Starling-May18 Projects/Katarina Stuart/KStuart.Starling-Aug18/Nc3_HihiSV/Analysis/2024-03-22.FitnessImpacts

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2024-03-22.FitnessImpacts



Fitness Impacts

```
module load R/4.1.0-gimkl-2020a
R
library(ggplot2)
library(data.table)
library(tidyr)
library(dplyr)
library(stringr)
library(lme4)
library(afex)
library(effects)
setwd("/nesi/nobackup/uoa00338/kstuart projects/Nc3 HihiSV/analysis/fitness")
#load metrics
data <- fread("/nesi/nobackup/uoa00338/kstuart projects/Nc3 HihiSV/data/individual ROH LOAD2 stats.txt")
#family data, in case it is needed
Fam <-(fread("/nesi/nobackup/uoa00338/kstuart_projects/Nc3_HihiSV/data/variant_calling/SV_curation/mendel/hihi_genofiltered.plink.fam",
header = F, sep = "\t"))[,c(1,2)]
Fam$V2 <- as.integer(Fam$V2)
#merge the data
allload2 <- merge(data,Fam, by.x = "IID", by.y = "V2")
names(allload2)[names(allload2) == "V1"] <- "FAM"
#Simple regression plots
modSNPreal <- Imer(Anna num offspring recorded~SNP prop real + SEX+(1|Anna Cohort), data=allload2[1:28,])
summary( modSNPreal )
effects modSNPreal <- effects::effect(term= "SNP prop real", mod= modSNPreal)
x modSNPreal <- as.data.frame(effects modSNPreal )
modSNPmask <- Imer(Anna_num_offspring_recorded~SNP_prop_mask + SEX+(1|Anna_Cohort), data=allload2[1:28,])
summary( modSNPmask )
effects modSNPmask <- effects::effect(term= "SNP prop mask", mod= modSNPmask)
x_modSNPmask <- as.data.frame(effects_modSNPmask)</pre>
modSNPnone <- Imer(Anna num offspring recorded~SNP prop none + SEX+(1|Anna Cohort), data=allload2[1:28,])
summary( modSNPnone )
effects_modSNPnone<- effects::effect(term= "SNP_prop_none", mod= modSNPnone)
x_modSNPnone <- as.data.frame(effects_modSNPnone )
pdf("Nc3_offspring_SNPreal.pdf", width=6, height=4)
ggplot() + geom point(data=allload2[1:28,], aes(x=SNP prop real, y=Anna num offspring recorded, col = SEX),size=5) +
```

```
geom_point(data=x_modSNPreal, aes(x=SNP_prop_real, y=fit), color="black") +
 geom line(data=x modSNPreal, aes(x=SNP prop real, y=fit), color="black") +
 geom ribbon(data= x modSNPreal, aes(x=SNP prop real, ymin=lower, ymax=upper), alpha= 0.3, fill="grey") +
 labs(x = "SNP Realised load", y = "Lifetime Fitness")+
 theme classic(base size = 18) +
 scale shape manual(values = c(18, 20))
dev.off()
pdf("Nc3 offspring SNPmask.pdf", width=6, height=4)
ggplot() + geom point(data=allload2[1:28,], aes(x=SNP prop mask ,y=Anna num offspring recorded, col = SEX),size=5) +
 geom point(data=x modSNPmask, aes(x=SNP prop mask, y=fit), color="black") +
 geom line(data=x modSNPmask, aes(x=SNP prop mask, y=fit), color="black") +
 geom ribbon(data= x modSNPmask, aes(x=SNP prop mask, ymin=lower, ymax=upper), alpha= 0.3, fill="grey") +
 labs(x = "SNP Masked load", y = "Lifetime Fitness")+
 theme classic(base size = 18) +
 scale_shape_manual(values = c(18, 20))
dev.off()
pdf("Nc3_offspring_SNPnone.pdf", width=6, height=4)
ggplot() + geom_point(data=allload2[1:28,], aes(x=SNP_prop_none,y=Anna_num_offspring_recorded, col = SEX),size=5) +
# geom point(data=x modSNPreal, aes(x=SNP prop real, y=fit), color="black") +
# geom_line(data=x_modSNPreal, aes(x=SNP_prop_real, y=fit), color="black") +
# geom_ribbon(data= x_modSNPreal, aes(x=SNP_prop_real, ymin=lower, ymax=upper), alpha= 0.3, fill="grey") +
 labs(x = "SNP Common allele homozygotes", y = "Lifetime Fitness")+
 theme classic(base size = 18) +
 scale shape manual(values = c(18, 20))
dev.off()
modSVreal <- Imer(Anna num offspring recorded~SV prop real + SEX+(1|Anna Cohort), data=allload2[1:28,])
summary( modSVreal )
effects modSVreal <- effects::effect(term= "SV prop real", mod= modSVreal)
x modSVreal <- as.data.frame(effects modSVreal )
modSVmask <- Imer(Anna_num_offspring_recorded~SV_prop_mask + SEX+(1|Anna_Cohort), data=allload2[1:28,])
summary( modSVmask )
effects modSVmask <- effects::effect(term= "SV prop mask", mod= modSVmask)
x modSVmask <- as.data.frame(effects modSVmask)
modSVnone <- lmer(Anna_num_offspring_recorded~SV_prop_none + SEX+(1|Anna_Cohort), data=allload2[1:28,])
summary( modSVnone )
effects modSVnone<- effects::effect(term= "SV prop none", mod= modSVnone)
x_modSVnone <- as.data.frame(effects_modSVnone )
pdf("Nc3 offspring SVreal.pdf", width=6, height=4)
ggplot() + geom point(data=allload2[1:28,], aes(x=SV prop real ,y=Anna num offspring recorded, col = SEX),size=5) +
 geom point(data=x modSVreal, aes(x=SV prop real, y=fit), color="black") +
 geom_line(data=x_modSVreal, aes(x=SV_prop_real, y=fit), color="black") +
 geom ribbon(data= x modSVreal, aes(x=SV prop real, ymin=lower, ymax=upper), alpha= 0.3, fill="grey") +
 labs(x = "SV Realised load", y = "Lifetime Fitness")+
 theme classic(base size = 18) +
 scale shape manual(values = c(18, 20))
dev.off()
pdf("Nc3_offspring_SVmask.pdf", width=6, height=4)
ggplot() + geom_point(data=allload2[1:28,], aes(x=SV_prop_mask,y=Anna_num_offspring_recorded, col = SEX),size=5) +
 geom point(data=x modSVmask, aes(x=SV prop mask, y=fit), color="black") +
 geom_line(data=x_modSVmask, aes(x=SV_prop_mask, y=fit), color="black") +
 geom ribbon(data= x modSVmask, aes(x=SV prop mask, ymin=lower, ymax=upper), alpha= 0.3, fill="grey") +
 labs(x = "SV Masked load", y = "Lifetime Fitness")+
```

```
theme_classic(base_size = 18) +
 scale shape manual(values = c(18, 20))
dev.off()
pdf("Nc3 offspring SVnone.pdf", width=6, height=4)
ggplot() + geom point(data=allload2[1:28,], aes(x=SNP prop none,y=Anna num offspring recorded, col = SEX),size=5) +
 geom_point(data=x_modSVnone, aes(x=SV_prop_none, y=fit), color="black") +
 geom line(data=x modSVnone, aes(x=SV prop none, y=fit), color="black") +
 geom ribbon(data= x modSVnone, aes(x=SV prop none, ymin=lower, ymax=upper), alpha= 0.3, fill="grey") +
 labs(x = "SV Common allele homozygotes", y = "Lifetime Fitness")+
 theme classic(base size = 18) +
 scale_shape_manual(values = c(18, 20))
dev.off()
#MASKED
summary(Imer(Anna num offspring recorded~SV prop mask +SNP prop mask + SEX+(1|Anna Cohort), data=allload2[1:28,] ))
anova(Imer(Anna num offspring recorded~SV prop mask+SNP prop mask+SEX+(1|Anna Cohort), data=allload2[1:28,] ))
#REALISED
summary(Imer(Anna num offspring recorded~SV prop real +SNP prop real + SEX+(1|Anna Cohort), data=allload2[1:28,] ))
anova(lmer(Anna_num_offspring_recorded~SV_prop_real +SNP_prop_real + SEX+(1|Anna_Cohort), data=allload2[1:28,] ))
```

Evolution

```
module load R/4.1.0-gimkl-2020a
library(ggplot2)
library(data.table)
library(tidyr)
library(dplyr)
library(stringr)
library(lme4)
library(afex)
setwd("/nesi/nobackup/uoa00338/kstuart_projects/Nc3_HihiSV/analysis/fitness")
#load metrics
fread("/nesi/nobackup/uoa00338/kstuart_projects/Nc3_HihiSV/analysis/evolution/AvianSeqfile_all_subset6/ALL_load_counts_evolution.txt")
#add metadata
population2 <- fread("/nesi/nobackup/uoa00338/kstuart_projects/Nc3_HihiSV/data/high_coverage_indiv_updated_metadata.txt", header = T,
sep = "\t")
#merge the data
allload2 <- merge(data,population2, by.x = "variable", by.y = "INDV")
#MASKED
summary(Imer(Anna_num_offspring_recorded~SV_evolprop_mask +SV_bothprop_mask +SEX+(1|Anna_Cohort), data=allload2[1:28,] ))
anova(lmer(Anna num offspring recorded~SV evolprop mask +SV bothprop mask +SEX+(1|Anna Cohort), data=allload2[1:28,] ))
```