visualise\_beta\_trends.R

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@title

visualise\_beta\_trends <- function() {  
  
 #How do each of the measures vary from 0 to 1  
 #i.e. location 1 has a allele frequency of (p = 0)  
 # and location 2 has a allele frequency of (p = 0 to 1)  
 #So differentiation should range from 0 (no differentiation)  
 # to 1 (complete differentiation)  
   
 p.start = 0.1  
 p.end = 0.9  
 n.samples = 10  
 n.loci = 1000  
 #Make a variable which is the distance between each value of d (distance)  
 increment.size = 0.01  
   
   
 #Create a table with   
 data <- tibble(  
 n.samples = n.samples,  
 i = increment.size,  
 p.start = p.start,  
 p.end = p.end,  
 d = seq(0, 1, increment.size)) %>% #Location of population along distance (0 to 1)  
 mutate(p = p.start + d\*(p.end - p.start))  
   
 #p.binom:  
 #Take n.samples from a binomial distribution around allele proportion p  
 #Divide by n.samples to get 'measured' allele frequency  
 #e.g. n.samples = 5, allele proportion p = 0.1  
 # rbinom(1,5,0.1) / 5  
 # Can only be 0, 0.2, 0.4, 0.6, 0.8, 1  
 # But would more likely be 0/0.2   
 # repeat over n.loci  
 data <- data %>%   
 .[rep(1:nrow(.), times = n.loci),] %>% #replicate over multiple loci with same p  
 rowwise() %>% #allows for mutate to work row by row (rather than as a vector)  
 mutate(p.binom = rbinom(1, n.samples, p)/n.samples) %>% #p.binom  
 ungroup() #stops rowwise operations  
  
 data <- data %>%  
   
 mutate(H0b = get.Hq.beta.per.locus(p.start, p.binom, 0),  
 H1b = get.Hq.beta.per.locus(p.start, p.binom, 1),  
 H2b.JOST = get.Hq.beta.per.locus(p.start, p.binom, 2),  
 H2b.GST = get.Hq.beta.per.locus(p.start, p.binom, 2, "Gst"),  
 D0b = get.Dq.beta.per.locus(p.start, p.binom, 0),  
 D1b = get.Dq.beta.per.locus(p.start, p.binom, 1),  
 D2b = get.Dq.beta.per.locus(p.start, p.binom, 2),  
 AFD = get.AFD(p.start, p.binom)  
 )  
   
 data\_summary <- data %>%  
 group\_by(d) %>%  
 summarise\_each(list(mean = mean, sd = sd)) %>%  
 as\_tibble()%>%  
 mutate(H0b = get.Hq.beta.per.locus(p.start\_mean, p\_mean, 0),  
 H1b = get.Hq.beta.per.locus(p.start\_mean, p\_mean, 1),  
 H2b.JOST = get.Hq.beta.per.locus(p.start\_mean, p\_mean, 2),  
 H2b.GST = get.Hq.beta.per.locus(p.start\_mean, p\_mean, 2, "Gst"),  
 D0b = get.Dq.beta.per.locus(p.start\_mean, p\_mean, 0),  
 D1b = get.Dq.beta.per.locus(p.start\_mean, p\_mean, 1),  
 D2b = get.Dq.beta.per.locus(p.start\_mean, p\_mean, 2),  
 AFD = get.AFD(p.start\_mean, p\_mean)  
 )  
   
 ggplot(data\_summary, aes(x = d))+  
 geom\_point(shape = 3, aes(y = H2b.GST\_mean), colour = "darkgreen")+  
 geom\_point(shape = 3, aes(y = H1b\_mean), colour = "lightblue")+  
 geom\_point(shape = 3, aes(y = H0b\_mean), colour = "red")+  
 geom\_point(shape = 3, aes(y = H2b.JOST\_mean), colour = "purple")+  
 geom\_point(shape = 3, aes(y = AFD\_mean), colour = "orange")+  
 geom\_point(shape = 3, aes(y = D1b\_mean-1), colour = "blue")+  
 geom\_point(aes(y = D1b-1), colour = "blue")+  
 geom\_point(aes(y = H2b.GST), colour = "darkgreen")+  
 geom\_point(aes(y = H1b), colour = "lightblue")+  
 geom\_point(aes(y = H0b), colour = "red")+  
 geom\_point(aes(y = H2b.JOST), colour = "purple")+  
 geom\_point(aes(y = AFD), colour = "orange")   
   
 ggplot(data\_summary)+  
 geom\_point(aes(x = H2b.GST, y = H2b.GST\_mean), colour = "darkgreen")+  
 geom\_point(aes(x = D1b-1, y = D1b\_mean-1), colour = "green")+  
 geom\_point(aes(x = D1b-1, y = D1b\_mean-1), colour = "blue")+  
 geom\_point(aes(x = H0b, y = H0b\_mean), colour = "pink")+  
 geom\_point(aes(x = D0b-1, y = D0b\_mean-1), colour = "red")+  
 geom\_point(aes(x = H1b, y = H1b\_mean), colour = "lightblue")+  
 geom\_point(aes(x = H2b.JOST, y = H2b.JOST\_mean), colour = "purple")+  
 geom\_point(aes(x = AFD, y = AFD\_mean), colour = "orange")+  
 geom\_abline(slope=1)+  
 xlab("True differentiation (0 to 1)")+  
 ylab("Measured differentiation (0 to 1)")  
   
   
   
}