count\_step\_detections.R

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Takes specific inputs of: step, n.samples, p.start, p.end, n.loci, n.pops and counts how many times each of the measures detects correct/incorrect steps repeats this “n\_reps” times

Simulates new data with these variables each time and returns the sum of correct/incorrect steps across all replicates

functions it calls: simulate\_data - main simulation and calculation script

count\_step\_detections <- function(step, n.samples, p.start, p.end,  
 n.loci, n.pops, n\_reps = 10) {  
   
 # Simple function for running a simulation, then extracting the no. of steps  
 extract\_steps <- function(x) {  
   
 sim\_results <- simulate\_data(step = step, #strength of step(s)  
 n.samples = n.samples, #number of samples from each site  
 p.start = p.start, #allele proportion at start  
 p.end = p.end, #allele proportion at end  
 n.loci = n.loci, #number of loci  
 n.pops = n.pops, #number of populations  
 detect\_step = T)  
   
 step\_results <- sim\_results$step\_results  
   
 total\_steps <- as.numeric(step\_results[[2]])  
   
 correct\_steps <- ifelse(step\_results[[3]] <= 0.5 & step\_results[[4]] >= 0.5, 1, 0)  
   
 correct\_steps <- ifelse(is.na(correct\_steps), 0, correct\_steps)  
   
 names(total\_steps) <- step\_results[[1]]  
   
 names(correct\_steps) <- paste0(step\_results[[1]], "\_correct")  
   
 output <- c(total\_steps, correct\_steps)  
   
 return(output)  
 }  
  
 # Add up total number of steps  
 number\_of\_steps <- summarise(map\_dfr(1:n\_reps, extract\_steps),   
 across(1:76, sum))  
  
 return(number\_of\_steps)  
}