

This exercise is about z -tests. For large sample sizes $n > 40$, by rule of thumb, the statistic

$$t = \frac{\bar{X} - \mu_0}{s/\sqrt{n}}$$

is approximately normal, and hypothesis tests can be made using critical z -values. In fact, for normal data, this statistic satisfies the t -distribution with $n - 1$ degrees of freedom, and the t -test, which is canned in **R** is usually used.

We analyze the birth weights observed by Secher in the **ISwR** package. For sake of concreteness, we ask: are the birthweights of European babies significantly above 6 pounds? (I don't know if anyone would ever want to do this!) We calculate the statistic and p -value "by hand" and find that the average is not significantly higher at all. Let $\mu_0 = 2721.6$ grams. This is 6 pounds times 453.6 grams per pound. the null and alternative hypotheses are

$$\begin{aligned} H_0 : & \quad \text{The mean } \mu \leq \mu_0; \\ H_a : & \quad \text{The mean } \mu > \mu_0. \end{aligned}$$

For this one-tailed test, we compute the statistic t and reject the null hypothesis if $t > z_\alpha$. At the $\alpha = .05$ significance level, $z_\alpha = \Phi^{-1}(1 - \alpha)$ or about $z_{.05} = 1.645$.

We then go on to find β , the probability of a Type II error. In the case of z tests, this can be computed using normal probabilities. If population mean is μ_1 instead, $\beta(\mu_1) = P(H_0 \text{ is accepted} | \mu = \mu_1)$. This becomes

$$\beta = P(T \leq z_\alpha | \mu = \mu_1) = P\left(\frac{\bar{X} - \mu_0}{s/\sqrt{n}} \leq z_\alpha | \mu = \mu_1\right) = \Phi\left(z = \frac{\bar{X} - \mu_1}{s/\sqrt{n}} \leq z_\alpha - d\right)$$

where the normalized difference is

$$d = \frac{\mu_1 - \mu_0}{s/\sqrt{n}}.$$

The two tailed situation is similar. This time $z_{.025} = 1.960$ and

$$\begin{aligned} \beta &= P(-z_{\alpha/2} \leq T \leq z_{\alpha/2} | \mu = \mu_1) \\ &= P\left(-z_{\alpha/2} \leq \frac{\bar{X} - \mu_0}{s/\sqrt{n}} \leq z_{\alpha/2} | \mu = \mu_1\right) \\ &= \Phi(z \leq z_{\alpha/2} - d) - \Phi(z \leq -z_{\alpha/2} - d) \end{aligned}$$

We plot curves showing how β depends on d . We also plot normal curve diagrams of the areas these probabilities correspond to.

R Session:

R version 2.11.1 (2010-05-31)
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[R.app GUI 1.34 (5589) i386-apple-darwin9.8.0]

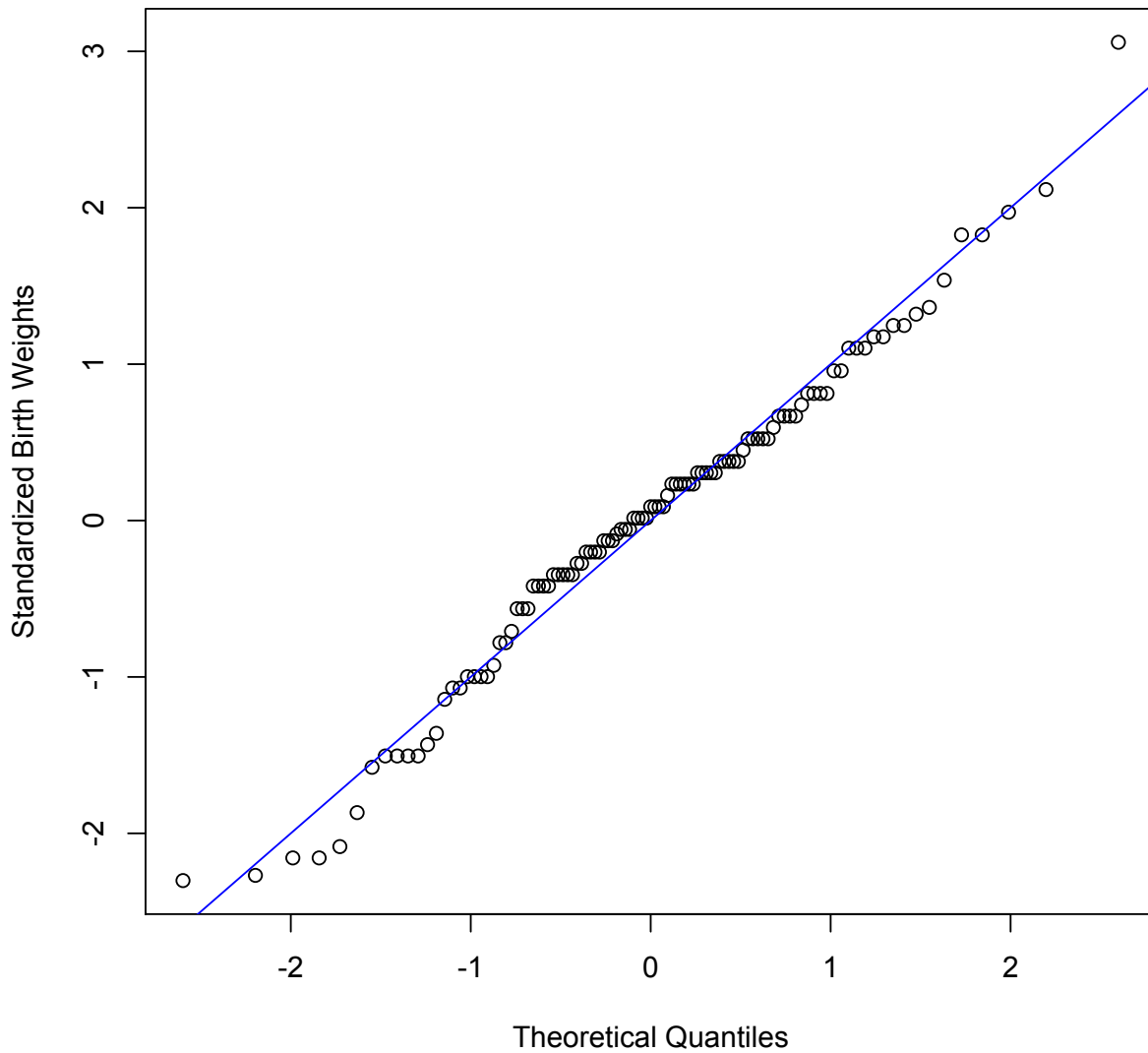
[Workspace restored from /home/1004/ma/treibergs/.RData]

```
> # Do random European babies exceed 6 lb birthweight?
> # Secher 1987 study of European babies is a canned dataset
> # secher in the package ISwR. Load the package and look at
> # the first few lines. The variable bwt is the birthweight.
>
> library(ISwR)
> head(secher)
  bwt bpd  ad no
1 2350  88  92  1
2 2450  91  98  2
3 3300  94 110  3
4 1800  84  89  4
5 2900  89  97  5
6 3500 100 110  6
>
> attach(secher)
> summary(bwt)
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 1150   2400   2800   2739   3125   4850

> n <- length(bwt);n
[1] 107

> xbar <- mean(bwt)
> s <- sd(bwt)
> # Standardizing means that the QQ points will line up on y = 0 + 1 * x:
> z <- (bwt-xbar)/s
> qqnorm(z,ylab="Standardized Birth Weights",main="QQ Plot of Birthweights")
> abline(0,1,col=4)
> # M3074BirthWeight1.pdf
```

QQ Plot of Birthweights



```
> # Looks pretty notmal!  
>  
> # there are 453.6 grams / pound so 6 lb is in grams  
> mu0 <- 6 * 453.6;mu0  
[1] 2721.6  
  
> # Do random European babies exceed 6 lb birthweight?  
> # Do random European babies significantly exceed 6 lb birthweight?  
> # Compute the T statistic and the p-value  
> T <- (xbar-mu0)/(s/sqrt(n)); T  
[1] 0.2621352
```

```

> pv <- pnorm(T,lower.tail=F); pv
[1] 0.3966086
>
> # So we can't reject the null hypothesis.
>
> # 95% lower CI for birthweight
> alp <- 0.05; alp
[1] 0.05
> zalp <- qnorm(alp,lower.tail=F); zalp
[1] 1.644854

> lci <- xbar - zalp * s/sqrt(n); lci
[1] 2629.325

> # We can make it look like R output.
>
> cat("  One Sample z-test\n\n z = ", T, ", p-value =", pv,
+ "\n alternative hypothesis: true mean is greater than", mu0,
+ "\n Level ",alp,"confidence interval:\n",lci,
+ "  Inf\n sample estimate:\n mean of x\n",xbar,"\n\n")

```

One Sample z-test

```

z = 0.2621352 , p-value = 0.3966086
alternative hypothesis: true mean is greater than 2721.6
Level 0.05 confidence interval:
2629.325      Inf
sample estimate:
mean of x
2739.093

```

```

> # Running the t-test yields almost the same.
>
> t.test(bwt,alternative="greater",mu = 2721.6)

```

One Sample t-test

```

data:  bwt
t = 0.2621, df = 106, p-value = 0.3969
alternative hypothesis: true mean is greater than 2721.6
95 percent confidence interval:
 2628.357      Inf
sample estimates:
mean of x
 2739.093

```

```

> ##### BETA COMPUTATIONS #####
>
> # If true mean weight was mu1 then for
> # d = (mu1-mu0)/(sigma/sqrt(n) ) we have
> # beta = P(z <= zalpha - d)
>
> d =seq(from=.1,to=2, by=.1);d
[1] 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1.0 1.1 1.2 1.3 1.4 1.5 1.6 1.7 1.8 1.9 2.0
> pnorm(zalphi-d)
[1] 0.9388092 0.9257505 0.9106637 0.8934072 0.8738651 0.8519547 0.8276332 0.8009037
[9] 0.7718199 0.7404890 0.7070729 0.6717872 0.6348978 0.5967151 0.5575868 0.5178880
[17] 0.4780109 0.4383530 0.3993050 0.3612400

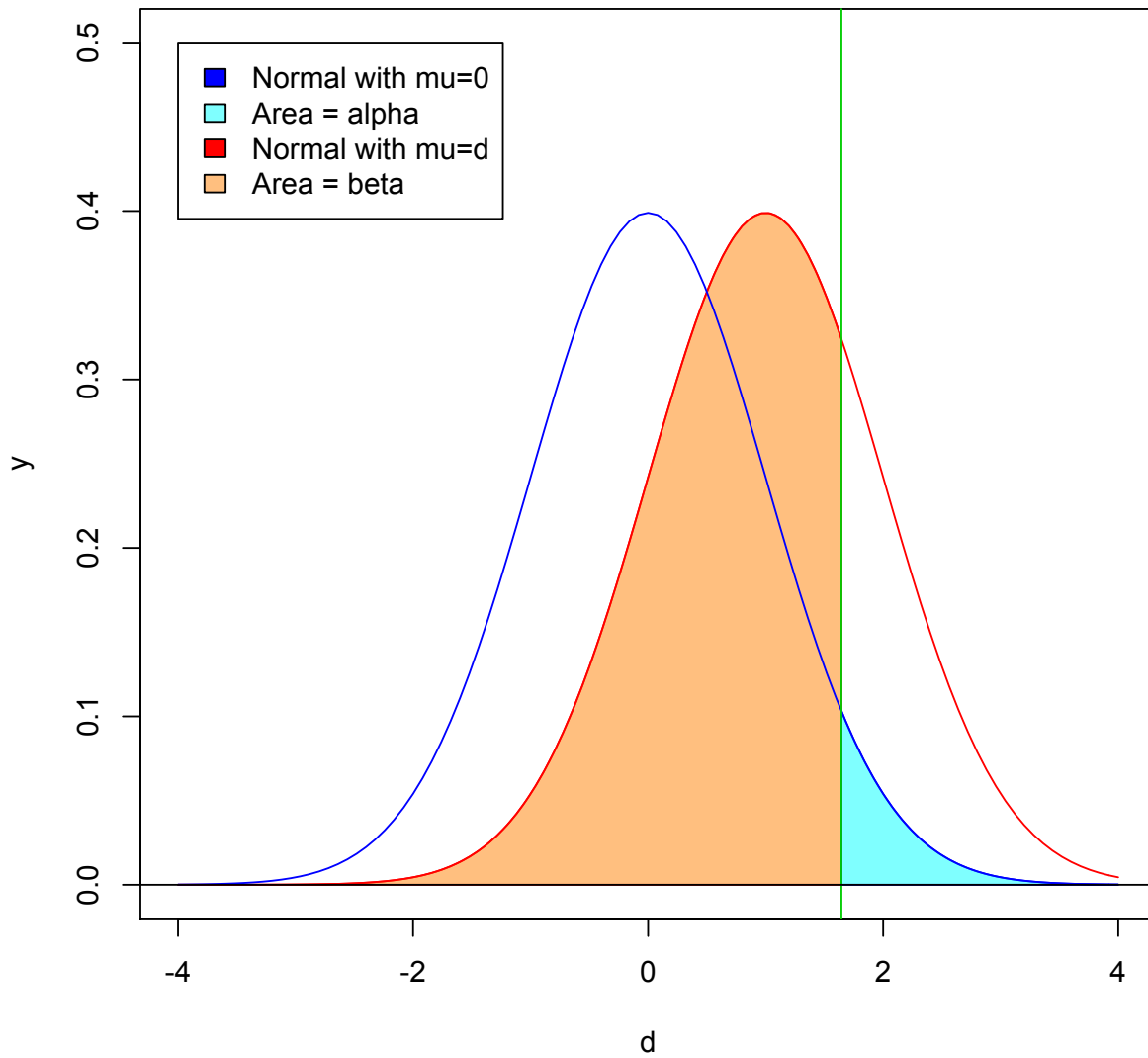
> # For example, if the actual mu = mu0 = 3628.8 gm (=8 lb) then the probability of
> # accepting mu <= 6 lb is
> pnorm(zalphi - (3628.8-2721.6)/(s/sqrt(n)))
[1] 3.273038e-33
> # For example, if the actual mu = mu0 = 3175.2 gm (= 7 lb) then the probability of
> # accepting mu <= 6 lb is
> pnorm(zalphi - (3175.2-2721.6)/(s/sqrt(n)))
[1] 1.287023e-07
> # for example, if the actual mu = mu0 = 2948.4 gm (= 6.5 lb) then the probability of
> # accepting mu <= 6 lb is
> pnorm(zalphi - (2948.4-2721.6)/(s/sqrt(n)))
[1] 0.0397419

> ##### NORMAL CURVES SHOWING ALPHA AND BETA #####
> # Make a function that inputs a,b,c , fill color and line color, and outputs a normal
> # density curve with mean c and sd = 1 and color in the region under the curve from
> # a to b. In fact, the coloring is done by making a polygon with 100 points along
> # the bell curve.
>
> plo <- function(a,b,c,co,cl){
+         xx <- c(a,seq(a,b,(b-a)/100),b,a)
+         yy <- c(0,dnorm(seq(a,b,(b-a)/100)-c),0,0)
+         curve(dnorm(x-c),-4,4,add=T,col=cl)
+         polygon(xx,yy,col=co,border=cl)
+     }
>
> # Now, plot the alpha and beta areas for two different d's. beta decreases as d increases.
> plot(x,y,type="n",xlim=c(-4,4),ylim=c(0,.5),main="beta for Upper-Tailed z-test",xlab="d")
> col1 <- rainbow(12,alpha=.5)[2];coll1 <- rainbow(12)[1]
> col2 <- rainbow(12,alpha=.5)[7];coll2 <- rainbow(12)[9]
> plo(-4,zalphi,1,col1,coll1)
> plo(zalphi,4,0,col2,coll2)
> legend(-4,.5,legend=c("Normal with mu=0","Area = alpha","Normal with mu=d","Area = beta"),
+ fill=c(coll2,col2,coll1,col1))
> abline(v=zalphi,col=3);abline(h=0)
> # M3074BirthWeight2.pdf
>
>
> plot(x,y,type="n",xlim=c(-4,4),ylim=c(0,.5),main="beta for Upper-Tailed z-test",xlab="d")

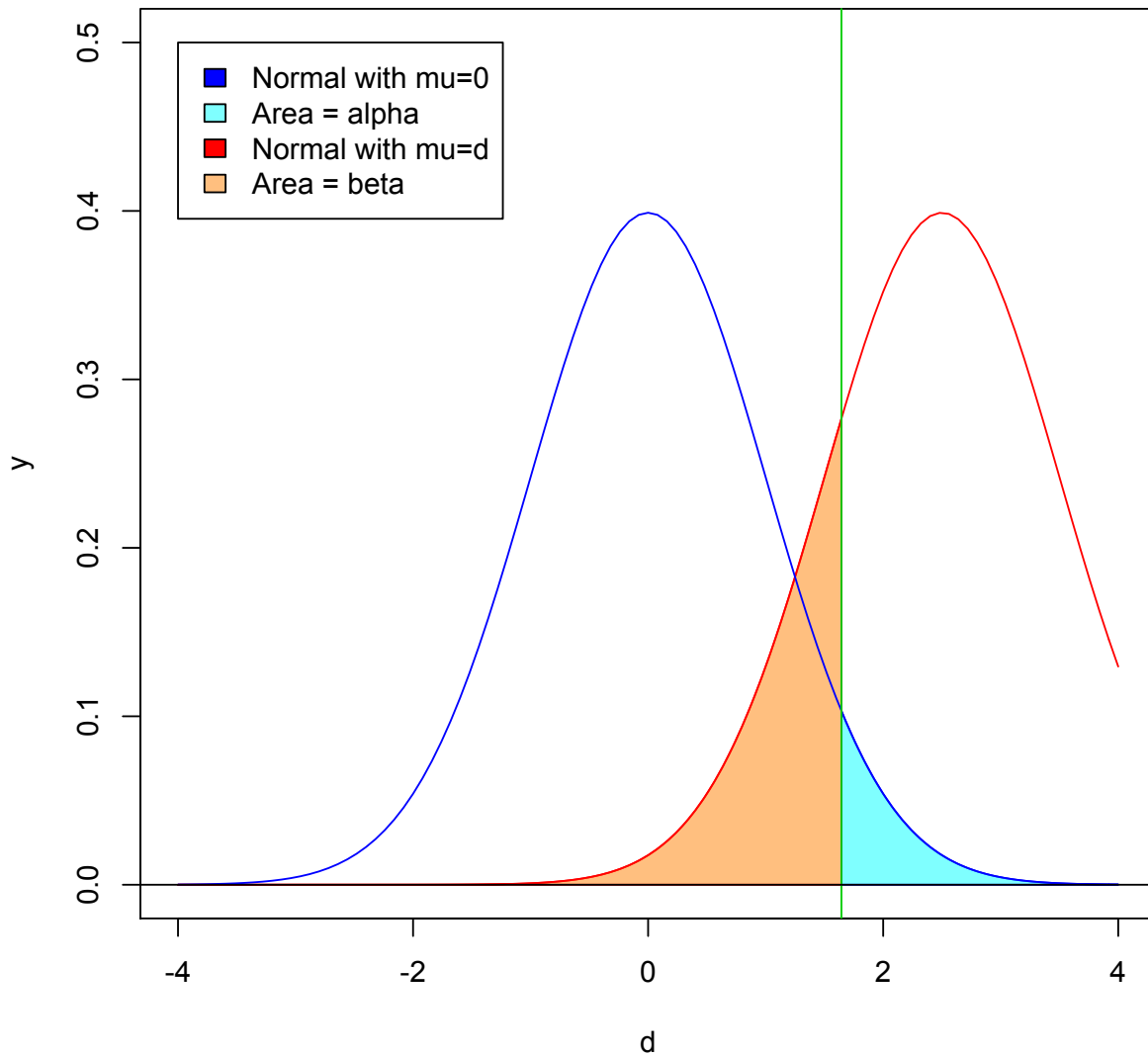
```

```
> plo(-4,zalpha,2.5,col1,col11)
> plo(zalpha,4,0,col2,col12)
> legend(-4,.5,legend=c("Normal with mu=0","Area = alpha","Normal with mu=d","Area = beta"),
+ fill=c(col12,col2,col11,col1))
> abline(v=zalpha,col=3);abline(h=0)
> # M3074BirthWeight3.pdf
```

beta for Upper-Tailed z-test



beta for Upper-Tailed z-test



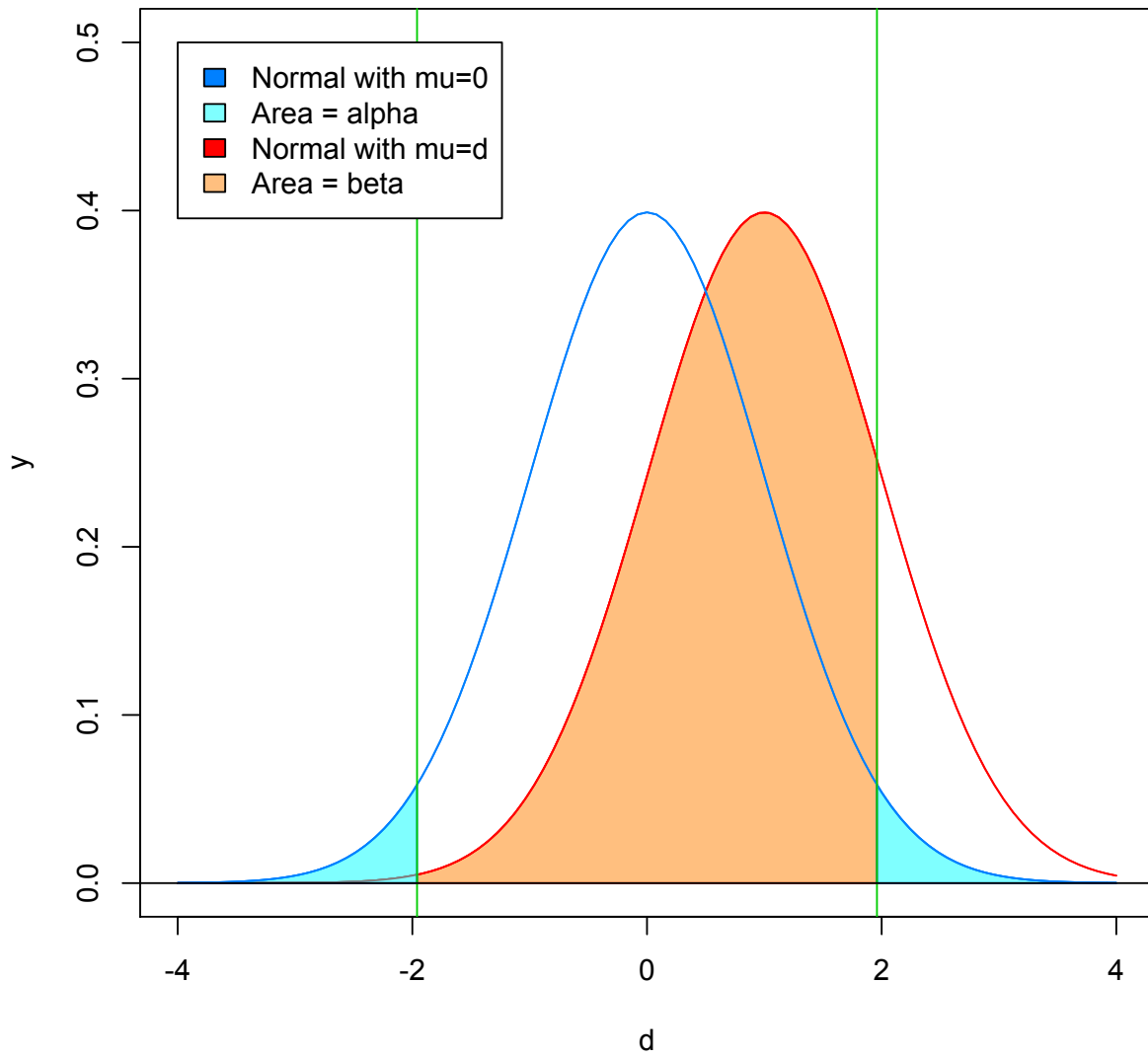
```
> # FOR THE TWO-TAILED TEST WE ALSO HAVE SIMILAR DIAGRAMS.
> za2 <- qnorm(.025,lower.tail=F)
> za2
[1] 1.959964
>
> plot(x,y,type="n",xlim=c(-4,4),ylim=c(0,.5),main="beta for Two-Tailed z-test,
+ alpha=.05",xlab="d")
> plo(-4,za2,1,col1,col11)
> plo(-4,-za2,1,"white",col11)
> plo(za2,4,0,col2,col12)
> plo(-4,-za2,0,col2,col12)
> abline(v=c(-za2,za2),col=3);abline(h=0)
```

```

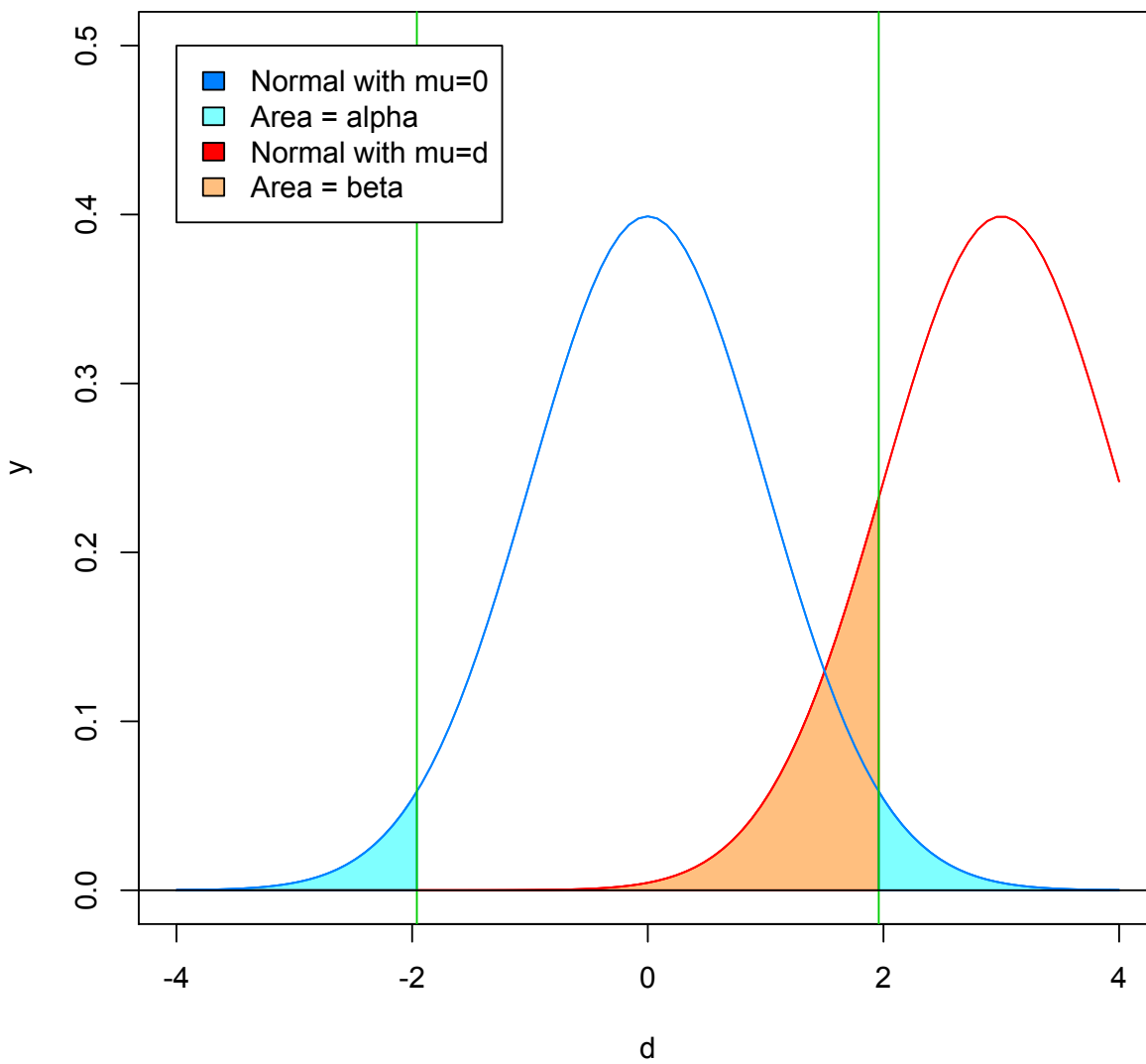
> legend(-4,.5,legend=c("Normal with mu=0","Area = alpha","Normal with mu=d","Area = beta"),
+ fill=c(coll2,col2,coll1,col1),bg="white")
> # M3074BirthWeight6.pdf
>
> plot(x,y,type="n",xlim=c(-4,4),ylim=c(0,.5),main="beta for Two-Tailed z-test,
+ alpha=.05",xlab="d")
> plo(-4,za2,3,col1,coll1)
> plo(-4,-za2,3,"white",coll1)
> plo(za2,4,0,col2,coll2)
> plo(-4,-za2,0,col2,coll2)
> abline(v=c(-za2,za2),col=3);abline(h=0)
> legend(-4,.5,legend=c("Normal with mu=0","Area = alpha","Normal with mu=d","Area = beta"),
+ fill=c(coll2,col2,coll1,col1),bg="white")
> # M3074BirthWeight7.pdf

```


beta for Two-Tailed z-test, alpha=.05



beta for Two-Tailed z-test, alpha=.05

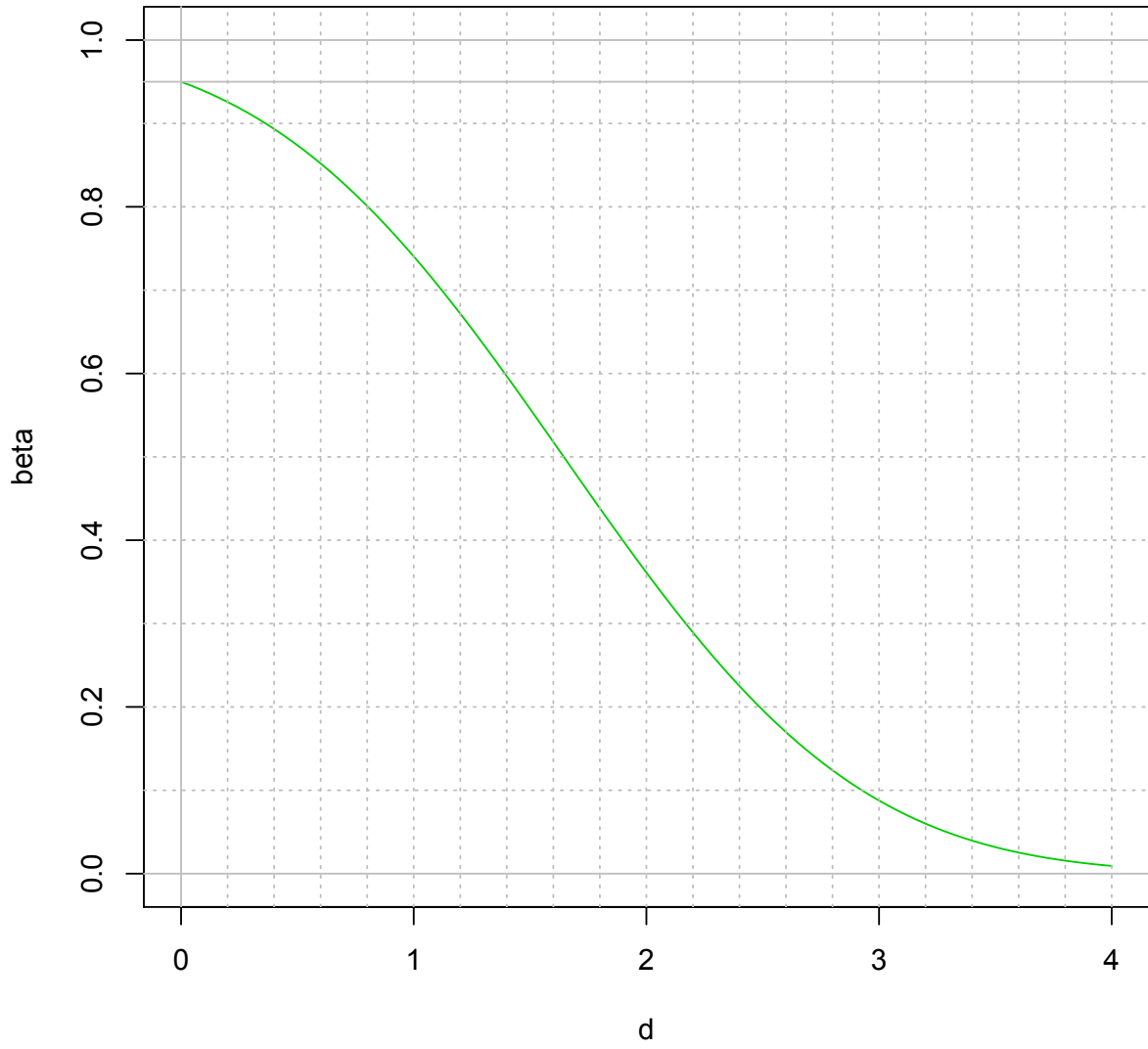


```

> ##### beta AS A FUNCTION OF d #####
> # One tailed computation beta computation.
> # If true mean weight was mu1
> # let d = (mu1-mu0)/(sigma/sqrt(n) ) then
> # beta = P(z <= zalpha - d)
>
> curve(pnorm(zalphi-x),0,4,main="beta Curve for One-Tailed z-test, alpha=.05",
+ xlim=c(0,4),ylim=0:1,col=3,ylab="beta",xlab="d")
> abline(v=0,col="gray");abline(v=1:20/5,col="gray",lty=3)
> abline(h=c(0,.95,1),col="gray");abline(h=1:9/10,col="gray",lty=3)
> # M3074BirthWeight4.pdf
>
> # Two tailed computation beta computation.
> # If true mean weight was mu1 then
> # beta = P( -za2 <= X <= za2 | mu = d) or
> # beta = P(-za2 - d <= z <= za2-d)
>
> d =seq(from=.1,to=2, by=.1);d
[1] 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1.0 1.1 1.2 1.3 1.4 1.5 1.6 1.7 1.8 1.9 2.0
>
> be <- function(x,za){pnorm(za-x)-pnorm(-za-x)}
> be(d,za2)
[1] 0.9488537 0.9454053 0.9396274 0.9314774 0.9209025 0.9078452 0.8922514 0.8740779
[9] 0.8533011 0.8299250 0.8039887 0.7755730 0.7448044 0.7118582 0.6769588 0.6403775
[17] 0.6024281 0.5634603 0.5238511 0.4839947
> col1 <- rainbow(12,alpha=.5)[4];col11 <- rainbow(12)[7]
> col2 <- rainbow(12,alpha=.5)[10];col12 <- rainbow(12)[11]
> curve(be(x,za2),0,4,main="beta Curve for Two-Tailed z-test, alpha=.05",
+ xlim=c(0,4),ylim=0:1,col=2,ylab="beta")
> abline(v=0,col="gray");abline(v=1:20/5,col="gray",lty=3)
> abline(h=c(0,.95,1),col="gray");abline(h=1:9/10,col="gray",lty=3)
> # M3074BirthWeight5.pdf

```

beta Curve for One-Tailed z-test, alpha=.05



beta Curve for Two-Tailed z-test, alpha=.05

