

Plots

Contents

Intro	1
Helper Functions	2
(): A wrapper to make image() more convenient	2
boot1M() and lboot(): wrappers for bootstrapping to get confidence intervals	3
plot1(): A function to plot the output of lboot()	4
The Data	5
Figure 2: facial and digital masculinity by age	7
TD male and female trends for digit ratio	8
TD male and AFF male trends for digit ratio	9
TD female and AFF female trends for digit ratio	10
TD male and female trends for facial masculinity	11
TD male and AFF male trends for facial masculinity	12
TD female and AFF female trends for facial masculinity	13
Figure 3: Relationships with diagnosis and parent-reported problems	14
Top: Boxplots showing masculinity scores distribution and barplots showing significance	14
Bottom: Parent-report Factors	16
Figure 4: PRS in devGenes	19
Left: PRS Associations	19
Right: Categorical PRS Comparison	23

Intro

This document illustrates the process used to create Figures 2-4 in from the paper *Genetic and morphological estimates of androgen exposure predict social deficits in multiple neurodevelopmental disorder cohorts*. These figures and data relate only to the study's DevGenes cohort, as raw data from the other cohort — SPARK — cannot be publicly released. SPARK data may be obtained by researchers approved by the Simons Foundation Autism Research Initiative, through SFARI Base: <https://www.sfari.org/resource/sfari-base>.

All code referenced in this document can be found in either `helper_functions.R` or `devGenes_final_figures_code.R`, and the data on which they are based can be found in `table_S1_final.txt` and `devGenes_final_factor_model_loadings.txt`.

Helper Functions

`img()`: A wrapper to make `image()` more convenient

```
img = function(x,ylab,xlab,axes,col,na.zero=F,breaks,do.breaks=T,...){
  cc = colorRampPalette(c("black","chartreuse"))
  if(any(x<0) & any(x>0)){
    cc = colorRampPalette(c("royalblue","royalblue4","black","orangered","goldenrod1"))
  }
  if(missing(ylab)) ylab=""
  if(missing(xlab)) xlab=""
  if(missing(axes)) axes=F
  if(missing(col)) col=cc(256)
  if(na.zero) x[is.na(x)] = 0
  if(do.breaks & missing(breaks)){
    mx = max(abs(x))
    qt = max(abs(quantile(x,c(0.01,0.99))))
    bk = c(-1*mx,seq(-1*qt,qt,length.out=255),mx)
    image(0:ncol(x),0:nrow(x),t(x),ylim=c(nrow(x),0),ylab=ylab,
      xlab=xlab,axes=axes,col=col,breaks=bk,...)
  }else{
    image(0:ncol(x),0:nrow(x),t(x),ylim=c(nrow(x),0),ylab=ylab,
      xlab=xlab,axes=axes,col=col,breaks=breaks,...)
  }
  box()
}
```

bootLM() and lboot(): wrappers for bootstrapping to get confidence intervals

```
bootLM = function(x,y){
  keep = !is.na(x) & !is.na(y)
  x0 = x[keep]
  y0 = y[keep]
  these = sample(length(x0),replace=T)
  x0 = x0[these]
  y0 = y0[these]

  approx(lowess(x0,y0),xout=seq(0,80,1),rule=2)$y
}

### with input x and y, generate a lowess trend with 95% confidence intervals
lboot = function(x,y,subset,nboot=1000,return.boot=F){
  if(length(x)!=length(y)) stop("x and y have different lengths")
  if(missing(subset)){
    subset=1:length(x)
  }
  x = x[subset]
  y = y[subset]

  ### generate nboot lowess fits
  b = replicate(nboot,bootLM(x,y))

  qu = apply(b,1,quantile,0.975)
  ql = apply(b,1,quantile,0.025)
  qm = rowMeans(b)
  xq = 0:80

  out = list()
  out$x = xq
  out$y = qm
  out$ci = list(upr=qu,lwr=ql)
  out$points = list(x=x,y=y)
  if(return.boot){
    out$boot = b
  }
  return(out)
}
```

plot1(): A function to plot the output of lboot()

```
plot1 = function(obj,pt.col,l.col,shade.col,plot.points=F,xlim=c(0,80),
  ylim,add=F,plot.ci=T,...){
  if(missing(ylim)){
    ylim=range(obj$y,na.rm=T)
    ylim = (c(-1,1)*abs(diff(ylim))) + ylim
  }
  if(!add){
    plot(obj,xlim=xlim,ylim=ylim,xlab="age (years)",type='l',col=l.col,...)
    if(plot.ci){
      polygon(c(obj$x,rev(obj$x)),c(obj$ci$lwr,rev(obj$ci$upr)),col=shade.col,border=l.col)
    }
  }else{
    lines(obj,col=l.col,...)
    if(plot.ci){
      polygon(c(obj$x,rev(obj$x)),c(obj$ci$lwr,rev(obj$ci$upr)),col=shade.col,border=l.col)
    }
  }
  if(plot.points){
    points(obj$points,pch=16,col=pt.col)
  }
}
```

The Data

Table 1: Factor Loadings

	Factor1	Factor2	Factor3	Factor4	Factor5	Factor6	Factor7	Factor8	Factor9	Factor10	Factor11
social.eyeccontact	0.1086367	0.4292602	0.0736042	0.1643372	0.1736255	0.2835086	0.3685458	0.0500302	0.3016591	-0.0381764	-0.1280986
social.init_conv	0.2852887	0.1512008	-0.0289435	0.2374517	0.1630843	0.1924666	0.3787394	0.1478946	0.3381085	-0.1800359	-0.0218842
social.uncomf_interact	0.0323974	0.1196371	0.1070747	0.0389679	0.1181215	-0.0130980	0.7039691	0.0786045	0.1543321	0.1342962	0.1714935
social.socializes	0.3813110	0.1493706	0.0620354	0.1495534	0.1271815	0.2526992	0.2149606	0.1206623	0.6884145	0.1012796	0.0045308
social.friends	0.3434447	0.1418500	0.0275180	0.2335482	0.1205117	0.2219378	0.3614091	0.0736616	0.4371931	0.0024861	0.1186012
social.soc_distress	0.1096375	0.4893621	0.1654568	0.2474608	0.1396017	0.0147531	0.2339567	0.3326524	0.1006547	0.2147951	0.0654177
rrb.rep_movies_music	0.1670886	0.2920419	-0.0919332	0.2194842	0.0383111	0.3441104	0.0827352	0.0789571	0.0574445	0.0407191	0.2013055
rrb.stim	0.0940111	0.0946858	0.1010345	0.1692635	0.0848560	0.6685771	-0.0039240	0.0493594	0.0793625	0.0849339	0.0940771
rrb.odd_beh	0.1920686	0.1746066	0.0410817	0.1308004	0.1261518	0.6093322	0.1252416	0.1198064	0.1153548	0.0220056	-0.0016797
rrb.needs_order	0.1072012	0.5804600	0.1458211	0.1302481	0.1316813	0.4224700	0.1504641	0.0069998	0.0805807	-0.0668679	0.0391601
rrb.mann_dis	0.2085801	0.4004670	0.2380111	0.2814674	0.1339018	0.2065598	0.1224160	0.2120164	0.2078487	-0.0718538	0.0339855
acad_abil.reading	0.7848285	-0.0728949	0.0362335	-0.0035160	0.0639259	0.0002604	0.0412783	0.1181537	-0.0802478	-0.0071809	0.0419540
acad_abil.writing	0.7846123	-0.0081306	0.0607637	0.1270829	0.0435566	0.1352355	0.0993364	0.0671456	0.0394453	0.0315433	0.0119071
acad_abil.math	0.7563774	-0.0338151	0.0059640	0.0075421	-0.0136599	0.0259029	-0.0296449	0.0331907	0.0727043	0.0293438	0.0651270
acad_abil.learn_new	0.7870456	0.0843797	0.0244262	0.1027442	0.0682323	0.2443105	0.0618290	0.0465394	0.1059697	0.0560536	0.0777145
language_level	0.3400045	0.0130433	0.0216755	0.0084760	0.0450168	-0.0001328	0.0560722	-0.0791267	0.1504180	0.0417985	-0.0546323
sensory.hugs	0.1222776	0.2781454	0.0307162	0.0001138	0.0805599	0.1131940	0.4283590	-0.0150713	0.0113038	0.0459380	-0.0261927
sensory.dizzy	0.0384089	0.2590796	0.0094119	-0.0782908	0.0850323	-0.0267729	-0.0426067	0.0648256	0.0563114	0.4826593	-0.0125189
sensory.clothing_atypical_temp	-0.0390338	0.3678003	0.1262807	0.1767642	0.1084653	0.2196858	0.1698069	0.0433369	0.0212022	0.1592841	0.0179347
sensory.haircut	0.2101859	0.1548386	0.0864475	0.4056075	0.0711193	0.1067211	-0.0284708	0.2599561	0.0451728	-0.1783465	0.1346923
sensory.sound	0.1398517	0.4147963	0.0862448	0.1823873	0.1136146	0.1883913	0.1382956	0.0570491	-0.0051759	-0.0393394	0.7303652
sensory.light	-0.0252027	0.4886829	0.1337168	0.1389714	0.1124484	0.0124121	0.1744358	0.0888327	0.0354690	0.1784304	0.2433216
sensory.odors	-0.0355109	0.6244332	0.2799430	-0.0409266	-0.0500753	-0.0192315	0.0718177	-0.0431105	0.0257336	0.2679002	0.1102792
sensory.tags	-0.1265136	0.5004148	0.0504564	0.1201747	0.0787497	0.0966972	0.0325400	0.0221242	0.0279833	0.0652394	0.0333144
sensory.sensory_distress	0.0684386	0.4845109	0.2534815	0.3501328	0.1500137	0.3044825	0.1266181	0.2022210	0.0810342	0.0174690	0.2931485
aggression.anger	0.0528586	0.1249831	0.9554577	0.1005087	0.1520969	0.0604562	0.0695452	-0.0275343	0.0657477	0.1146180	0.0611632
aggression.violence	0.0661081	0.2906201	0.5465781	0.1746469	0.1326751	0.0623793	0.0564477	0.2158469	-0.0436690	-0.0161480	-0.0258320
aggression.aggression_social_impact	0.0199923	0.2912773	0.6635470	0.1480428	0.1527398	0.0612080	0.0485477	0.2797050	0.0287037	0.1894996	0.0444737
selfharm.cutting	0.0399613	0.0877897	0.2340288	-0.0368726	0.3146753	0.2450929	0.0672675	0.4197677	0.1298342	0.0982396	-0.0057725
selfharm.hitting	0.0797972	0.0858401	0.1367376	0.0445167	0.8390454	0.0929194	0.0064543	0.0318419	0.1594575	0.1839177	0.1189593
selfharm.banging_head	0.0807096	0.0983643	0.0572073	0.0092898	0.7102043	0.1095340	0.0749824	0.0861172	0.0622817	0.0834091	0.0316940
selfharm.throwing_self	0.0449241	0.1546198	0.1532955	0.0758152	0.5785241	0.0367246	0.2636664	0.1271626	-0.0926529	-0.1439024	-0.0427580
selfharm.self_harm_distressing	0.1064328	0.0671795	0.3480908	0.0962328	0.3101966	0.1344785	0.1155804	0.6190053	0.0372422	0.3273024	0.0738414
eating_GL.eatnorm	0.0403232	0.1350088	0.0722995	0.7802575	0.0716180	0.2193817	-0.0071309	-0.0537625	0.1281635	0.0888874	0.0522333
eating_GL.eat_impact	0.0264519	0.1603731	0.1436861	0.7767861	-0.0006521	0.0813644	0.1240521	0.0083003	0.0056154	0.1118477	0.0158114
eating_GL.constipated	0.0796142	0.0645222	0.1765971	0.1482022	-0.0069866	0.0723587	0.0922520	0.0378867	-0.0410081	0.3774085	0.0243725
eating_GL.GL_distress	0.0473416	0.0822622	0.0445915	0.1934545	0.2245463	0.1958065	0.2322892	0.1143314	0.0423597	0.3633752	-0.0659286
sleep_impact	0.1206532	0.1246777	0.1821075	0.2781920	-0.0321715	0.1153745	0.0484484	0.2086078	0.0985251	0.0364789	0.0884538

9.

[illegible]

Figure 2: facial and digital masculinity by age

```
### lboot() returns the lowess trend of the
### data as well as its 95% CI; the object returned by lboot()
### can be visualized using plotl() as shown below

set.seed(1283)
### get the trends for TD males
idx = !dat$affected & dat$sex_male==1
tdM_flm = lboot(dat$ageyears, dat$facial_masc_raw, subset=idx, return.boot=T)
tdM_drm = lboot(dat$ageyears, dat$digit_ratio_raw, subset=idx, return.boot=T)

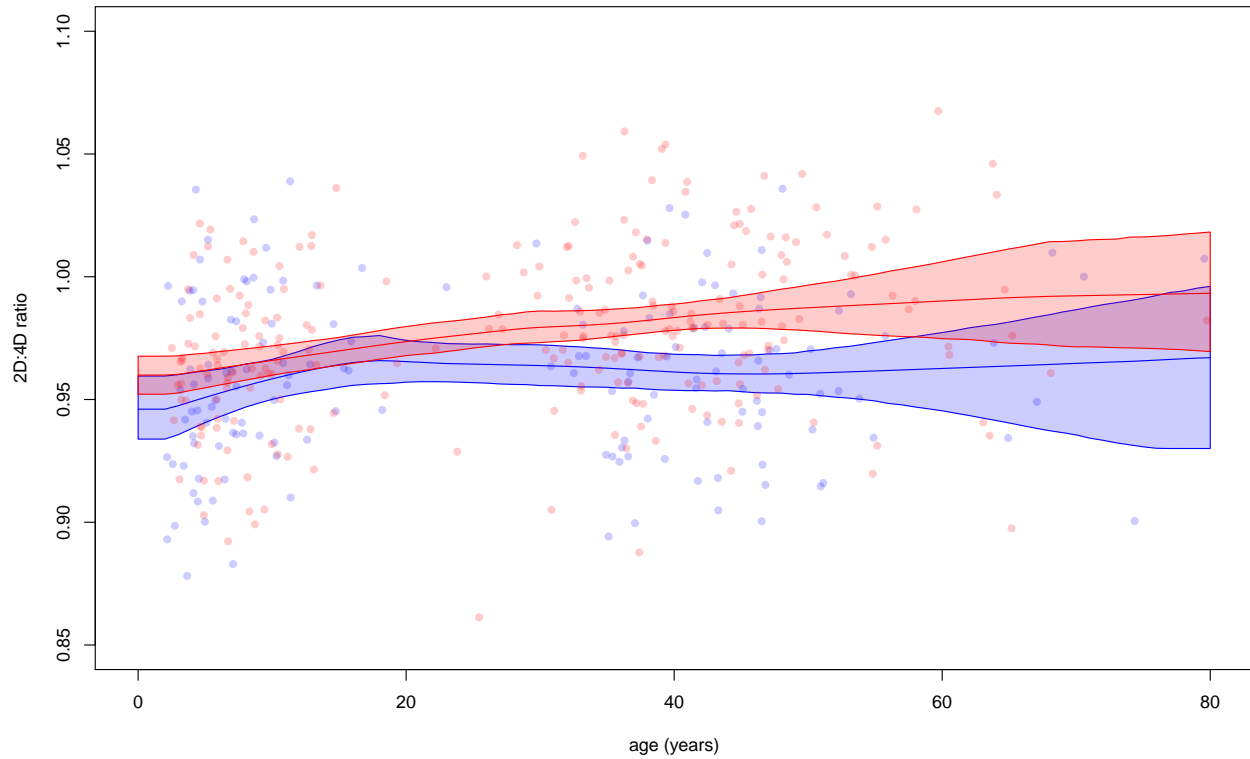
### get the trends for TD females
idx = !dat$affected & dat$sex_male==0
tdF_flm = lboot(dat$ageyears, dat$facial_masc_raw, subset=idx, return.boot=T)
tdF_drm = lboot(dat$ageyears, dat$digit_ratio_raw, subset=idx, return.boot=T)

set.seed(7751)
### get the trends for affected males
idx = dat$affected & dat$sex_male==1
affM_flm = lboot(dat$ageyears, dat$facial_masc_raw, subset=idx, return.boot=T)
affM_drm = lboot(dat$ageyears, dat$digit_ratio_raw, subset=idx, return.boot=T)

### get the trends for affected females
idx = dat$affected & dat$sex_male==0
affF_flm = lboot(dat$ageyears, dat$facial_masc_raw, subset=idx, return.boot=T)
affF_drm = lboot(dat$ageyears, dat$digit_ratio_raw, subset=idx, return.boot=T)
```

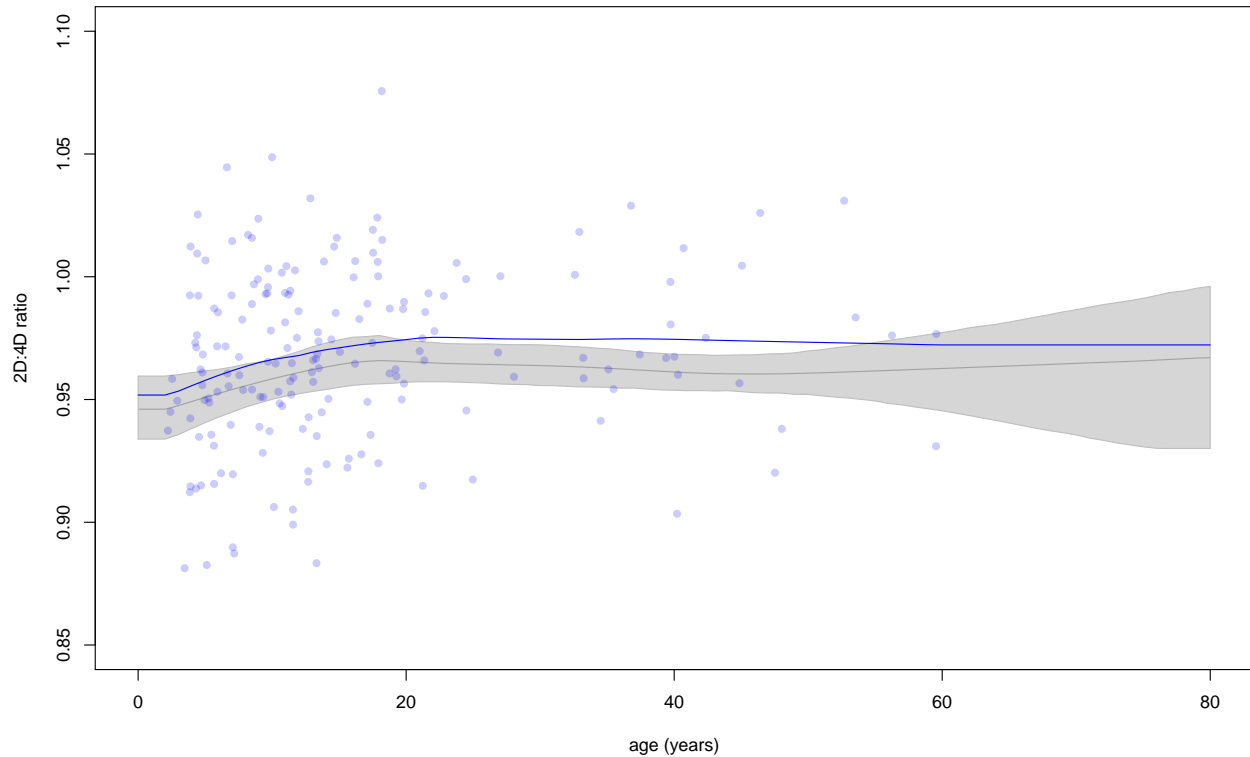
TD male and female trends for digit ratio

```
plot1(tdM_drm,l.col="blue",shade.col=rgb(0,0,1,0.2),pt.col=rgb(0,0,1,0.2),  
plot.points=T,ylab="2D:4D ratio",ylim=c(0.85,1.1))  
plot1(tdF_drm,l.col="red",shade.col=rgb(1,0,0,0.2),pt.col=rgb(1,0,0,0.2),  
plot.points=T,ylab="2D:4D ratio",ylim=c(0.85,1.1),add=T)
```



TD male and AFF male trends for digit ratio

```
plot1(tdM_drm,l.col="grey",shade.col=rgb(0.2,0.2,0.2,0.2),pt.col=rgb(0.2,0.2,0.2,0.2),
plot.points=F,ylab="2D:4D ratio",ylim=c(0.85,1.1))
plot1(affM_drm,l.col="blue",shade.col=rgb(0,0,1,0.2),pt.col=rgb(0,0,1,0.2),
plot.points=T,ylab="2D:4D ratio",ylim=c(0.85,1.1),add=T,plot.ci=F)
```

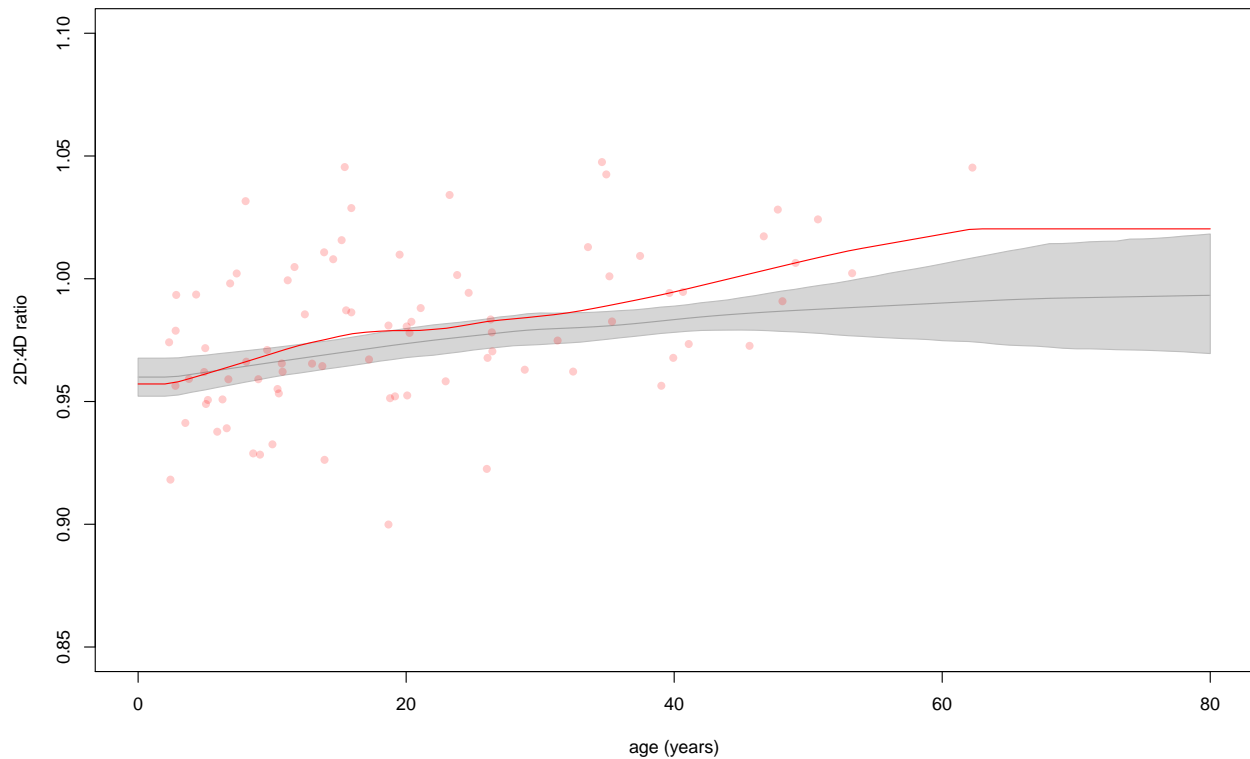


```
### look at the empirical p value for Ha: aff > masc. than TD
### (for digit ratio, lower value is more masculine)
sum(colSums(tdM_drm$b)<sum(affM_drm$y))/1000 ### this is the empirical p-value
```

```
## [1] 0.991
```

TD female and AFF female trends for digit ratio

```
plot1(tdF_drm,l.col="grey",shade.col=rgb(0.2,0.2,0.2,0.2),pt.col=rgb(0.2,0.2,0.2,0.2),
plot.points=F,ylab="2D:4D ratio",ylim=c(0.85,1.1))
plot1(affF_drm,l.col="red",shade.col=rgb(1,0,0,0.2),pt.col=rgb(1,0,0,0.2),
plot.points=T,ylab="2D:4D ratio",ylim=c(0.85,1.1),add=T,plot.ci=F)
```

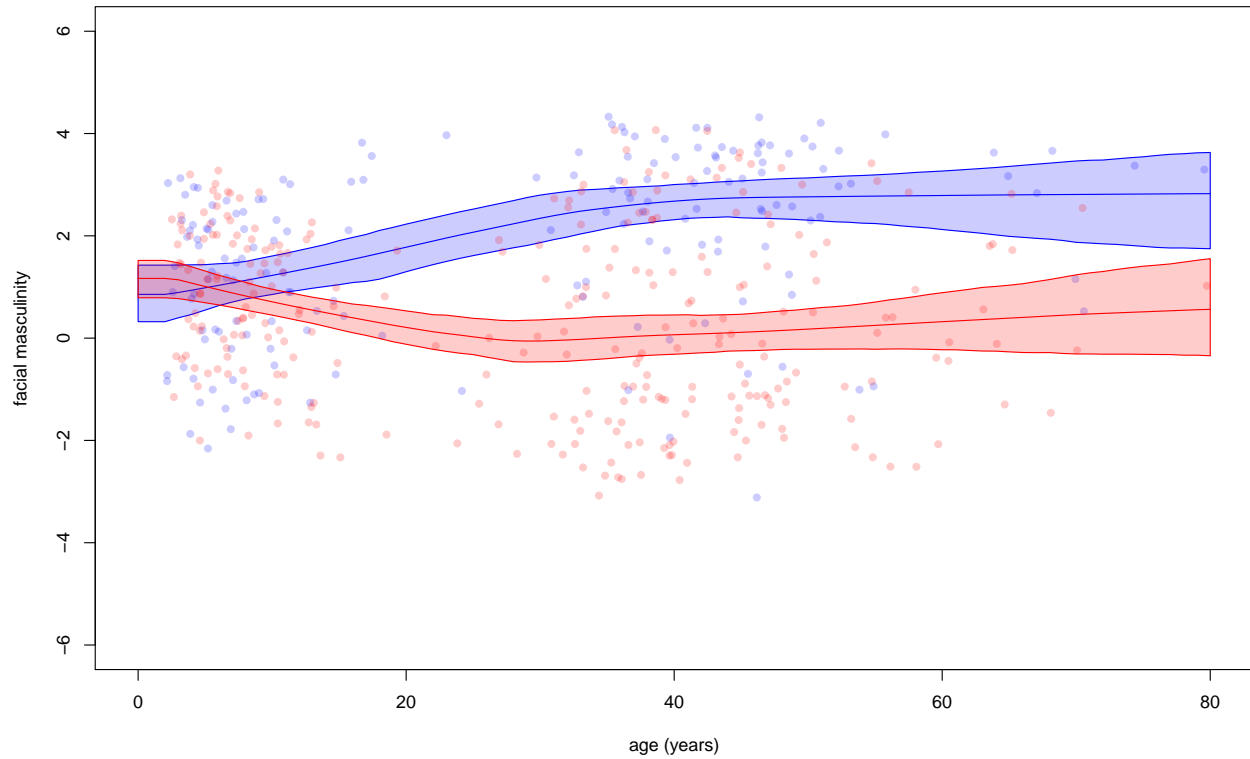


```
### look at the empirical p value for Ha: aff > masc. than TD
### (for digit ratio, lower value is more masculine)
sum(colSums(tdF_drm$b)<sum(affF_drm$y))/1000 ### this is the empirical p-value
```

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

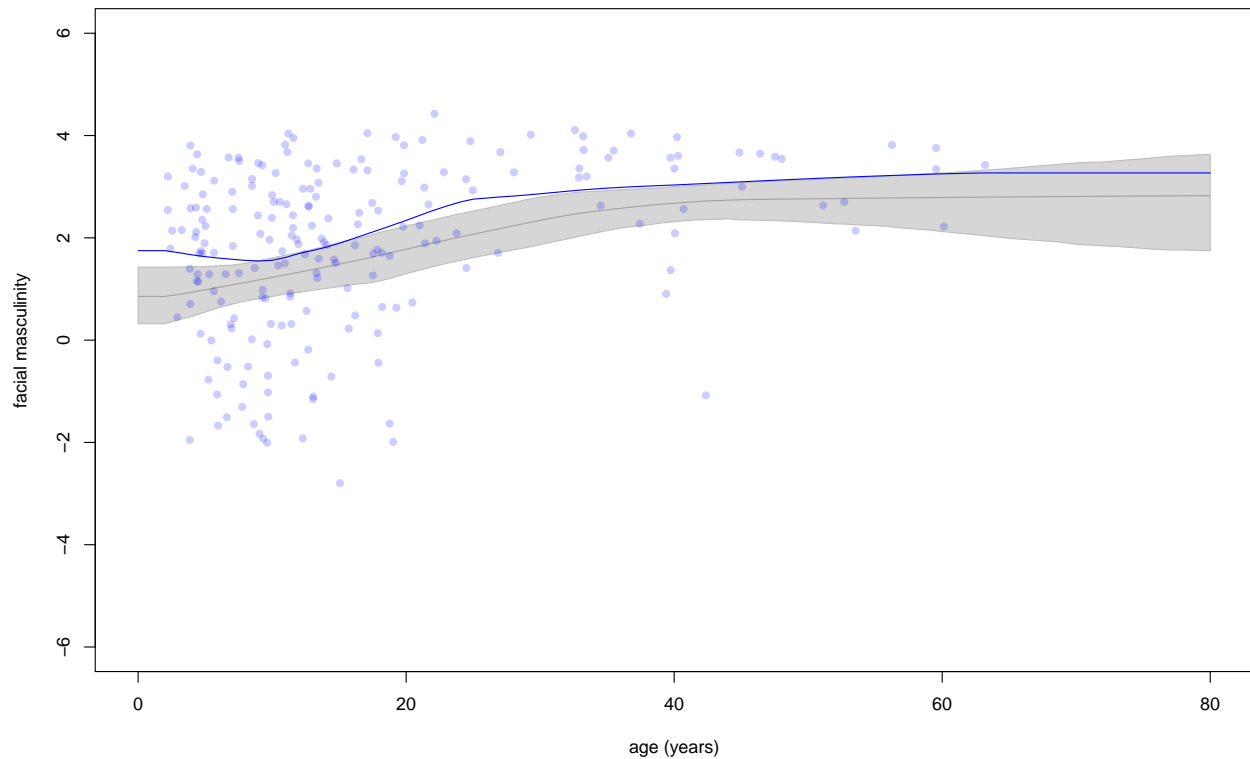
TD male and female trends for facial masculinity

```
plot1(tdM_flm,l.col="blue",shade.col=rgb(0,0,1,0.2),pt.col=rgb(0,0,1,0.2),  
plot.points=T,ylab="facial masculinity",ylim=c(-6,6))  
plot1(tdF_flm,l.col="red",shade.col=rgb(1,0,0,0.2),pt.col=rgb(1,0,0,0.2),  
plot.points=T,ylab="facial masculinity",ylim=c(-6,6),add=T)
```



TD male and AFF male trends for facial masculinity

```
plot1(tdM_flm,l.col="grey",shade.col=rgb(0.2,0.2,0.2,0.2),pt.col=rgb(0.2,0.2,0.2,0.2),  
plot.points=F,ylab="facial masculinity",ylim=c(-6,6))  
plot1(affM_flm,l.col="blue",shade.col=rgb(0,0,1,0.2),pt.col=rgb(0,0,1,0.2),  
plot.points=T,ylab="facial masculinity",ylim=c(-6,6),add=T,plot.ci=F)
```

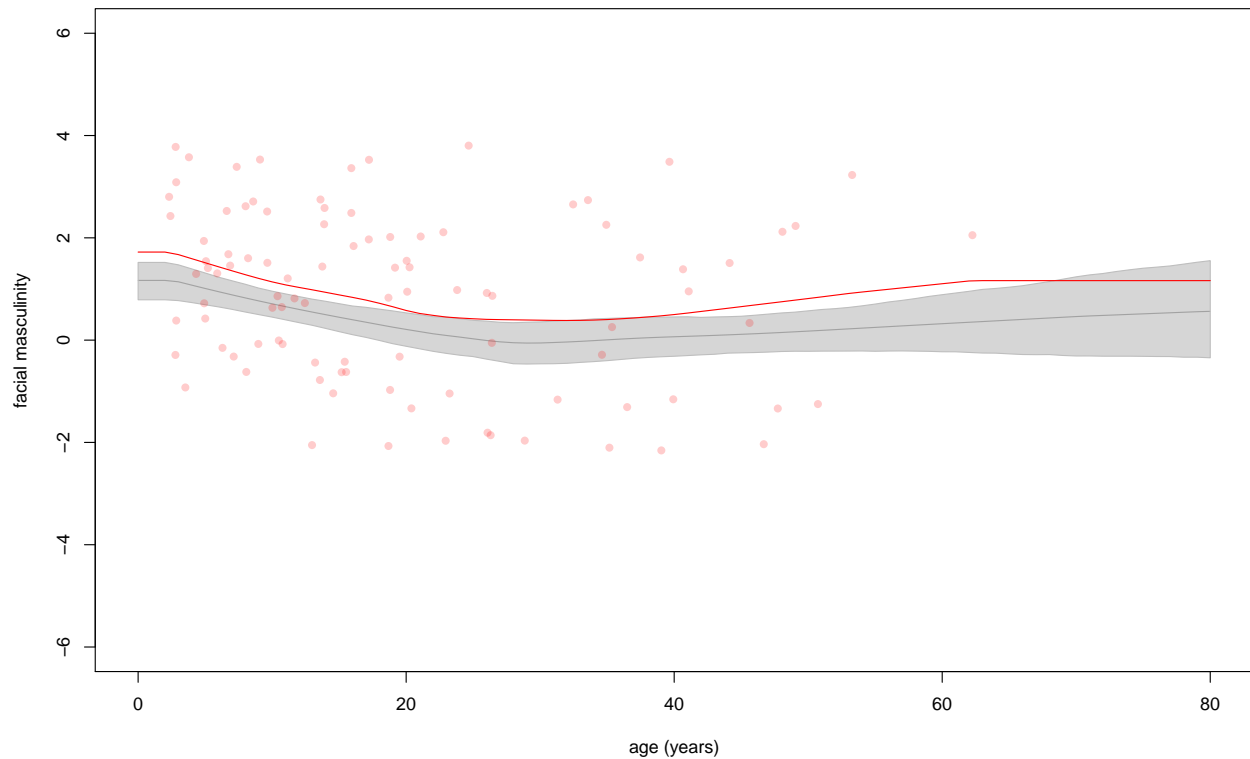


```
### look at the empirical p value for Ha: aff > masc. than TD  
sum(colSums(tdM_flm$b)>sum(affM_flm$y))/1000 ### this is the empirical p-value
```

```
## [1] 0.002
```

TD female and AFF female trends for facial masculinity

```
plot1(tdF_flm,l.col="grey",shade.col=rgb(0.2,0.2,0.2,0.2),pt.col=rgb(0.2,0.2,0.2,0.2),
plot.points=F,ylab="facial masculinity",ylim=c(-6,6))
plot1(affF_flm,l.col="red",shade.col=rgb(1,0,0,0.2),pt.col=rgb(1,0,0,0.2),
plot.points=T,ylab="facial masculinity",ylim=c(-6,6),add=T,plot.ci=F)
```



```
### look at the empirical p value for Ha: aff > masc. than TD
sum(colSums(tdF_flm$b)>sum(affF_flm$y))/1000 ### this is the empirical p-value
```

```
## [1] 0
```

Figure 3: Relationships with diagnosis and parent-reported problems

Top: Boxplots showing masculinity scores distribution and barplots showing significance

```
### pull out the Dx indicators
dxlab = c("adhd","asd","ID","lang","epilepsy","depression","bipolar","anxiety")
dx = as.data.frame(sapply(dat[,dxlab],as.integer))
rownames(dx) = rownames(dat)

cc = c("grey",rep("orangered",5),rep("mistyrose",3))

### structure the masculinity data according to Dx
ll = lapply(dx,function(x) dat$Zdrm[x==1])
ll = c(list(TD=dat$Zdrm[rowSums(dx)==0]),ll)
ll_drm = ll
ll = lapply(dx,function(x) dat$Zflm[x==1])
ll = c(list(TD=dat$Zflm[rowSums(dx)==0]),ll)
ll_flm = ll

## t-tests comparing TD to all other Dxs
td_vs_dx = function(x) {
  p = sapply(x[-1],function(y) t.test(x[[1]],y)$p.v)
  fdr = p.adjust(p, 'fdr')
  out = cbind(p,fdr)
  rownames(out) = names(x)[-1]
  return(out)
}

p_drm = td_vs_dx(ll_drm)
p_flm = td_vs_dx(ll_flm)
```

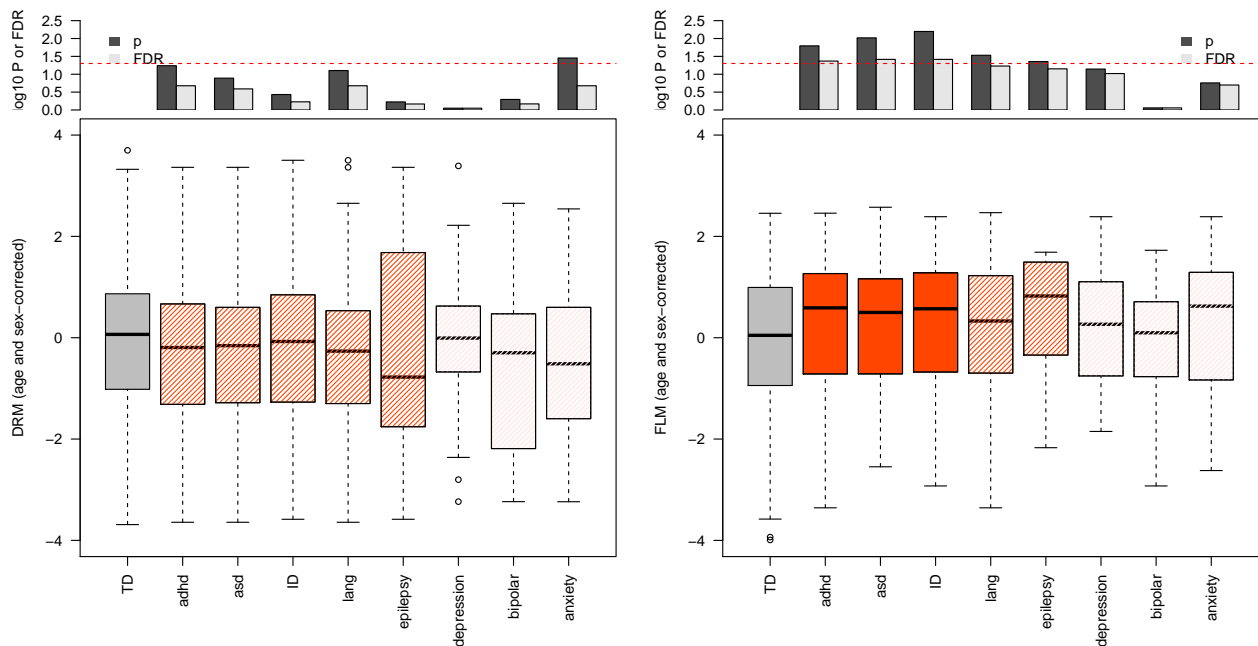
```
layout(matrix(c(1,3,2,4),2,2),heights=c(1,5))
par(mar=c(0,4,1,2))
  barplot(-log10(t(rbind(c(NA,NA),p_drm))),
    beside=T,
    las=2,
    ylim=c(0,2.5),
    ylab="-log10 P or FDR",
    names.arg=rep("",9),
    legend.text=c("p","FDR"),
    args.legend=list(x="topleft",bty="n",border=NA,inset=0.03))
  abline(h=-log10(0.05),col='red',lty=2)
  barplot(-log10(t(rbind(c(NA,NA),p_flm))),
    beside=T,
    las=2,
    ylim=c(0,2.5),
    ylab="-log10 P or FDR",
    names.arg=rep("",9),
    legend.text=c("p","FDR"),
    args.legend=list(x="topright",bty="n",border=NA,inset=0.03))
```

```

abline(h=-log10(0.05),col='red',lty=2)

## the boxplots showing the distribution of the masculinity scores within
par(mar=c(5,4,0.5,2))
bp = boxplot(l1_drm,las=2,ylim=c(-4,4),
  col=c("grey",rep("white",8)),
  ylab="DRM (age and sex-corrected)",
  xaxs="i")
### pattern fills to emphasize (non)significance
rect((2:9)-.4,
bp$stats[2,-1],
(2:9)+.4,
bp$stats[4,-1],
density=c(rep(30,8)), ## tweaked according to which comparisons are sig.
col=cc[-1],border="black")
bp = boxplot(l1_flm,las=2,ylim=c(-4,4),
  col=c("grey",rep("orangered",3),rep("white",5)),
  ylab="FLM (age and sex-corrected)",
  xaxs="i")
### pattern fills to emphasize (non)significance
rect((2:9)-.4,
bp$stats[2,-1],
(2:9)+.4,
bp$stats[4,-1],
density=c(0,0,0,rep(30,6)), ## tweaked according to which comparisons are sig.
col=cc[-1],border="black")

```



Bottom: Parent-report Factors

```
# Xs is the matrix of parent-reported items (we are only distributing factor scores)
# fac = factanal(scale(Xs),factors=11,scores="regression")

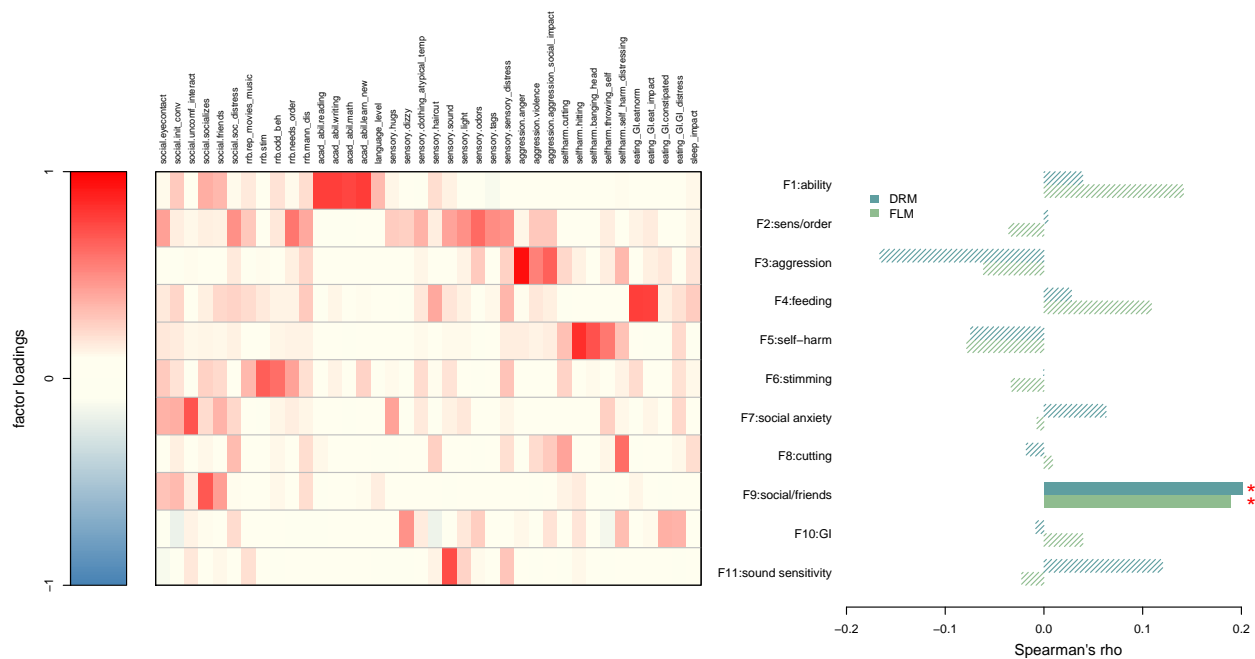
### grab the factor scores from the supplemental table
S = dat[,grep("Factor",colnames(dat))]
### look at the correlations
cors = cor(dat[,c("Zdrm", "Zflm")],S,use="pairwise.complete.obs",method="spearman")

### set layout
layout(matrix(c(1,2,3),1,3),widths=c(1.5,5,5))
### set colors, labels, and breaks for loadings
cp = colorRampPalette(c("steelblue","ivory","red"))
flab = c("F1:ability","F2:sens/order","F3:aggression","F4:feeding",
        "F5:self-harm","F6:stimming","F7:social anxiety","F8:cutting",
        "F9:social/friends","F10:GI","F11:sound sensitivity")
bk = c(-1,seq(-1,-0.1,length.out=127),0,seq(0.1,1,length.out=127),1)

### the key for the factor loadings
par(mar=c(5,7,12,1))
img(as.matrix(seq(1,-1,length.out=256)),col=cp(256),breaks=bk)
axis(2,at=c(0,256/2,256),labels=c(1,0,-1))
mtext("factor loadings",side=2,at=256/0,line=3,cex=0.8)

### the factor loadings
par(mar=c(5,1,12,1))
img(t(1),breaks=bk,col=cp(256))
mtext(rownames(1),side=3,at=c(1:nrow(1))-0.5,las=2,line=0.5,cex=0.5)
abline(h=c(0:12),col='grey')
box()

### the barplot of correlations w/ factor scores
par(mar=c(5,9,12,2))
bp = barplot(cors[2:1,11:1],beside=T,las=2,yaxs="i",names.arg=flab[11:1],axes=F,
            ylab="",col=c("darkseagreen","cadetblue"),
            legend.text=c("FLM","DRM"),
            args.legend=list(x="topleft",inset=0.03,border=NA,bty='n',density=-1),
            border=NA,xlim=c(-0.2,0.22),
            density=rev(c(rep(30,16),-1,-1,rep(30,4))),horiz=T)
axis(1,line=1.5)
mtext("Spearman's rho",side=1,at=0.025,line=4,cex=0.8)
text(c(0.21,0.21),bp[1:2,3],rep(" ",2),col='red',cex=2)
```

Bottom: Statistics

Table 3: Digit Ratio Masculinity

Factor	ρ	FDR
Factor1	0.0393443	0.9946875
Factor2	0.0041213	0.9946875
Factor3	-0.1663960	0.0976235
Factor4	0.0279256	0.9946875
Factor5	-0.0743621	0.8014244
Factor6	-0.0004705	0.9946875
Factor7	0.0629893	0.8176376
Factor8	-0.0179701	0.9946875
Factor9	0.2012962	0.0444052
Factor10	-0.0083417	0.9946875
Factor11	0.1202564	0.3206328

Table 4: Facial Landmark Masculinity

Factor	ρ	FDR
Factor1	0.1413869	0.1648585
Factor2	-0.0356959	0.8390477
Factor3	-0.0612753	0.7664615
Factor4	0.1089886	0.3476934
Factor5	-0.0783222	0.6338121
Factor6	-0.0333277	0.8390477
Factor7	-0.0071165	0.9133422
Factor8	0.0088366	0.9133422
Factor9	0.1886747	0.0403774
Factor10	0.0394948	0.8390477
Factor11	-0.0226260	0.8913875

Figure 4: PRS in devGenes

Left: PRS Associations

```
### pull out the PRS and covariates from the main table for convenience
prs = dat[,grep("p0",colnames(dat))]
covars = dat[,c(2:3,grep("PC",colnames(dat)))]
covars[[1]] = log(covars[[1]])

### wrapper to grab the PRS-related effect (x) and associated statistics
### from a linear model
fsig = function(x,y) summary(lm(y~.,data=data.frame(covars,x)))$coef[9,]

cfsoc = t(apply(prs,2,fsig,S[,9]))
cfdrm = t(apply(prs,2,fsig,dat$Zdrm))
cfflm = t(apply(prs,2,fsig,dat$Zflm))

### add FDR
cfsoc = cbind(cfsoc,FDR = p.adjust(cfsoc[,4],'fdr'))
cfdrm = cbind(cfdrm,FDR = p.adjust(cfdrm[,4],'fdr'))
cfflm = cbind(cfflm,FDR = p.adjust(cfflm[,4],'fdr'))

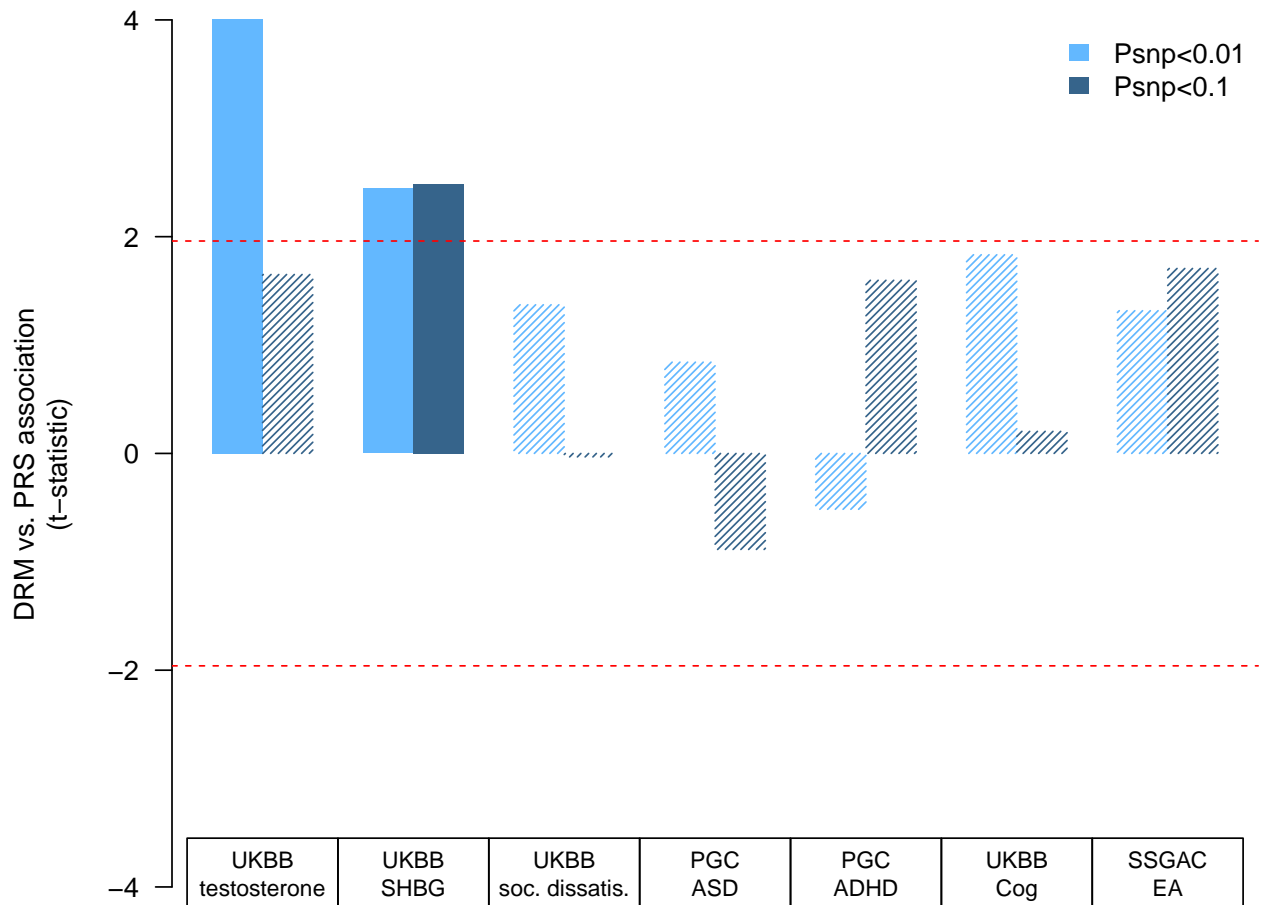
### assemble the t-statistics and arrange for the barplot
p1 = cbind(drm=cfdrm[grep("0\\.1$",rownames(cfdrm)),3],
           flm=cfflm[grep("0\\.1$",rownames(cfflm)),3],
           F9=cfsoc[grep("0\\.1$",rownames(cfsoc)),3])
p01 = cbind(drm=cfdrm[grep("0\\.01$",rownames(cfdrm)),3],
            flm=cfflm[grep("0\\.01$",rownames(cfflm)),3],
            F9=cfsoc[grep("0\\.01$",rownames(cfsoc)),3])

### this is what will be plotted
pdrm = cbind(p01[,1],p1[,1])
pflm = cbind(p01[,2],p1[,2])
psoc = cbind(p01[,3],p1[,3])

### helper function to pattern fill according to significance
fdens = function(x) ifelse(t(abs(x))>=1.96),-1,30)
### define colors and labels
cc = c("steelblue1","steelblue4")
plab = c("UKBB\\ntestosterone","UKBB\\nSHBG","UKBB\\nsoc. dissatis.", "PGC\\nASD", "PGC\\nADHD", "UKBB\\nCog", "S
```

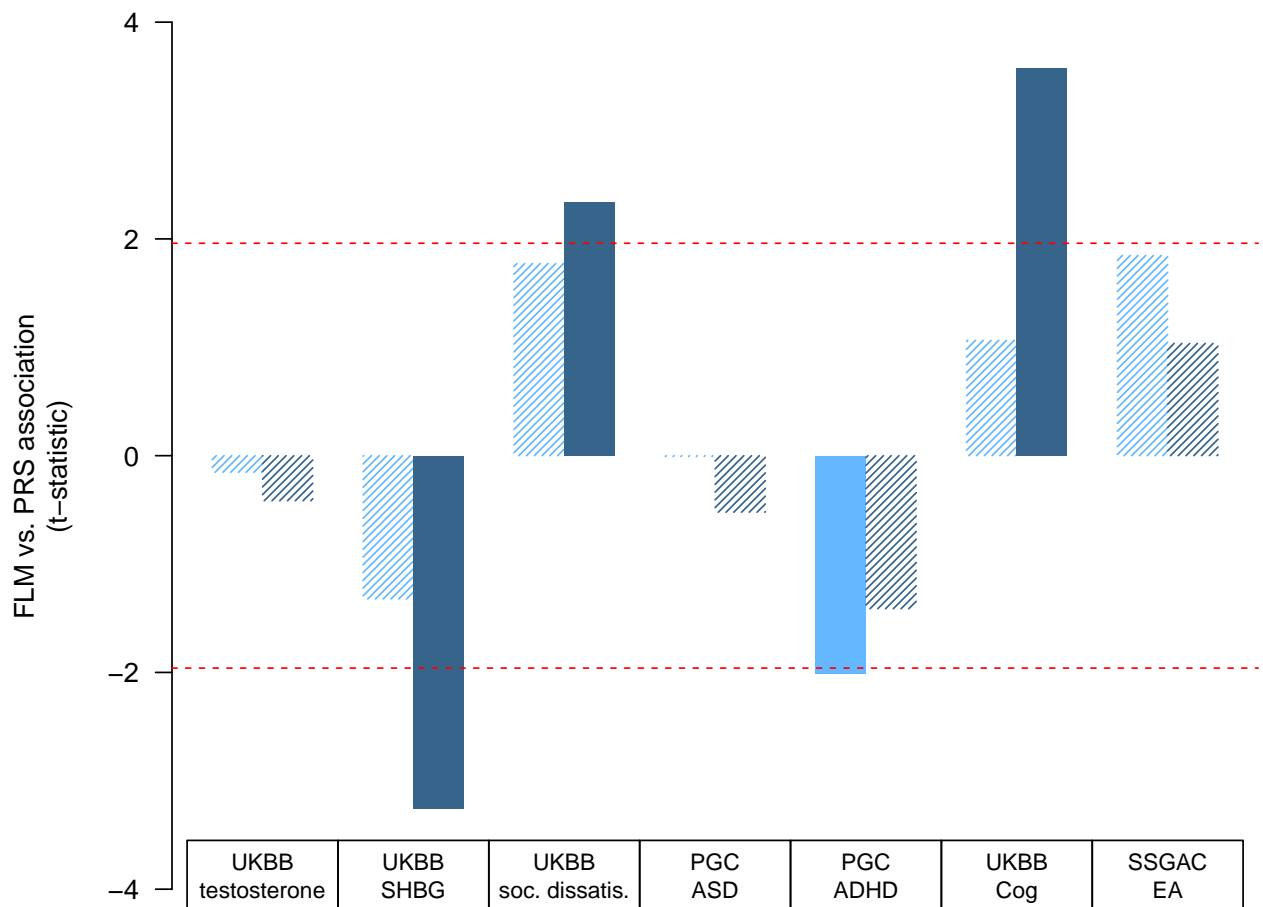
Digit Ratio Masculinity

```
par(mar=c(1,5,2,2))
bp = barplot(t(pdrm),
  beside=T,
  las=2,
  ylim=c(-4.2,4),
  names.arg=rep("",7),
  density=fdens(pdrm),
  col=cc,border=NA,
  legend.text=c("Psn<0.01","Psn<0.1"),
  args.legend=list(x="topright",bty='n',border=NA,density=-1),
  ylab="DRM vs. PRS association\n(t-statistic)")
rect(t(bp)[,1]-1,-4.20,t(bp)[,2]+1,-3.55)
text(bp[1,]+0.5,rep(-3.88,7),plab,cex=0.85)
abline(h=c(-1.96,1.96),col='red',lty=2)
```



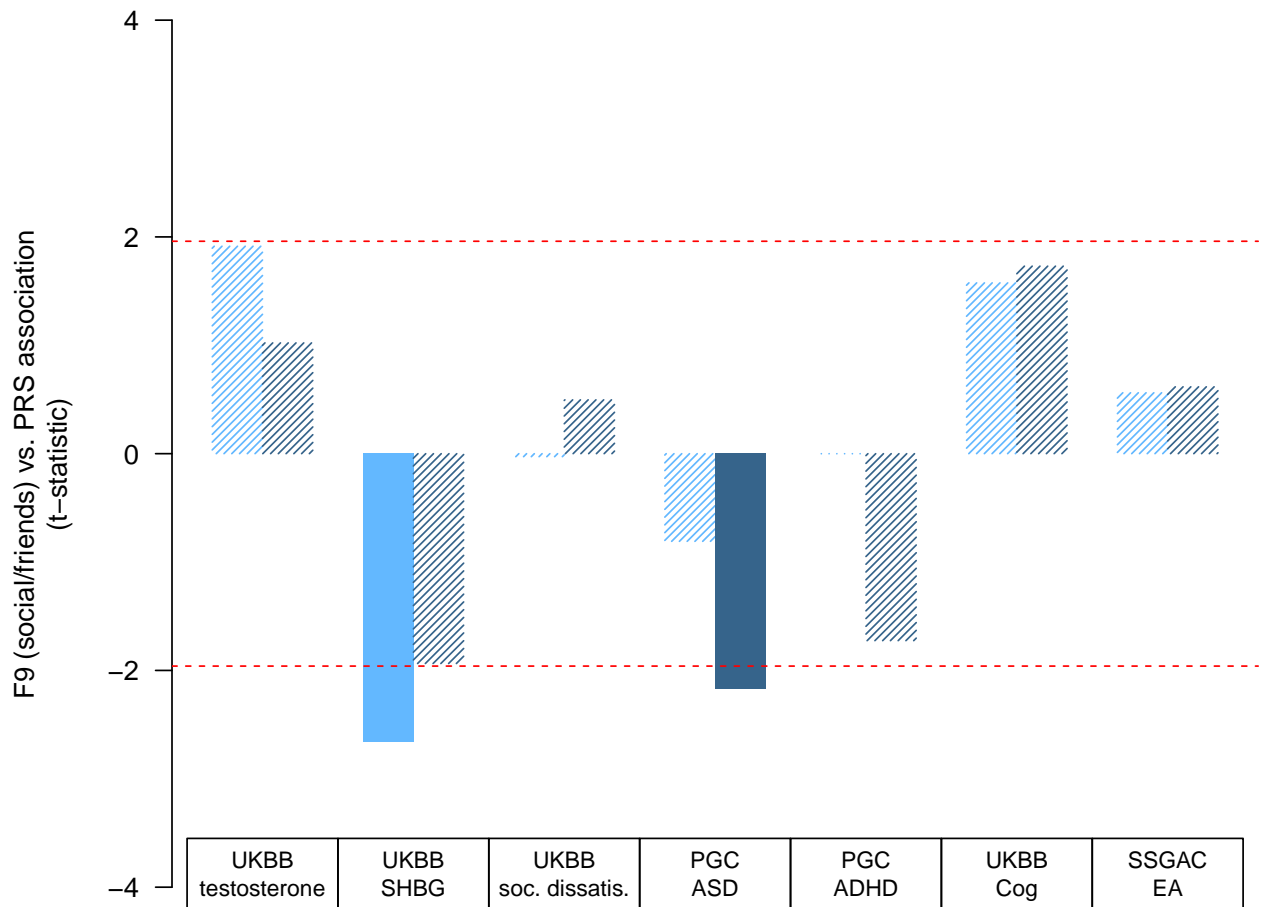
Facial Landmark Masculinity

```
par(mar=c(1,5,2,2))
barplot(t(pflm),
  beside=T,
  las=2,
  ylim=c(-4.2,4),
  names.arg=rep("",7),
  density=fdens(pflm),
  col=cc,border=NA,
  ylab="FLM vs. PRS association\n(t-statistic)")
abline(h=c(-1.96,1.96),col='red',lty=2)
rect(t(bp)[,1]-1,-4.20,t(bp)[,2]+1,-3.55)
text(bp[1,]+0.5,rep(-3.88,7),plab,cex=0.85)
```



Factor 9 (social)

```
par(mar=c(1,5,2,2))
barplot(t(psoc),
  beside=T,
  las=2,
  ylim=c(-4.2,4),
  names.arg=rep("",7),
  density=fdens(psoc),
  col=cc,border=NA,
  ylab="F9 (social/friends) vs. PRS association\n(t-statistic)")
abline(h=c(-1.96,1.96),col='red',lty=2)
rect(t(bp)[,1]-1,-4.20,t(bp)[,2]+1,-3.55)
text(bp[1,]+0.5,rep(-3.88,7),plab,cex=0.85)
```



Right: Categorical PRS Comparison

```
## set up colors, layout, and labels
par(mfrow=c(3,2),mar=c(4,4,3,2))
cc1 = colorRampPalette(c("ivory", "orangered1"))(3)
cc2 = colorRampPalette(c("ivory", "paleturquoise3"))(3)
nn = c("bottom 20%", "middle 60%", "top 20%")

boxplot(dat$Zdrm~prs[,1],
        names=nn,
        ylab="DRM",
        main="testosterone PRS",
        col=cc1)
boxplot(dat$Zdrm~prs[,9],
        names=nn,
        ylab="DRM",
        main="SHBG PRS",
        col=cc2)
boxplot(dat$Zflm~prs[,1],
        names=nn,
        ylab="FLM",
        main="testosterone PRS",
        col=cc1)
boxplot(dat$Zflm~prs[,9],
        names=nn,
        ylab="FLM",
        main="SHBG PRS",
        col=cc2)
boxplot(S[,9]~prs[,1],
        names=nn,
        ylab="Factor 9 (social)",
        main="testosterone PRS",
        col=cc1)
boxplot(S[,9]~prs[,9],
        names=nn,
        ylab="Factor 9 (social)",
        main="SHBG PRS",
        col=cc2)
```

