measure\_step\_detection\_sensitivity.R

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Takes inputs of: step, n.samples, p.start, p.end, n.samples, n.loci, n.pops, n\_reps

And tallies number of correct and incorrect steps detected for each diversity measure

If any input is a vector, runs a set of simulations for each combination

and checks for a step 1000 times for each sample size returns data and plot

To allow rerunning of later functions, this is skipped if “merged\_results” already exists

@param step Intensity of step (default = 0). Can be vector of values. @param p.start Starting allele proportion (default = 0). Can be vector of values. @param p.end End allele proportion (default = 1). Can be vector of values. @param n.samples Number of genomes sampled (default = 0). Can be vector of values. @param n.loci Number of loci (default = 1000). Can be vector of values. @param n.pops Number of localities (default = 10). Can be vector of values. @param n\_reps Number of times to repeat simulation (default = 10). Can be vector of values.

measure\_step\_detection\_sensitivity <- function(step = 0, p.start = 0, p.end = 1,   
 n.samples = 20, n.loci = 1000,   
 n.pops = 10, n\_reps = 10) {  
  
 #Create a data frame of every possible combination of input variables  
 input\_combinations <- purrr::cross\_df(list(step = step,   
 n.samples = n.samples,   
 p.start = p.start,   
 p.end = p.end,   
 n.loci = n.loci,  
 n.pops = n.pops,  
 n\_reps = n\_reps))  
   
   
 # Count number of steps detected for each combinations (run n\_reps times)  
 # Create a table with the model inputs, number of model replicates  
 # steps detected for each measure and correct steps detected for each measure  
 replication\_table\_step <- future\_pmap\_dfr(input\_combinations,  
 count\_step\_detections) %>%  
 add\_column(input\_combinations, .before = 1)  
   
 return(replication\_table\_step)  
  
}