```
## Johnson SU distribution
## MLE (Maximum Likelihood Estimate) fit to determine parameters
## LR (Likelihood Ratio) approach to find tolerance limit

##------------------------------------------------------------------------------
## GIVEN
x     <- iris$Sepal.Width
P     <- 0.99  # proportion or coverage
alpha <- 0.01
sided <- 1
```

```
> x
  [1] 3.5 3.0 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 3.7 3.4 3.0 3.0 4.0 4.4 3.9 3.5 3.8 3.8
 [21] 3.4 3.7 3.6 3.3 3.4 3.0 3.4 3.5 3.4 3.2 3.1 3.4 4.1 4.2 3.1 3.2 3.5 3.6 3.0 3.4
 [41] 3.5 2.3 3.2 3.5 3.8 3.0 3.8 3.2 3.7 3.3 3.2 3.2 3.1 2.3 2.8 2.8 3.3 2.4 2.9 2.7
 [61] 2.0 3.0 2.2 2.9 2.9 3.1 3.0 2.7 2.2 2.5 3.2 2.8 2.5 2.8 2.9 3.0 2.8 3.0 2.9 2.6
 [81] 2.4 2.4 2.7 2.7 3.0 3.4 3.1 2.3 3.0 2.5 2.6 3.0 2.6 2.3 2.7 3.0 2.9 2.9 2.5 2.8
[101] 3.3 2.7 3.0 2.9 3.0 3.0 2.5 2.9 2.5 3.6 3.2 2.7 3.0 2.5 2.8 3.2 3.0 3.8 2.6 2.2
[121] 3.2 2.8 2.8 2.7 3.3 3.2 2.8 3.0 2.8 3.0 2.8 3.8 2.8 2.8 2.6 3.0 3.4 3.1 3.0 3.1
[141] 3.1 3.1 2.7 3.2 3.3 3.0 2.5 3.0 3.4 3.0
```

```
## Following results executed with:
out <- mle.johnsonsu(x, plots=TRUE)
out <- hist_nwj(x, type='j')

##------------------------------------------------------------------------------
## DETERMINE JOHNSON SU PARAMETERS (this step not needed other than for comparison)

## define nll (negative log likelihood) function to fit
## parameters: gamma, delta, xi, lambda
nll <- function() {
    pdf <- delta /( lambda * sqrt(2 * pi)    ) *
        1 / sqrt(1 +                    ( (x-xi)/lambda )^2)   *
        exp( -0.5*(gamma + delta * asinh( (x-xi)/lambda ))^2 )
    nll <- -sum(log(pdf))
}
## MLE fit on nnl() returns values for gamma, delta, xi, and lambda
params
```

	gamma	delta	xi	lambda	quant
standard fit	-3.306484	5.319412	1.784619	1.887725	NA

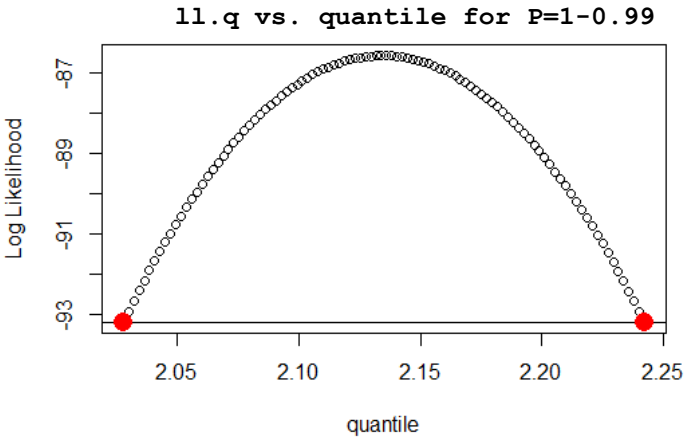
```
##------------------------------------------------------------------------------
## DETERMINE EQUIVALENT JOHNSON SU FIT USING QUANTILE AS A PARAMETER INSTEAD OF GAMMA

## define nll.q function to fit alternate parameters: quant, delta, xi, lambda
## where P     = coverage
##       quant = quantile associated with coverage
nll.q <- function() {
    gamma <- qnorm(P) - delta * asinh( (quant-xi)/lambda )
    pdf <- delta /( lambda * sqrt(2 * pi)    ) *
        1 / sqrt(1 +                    ( (x-xi)/lambda    )^2)   *
        exp( -0.5*(gamma + delta * asinh( (x-xi)/lambda ) )^2 )
    nll.q <- -sum(log(pdf))
}
## MLE fit on nll.q() returns values for quant, delta, xi, and lambda for given P
params.q
```

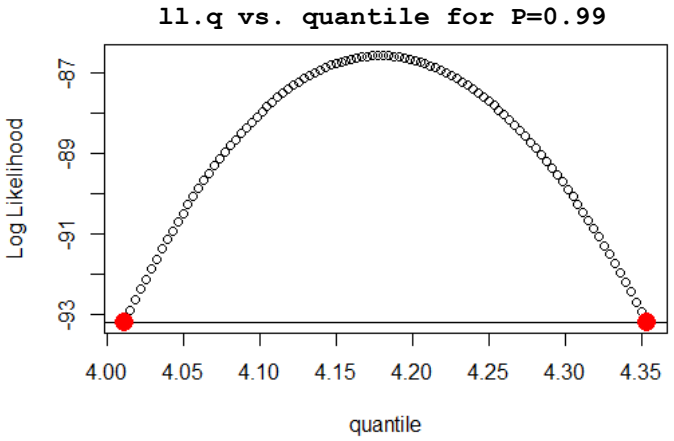
	gamma	delta	xi	lambda	quant
standard fit	-3.306484	5.319412	1.784619	1.887725	NA
fit on quantile at 1-P	-3.306500	5.319415	1.784613	1.887714	2.134413
fit on quantile at P	-3.307633	5.319502	1.784351	1.887396	4.178574

```
##-----------------------------------------------------------------------------
## CALCULATE CONFIDENCE LIMITS USING LR (LIKELIHOOD RATIO)

## Find peak of log likelihood
ll.max.P <- -nll.max.bestfit

## Reduce peak by chi-squared
ll.tol <-  ll.max.P - qchisq(1 - alpha/sided, 1)  # qchisq(1-0.01/1, 1) = 6.634897
```

```
ll.max.P = -86.55915 ; ll.tol = -93.19405 for P= 0.01
ll.max.P = -86.55915 ; ll.tol = -93.19405 for P= 0.99
```

```
## confidence limits are the intersection of ll.tol and the log likelihood function
## for given level of coverage, P
ll.q <- -nll.q(x, P, quantile, delta, xi, lambda)
```






```
Final confidence interval for P= 0.01
2.027558 2.242365
```

```
Final confidence interval for P= 0.99
4.011839 4.352955
```

```
## Based on the above:
  alpha    P sided tol.lower tol.upper
1  0.01 0.99     1  2.027558  4.352955
```

```
##-----------------------------------------------------------------------------
## HISTOGRAM WITH TOLERANCE LIMIT
```