

Supplement 3 with subjects omitted as suggested by the HCP

source and input files available at <https://osf.io/p6msu/>

compiled May 12, 2020

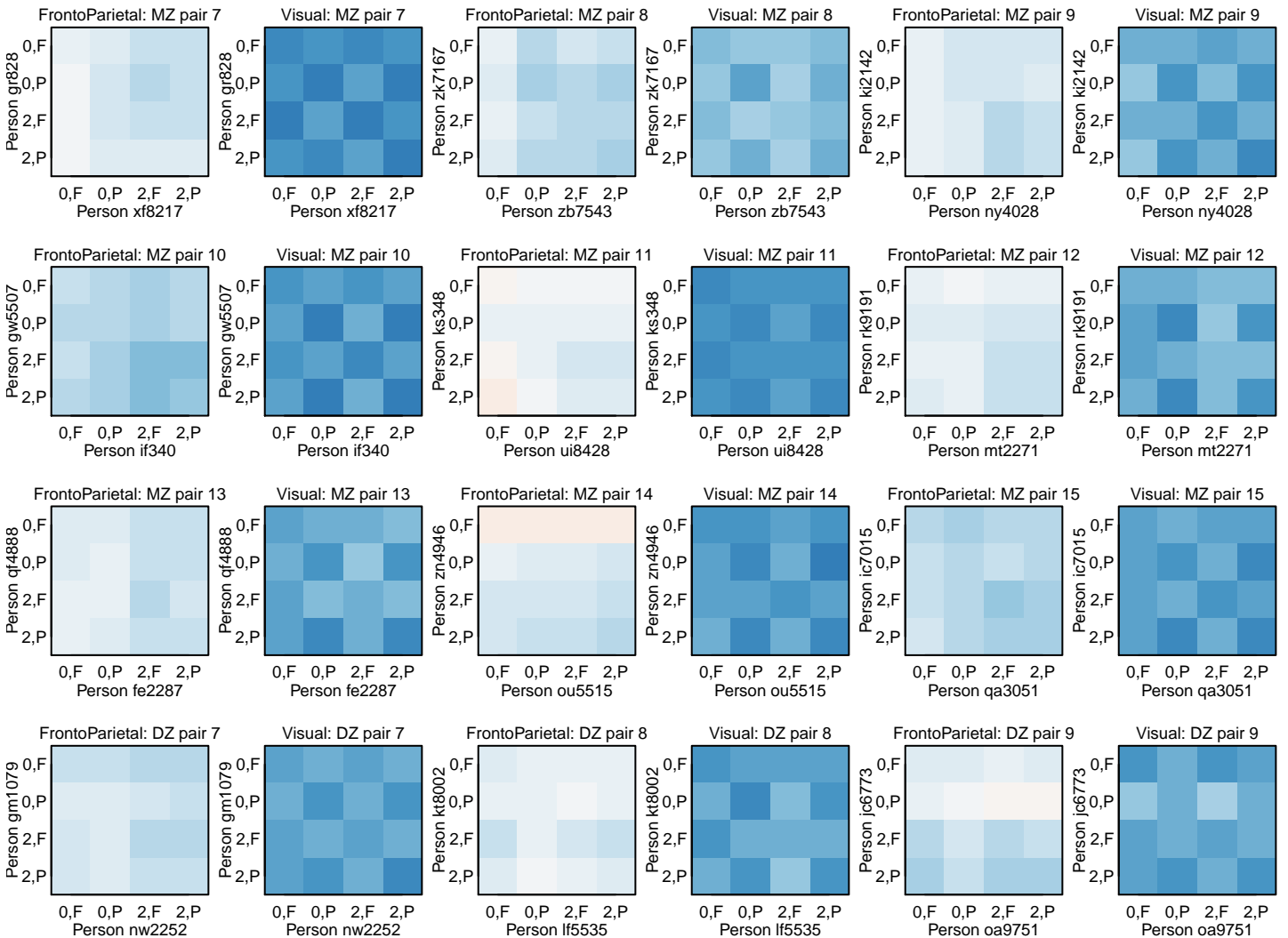
Supplement 3 for “Pattern similarity analyses of frontoparietal task coding: Individual variation and genetic influences” by Joset A. Etzel, Ya’el Courtney, Caitlin E. Carey, Maria Z. Gehred, Arpana Agrawal, and Todd S. Braver.

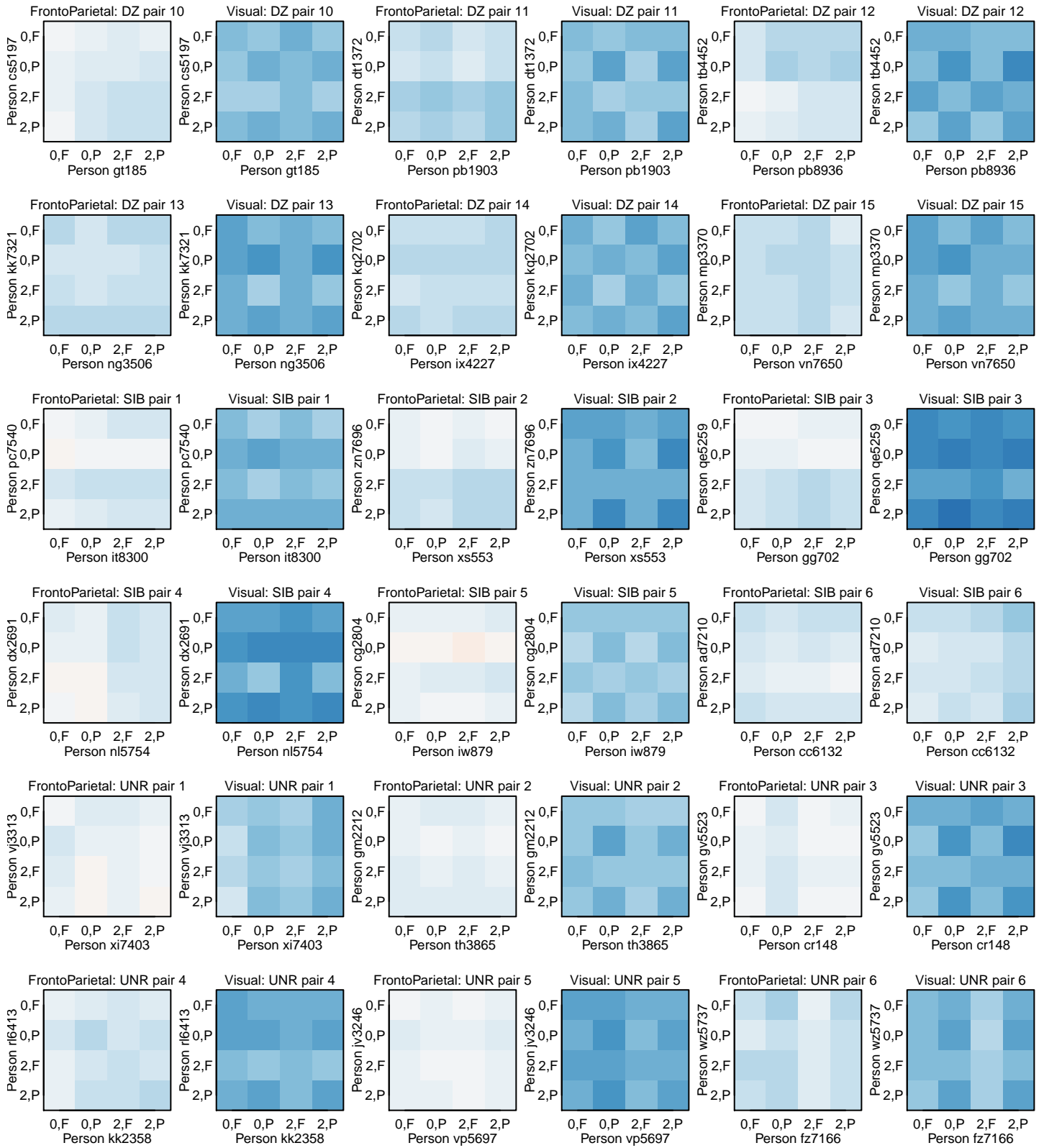
Cerebral Cortex, Volume 30, Issue 5, May 2020, doi:10.1093/cercor/bhz301

This is a knitr file (<https://yihui.name/knitr/>); see the .rnw file with the same name as this .pdf for the R code to generate all figures and results. To compile, change the in.path variable to the location of the input directory downloaded from <https://osf.io/p6msu/>.

NOTE: This knitr was compiled using a subset of the participants in the published paper: 20 (as of 11 May 2020) people included in the original analysis were later flagged by the HCP as having problematic WM task fMRI data (11 MZ, 3 DZ, 2 SIB, 4 UNR). Omitting pairs in which at least one member was flagged by the HCP leaves 94 MZ pairs, 75 DZ pairs, 97 SIB pairs, and 96 UNR pairs for these analyses.

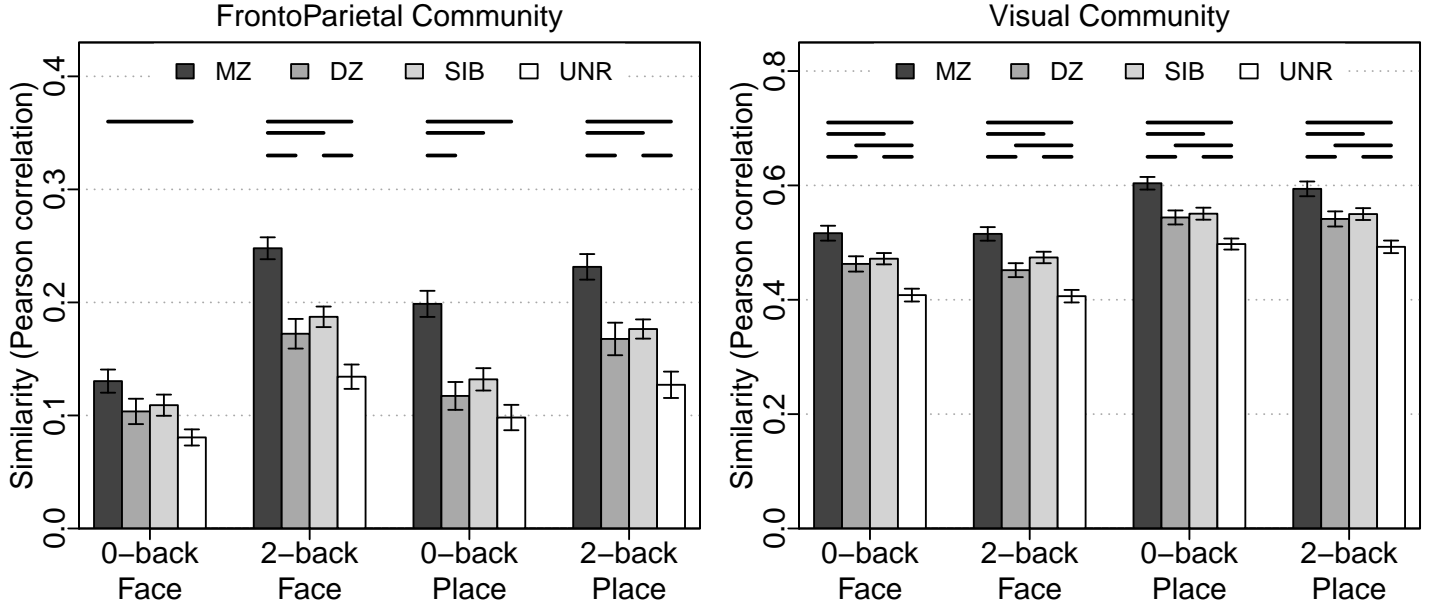
S3.1 Example pairwise similarity matrices and group average





S3.2 Pairwise similarity of matched conditions

Mean similarity of each stimulus type separately; error bars are standard error of the mean (SEM). Both are robust statistics, trimmed at 0.1. Horizontal lines indicate bars that significantly ($p < .0083$, Bonferroni correction of .05 for 6 comparisons) differ in a t-test; see below for t-test t and p values. Note that the y-axis scaling differs between the two plots.



Mean (SEM) of each stimulus type separately, as plotted above and Figure 7. Both are robust statistics, trimmed at 0.1.

Community	Condition	MZ	DZ	SIB	UNR
Frontoparietal	0-back,Face	.13 { .0102 }	.104 { .0112 }	.109 { .0094 }	.081 { .0071 }
Frontoparietal	2-back,Face	.248 { .0097 }	.172 { .0131 }	.187 { .0091 }	.134 { .0108 }
Frontoparietal	0-back,Place	.199 { .0115 }	.117 { .0123 }	.132 { .0099 }	.098 { .0112 }
Frontoparietal	2-back,Place	.231 { .0113 }	.168 { .0144 }	.176 { .0085 }	.127 { .0117 }
Visual	0-back,Face	.516 { .013 }	.463 { .0134 }	.472 { .0099 }	.408 { .0112 }
Visual	2-back,Face	.515 { .0119 }	.452 { .0122 }	.474 { .01 }	.406 { .011 }
Visual	0-back,Place	.604 { .011 }	.544 { .0123 }	.551 { .0105 }	.497 { .0097 }
Visual	2-back,Place	.594 { .0129 }	.541 { .0132 }	.55 { .0104 }	.493 { .011 }

t and p (in parentheses) values from two-sided t-tests of the difference between the (z-transformed) correlations in each subject group. Asterisks and shading mark differences with $p < .008$, Bonferroni-corrected threshold for $p < .05$ with 6 comparisons.

FrontoParietal, 0-back Face

	MZ	DZ	SIB	UNR
MZ				
DZ	1.83 (.07)			
SIB	1.61 (.111)	-.4 (.69)		
UNR	4.13 (<.001)***	1.79 (.077)	2.56 (.012)	

FrontoParietal, 0-back Place

	MZ	DZ	SIB	UNR
MZ				
DZ	5.1 (<.001)***			
SIB	4.69 (<.001)***	-.99 (.323)		
UNR	6.56 (<.001)***	1.19 (.236)	2.38 (.019)	

Visual, 0-back Face

	MZ	DZ	SIB	UNR
MZ				
DZ	3.79 (<.001)**			
SIB	3.58 (<.001)**	-.75 (.456)		
UNR	8.11 (<.001)***	3.96 (<.001)***	5.39 (<.001)***	

Visual, 0-back Place

	MZ	DZ	SIB	UNR
MZ				
DZ	5.43 (<.001)***			
SIB	5.42 (<.001)***	-.61 (.541)		
UNR	10.76 (<.001)***	4.13 (<.001)***	5.32 (<.001)***	

FrontoParietal, 2-back Face

	MZ	DZ	SIB	UNR
MZ				
DZ	4.95 (<.001)***			
SIB	4.89 (<.001)***	-1.01 (.313)		
UNR	8.29 (<.001)***	2.35 (.02)	3.97 (<.001)***	

FrontoParietal, 2-back Place

	MZ	DZ	SIB	UNR
MZ				
DZ	3.7 (<.001)**			
SIB	4.17 (<.001)***	-.6 (.551)		
UNR	6.77 (<.001)***	2.28 (.024)	3.65 (<.001)**	

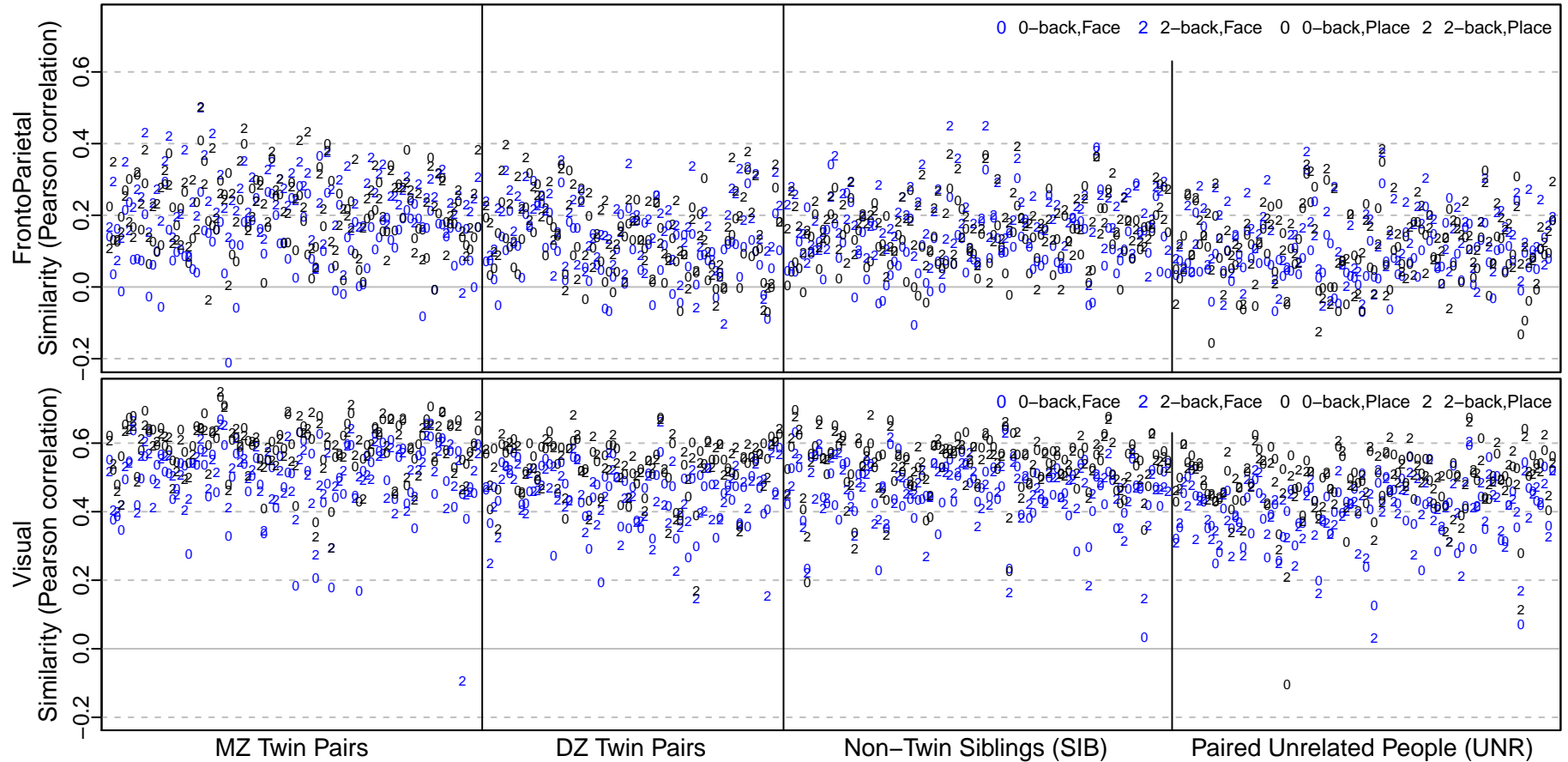
Visual, 2-back Face

	MZ	DZ	SIB	UNR
MZ				
DZ	4.91 (<.001)***			
SIB	3.48 (.001)**	-1.86 (.066)		
UNR	8.64 (<.001)***	3.46 (.001)**	5.72 (<.001)***	

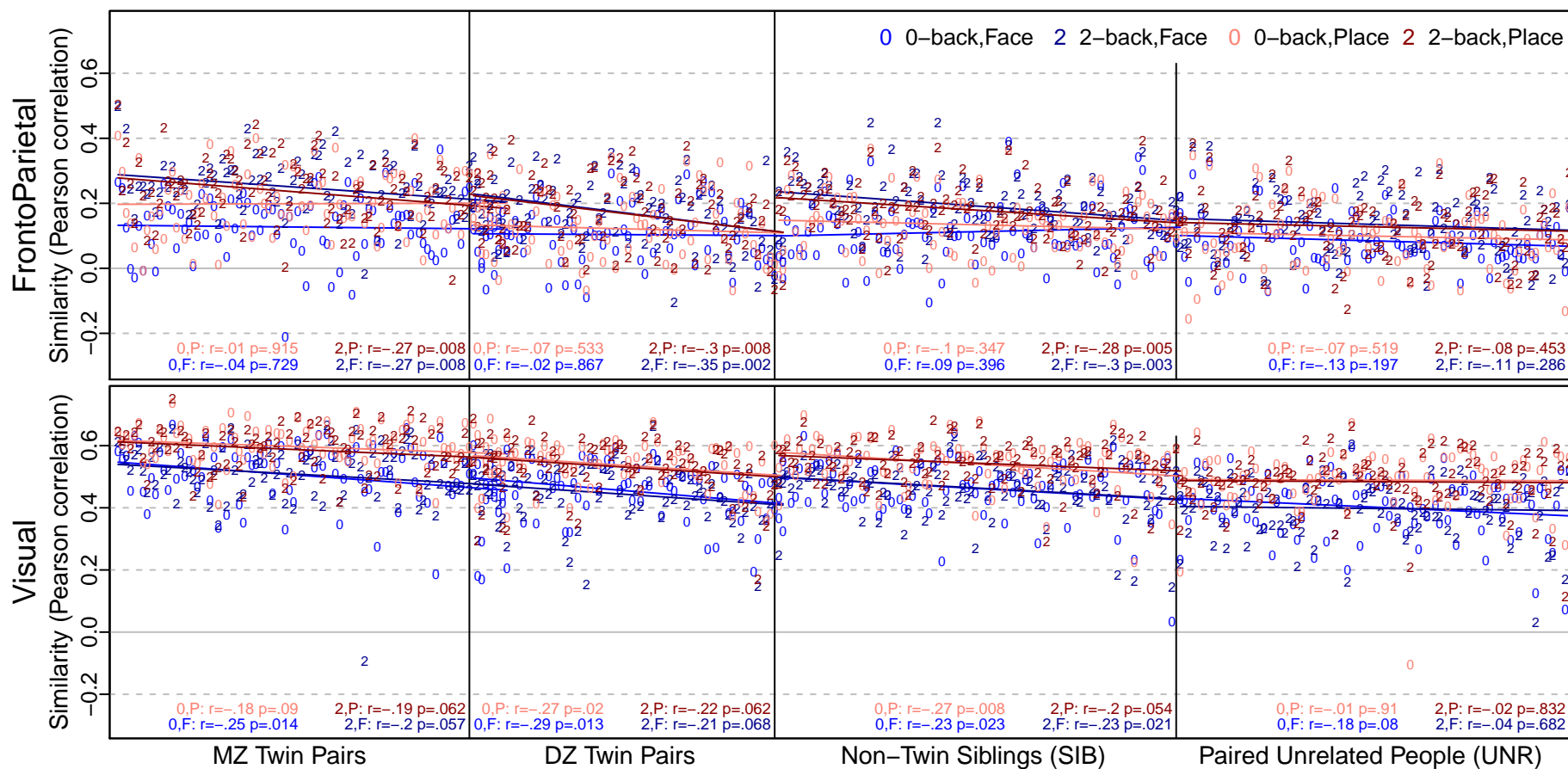
Visual, 2-back Place

	MZ	DZ	SIB	UNR
MZ				
DZ	4.19 (<.001)***			
SIB	3.93 (<.001)***	-.76 (.448)		
UNR	8.63 (<.001)***	3.99 (<.001)***	5.35 (<.001)***	

Similarity on matching stimulus types, full dataset. The paired participants are arrayed along the x-axis in **arbitrary order** within each type (MZ, DZ, SIB, UNR), with their four similarities (0-back Face, 2-back Face, 0-back Place, 2-back Place) shown in each column. Note the higher overall similarity in Visual, with Place (black symbols) more similar than Face (blue symbols); in FrontoParietal 2-back tends to be higher. In both FrontoParietal and Visual the variability of similarities in each pair of people is approximately the same (e.g., SIB pairs are not noticeably more variable than DZ pairs), with the band of similarities decreasing from left to right (UNR pairs tend to be less similar than MZ pairs).



Similarity on matching stimulus types, full dataset. The paired participants are arrayed along the x-axis **by decreasing d'** within each type (MZ, DZ, SIB, UNR). Regression against rank ordering, not actual d'.



S3.3 Similarity of matched conditions: Linear mixed models

Unlike the previous pairwise t-tests, these have all four pairs (0-back face to 0-back face, etc.) analyzed together. Beginning with a model of the entire dataset, there's a 3-way interaction between community.id, pair.group, and condition.id, so need to investigate subsets.

In Visual: All pair groups except SIB and DZ are significantly different, in the expected directions (e.g., MZ more similar than UNR). The same-category contrasts (2,P-0,P; 2,F-0,F) are not significantly different, but all those that mix categories are, in the direction of Place more similar than Face.

In FrontoParietal: Within each pair.group (MZ, DZ, SIB, UNR), all the contrasts mixing 0-back and 2-back are significant, with 2-back more similar than 0-back. Further, the 2,P-2,F contrast is not significant in any pair.group, and 0,P-0,F only significant (0,P higher) in MZ. Consistent with the pairwise tests, the SIB-DZ contrast (only) is always highly non-significant. The other pairwise contrasts are all significantly different in 2,P and 2,F, and some in 0,F and 0,P.

```
head(mm.tbl); # show dataframe structure

##      pair.id pair.group  community.id condition.id similarity
## 1 up8860.th4838      MZ FrontoParietal          0,F  0.1406666
## 2 up8860.th4838      MZ FrontoParietal          2,F  0.1665236
## 3 up8860.th4838      MZ FrontoParietal          0,P  0.2253955
## 4 up8860.th4838      MZ FrontoParietal          2,P  0.1081610
## 5 ei1052.ss2996      MZ FrontoParietal          0,F  0.0360331
## 6 ei1052.ss2996      MZ FrontoParietal          2,F  0.2937225

# everything in the model: three-way interaction
anova(lme(fixed=similarity~pair.group*community.id*condition.id,
          random=list(pair.id=~1, community.id=~1), data=mm.tbl));

##                                numDF denDF  F-value p-value
## (Intercept)                      1   2148 9879.042 <.0001
## pair.group                        3    358   39.111 <.0001
## community.id                     1    358 5137.032 <.0001
## condition.id                     3   2148  238.294 <.0001
## pair.group:community.id          3    358    0.767  0.5131
## pair.group:condition.id          9   2148    4.206 <.0001
## community.id:condition.id        3   2148  179.354 <.0001
## pair.group:community.id:condition.id 9   2148    2.296  0.0146
```

Visual only.

```
stbl <- subset(mm.tbl, mm.tbl$community.id == "Visual"); # visual only
lme.out <- lme(fixed=similarity~pair.group*condition.id, random=~1|pair.id, data=stbl);
anova(lme.out); # no interaction but significant main effects, so do contrasts:

##                                numDF denDF  F-value p-value
## (Intercept)                      1   1074 14849.325 <.0001
## pair.group                        3    358   28.819 <.0001
## condition.id                     3   1074  354.900 <.0001
## pair.group:condition.id          9   1074    0.633  0.7695

summary(glht(lme.out, mcp(pair.group="Tukey"))); # Visual: all but SIB-DZ significantly different

##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
## Fit: lme.formula(fixed = similarity ~ pair.group * condition.id, data = stbl,
##      random = ~1 | pair.id)
##
## Linear Hypotheses:
```



```
##               Estimate Std. Error z value Pr(>|z|)
## MZ - DZ == 0    0.047197   0.013675   3.451  0.00322 **
## SIB - DZ == 0    0.007258   0.013581   0.534  0.95061
## UNR - DZ == 0   -0.052900   0.013612  -3.886 < 0.001 ***
## SIB - MZ == 0   -0.039939   0.012783  -3.124  0.00936 **
## UNR - MZ == 0   -0.100097   0.012816  -7.810 < 0.001 ***
## UNR - SIB == 0  -0.060158   0.012716  -4.731 < 0.001 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)

summary(glht(lme.out, mcp(condition.id="Tukey"))); # Visual: same-category contrasts not significantly different

##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lme.formula(fixed = similarity ~ pair.group * condition.id, data = stbl,
## random = ~1 | pair.id)
##
## Linear Hypotheses:
##               Estimate Std. Error z value Pr(>|z|)
## 0,P - 0,F == 0  0.081213   0.008026  10.118 <1e-04 ***
## 2,F - 0,F == 0 -0.011726   0.008026  -1.461   0.461
## 2,P - 0,F == 0  0.075647   0.008026   9.425 <1e-04 ***
## 2,F - 0,P == 0 -0.092938   0.008026 -11.579 <1e-04 ***
## 2,P - 0,P == 0 -0.005565   0.008026  -0.693   0.900
## 2,P - 2,F == 0  0.087373   0.008026  10.886 <1e-04 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

FrontoParietal only.

```
stbl <- subset(mm.tbl, mm.tbl$community.id == "FrontoParietal"); # FrontoParietal only
anova(lme(fixed=similarity~pair.group*condition.id, random=~1|pair.id, data=stbl)); # significant interaction

##               numDF denDF    F-value p-value
## (Intercept)         1  1074 1427.2316 <.0001
## pair.group          3   358  22.3881 <.0001
## condition.id        3  1074 119.9490 <.0001
## pair.group:condition.id  9  1074   4.8441 <.0001

#####
# Frontoparietal, MZ only
stbl <- subset(mm.tbl, mm.tbl$community.id == "FrontoParietal" & mm.tbl$pair.group == "MZ");
lme.out <- lme(fixed=similarity~condition.id, random=~1|pair.id, data=stbl);
#anova(lme.out);
summary(glht(lme.out, mcp(condition.id="Tukey")));

##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lme.formula(fixed = similarity ~ condition.id, data = stbl, random = ~1 |
## pair.id)
##
## Linear Hypotheses:
```

```
##              Estimate Std. Error z value Pr(>|z|)
## 0,P - 0,F == 0  0.072355   0.009851   7.345   <0.001 ***
## 2,F - 0,F == 0  0.119739   0.009851  12.155   <0.001 ***
## 2,P - 0,F == 0  0.104693   0.009851  10.627   <0.001 ***
## 2,F - 0,P == 0  0.047384   0.009851   4.810   <0.001 ***
## 2,P - 0,P == 0  0.032339   0.009851   3.283   0.0057 **
## 2,P - 2,F == 0 -0.015046   0.009851  -1.527   0.4211
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)

#####
# FrontoParietal, DZ only
stbl <- subset(mm.tbl, mm.tbl$community.id == "FrontoParietal" & mm.tbl$pair.group == "DZ");
lme.out <- lme(fixed=similarity~condition.id, random=~1|pair.id, data=stbl);
#anova(lme.out);
summary(glht(lme.out, mcp(condition.id="Tukey")));

##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lme.formula(fixed = similarity ~ condition.id, data = stbl, random = ~1 |
## pair.id)
##
## Linear Hypotheses:
##              Estimate Std. Error z value Pr(>|z|)
## 0,P - 0,F == 0  0.017675   0.010147   1.742   0.302
## 2,F - 0,F == 0  0.065853   0.010147   6.490   <1e-04 ***
## 2,P - 0,F == 0  0.063491   0.010147   6.257   <1e-04 ***
## 2,F - 0,P == 0  0.048179   0.010147   4.748   <1e-04 ***
## 2,P - 0,P == 0  0.045816   0.010147   4.515   <1e-04 ***
## 2,P - 2,F == 0 -0.002362   0.010147  -0.233   0.996
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)

#####
# FrontoParietal, SIB only
stbl <- subset(mm.tbl, mm.tbl$community.id == "FrontoParietal" & mm.tbl$pair.group == "SIB");
lme.out <- lme(fixed=similarity~condition.id, random=~1|pair.id, data=stbl);
#anova(lme.out);
summary(glht(lme.out, mcp(condition.id="Tukey")));

##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lme.formula(fixed = similarity ~ condition.id, data = stbl, random = ~1 |
## pair.id)
##
## Linear Hypotheses:
##              Estimate Std. Error z value Pr(>|z|)
## 0,P - 0,F == 0  0.020856   0.008341   2.500   0.0602 .
## 2,F - 0,F == 0  0.078003   0.008341   9.352   <0.001 ***
## 2,P - 0,F == 0  0.065378   0.008341   7.838   <0.001 ***
## 2,F - 0,P == 0  0.057147   0.008341   6.852   <0.001 ***
## 2,P - 0,P == 0  0.044523   0.008341   5.338   <0.001 ***
## 2,P - 2,F == 0 -0.012625   0.008341  -1.514   0.4292
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)

#####
# FrontoParietal, UNR only
stbl <- subset(mm.tbl, mm.tbl$community.id == "FrontoParietal" & mm.tbl$pair.group == "UNR");
lme.out <- lme(fixed=similarity~condition.id, random=~1|pair.id, data=stbl);
anova(lme.out);

##          numDF denDF    F-value p-value
## (Intercept)      1   285 199.84698 <.0001
## condition.id     3   285  13.32448 <.0001

summary(glht(lme.out, mcp(condition.id="Tukey")));

##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
## Fit: lme.formula(fixed = similarity ~ condition.id, data = stbl, random = ~1 |
##      pair.id)
##
## Linear Hypotheses:
##              Estimate Std. Error z value Pr(>|z|)
## 0,P - 0,F == 0  0.014906   0.009220   1.617   0.3691
## 2,F - 0,F == 0  0.050618   0.009220   5.490 <0.001 ***
## 2,P - 0,F == 0  0.043313   0.009220   4.698 <0.001 ***
## 2,F - 0,P == 0  0.035712   0.009220   3.873 <0.001 ***
## 2,P - 0,P == 0  0.028407   0.009220   3.081  0.0114 *
## 2,P - 2,F == 0 -0.007305   0.009220  -0.792   0.8580
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)

#####
# FrontoParietal, 0,F only
stbl <- subset(mm.tbl, mm.tbl$community.id == "FrontoParietal" & mm.tbl$condition.id == "0,F");
lme.out <- lme(fixed=similarity~pair.group, random=~1|pair.id, data=stbl);
#anova(lme.out);
summary(glht(lme.out, mcp(pair.group="Tukey")));

##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
## Fit: lme.formula(fixed = similarity ~ pair.group, data = stbl, random = ~1 |
##      pair.id)
##
## Linear Hypotheses:
##              Estimate Std. Error z value Pr(>|z|)
## MZ - DZ == 0    0.02289   0.01354   1.690  0.32846
## SIB - DZ == 0    0.00936   0.01345   0.696  0.89859
## UNR - DZ == 0   -0.01963   0.01348  -1.456  0.46389
## SIB - MZ == 0   -0.01353   0.01266  -1.069  0.70829
## UNR - MZ == 0   -0.04253   0.01269  -3.350  0.00442 **
## UNR - SIB == 0  -0.02899   0.01260  -2.302  0.09742 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```
#####
# FrontoParietal, 2,F only
stbl <- subset(mm.tbl, mm.tbl$community.id == "FrontoParietal" & mm.tbl$condition.id == "2,F");
lme.out <- lme(fixed=similarity~pair.group, random=~1|pair.id, data=stbl);
#anova(lme.out);
summary(glht(lme.out, mcp(pair.group="Tukey")));

##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lme.formula(fixed = similarity ~ pair.group, data = stbl, random = ~1 |
## pair.id)
##
## Linear Hypotheses:
## Estimate Std. Error z value Pr(>|z|)
## MZ - DZ == 0 0.07678 0.01446 5.311 <0.001 ***
## SIB - DZ == 0 0.02151 0.01436 1.498 0.4382
## UNR - DZ == 0 -0.03487 0.01439 -2.423 0.0727 .
## SIB - MZ == 0 -0.05527 0.01351 -4.090 <0.001 ***
## UNR - MZ == 0 -0.11165 0.01355 -8.240 <0.001 ***
## UNR - SIB == 0 -0.05638 0.01344 -4.194 <0.001 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)

#####
# FrontoParietal, 0,P only
stbl <- subset(mm.tbl, mm.tbl$community.id == "FrontoParietal" & mm.tbl$condition.id == "0,P");
lme.out <- lme(fixed=similarity~pair.group, random=~1|pair.id, data=stbl);
anova(lme.out);

## numDF denDF F-value p-value
## (Intercept) 1 358 747.5250 <.0001
## pair.group 3 358 18.4717 <.0001

summary(glht(lme.out, mcp(pair.group="Tukey")));

##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lme.formula(fixed = similarity ~ pair.group, data = stbl, random = ~1 |
## pair.id)
##
## Linear Hypotheses:
## Estimate Std. Error z value Pr(>|z|)
## MZ - DZ == 0 0.07757 0.01496 5.185 <0.001 ***
## SIB - DZ == 0 0.01254 0.01486 0.844 0.8332
## UNR - DZ == 0 -0.02240 0.01489 -1.504 0.4345
## SIB - MZ == 0 -0.06503 0.01399 -4.650 <0.001 ***
## UNR - MZ == 0 -0.09998 0.01402 -7.130 <0.001 ***
## UNR - SIB == 0 -0.03494 0.01391 -2.512 0.0581 .
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)

#####
# FrontoParietal, 2,P only
```

```

stbl <- subset(mm.tbl, mm.tbl$community.id == "FrontoParietal" & mm.tbl$condition.id == "2,P");
lme.out <- lme(fixed=similarity~pair.group, random=~1|pair.id, data=stbl);
#anova(lme.out);
summary(glht(lme.out, mcp(pair.group="Tukey")));

##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lme.formula(fixed = similarity ~ pair.group, data = stbl, random = ~1 |
## pair.id)
##
## Linear Hypotheses:
## Estimate Std. Error z value Pr(>|z|)
## MZ - DZ == 0 0.06410 0.01519 4.218 < 0.001 ***
## SIB - DZ == 0 0.01125 0.01509 0.745 0.87852
## UNR - DZ == 0 -0.03981 0.01512 -2.632 0.04218 *
## SIB - MZ == 0 -0.05285 0.01420 -3.721 0.00104 **
## UNR - MZ == 0 -0.10391 0.01424 -7.297 < 0.001 ***
## UNR - SIB == 0 -0.05106 0.01413 -3.614 0.00167 **
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)

```

S3.4 Similarity of matched conditions: ACE modeling

For MZ and DZ.

Community	Condition	h2	c2	e2
FrontoParietal	0-back,Face	0.05 [-0.01,0.1]	0.08 [0.04,0.13]*	0.87 [0.85,0.89]*
FrontoParietal	2-back,Face	0.15 [0.1,0.21]*	0.09 [0.04,0.14]*	0.75 [0.73,0.77]*
FrontoParietal	0-back,Place	0.16 [0.1,0.22]*	0.04 [0,0.09]	0.8 [0.78,0.82]*
FrontoParietal	2-back,Place	0.13 [0.07,0.19]*	0.1 [0.05,0.16]*	0.77 [0.75,0.79]*
Visual	0-back,Face	0.1 [0.04,0.15]*	0.41 [0.37,0.45]*	0.49 [0.47,0.51]*
Visual	2-back,Face	0.13 [0.07,0.19]*	0.38 [0.34,0.43]*	0.49 [0.47,0.51]*
Visual	0-back,Place	0.12 [0.08,0.16]*	0.48 [0.44,0.51]*	0.4 [0.39,0.42]*
Visual	2-back,Place	0.11 [0.06,0.16]*	0.48 [0.44,0.52]*	0.41 [0.39,0.43]*

For MZ and DZ+SIB.

Community	Condition	h2	c2	e2
FrontoParietal	0-back,Face	0.04 [-0.01,0.08]	0.09 [0.06,0.13]*	0.87 [0.85,0.89]*
FrontoParietal	2-back,Face	0.13 [0.08,0.18]*	0.12 [0.08,0.15]*	0.75 [0.73,0.77]*
FrontoParietal	0-back,Place	0.14 [0.09,0.19]*	0.06 [0.02,0.09]*	0.8 [0.78,0.82]*
FrontoParietal	2-back,Place	0.12 [0.07,0.17]*	0.12 [0.08,0.15]*	0.77 [0.75,0.79]*
Visual	0-back,Face	0.09 [0.04,0.14]*	0.42 [0.38,0.45]*	0.49 [0.47,0.51]*
Visual	2-back,Face	0.11 [0.06,0.15]*	0.41 [0.37,0.44]*	0.49 [0.47,0.51]*
Visual	0-back,Place	0.11 [0.08,0.15]*	0.49 [0.46,0.51]*	0.4 [0.39,0.41]*
Visual	2-back,Place	0.1 [0.06,0.14]*	0.49 [0.46,0.52]*	0.41 [0.39,0.43]*

S3.5 Comparison of variance components with other studies

Reference	Mean Age	MZ similarity (Npairs)	DZ similarity (Npairs)	UNR similarity (Npairs)	a2	c2	e2	Reference table or figure
Etzel FPN	22-36 Avg 29.2	.13-.25 (105)	.11-.19 (78+99 SIB)	.08-.13 (100)	5-15%**	5-11%	75-87%	Figure 7, S3.2, S3.4
Etzel Visual	22-36 Avg 29.2	.51-.60 (105)	.46-.55 (78+99 SIB)	.40-.55 (100)	9-11%**	40-49%**	41-49%**	Figure 7, S3.2, S3.4
Polk (2007)	18-29	~.73 (13)	~.63 (11)	~.62 (22)	20%*	53%*	27%*	Figure 2 (faces)
Pinel (2015)	Avg 21.7	~.40 (16)	~.25 (13)	~.27#	30%*	10%*	60%*	Figure 6 (faces)
Pinel (2015)	Avg 21.7	.489 (16)	.202 (13)	-	55%** [0-82%]	0%** [0-47%]	45%** [18-100%]	Tables 3, 4 (OFAface, L.I.)
Blokland (2008)	21-27	.19-.42 (29)	-.24-.20 (31)	-	11-36.5%**	0-19.3%	63.5-81.4%	Table 2
Blokland (2011)	20-30	Fig2b (75)	Fig2b (66)	-	33%** (average across regions)	-	67%	Figure 2b, 3
Blokland (2017)	16-30	.09-.54 (110)	-.05-.33 (138)	-	41%** (average across regions)	-	59%	Supplement Table 1

N.B. MZ and DZ similarity coefficients (typically, correlations) prefaced by a \sim represent approximations from Figures where a precise estimate of the correlation was not provided; similarly, the * in the estimate of additive genetic (a2), common environment (c2) and individual-specific environment (e2) denotes that those estimates were computed for the purpose of this table, based on: $e2=1-rMZ$; $a2=2(rMZ-rDZ)$; and $c2=rMZ-a2$, and were not provided in the study either using such equations or via formal model-fitting (latter denoted by **); # study does not specify number of unrelated pairs.

The table above outlines variance components estimates for brain activation during a working memory task across multiple studies of MZ and DZ twins. The current study (Etzel) is among the largest. Based the table above, we see similarities and distinctions across the studies with regards to each variance component:

- Individual-specific environment: The estimate of individual-specific environment (e2) is roughly derived from subtracting the MZ correlation from unity; this estimate is typically estimated with reasonable power even in smaller samples and includes an estimate of measurement error. With the exception of Polk (2007), which includes the fewest MZ pairs and thus may have derived a higher rMZ (the feature selection procedure may also have increased the rMZ), estimates of e2 are >40%, and often >60%, although less so for Visual in the current study. The observation that e2 estimates are the highest for FPN also support our hypothesis of that this network's structure is more idiosyncratic (and so has additional sources of person-specific variance).
- Additive genetics, or heritability: Despite the larger sample size of the current study, estimates of heritability (a2) were lower for both FrontoParietal (FPN) and Visual in the current study, although when compared to Blokland (2011), heritability of behavioral performance (accuracy and mean reaction time, see Table 2 in Blokland and S1.6 in current study) were quite comparable especially for the 2-back in Blokland (2011) suggesting that the lower heritability in our study may be attributed to our analytic approach and our communities of interest.
- Common environment: Importantly, unlike a majority of the other studies, we were able to parse familial effects (i.e., rMZ) into its heritable and common environmental sources, where the latter reflects those environments that are received or perceived equivalently by members of MZ and DZ pairs (and, in our case, non-twin siblings as our analyses did not reveal any evidence for special twin environment). The only other study to hint at common environmental influence is Polk (2007) although we arrive at this estimate via approximation based on the relative magnitude of their MZ and DZ correlations where the latter appears considerably greater than half the former. Interestingly, our choice to contrast the FPN and Visual communities further underscored the role of c2. For instance, while familial effects (i.e., MZ similarity) on Visual were greater than those on FPN, the greater familiarity in Visual was primarily attributable to common environment. We might speculate that our estimates deviate from those reported by other studies due to

our analytic approach to examine patterns of similarity, due to greater precision afforded by our larger sample size, especially for the DZ+SIB pair set, or due to age-effects (as our sample includes twins that are potentially somewhat older than those in prior studies), or further due to unmeasured positive gene-common environment covariance or primary assortative mating.

- Non-additive genetics: Unlike Blokland (2008, 2011, 2017), we did not notice any evidence for non-additive genetic effects as our DZ+SIB (and DZ alone) correlations were rarely less than half that of the MZ pairs.