extract\_relative\_senstivities.R

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@title @param merged\_results

extract\_relative\_senstivities <- function(merged\_results) {  
  
 #Get full data set of all simulations  
 data <- merged\_results  
   
 #Vector stating the order you want the measures to be displayed  
 measure\_order <- c("H1b.MI.AvLast", "H1b.MI.AvFirst",  
 "H2b.GST.AvLast", "H2b.GST.AvFirst",  
 "D2b.A.AvFirst","BC.AvLast")  
   
 #Filter down to the six best measures  
 data <- data %>%  
 filter(Measure %in% measure\_order)  
   
 #Make a column for false positives  
 #When step is zero, all steps detected are false  
 #Otherwise only those not at 0.5 are false  
 data <- data %>%  
 mutate(false\_pos = ifelse(step == 0, Total.Steps, Incorrect.Steps),  
 true\_pos = ifelse(step == 0, NA, Correct.Steps))  
   
 #Split into individual allele proportion treatments  
 data\_0\_1 <- data %>%  
 filter(p.start == 0) %>%  
 filter(p.end == 1) %>%  
 group\_by(Measure, step) %>%  
 summarise(true\_pos = round(sum(true\_pos)/(n()), digits = 1),   
 false\_pos = round(sum(false\_pos)/(n()), digits = 1)) %>%  
 pivot\_longer(names\_to = "step\_type", cols = c(true\_pos, false\_pos)) %>%  
 pivot\_wider(names\_from = step, values\_from = value) %>%  
 rename\_with(.cols = -c(Measure, step\_type), ~ paste(.x, "0\_1", sep = "\_"))  
   
 data\_0.1\_0.9 <- data %>%  
 filter(p.start == 0.1) %>%  
 filter(p.end == 0.9) %>%  
 group\_by(Measure, step) %>%  
 summarise(true\_pos = round(sum(true\_pos)/(n()), digits = 1),   
 false\_pos = round(sum(false\_pos)/(n()), digits = 1)) %>%  
 pivot\_longer(names\_to = "step\_type", cols = c(true\_pos, false\_pos)) %>%  
 pivot\_wider(names\_from = step, values\_from = value) %>%  
 rename\_with(.cols = -c(Measure, step\_type), ~ paste(.x, "0.1\_0.9", sep = "\_"))  
   
   
 data\_0\_0.5 <- data %>%  
 filter(p.start == 0) %>%  
 filter(p.end == 0.5)%>%  
 group\_by(Measure, step) %>%  
 summarise(true\_pos = round(sum(true\_pos)/(n()), digits = 1),   
 false\_pos = round(sum(false\_pos)/(n()), digits = 1)) %>%  
 pivot\_longer(names\_to = "step\_type", cols = c(true\_pos, false\_pos)) %>%  
 pivot\_wider(names\_from = step, values\_from = value) %>%  
 rename\_with(.cols = -c(Measure, step\_type), ~ paste(.x, "0\_0.5", sep = "\_"))  
   
   
 data\_0\_0.2 <- data %>%  
 filter(p.start == 0) %>%  
 filter(p.end == 0.2) %>%  
 group\_by(Measure, step) %>%  
 summarise(true\_pos = round(sum(true\_pos)/(n()), digits = 1),   
 false\_pos = round(sum(false\_pos)/(n()), digits = 1)) %>%  
 pivot\_longer(names\_to = "step\_type", cols = c(true\_pos, false\_pos)) %>%  
 pivot\_wider(names\_from = step, values\_from = value) %>%  
 rename\_with(.cols = -c(Measure, step\_type), ~ paste(.x, "0\_0.2", sep = "\_"))  
   
   
 data\_0.3\_0.5 <- data %>%  
 filter(p.start == 0.3) %>%  
 filter(p.end == 0.5) %>%  
 group\_by(Measure, step) %>%  
 summarise(true\_pos = round(sum(true\_pos)/(n()), digits = 1),   
 false\_pos = round(sum(false\_pos)/(n()), digits = 1)) %>%  
 pivot\_longer(names\_to = "step\_type", cols = c(true\_pos, false\_pos)) %>%  
 pivot\_wider(names\_from = step, values\_from = value) %>%  
 rename\_with(.cols = -c(Measure, step\_type), ~ paste(.x, "0.3\_0.5", sep = "\_"))  
   
   
 #Put all the data back together  
 data\_merge <- data\_0\_1 %>%  
 left\_join(data\_0.1\_0.9, by = c("Measure", "step\_type"))%>%  
 left\_join(data\_0\_0.5, by = c("Measure", "step\_type"))%>%  
 left\_join(data\_0\_0.2, by = c('Measure', "step\_type"))%>%  
 left\_join(data\_0.3\_0.5, by = c("Measure", "step\_type")) %>%  
 rename\_with(.cols = -c(Measure, step\_type), ~ paste("step", .x, sep = "\_"))  
  
   
   
   
 data\_merge\_format <- data\_merge  
   
   
 data\_merge\_format <- data\_merge\_format %>%  
 mutate(Measure = factor(Measure, levels = measure\_order)) %>%  
 # mutate(Measure = fct\_relevel(Measure, measure\_order)) %>%  
 arrange(Measure)  
   
   
 data\_merge\_format$Measure <- c("MI \n (AvLast)", " ", "MI \n (AvFirst)", " ",   
 "GST \n (AvLast)", " ", "GST \n (AvFirst)", " ",   
 "D2b.A (AvFirst)", " ", "BC (AvLast)", " ")  
   
 data\_merge\_format <- data\_merge\_format %>%  
 mutate\_all(~replace(., is.na(.), "-"))  
   
   
 data\_merge\_format$step\_type[data\_merge\_format$step\_type == "true\_pos"] <- "True Positives"  
   
   
 data\_merge\_format$step\_type[data\_merge\_format$step\_type == "false\_pos"] <- "False Positives"  
   
   
   
 #correct steps formatting  
 data\_merge\_format[3:22] <- lapply(data\_merge\_format[3:22], function(x) {  
 v <- 1:14  
 v[c(1,3,5,7,9,11,13,14)] <- color\_tile("transparent", "green")(c(x[c(1,3,5,7,9,11)], 0, 100))  
 v[c(2,4,6,8,10,12,13,14)] <- color\_tile("transparent", "red")(c(x[c(2,4,6,8,10,12)], 0, 100))  
   
 return(v[1:12])   
 })  
   
   
   
 options(knitr.kable.NA = '-')  
   
   
 #create basic table  
 results\_table <- data\_merge\_format %>%  
 kbl(col.names = c("Measure", "Type of Step", "0", "1", "5", "50", "0", "1", "5", "50",  
 "0", "1", "5", "50", "0", "1", "5", "50", "0", "1", "5", "50"),  
 escape = FALSE) %>%  
 kable\_classic(full\_width = F, html\_font = "Cambria") %>%  
 #Add heading  
   
 #Remove every second Measure name  
   
 #Replace Measure name with better formatting  
 #Add stub head for each allele treatment  
 add\_header\_above(c(" " = 2,   
 "Maximal \n range: \n p = 0 - 1" = 4,   
 "Maximal range \n without fixation: \n p = 0.1 - 0.9" = 4,   
 "Halfmaximal \n range: \n p = 0 - 0.5" = 4,  
 "Narrow range \n near fixation: \n p = 0 - 0.2" = 4,  
 "Narrow range \n far from fixation: \n p = 0.3 - 0.5" = 4)  
 )  
 #Make Step names shorter  
 #Add conditional formatting  
   
 results\_table  
   
 save\_kable(results\_table, file = "./Outputs/relative\_sensitivities\_table.html")  
   
   
 return(results\_table)  
}