plan.R

z3254626

2021-07-07

#The plan - runs all of the code for this project  
  
the\_plan <- drake\_plan(  
   
 #Default variables for step sensitivity tests  
 default\_values = list(  
 step = c(0, 1, 5, 50), #4 levels of step  
 n.samples = 20, #default  
 p.start = c(0, 0.1, 0.3), #Different allele proportion treatments  
 p.end = c(0.2, 0.5, 0.9, 1), #Different allele proportion treatments  
 n.loci = 1000, #default  
 n.pops = 10, #default  
 n\_reps = 100 #replication number  
 ),  
   
 #Run simulations of all combinations of default values and varied n.samples  
 step\_sensitivities\_samples = measure\_step\_detection\_sensitivity(  
 step = default\_values$step,  
 n.samples = seq(2, 30, 2), #varied input  
 p.start = default\_values$p.start,  
 p.end = default\_values$p.end,  
 n.loci = default\_values$n.loci,  
 n.pops = default\_values$n.pops,  
 n\_reps = default\_values$n\_reps  
 ),  
   
 # Run simulations of all combinations of default values and varied n.loci  
 step\_sensitivities\_loci = measure\_step\_detection\_sensitivity(  
 step = default\_values$step,  
 n.samples = default\_values$n.samples,  
 p.start = default\_values$p.start,  
 p.end = default\_values$p.end,  
 n.loci = seq(100, 2000, 100), #varied input  
 n.pops = default\_values$n.pops,  
 n\_reps = default\_values$n\_reps  
 ),   
   
 # Run simulations of all combinations of default values and varied n.pops  
 step\_sensitivities\_pops = measure\_step\_detection\_sensitivity(  
 step = default\_values$step,  
 n.samples = default\_values$n.samples,  
 p.start = default\_values$p.start,  
 p.end = default\_values$p.end,  
 n.loci = default\_values$n.loci,  
 n.pops = seq(4, 15, 1), #varied input  
 n\_reps = default\_values$n\_reps  
 ),  
   
 #Merge results into a single data frame  
 merged\_results = merge\_results(step\_sensitivities\_samples,  
 step\_sensitivities\_loci,  
 step\_sensitivities\_pops),  
   
 #Turn results into tables for publication, including all formatting  
 #Standard treatment results for q = 0, q = 1,q = 2 and BC)  
 results\_table = get\_results\_table(merged\_results),   
   
 #Percentage of all step sensitivities for best 6 measures  
 relative\_sensitivities = extract\_relative\_senstivities(merged\_results),  
   
 #Summary of measures' properties, all treatments  
 properties\_table = make\_properties\_summary\_table(merged\_results),  
   
 #Creates supplementary figures for all tested measures  
 individual\_figures = generate\_sensitivity\_figures(merged\_results),  
   
 #Creates supplementary figures comparing the best 6 measures  
 comparison\_figures = create\_comparison\_figures(),  
   
 alpha\_peaks = vis\_alpha\_peaks()  
   
 )