

# Multipopulation Statistical Test

Weihaio Lu

2018/3/30

Reference: Wang. J. L., Non-parametric statistical analysis, 2006.4

## Kruskal-Wallis One-way ANOVA

page 92

*When number of groups  $k=2$ , equivalent to Wilcoxon-Mann-Whitney  $U$  test*

```
medicine=c(80,203,235,252,284,368,457,393,
           133,180,100,160,
           156,295,320,448,465,481,279,
           194,214,272,330,386,475)
group=rep(1:4, c(8,4,7,6))
kruskal.test(medicine, group)

##
## Kruskal-Wallis rank sum test
##
## data:  medicine and group
## Kruskal-Wallis chi-squared = 8.0721, df = 3, p-value = 0.04455
```

## Trend-Rank-Test

page 99

```
trendrank.test=function(x, group, fixed.knot=TRUE){
  rankx=rank(x)

  k=length(unique(group))
  N=length(group)

  Rimean=rep(0, k)
  wi=rep(0, k+1)
  ni=rep(0, k+1)
  for(i in 1:k){
    Rimean[i]=sum(rankx[group==i])
    ni[i+1]=sum(group==i)
    wi[i+1]=wi[i]+ni[i+1]+ni[i]
  }
  wi=wi[-1]
  ni=ni[-1]
  T.stat=sum(Rimean*wi)
  ET.HO=N^2*(N+1)/2
  if(!fixed.knot){
    DT.HO=N*(N+1)*(sum(ni*wi^2)-N^3)/12
  }else{
    knot=as.numeric(table(rankx[duplicated(rankx)]))+1
    DT.HO=(N*(N^2-1)-sum(knot^3-knot))*(sum(ni*wi^2)-N^3)/(12*(N-1))
  }
}
```

```

}
p.value=pnorm((T.stat-ET.H0)/sqrt(DT.H0), lower.tail = F)
names(T.stat) <- "Trend-Rank-Test statistics"
RVAL <- list(statistic=T.stat, p.value=p.value, method="Trend-Rank-Test",
            data.name=deparse(substitute(x)))
class(RVAL) <- "htest"
return(RVAL)
}

```

```

Beta.lipoprotein=c(260,200,240,170,270,205,190,200,250,200,
                  310,310,190,225,170,210,280,210,280,240,
                  320,260,360,310,270,380,240,295,260,250)
group=gl(3,10)
trendrank.test(Beta.lipoprotein, group)

```

```

##
## Trend-Rank-Test
##
## data: Beta.lipoprotein
## Trend-Rank-Test statistics = 16430, p-value = 0.0007961
trendrank.test(Beta.lipoprotein, group, fixed.knot = FALSE)

```

```

##
## Trend-Rank-Test
##
## data: Beta.lipoprotein
## Trend-Rank-Test statistics = 16430, p-value = 0.0008175

```

## Jonckheere Terpstra Test

page 101

*When number of groups  $k=2$ , equivalent to Wilcoxon-Mann-Whitney  $U$  test*

*The following code is modified by trendrank.test()*

```

jonckheere.test=function(x, group, fixed.knot=TRUE){
  rankx=rank(x)

  k=length(unique(group))
  N=length(group)

  ni=rep(0, k)
  J.stat=0
  for(m in 1:k){
    ni[m]=sum(group==m)
  }
  csum.ni=c(0,cumsum(ni))
  for(j in 2:k){
    for(i in 1:(j-1)){
      J.stat=J.stat+sum(
        sapply(x[(csum.ni[i]+1):csum.ni[i+1]],
              "<",
              x[(csum.ni[j]+1):csum.ni[j+1]]))
    }
  }
}

```

```

}
EJ.H0=(N^2-sum(ni^2))/4
if(!fixed.knot){
  DJ.H0=(N^2*(2*N+3)-2*sum(ni^3)-3*sum(ni^2))/72
}else{
  knot=as.numeric(table(rankx[duplicated(rankx)]))+1
  DJ.H0=(N^2*(2*N+3)-2*sum(ni^3)-3*sum(ni^2)-sum(knot*(knot-1)*(2*knot+5)))/72+
    sum(ni*(ni-1)*(ni-2))*sum(knot*(knot-1)*(knot-2))/(36*N*(N-1)*(N-2))+
    sum(ni*(ni-1))*sum(knot*(knot-1))/(8*N*(N-1))
}
p.value=pnorm((J.stat-EJ.H0)/sqrt(DJ.H0), lower.tail = F)
names(J.stat) <- "Jonckheere-Terpstra-Test statistics"
RVAL <- list(statistic=J.stat, p.value=p.value, method="Jonckheere-Terpstra-Test",
  data.name=deparse(substitute(x)))
class(RVAL) <- "htest"
return(RVAL)
}

```

```

heartbeat=c(125,136,116,101,105,109,
            122,114,131,120,119,127,
            128,142,128,134,135,131,140,129)
group=rep(1:3, c(6,6,8))
jonckheere.test(heartbeat, group)

```

```

##
## Jonckheere-Terpstra-Test
##
## data: heartbeat
## Jonckheere-Terpstra-Test statistics = 111, p-value = 0.000873
jonckheere.test(heartbeat, group, fixed.knot = FALSE)

```

```

##
## Jonckheere-Terpstra-Test
##
## data: heartbeat
## Jonckheere-Terpstra-Test statistics = 111, p-value = 0.0008809

```