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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]

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>
> ##### MUNICH #####
>
> table11 <- matrix(c(16, 4, 3, 13),
+   2, 2, byrow = TRUE,
+   dimnames = list(Alice = c("+", "-"), Bob = c("+", "-")))
> table12 <- matrix(c(11, 4, 2, 17),
+   2, 2, byrow = TRUE,
+   dimnames = list(Alice = c("+", "-"), Bob = c("+", "-")))
> table21 <- matrix(c(19, 4, 3, 16),
+   2, 2, byrow = TRUE,
+   dimnames = list(Alice = c("+", "-"), Bob = c("+", "-")))
> table22 <- matrix(c(4, 22, 10, 2),
+   2, 2, byrow = TRUE,
+   dimnames = list(Alice = c("+", "-"), Bob = c("+", "-")))
>
> table11
  Bob
Alice + -
  + 16 4
  - 3 13
> table12
  Bob
Alice + -
  + 11 4
  - 2 17
> table21
  Bob
Alice + -
  + 19 4
  - 3 16
> table22
  Bob
Alice + -
  + 4 22
  - 10 2
>
> 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
  ++ 16 11 19 4
  +- 4 4 4 22
  -+ 3 2 3 10
  -- 13 17 16 2
>
> Ns <- apply(tables, 2, sum)
> Ns
11 12 21 22
36 34 42 38
>
> rawProbsMat <- tables / outer(rep(1,4), Ns)
> rawProbsMat
  settings
outcomes 11 12 21 22
  ++ 0.44444444 0.32352941 0.45238095 0.10526316
  +- 0.11111111 0.11764706 0.09523810 0.57894737
  -+ 0.08333333 0.05882353 0.07142857 0.26315789
  -- 0.36111111 0.50000000 0.38095238 0.05263158
>
> VecNames <- as.vector(t(outer(colnames(rawProbsMat), rownames(rawProbsMat), paste, sep = "")))

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> 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-+    21--    22++    22+-    22-+
0.44444444 0.11111111 0.08333333 0.36111111 0.32352941 0.11764706 0.05882353 0.50000000 0.45238095 0.09523810 0.07142857
   21--    22++    22+-    22-+
0.38095238 0.10526316 0.57894737 0.26315789 0.05263158
>
> 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 = 150"
> sum(NS)
[1] 150
>
> 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] 2.609047
>
> 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,] 0.0617252
> sqrt(varCHSH / varCHSHopt)
   [,1]
[1,] 1.01325
> covSN %*% solve(covNN)
NSa1    NSa2    NSb1    NSb2
[1,] 0.279026 0.071646 -0.04462686 0.3469921
> Sopt <- S - covSN %*% InvCovNN %*% t(NS)
> Sopt

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      11++     11+-     11-+    11--     12++     12+-     12-+    12--     21++     21+-     21-+    21--
[1,] 0.7656009 -1.279026 -0.9553731   1 0.9320339 -0.720974 -1.346992   1 0.8837271 -1.071646 -1.044627   1
      22++     22+-     22-+    22--
[1,] -0.5813619 1.071646 1.346992   -1
>
> CHSH <- sum(S * rawProbsVec)
> CHSH
[1] 2.609047
>
> CHSHopt <- sum(Sept * rawProbsVec)
> CHSHopt
[1] 2.582261
>
> pnorm((CHSH - 2)/ sqrt(varCHSH), lower.tail = FALSE)
[1]
[1,] 0.007114475
> pnorm((CHSHopt - 2)/ sqrt(varCHSHopt), lower.tail = FALSE)
[1]
[1,] 0.008782296
>
> 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] 0.1501057
>
> varJ <- t(J) %*% Cov %*% J
> sum(J * rawProbsVec) / sqrt(varJ)
[1]
[1,] 1.270007
> pnorm(sum(J * rawProbsVec) / sqrt(varJ), lower.tail = FALSE)
[1]
[1,] 0.1020411
>
> covNN <- t(NS) %*% Cov %*% NS
> covJN <- t(J) %*% Cov %*% NS
> covNJ <- t(covJN)
> varJ - covJN %*% InvCovNN %*% covNJ
[1]
[1,] 0.003757588
> varJ
[1]
[1,] 0.01396953
> sqrt(varJ / (varJ - covJN %*% InvCovNN %*% covNJ))
[1]
[1,] 1.92813
> covJN %*% InvCovNN
      NSa1      NSa2      NSb1      NSb2
[1,] 0.5697565 0.5179115 0.4888433 0.586748
>
> Jopt <- J - covJN %*% InvCovNN %*% t(NS)
> Jopt
      11++     11+-     11-+    11--     12++     12+-     12-+    12--     21++     21+-     21-+    21--
[1,] -0.05859978 -0.5697565 -0.4888433   0 -0.01699153 -0.4302435 -0.586748   0 -0.02906821 -0.5179115 -0.5111567   0
      22++     22+-     22-+    22--
[1,] 0.1046595 0.5179115 0.586748   0
>
> sum(J * rawProbsVec)
[1] 0.1501057
>
> sum(Jopt * rawProbsVec)
[1] 0.1455654
>
> varJ / (varJ - covJN %*% InvCovNN %*% covNJ)
[1]
[1,] 3.717686
> varJopt <- varJ - covJN %*% InvCovNN %*% covNJ
> (varJ - covJN %*% InvCovNN %*% covNJ) / varJ
[1]
[1,] 0.2689845
> sqrt( (varJ - covJN %*% InvCovNN %*% covNJ) / varJ )
[1]
[1,] 0.5186372
>
> pnorm(sum(J * rawProbsVec) / sqrt(varJ), lower.tail = FALSE)
[1]
[1,] 0.1020411
> pnorm(sum(Jopt * rawProbsVec) / sqrt(varJopt), lower.tail = FALSE)
[1]
[1,] 0.008782296
>
>

```