generate\_sensitivity\_figures.R

z3254626

2021-07-07

.. content for (no empty lines) ..

.. content for ..

@title

generate\_sensitivity\_figures <- function(step\_sensitivities\_samples,  
 step\_sensitivities\_loci,  
 step\_sensitivities\_pops) {  
   
 measures <- c("H0b.Jac.AvLast", "H0b.Sor.AvLast",  
 "D0b.A.AvLast", "D0b.B.AvLast",  
 "H0b.Jac.AvFirst", "H0b.Sor.AvFirst",  
 "D0b.A.AvFirst", "D0b.B.AvFirst",  
 "H1b.MI.AvLast", "H1b.ShD.AvLast",   
 "D1b.A.AvLast", "D1b.B.AvLast",   
 "H1b.MI.AvFirst", "H1b.ShD.AvFirst",   
 "D1b.A.AvFirst", "D1b.B.AvFirst",  
 "H2b.GST.AvLast", "H2b.JOST.AvLast",   
 'D2b.A.AvLast', 'D2b.B.AvLast',  
 "H2b.GST.AvFirst", "H2b.JOST.AvFirst",   
 'D2b.A.AvFirst', 'D2b.B.AvFirst',  
 "BC.AvLast") #skip relative measures  
   
 #Create pdf of results for each measure, for each allele treatment  
 figs1 <- map(measures, create\_sensitivities\_figure, p.start = 0, p.end = 1)  
   
 figs2 <- map(measures, create\_sensitivities\_figure, p.start = 0.1, p.end = 0.9)  
   
 figs3 <- map(measures, create\_sensitivities\_figure, p.start = 0, p.end = 0.5)  
   
 figs4 <- map(measures, create\_sensitivities\_figure, p.start = 0, p.end = 0.2)  
   
 figs5 <- map(measures, create\_sensitivities\_figure, p.start = 0.3, p.end = 0.5)  
   
 #After saving the initial files, put them all together in one pdf (130 pages)  
   
 #add them all to a list  
 l <- c(figs1, figs2, figs3, figs4, figs5)  
   
 pdf("Outputs/all\_supp\_figs.pdf")  
 invisible(lapply(l, print))  
 dev.off()  
   
}