

Using the GenoDive output in the functions:

dlr and *plot_assignment_dlr*

number.individuals = 394

number.pop = 9

l.skip = 33

we want to read this part of the file

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GenoDive 2.27, 2015-09-29 20:32:11 +0000
Population Assignment.
File: genpop.12pop-9pop.30max_imputed.gen
394 of 394 individuals included, 5592 of 5592 loci included.
~
~2 individuals were tagged as migrants, based on the per-population thresholds.
~
Individual Current Inferred Lik_max Lik_home Lik_ratio Threshold
EST-LAN-ADU-2013-003 EST-LAN-ADU-2013-001 EST-ANG-ADU-2013-001 -3252.451165 -3272.447850 39.993371 -3254.926745
EST-CHU-ADU-2013-017 EST-CHU-ADU-2013-002 EST-GRA-ADU-2013-001 -2924.782642 -3891.870554 1934.175823 -3866.762481
~
~Home likelihood thresholds for all 9 populations based on the Monte Carlo test, with an alpha of 0.00200.
~3000 replicated datasets, with a total of 1182000 resampled individuals.
~
PopName Lik_home
1Δ EST-JEN-ADU-2014-005Δ -3607.268857
2Δ EST-LAN-ADU-2013-001Δ -3254.926745
3Δ EST-GRA-ADU-2013-001Δ -3155.750285
4Δ EST-BUR-ADU-2013-001Δ -3160.311005
5Δ EST-GUL-ADU-2013-001Δ -3165.234524
6Δ EST-ANG-ADU-2013-001Δ -3125.735057
7Δ EST-FOX-ADU-2014-001Δ -3304.267038
8Δ EST-GOD-ADU-2013-001Δ -3251.260944
9Δ EST-CHU-ADU-2013-002Δ -3866.762481
OverallΔ -3260.446650
~
~
~Current and inferred population membership for all individuals, as well as ln(likelihood) for population membership for all individuals and all po
~
Individual Current Inferred Lik_max Lik_home Lik_ratio EST-JEN-ADU-2014-005 EST-LAN-ADU-2013-001 EST-GRA-ADU-2013-001 EST-BUR-ADU-
EST-JEN-ADU-2014-005 EST-JEN-ADU-2014-005 EST-LAN-ADU-2013-001 -2660.138042 -2804.357312 288.438540 -2804.357312 -2660.138042
EST-JEN-ADU-2014-006 EST-JEN-ADU-2014-005 EST-JEN-ADU-2014-005 -2774.592918 -2774.592918 0.000000 -2774.592918 -2949.354100
EST-JEN-ADU-2014-007 EST-JEN-ADU-2014-005 EST-JEN-ADU-2014-005 -2814.841158 -2814.841158 0.000000 -2814.841158 -2920.094303
EST-JEN-ADU-2014-009 EST-JEN-ADU-2014-005 EST-LAN-ADU-2013-001 -2478.859147 -2927.800672 897.883051 -2927.800672 -2478.859147
EST-JEN-ADU-2014-014 EST-JEN-ADU-2014-005 EST-JEN-ADU-2014-005 -2721.237286 -2721.237286 0.000000 -2721.237286 -2923.605814
EST-JEN-ADU-2014-016 EST-JEN-ADU-2014-005 EST-LAN-ADU-2013-001 -2928.464368 -3314.972629 773.016522 -3314.972629 -2928.464368
EST-JEN-ADU-2014-018 EST-JEN-ADU-2014-005 EST-LAN-ADU-2013-001 -2841.826950 -3261.324738 838.995576 -3261.324738 -2841.826950
EST-JEN-ADU-2014-019 EST-JEN-ADU-2014-005 EST-JEN-ADU-2014-005 -2621.580476 -2621.580476 0.000000 -2621.580476 -2811.872907
EST-JEN-ADU-2014-021 EST-JEN-ADU-2014-005 EST-LAN-ADU-2013-001 -2878.249012 -3345.890681 935.283338 -3345.890681 -2878.249012
EST-JEN-ADU-2014-023 EST-JEN-ADU-2014-005 EST-LAN-ADU-2013-001 -2844.390170 -3278.711101 868.641862 -3278.711101 -2844.390170
EST-LAN-ADU-2013-001 EST-LAN-ADU-2013-001 EST-LAN-ADU-2013-001 -3126.025542 -3126.025542 0.000000 -3126.025542 -3126.025542
EST-LAN-ADU-2013-002 EST-LAN-ADU-2013-001 EST-LAN-ADU-2013-001 -2565.169552 -2565.169552 0.000000 -3047.908890 -2565.169552
EST-LAN-ADU-2013-003 EST-LAN-ADU-2013-001 EST-ANG-ADU-2013-001 -3252.451165 -3272.447850 39.993371 -3768.541506 -3272.447850
EST-LAN-ADU-2013-004 EST-LAN-ADU-2013-001 EST-GRA-ADU-2013-001 -3110.939226 -3185.494708 149.110964 -3659.887957 -3185.494708
EST-LAN-ADU-2014-070 EST-LAN-ADU-2013-001 EST-LAN-ADU-2013-001 -2899.954541 -2899.954541 0.000000 -3303.617957 -2899.954541

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

arguments: pop.levels and pop.labels

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

↑ ↑
5 7

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

On 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, 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