

## Probability Distributions and CI for Correlation

### Probability Distributions

One convenient use of R is to provide a comprehensive set of statistical tables. Functions are provided to evaluate the cumulative distribution function  $P(X \leq x)$ , the probability density function and the quantile function (given  $q$ , the smallest  $x$  such that  $P(X \leq x) > q$ ), and to simulate from the distribution.

| <u>Distribution</u> | <u>R name</u> | <u>Additional arguments</u> |
|---------------------|---------------|-----------------------------|
| Binomial            | binom         | size, prob                  |
| Chi-squared         | chisq         | df, ncp                     |
| Exponential         | exp           | rate                        |
| F                   | f             | df1, df2, ncp               |
| Normal              | norm          | mean, sd                    |
| Poisson             | pois          | lambda                      |
| Student's t         | t             | df, ncp                     |
| Uniform             | unif          | min, max                    |

Prefix the name given here by 'd' --- for the density;  
 'p' --- for the CDF;  
 'q' --- for the quantile function;  
 'r' --- for simulation (random numbers).

Here are some examples.

```
> ## 2-tailed p-value for t(13) distribution
> 2*pt(-2.43, df = 13)

> ## upper 1% point for an F(2, 7) distribution
> qf(0.99, df1 = 2, df2 = 7)

> # To generate 100 random numbers from N(0,2) distribution
> x <- rnorm(100, mean = 0, sd = 2); x
> # by default, rnorm generates numbers from N(0, 1).

> # to compute  $P(X=12)$ , where  $X \sim \text{Binomial}(20,.45)$ 
> pbinom(12, size = 20, prob = 0.45)
[1] 0.942
```

## A Confidence Interval for Correlation Coefficient

The following function is written to construct a  $p\%$  (by default, 95%) confidence interval for the population correlation coefficient between two random variables, say,  $X$  and  $Y$ .

```
ci.corr <- function(x, y, p=.95)
{ r <- cor(x, y); # compute the sample correlation
  n <- length(x) # sample size
  z <- 0.5*log((1+r)/(1-r)) # Fisher's Z transformation
  width <- qnorm(1-(1-p)/2)/sqrt(n-3) # half width of the CI
  L <- z - width # Lower bound for z
  U <- z + width # Upper bound for z
  cbind(lower.bound=(exp(2*L)-1)/(exp(2*L)+1),
        upper.bound=(exp(2*U)-1)/(exp(2*U)+1))
}
```

To apply the above function, consider the following artificial data.

```
> n <- 100 # sample size
> x <- rexp(n, rate = 1)
> y <- 2.5 * x^2 + rnorm(n, mean = 0, sd = 0.5)
> ci.corr(x, y, p = 0.9)
      lower.bound upper.bound
[1,]      0.9013      0.9482
```