(1-\alpha/2, N-1) \)]. For a very large sample, the 95% CI are well approximated by 1.96×SE. For the Fig.-1 data, \( \bar{y} = 2.60 \, g \), \( SE = 1.477 \), \( N = 24 \), and \( t_{0.05} = 2.069 \); so the 95% CI = 2.60 ± 3.05 g.

The one-sample Student’s \( t \) statistic tests the compatibility of the data with a refutable null hypothesis: \( H_0 = \mu \). The data give \( t = (\bar{y} - \mu)/SE \), with \( N-1 \) degrees of freedom. The probability, \( P \), of Type-I error (rejecting a true null hypothesis) can be found by evaluating \( t \) against its \( \alpha \)-quantile, \( t_{\alpha\frac{N}{2}} \) for a two-tailed test (obtained either with the R command given above, or from a table of \( \alpha \)-quantiles of the Student’s \( t \) distribution). If \( t \) exceeds the critical value, then \( P < \alpha \) and we reject \( H_0 \). Alternatively, \( P \) is obtained directly with the R command: \( 2 \times (1 - pt(abs(t), N-1)) \). For example, an analysis of the Fig.-1 data fails to refute the null hypothesis of zero growth (\( t_3 = 1.76, P = 0.09 \)). The value of \( P \) is the probability of data at least as deviant given the null hypothesis, and thus the probability of making a mistake by rejecting a true \( H_0 \). In other words, a normally distributed population with mean \( \mu = 0 \, g \) has 9% probability of yielding a sample mean at least as deviant as the observed \( \bar{y} = 2.60 \, g \). At > 5%, this is too high a probability for us to reject the possibility of zero growth in the population. The result accords perfectly with the inference we drew from the 95% CI (page 1 above and Fig. 1).
R commands for plotting Fig. 1

```r
# Plot of a single sample mean with 95% CI.

library(gplots) # *** requires installation of package 'gplots' ***

mu <- 0 # the null hypothesis for the value of the population mean
alpha <- 0.05 # critical threshold for Type-I error

y <- c(-3.4076, -8.5488, -1.8395, -5.6626, -2.8127, -4.6241, -1.6908, -4.7169, -0.6191, 1.2085, 5.1147, 7.2654, 4.4188, 6.3951, 0.5986, -4.5985, 13.322, 17.0426, 14.66, 16.1283, 8.5927, 2.2129, 1.8934, 2.0203) # the data

N <- length(y) ; DF <- N - 1
x <- c(rep("1", N)) # single sample x = 1
SE <- sqrt(var(y)/N) # SE = sqrt(v/N)
Cl <- SE*qt(1-alpha/2, DF) # confidence limits either side of mean

par(cex = setcex) # set the font size for labels

# Add reference line, axis labels, and legend

windowsFonts( A = windowsFont("Times"),
            B = windowsFont("Arial"),
            C = windowsFont("Cambria"))

abline(h = mu, lty = 3) # reference line for null hypothesis

if (mu > (mean(y)+qt(1-alpha/2,DF))*0.9) {ps = 1} else {ps = 3} # text below/above Line

text(1.3, mu, substitute(paste(italic("H"), "[0], "~italic("\u03bc")~", v), list(v=mu)),
     pos=ps, cex=setcex/2, family = "A")

mtext("x", font = 3, side = 1, line = 0.5,
      las = 1, cex = setcex, family = "A")

mtext(substitute(paste("Response mean and ",v,"% CI"), list(v=100*(1-alpha))),
      side = 2, line = 2.5, las = 0, cex = setcex, family = "B")

mtext(expression(" ~italic("y")~"),
      side = 2, line = 2.5, las = 0, cex = setcex, family = "A")

mtext(expression(~ bold("Fig. 1."~~ Sample from a population with unknown"~italic("\u03bc\. "))),
      side = 1, line = 1.5, cex = setcex, family = "C")

# Report statistics

writeLines(sprintf("Sample mean = %.2f g.",mean(y))) # mean (with trailing zero)

## Sample mean = 2.60 g.

t <- (mean(y)-mu)/SE ; P <- 2*(1-pt(abs(t),DF)) # Student's t test
tcrit <- qt(1-alpha/2, DF) # critical t at alpha for a two-tailed test

if (abs(t) > tcrit) {result <- "Reject"} else {result <- "Fail to reject"}
writeLines(c(result, " \ H0: mu = \), mu, sprintf(" (t = %.3f, \),t),
    sprintf("DF = %.3f, \),DF),
    sprintf("P = %.3f; \),P),
    sprintf("[t[alpha=\%.2f \],alpha),
    sprintf(" = %.3f).",tcrit)

## Fail to reject H0: mu = 0 (t = 1.762, DF = 23, P = 0.091; t[alpha=0.05] = 2.069).

# rm(list = ls())

par(par(no.readonly = TRUE))
```