# Statistical Inference for Counts and proportions

## A) proportions parameter for one population

**Null Hypothesis** $H_0$: $p = p_0$

**Assumptions**: random sample, large n and p is around .5.

**R function:**

**binom.test ():** Test hypothesis about ONE parameter p in a Binomial (n,p) model given x, the number of successes out of n trials.

## binom.test(x, n, p=0.5, alternative ="two . sided")

where x is number of successes, n is the number of the independent trials, p is the success probability to be tested.

**Possible output for binom.test( ) are:**

| | |
|---|---|
| statistic | number of successes |
| parameters | number of trials. |
| p.value | the p-value. |
| null.value | null hypothesis value of the probability of success. |
| alternative | alternative hypothesis |
| method | the string "Exact binomial test". |
| data.name | a chararter vector describing the data used for the test. |

Each of these values can be accessed by $"name".

**B)** **proportions parameters for two or more populations:**
   **Null Hypothesis $H_0$: $p_1 = p_2$  or $H_0$: $p_1 = p_2$**
   **Assumptions: random independent samples, min (np, n(1-p)) >=5**

# R function:
**prop.test(x, n, p, alternative = "two . sided", conf . level= .95, correct=T)**

**x: a vector of counts of successes or a matrix with 2 columns**
        **giving the counts of successes and failures, espectively.**
**n: a vector of counts of trials; ignored if 'x' is a matrix.**
**p: a vector of probabilities of success.  The length of 'p' must be the same as the number of groups specified by 'x', and its elements must be greater than 0 and less than 1.**

**prop.test ():**
   **Compares proportions against hypothesized values. Alternately, tests whether underlying proportions are equal. Where x, n are vectors of counts of successes and trials respectively. The elements of n must be positive; those of x must be nonnegative and no greater than the corresponding values in n. Both vectors must have the same length. p is a vector of probabilities of success specified in the null hypothesis.**

## Example:
## H0: The null hypothesis is that the four populations from which the patients were drawn have the same true proportion of smokers.
## H1:  The alternative is that this proportion is different in at least one of the populations.

```
smokers  <- c( 83, 90, 129, 70 )
patients <- c( 86, 93, 136, 82 )
   prop.test(smokers, patients)         #   p=c(.25,.25,.25,.25)
```

**possible output for prop.test ( ) are:**

| | |
|---|---|
| statistic | Pearson's X-squared statistic |
| parameters | the degrees of freedom |
| p.value | the asymptotic p-value for the test. |
| conf.int | a confidence interval for the true probability of success (1, 2 groups only) |
| estimate | vector giving the sample proportions x / n; |
| null.value | probabilities of success specified in null hypothesis. |
| alternative | one of "greater", "less" or "two.sided". |
| method | character string giving the name of the method used, including whether Yates' continuity correction was applied. |
| data.name | a character string containing the actual names of the input vectors x and n , and of p if given. |

Each of these can be accessed by $ "name".