Mphar_Amel

Loading libraries, themes

Loading previous results

```r
setwd("~/GitHub/devnetwork/")
load("results/DEtests.RData")
load("results/collectedPhylo.RData")
antPlaid <- read.csv("results/antPlaidGenes.csv")
beePlaid <- read.csv("results/beePlaidGenes.csv")
tau <- read.csv("results/bee_tau.csv")
sexGenes <- read.csv("results/dmel_sexGenes.csv")
antConn <- read.csv("results/antConnectivity.csv")
beeConn <- read.csv("results/beeConnectivity.csv")

beeT <- read.table("data/bees.tpm.txt",header=TRUE)
antT <- read.table("data/ants.tpm.txt",header=TRUE)
modifyDF <- function(data){
  rownames(data)=data[,1]
  return(data[!grepl("ERCC",rownames(data)),-c(1)])
}
beeT <- modifyDF(beeT)
antT <- modifyDF(antT)
antT = antT[rowSums(antT) > 0,]
beeT = beeT[rowSums(beeT) > 0,]

TGmap <- read.table("phylostratigraphy/out/TGmap_Amel.txt")
TNmap <- as.data.frame(fread("data/AmelTranName.txt",sep="~",header=FALSE))

AmelName <- merge(TGmap,TNmap,by.x = "V2",by.y = "V1")[,c(2,3)]
```

```
## Warning in merge.data.frame(TGmap, TNmap, by.x = "V2", by.y = "V1"): column
## name 'V2' is duplicated in the result
```

```r
colnames(AmelName) = c("Gene","GeneName")
AmelName$GeneName = gsub(" isoform X[0-9]","",AmelName$GeneName)
aName = AmelName[!duplicated(AmelName$Gene),]
```

0.1 Number of times a gene is queen- and worker-biased across development

```r
#Summarize number of times DE
sumDE <- function(dfDE,type1,type2){
  dfDE$numQueen = apply(dfDE[,c(2:ncol(dfDE))],1,function(x) sum(x == type1))
  dfDE$numWorker = apply(dfDE[,c(2:ncol(dfDE))],1,function(x) sum(x == type2))
  d = table(dfDE$numQueen,dfDE$numWorker)
  m = melt(d)
  colnames(m)[c(1,2)] = c(type1,type2)
  return(m)
}
```

```
m1 = sumDE(antRes[[2]],"queen","worker")
m2 = sumDE(beeRes[[2]],"queen","worker")

#Add these since there are no genes DE all five times in Apis
m2E = t(sapply(seq(0,5),function(i) c(queen=i,worker=5,value=0)))
m2Eb = t(sapply(seq(0,5),function(i) c(queen=5,worker=i,value=0)))
m2E = rbind(m2Eb,m2E)
m2 = rbind(m2,m2E)

m1$species = "M. pharaonis"
m2$species = "A. mellifera"
mA = rbind(m1,m2)
mA$species = factor(mA$species,levels= c("M. pharaonis","A. mellifera"))


#Create heatmap of differential expression (number of times DE for queens and workers)
p <- ggplot(mA,aes(x=queen,y=worker))+
  geom_tile(aes(fill = value))+
  facet_grid(. ~ species)+
  scale_fill_gradient(name = "number of genes",trans = "log",
                      breaks = c(1,10,100,1000),
                      limits = c(1,10000),
                      labels = c(1,10,100,1000))+
  geom_text(aes(x = queen,y = worker,label = value),color="white")+
  main_theme+
  scale_y_continuous(name = "number of times worker-biased",
                     breaks  = seq(0,5),
                     expand = c(0,0))+
  scale_x_continuous(name = "number of times queen-biased",
                     breaks = seq(0,5),
                     expand = c(0,0))+
  theme(legend.position = "right",
        axis.line=element_line(color="black"),
        axis.text = element_text(size=16),
        axis.title = element_text(size = 22,face="bold"),
        strip.text = element_text(size=22,face="bold"),
        legend.title = element_blank(),
        strip.background = element_rect(color=NA,fill=NA),
        plot.title = element_text(hjust = 0.5,size=25,face = "bold"),
        panel.border = element_rect(size = 1, color = "black",fill = NA))
```
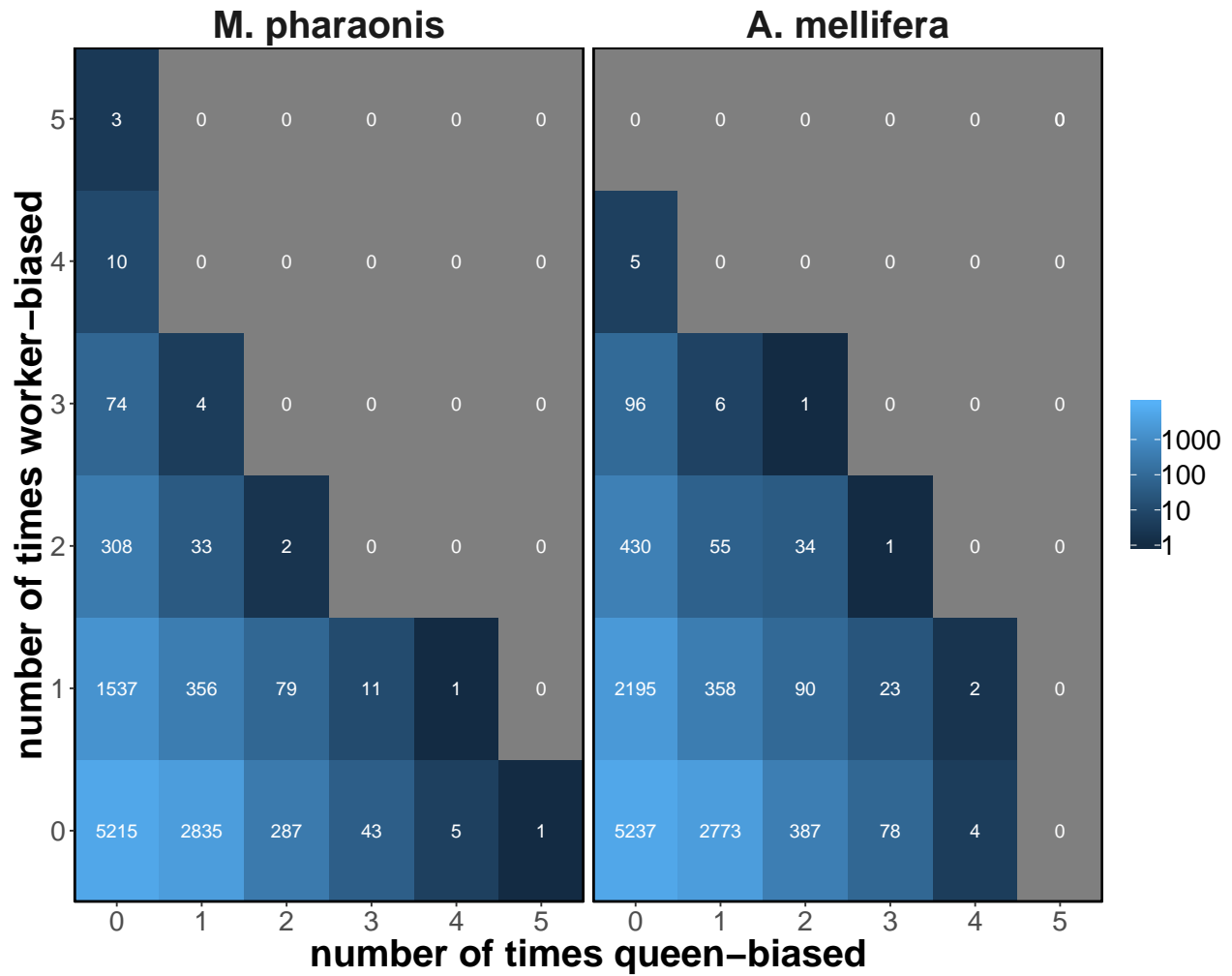
0.1 Number of times a gene is queen- and worker-biased across development

```
## Warning: Transformation introduced infinite values in discrete y-axis
```

0.2 Correlation of log fold-change across stages

```r
#Correlation of log fold change across development
lfcCor <- function(antD,beeD){
  nStage = ncol(antD) - 1
  antD <- merge(antD,ACUogg,by.x = "Gene",by.y = "gene_Mphar")
  beeD <- merge(beeD,ACUogg,by.x = "Gene",by.y = "gene_Amel")
  antD = antD[antD$OGG %in% beeD$OGG,]
  beeD = beeD[beeD$OGG %in% antD$OGG,]
  antD = antD[order(antD$OGG),]
  beeD = beeD[order(beeD$OGG),]
  d = data.frame(stage = colnames(antD)[c(2:(nStage+1))])
  dAbs = data.frame(stage = colnames(antD)[c(2:(nStage+1))])
  for (i in 1:nStage){
    t = cor.test(antD[,i+1],beeD[,i+1])
    d[i,2] = t$estimate
    d[i,3] = t$conf.int[1]
    d[i,4] = t$conf.int[2]
    t = cor.test(abs(antD[,i+1]),abs(beeD[,i+1]))
    dAbs[i,2] = t$estimate
```

```
    dAbs[i,3] = t$conf.int[1]
    dAbs[i,4] = t$conf.int[2]
  }
  colnames(d) = colnames(dAbs) = c("Stage","cor","c1","c2")
  return(list(d,dAbs))
}
CasteCor <- lfcCor(antRes[[1]],beeRes[[1]])
CasteCor_allStage <- lfcCor(antRes_allstage[[1]],beeRes_allstage[[1]])
BehavCor <- lfcCor(antSocRes[[1]],beeSocRes[[1]])

CasteCor[[1]]$Stage = as.character(CasteCor[[1]]$Stage)
CasteCor[[1]]$Stage[1] = "larva*"
CasteCor_allStage[[1]]$Stage = c("L2","L3","L4","L5","pupa","head","thorax","abdomen")
BehavCor[[1]]$Stage = c("head","thorax","abdomen")
CasteCor[[1]]$Stage = factor(CasteCor[[1]]$Stage,levels = CasteCor[[1]]$Stage)
CasteCor_allStage[[1]]$Stage = factor(CasteCor_allStage[[1]]$Stage,levels = CasteCor_allStage[[1]]$Stag
BehavCor[[1]]$Stage = factor(BehavCor[[1]]$Stage,levels = BehavCor[[1]]$Stage)


pl <- lapply(list(CasteCor[[1]],CasteCor_allStage[[1]],BehavCor[[1]]), function(x){
  ggplot(x,aes(x = Stage,y=cor))+
    geom_bar(stat="identity")+main_theme+
    xlab("stage/tissue")+
    geom_errorbar(aes(ymin=c1,ymax=c2),width=0.2)+
    ylab("correlation of queen/worker\nlog2 fold-change")+
    theme(plot.margin=unit(c(0.5,1.5,0.5,0.5),"cm"),
          axis.text.x = element_text(hjust=0,angle=-25))
})
pl[[3]] = pl[[3]] + ylab("correlation of nurse/forager\nlog2 fold-change")
```
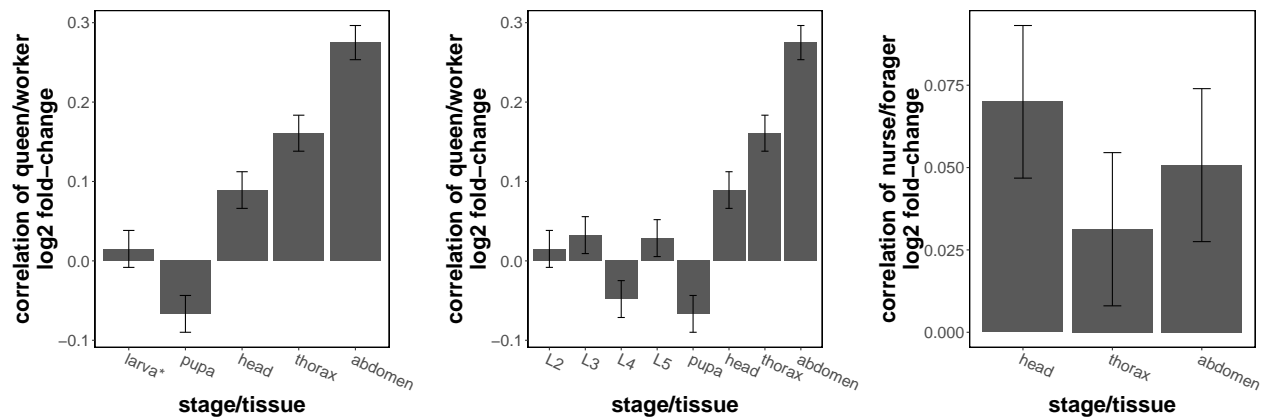
0.2 Correlation of log fold-change across stages

1.1 Caste-bias across development

```
compDef <- function(antR,beeR){

  #Define whether or not orthologs exist
  antR$ortholog_found = antR$OGG_found = FALSE
  antR$ortholog_found[antR$Gene %in% AllPS$Gene.x] = TRUE
  antR$OGG_found[antR$Gene %in% ACUogg$gene_Mphar] = TRUE
```

4

```r
    aM = melt(antR,id.vars = c("Gene","ortholog_found","OGG_found"))
    aD = ddply(aM,~variable,summarize,
               NDE = sum(value=="nonDE"),
               no_ortholog = sum(value!="nonDE" & !ortholog_found),
               dup = sum(value!="nonDE" & ortholog_found & !OGG_found),
               OGG = sum(value!="nonDE" & OGG_found))

    #Do same thing for apis
    beeR$ortholog_found = beeR$OGG_found = FALSE
    beeR$ortholog_found[beeR$Gene %in% AllPS$Gene.y] = TRUE
    beeR$OGG_found[beeR$Gene %in% ACUogg$gene_Amel] = TRUE
    bM = melt(beeR,id.vars = c("Gene","ortholog_found","OGG_found"))
    bD = ddply(bM,~variable,summarize,
               NDE = sum(value=="nonDE"),
               no_ortholog = sum(value!="nonDE" & !ortholog_found),
               dup = sum(value!="nonDE" & ortholog_found & !OGG_found),
               OGG = sum(value!="nonDE" & OGG_found))
    colnames(bM)[5] = "value_apis"

    #Getting all results together, tabulating
    aM = merge(aM[,-c(2,3)], ACUogg,by.x="Gene",by.y="gene_Mphar")
    bM = merge(bM[,-c(2,3)], ACUogg,by.x="Gene",by.y="gene_Amel")
    allM = merge(aM,bM,by=c("OGGacu","variable"))
    allD = ddply(allM,~variable,summarize,
                 DEboth = sum(value_apis!="nonDE" & value != "nonDE"))

    #Calculate number of genes which are DE, have ortholog, and aren't commonly DEG
    aD$DEboth = bD$DEboth = allD$DEboth
    aD$OGG = aD$OGG - aD$DEboth
    bD$OGG = bD$OGG - bD$DEboth

    aDM = melt(aD,id.vars = "variable")
    bDM = melt(bD,id.vars = "variable")
    colnames(aDM) = colnames(bDM) = c("stage","DEtype","value")
    aDM$species = "ant"
    bDM$species = "bee"

    #Get data back together
    d = rbind(aDM,bDM)
    d$species=as.factor(d$species)
    levels(d$species) = c("M. pharaonis","A. mellifera")
    levels(d$DEtype) = c("NDE","no ortholog","paralogs present","ortholog present,\nnon-conserved caste-bi
    return(d)
}

d = compDef(antRes[[2]],beeRes[[2]])

levels(d$stage)[1] = "larva*"

levels(d$species) = c("ant","bee")
p1m <- ggplot(d[d$DEtype!="NDE",],
              aes(x = stage, y = value, fill = DEtype))+
    geom_bar(stat="identity")+
```

```r
  plot2theme+
  ylim(0,5500)+
  facet_grid(. ~ species)+
  xlab("stage/tissue")+
  scale_fill_manual(values = DE_palette[c(3,5,7,9)])+
  ylab("number of\ncaste-biased genes")+
  theme(axis.text.x = element_text(angle=-25,hjust=0.1),
        legend.position = "top",
        strip.text = element_text(size=22,face="bold"),
        legend.title = element_blank(),
        strip.background = element_rect(color=NA,fill=NA),
        plot.margin = margin(0.5,2,0.5,0.5,"cm"))+
  theme(panel.spacing = unit(2, "lines"))

p2 <- ggplot(d[d$DEtype!="NDE" & d$species=="ant",],
             aes(x = stage, y = value, fill = DEtype))+
  geom_bar(stat="identity",position = "fill")+
  main_theme+
  scale_fill_manual(values = DE_palette[c(3,5,7,9)])+
  theme(axis.text = element_text(size = 8.5),axis.ticks = element_blank())+
  xlab("")+
  ylab("proportion")+
  scale_y_continuous(breaks = c(0,0.5,1))+
  theme(axis.text.x = element_blank(),
        axis.ticks.x = element_blank(),
        rect = element_rect(fill="transparent"),
        legend.position = "none",
        panel.border = element_blank(),
        panel.background = element_blank(),
        legend.title = element_blank(),
        axis.title.y = element_text(margin=margin(t=0,r=0,l=0,b=0)),
        axis.text.y = element_text(margin=margin(t=0,r=-3,l=0,b=0)),
        axis.title = element_text(size=10),
        plot.margin = margin(0,0,0,0,"cm"))


p3 <- ggplot(d[d$DEtype!="NDE" & d$species=="bee",],
             aes(x = stage, y = value, fill = DEtype))+
  geom_bar(stat="identity",position = "fill")+
  main_theme+
  theme(axis.text = element_text(size = 8.5),axis.ticks = element_blank())+
  xlab("")+
  scale_fill_manual(values = DE_palette[c(3,5,7,9)])+
  ylab("proportion")+
  scale_y_continuous(breaks = c(0,0.5,1))+
  theme(axis.text.x = element_blank(),
        axis.ticks.x = element_blank(),
        rect = element_rect(fill="transparent"),
        legend.position = "none",
        panel.border = element_blank(),
        panel.background = element_blank(),
        legend.title = element_blank(),
        axis.title.y = element_text(margin=margin(t=0,r=0,l=0,b=0)),
```
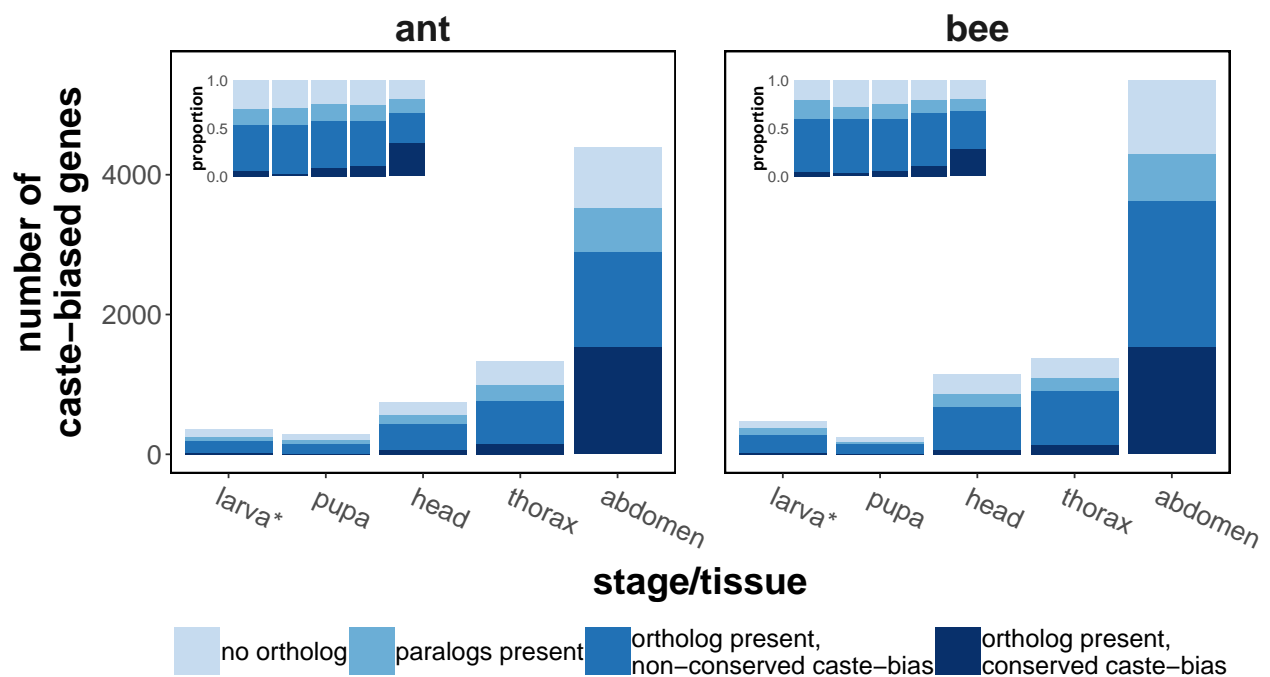
```
        axis.text.y = element_text(margin=margin(t=0,r=-3,l=0,b=0)),
        axis.title = element_text(size=10),
        plot.margin = margin(0,0,0,0,"cm"))

pQ <- ggdraw()+
  draw_plot(p1m+
              theme(legend.text = element_text(size=15),
                    legend.key.width = unit(1,"cm"),
                    legend.position = "bottom"))+
  draw_plot(p2,x=0.15,y=0.69,height=0.18,width=0.18)+
  draw_plot(p3,x=0.57,y=0.69,height=0.18,width=0.18)
```

1.1 Caste bias across development

1.2 Nurse/forager bias

```
d = compDef(antSocRes[[2]],beeSocRes[[2]])

p1 <- ggplot(d[d$DEtype!="NDE",],
             aes(x = stage, y = value, fill = DEtype))+
  geom_bar(stat="identity")+
  main_theme+
  xlab("tissue")+
  ylim(0,4500)+
  facet_grid(. ~ species)+
  scale_fill_manual(values = DE_palette[c(3,5,7,9)])+
  ylab("number of behavior-biased genes")+
  theme(axis.text.x = element_text(angle=-25,hjust=0.1),
        legend.position = "top",
```

```r
          strip.text = element_text(size=20,face="bold.italic"),
          axis.title.y=element_text(margin=margin(t=0,l=0,r=10,b=0)),
          legend.title = element_blank(),
          strip.background = element_rect(color="black",fill="darkgrey"),
          plot.margin = margin(0,2,2,2,"cm"))

p2 <- ggplot(d[d$DEtype!="NDE" & d$species=="M. pharaonis",],
             aes(x = stage, y = value, fill = DEtype))+
  geom_bar(stat="identity",position = "fill")+
  main_theme+
  scale_fill_manual(values = DE_palette[c(3,5,7,9)])+
  theme(axis.text = element_text(size = 8.5),axis.ticks = element_blank())+
  xlab("")+
  ylab("proportion")+
  scale_y_continuous(breaks = c(0,0.5,1))+
  theme(axis.text.x = element_blank(),
        axis.ticks.x = element_blank(),
        rect = element_rect(fill="transparent"),
        legend.position = "none",
        panel.border = element_blank(),
        panel.background = element_blank(),
        legend.title = element_blank(),
        axis.title.y = element_text(margin=margin(t=0,r=0,l=0,b=0)),
        axis.text.y = element_text(margin=margin(t=0,r=-3,l=0,b=0)),
        axis.title = element_text(size=10),
        plot.margin = margin(0,0,0,0,"cm"))


p3 <- ggplot(d[d$DEtype!="NDE" & d$species=="A. mellifera",],
             aes(x = stage, y = value, fill = DEtype))+
  geom_bar(stat="identity",position = "fill")+
  main_theme+
  theme(axis.text = element_text(size = 8.5),axis.ticks = element_blank())+
  xlab("")+
  scale_fill_manual(values = DE_palette[c(3,5,7,9)])+
  ylab("proportion")+
  scale_y_continuous(breaks = c(0,0.5,1))+
  theme(axis.text.x = element_blank(),
        axis.ticks.x = element_blank(),
        rect = element_rect(fill="transparent"),
        legend.position = "none",
        panel.border = element_blank(),
        panel.background = element_blank(),
        legend.title = element_blank(),
        axis.title.y = element_text(margin=margin(t=0,r=0,l=0,b=0)),
        axis.text.y = element_text(margin=margin(t=0,r=-3,l=0,b=0)),
        axis.title = element_text(size=10),
        plot.margin = margin(0,0,0,0,"cm"))

pSoc <- ggdraw()+
  draw_plot(p1+
              theme(legend.text = element_text(size=13),
                    legend.key.width = unit(1,"cm")))+
```
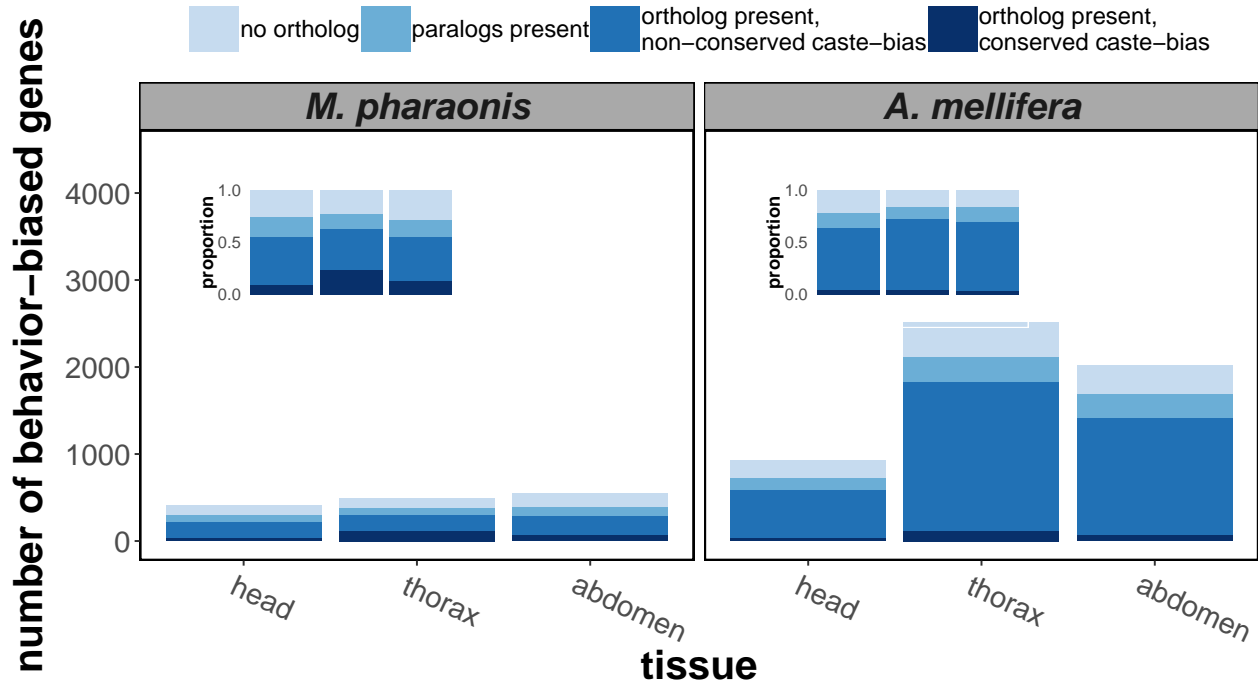
```
    draw_plot(p2,x=0.2,y=0.58,height=0.18,width=0.18)+
    draw_plot(p3,x=0.59,y=0.58,height=0.18,width=0.18)
```

1.2 nurse/forager bias

1.3 Phylostrata of genes with conserved abdominal caste bias

```
psO = merge(AllPS_sum,ACUogg,by="OGGacu")
psO$a2 = "non-DE/non-conserved"

#Find genes with conserved queen or worker bias
psO$a2[psO$gene_Amel %in% beeRes[[2]]$Gene[beeRes[[2]]$abdomen=="worker"] &
       psO$gene_Mphar %in% antRes[[2]]$Gene[antRes[[2]]$abdomen=="worker"]] = "conserved worker"
psO$a2[psO$gene_Amel %in% beeRes[[2]]$Gene[beeRes[[2]]$abdomen=="queen"] &
       psO$gene_Mphar %in% antRes[[2]]$Gene[antRes[[2]]$abdomen=="queen"]] = "conserved queen"

levels(psO$psName)[1] = "ancient"

p <- ggplot(psO,aes(x = a2,fill = forcats::fct_rev(psName)))+
  ylab("proportion")+
  geom_bar(stat = "count",position = "fill")+
  scale_fill_manual(values = mypalette2[c(2,4,5,6)],name = "phylostrata")+
  main_theme+
  coord_flip()+
  xlab("abdominal DEG type")+
  scale_x_discrete(expand=c(0,0))+
  guides(fill = guide_legend(reverse=T))+
  scale_y_continuous(expand=c(0,0))+
```
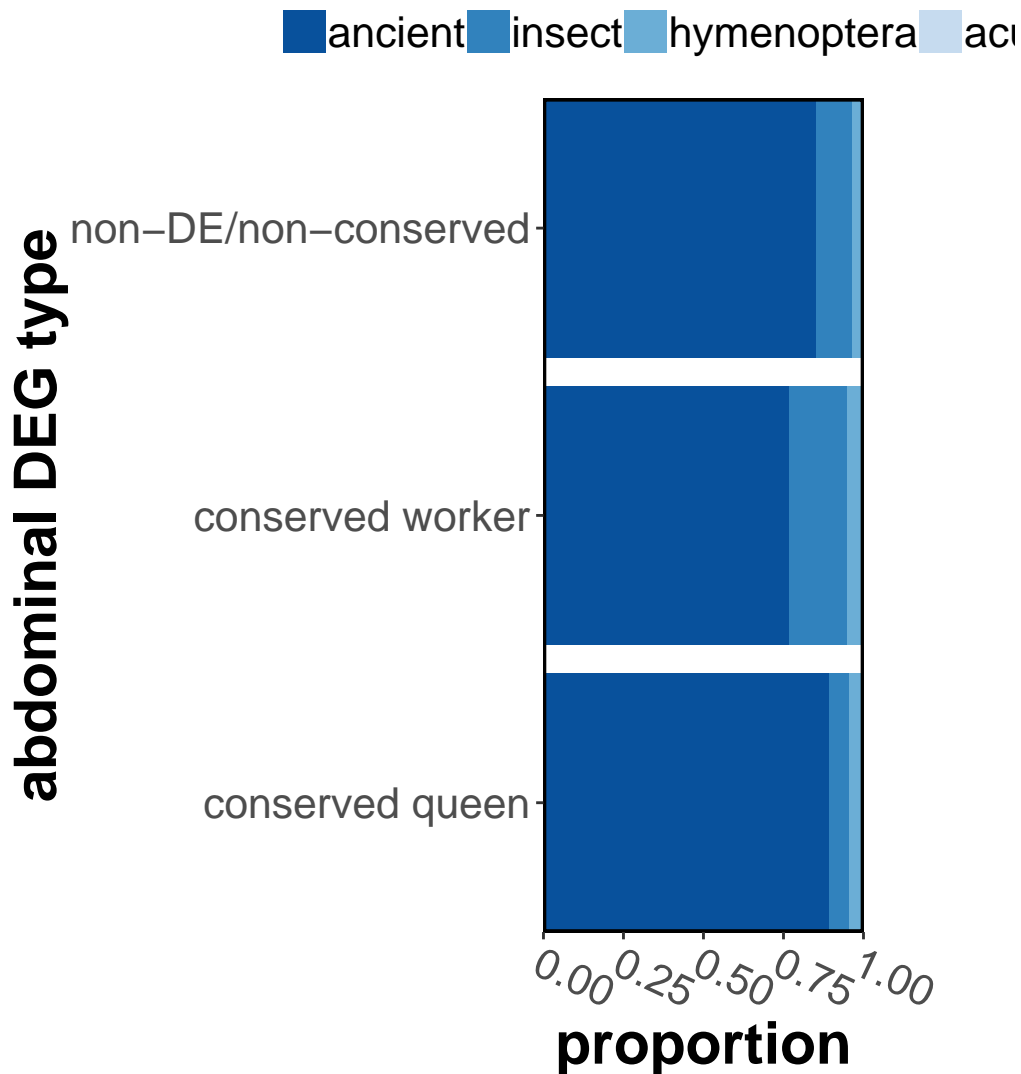
```
theme(axis.text.x = element_text(angle=-25,hjust=0),
      legend.position = "top",
      legend.title = element_blank(),
      plot.margin = unit(c(0.5,2,0.5,2),"cm"))
```

1.3 Estimated evolutionary age of genes with abdominal caste bias

2.1 Bicluster associated with queen abdominal expression

-Previously performed plaid clustering and extracted genes commonly found in a queen abdomen-specific bicluster.

```
#Find out what the genes are
antGrC = merge(antPlaid,Aps,by="Gene")
beeGrC = merge(beePlaid,Bps,by="Gene")
antGrC$species = "ant"
beeGrC$species = "bee"
```

```
#Make general plot
allC = rbind(antGrC,beeGrC)
allC$DEcat = factor(allC$DEcat,levels = c("queen","worker","non-DE"))

#Note -abdomen because we want queen genes to be upregulated
p1 <- ggplot(allC,aes(x = conn,y=-abdomen))+
  geom_point(aes(fill = DEcat),pch=21,color="black")+
  scale_fill_manual(values = SexPal[c(1,2,5)],name="DEG type")+
  scale_alpha_continuous(guide="none")+
  ylab("abdominal caste bias")+
  xlab("scaled connectivity in abdominal module")+
  plot2theme+
  facet_grid(. ~ species)+
  theme(panel.spacing = unit(2, "lines"))+
  guides(fill = guide_legend(override.aes = list(size=4)))+
  scale_x_log10()+
  theme(legend.position ="none",
        legend.text = element_text(size=15),
        strip.text = element_text(size=22,face="bold"),
        axis.title.y=element_text(margin=margin(t=0,l=0,r=10,b=0)),
        legend.title = element_blank(),
        plot.margin = unit(rep(1,4),"cm"),
        strip.background = element_rect(color=NA,fill=NA))

p1
```
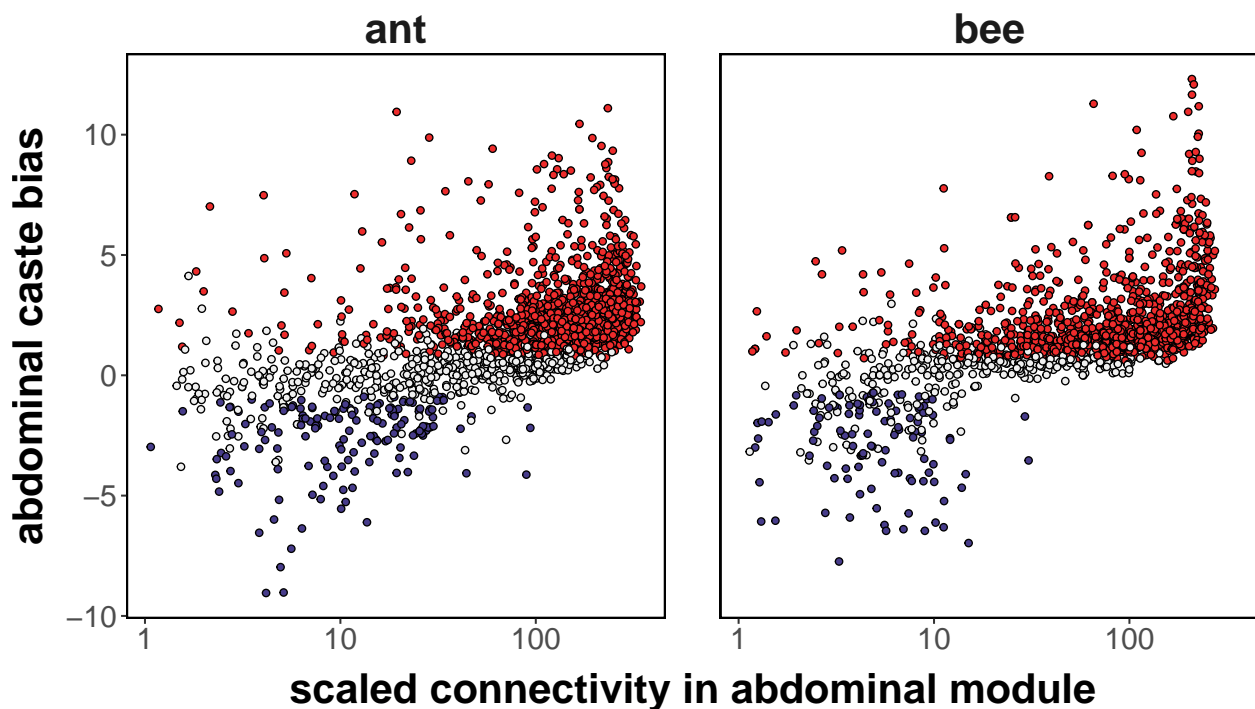

2.2 Specific genes within the bicluster

- holding off plotting specific genes for now

```r
beeAnn <- read.csv("data/Amel_Gene_Names.csv")
ann <- read.csv("data/MpharAnn.csv")

#Pick genes with connectivity in the top 90% that are four-fold upregulated in queens
antGenes = antGrC$Gene[antGrC$conn > quantile(antGrC$conn,0.9) &
                        antGrC$abdomen < -2]
beeGenes = beeGrC$Gene[beeGrC$conn > quantile(beeGrC$conn,0.9) &
                        beeGrC$abdomen < -2]
annSwiss = ann$SwissProt[ann$Gene %in% antGenes]
beeSwiss = beeAnn$GeneName[beeAnn$Gene %in% beeGenes]
```

ant Genes

```r
annSwiss[!grepl("ncharacterized",annSwiss) & annSwiss!="-"]
```

```
##    [1] JNK1/MAPK8-associated membrane protein
##    [2] Protein halfway
##    [3] Protein aubergine
##    [4] DnaJ homolog subfamily C member 2
##    [5] REST corepressor 3
##    [6] Nucleoporin GLE1
##    [7] Peroxisomal N(1)-acetyl-spermine/spermidine oxidase
##    [8] PRKCA-binding protein
##    [9] Double-strand-break repair protein rad21 homolog
##   [10] Importin subunit alpha-7
##   [11] Histone RNA hairpin-binding protein
##   [12] Protein abnormal spindle
##   [13] RNA exonuclease 4
##   [14] Enhancer of mRNA-decapping protein 3
##   [15] Probable phenylalanine--tRNA ligase alpha subunit
##   [16] N-alpha-acetyltransferase 25  NatB auxiliary subunit
##   [17] Protein CNPPD1
##   [18] Gephyrin
##   [19] FACT complex subunit spt16
##   [20] Rho GTPase-activating protein 11B
##   [21] Protein Smaug homolog 1
##   [22] Coiled-coil domain-containing protein 22 homolog
##   [23] ATP-binding cassette sub-family G member 4
##   [24] Maternal embryonic leucine zipper kinase
##   [25] Histone H2B
##   [26] Nuclear pore complex protein Nup160 homolog
##   [27] Dystrophin  isoform B
##   [28] E3 ubiquitin-protein ligase UHRF1
##   [29] Apoptosis inhibitor IAP
##   [30] CCR4-NOT transcription complex subunit 1
##   [31] Polynucleotide 5'-hydroxyl-kinase NOL9
##   [32] S-phase kinase-associated protein 2
##   [33] WD repeat-containing protein 44
##   [34] Transcriptional regulator ATRX
##   [35] Male-specific lethal 3 homolog
##   [36] U4/U6 small nuclear ribonucleoprotein Prp4
##   [37] WD repeat-containing protein 3
##   [38] Pre-mRNA 3'-end-processing factor FIP1
##   [39] Importin subunit alpha-1
```

```
##  [40] Probable DNA mismatch repair protein Msh6
##  [41] CSC1-like protein 2
##  [42] NCK-interacting protein with SH3 domain
##  [43] snRNA-activating protein complex subunit 4
##  [44] Protein dispatched
##  [45] Glycylpeptide N-tetradecanoyltransferase 1
##  [46] Probable nucleolar GTP-binding protein 1
##  [47] E3 ubiquitin-protein ligase SIAH1
##  [48] Protein TSSC4
##  [49] DNA-directed RNA polymerase I subunit RPA1
##  [50] Zinc finger protein 800
##  [51] Activated CDC42 kinase 1
##  [52] Symplekin
##  [53] Probable histone-binding protein Caf1
##  [54] Lipase 3
##  [55] Probable nucleoporin Nup58
##  [56] Ribonucleoside-diphosphate reductase large subunit
##  [57] Chromosome-associated kinesin KIF4
##  [58] COP9 signalosome complex subunit 1
##  [59] Squamous cell carcinoma antigen recognized by T-cells 3
##  [60] Integrator complex subunit 11
##  [61] Structural maintenance of chromosomes protein 5
##  [62] Macoilin
##  [63] Pogo transposable element with ZNF domain
##  [64] Zinc finger protein 346
##  [65] DNA replication licensing factor Mcm2
##  [66] Piwi-like protein 1
##  [67] HEAT repeat-containing protein 1
##  [68] Gephyrin
##  [69] Protein LSM14 homolog B
##  [70] WD repeat-containing protein 89
##  [71] Nuclear RNA export factor 1
##  [72] Cell division control protein 6 homolog
##  [73] Fanconi-associated nuclease 1
##  [74] Putative bifunctional UDP-N-acetylglucosamine transferase and deubiquitinase ALG13
##  [75] Putative ATP-dependent RNA helicase me31b
##  [76] Erythroid differentiation-related factor 1
##  [77] Mediator of RNA polymerase II transcription subunit 8
##  [78] CCR4-NOT transcription complex subunit 2
##  [79] Probable malonyl-CoA-acyl carrier protein transacylase  mitochondrial
##  [80] MKL/myocardin-like protein 1
##  [81] Phosphatidylinositide phosphatase SAC1
##  [82] STIP1 homology and U box-containing protein 1
##  [83] Ubiquitin-like-conjugating enzyme ATG3
##  [84] Glucose-fructose oxidoreductase domain-containing protein 1
##  [85] Protein misato
##  [86] Serine/threonine-protein kinase 3
##  [87] Zinc finger protein-like 1
##  [88] Nuclear RNA export factor 1
##  [89] Methionine--tRNA ligase  cytoplasmic
##  [90] Cytoplasmic phosphatidylinositol transfer protein 1
##  [91] Glyoxylate reductase
##  [92] Histone H2B
##  [93] LisH domain and HEAT repeat-containing protein KIAA1468 homolog
```

```
##    [94] RCC1 and BTB domain-containing protein 1
##    [95] BRCA1-associated protein
##    [96] Rho GTPase-activating protein 19
##    [97] Digestive organ expansion factor homolog
##    [98] tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6
##    [99] Transcription factor SPT20 homolog
## [100] Serine protease nudel
## [101] Ubiquitin-conjugating enzyme E2 5A
## [102] Rab5 GDP/GTP exchange factor
## [103] Serine/threonine-protein phosphatase 2A regulatory subunit B'' subunit gamma
## [104] Protein brambleberry
## [105] Cell division cycle protein 27 homolog
## [106] Probable E3 ubiquitin-protein ligase makorin-1
## [107] Segment polarity protein dishevelled homolog DVL-3
## [108] DNA replication complex GINS protein PSF2
## [109] GPI mannosyltransferase 4
## [110] Protein FAM60A
## [111] ATP-dependent RNA helicase Ddx1
## [112] Leukocyte elastase inhibitor A
## [113] Rac GTPase-activating protein 1
## [114] DNA repair and recombination protein RAD54-like (Fragment)
## [115] DNA mismatch repair protein Msh2
## [116] Sentrin-specific protease 1
## [117] Maternal protein tudor
## [118] Nucleoporin NDC1
## [119] Ankyrin-2
## [120] Metallophosphoesterase 1
## [121] Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16
## [122] Serine/threonine-protein phosphatase 6 catalytic subunit
## [123] UPF0586 protein C9orf41 homolog
## [124] Ubiquitin carboxyl-terminal hydrolase 36
## [125] Nucleoporin NUP53
## [126] Macrophage erythroblast attacher
## [127] Multiple PDZ domain protein
## [128] Structural maintenance of chromosomes protein 6
## [129] U1 small nuclear ribonucleoprotein 70 kDa
## [130] Cullin-associated NEDD8-dissociated protein 1
## [131] Microspherule protein 1
## [132] Transcription factor SOX-14
## [133] Zinc finger protein 184
## [134] Pyridine nucleotide-disulfide oxidoreductase domain-containing protein 1
## [135] Cell division cycle 5-like protein
## [136] Spondin-1
## [137] Brahma-associated protein of 60 kDa
## [138] Broad-complex core protein isoform 6
## [139] DNA polymerase alpha catalytic subunit
## [140] Probable ATP-dependent RNA helicase DDX43
## [141] Tudor domain-containing protein 5
## [142] G2/M phase-specific E3 ubiquitin-protein ligase
## [143] Putative tRNA (cytidine(32)/guanosine(34)-2'-O)-methyltransferase
## [144] Eukaryotic translation initiation factor 3 subunit C
## [145] N-acetyltransferase 10
## [146] G2/mitotic-specific cyclin-B3
## [147] N6-adenosine-methyltransferase subunit METTL3
```

```
## [148] Rho guanine nucleotide exchange factor 3
## [149] Importin-4
## [150] Rho GTPase-activating protein 18
## [151] ATP-dependent RNA helicase vasa  isoform A
## [152] Checkpoint protein HUS1
## [153] Pre-mRNA-splicing factor RBM22
## [154] Transmembrane protein 209
## [155] Translation initiation factor eIF-2B subunit delta
## [156] Protein ariadne-2
## [157] Acidic repeat-containing protein
## [158] ATPase family AAA domain-containing protein 5
## 7725 Levels:  Pyruvate dehydrogenase  acetyl-transferring  -phosphatase 1  mitochondrial ...
```

bee Genes

```
beeSwiss[!grepl("ncharacterized",beeSwiss) & beeSwiss!="-"]
```

```
##  [1] ATP-dependent RNA helicase vasa
##  [2] PREDICTED: kinesin-like protein KIF18A
##  [3] PREDICTED: prion-like-(Q/N-rich) domain-bearing protein 25
##  [4] PREDICTED: disks large-associated protein 5-like
##  [5] PREDICTED: E3 ubiquitin-protein ligase TRIM71
##  [6] PREDICTED: zinc finger protein 470-like
##  [7] PREDICTED: CDC42 small effector protein homolog
##  [8] PREDICTED: NF-kappa-B inhibitor cactus-like
##  [9] PREDICTED: hyaluronan mediated motility receptor
## [10] PREDICTED: ADP-ribosylation factor-like protein 1
## [11] PREDICTED: facilitated trehalose transporter Tret1-like
## [12] PREDICTED: histone H2B-like
## [13] PREDICTED: protein claret segregational
## [14] PREDICTED: dual specificity protein kinase TTK
## [15] PREDICTED: prolyl 3-hydroxylase OGFOD1
## [16] PREDICTED: targeting protein for Xklp2 homolog
## [17] PREDICTED: zinc finger protein 480
## [18] PREDICTED: kinetochore protein ndc80
## [19] PREDICTED: SET and MYND domain-containing protein 4-like
## [20] PREDICTED: rhoGEF domain-containing protein gxcJ-like
## [21] PREDICTED: helix-loop-helix protein delilah-like
## [22] PREDICTED: nucleoredoxin-like
## [23] PREDICTED: interaptin-like
## [24] PREDICTED: polycomb protein Asx
## [25] PREDICTED: F-BAR domain only protein 2
## [26] PREDICTED: glucose-6-phosphate 1-epimerase
## [27] PREDICTED: kanadaptin
## [28] PREDICTED: S-phase kinase-associated protein 2
## [29] PREDICTED: protein kintoun
## [30] PREDICTED: WW domain-containing adapter protein with coiled-coil
## [31] PREDICTED: citron Rho-interacting kinase-like
## [32] PREDICTED: maternal embryonic leucine zipper kinase-like
## [33] PREDICTED: spindle and kinetochore-associated protein 1-like, partial
## [34] PREDICTED: protein LSM14 homolog A
## [35] PREDICTED: geminin
## [36] PREDICTED: protein kinase 4-like
## [37] PREDICTED: ankyrin repeat domain-containing protein 54
## [38] PREDICTED: protein Smaug homolog 1
```

```
## [39] PREDICTED: transformation/transcription domain-associated protein
## [40] PREDICTED: serine protease gd
## [41] PREDICTED: golgin subfamily A member 6-like protein 22
## [42] PREDICTED: RWD domain-containing protein 1
## [43] PREDICTED: PERQ amino acid-rich with GYF domain-containing protein CG11148
## [44] PREDICTED: N-acetylglucosamine-1-phosphotransferase subunits alpha/beta
## [45] PREDICTED: cyclin-A2
## [46] PREDICTED: protein groucho
## [47] PREDICTED: CCR4-NOT transcription complex subunit 1
## [48] PREDICTED: enhancer of mRNA-decapping protein 3
## [49] PREDICTED: mitotic spindle assembly checkpoint protein MAD2A
## [50] PREDICTED: G2/mitotic-specific cyclin-B3
## [51] PREDICTED: micronuclear linker histone polyprotein-like
## [52] PREDICTED: polycomb protein Pcl
## [53] PREDICTED: KAT8 regulatory NSL complex subunit 1
## [54] PREDICTED: UBX domain-containing protein 7
## [55] PREDICTED: ankyrin repeat domain-containing protein 17
## [56] PREDICTED: MAU2 chromatid cohesion factor homolog
## [57] PREDICTED: macoilin
## [58] PREDICTED: probable helicase with zinc finger domain
## [59] PREDICTED: DNA replication factor Cdt1
## [60] PREDICTED: DNA repair protein complementing XP-G cells
## [61] PREDICTED: ras GTPase-activating-like protein IQGAP1
## [62] PREDICTED: histone H1.2-like
## [63] PREDICTED: protein maelstrom 2
## [64] PREDICTED: LOW QUALITY PROTEIN: protein lin-9 homolog
## [65] PREDICTED: lachesin-like
## [66] PREDICTED: protein Daple
## [67] PREDICTED: protein split ends-like
## [68] PREDICTED: LOW QUALITY PROTEIN: bromodomain-containing protein 4
## [69] PREDICTED: SPX and EXS domain-containing protein 4-like
## [70] PREDICTED: zinc finger CCHC domain-containing protein 10-like
## [71] PREDICTED: protein distal antenna
## [72] PREDICTED: vitellogenin receptor
## [73] PREDICTED: homeobox protein OTX1 A
## [74] PREDICTED: eukaryotic translation initiation factor 4E transporter
## [75] PREDICTED: E3 ubiquitin-protein ligase TRAIP-like
## [76] PREDICTED: poly(A) RNA polymerase gld-2 homolog A
## [77] PREDICTED: serine/threonine-protein kinase polo
## [78] PREDICTED: importin subunit alpha
## [79] PREDICTED: centrosomal protein of 162 kDa-like
## [80] PREDICTED: LOW QUALITY PROTEIN: meiosis arrest female protein 1
## [81] PREDICTED: protein ovo
## [82] PREDICTED: P protein-like
## [83] PREDICTED: suppressor protein SRP40
## [84] PREDICTED: male-specific lethal 1 homolog
## [85] PREDICTED: GRB2-associated-binding protein 2
## [86] PREDICTED: enolase-phosphatase E1
## [87] PREDICTED: G kinase-anchoring protein 1-like
## [88] PREDICTED: histone-lysine N-methyltransferase pr-set7
## [89] PREDICTED: myotubularin-related protein 14
## [90] PREDICTED: TATA-box-binding protein
## [91] PREDICTED: coiled-coil domain-containing protein 43
## [92] PREDICTED: serine/threonine-protein kinase VRK1-like
```

```
## [93] PREDICTED: putative ATP-dependent RNA helicase me31b
## 9976 Levels: 18-wheeler precursor ... zinc finger protein 629-like
```

3.1 Comparing caste bias to sex bias

```
extractBias <- function(DEres){
  sexQ <- rownames(DEres)[DEres$FDR < 0.1 & DEres$logFC < 0]
  sexM <- rownames(DEres)[DEres$FDR < 0.1 & DEres$logFC > 0]
  sexFC <- data.frame(Gene = rownames(DEres), FC = DEres$logFC)
  return(list(FC = sexFC,Queen = sexQ,nonQueen = sexM))
}


AsexRes <- lapply(ant_sexDE,extractBias)
AcasteRes <- lapply(antTests_oneLarv[c(3:5)],extractBias)
BsexRes <- lapply(bee_sexDE,extractBias)
BcasteRes <- lapply(beeTests_oneLarv[c(3:5)],extractBias)
```

Identify genes with conserved bias for plotting

```
ogg11 = ACUogg
ogg11$abdDE = "non-conserved/non-DE"
ogg11$abdDE[(ogg11$gene_Amel %in% BcasteRes[[3]][[2]] & ogg11$gene_Mphar %in% AcasteRes[[3]][[2]])] = "
ogg11$abdDE[(ogg11$gene_Amel %in% BcasteRes[[3]][[3]] & ogg11$gene_Mphar %in% AcasteRes[[3]][[3]])] = "
```

3.1 Construct sex bias vs caste bias plots

```
biasPlot <- function(d1,d2,spec){

  FC = merge(d1,d2,by = "Gene")
  FC = merge(FC,ogg11,by.x = "Gene",by.y=spec,all.x=TRUE)
  FC$abdDE[is.na(FC$abdDE)] = "non-conserved/non-DE"
  FC$abdDE = factor(FC$abdDE,levels = c("conserved queen","conserved worker","non-conserved/non-DE"))
  FC$alpha = 0.2
  FC$alpha[FC$abdDE!="non-conserved/non-DE"]=0.8

  p1 <- ggplot(FC,aes(x = -FC.x,y = -FC.y))+ #Queen-up will be positive
    geom_point(aes(fill = abdDE,alpha=alpha),pch=21,color="black",size=2)+
    geom_smooth(method="lm",se=FALSE,color="black")+
    scale_fill_manual(values = SexPal[c(1,2,5)],name = "abdominal caste bias")+
    guides(fill = guide_legend(override.aes = list(size=4)))+
    scale_alpha_continuous(guide="none")+
    main_theme+
    ylab("caste bias (queen/worker)")+
    xlab("sex bias (queen/male)")+
    ylim(-10,10)+xlim(-10,10)+
    theme(axis.title.y=element_text(margin = margin(t=0,l=15,r=-5,b=0)))+
    theme(legend.position="none",
          legend.text = element_text(size=17),
          legend.title = element_text(size=19,face="bold"))
```

```
    return(p1)


}

p1 = biasPlot(AsexRes[[3]][[1]],AcasteRes[[3]][[1]],"gene_Mphar")+
  ylab("ant caste bias (queen/worker)")+
  xlab("ant sex bias (queen/male)")
p2 = biasPlot(BsexRes[[3]][[1]],BcasteRes[[3]][[1]],"gene_Amel")+
  ylab("bee caste bias (queen/worker)")+
  xlab("bee sex bias (queen/male)")
grid.arrange(p1,p2,nrow=1)
```

```
## Warning: Removed 54 rows containing non-finite values (stat_smooth).

## Warning: Removed 54 rows containing missing values (geom_point).

## Warning: Removed 47 rows containing non-finite values (stat_smooth).

## Warning: Removed 47 rows containing missing values (geom_point).
```
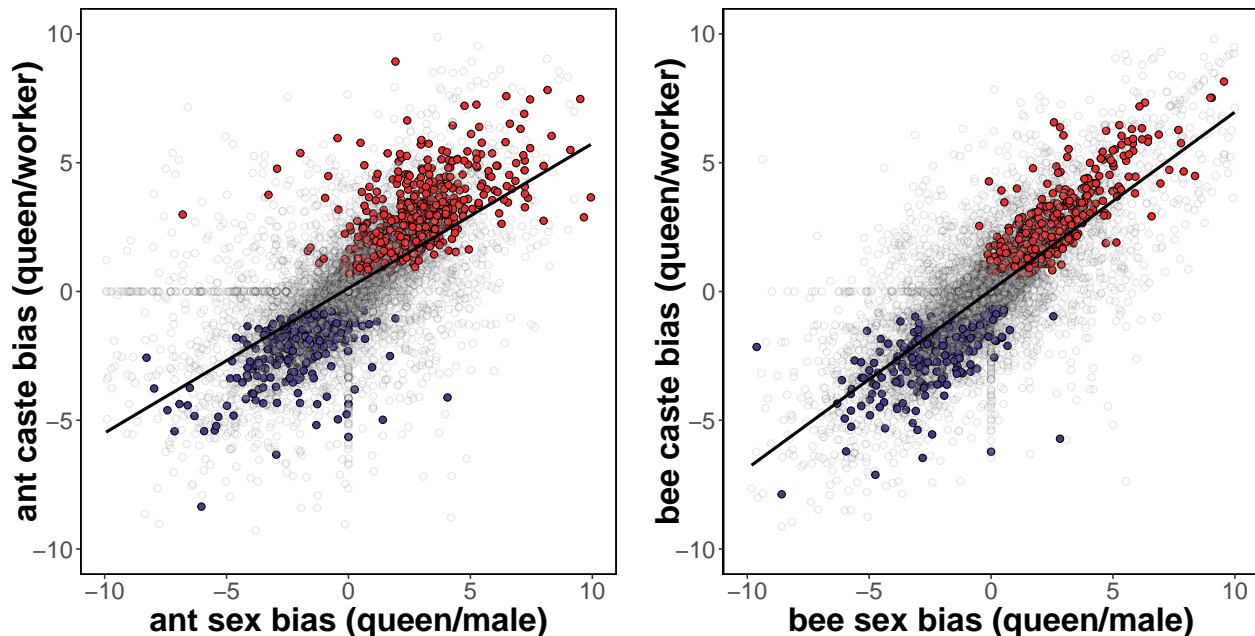

3.2 Comparison to D. melanogaster

```
DmelSC = merge(sexGenes,ogg11,by="gene_Amel")
DmelSC$abdDE = factor(DmelSC$abdDE,levels = c("conserved queen","conserved worker","non-DE/inconsistent

p4 <- ggplot(DmelSC[grepl("conserved",DmelSC$abdDE),],aes(x = abdDE,y=-logFC))+
  geom_violin(fill="grey90",trim=FALSE)+
  geom_jitter(width = 0.1,size=0.5,aes(color=abdDE))+
  geom_boxplot(width=0.05,outlier.shape = NA,fill="black",color="black",notch=TRUE,notchwidth = 0.7)+
  plot2theme+
  ylab("fly sex bias")+
  ylim(-10,10)+
  theme(axis.title.y=element_text(margin = margin(t=0,l=15,r=0,b=0)))+
```
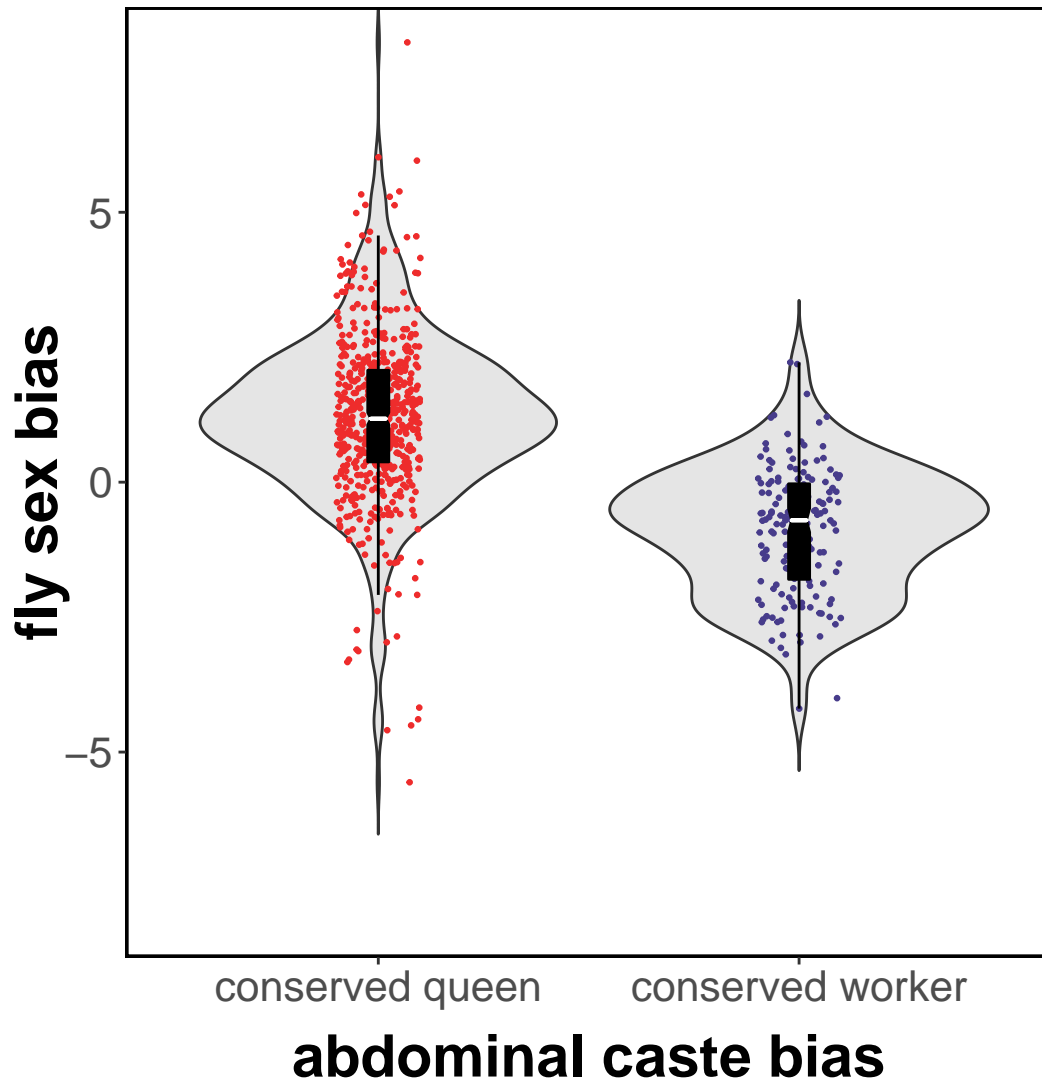
```
  xlab("abdominal caste bias")+
  scale_fill_manual(values=SexPal)+
  scale_color_manual(values=SexPal)+
  theme(legend.position="none")+
  stat_summary(geom = "crossbar", width=0.035, fatten=0, size=0.7,color="white",
               fun.data = function(x){c(y=median(x), ymin=median(x), ymax=median(x))})+
  coord_cartesian(ylim = c(-8,8))
p4
```


Comparison to development

```
DmelSC = merge(sexGenes,ogg11,by="gene_Amel")
key <- read.table("data/DmelKey.txt") #Generated from Drosophila melanogaster gff file
key2 <- read.table("data/Dmel_CDStoGene_key.txt")
devel <- read.table("data/Dmel_Devel_IDs.txt")
sex <- read.table("data/Dmel_Sex_IDs.txt")

key3 = merge(key,key2,by="V1")
DmelSC = merge(DmelSC,key3,by.x="Gene",by.y="V2.y")
DmelSC$develSex = "nonDE"
```

```
DmelSC$develSex[DmelSC$V2.x %in% devel$V1] = "devel"
DmelSC$develSex[DmelSC$V2.x %in% sex$V1] = "sex"
DmelSC$develSex[DmelSC$V2.x %in% sex$V1 & DmelSC$V2.x %in% devel$V1] = "sex and devel"

DmelSC$develSex = factor(DmelSC$develSex,levels = c("nonDE","sex and devel","devel","sex"))
ggplot(DmelSC[!grepl("ant",DmelSC$abdDE),],aes(x = abdDE,fill=develSex))+
  geom_bar(stat="count",position="fill")+
  ylab("proportion")+
  xlab("abdominal caste bias")
```



```
antDevel2$Gene=rownames(antDevel2)
aD = merge(ogg11,antDevel2,by.x="gene_Mphar",by.y="Gene")
```

```
p1 <- ggplot(aD[!grepl("ant",aD$abdDE),],aes(x = abdDE,y=-log(FDR)))+
  geom_boxplot(notch = T)+
  scale_y_log10()+
  ggtitle("devel measured in ant")

beeDevel2$Gene=rownames(beeDevel2)
bD = merge(ogg11,beeDevel2,by.x="gene_Amel",by.y="Gene")

p2 <- ggplot(bD[!grepl("ant",bD$abdDE),],aes(x = abdDE,y=-log(FDR)))+
  geom_boxplot(notch = T)+
  scale_y_log10()+
  ggtitle("devel measured in bee")

grid.arrange(p1,p2,nrow=1)
```
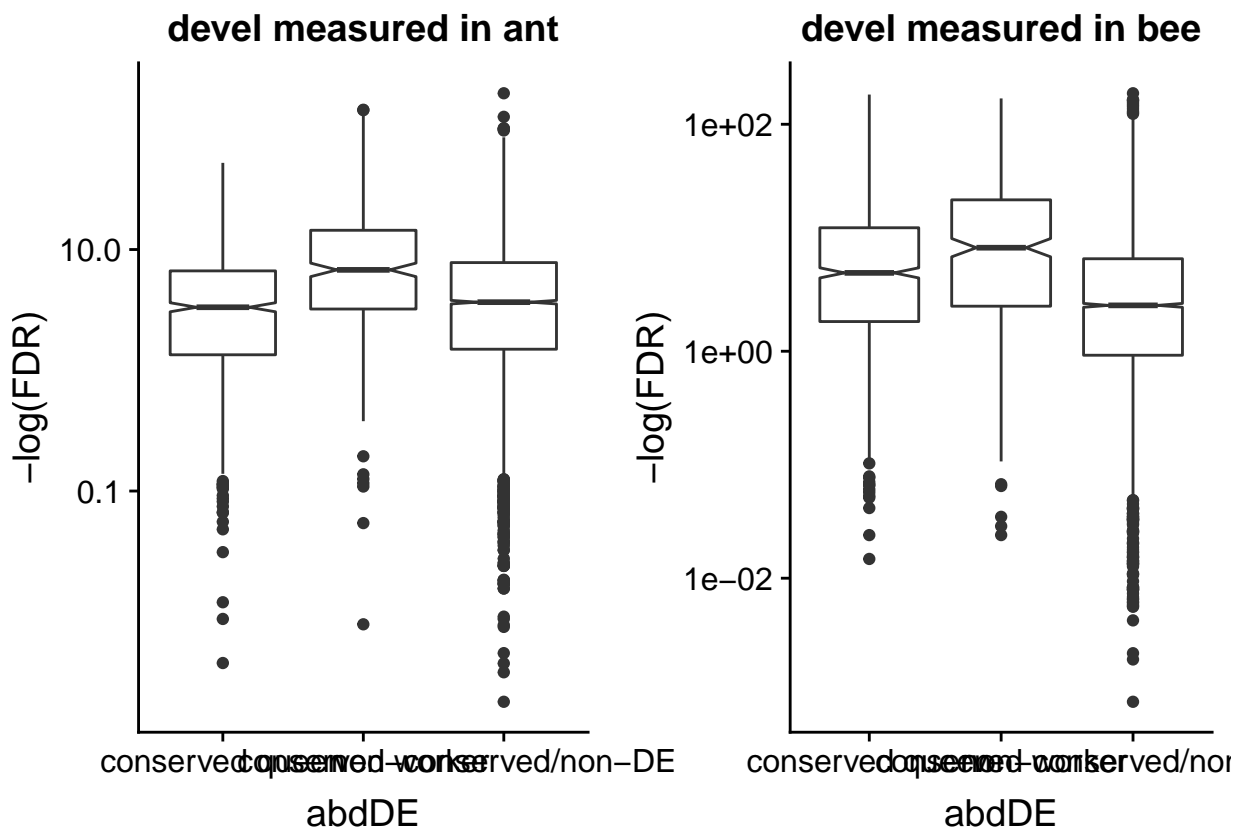
```
## Warning: Transformation introduced infinite values in continuous y-axis

## Warning: Removed 14 rows containing non-finite values (stat_boxplot).

## Warning: Transformation introduced infinite values in continuous y-axis

## Warning: Removed 12 rows containing non-finite values (stat_boxplot).
```


4.1 Calculation of overall caste bias

```
#Calculate euclidean distance
euclDist <- function(res){
```

```
  cb = apply(res[,-c(1)],1,function(x) sqrt(sum(x^2))/length(x))
  cb_noAbd = apply(res[,-c(1,ncol(res))],1,function(x) sqrt(sum(x^2))/length(x))
  cb_noAdult = apply(res[,-c(1,(ncol(res) - 2):ncol(res))],1,function(x) sqrt(sum(x^2))/length(x))
  cb_larva = apply(res[,-c(1,(ncol(res) - 3):ncol(res))],1,function(x) sqrt(sum(x^2))/length(x))
  cb_adult = apply(res[,-c(1:(ncol(res) - 3))],1,function(x) sqrt(sum(x^2))/length(x))
  cb_abd = apply(as.data.frame(res[,-c(1:(ncol(res) - 1))]),1,function(x) sqrt(sum(x^2))/length(x))
  results = data.frame(Gene = res$Gene,cb=cb,cb_noAbd=cb_noAbd,cb_noAdult=cb_noAdult,cb_larva=cb_larva,
  return(results)
}

#For this analysis, we include all larval stages

antCB = euclDist(antRes_allstage[[1]])
beeCB = euclDist(beeRes_allstage[[1]])
antSB = euclDist(antSocRes[[1]])
beeSB = euclDist(beeSocRes[[1]])

antSB$type=beeSB$type="behavior"
antCB$type=beeCB$type="caste"
antBias2 = rbind(antCB,antSB)
beeBias2 = rbind(beeCB,beeSB)
```

4.1 Caste/Behavior bias vs connectivity

```
cbAps = merge(antBias2,Aps,by="Gene")
cbBps = merge(beeBias2,Bps,by="Gene")
cbAps = merge(antConn,cbAps,by="Gene")
cbBps = merge(beeConn,cbBps,by="Gene")

cbBps$kTotal = cbBps$kTotal/max(cbBps$kTotal)
cbAps$kTotal = cbAps$kTotal/max(cbAps$kTotal)
levels(cbAps$psName)[1] = levels(cbBps$psName)[1]= "ancient"

cbPlot <- function(data,type,spec){
  p1C <- ggplot(data[data$type==type,],aes(x = kTotal,y=cb))+
  geom_hex(bins=70)+
  scale_fill_gradient(low = "blue",high="red")+
  plot2theme+
  ylim(0,2.5)+
  geom_smooth(method="lm",size=1.5,se=FALSE,color="black")+
  xlab("scaled network connectivity")+
  ggtitle(spec)+
  ylab(paste("overall",type,"bias",sep = " "))+
  scale_x_log10(breaks = c(0.01,0.1,1))+
  theme(legend.position="none")
  return(p1C)
}

p1 <- cbPlot(cbAps,"caste","ant")
p2 <- cbPlot(cbAps,"behavior","ant")
p3 <- cbPlot(cbBps,"caste","bee")
p4 <- cbPlot(cbBps,"behavior","bee")
```
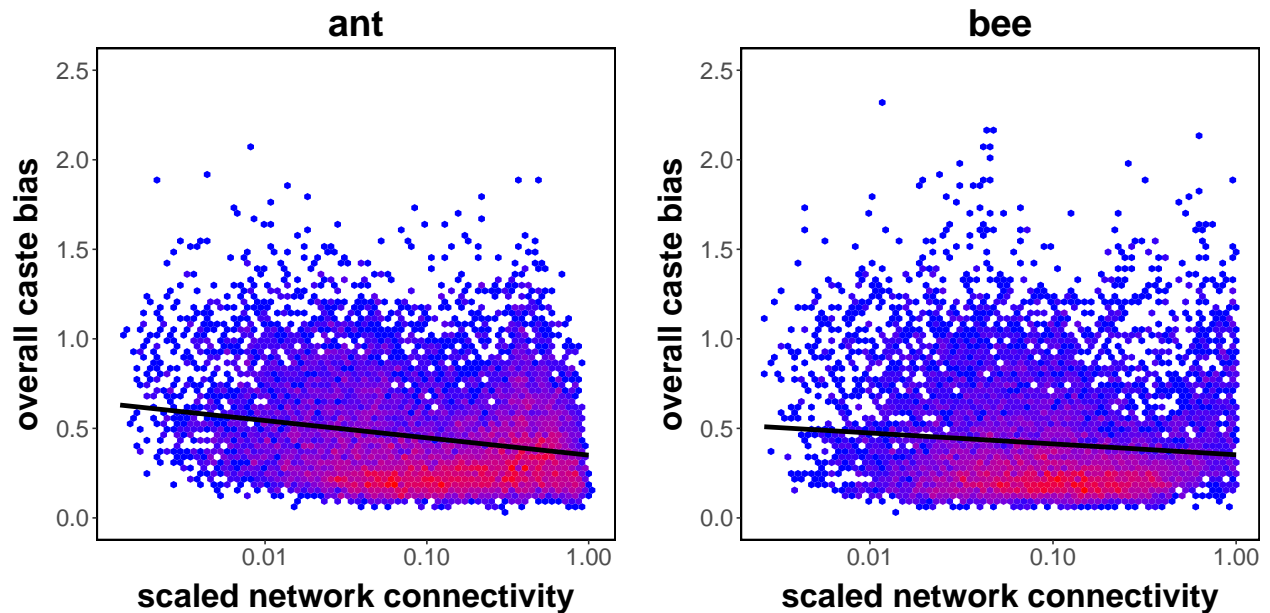
```
grid.arrange(p1,p3,nrow=1)
```

Warning: package 'hexbin' was built under R version 3.4.3

Warning: Removed 7 rows containing missing values (geom_hex).

Warning: Removed 6 rows containing missing values (geom_hex).


```
grid.arrange(p2,p4,nrow=1)
```

## Warning: Removed 56 rows containing non-finite values (stat_binhex).

Warning: Removed 56 rows containing non-finite values (stat_smooth).

Warning: Removed 47 rows containing missing values (geom_hex).

Warning: Removed 156 rows containing non-finite values (stat_binhex).

Warning: Removed 156 rows containing non-finite values (stat_smooth).

## Warning: Removed 37 rows containing missing values (geom_hex).
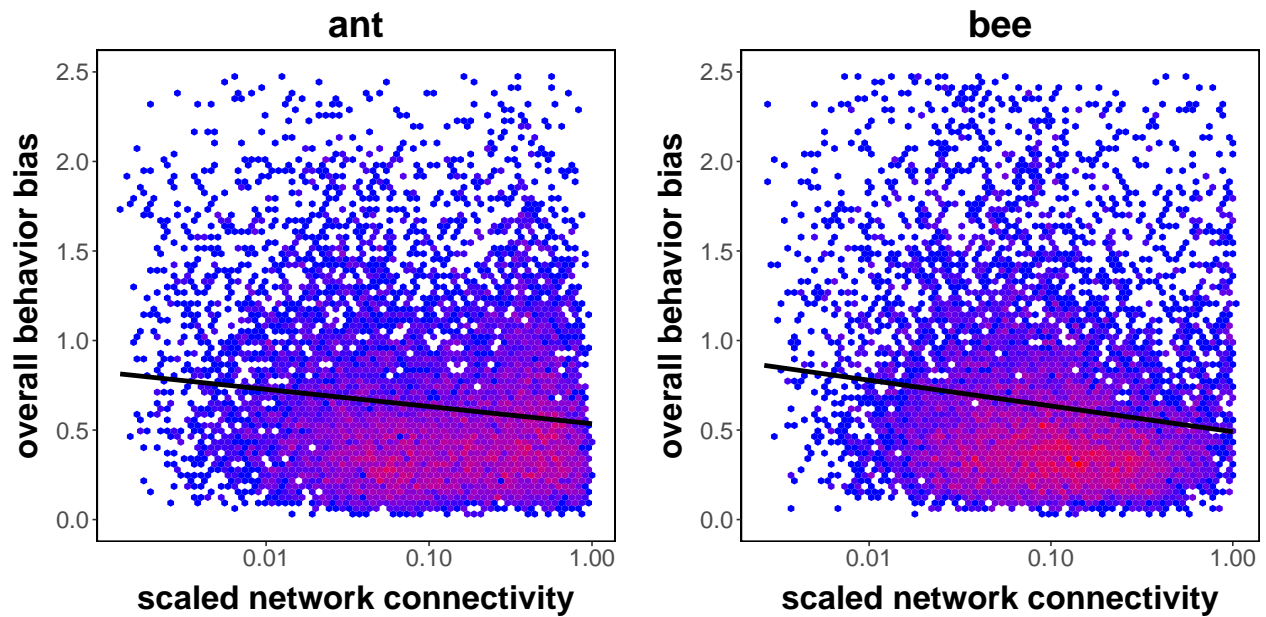
## 4.2 Caste/Behavior bias vs phylostrata

```
phPlot <- function(data,type,spec){
  pA <- ggplot(data[data$type==type & !is.na(data$psName),],aes(x = psName,y=cb,fill=psName))+
  geom_boxplot(notch=TRUE,outlier.shape=NA)+
  plot2theme+
  ggtitle(spec)+
  xlab("")+
  coord_cartesian(ylim=c(0,2))+
  scale_y_continuous(breaks = c(0,1,2,3))+
  scale_fill_manual(values = rev(mypalette2),name = "phylostrata",guide=guide_legend(title.position="top
  ylab(paste("overall",type,"bias",sep = " "))+
  theme(axis.text.x = element_text(angle = -25,hjust=0),
        legend.position="none")
  return(pA)
}

p1 <- phPlot(cbAps,"caste","ant")
p2 <- phPlot(cbAps,"behavior","ant")
p3 <- phPlot(cbBps,"caste","bee")
p4 <- phPlot(cbBps,"behavior","bee")

grid.arrange(p1,p3,nrow=1)
```
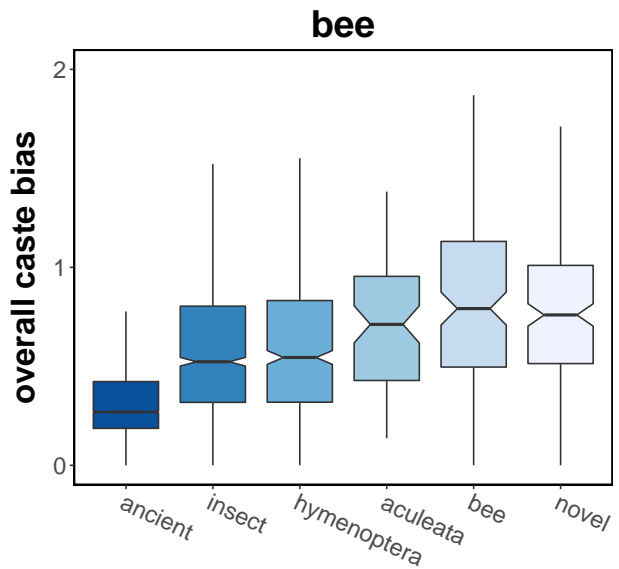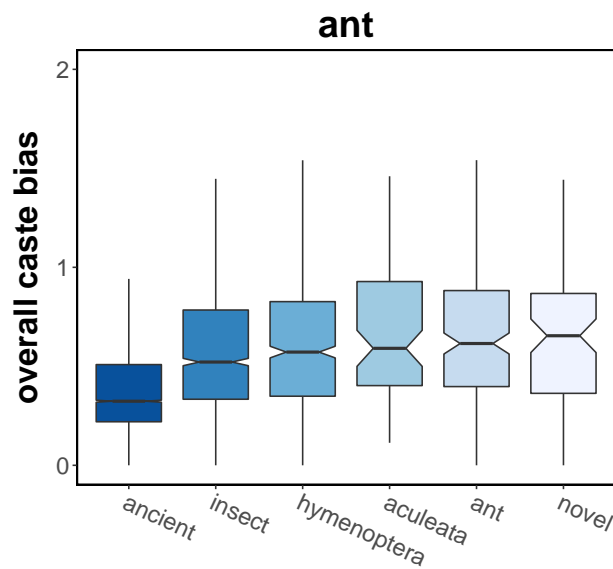
```
grid.arrange(p2,p4,nrow=1)
```
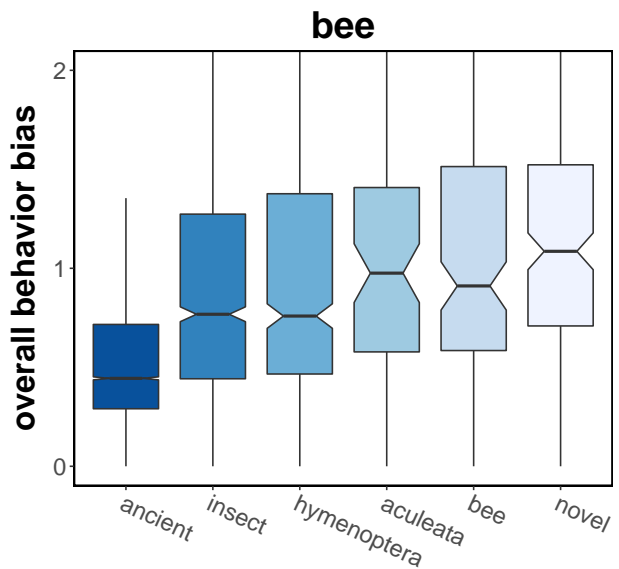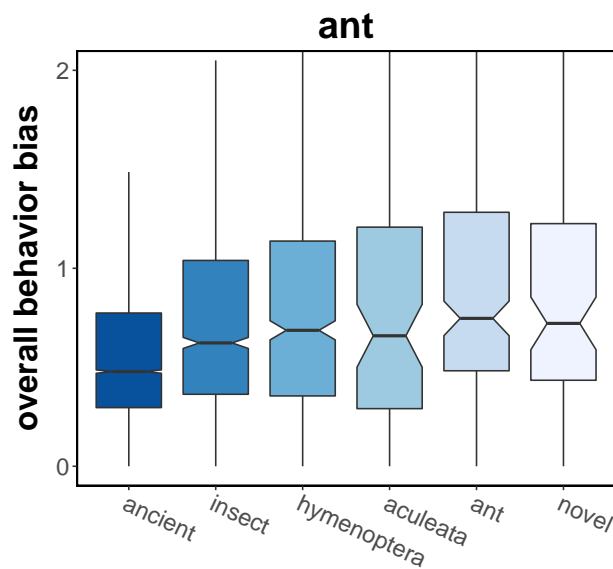

4.3 Caste bias vs tissue specificity -tissue specificity is estimated across 12 honey bee tissues.

```
bT = merge(tau,beeBias2,by="Gene")
bT$species = "bee"
bT$type = factor(bT$type,levels = c("caste","behavior"))
levels(bT$type) = c("caste bias","behavior bias")

p1 <- ggplot(bT,aes(x=tau,y=cb))+
  geom_point(size=1,alpha=0.6,pch=21,aes(fill=type),color="grey60")+
  geom_smooth(se=FALSE,aes(color=type))+
  scale_color_manual(values = SexPal)+
  scale_fill_manual(values = SexPal)+
  main_theme+xlab("tissue specificity")+ylab("bee bias")+
  theme(legend.position=c(0.2,0.6),
        legend.text = element_text(size=20),
        legend.title=element_blank())
p1
```

```
## `geom_smooth()` using method = 'gam' and formula 'y ~ s(x, bs = "cs")'
```
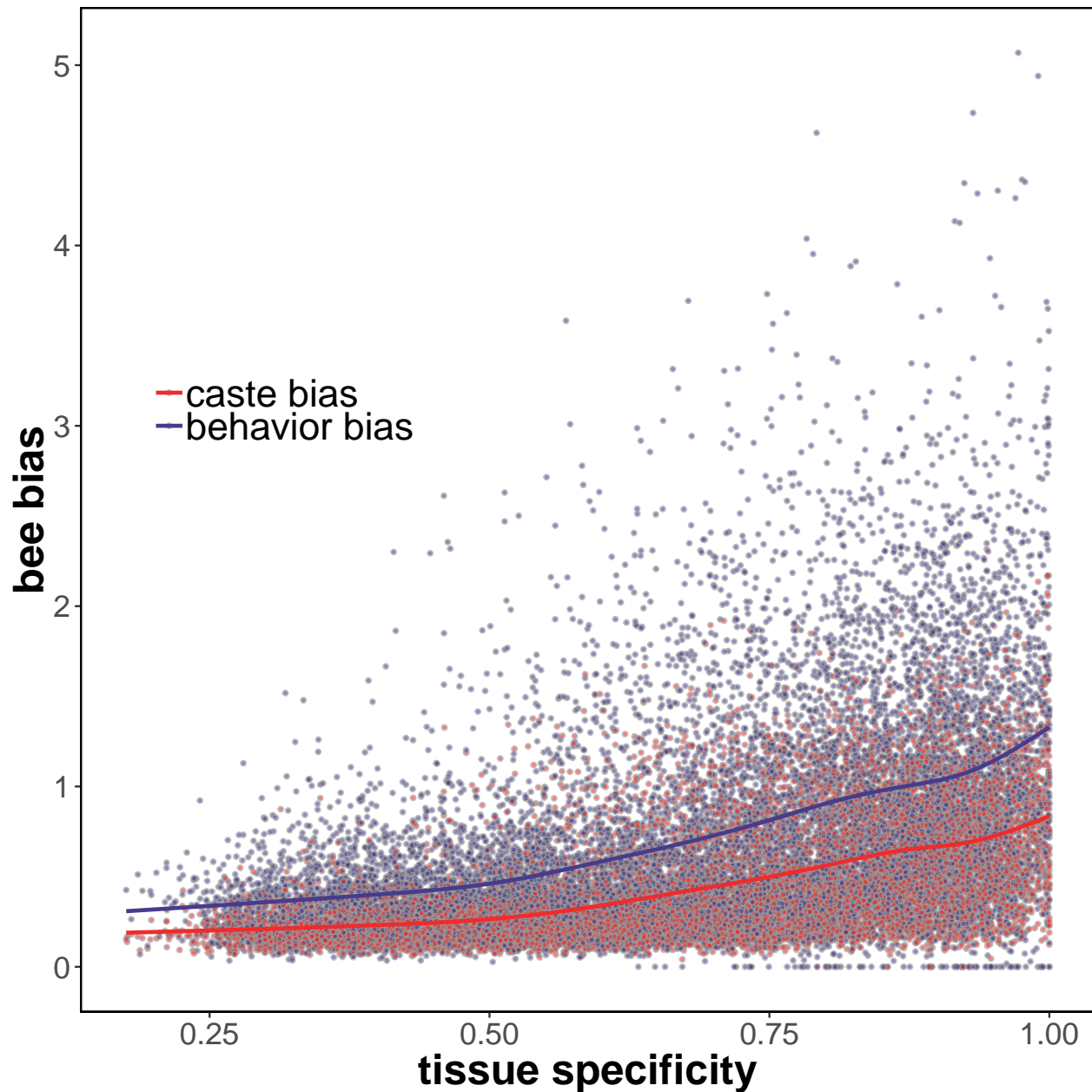

Development section

Comparison to pre-defined sex and development genes

```
DmelSC = merge(sexGenes,ogg11,by="gene_Amel")
key <- read.table("data/DmelKey.txt") #protein-CDS
key2 <- read.table("data/Dmel_CDStoGene_key.txt") #Gene-CDS
devel <- read.table("data/Dmel_Devel_IDs.txt") #Downloaded from flybase, genes with developmental terms
sex <- read.table("data/Dmel_Sex_IDs.txt") #Downloaded from flybase, genes with sex terms
key3 = merge(key,key2,by="V1")
```

```
DmelSC = merge(DmelSC,key3,by.x="Gene",by.y="V2.y")
DmelSC$develSex = "nonDE"
DmelSC$develSex[DmelSC$V2.x %in% devel$V1] = "devel"
DmelSC$develSex[DmelSC$V2.x %in% sex$V1] = "sex"
DmelSC$develSex[DmelSC$V2.x %in% sex$V1 & DmelSC$V2.x %in% devel$V1] = "sex and devel"

DmelSC$develSex = factor(DmelSC$develSex,levels = c("nonDE","sex and devel","devel","sex"))
p <- ggplot(DmelSC[!grepl("ant",DmelSC$abdDE),],aes(x = abdDE,fill=develSex))+
  geom_bar(stat="count",position="fill")+
  ylab("proportion")+
  xlab("abdominal caste bias")
p
```
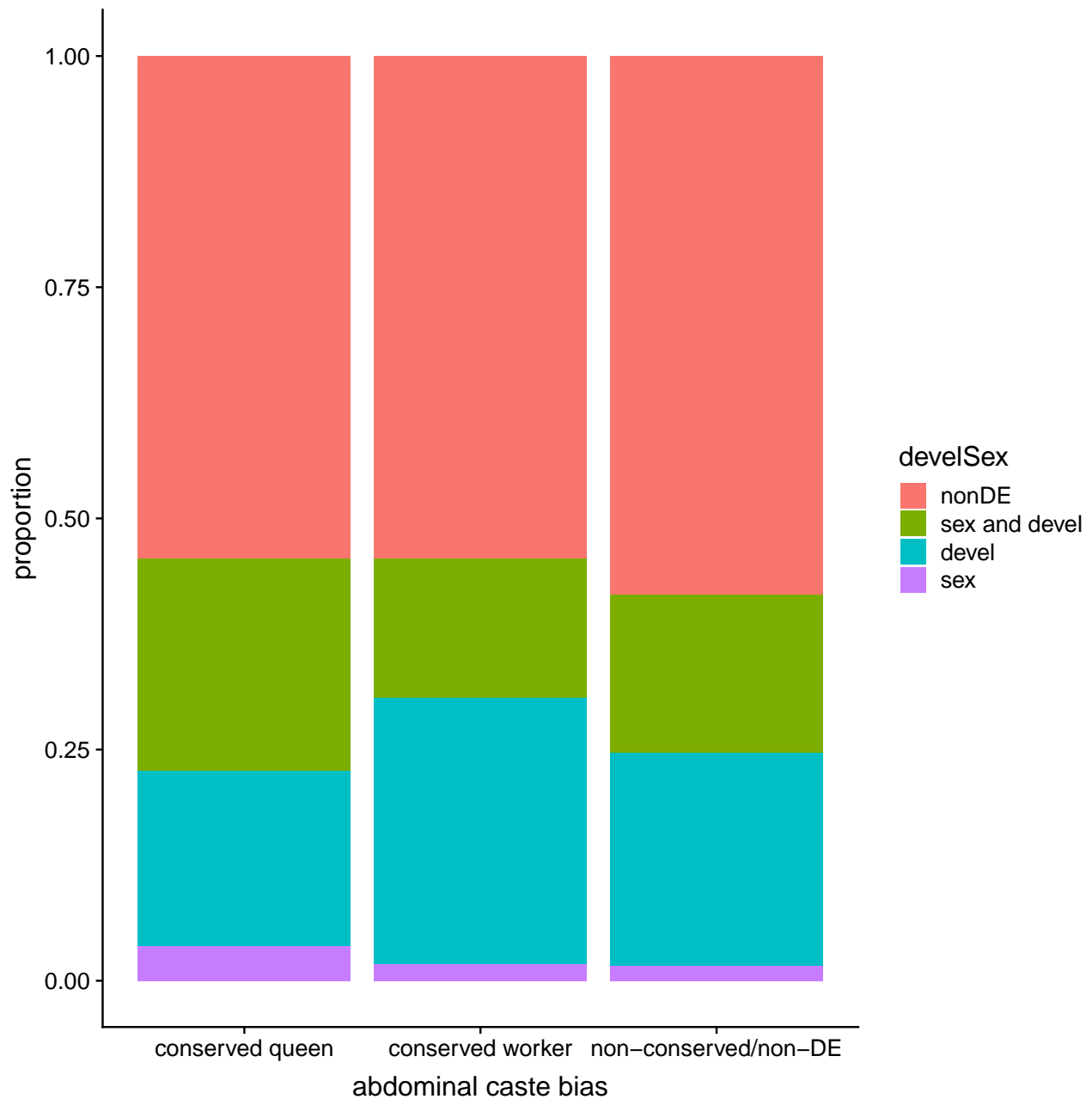
-log(P-value) for genes with conserved abdominal differential expression

```r
#using DE results
antDevel2$Gene=rownames(antDevel2)
aD = merge(ogg11,antDevel2,by.x="gene_Mphar",by.y="Gene")

p1 <- ggplot(aD[!grepl("ant",aD$abdDE),],aes(x = abdDE,y=-log(FDR)))+
  geom_boxplot(notch = T)+
  scale_y_log10()+
  theme(axis.text.x = element_text(angle=90))+
  ggtitle("devel measured in ant")

beeDevel2$Gene=rownames(beeDevel2)
bD = merge(ogg11,beeDevel2,by.x="gene_Amel",by.y="Gene")

p2 <- ggplot(bD[!grepl("ant",bD$abdDE),],aes(x = abdDE,y=-log(FDR)))+
  geom_boxplot(notch = T)+
  scale_y_log10()+
  theme(axis.text.x = element_text(angle=90))+
  ggtitle("devel measured in bee")

grid.arrange(p1,p2,nrow=1)
```

```
## Warning: Transformation introduced infinite values in continuous y-axis

## Warning: Removed 14 rows containing non-finite values (stat_boxplot).

## Warning: Transformation introduced infinite values in continuous y-axis

## Warning: Removed 12 rows containing non-finite values (stat_boxplot).
```

devel measured in ant

devel measured in bee

−log(FDR)

10.0

0.1

−log(FDR)

1e+02

1e+00

1e−02

conserved queen

conserved worker

non−conserved/non−DE

abdDE

conserved queen

conserved worker

non−conserved/non−DE

abdDE