```
R version 3.6.0 (2019-04-26) -- "Planting of a Tree"
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Platform: x86_64-apple-darwin15.6.0 (64-bit)

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[R.app GUI 1.70 (7657) x86_64-apple-darwin15.6.0]

[Workspace restored from /Users/richard/.RData]
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>
> ############# DELFT #############
>
> table11 <- matrix(c(23,  3,  4, 23),
+     2, 2, byrow = TRUE,
+     dimnames = list(Alice = c("+", "-"), Bob = c("+", "-")))
> table12 <- matrix(c(33, 11,  5, 30),
+     2, 2, byrow = TRUE,
+     dimnames = list(Alice = c("+", "-"), Bob = c("+", "-")))
> table21 <- matrix(c(22, 10,  6, 24),
+     2, 2, byrow = TRUE,
+     dimnames = list(Alice = c("+", "-"), Bob = c("+", "-")))
> table22 <- matrix(c(4, 20, 21,  6),
+     2, 2, byrow = TRUE,
+     dimnames = list(Alice = c("+", "-"), Bob = c("+", "-")))
>
> table11
     Bob
Alice  +  -
    + 23  3
    -  4 23
> table12
     Bob
Alice  +  -
    + 33 11
    -  5 30
> table21
     Bob
Alice  +  -
    + 22 10
    -  6 24
> table22
     Bob
Alice  +  -
    +  4 20
    - 21  6
>
> tables <- cbind(as.vector(t(table11)), as.vector(t(table12)), as.vector(t(table21)), as.vector(t(table22)))
> dimnames(tables) = list(outcomes = c("++", "+-", "-+", "--"),
+                         settings = c(11, 12, 21, 22))
> tables
        settings
outcomes 11 12 21 22
      ++ 23 33 22  4
      +-  3 11 10 20
      -+  4  5  6 21
      -- 23 30 24  6
>
> Ns <- apply(tables, 2, sum)
> Ns
11 12 21 22
53 79 62 51
>
> rawProbsMat <- tables / outer(rep(1,4), Ns)
> rawProbsMat
        settings
outcomes         11         12         21         22
      ++ 0.43396226 0.41772152 0.35483871 0.07843137
      +- 0.05660377 0.13924051 0.16129032 0.39215686
      -+ 0.07547170 0.06329114 0.09677419 0.41176471
      -- 0.43396226 0.37974684 0.38709677 0.11764706
>
> VecNames <- as.vector(t(outer(colnames(rawProbsMat), rownames(rawProbsMat), paste, sep = "")))
```

```
> VecNames
 [1] "11++" "11+-" "11-+" "11--" "12++" "12+-" "12-+" "12--" "21++" "21+-" "21-+" "21--" "22++" "22+-" "22-+" "22--"
>
> rawProbsVec <- as.vector(rawProbsMat)
> names(rawProbsVec) <- VecNames
>
> VecNames
 [1] "11++" "11+-" "11-+" "11--" "12++" "12+-" "12-+" "12--" "21++" "21+-" "21-+" "21--" "22++" "22+-" "22-+" "22--"
> rawProbsVec
      11++       11+-       11-+       11--       12++       12+-       12-+       12--       21++       21+-       21-+
0.43396226 0.05660377 0.07547170 0.43396226 0.41772152 0.13924051 0.06329114 0.37974684 0.35483871 0.16129032 0.09677419
      21--       22++       22+-       22-+       22--
0.38709677 0.07843137 0.39215686 0.41176471 0.11764706
>
> Aplus <- c(1, 1, 0, 0)
> Aminus <- - Aplus
> Bplus <- c(1, 0, 1, 0)
> Bminus <- - Bplus
> zero <- c(0, 0, 0, 0)
> NSa1 <- c(Aplus, Aminus, zero, zero)
> NSa2 <- c(zero, zero, Aplus, Aminus)
> NSb1 <- c(Bplus, zero, Bminus, zero)
> NSb2 <- c(zero, Bplus, zero, Bminus)
> NS <- cbind(NSa1 = NSa1, NSa2 = NSa2, NSb1 = NSb1, NSb2 = NSb2)
> rownames(NS) <- VecNames
> NS
     NSa1 NSa2 NSb1 NSb2
11++    1    0    1    0
11+-    1    0    0    0
11-+    0    0    1    0
11--    0    0    0    0
12++   -1    0    0    1
12+-   -1    0    0    0
12-+    0    0    0    1
12--    0    0    0    0
21++    0    1   -1    0
21+-    0    1    0    0
21-+    0    0   -1    0
21--    0    0    0    0
22++    0   -1    0   -1
22+-    0   -1    0    0
22-+    0    0    0   -1
22--    0    0    0    0
>
> # "The number of valid trials is N = 245"
> sum(Ns)
[1] 245
>
> cov11 <- diag(rawProbsMat[ , "11"]) - outer(rawProbsMat[ , "11"], rawProbsMat[ , "11"])
> cov12 <- diag(rawProbsMat[ , "12"]) - outer(rawProbsMat[ , "12"], rawProbsMat[ , "12"])
> cov21 <- diag(rawProbsMat[ , "21"]) - outer(rawProbsMat[ , "21"], rawProbsMat[ , "21"])
> cov22 <- diag(rawProbsMat[ , "22"]) - outer(rawProbsMat[ , "22"], rawProbsMat[ , "22"])
>
> Cov <- matrix(0, 16, 16)
> rownames(Cov) <- VecNames
> colnames(Cov) <- VecNames
> Cov[1:4, 1:4] <- cov11/Ns["11"]
> Cov[5:8, 5:8] <- cov12/Ns["12"]
> Cov[9:12, 9:12] <- cov21/Ns["21"]
> Cov[13:16, 13:16] <- cov22/Ns["22"]
>
> S <- c(c(1, -1, -1 ,1), c(1, -1, -1 , 1), c(1, -1, -1, 1), - c(1, -1, -1, 1))
> names(S) <- VecNames
> sum(S * rawProbsVec)
[1] 2.4225
>
> varS <- t(S) %*% Cov %*% S
> covNN <- t(NS) %*% Cov %*% NS
> covSN <- t(S) %*% Cov %*% NS
> covNS <- t(covSN)
>
> InvCovNN <- solve(covNN)
>
> varCHSH <- varS
>
> varCHSHopt <- varS - covSN %*% InvCovNN %*% covNS
> varS
           [,1]
[1,] 0.04154528
> sqrt(varCHSH / varCHSHopt)
         [,1]
[1,] 1.009601
> covSN %*% solve(covNN)
         NSa1       NSa2       NSb1         NSb2
[1,] 0.2352838 -0.2197461 -0.2520529 -0.004879677
> Sopt <- S - covSN %*% InvCovNN %*% t(NS)
> Sopt
```

```
         11++      11+-       11-+ 11--     12++       12+-       12-+ 12--      21++       21+-      21-+ 21--
[1,] 1.016769 -1.235284 -0.7479471    1 1.240163 -0.7647162 -0.9951203    1 0.9676932 -0.7802539 -1.252053    1
          22++      22+-      22-+ 22--
[1,] -1.224626 0.7802539 0.9951203   -1
>
> CHSH <- sum(S * rawProbsVec)
> CHSH
[1] 2.4225
>
> CHSHopt <- sum(Sopt * rawProbsVec)
> CHSHopt
[1] 2.462658
>
> pnorm((CHSH - 2)/ sqrt(varCHSH), lower.tail = FALSE)
           [,1]
[1,] 0.0190936
> pnorm((CHSHopt - 2)/ sqrt(varCHSHopt), lower.tail = FALSE)
           [,1]
[1,] 0.01096277
>
> J <- c(c(1, 0, 0 ,0), c(0, -1, 0 ,0), c(0, 0, -1, 0), c(-1, 0, 0, 0))
> names(J) <- VecNames
> sum(J * rawProbsVec)
[1] 0.1195162
>
> varJ <- t(J) %*% Cov %*% J
> sum(J * rawProbsVec) / sqrt(varJ)
         [,1]
[1,] 1.261291
> pnorm(sum(J * rawProbsVec) / sqrt(varJ), lower.tail = FALSE)
         [,1]
[1,] 0.103602
>
> covNN <- t(NS) %*% Cov %*% NS
> covJN <- t(J) %*% Cov %*% NS
> covNJ <- t(covJN)
> varJ - covJN %*% InvCovNN %*% covNJ
            [,1]
[1,] 0.002547429
> varJ
           [,1]
[1,] 0.008978894
> sqrt(varJ / (varJ - covJN %*% InvCovNN %*% covNJ))
         [,1]
[1,] 1.877415
> covJN %*% InvCovNN
          NSa1      NSa2      NSb1      NSb2
[1,] 0.5588209 0.4450635 0.4369868 0.4987801
>
> Jopt <- J - covJN %*% InvCovNN %*% t(NS)
> Jopt
           11++       11+-       11-+ 11--       12++       12+-       12-+ 12--         21++       21+-       21-+
[1,] 0.004192268 -0.5588209 -0.4369868    0 0.06004087 -0.4411791 -0.4987801    0 -0.008076702 -0.4450635 -0.5630132
     21--        22++      22+-      22-+ 22--
[1,]    0 -0.05615644 0.4450635 0.4987801    0
>
> sum(J * rawProbsVec)
[1] 0.1195162
>
> sum(Jopt * rawProbsVec)
[1] 0.1156646
>
> varJ / (varJ - covJN %*% InvCovNN %*% covNJ)
         [,1]
[1,] 3.524688
> varJopt <- varJ - covJN %*% InvCovNN %*% covNJ
> (varJ - covJN %*% InvCovNN %*% covNJ) / varJ
         [,1]
[1,] 0.283713
> sqrt( (varJ - covJN %*% InvCovNN %*% covNJ) / varJ )
          [,1]
[1,] 0.5326472
>
> pnorm(sum(J * rawProbsVec) / sqrt(varJ), lower.tail = FALSE)
         [,1]
[1,] 0.103602
> pnorm(sum(Jopt * rawProbsVec) / sqrt(varJopt), lower.tail = FALSE)
           [,1]
[1,] 0.01096277
>
>
>
############# DELFT #############

table11 <- matrix(c(23,  3,  4, 23),
    2, 2, byrow = TRUE,
    dimnames = list(Alice = c("+", "-"), Bob = c("+", "-")))
```

```
table12 <- matrix(c(33, 11,  5, 30),
    2, 2, byrow = TRUE,
    dimnames = list(Alice = c("+", "-"), Bob = c("+", "-")))
table21 <- matrix(c(22, 10,  6, 24),
    2, 2, byrow = TRUE,
    dimnames = list(Alice = c("+", "-"), Bob = c("+", "-")))
table22 <- matrix(c(4, 20, 21,  6),
    2, 2, byrow = TRUE,
    dimnames = list(Alice = c("+", "-"), Bob = c("+", "-")))

table11
table12
table21
table22

tables <- cbind(as.vector(t(table11)), as.vector(t(table12)), as.vector(t(table21)), as.vector(t(table22)))
dimnames(tables) = list(outcomes = c("++", "+-", "-+", "--"),
                        settings = c(11, 12, 21, 22))
tables

Ns <- apply(tables, 2, sum)
Ns

rawProbsMat <- tables / outer(rep(1,4), Ns)
rawProbsMat

VecNames <- as.vector(t(outer(colnames(rawProbsMat), rownames(rawProbsMat), paste, sep = "")))
VecNames

rawProbsVec <- as.vector(rawProbsMat)
names(rawProbsVec) <- VecNames

VecNames
rawProbsVec

Aplus <- c(1, 1, 0, 0)
Aminus <- - Aplus
Bplus <- c(1, 0, 1, 0)
Bminus <- - Bplus
zero <- c(0, 0, 0, 0)
NSa1 <- c(Aplus, Aminus, zero, zero)
NSa2 <- c(zero, zero, Aplus, Aminus)
NSb1 <- c(Bplus, zero, Bminus, zero)
NSb2 <- c(zero, Bplus, zero, Bminus)
NS <- cbind(NSa1 = NSa1, NSa2 = NSa2, NSb1 = NSb1, NSb2 = NSb2)
rownames(NS) <- VecNames
NS

# "The number of valid trials is N = 245"
sum(Ns)

cov11 <- diag(rawProbsMat[ , "11"]) - outer(rawProbsMat[ , "11"], rawProbsMat[ , "11"])
cov12 <- diag(rawProbsMat[ , "12"]) - outer(rawProbsMat[ , "12"], rawProbsMat[ , "12"])
cov21 <- diag(rawProbsMat[ , "21"]) - outer(rawProbsMat[ , "21"], rawProbsMat[ , "21"])
cov22 <- diag(rawProbsMat[ , "22"]) - outer(rawProbsMat[ , "22"], rawProbsMat[ , "22"])

Cov <- matrix(0, 16, 16)
rownames(Cov) <- VecNames
colnames(Cov) <- VecNames
Cov[1:4, 1:4] <- cov11/Ns["11"]
Cov[5:8, 5:8] <- cov12/Ns["12"]
Cov[9:12, 9:12] <- cov21/Ns["21"]
Cov[13:16, 13:16] <- cov22/Ns["22"]

S <- c(c(1, -1, -1 ,1), c(1, -1, -1 , 1), c(1, -1, -1, 1), - c(1, -1, -1, 1))
names(S) <- VecNames
sum(S * rawProbsVec)

varS <- t(S) %*% Cov %*% S
covNN <- t(NS) %*% Cov %*% NS
covSN <- t(S) %*% Cov %*% NS
covNS <- t(covSN)

InvCovNN <- solve(covNN)

varCHSH <- varS

varCHSHopt <- varS - covSN %*% InvCovNN %*% covNS
varS
sqrt(varCHSH / varCHSHopt)
covSN %*% solve(covNN)
Sopt <- S - covSN %*% InvCovNN %*% t(NS)
Sopt

CHSH <- sum(S * rawProbsVec)
CHSH
```

```
CHSHopt <- sum(Sopt * rawProbsVec)
CHSHopt

pnorm((CHSH - 2)/ sqrt(varCHSH), lower.tail = FALSE)
pnorm((CHSHopt - 2)/ sqrt(varCHSHopt), lower.tail = FALSE)

J <- c(c(1, 0, 0 ,0), c(0, -1, 0 ,0), c(0, 0, -1, 0), c(-1, 0, 0, 0))
names(J) <- VecNames
sum(J * rawProbsVec)

varJ <- t(J) %*% Cov %*% J
sum(J * rawProbsVec) / sqrt(varJ)
pnorm(sum(J * rawProbsVec) / sqrt(varJ), lower.tail = FALSE)

covNN <- t(NS) %*% Cov %*% NS
covJN <- t(J) %*% Cov %*% NS
covNJ <- t(covJN)
varJ - covJN %*% InvCovNN %*% covNJ
varJ
sqrt(varJ / (varJ - covJN %*% InvCovNN %*% covNJ))
covJN %*% InvCovNN

Jopt <- J - covJN %*% InvCovNN %*% t(NS)
Jopt

sum(J * rawProbsVec)

sum(Jopt * rawProbsVec)

varJ / (varJ - covJN %*% InvCovNN %*% covNJ)
varJopt <- varJ - covJN %*% InvCovNN %*% covNJ
(varJ - covJN %*% InvCovNN %*% covNJ) / varJ
sqrt( (varJ - covJN %*% InvCovNN %*% covNJ) / varJ )

pnorm(sum(J * rawProbsVec) / sqrt(varJ), lower.tail = FALSE)
pnorm(sum(Jopt * rawProbsVec) / sqrt(varJopt), lower.tail = FALSE)
```