

```
> t = table(dti2$used, dti2$DX)
> chisq.test(t)
```

Pearson's Chi-squared test with Yates' continuity correction

```
data: t
X-squared = 5.9558, df = 1, p-value = 0.01467
```

```
> print(t)
```

```
      ADHD  NV
FALSE  272 178
TRUE   264 240
```

```
> t = table(fmri2$used, fmri2$DX)
> chisq.test(t)
```

Pearson's Chi-squared test with Yates' continuity correction

```
data: t
X-squared = 0.58854, df = 1, p-value = 0.443
```

```
> print(t)
```

```
      ADHD  NV
FALSE  133 141
TRUE   234 218
```

```
> t = table(data2$used, data2$DX)
> chisq.test(t)
```

Pearson's Chi-squared test with Yates' continuity correction

```
data: t
X-squared = 2.1276, df = 1, p-value = 0.1447
```

```
> print(t)
```

```
      ADHD  NV
FALSE  413 311
TRUE   510 446
```

```
dti =
read.csv('~data/heritability_change_rev/dti_JHUtracts_ADRDonly_0D0.95_two
TimePoints_noOtherDX.csv')
fmri =
read.csv('~data/heritability_change_rev/rsfmri_7by7from100_4nets_p05SigSu
m_0D0.95_12052019_twoTimePoints.csv')
cnames = c('ID', 'sex', 'race', 'ethn', 'age', 'SX_inatt', 'SX_HI')
a = dti[, c(1, 4:6, 9, 96:97)]
b = fmri[, c(1, 41, 44, 43, 45, 52:53)]
colnames(a) = cnames
```

```

colnames(b) = cnames
data = rbind(a,b)
data2 = add_DX(data, 'age')
data2 = data2[!duplicated(data2$ID), ]

dti =
read.csv('~data/heritability_change_rev/dti_JHUtracts_ADRDonly_0D0.95_SES
andIQ.csv')
colnames(dti)[1] = 'ID'
fmri =
read.csv('~data/heritability_change_rev/rsfmri_7by7from100_4nets_p05SigSu
m_0D0.95_12052019_clean_SESandIQ.csv')
colnames(fmri)[1] = 'ID'
ses_iq = rbind(dti[, c('ID', 'SES', 'FSIQ')], fmri[, c('ID', 'SES',
'FSIQ')])
ses_iq = ses_iq[!duplicated(ses_iq$ID), ]
m = merge(data2, ses_iq, by='ID', all.x=T, all.y=F)

```

```
> table(m$DX)
```

```
ADHD  NV
150  138
```

```
> table(m$DX, m$sex)
```

```

      Female Male
ADHD      47  103
NV        53   85

```

```
> t.test(m[m$DX=='NV', 'SES'], m[m$DX=='ADHD', 'SES'])
```

Welch Two Sample t-test

```

data:  m[m$DX == "NV", "SES"] and m[m$DX == "ADHD", "SES"]
t = -1.3432, df = 278.96, p-value = 0.1803
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -6.403468  1.209032
sample estimates:
mean of x mean of y
 31.47761  34.07483

```

```
> t.test(m[m$DX=='NV', 'FSIQ'], m[m$DX=='ADHD', 'FSIQ'])
```

Welch Two Sample t-test

```

data:  m[m$DX == "NV", "FSIQ"] and m[m$DX == "ADHD", "FSIQ"]
t = 2.6923, df = 245.53, p-value = 0.007585
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
  1.479050  9.542328
sample estimates:
mean of x mean of y

```

```

114.8258  109.3151

> table(m$DX, m$race)

      [American Indian or Alaska Native] [Asian] [Black or African
American]
ADHD                                   1         4
17
NV                                   0         11
14

      [Mixed] [White]
ADHD       13     115
NV         13     100
> table(m$DX, m$eth)

      Hispanic or Latino Not Hispanic or Latino
ADHD                   18                   132
NV                      9                   129
> t = table(m$DX, m$eth)
> print(t)

      Hispanic or Latino Not Hispanic or Latino
ADHD                   18                   132
NV                      9                   129
> chisq.test(t)

      Pearson's Chi-squared test with Yates' continuity correction

data:  t
X-squared = 1.935, df = 1, p-value = 0.1642

```

Now, for within modality ages and number of scans:

```

dti =
read.csv('~data/heritability_change_rev/dti_JHUtracts_ADRDonly_0D0.95_two
TimePoints_no0therDX.csv')
fmri =
read.csv('~data/heritability_change_rev/rsfmri_7by7from100_4nets_p05SigSu
m_0D0.95_12052019_twoTimePoints.csv')
cnames = c('ID', 'sex', 'race', 'ethn', 'age', 'SX_inatt', 'SX_HI')
a = dti[, c(1, 4:6, 9, 96:97)]
b = fmri[, c(1, 41, 44, 43, 45, 52:53)]
colnames(a) = cnames
colnames(b) = cnames
dti2 = add_DX(a, 'age')
fmri2 = add_DX(b, 'age')

```

```
> table(dti2$DX)

ADHD   NV
250  254
> table(fmri2$DX)

ADHD   NV
226  226
```

```
add_baseline = function(df) {
  df$is_baseline = T
  for (m in df$ID) {
    subj_rows = which(df$ID==m)
    last = which.max(df[subj_rows, 'age'])
    df[subj_rows[last], 'is_baseline'] = F
  }
  return(df)
}
dti3 = add_baseline(dti2)
fmri3 = add_baseline(fmri2)
```

```
> idx = fmri3$DX=='NV' & fmri3$is_baseline
> mean(fmri3[idx, 'age'])
[1] 10.45529
> sd(fmri3[idx, 'age'])
[1] 2.562922
> min(fmri3[idx, 'age'])
[1] 4.492813
> max(fmri3[idx, 'age'])
[1] 16.71458
> idx = fmri3$DX=='ADHD' & fmri3$is_baseline
> mean(fmri3[idx, 'age'])
[1] 10.31923
> sd(fmri3[idx, 'age'])
[1] 2.474852
> min(fmri3[idx, 'age'])
[1] 4.867899
> max(fmri3[idx, 'age'])
[1] 16.0219
> idx = fmri3$DX=='NV' & !fmri3$is_baseline
> mean(fmri3[idx, 'age'])
[1] 12.56024
> sd(fmri3[idx, 'age'])
[1] 2.470571
> min(fmri3[idx, 'age'])
[1] 8.095825
> max(fmri3[idx, 'age'])
[1] 17.84531
```

```
> idx = fmri3$DX=='ADHD' & !fmri3$is_baseline
> mean(fmri3[idx,'age'])
[1] 12.92944
> sd(fmri3[idx,'age'])
[1] 2.449058
> min(fmri3[idx,'age'])
[1] 6.847365
> max(fmri3[idx,'age'])
[1] 17.46201
> t.test(fmri3[fmri3$DX=='ADHD' & !fmri3$is_baseline, 'age'],
fmri3[fmri3$DX=='NV' & !fmri3$is_baseline, 'age'])
```

Welch Two Sample t-test

```
data: fmri3[fmri3$DX == "ADHD" & !fmri3$is_baseline, "age"] and
fmri3[fmri3$DX == "NV" & !fmri3$is_baseline, "age"]
t = 1.1282, df = 223.98, p-value = 0.2605
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -0.2756887  1.0140846
sample estimates:
mean of x mean of y
 12.92944  12.56024

> t.test(fmri3[fmri3$DX=='ADHD' & fmri3$is_baseline, 'age'],
fmri3[fmri3$DX=='NV' & fmri3$is_baseline, 'age'])
```

Welch Two Sample t-test

```
data: fmri3[fmri3$DX == "ADHD" & fmri3$is_baseline, "age"] and
fmri3[fmri3$DX == "NV" & fmri3$is_baseline, "age"]
t = -0.40598, df = 223.73, p-value = 0.6851
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -0.7965411  0.5244035
sample estimates:
mean of x mean of y
 10.31923  10.45529
```

```
> idx = dti3$DX=='ADHD' & !dti3$is_baseline
> mean(dti3[idx,'age'])
[1] 11.51936
> sd(dti3[idx,'age'])
[1] 2.295731
> min(dti3[idx,'age'])
[1] 6.7
> max(dti3[idx,'age'])
[1] 16.99
> idx = dti3$DX=='NV' & !dti3$is_baseline
> mean(dti3[idx,'age'])
[1] 11.19315
> sd(dti3[idx,'age'])
[1] 2.51356
```

```

> min(dti3[idx,'age'])
[1] 5.14
> max(dti3[idx,'age'])
[1] 17.91
> idx = dti3$DX=='NV' & dti3$is_baseline
> mean(dti3[idx,'age'])
[1] 9.43252
> sd(dti3[idx,'age'])
[1] 2.404655
> min(dti3[idx,'age'])
[1] 4.14
> max(dti3[idx,'age'])
[1] 16.49
> idx = dti3$DX=='ADHD' & dti3$is_baseline
> mean(dti3[idx,'age'])
[1] 9.23264
> sd(dti3[idx,'age'])
[1] 2.052029
> min(dti3[idx,'age'])
[1] 5.19
> max(dti3[idx,'age'])
[1] 14.9

> t.test(dti3[dti3$DX=='ADHD' & dti3$is_baseline, 'age'],
dti3[dti3$DX=='NV' & dti3$is_baseline, 'age'])

```

Welch Two Sample t-test

```

data: dti3[dti3$DX == "ADHD" & dti3$is_baseline, "age"] and dti3[dti3$DX
== "NV" & dti3$is_baseline, "age"]
t = -0.71017, df = 245.09, p-value = 0.4783
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -0.7542593  0.3544999
sample estimates:
mean of x mean of y
  9.23264  9.43252

```

```

> t.test(dti3[dti3$DX=='ADHD' & !dti3$is_baseline, 'age'],
dti3[dti3$DX=='NV' & !dti3$is_baseline, 'age'])

```

Welch Two Sample t-test

```

data: dti3[dti3$DX == "ADHD" & !dti3$is_baseline, "age"] and dti3[dti3$DX
== "NV" & !dti3$is_baseline, "age"]
t = 1.076, df = 248.62, p-value = 0.283
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -0.2708949  0.9233157
sample estimates:
mean of x mean of y
 11.51936 11.19315

```