read\_specific\_plot.R

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Get a plot of beta diversities from one\_locus\_data

@title

read\_specific\_plot <- function(step, n.samples, p.start, p.end, n.loci,   
 n.pops, ...) {  
  
  
plot\_index <- detect\_index(one\_locus\_data[c(T,F,F)], ~   
 ((.x$step == step) & #options: 0, 1, 5, 10, 50  
 (.x$n.samples == n.samples) & #options: 5, 10, 25  
 (.x$p.start == p.start) & #options: 0, 0.1, 0.3  
 (.x$p.end == p.end) & #options: 0.4, 0.5, 0.9, 1  
 (.x$n.loci == n.loci) & #options: 10, 50, 1000  
 (.x$n.pops == n.pops))) #options: 4, 5, 6, 7, 10, 11  
  
  
beta\_plot <- get.one.locus.plot(readd(one\_locus\_data, subtargets = plot\_index), ...)$beta\_plot  
  
return(beta\_plot)  
}  
  
  
#read\_specific\_plot(step = 0, n.samples = 10, p.start = 0.3,   
 # p.end = 0.4, n.loci = 1000, n.pops = 11,   
 # div\_type = "D", expected = T, errorbars = T, ratios = F)