

fMRI Scans and Clinical Data Analysis

Setup

```
# load packages
packages <- c("here", "dplyr", "data.table", "psych", "FSA")

lapply(packages, library, character.only = TRUE)
```

Read in toddler data

```
# read in data
tidy_fMRI_clinical_toddlers <- read.table(here::here("data", "tidy_fMRI_clinical_toddlers.txt"),
                                         header = T, sep = "\t", stringsAsFactors = F)

# toddler sample
toddler_sample <- tidy_fMRI_clinical_toddlers[!duplicated(tidy_fMRI_clinical_toddlers$subjid), ]
dim(toddler_sample)[1]
```

```
## [1] 71
```

Toddler fMRI scans and sample size

```
# total scans
Story_scans <- tidy_fMRI_clinical_toddlers[!is.na(tidy_fMRI_clinical_toddlers$Story_Lang),]
Karen_scans <- tidy_fMRI_clinical_toddlers[!is.na(tidy_fMRI_clinical_toddlers$Karen_Lang),]
Motherese_scans <- tidy_fMRI_clinical_toddlers[!is.na(tidy_fMRI_clinical_toddlers$Motherese),]

knitr::kable(rbind(Story_Lang = table(Story_scans$group),
                   Karen_Lang = table(Karen_scans$group),
                   Motherese = table(Motherese_scans$group)))
```

	ASD	TD
Story_Lang	33	26
Karen_Lang	40	33
Motherese	39	29

```
# sample size
knitr::kable(rbind(Story_Lang = table(Story_scans$group[!duplicated(Story_scans$subj)]),
  Karen_Lang = table(Karen_scans$group[!duplicated(Karen_scans$subj)]),
  Motherese = table(Motherese_scans$group[!duplicated(Motherese_scans$subj)])))
```

	ASD	TD
Story_Lang	31	23
Karen_Lang	36	28
Motherese	37	25

Adult scans and sample size

```
# read adult data
adult_scans <- read.table(here::here("data", "tidy_fMRI_adults.txt"),
  header = T, sep = "\t", stringsAsFactors = F)
```

```
# adult sample
adult_sample <- adult_scans[!duplicated(adult_scans$Subj), ]
dim(adult_sample)[1]
```

```
## [1] 14
```

```
table(adult_sample$gender)
```

```
##
## F M
## 8 6
```

```
# adult fMRI scans and sample size
Story_scans_adult <- adult_scans[!is.na(adult_scans$Story_Lang),]
Karen_scans_adult <- adult_scans[!is.na(adult_scans$Karen_Lang),]
Motherese_scans_adult <- adult_scans[!is.na(adult_scans$Motherese),]
```

```
knitr::kable(cbind(Story_Lang = dim(Story_scans_adult)[1],
  Karen_Lang = dim(Karen_scans_adult)[1],
  Motherese = dim(Motherese_scans_adult)[1]))
```

Story_Lang	Karen_Lang	Motherese
18	12	11

```
# sample size
knitr::kable(cbind(Story_Lang = dim(Story_scans_adult[!duplicated(Story_scans_adult$Subj),])[1],
  Karen_Lang = dim(Karen_scans_adult[!duplicated(Karen_scans_adult$Subj),])[1],
  Motherese = dim(Motherese_scans_adult[!duplicated(Motherese_scans_adult$Subj),])[1]))
```

Story_Lang	Karen_Lang	Motherese
13	12	8

Head motion for each language paradigm

mean and sd in toddlers

```
describeBy(Story_scans[, c("group", "Story_meanFD")], group = "group",
           mat = TRUE, digits = 2)
```

```
##           item group1 vars  n mean  sd median trimmed  mad  min  max range
## group*1      1    ASD   1 33 1.00 0.00   1.00   1.00 0.00 1.00 1.00  0.00
## group*2      2    TD    1 26 1.00 0.00   1.00   1.00 0.00 1.00 1.00  0.00
## Story_meanFD1 3    ASD   2 33 0.09 0.06   0.07   0.08 0.02 0.03 0.30  0.27
## Story_meanFD2 4    TD    2 26 0.11 0.10   0.07   0.09 0.05 0.04 0.46  0.42
##           skew kurtosis  se
## group*1      NaN      NaN 0.00
## group*2      NaN      NaN 0.00
## Story_meanFD1 1.97      3.47 0.01
## Story_meanFD2 2.23      4.63 0.02
```

```
describeBy(Karen_scans[, c("group", "Karen_meanFD")], group = "group",
           mat = TRUE, digits = 2)
```

```
##           item group1 vars  n mean  sd median trimmed  mad  min  max range
## group*1      1    ASD   1 40 1.00 0.00   1.00   1.00 0.00 1.00 1.00  0.00
## group*2      2    TD    1 33 1.00 0.00   1.00   1.00 0.00 1.00 1.00  0.00
## Karen_meanFD1 3    ASD   2 40 0.09 0.06   0.07   0.08 0.03 0.03 0.33  0.30
## Karen_meanFD2 4    TD    2 33 0.10 0.05   0.09   0.10 0.06 0.03 0.22  0.19
##           skew kurtosis  se
## group*1      NaN      NaN 0.00
## group*2      NaN      NaN 0.00
## Karen_meanFD1 2.20      5.78 0.01
## Karen_meanFD2 0.55     -0.85 0.01
```

```
describeBy(Motherese_scans[, c("group", "Motherese_meanFD")], group = "group",
           mat = TRUE, digits = 2)
```

```
##           item group1 vars  n mean  sd median trimmed  mad  min  max
## group*1      1    ASD   1 39 1.00 0.00   1.00   1.00 0.00 1.00 1.00
## group*2      2    TD    1 29 1.00 0.00   1.00   1.00 0.00 1.00 1.00
## Motherese_meanFD1 3    ASD   2 39 0.11 0.14   0.07   0.09 0.04 0.03 0.87
## Motherese_meanFD2 4    TD    2 29 0.09 0.06   0.06   0.09 0.04 0.03 0.21
##           range skew kurtosis  se
## group*1      0.00 NaN      NaN 0.00
## group*2      0.00 NaN      NaN 0.00
## Motherese_meanFD1 0.84 4.32    20.51 0.02
## Motherese_meanFD2 0.18 0.76    -0.91 0.01
```

```

# ASD vs. TD toddlers
t.test(Story_scans$Story_meanFD[Story_scans$group == "TD"],
       Story_scans$Story_meanFD[Story_scans$group == "ASD"])

##
## Welch Two Sample t-test
##
## data: Story_scans$Story_meanFD[Story_scans$group == "TD"] and Story_scans$Story_meanFD[Story_scans$group == "ASD"]
## t = 0.87889, df = 40.133, p-value = 0.3847
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.02541549 0.06453575
## sample estimates:
## mean of x mean of y
## 0.11125759 0.09169746

t.test(Karen_scans$Story_meanFD[Karen_scans$group == "TD"],
       Karen_scans$Story_meanFD[Karen_scans$group == "ASD"])

##
## Welch Two Sample t-test
##
## data: Karen_scans$Story_meanFD[Karen_scans$group == "TD"] and Karen_scans$Story_meanFD[Karen_scans$group == "ASD"]
## t = 1.2763, df = 33.38, p-value = 0.2106
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.01665545 0.07279804
## sample estimates:
## mean of x mean of y
## 0.11313742 0.08506613

t.test(Motherese_scans$Story_meanFD[Motherese_scans$group == "TD"],
       Motherese_scans$Story_meanFD[Motherese_scans$group == "ASD"])

##
## Welch Two Sample t-test
##
## data: Motherese_scans$Story_meanFD[Motherese_scans$group == "TD"] and Motherese_scans$Story_meanFD[Motherese_scans$group == "ASD"]
## t = -0.60862, df = 50.905, p-value = 0.5455
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.03868958 0.02068921
## sample estimates:
## mean of x mean of y
## 0.08406022 0.09306040

# mean and sd in adults
Summarize(Story_scans_adult$Story_meanFD)[2:3]

##      mean      sd
## 0.0817588 0.0245075

```

```
Summarize(Karen_scans_adult$Karen_meanFD)[2:3]
```

```
##      mean      sd
## 0.0808412 0.0404793
```

```
Summarize(Motherese_scans_adult$Motherese_meanFD)[2:3]
```

```
##      mean      sd
## 0.0746597 0.0300425
```

```
# adults vs. TD toddlers
```

```
t.test(Story_scans_adult$Story_meanFD,
       Story_scans$Story_meanFD[Story_scans$group == "TD"])
```

```
##
## Welch Two Sample t-test
##
## data: Story_scans_adult$Story_meanFD and Story_scans$Story_meanFD[Story_scans$group == "TD"]
## t = -1.4569, df = 29.288, p-value = 0.1558
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.07089122 0.01189373
## sample estimates:
## mean of x mean of y
## 0.08175885 0.11125759
```

```
t.test(Karen_scans_adult$Karen_meanFD,
       Karen_scans$Karen_meanFD[Karen_scans$group == "TD"])
```

```
##
## Welch Two Sample t-test
##
## data: Karen_scans_adult$Karen_meanFD and Karen_scans$Karen_meanFD[Karen_scans$group == "TD"]
## t = -1.3221, df = 25.522, p-value = 0.1979
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.05027957 0.01093995
## sample estimates:
## mean of x mean of y
## 0.0808412 0.1005110
```

```
t.test(Motherese_scans_adult$Motherese_meanFD,
       Motherese_scans$Motherese_meanFD[Motherese_scans$group == "TD"])
```

```
##
## Welch Two Sample t-test
##
## data: Motherese_scans_adult$Motherese_meanFD and Motherese_scans$Motherese_meanFD[Motherese_scans$g
## t = -1.3092, df = 33.15, p-value = 0.1995
## alternative hypothesis: true difference in means is not equal to 0
```

```
## 95 percent confidence interval:
## -0.046098527 0.009996017
## sample estimates:
## mean of x mean of y
## 0.07465973 0.09271098
```

```
# adults vs. ASD toddlers
t.test(Story_scans_adult$Story_meanFD,
       Story_scans$Story_meanFD[Story_scans$group == "ASD"])
```

```
##
## Welch Two Sample t-test
##
## data: Story_scans_adult$Story_meanFD and Story_scans$Story_meanFD[Story_scans$group == "ASD"]
## t = -0.80587, df = 45.717, p-value = 0.4245
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.03476738 0.01489016
## sample estimates:
## mean of x mean of y
## 0.08175885 0.09169746
```

```
t.test(Karen_scans_adult$Karen_meanFD,
       Karen_scans$Karen_meanFD[Karen_scans$group == "ASD"])
```

```
##
## Welch Two Sample t-test
##
## data: Karen_scans_adult$Karen_meanFD and Karen_scans$Karen_meanFD[Karen_scans$group == "ASD"]
## t = -0.67748, df = 26.036, p-value = 0.5041
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.04064170 0.02049152
## sample estimates:
## mean of x mean of y
## 0.08084120 0.09091629
```

```
t.test(Motherese_scans_adult$Motherese_meanFD,
       Motherese_scans$Motherese_meanFD[Motherese_scans$group == "ASD"])
```

```
##
## Welch Two Sample t-test
##
## data: Motherese_scans_adult$Motherese_meanFD and Motherese_scans$Motherese_meanFD[Motherese_scans$group == "ASD"]
## t = -1.6601, df = 46.817, p-value = 0.1036
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.08771817 0.00840488
## sample estimates:
## mean of x mean of y
## 0.07465973 0.11431637
```

Demographic information and clinical test scores

```
colnames(select(toddler_sample, contains("final")))
```

```
## [1] "final_Dx" "final_ados_CoSoTot"
## [3] "final_ados_RRTot" "final_ados_CoSoTotRRTot"
## [5] "final_vine_ComTotal_DomStd" "final_vine_DlyTotal_DomStd"
## [7] "final_vine_SocTotal_DomStd" "final_vine_MtrTotal_DomStd"
## [9] "final_vine_AdapBehav_DomStd" "final_vine_DomStdTotal"
## [11] "final_mullen_VRT" "final_mullen_FMT"
## [13] "final_mullen_RLT" "final_mullen_ELT"
## [15] "final_mullen_ELC_Std"
```

```
describeBy(toddler_sample[, c("group", "Gender", "scan_age", "test_age", colnames(select(toddler_sample, 
group = "group", mat = TRUE, digits = 3))
```

	item	group1	vars	n	mean	sd	median	trimmed
## group*1	1	ASD	1 41	1.000	0.000	1.0	1.000	
## group*2	2	TD	1 30	1.000	0.000	1.0	1.000	
## Gender*1	3	ASD	2 41	1.854	0.358	2.0	1.939	
## Gender*2	4	TD	2 30	1.600	0.498	2.0	1.625	
## scan_age1	5	ASD	3 41	28.805	9.732	27.0	28.000	
## scan_age2	6	TD	3 30	23.700	5.984	22.0	23.292	
## test_age1	7	ASD	4 41	28.879	8.416	33.0	29.004	
## test_age2	8	TD	4 30	26.267	8.136	27.0	26.458	
## final_Dx*1	9	ASD	5 41	1.024	0.156	1.0	1.000	
## final_Dx*2	10	TD	5 30	4.700	2.535	4.5	4.667	
## final_ados_CoSoTot1	11	ASD	6 41	12.854	4.059	13.0	13.000	
## final_ados_CoSoTot2	12	TD	6 30	2.700	1.489	3.0	2.708	
## final_ados_RRTot1	13	ASD	7 41	5.341	2.128	6.0	5.455	
## final_ados_RRTot2	14	TD	7 30	1.233	1.165	1.0	1.125	
## final_ados_CoSoTotRRTot1	15	ASD	8 41	18.195	5.372	18.0	18.394	
## final_ados_CoSoTotRRTot2	16	TD	8 30	3.933	1.799	4.0	3.833	
## final_vine_ComTotal_DomStd1	17	ASD	9 41	82.927	16.626	85.0	84.030	
## final_vine_ComTotal_DomStd2	18	TD	9 30	97.167	11.859	96.0	96.583	
## final_vine_DlyTotal_DomStd1	19	ASD	10 41	86.366	11.764	85.0	85.758	
## final_vine_DlyTotal_DomStd2	20	TD	10 30	97.533	12.227	96.5	97.250	
## final_vine_SocTotal_DomStd1	21	ASD	11 41	82.951	12.586	84.0	83.455	
## final_vine_SocTotal_DomStd2	22	TD	11 30	98.567	10.311	99.0	98.000	
## final_vine_MtrTotal_DomStd1	23	ASD	12 41	89.829	17.943	89.0	91.212	
## final_vine_MtrTotal_DomStd2	24	TD	12 30	94.633	20.769	97.5	97.750	
## final_vine_AdapBehav_DomStd1	25	ASD	13 41	82.366	11.510	83.0	81.667	
## final_vine_AdapBehav_DomStd2	26	TD	13 30	96.800	10.889	97.5	96.333	
## final_vine_DomStdTotal1	27	ASD	14 41	341.829	44.069	344.0	341.030	
## final_vine_DomStdTotal2	28	TD	14 30	388.200	34.035	392.0	388.208	
## final_mullen_VRT1	29	ASD	15 41	38.610	12.730	40.0	39.000	
## final_mullen_VRT2	30	TD	15 30	54.300	11.621	55.0	54.000	
## final_mullen_FMT1	31	ASD	16 41	39.951	11.853	42.0	40.455	
## final_mullen_FMT2	32	TD	16 30	50.000	8.154	49.0	49.917	
## final_mullen_RLT1	33	ASD	17 41	32.293	14.780	26.0	31.667	
## final_mullen_RLT2	34	TD	17 30	48.200	11.493	47.5	48.042	

```

## final_mullen_ELT1      35    ASD   18 41   33.098 16.143   30.0 32.879
## final_mullen_ELT2      36     TD   18 30   43.767 12.204   42.0 43.042
## final_mullen_ELC_Std1  37    ASD   19 41   74.073 21.979   72.0 74.818
## final_mullen_ELC_Std2  38     TD   19 30   98.367 16.587   97.5 98.042
##
##      mad min max range   skew kurtosis   se
## group*1      0.000   1   1     0    NaN      NaN 0.000
## group*2      0.000   1   1     0    NaN      NaN 0.000
## Gender*1      0.000   1   2     1 -1.928    1.764 0.056
## Gender*2      0.000   1   2     1 -0.388   -1.910 0.091
## scan_age1     10.378  14  55    41  0.727    0.002 1.520
## scan_age2      6.672  14  38    24  0.511   -0.571 1.092
## test_age1      4.448  12  51    39 -0.025   -0.205 1.314
## test_age2     10.378  13  37    24 -0.163   -1.548 1.486
## final_Dx*1      0.000   1   2     1  5.942   34.145 0.024
## final_Dx*2      3.706   1   8     7 -0.005   -1.817 0.463
## final_ados_CoSoTot1   4.448   0  20    20 -0.621    0.669 0.634
## final_ados_CoSoTot2   1.483   0   6     6  0.078   -0.361 0.272
## final_ados_RRTot1     2.965   0   9     9 -0.347   -0.711 0.332
## final_ados_RRTot2     1.483   0   4     4  0.444   -0.895 0.213
## final_ados_CoSoTotRRTot1 5.930   5  27    22 -0.334   -0.372 0.839
## final_ados_CoSoTotRRTot2 1.483   1   8     7  0.474   -0.539 0.328
## final_vine_ComTotal_DomStd1 14.826  35 126   91 -0.475    0.875 2.597
## final_vine_ComTotal_DomStd2 10.378  70 122   52  0.231   -0.135 2.165
## final_vine_DlyTotal_DomStd1 14.826  68 116   48  0.469   -0.423 1.837
## final_vine_DlyTotal_DomStd2 11.119  76 122   46  0.208   -1.019 2.232
## final_vine_SocTotal_DomStd1 16.309  57 108   51 -0.205   -0.871 1.966
## final_vine_SocTotal_DomStd2  8.896  79 126   47  0.526    0.463 1.883
## final_vine_MtrTotal_DomStd1 10.378   0 117  117 -2.845   12.703 2.802
## final_vine_MtrTotal_DomStd2  9.637   0 119  119 -3.081   11.578 3.792
## final_vine_AdapBehav_DomStd1  8.896  58 111   53  0.445    0.206 1.798
## final_vine_AdapBehav_DomStd2 10.378  79 128   49  0.587    0.561 1.988
## final_vine_DomStdTotal1    51.891 250 445  195  0.099   -0.515 6.882
## final_vine_DomStdTotal2    24.463 315 483  168  0.188    0.675 6.214
## final_mullen_VRT1     11.861   1  63    62 -0.512    0.241 1.988
## final_mullen_VRT2     13.343  30  77    47  0.078   -0.746 2.122
## final_mullen_FMT1     11.861  20  57    37 -0.495   -1.074 1.851
## final_mullen_FMT2     10.378  35  64    29  0.089   -1.075 1.489
## final_mullen_RLT1     10.378   1  59    58  0.253   -1.095 2.308
## final_mullen_RLT2     12.602  23  72    49  0.093   -0.528 2.098
## final_mullen_ELT1     14.826   1  63    62  0.228   -1.011 2.521
## final_mullen_ELT2     14.085  25  70    45  0.367   -0.802 2.228
## final_mullen_ELC_Std1    22.239   7 115   108 -0.467    0.545 3.433
## final_mullen_ELC_Std2    15.567  71 127    56  0.191   -1.063 3.028

```

```
# Chi-squared test on gender by group
```

```
gender_diff <- table(toddler_sample$Gender, toddler_sample$group)
knitr::kable(gender_diff)
```

	ASD	TD
F	6	12
M	35	18


```
chisq.test(gender_diff)
```

```
##  
## Pearson's Chi-squared test with Yates' continuity correction  
##  
## data: gender_diff  
## X-squared = 4.6259, df = 1, p-value = 0.03149
```

```
# group differences between ASD and TD
```

```
lapply(toddler_sample[, c("scan_age", "test_age", colnames(select(toddler_sample, contains("final")))[-1]),  
       function(x) t.test(x ~ toddler_sample$group, var.equal = TRUE))
```

```
## $scan_age  
##  
## Two Sample t-test  
##  
## data: x by toddler_sample$group  
## t = 2.5404, df = 69, p-value = 0.01333  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## 1.096119 9.113638  
## sample estimates:  
## mean in group ASD mean in group TD  
## 28.80488 23.70000  
##  
##  
## $test_age  
##  
## Two Sample t-test  
##  
## data: x by toddler_sample$group  
## t = 1.3098, df = 69, p-value = 0.1946  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## -1.366141 6.589881  
## sample estimates:  
## mean in group ASD mean in group TD  
## 28.87854 26.26667  
##  
##  
## $final_ados_CoSoTot  
##  
## Two Sample t-test  
##  
## data: x by toddler_sample$group  
## t = 13.052, df = 69, p-value < 2.2e-16  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## 8.601704 11.705613  
## sample estimates:  
## mean in group ASD mean in group TD
```

```

##          12.85366          2.70000
##
##
## $final_ados_RRTot
##
## Two Sample t-test
##
## data: x by toddler_sample$group
## t = 9.5632, df = 69, p-value = 2.845e-14
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  3.251147 4.965113
## sample estimates:
## mean in group ASD mean in group TD
##      5.341463      1.233333
##
##
## $final_ados_CoSoTotRRTot
##
## Two Sample t-test
##
## data: x by toddler_sample$group
## t = 13.956, df = 69, p-value < 2.2e-16
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 12.22313 16.30044
## sample estimates:
## mean in group ASD mean in group TD
##      18.195122      3.933333
##
##
## $final_vine_ComTotal_DomStd
##
## Two Sample t-test
##
## data: x by toddler_sample$group
## t = -4.0019, df = 69, p-value = 0.0001559
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -21.338451 -7.141224
## sample estimates:
## mean in group ASD mean in group TD
##      82.92683      97.16667
##
##
## $final_vine_DlyTotal_DomStd
##
## Two Sample t-test
##
## data: x by toddler_sample$group
## t = -3.8862, df = 69, p-value = 0.000231
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -16.900232 -5.434727

```

```

## sample estimates:
## mean in group ASD   mean in group TD
##           86.36585           97.53333
##
##
## $final_vine_SocTotal_DomStd
##
## Two Sample t-test
##
## data:  x by toddler_sample$group
## t = -5.5628, df = 69, p-value = 4.692e-07
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -21.21549 -10.01540
## sample estimates:
## mean in group ASD   mean in group TD
##           82.95122           98.56667
##
##
## $final_vine_MtrTotal_DomStd
##
## Two Sample t-test
##
## data:  x by toddler_sample$group
## t = -1.0424, df = 69, p-value = 0.3008
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -13.997691   4.389561
## sample estimates:
## mean in group ASD   mean in group TD
##           89.82927           94.63333
##
##
## $final_vine_AdapBehav_DomStd
##
## Two Sample t-test
##
## data:  x by toddler_sample$group
## t = -5.3386, df = 69, p-value = 1.132e-06
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -19.827972  -9.040321
## sample estimates:
## mean in group ASD   mean in group TD
##           82.36585           96.80000
##
##
## $final_vine_DomStdTotal
##
## Two Sample t-test
##
## data:  x by toddler_sample$group
## t = -4.8061, df = 69, p-value = 8.672e-06
## alternative hypothesis: true difference in means is not equal to 0

```

```

## 95 percent confidence interval:
## -65.61853 -27.12293
## sample estimates:
## mean in group ASD mean in group TD
## 341.8293 388.2000
##
##
## $final_mullen_VRT
##
## Two Sample t-test
##
## data: x by toddler_sample$group
## t = -5.3199, df = 69, p-value = 1.218e-06
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -21.574061 -9.806427
## sample estimates:
## mean in group ASD mean in group TD
## 38.60976 54.30000
##
##
## $final_mullen_FMT
##
## Two Sample t-test
##
## data: x by toddler_sample$group
## t = -3.999, df = 69, p-value = 0.0001575
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -15.061763 -5.035798
## sample estimates:
## mean in group ASD mean in group TD
## 39.95122 50.00000
##
##
## $final_mullen_RLT
##
## Two Sample t-test
##
## data: x by toddler_sample$group
## t = -4.9056, df = 69, p-value = 5.967e-06
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -22.376336 -9.438298
## sample estimates:
## mean in group ASD mean in group TD
## 32.29268 48.20000
##
##
## $final_mullen_ELIT
##
## Two Sample t-test
##
## data: x by toddler_sample$group

```

```

## t = -3.038, df = 69, p-value = 0.003361
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -17.675195  -3.663016
## sample estimates:
## mean in group ASD  mean in group TD
##           33.09756           43.76667
##
##
## $final_mullen_ELC_Std
##
## Two Sample t-test
##
## data:  x by toddler_sample$group
## t = -5.0833, df = 69, p-value = 3.037e-06
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -33.82757 -14.75943
## sample estimates:
## mean in group ASD  mean in group TD
##           74.07317           98.36667

```

ROI Analysis

Setup

```
# load packages
packages <- c("here", "dplyr", "WGCNA", "factoextra", "ggplot2", "effsize", "data.table", "lme4", "lmerTest", "p  
source(here::here("code", "Mods2table.R"))
source(here::here("code", "ROI_psc_plot.R"))
source(here::here("code", "ROI_behavior_plot.R"))
source(here::here("code", "test_retest_plot.R"))
lapply(packages, library, character.only = TRUE)
```

Read in toddler data

```
# read in data
tidy_fMRI_clinical_toddlers <- read.table(here::here("data", "tidy_fMRI_clinical_toddlers.txt"),
                                         header = T, sep = "\t", stringsAsFactors = F)

# scans for each language paradigm
Story_scans <- tidy_fMRI_clinical_toddlers[!is.na(tidy_fMRI_clinical_toddlers$Story_Lang),]
Karen_scans <- tidy_fMRI_clinical_toddlers[!is.na(tidy_fMRI_clinical_toddlers$Karen_Lang),]
Motherese_scans <- tidy_fMRI_clinical_toddlers[!is.na(tidy_fMRI_clinical_toddlers$Motherese),]
```

Read in adult data

```
# read in data
adult_scans <- read.table(here::here("data", "tidy_fMRI_adults.txt"),
                          header = T, sep = "\t", stringsAsFactors = F)

# scans for each language paradigm
Story_scans_adult <- adult_scans[!is.na(adult_scans$Story_Lang),]
Karen_scans_adult <- adult_scans[!is.na(adult_scans$Karen_Lang),]
Motherese_scans_adult <- adult_scans[!is.na(adult_scans$Motherese),]
```

Plots for test-retest percent signal changes in each language paradigm

```

# organize data file
Story_tmp <- Story_scans$subjid[duplicated(Story_scans$subjid)]
Story_retest <- Story_scans[Story_scans$subjid %in% Story_tmp,
  colnames(Story_retest)[4:5] <- c("LHtemporal_psc", "RHtemporal_psc")
Story_retest$task <- "Story_Lang"
Story_retest$grp <- rep(1:length(Story_tmp), each=2)

Karen_tmp <- Karen_scans$subjid[duplicated(Karen_scans$subjid)]
Karen_retest <- Karen_scans[Karen_scans$subjid %in% Karen_tmp,
  c("subjid", "group", "scan_age", "Karen_LHtemporal_psc", "Karen_RHtemporal_psc")]
colnames(Karen_retest)[4:5] <- c("LHtemporal_psc", "RHtemporal_psc")
Karen_retest$task <- "Karen_Lang"
Karen_retest$grp <- rep(1:length(Karen_tmp), each=2)

Motherese_tmp <- Motherese_scans$subjid[duplicated(Motherese_scans$subjid)]
Motherese_retest <- Motherese_scans[Motherese_scans$subjid %in% Motherese_tmp,
  c("subjid", "group", "scan_age", "Motherese_LHtemporal_psc", "Motherese_RHtemporal_psc")]
colnames(Motherese_retest)[4:5] <- c("LHtemporal_psc", "RHtemporal_psc")
Motherese_retest$task <- "Motherese"
Motherese_retest$grp <- rep(1:length(Motherese_tmp), each=2)

combined_retest <- rbind.data.frame(Story_retest, Karen_retest, Motherese_retest)

# add test-retest scan interval
for (i in seq(2, length(combined_retest$subjid), 2)) {
  combined_retest$interval[i-1] <- "initial scan"
  combined_retest$interval[i] <- combined_retest$scan_age[i] -
    combined_retest$scan_age[i-1]
}

Summarize(as.numeric(combined_retest$interval[seq(2, length(combined_retest$subjid), 2)]), digits = 2)

##      n   mean    sd   min    Q1 median    Q3    max
## 20.00  7.60   5.58   1.00   3.50   4.00  13.00  15.00

# group retest scans into short-term and long-term scans
combined_retest$scan_group <- combined_retest$interval
combined_retest$scan_group[which(as.numeric(combined_retest$interval) <=4)] <- "short-term retest"
combined_retest$scan_group[which(as.numeric(combined_retest$interval) >4)] <- "long-term retest"

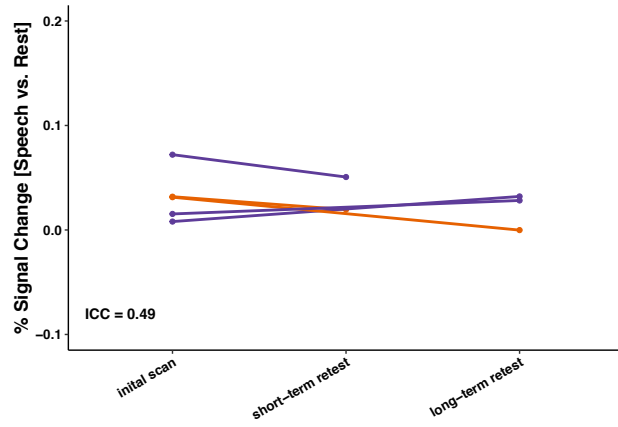
# plot line graphs with intraclass correlation coefficients
combined_retest$scan_group <- factor(combined_retest$scan_group, levels = c("initial scan", "short-term retest", "long-term retest"))

combined_retest$group <- as.factor(combined_retest$group)
test_retest_plot(combined_retest, "Story_Lang", "LHtemporal_psc")

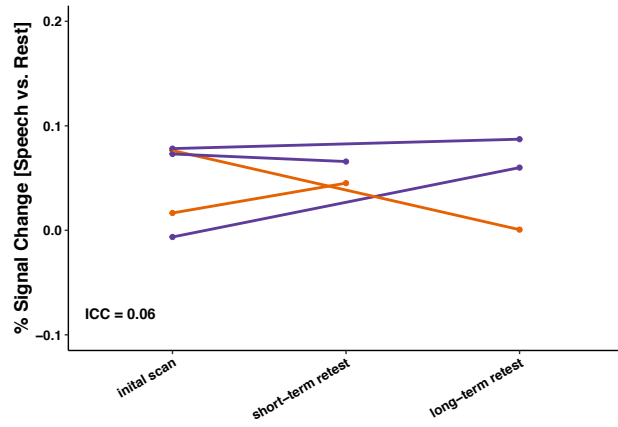
## Loading required package: irr

## Loading required package: lpSolve

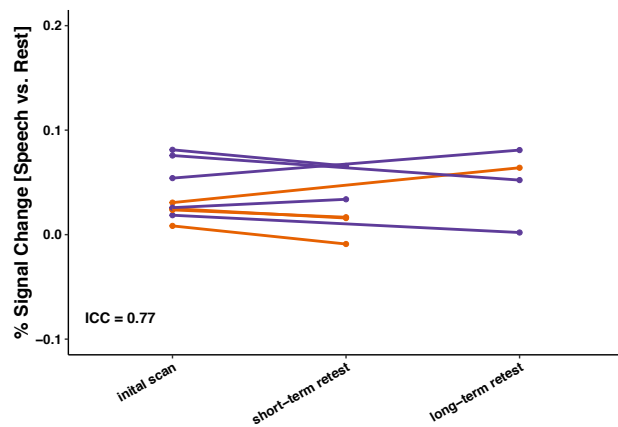
```



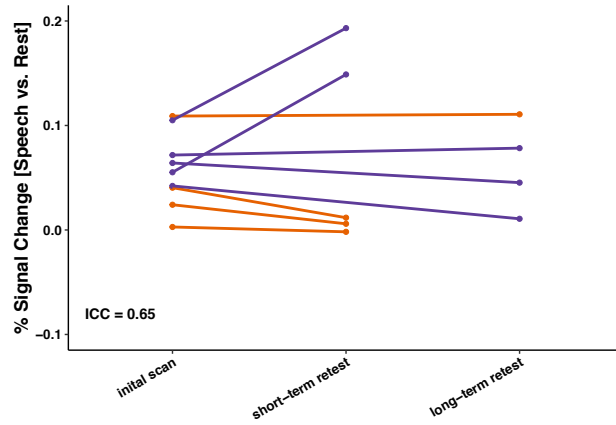
```
test_retest_plot(combined_retest, "Story_Lang", "RHtemporal_psc")
```



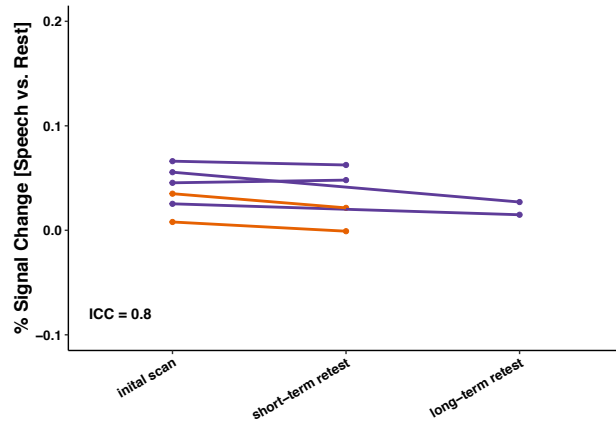
```
test_retest_plot(combined_retest, "Karen_Lang", "LHtemporal_psc")
```



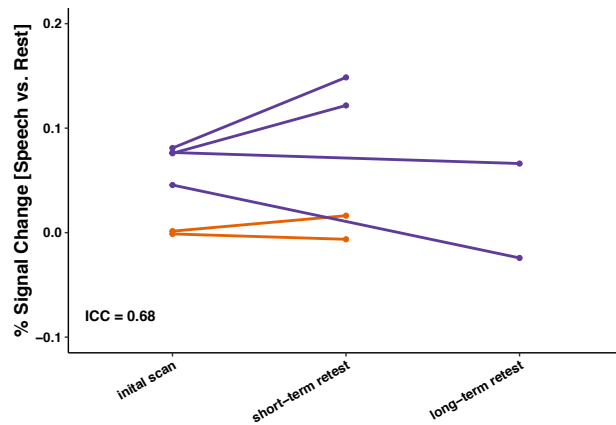
```
test_retest_plot(combined_retest, "Karen_Lang", "RHtemporal_psc")
```

```
test_retest_plot(combined_retest, "Motherese", "LHtemporal_psc")
```



```
test_retest_plot(combined_retest, "Motherese", "RHtemporal_psc")
```



Percent signal changes in TD and ASD across three language paradigms

```
# organize data file
Story_psc <- Story_scans[,c("subjid", "scan_age", "group", "Story_LHtemporal_psc",
                           "Story_RHtemporal_psc")]
colnames(Story_psc)[4:5] <- c("LHtemporal_psc", "RHtemporal_psc")
Story_psc$task <- "Story language"

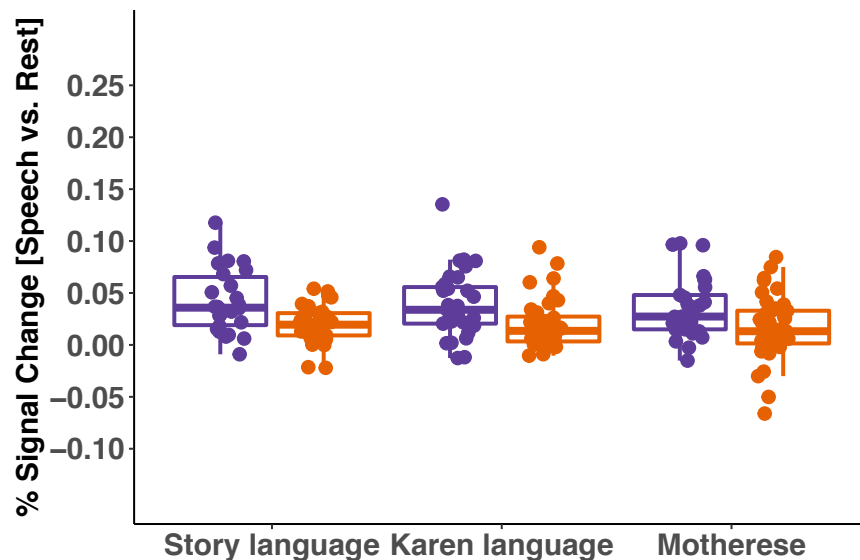
Karen_psc <- Karen_scans[,c("subjid", "scan_age", "group", "Karen_LHtemporal_psc",
                           "Karen_RHtemporal_psc")]
colnames(Karen_psc)[4:5] <- c("LHtemporal_psc", "RHtemporal_psc")
Karen_psc$task <- "Karen language"

Motherese_psc <- Motherese_scans[,c("subjid", "scan_age", "group", "Motherese_LHtemporal_psc",
                                    "Motherese_RHtemporal_psc")]
colnames(Motherese_psc)[4:5] <- c("LHtemporal_psc", "RHtemporal_psc")
Motherese_psc$task <- "Motherese"

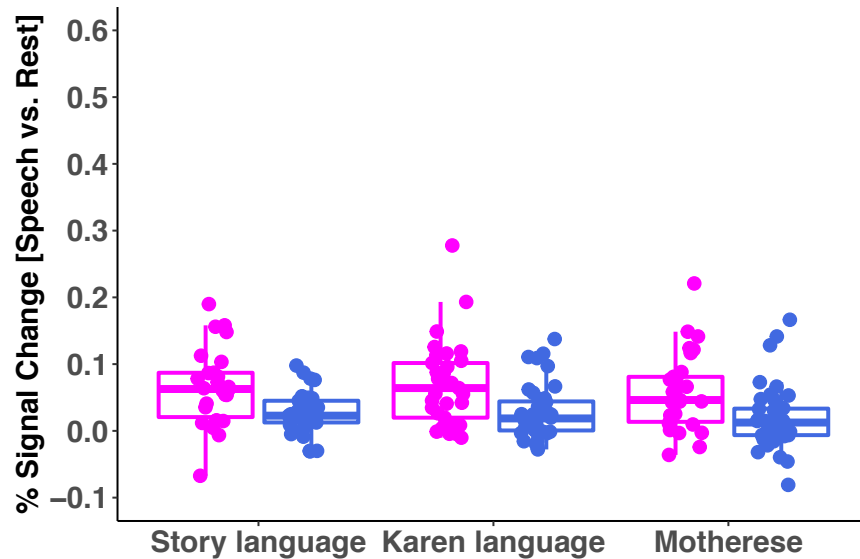
combined_psc <- rbind.data.frame(Story_psc, Karen_psc, Motherese_psc)

combined_psc$task <- factor(combined_psc$task, levels = unique(combined_psc$task))
combined_psc$group <- factor(combined_psc$group, levels = unique(combined_psc$group))

# boxplots
ROI_psc_plot(combined_psc, "LHtemporal_psc", "TDvsASD")
```



```
ROI_psc_plot(combined_psc, "RHtemporal_psc", "TDvsAdults")
```



```
# t-tests and effect sizes
tasks <- c("Story language", "Karen language", "Motherese")

es_mat <- matrix(1:12, nrow = 3, ncol = 4)
rownames(es_mat) <- c("Story language", "Karen language", "Motherese")
colnames(es_mat) <- c("left temporal", "right temporal", "left temporal", "right temporal")

i <- 0
for (task in tasks) {
  i <- i + 1
  aa <- effsize::cohen.d(combined_psc[combined_psc$task == task, "LHtemporal_psc"],
    combined_psc[combined_psc$task == task, "group"],
    pooled = T)

  bb <- effsize::cohen.d(combined_psc[combined_psc$task == task, "RHtemporal_psc"],
    combined_psc[combined_psc$task == task, "group"],
    pooled = T)

  tt1 <- t.test(combined_psc[combined_psc$task == task & combined_psc$group == "TD",
    "LHtemporal_psc"],
    combined_psc[combined_psc$task == task & combined_psc$group == "ASD",
    "LHtemporal_psc"])

  tt2 <- t.test(combined_psc[combined_psc$task == task & combined_psc$group == "TD",
    "RHtemporal_psc"],
    combined_psc[combined_psc$task == task & combined_psc$group == "ASD",
    "RHtemporal_psc"])

  es_mat[i, 1] <- round(abs(aa$estimate), 2)
  es_mat[i, 2] <- round(abs(bb$estimate), 2)
  es_mat[i, 3] <- round(abs(tt1$p.value), 3)
```

```

    es_mat[i, 4] <- round(abs(tt2$p.value),3)
  }

# t-tests results
knitr::kable(es_mat[,3:4])

```

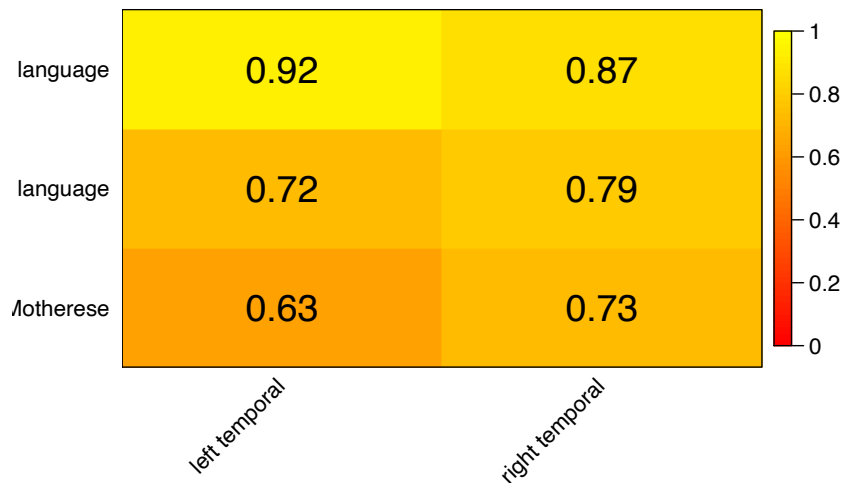
	left temporal	right temporal
Story language	0.002	0.004
Karen language	0.004	0.002
Motherese	0.011	0.006

```

# plot the effect size matrix as a heatmap
eff <- es_mat[,1:2]
colfunc <- colorRampPalette(c("red", "yellow"))

WGCNA::labeledHeatmap(Matrix = eff, xLabels = colnames(eff),
  yLabels = rownames(eff), ySymbols = NULL, colorLabels = F,
  colors = colfunc(50), textMatrix = round(eff, digits = 2),
  setStdMargins = F, cex.text = 1.7, zlim = c(0, 1))

```



Group differences in percent signal changes between TD toddlers vs. adults across three language paradigms

```

# organize data file: TD toddler
combined_psc_TD <- combined_psc[combined_psc$group == "TD", c("subjid", "LHtemporal_psc", "RHtemporal_psc")]
combined_psc_TD$group <- "TD Toddlers"

# organize data file: adults

```

```

Story_adult_tstats <- Story_scans_adult[, c("fMRI_Subj", "Story_LHtemporal_psc", "Story_RHtemporal_psc")]
colnames(Story_adult_tstats)[2:3] <- c("LHtemporal_psc", "RHtemporal_psc")
Story_adult_tstats$task <- "Story language"

Karen_adult_tstats <- Karen_scans_adult[, c("fMRI_Subj", "Karen_LHtemporal_psc", "Karen_RHtemporal_psc")]
colnames(Karen_adult_tstats)[2:3] <- c("LHtemporal_psc", "RHtemporal_psc")
Karen_adult_tstats$task <- "Karen language"

Motherese_adult_tstats <- Motherese_scans_adult[, c("fMRI_Subj", "Motherese_LHtemporal_psc", "Motherese_RHtemporal_psc")]
colnames(Motherese_adult_tstats)[2:3] <- c("LHtemporal_psc", "RHtemporal_psc")
Motherese_adult_tstats$task <- "Motherese"

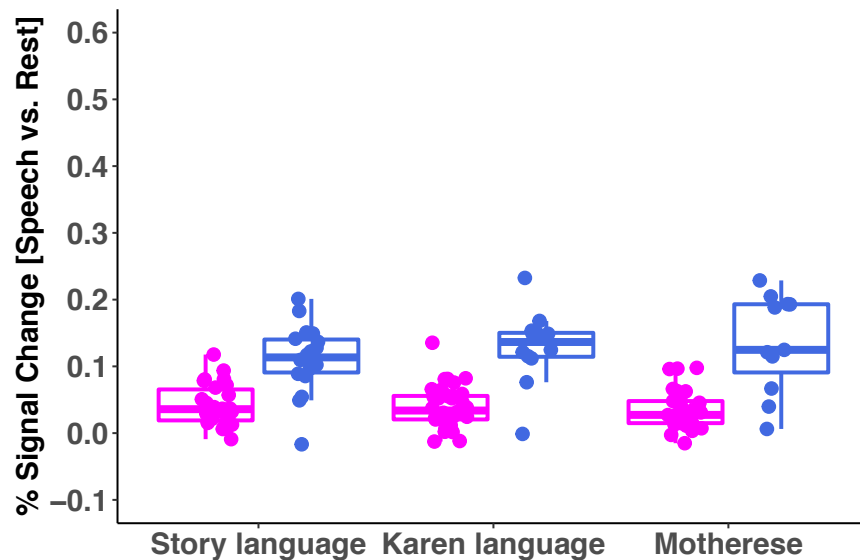
combined_psc_adults <- rbind.data.frame(Story_adult_tstats, Karen_adult_tstats, Motherese_adult_tstats)
combined_psc_adults$group <- "TD Adults"

# combine TD toddlers and adults
colnames(combined_psc_adults)[1] <- "subjid"
combined_psc_all <- rbind(combined_psc_TD, combined_psc_adults)

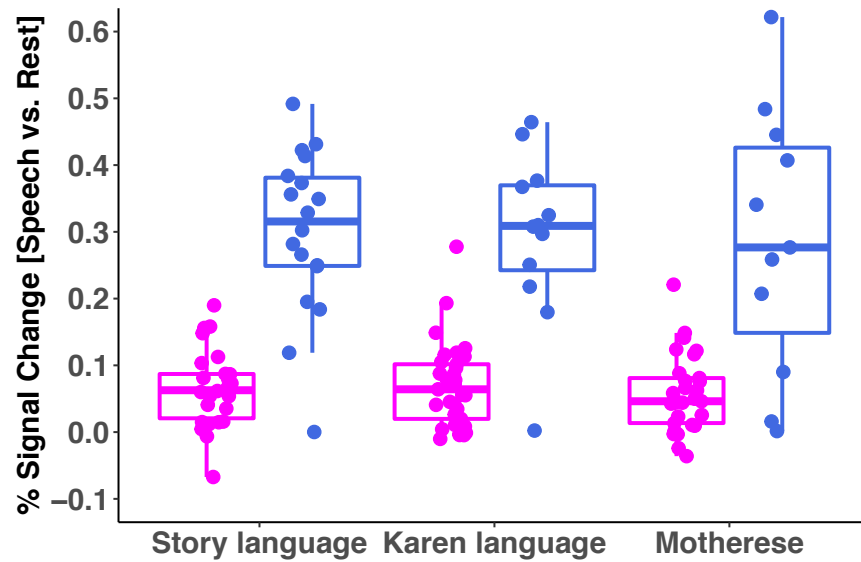
combined_psc_all$task <- factor(combined_psc_all$task, levels = unique(combined_psc_all$task))
combined_psc_all$group <- factor(combined_psc_all$group, levels = unique(combined_psc_all$group))

# boxplots
ROI_psc_plot(combined_psc_all, "LHtemporal_psc", "TDvsAdults")

```



```
ROI_psc_plot(combined_psc_all, "RHtemporal_psc", "TDvsAdults")
```



```
# t-tests
tasks <- c("Story language", "Karen language", "Motherese")

ttest <- matrix(1:6,nrow = 3, ncol = 2)
rownames(ttest) <- c("Story language", "Karen language", "Motherese")
colnames(ttest) <- c("LHtemporal", "RHtemporal")

i <- 0
for (task in tasks) {
  i <- i + 1
  tt1 <- t.test(combined_psc_all[combined_psc_all$task == task & combined_psc_all$group == "TD Toddlers", "LHtemporal"],
               combined_psc_all[combined_psc_all$task == task & combined_psc_all$group == "TD Adults", "LHtemporal"])

  tt2 <- t.test(combined_psc_all[combined_psc_all$task == task & combined_psc_all$group == "TD Toddlers", "RHtemporal"],
               combined_psc_all[combined_psc_all$task == task & combined_psc_all$group == "TD Adults", "RHtemporal"])

  ttest[i, 1:2] <- c(round(abs(tt1$p.value),3),round(abs(tt2$p.value),3))
}

# t-tests results
knitr::kable(ttest)
```

	LHtemporal	RHtemporal
Story language	0.000	0.000
Karen language	0.000	0.000
Motherese	0.001	0.003

Mixed effects model analysis

```
# orgnize datafile
Story_datafile <- Story_scans[,c("subj", "subjid", "scan_age", "gender", "group", "Story_meanFD",
    "Story_LHtemporal_psc", "Story_RHtemporal_psc", "final_vine_ComTotal_DomStd",
    "final_vine_SocTotal_DomStd")]
Story_datafile$task <- "Story_Lang"
colnames(Story_datafile)[6:8] <- c("meanFD", "LHtemporal_psc", "RHtemporal_psc")

Karen_datafile <- Karen_scans[,c("subj", "subjid", "scan_age", "gender", "group", "Karen_meanFD",
    "Karen_LHtemporal_psc", "Karen_RHtemporal_psc", "final_vine_ComTotal_DomStd",
    "final_vine_SocTotal_DomStd")]
Karen_datafile$task <- "Karen_Lang"
colnames(Karen_datafile)[6:8] <- c("meanFD", "LHtemporal_psc", "RHtemporal_psc")

Motherese_datafile <- Motherese_scans[,c("subj", "subjid", "scan_age", "gender", "group", "Motherese_meanFD",
    "Motherese_LHtemporal_psc", "Motherese_RHtemporal_psc", "final_vine_ComTotal_DomStd",
    "final_vine_SocTotal_DomStd")]
Motherese_datafile$task <- "Motherese"
colnames(Motherese_datafile)[6:8] <- c("meanFD", "LHtemporal_psc", "RHtemporal_psc")

combined_datafile <- rbind.data.frame(Story_datafile, Karen_datafile, Motherese_datafile)

# run mixed effects models
ROIs <- c("LHtemporal_psc", "RHtemporal_psc")
clins <- c("final_vine_ComTotal_DomStd", "final_vine_SocTotal_DomStd")
cnames <- c("Estimate", "Std. Error", "t value", "p value", "R2")

Mods2table(combined_datafile, ROIs, clins, cnames) %>%
  as.data.frame()

##           Variables Estimate Std. Error t value p value    R2
## 1 Communication scores  0.00037   0.00016   2.397   0.02 0.068
## 2      Social scores    5e-04   0.00018   2.727   0.009 0.08
## 3 Communication scores  0.00081   0.00032   2.577   0.013 0.094
## 4      Social scores  0.00118   0.00037   3.227   0.002 0.125

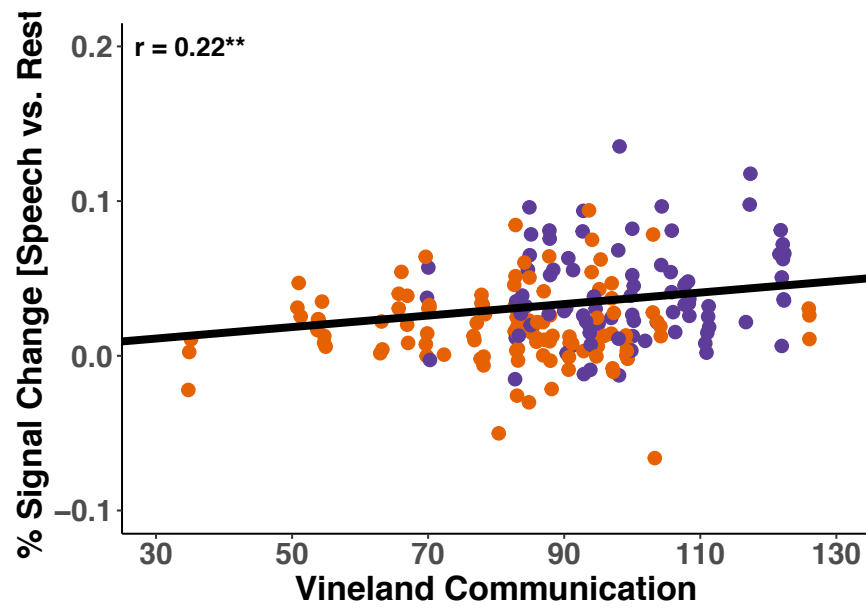
# fdr correction
p.adjust(as.numeric(Mods2table(combined_datafile, ROIs, clins, cnames)[, "p value"]),
  method = "fdr")

## [1] 0.02000000 0.01733333 0.01733333 0.00800000
```

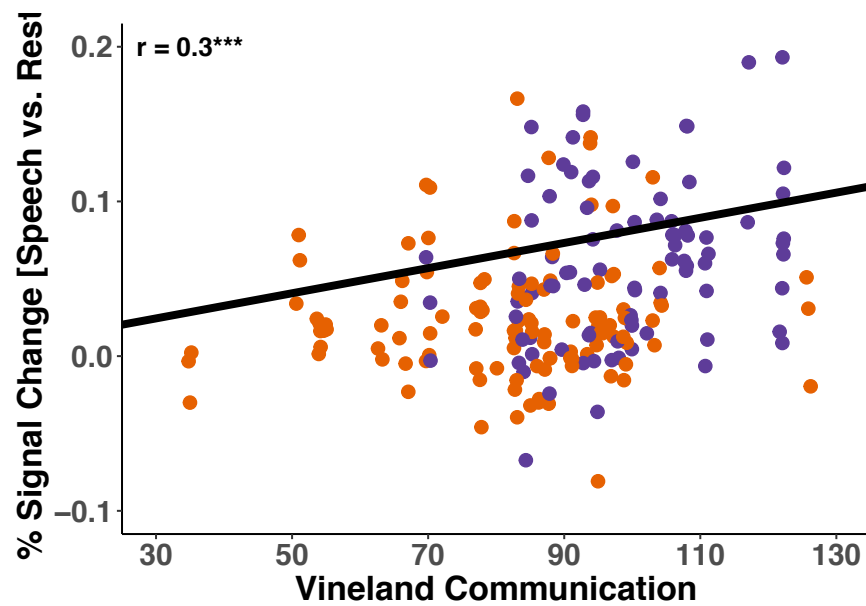
Scatterplots: ROI activation and Vineland communication and social scores

```
dat <- combined_datafile

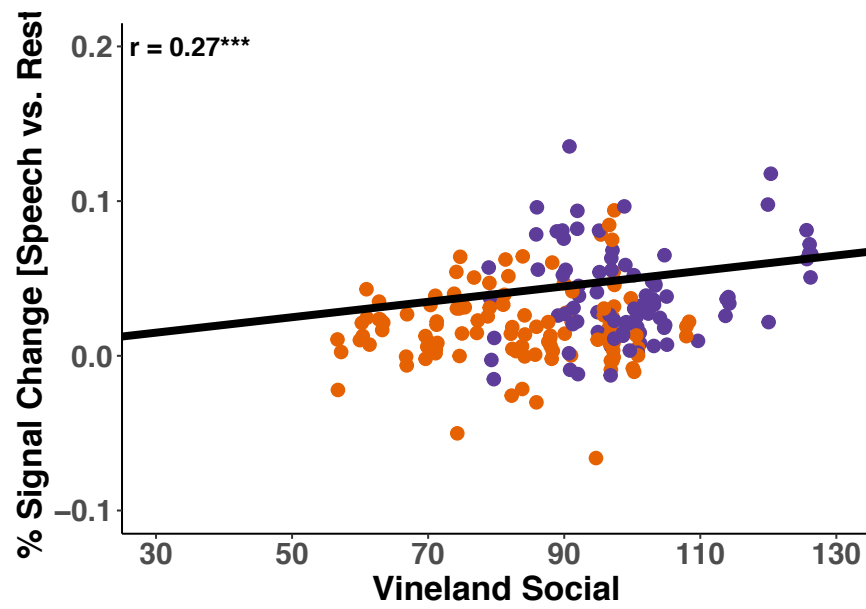
ROI_behavior_plot(dat, "final_vine_ComTotal_DomStd", "LHtemporal_psc",
  "Vineland Communication")
```



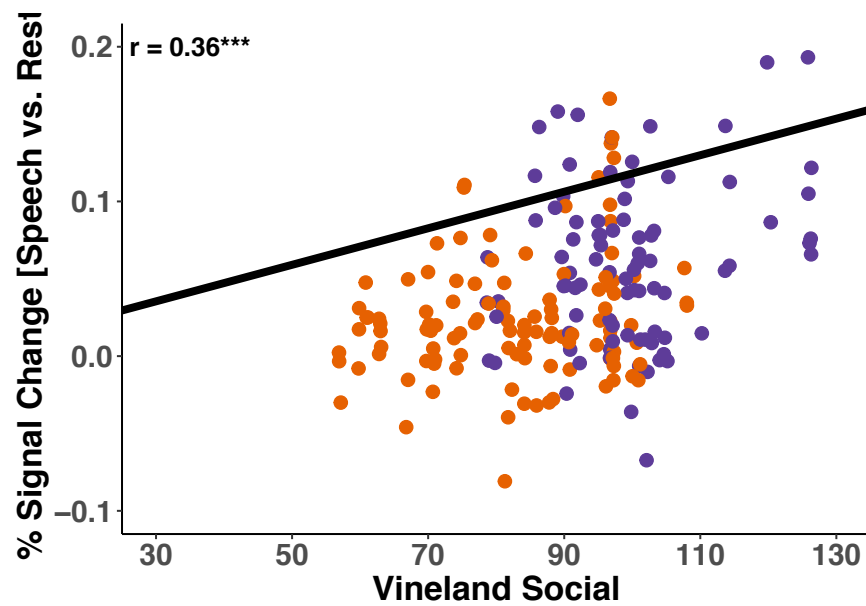
```
ROI_behavior_plot(dat, "final_vine_ComTotal_DomStd", "RHtemporal_psc",
                  "Vineland Communication")
```



```
ROI_behavior_plot(dat, "final_vine_SocTotal_DomStd", "LHtemporal_psc",
                  "Vineland Social")
```

```
ROI_behavior_plot(dat, "final_vine_SocTotal_DomStd", "RHtemporal_psc",
                  "Vineland Social")
```



SNF/Clustering and Motherese Eye-Tracking Analysis

Setup

```
# load packages
packages <- c("here", "tidyr", "WGCNA", "dplyr", "SNFtool", "ggplot2", "effsize", "data.table",
              "psych", "FSA")
source(here::here("code", "SNF_Louvain.R"))
source(here::here("code", "clusters_plot.R"))
source(here::here("code", "ET_clusters.R"))
lapply(packages, library, character.only = TRUE)
```

Read in toddler data

```
tidy_fMRI_clinical_toddlers <- read.table(here::here("data", "tidy_fMRI_clinical_toddlers.txt"),
                                         header = T, sep = "\t", stringsAsFactors = F)
# subjects with all three language paradigms
fMRI_clinical_all <- tidy_fMRI_clinical_toddlers[!is.na(tidy_fMRI_clinical_toddlers$Story_Lang) &
                                                !is.na(tidy_fMRI_clinical_toddlers$Karen_Lang) &
                                                !is.na(tidy_fMRI_clinical_toddlers$Motherese), ]

dim(fMRI_clinical_all)[1]
```

```
## [1] 52
```

```
table(fMRI_clinical_all$group)
```

```
##
## ASD  TD
## 30  22
```

Run Similarity Network Fusion analysis

```
dat <- fMRI_clinical_all
ROI_var <- colnames(select(fMRI_clinical_all, contains("psc")))
clinic_var <- colnames(select(fMRI_clinical_all, contains("final")))[-1]

cluster_results <- SNF_Louvain(dat, ROI_var, clinic_var)
```

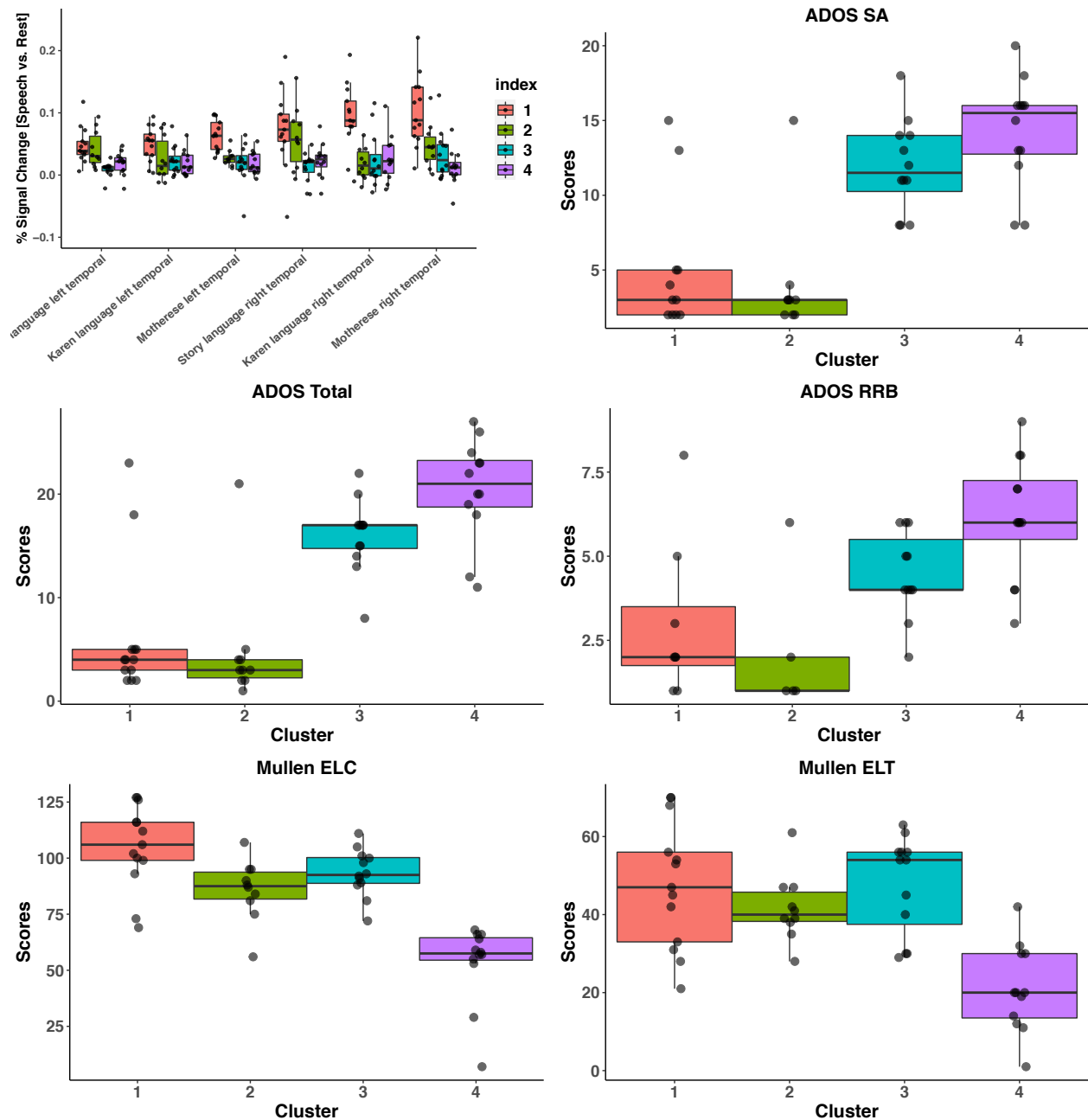
```
## [1] "There are 5 clusters"
```

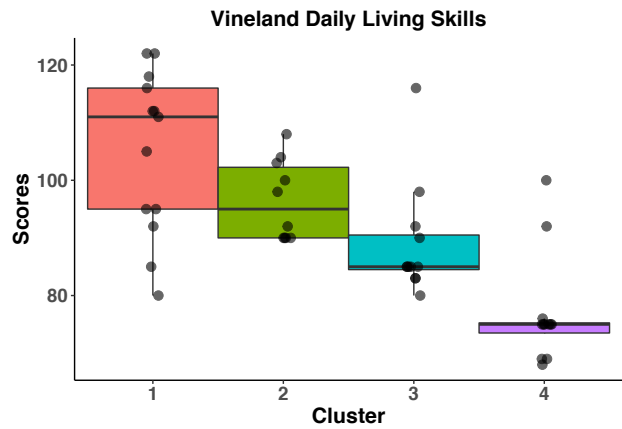
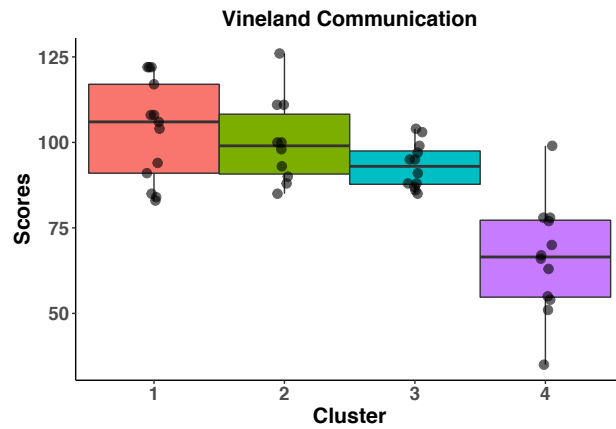
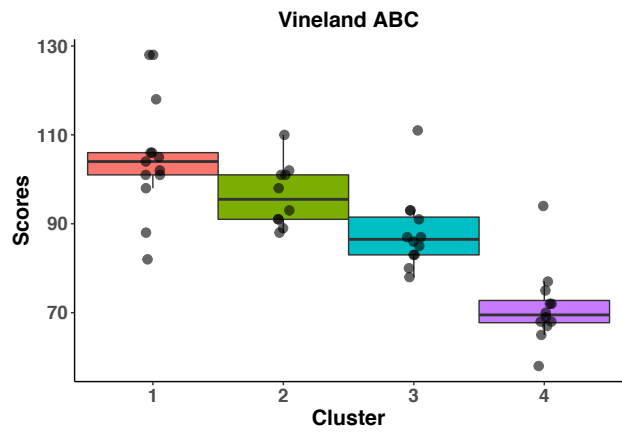
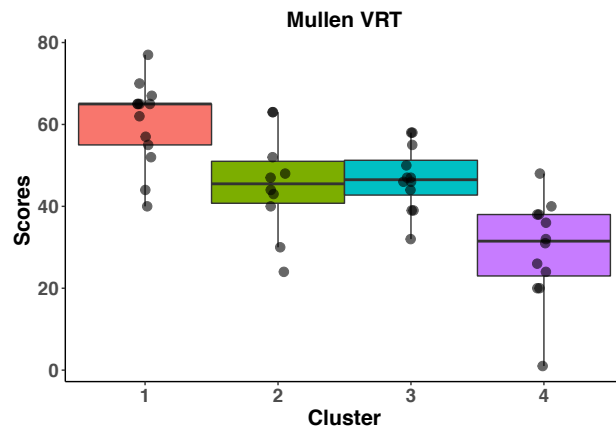
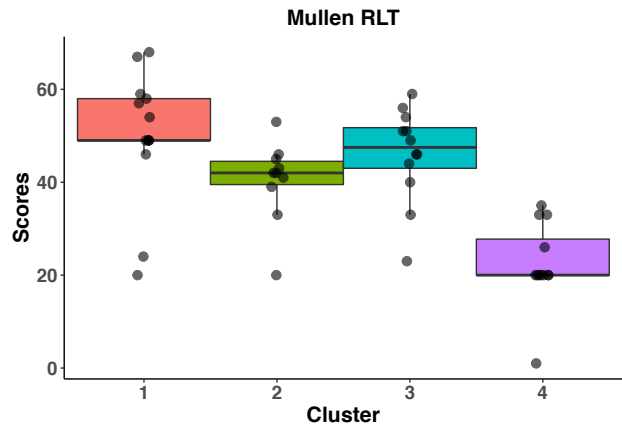
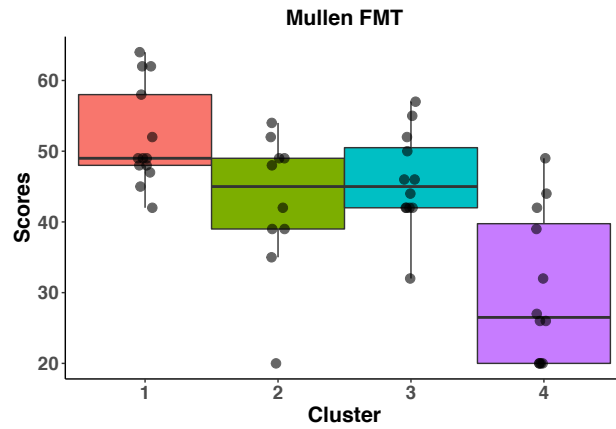
```
SNF_clusters <- cluster_results[[2]]
```

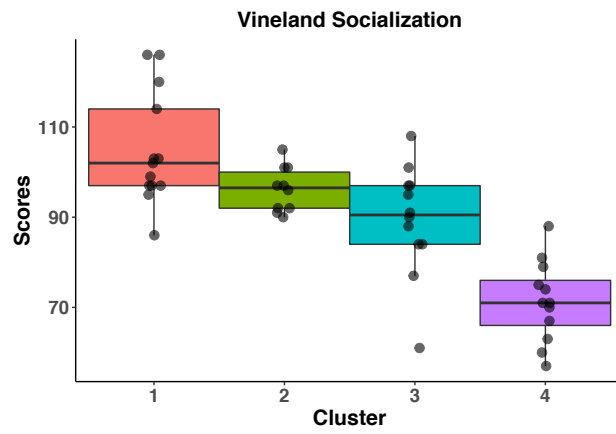
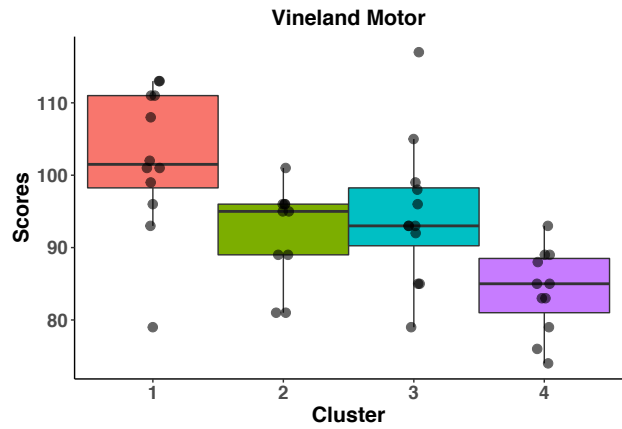
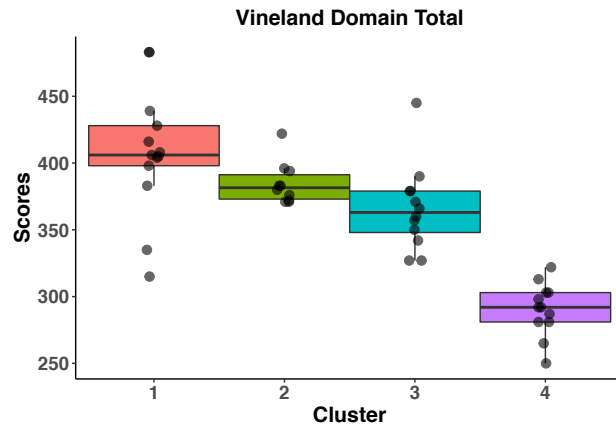
Plot fMRI and clinical data across clusters

```
# only plot 4 main clusters
```

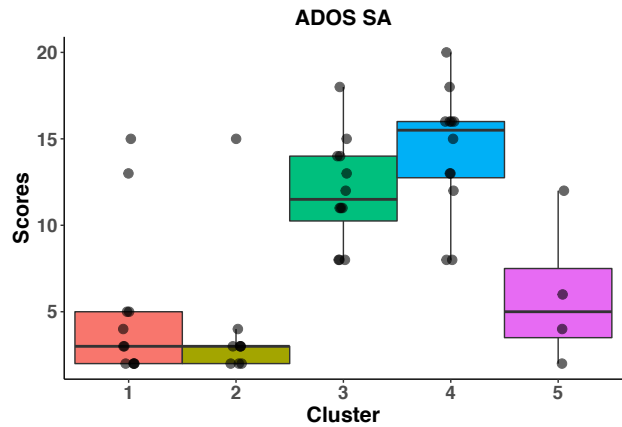
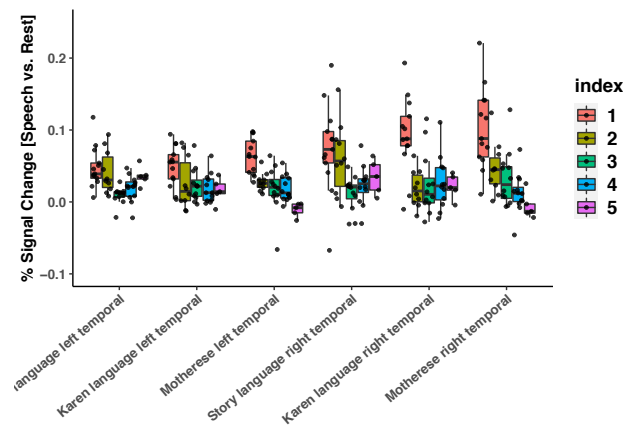
```
ROI_clinic_clusters = clusters_plot(fMRI_clinical_all, SNF_clusters, ROI_var, clinic_var,  
  plotAll = FALSE)
```

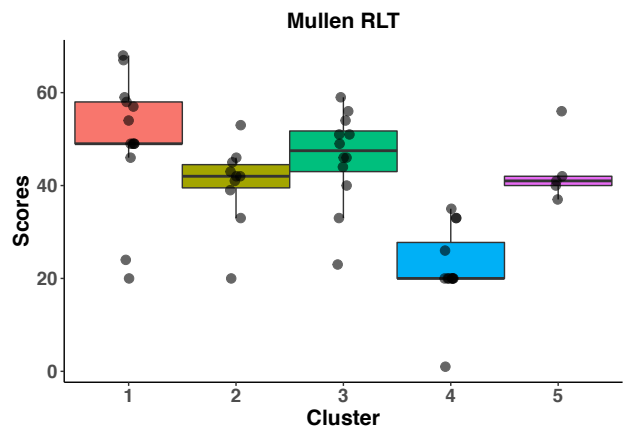
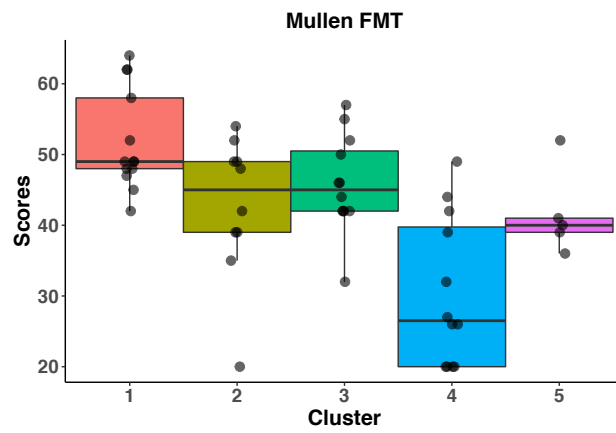
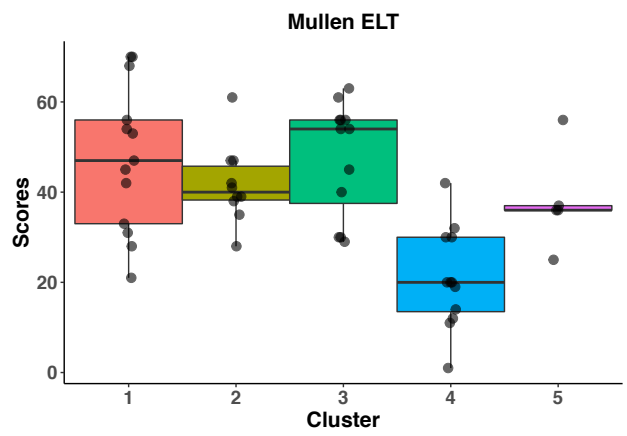
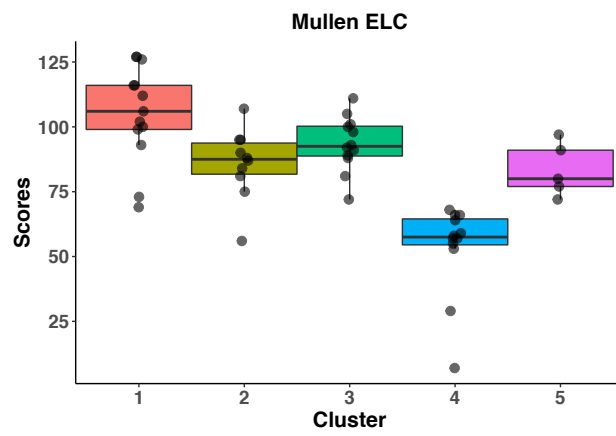
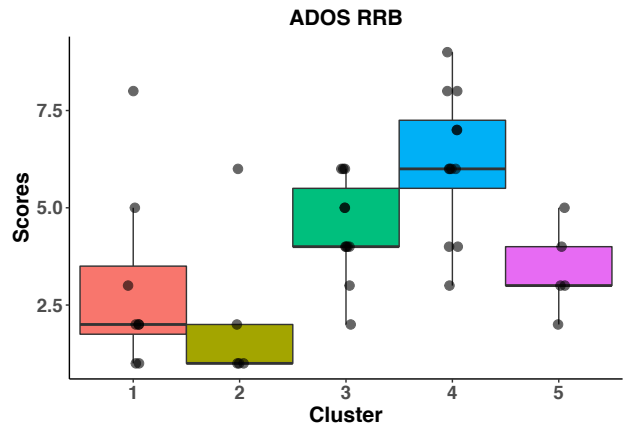
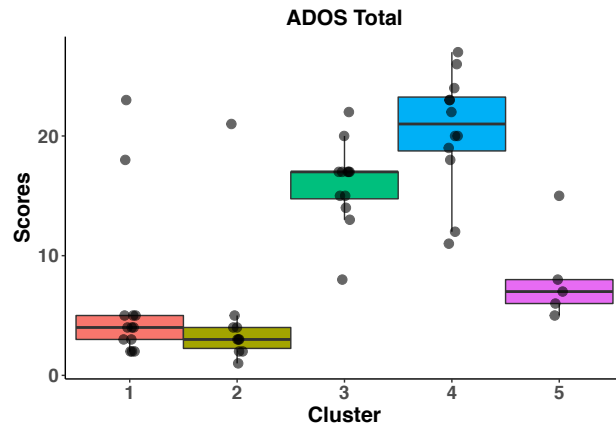


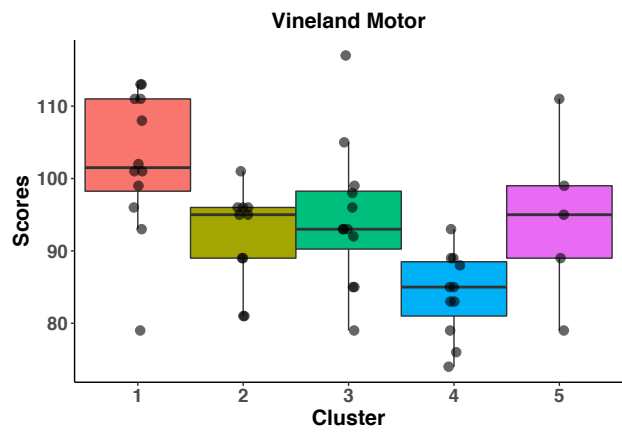
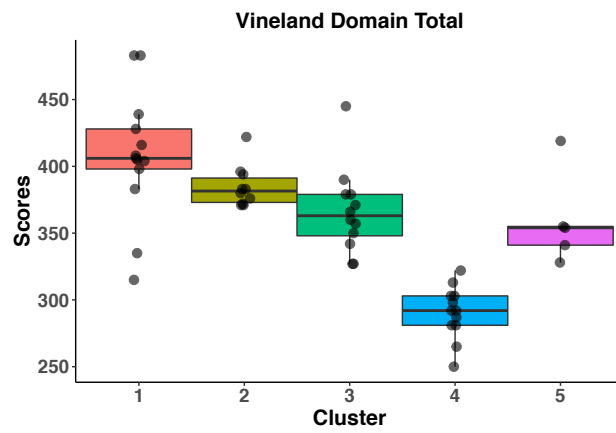
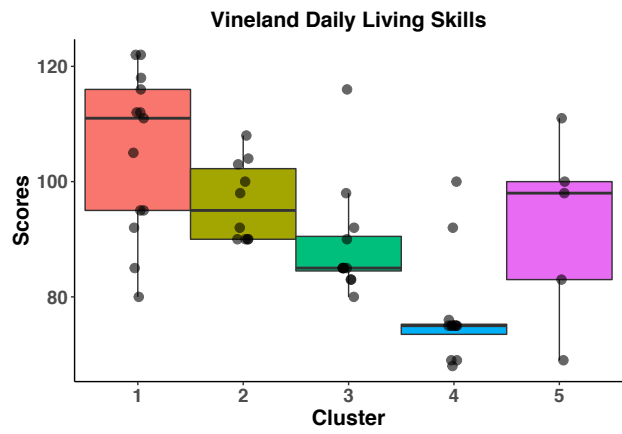
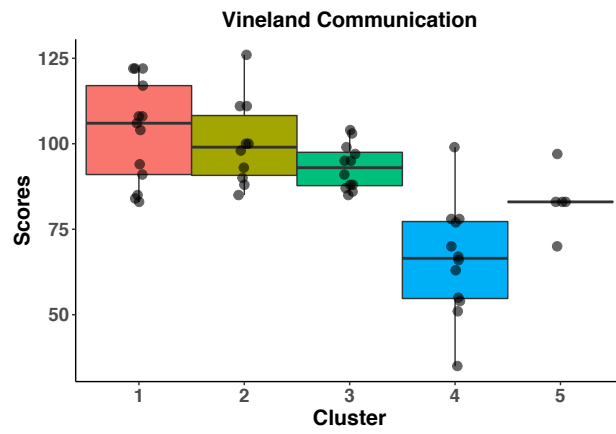
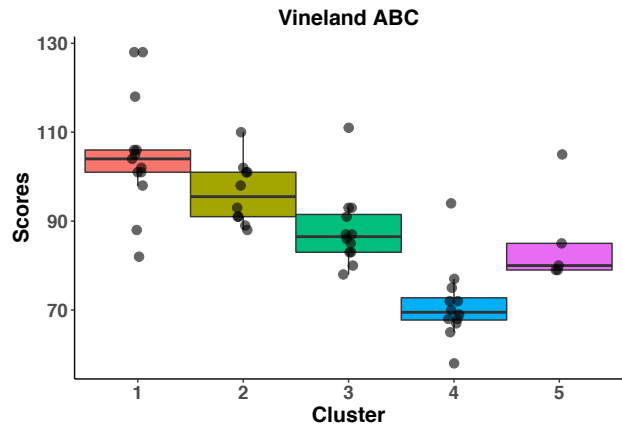
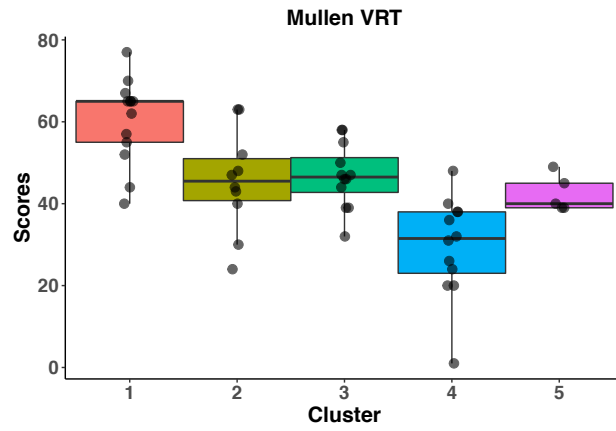


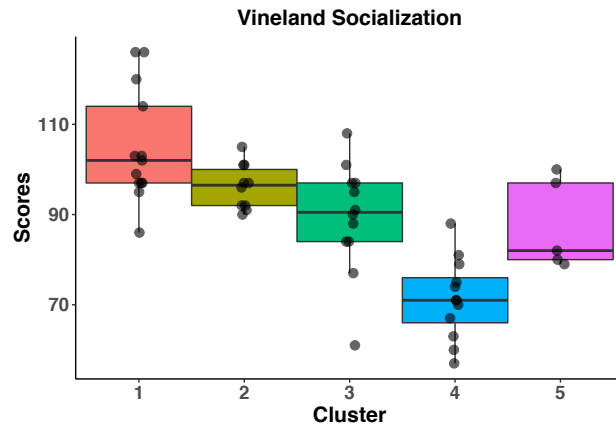


```
# plot all clusters
ROI_clinic_clusters = clusters_plot(fmri_clinical_all, SNF_clusters, ROI_var, clinic_var,
                                   plotAll = TRUE)
```









```
# distribution of clusters
knitr::kable(ROI_clinic_clusters[[1]])
```

	1	2	3	4	5
ASD	12	1	12	3	2
TD	0	9	0	2	11

Motherese eye-tracking data

```
# read in data
Motherese_ET <- read.table(here::here("data", "tidy_Motherese_ET.txt"), header = T,
  sep = "\t", stringsAsFactors = F)
dim(Motherese_ET)[1]
```

```
## [1] 54
```

```
# Motherese eye-tracking test: how many completed before the scan and how many after the scan
dim(Motherese_ET[as.Date(Motherese_ET$ScanDate) > as.Date(Motherese_ET$LK_Date),])[1]
```

```
## [1] 38
```

```
dim(Motherese_ET[as.Date(Motherese_ET$ScanDate) < as.Date(Motherese_ET$LK_Date),])[1]
```

```
## [1] 16
```

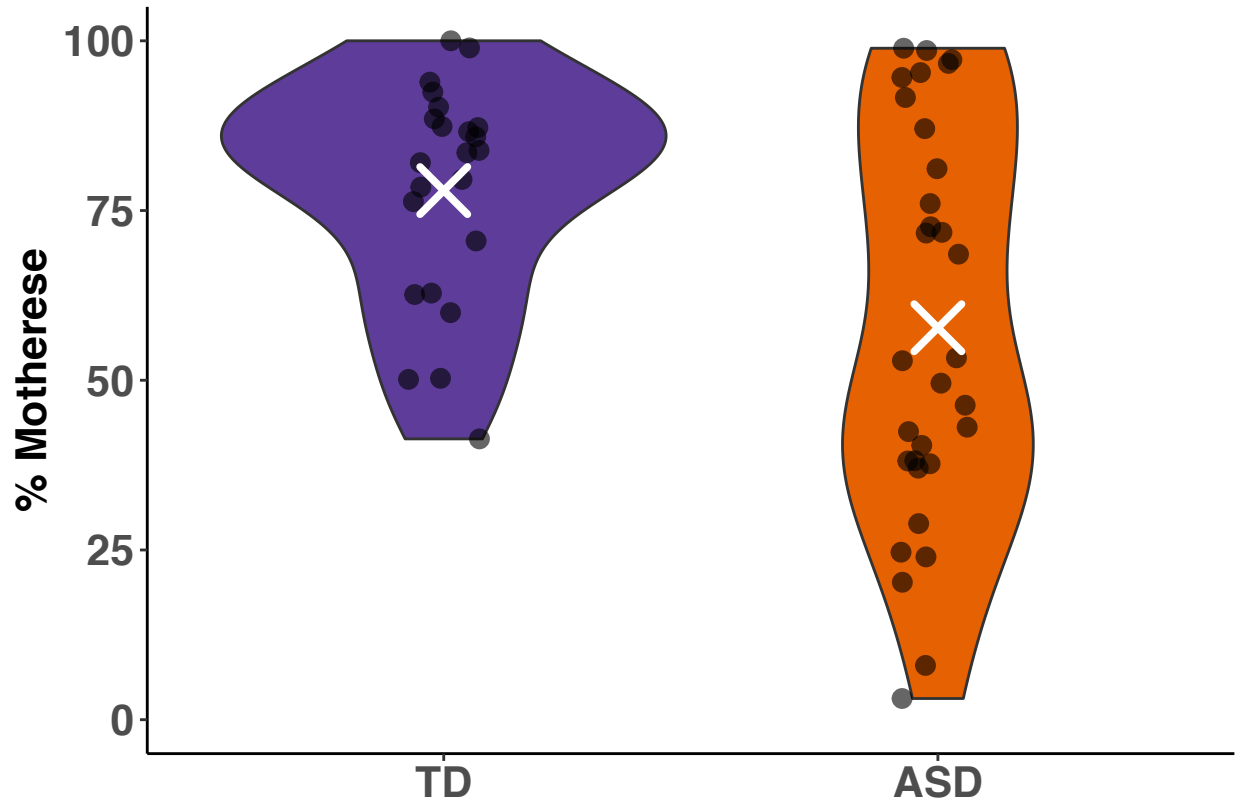
```
# group differences in Motherese eye-tracking between ASD and TD
eff <- effsize::cohen.d(Motherese_ET$LK_.fixation.Motherese, Motherese_ET$group, pooled = T)
tvalue <- t.test(Motherese_ET$LK_.fixation.Motherese ~ Motherese_ET$group)

knitr::kable(cbind(effect_size = eff$estimate, t_value = tvalue$p.value))
```


effect_size	t_value
-0.8258775	0.0021

```
# plot Motherese eye-tracking data in ASD and TD
Motherese_ET$group <- factor(Motherese_ET$group, levels = unique(Motherese_ET$group))

ggplot(Motherese_ET, aes(x = group, y = 'LK_.fixation.Motherese')) +
  geom_violin(aes(fill = group), position = "dodge", trim = T) +
  geom_point(aes(fill = group), size = 3, alpha = 0.6, position =
    position_jitterdodge(jitter.width = 0.3)) +
  stat_summary(fun = "mean", geom = "point", shape = 4, size = 7,
    color = "white", stroke = 2) +
  scale_fill_manual(values = c("#5e3c99", "#e66101")) +
  labs(y = "% Motherese", x = "") +
  guides(color = F, fill = F) +
  theme(plot.title = element_text(hjust = 0.5, size = 16, face = "bold"),
    axis.text = element_text(size = 16, face = "bold"),
    axis.title.y = element_text(size = 16, face = "bold")) +
  theme(panel.border = element_blank(),
    panel.background = element_blank(),
    panel.grid = element_blank(),
    axis.line = element_line(colour = "black")) +
  coord_cartesian(ylim=c(00, 100)) +
  scale_y_continuous(breaks = seq(0, 100, 25))
```



Association of clusters and gaze preference for motherese

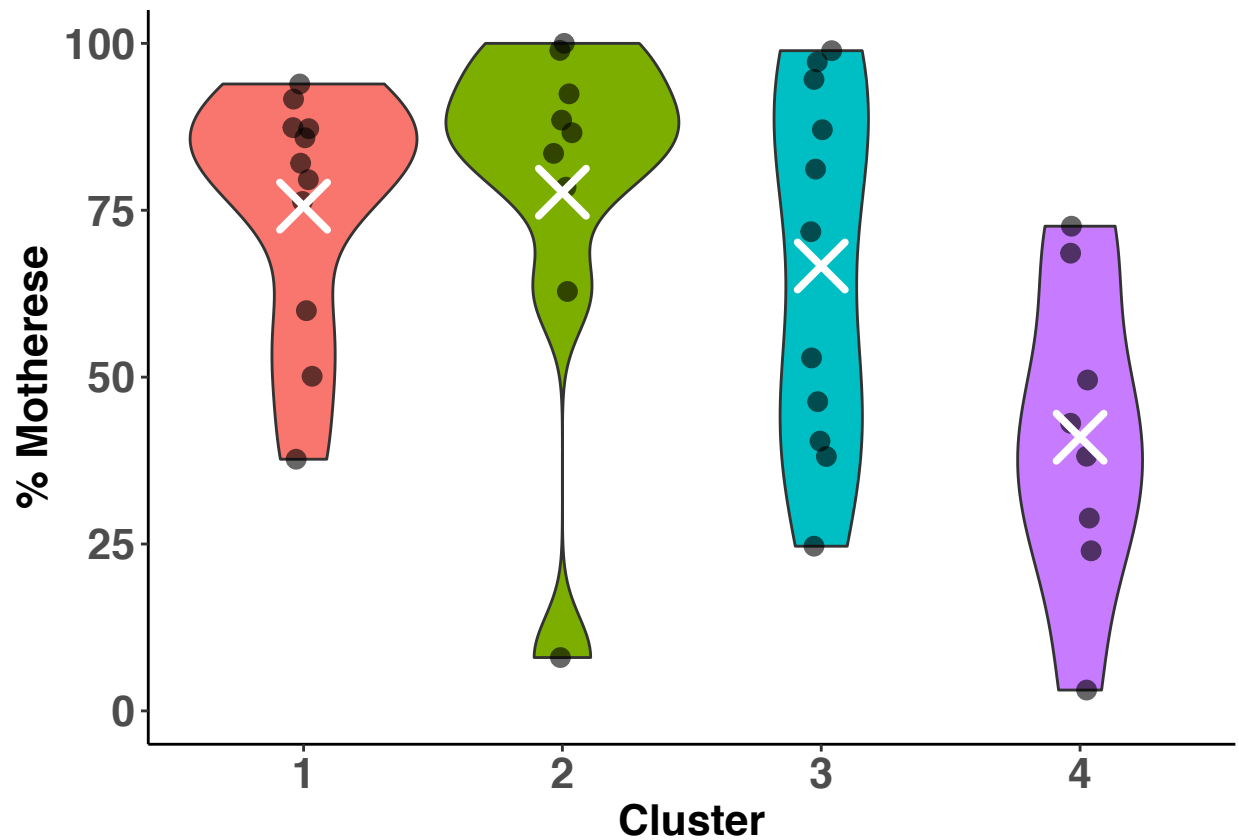
```
# organize datafile
clusters <- ROI_clinic_clusters[[2]][,c("subj","Clustering","index")]
colnames(Motherese_ET)[1] <- "subj"
Motherese_ET_clusters <- merge(Motherese_ET, clusters, by = "subj")

dim(Motherese_ET_clusters)[1]
```

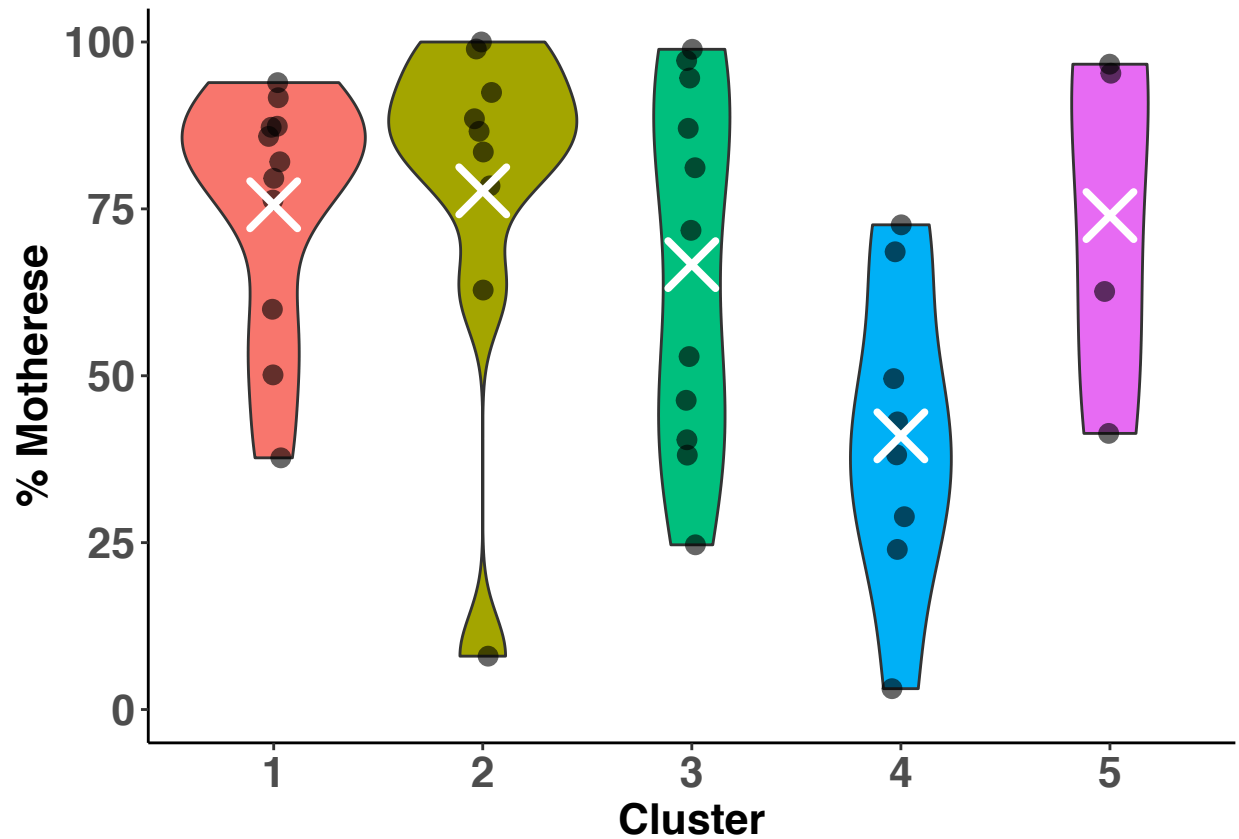
```
## [1] 43
```

```
Motherese_ET_clusters$index <- as.factor(Motherese_ET_clusters$index)

# violin plots
ET_clusters(Motherese_ET_clusters, plotAll = FALSE)
```



```
ET_clusters(Motherese_ET_clusters, plotAll = TRUE)
```



```
# t-tests and effect sizes
cohen <- matrix(1:25, 5, 5)
ttest <- matrix(1:25, 5, 5)
rownames(cohen) <- c("Cluster 1", "Cluster 2", "Cluster 3", "Cluster 4", "Cluster 5")
colnames(cohen) <- c("Cluster 1", "Cluster 2", "Cluster 3", "Cluster 4", "Cluster 5")
rownames(ttest) <- c("Cluster 1", "Cluster 2", "Cluster 3", "Cluster 4", "Cluster 5")
colnames(ttest) <- c("Cluster 1", "Cluster 2", "Cluster 3", "Cluster 4", "Cluster 5")

for (i in 1:5) {
  for (j in 1:5) {
    if (i == j) {
      cohen[i, j] <- NA
      ttest[i, j] <- NA
    } else {
      aa <- effsize::cohen.d(Motherese_ET_clusters$LK_.fixation.Motherese[Motherese_ET_clusters$index == i],
                             Motherese_ET_clusters$LK_.fixation.Motherese[Motherese_ET_clusters$index == j])
      bb <- t.test(Motherese_ET_clusters$LK_.fixation.Motherese[Motherese_ET_clusters$index == i],
                   Motherese_ET_clusters$LK_.fixation.Motherese[Motherese_ET_clusters$index == j])

      cohen[i, j] <- abs(round(aa$estimate, 2))
      ttest[i, j] <- abs(round(bb$p.value, 3))
    }
  }
}
```

```
knitr::kable(cohen)
```

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Cluster 1	NA	0.09	0.39	1.70	0.08
Cluster 2	0.09	NA	0.40	1.41	0.13
Cluster 3	0.39	0.40	NA	1.01	0.27
Cluster 4	1.70	1.41	1.01	NA	1.36
Cluster 5	0.08	0.13	0.27	1.36	NA

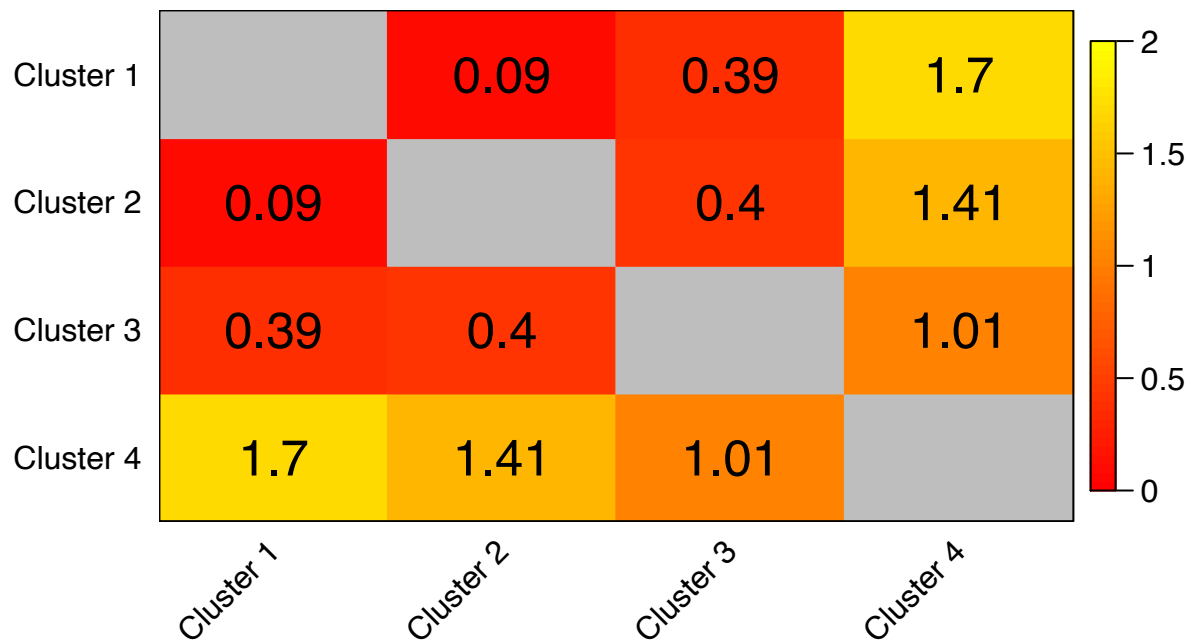
```
knitr::kable(ttest)
```

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Cluster 1	NA	0.852	0.374	0.004	0.916
Cluster 2	0.852	NA	0.389	0.010	0.829
Cluster 3	0.374	0.389	NA	0.040	0.658
Cluster 4	0.004	0.010	0.040	NA	0.086
Cluster 5	0.916	0.829	0.658	0.086	NA

```
# plot the effect size matrix as a heatmap: 4 clusters
```

```
colfunc <- colorRampPalette(c("red", "yellow"))
```

```
WGCNA::labeledHeatmap(Matrix = cohen[1:4,1:4], xLabels = colnames(cohen)[1:4],
  yLabels = rownames(cohen)[1:4], ySymbols = NULL, colorLabels = F,
  colors = colfunc(50), textMatrix = round(cohen[1:4,1:4], digits = 2),
  setStdMargins = F, cex.text = 1.6, zlim = c(0, 2))
```



```
# plot the effect size matrix as a heatmap: 5 clusters
WGCNA::labeledHeatmap(Matrix = cohen, xLabels = colnames(cohen),
  yLabels = rownames(cohen), ySymbols = NULL, colorLabels = F,
  colors = colfunc(50), textMatrix = round(cohen, digits = 2),
  setStdMargins = F, cex.text = 1.6, zlim = c(0, 2))
```

