

## 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).

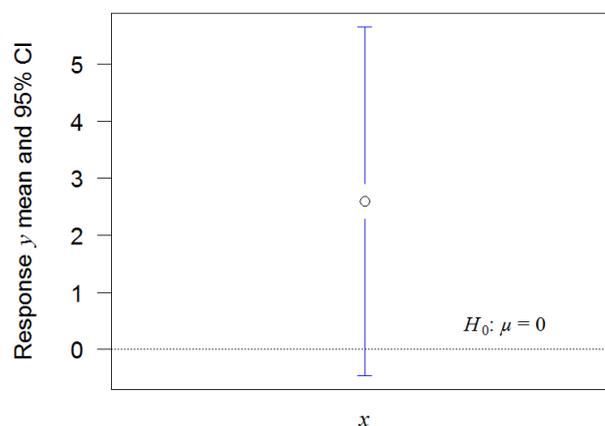
The sample *variance* ( $v$ ) is a measure of the spread of data around the sample mean, given by the mean square deviation of the data (the average squared deviation from the mean per degree of freedom<sup>1</sup>). In an Analysis of Variance on two or more samples, the variance equals the MS[Error], 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  $\pm 1$ SD.

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:  $\sqrt{v/N} = \text{SD}/\sqrt{N}$ . An analysis of variance is often illustrated by means  $\pm 1$ SE.

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.



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

<sup>1</sup> 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

$$\text{Sample mean: } \bar{y} = \sum_{i=1}^N y_i / N$$

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

$$\text{Standard deviation: } SD = \sqrt{v}$$

$$\text{Standard error of the mean: } SE = SD / \sqrt{N}$$

$$\text{Confidence interval: } CI = \bar{y} \pm t_{[\alpha] N-1} \cdot SE$$

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

The confidence interval, CI, for a threshold Type-I error  $\alpha$ , lies either side of the sample mean between limits  $\bar{y} \pm t_{[\alpha] N-1} \cdot SE$ , where the quantile  $t_{[\alpha] N-1}$  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  $1.96 \times SE$ . For the Fig.-1 data,  $\bar{y} = 2.60$  g,  $SE = 1.477$ ,  $N = 24$ , and  $t_{[0.05] 23} = 2.069$ ; so the 95% CI =  $2.60 \pm 3.05$  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,  $t_{[\alpha] N-1}$  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*(1 - pt(abs(t), N-1))`. For example, an analysis of the Fig.-1 data fails to refute the null hypothesis of zero growth ( $t_{23} = 1.76$ ,  $P = 0.09$ ). 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

```
# 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, -4.6421,
      -1.6908, -4.7169, -0.6191, 1.2085, 5.1147, 7.2654, 4.4188,
      6.3951, 0.5986, -4.5055, 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
setcex <- 1.8           # set the font size for labels
par(cex = setcex, mar = c(4, 4, 1, 2) + 0.1) # define plot margins
# Plot the mean and CI using 'plotmeans' from the 'gplots' library
plotmeans(y ~ x, p = 1-alpha, las = 1, xlab = "", ylab = "", n.label = FALSE, xaxt = "n")
# 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 .")),
      outer = TRUE, 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 = %.0f, ",DF), sprintf("P = %.3f; ",P),
        sprintf("t[alpha=%.2f] ",alpha), sprintf("= %.3f).",tcrit)
        ),sep = "")

## 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))
```