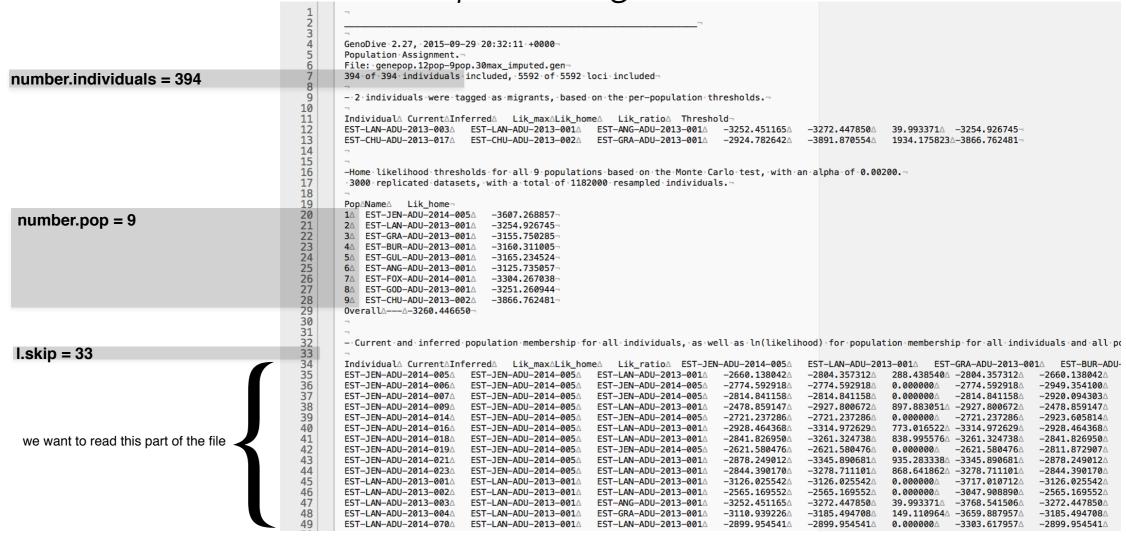
Using the GenoDive output in the functions:

dlr and plot_assignment_dlr



pop.id.start = 5 pop.id.end = 7

My individual's id: EST-GRA-ADU-2013-015

note: No pop id constant in your individual's name? use the strata argument

arguments: pop.levels and pop.labels

lon the example of the GenoDive assignment analysis output file, I had combined sampling sites into populations. Sites: JEN, LAN, GRA, BUR, GUL, ANG, LLI, WEI, FOX, GOD, HAY, CHU Pop: JEN, LAN, GRA, BUR, GUL, LNR, LNR, FOX, HAY, HAY, CHU

ANG+LLI+WEI are regrouped into LNR GOD + HAY are regrouped into HAY

How to handle this?

option 1: With the pop.id.start, pop.id.end argument and levels and labels. pop.levels = c("JEN", "LAN", "GRA", "BUR", "GUL", "ANG", "LLI", "WEI", "FOX", "GOD", "HAY", "CHU") pop.labels = c("JEN", "LAN", "GRA", "BUR", "GUL", "LNR", "LNR", "LNR", "FOX", "HAY", "HAY", "CHU")

option 2: use the strata argument in the functions