

# Social Associations

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In this markdown I will:

1. Subset data to easily visualize analytical steps. Then, create an association matrix from the gambit of the group assumption using the simple-ratio index function.
2. Form repeated permutations from the true association matrix to create a null distribution of their coefficients of variations (CV). This will determine if the true CV ranges outside of what is expected by chance associations.

## PART 1: *Social Association Matrix*

```
##      F24A FB26 FB04 F154 FB58 UOU0 R3R3
## 1      1      1      0      0      0      0      0
## 2      0      0      1      0      0      0      0
## 3      0      0      0      1      1      0      0
## 4      0      0      0      0      0      1      0
## 5      0      0      0      0      0      0      1
## 6      1      1      0      0      1      0      0
```

Calculate simple-ratio index with group by individual matrix above.

```
##           F24A      FB26 FB04 F154      FB58 UOU0 R3R3
## F24A 1.0000000 1.0000000      0 0.0 0.3333333      0      0
## FB26 1.0000000 1.0000000      0 0.0 0.3333333      0      0
## FB04 0.0000000 0.0000000      1 0.0 0.0000000      0      0
## F154 0.0000000 0.0000000      0 1.0 0.5000000      0      0
## FB58 0.3333333 0.3333333      0 0.5 1.0000000      0      0
## UOU0 0.0000000 0.0000000      0 0.0 0.0000000      1      0
## R3R3 0.0000000 0.0000000      0 0.0 0.0000000      0      1
```

## PART 2: Permutations

True association index coefficient of variation

$CV = (SD/\text{mean}) * 100$

```
## [1] 168.8753
```

## Create 1000 repeated matrices from true matrix to form null distribution

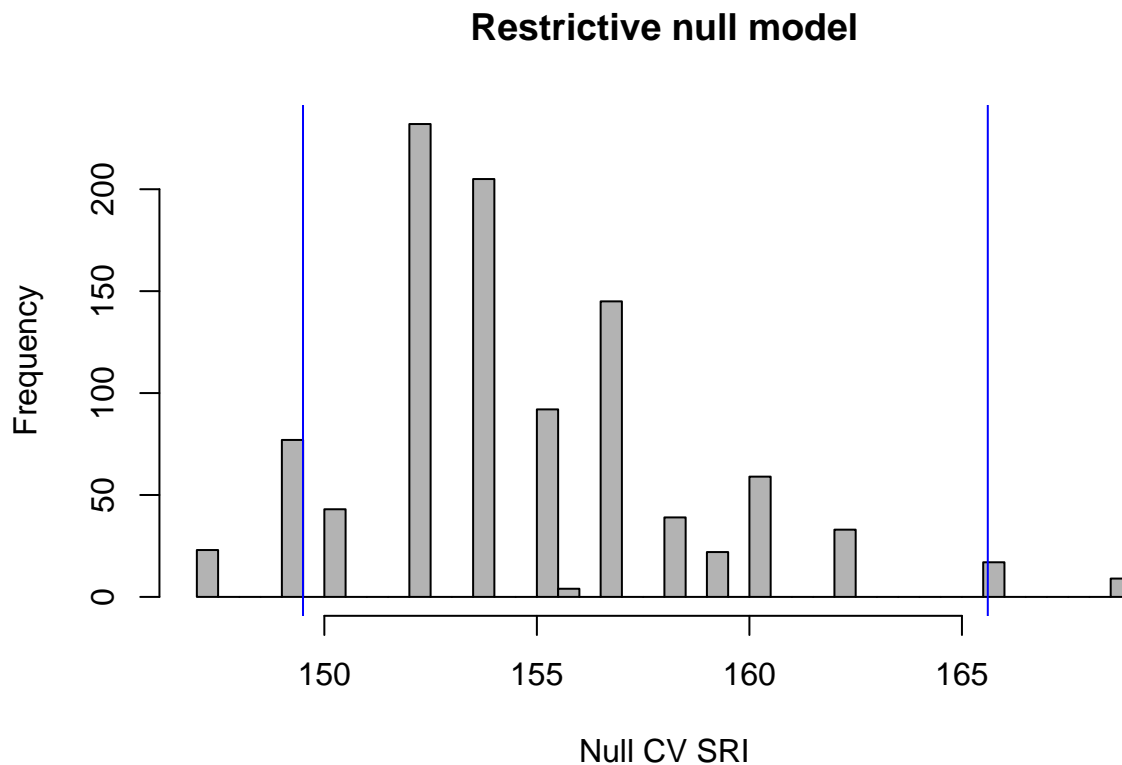
```
# Create 1000 random group-by-individual binary matrices
nF <- null(gbi, iter=1000)

# Calculate the association and CV for each of the 1000 permuted matrices to
# create null distribution
cv_null <- rep(NA,1000)

for (i in 1:1000) {
  sri_null = as.matrix(SRI.func(nF[[i]]))
  cv_null[i] <- ( sd(sri_null) / mean(sri_null) ) * 100
}

# remove NAs, if any
cv_null = cv_null[!is.na(cv_null)]
```

## Form CV distribution



We can reject the null hypothesis that individuals associate at random and conclude that there is evidence that associations are different from what we would expect by chance. Since the CV(TAI) is lower than the other CV, the associations are lower than expected.