Non-parametric tests

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Inhoud

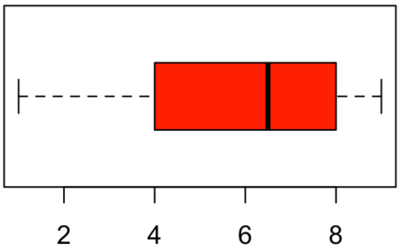
Nonparametric tests

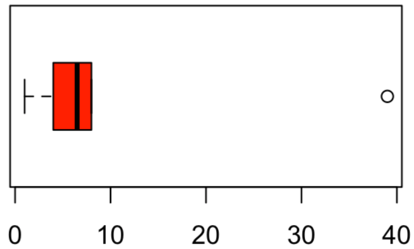
Parametric vs Nonparametric

Attribute	Parametric	Nonparametric
distribution	normaly distributed	any distribution
sampling	random sample	random sample
sensitivity to outliers	yes	no
works with	large data sets	small and large data sets
speed	fast	slow

Ranking

```
x = c(1, 4, 6, 7, 8, 9)
y = c(1, 4, 6, 7, 8, 39)

layout(matrix(1:2, 1, 2))
boxplot(x, horizontal=T, col='red')
boxplot(y, horizontal=T, col='red')
```






```
rbind(rx = rank(x), ry = rank(y))
```

```
##    [,1] [,2] [,3] [,4] [,5] [,6]
## rx    1    2    3    4    5    6
## ry    1    2    3    4    5    6
```

Ties

```
x = c(1, 4, 6, 7, 8, 8, 4, 7, 9)
```

```
rbind(x, ordered = sort(x), non.tied.rank = 1:length(x), ran
```

```
##                 [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9
## x                  1  4.0  6.0    7  8.0  8.0  4.0  7.0
## ordered            1  4.0  4.0    6  7.0  7.0  8.0  8.0
## non.tied.rank      1  2.0  3.0    4  5.0  6.0  7.0  8.0
## ranked             1  2.5  2.5    4  5.5  5.5  7.5  7.5
```

$$\frac{2+3}{2} = 2.5, \frac{5+6}{2} = 5.5, \frac{7+8}{2} = 7.5$$

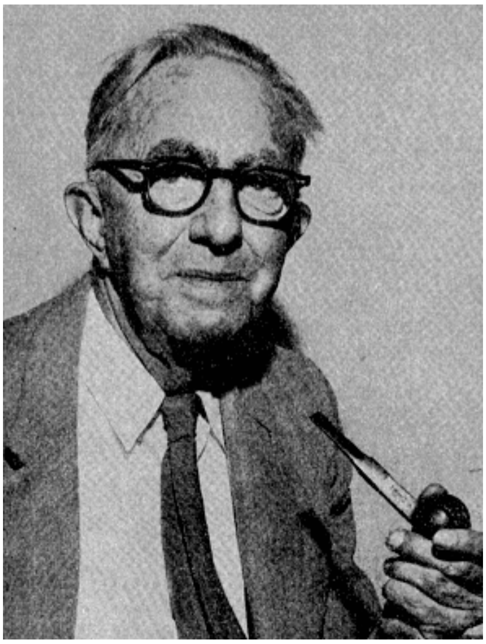
Procedure

1. Assumption: independent random samples.
2. Hypothesis:
   H_0 : equal population distributions (implies equal mean ranking)
   H_A : unequal mean ranking (two sided)
   H_A : higher mean ranking for one group.
3. Test statistic is difference between mean or sum of ranking.
4. Standardise test statistic
5. Calculate *P*-value one or two sided.
6. Conclude to reject H_0 if $p < \alpha$.

Independent 2 samples

Wilcoxon rank-sum test

Wilcoxon rank-sum test



Developed by Frank Wilcoxon the rank-sum test is a nonparametric alternative to the independent samples t-test.

By first ranking x and then sum these ranks per group one would expect, under the null hypothesis, equal values for both groups.

After standardising this difference one can test using a standard normal distribution.

Simulate data

```
n      = 20
factor = rep(c("Ecstasy","Alcohol"),each=n/2)
dummy  = ifelse(factor == "Ecstacy", 0, 1)
b.0    = 23
b.1    = 5
error  = rnorm(n, 0, 1.7)
depres = b.0 + b.1*dummy + error
depres = round(depres)

data <- data.frame(factor, depres)

## add the ranks
data$R <- rank(data$depres)
```

Example

Calculate the sum of ranks per group

```
R <- aggregate(R ~ factor, data, sum)
R
```

```
##    factor   R
## 1 Alcohol  88
## 2 Ecstasy 122
```

So W is the lowest

$$W = min\left(\sum R_1, \sum R_2\right)$$

```
W <- min(R$R)
W
```

```
## [1] 88
```

Standardise W

To calculate the Z score we need to standardise the W. To do so we need the mean W and the standard error of W.

For this we need the sample sizes for each group.

```
n <- aggregate(R ~ factor, data, length)

n.1 = n$R[1]
n.2 = n$R[2]

cbind(n.1, n.2)
```

```
##      n.1 n.2
## [1,]  10  10
```

Mean W

$$\bar{W}_s = \frac{n_1(n_1 + n_2 + 1)}{2}$$

```
W.mean = (n.1*(n.1+n.2+1))/2
W.mean
```

```
## [1] 105
```

SE W

$$SE_{\bar{W}_s} = \sqrt{\frac{n_1 n_2 (n_1 + n_2 + 1)}{12}}$$

```
W.se = sqrt((n.1*n.2*(n.1+n.2+1))/12)
W.se
```

```
## [1] 13.22876
```

Calculate Z

$$z = \frac{W - \bar{W}}{SE_W}$$

Which looks a lot like

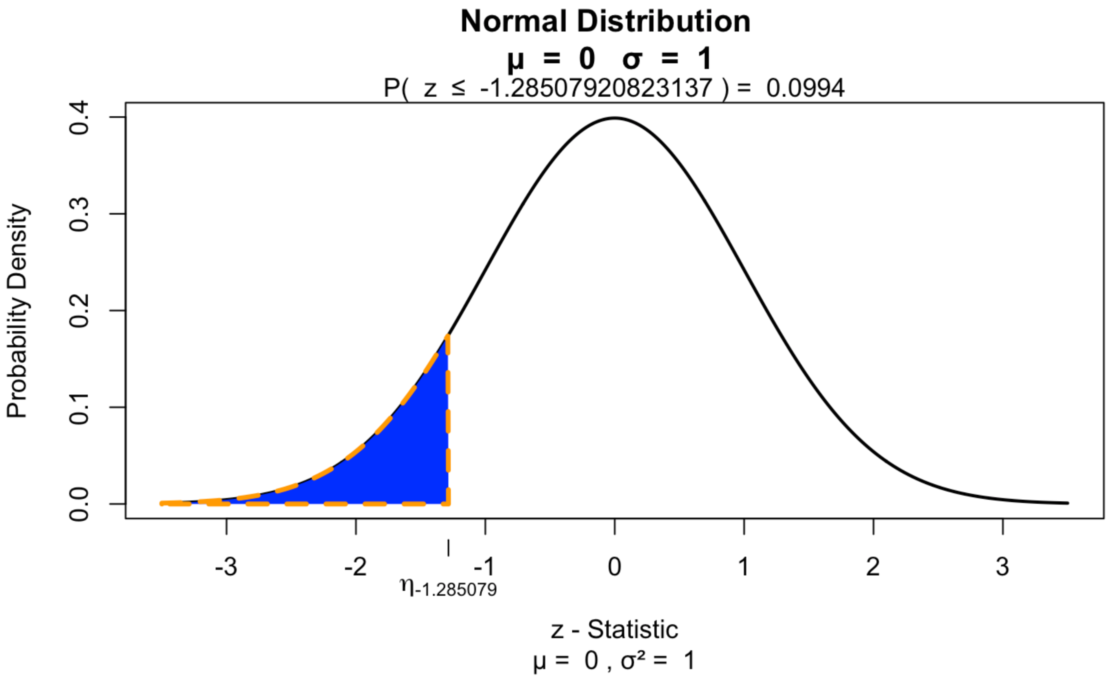
$$\frac{X - \bar{X}}{SE_X} \text{or} \frac{b - \mu_b}{SE_b}$$

```
z = (W - W.mean) / W.se
z
```

```
## [1] -1.285079
```

Test for significance 1 sided

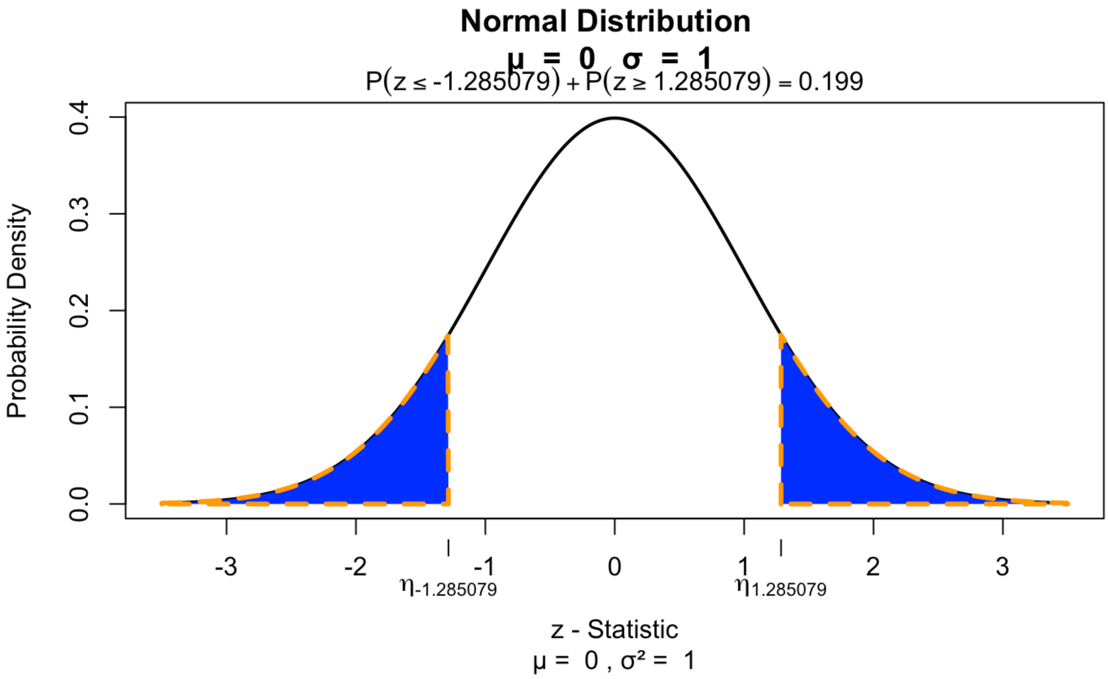
```
if(!"visualize" %in% installed.packages()){ install.packages
library("visualize")

visualize.norm(z, section="lower")
```



Normal Distribution
μ = 0 σ = 1
P(z ≤ -1.28507920823137) = 0.0994
Probability Density
0.0
0.1
0.2
0.3
0.4
-3
-2
-1
0
1
2
3
η-1.285079
z - Statistic
μ = 0 , σ² = 1

Test for significance 2 sided

```
visualize.norm(c(z,-z), section="tails")
```


Normal Distribution
μ = 0 σ = 1
P(z ≤ -1.285079) + P(z ≥ 1.285079) = 0.199
Probability Density
0.0
0.1
0.2
0.3
0.4
-3
-2
-1
0
1
2
3
η-1.285079
η1.285079
z - Statistic
μ = 0 , σ² = 1

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Effect size

$$r = \frac{z}{\sqrt{N}}$$

```
N = sum(n$R)
r = z / sqrt(N)
r
```

```
## [1] -0.2873524
```

Mann–Whitney test

$$U = n_1 n_2 + \frac{n_1(n_1 + 1)}{2} - R_1$$

```
U = (n.1*n.2)+(n.1*(n.1+1))/2-R$R[1]
U
```

```
## [1] 67
```

$\bar{U}$ and SE_U for non tied ranks

$$\bar{U} = \frac{n_1 n_2}{2}$$

```
(n.1*n.2)/2
```

```
## [1] 50
```

$$SE_U = \sqrt{\frac{n_1 n_2 (n_1 + n_2 + 1)}{12}}$$

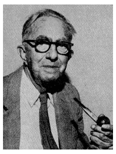
```
sqrt((n.1*n.2*(n.1+n.2+1))/12)
```

```
## [1] 13.22876
```

Paired 2 samples

Wilcoxon signed-rank test

Wilcoxon signed-rank test



The Wilcoxon signed-rank test is a nonparametric alternative to the paired samples t-test. It assigns + or - signs to the difference between two repeated measures. By ranking the differences and summing these ranks for the positive group, the null hypothesis is tested that both positive and negative differences are equal.

Simulate data

```
n      = 20
factor = rep(c("Ecstasy","Alcohol"),each=n/2)
dummy  = ifelse(factor == "Ecstacy", 0, 1)
b.0    = 23
b.1    = 5
error  = rnorm(n, 0, 1.7)
depres = b.0 + b.1*dummy + error
depres = round(depres)

data <- data.frame(factor, depres)

Ecstasy <- subset(data, factor=="Ecstasy")$depres
Alcohol <- subset(data, factor=="Alcohol")$depres

data <- data.frame(Ecstasy, Alcohol)
```

Example

Calculate T

```
# Calculate difference in scores between first and second measure
data$difference = data$Ecstasy - data$Alcohol

# Calculate difference in scores between first and second measure
data$abs.difference = abs(data$Ecstasy - data$Alcohol)

# Create rank variable with place holder NA
data$rank <- NA

# Rank only the difference scores
data[which(data$difference != 0),'rank'] <- rank(data[which(data$differer
                                                      'abs.difference'])

# Assign a '+' or a '-' to those values
data$sign = sign(data$Ecstasy - data$Alcohol)

# Add positive and negative rank to     test  if    else
data$rank_pos = with(data, ifelse(sign ==  1, rank, 0   ))
data$rank_neg = with(data, ifelse(sign == -1, rank, 0   ))
```

The data

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Calculate T_+

```
# Calculate the sum of the positive ranks
T_pos = sum(data$rank_pos)
T_pos
```

```
## [1] 18.5
```

```
# Calculate N without 0 (no differences).
n = sum(abs(data$sign))
n
```

```
## [1] 7
```

Calculate $\bar{T}$ and SE_T

$$\bar{T} = \frac{n(n+1)}{4}$$

```
T_mean = (n*(n+1))/4
T_mean
```

```
## [1] 14
```

$$SE_T = \sqrt{\frac{n(n+1)(2n+1)}{24}}$$

```
SE_T = sqrt( (n*(n+1)*(2*n+1)) / 24 )
```

Calculate Z

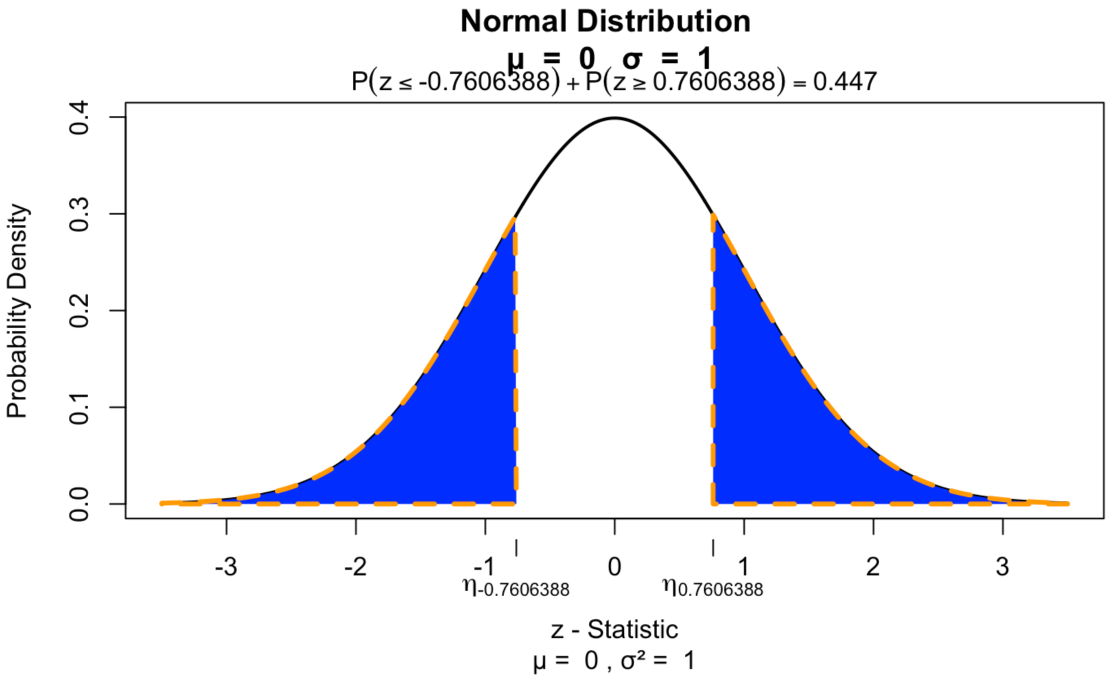
$$z = \frac{T_+ - \bar{T}}{SE_T}$$

```
z = (T_pos - T_mean)/SE_T
z
```

```
## [1] 0.7606388
```

Test for significance

```
visualize.norm(c(z,-z), section="tails")
```


Normal Distribution
μ = 0 σ = 1
P(z ≤ -0.7606388) + P(z ≥ 0.7606388) = 0.447
Probability Density
0.0
0.1
0.2
0.3
0.4
-3
-2
-1
0
1
2
3
η-0.7606388
η0.7606388
z - Statistic
μ = 0 , σ² = 1

Effect size

$$r = \frac{z}{\sqrt{N}}$$

Here N is the number of observations.

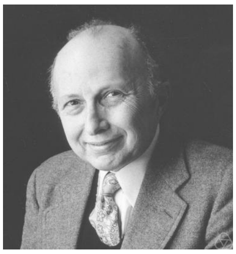
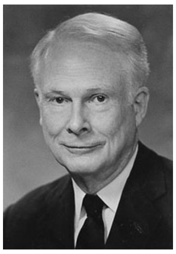
```
N = 20
r = z / sqrt(N)
r
```

```
## [1] 0.170084
```

Independent >2 samples

Kruskal–Wallis test

Kruskal–Wallis test

Created by William Henry Kruskal (L) and Wilson Allen Wallis (R), the Kruskal-Wallis test is a nonparametric alternative to the independent one-way ANOVA.

The Kruskal-Wallis test essentially subtracts the expected mean ranking from the calculated oberved mean ranking, which is χ^2 distributed.

Simulate data

```
n      = 30
factor = rep(c("ecstasy","alcohol","control"), each=n/3)

dummy.1 = ifelse(factor == "alcohol", 1, 0)
dummy.2 = ifelse(factor == "ecstasy", 1, 0)
b.0     = 23
b.1     = 0
b.2     = 0
error   = rnorm(n, 0, 1.7)

# Model
depres  = b.0 + b.1*dummy.1 + b.2*dummy.2 + error
depres  = round(depres)

data <- data.frame(factor, depres)
```

Assign ranks

```
# Assign ranks
data$ranks = rank(data$depres)
```

The data

Calculate H

$$H = \frac{12}{N(N+1)} \sum_{i=1}^{k} \frac{R_i^2}{n_i} - 3(N+1)$$

- N total sample size
- n_i sample size per group
- k number of groups
- R_i rank sums per group

Calculate H

```
# Now we need the sum of the ranks per group.
R.i = aggregate(ranks ~ factor, data = data, sum)$ranks
R.i
```

```
## [1] 207.0 121.5 136.5
```

```
# De total sample size N is:
N = nrow(data)

# And the sample size per group is n_i:
n.i = aggregate(depres ~ factor, data=data, length)$depres
n.i
```

```
## [1] 10 10 10
```

Calculate H

$$H = \frac{12}{N(N+1)} \sum_{i=1}^{k} \frac{R_i^2}{n_i} - 3(N+1)$$

```
H = ( 12/(N*(N+1)) ) * sum(R.i^2/n.i) - 3*(N+1)
H
```

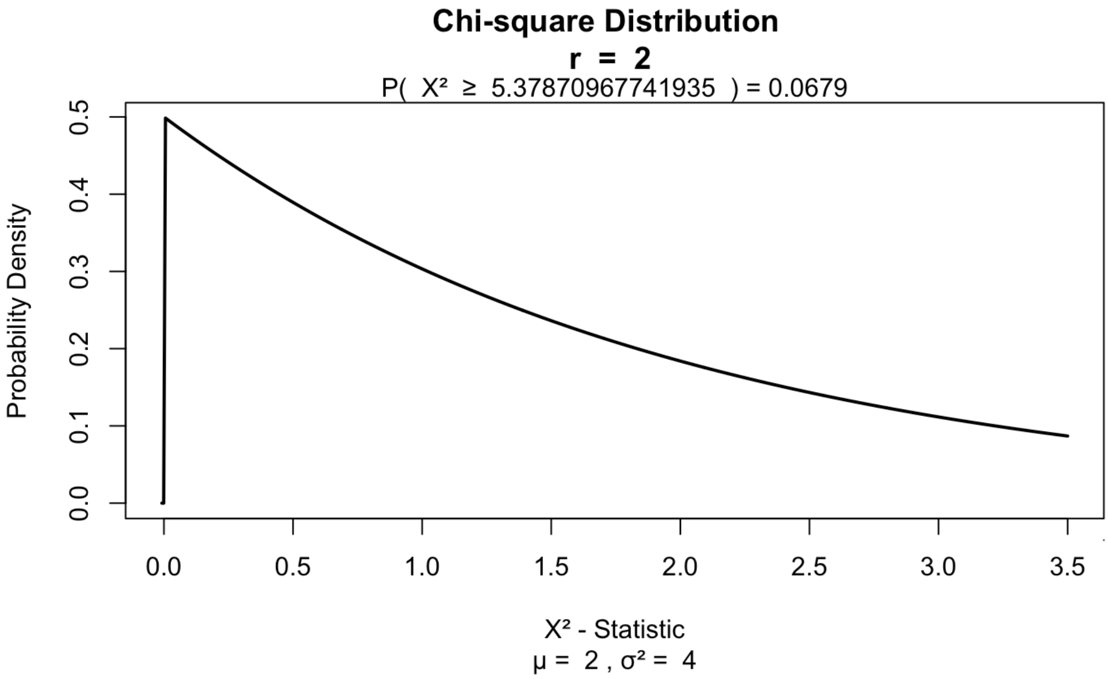
```
## [1] 5.37871
```

And the degrees of freedom

```
k  = 3
df = k - 1
```

Test for significance

```
visualize.chisq(H, df, section="upper")
```


Chi-square Distribution
r = 2
P(X² ≥ 5.37870967741935) = 0.0679
Probability Density
0.0
0.1
0.2
0.3
0.4
0.5
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
X² - Statistic
μ = 2 , σ² = 4

Paired >2 samples

Friedman's ANOVA

Friedman's ANOVA

Created by William Frederick Friedman the Friedman's ANOVA is a nonparametric alternative to the repeated one-way ANOVA.

Just like the Kruskal-Wallis test, Friedman's ANOVA, subtracts the expected mean ranking from the calculated oberved mean ranking, which is also χ^2 distributed.

Simulate data

```
n      = 30
factor = rep(c("ecstasy","alcohol","control"), each=n/3)

dummy.1 = ifelse(factor == "alcohol", 1, 0)
dummy.2 = ifelse(factor == "ecstasy", 1, 0)
b.0     = 23
b.1     = 0
b.2     = 0
error   = rnorm(n, 0, 1.7)

# Model
depres  = b.0 + b.1*dummy.1 + b.2*dummy.2 + error
depres  = round(depres)

data <- data.frame(factor, depres)
```

Simulate data

```
ecstasy <- subset(data, factor=="ecstasy")$depres
alcohol <- subset(data, factor=="alcohol")$depres
control <- subset(data, factor=="control")$depres

data <- data.frame(ecstasy, alcohol, control)
```

The data

Assign ranks

Rank each row.

```
# Rank for each person
ranks = t(apply(data, 1, rank))
```

The data with ranks

Calculate F_r

$$F_r = \left[\frac{12}{Nk(k+1)} \sum_{i=1}^{k} R_i^2\right] - 3N(k+1)$$

- N total number of subjects
- k number of groups
- R_i rank sums for each group

Calculate F_r

Calculate ranks sum per condition and N.

```
R.i = apply(ranks, 2, sum)
R.i
```

```
## ecstasy alcohol control
##    20.0    19.5    20.5
```

```
# N is number of participants
N = 10
```

Calculate F_r

$$F_r = \left[\frac{12}{Nk(k+1)} \sum_{i=1}^{k} R_i^2 \right] - 3N(k+1)$$

```
k = 3
F.r = ( ( 12/(N*k*(k+1)) ) * sum(R.i^2) ) - ( 3*N*(k+1) )
F.r
```

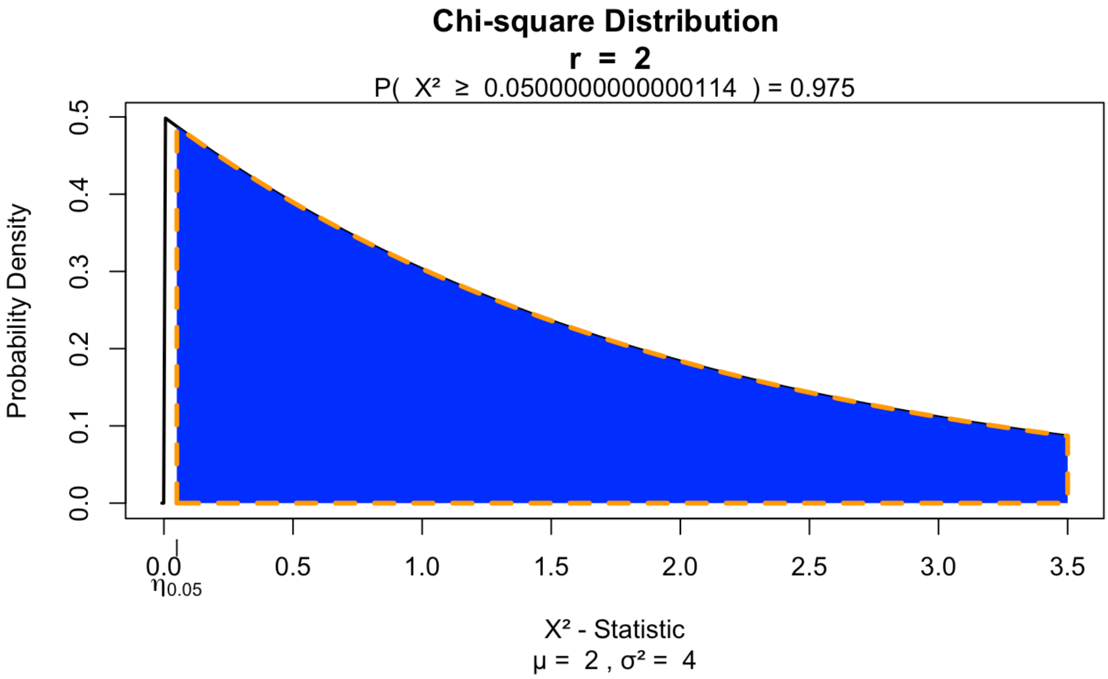
```
## [1] 0.05
```

And the degrees of freedom

```
df = k - 1
```

Test for significance

```
visualize.chisq(F.r, df, section="upper")
```


Chi-square Distribution
r = 2
P(X² ≥ 0.0500000000000114) = 0.975
Probability Density
0.0
0.1
0.2
0.3
0.4
0.5
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
η0.05
X² - Statistic
μ = 2 , σ² = 4

@shklinkenberg

END