

Vignette for package `resamplediversity`

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This vignette documents workflow from our paper^[1].

Installing the package

On Windows, you can install the R package `diversitycompare` with the following command

```
install.packages(file.choose(), repos = NULL)
```

whereupon a window will pop-up. You can now select the package binary (.zip). Instead of `file.choose()` you can specify a (full) path to the .zip file. Ultimately, you can build from the **source** tarball on any operating system platform.

Contact the author if you have a problem installing the package.

```
install.packages(pkgs = "/diversitycompare.tar.gz",  
                 repos = NULL,  
                 type = "source")
```

The Dinaric bears are used as the reference population. We can make a quick summary of the data and look at the loci that were used.

```
data(dinaric.genotypes)
```

```
summary(dinaric.genotypes)  
  
##  
## # Total number of genotypes: 513  
##  
## # Population sample sizes:  
##  
## 513  
##  
## # Number of alleles per locus:  
## L01 L02 L03 L04 L05 L06 L07 L08 L09 L10 L11 L12 L13 L14 L15  
## 6 9 9 7 7 7 6 10 10 6 8 10 6 8 7  
## L16 L17 L18 L19 L20  
## 8 7 6 10 7  
##  
## # Number of alleles per population:  
## 1  
## 136
```

```
##
## # Percentage of missing data:
## [1] 0.01949
##
## # Observed heterozygosity:
##      L01      L02      L03      L04      L05      L06      L07      L08
## 0.7680 0.7290 0.7602 0.7973 0.6530 0.6316 0.7563 0.7739
##      L09      L10      L11      L12      L13      L14      L15      L16
## 0.8187 0.6589 0.6250 0.6953 0.6842 0.7232 0.7817 0.7914
##      L17      L18      L19      L20
## 0.8012 0.5673 0.8674 0.7563
##
## # Expected heterozygosity:
##      L01      L02      L03      L04      L05      L06      L07      L08
## 0.7574 0.7107 0.7416 0.7889 0.6853 0.6371 0.7563 0.7798
##      L09      L10      L11      L12      L13      L14      L15      L16
## 0.8407 0.6478 0.6620 0.7222 0.6821 0.7409 0.7676 0.8097
##      L17      L18      L19      L20
## 0.8004 0.5911 0.8485 0.7793

locNames(dinaric.genotypes)

##      L01      L02      L03      L04      L05      L06      L07
## "Cxx20" "G10B" "G10C" "G10D" "G10J" "G10L" "G10M"
##      L08      L09      L10      L11      L12      L13      L14
## "G10P" "G10X" "G1A" "Mu05" "Mu09" "Mu10" "Mu11"
##      L15      L16      L17      L18      L19      L20
## "Mu15" "Mu23" "Mu50" "Mu51" "Mu59" "Mu61"
```

To compare genetic diversity indices between two populations, we need to have a common set of loci and provide correction for unequal sample sizes. The latter is especially important for estimates of allelic richness, as this parameter is heavily dependent on sample size (rare alleles will not make it when sample size is low). Expected heterozygosity is much more robust.

We first need a list of common markers. Let's look at a table of diversity parameters from different brown bear populations around the world (see table 1):

```
data(bear.diversity)
bear.diversity
```

Let's compare genetic diversity between Dinaric bears and bears in Kluane, Yukon. They were studied in study 2:

```
data(included.studies)
```

```
bear.diversity[4, ]
```

```
##      Population N Study      A  SEA  He  SEHe
## 4 Kluane, Yukon 50      2 7.38 0.56 0.76 0.025
```

```
included.studies[included.studies$ID == 2, ]
```

```
##      ID      Reference      GeoArea
## 2 2 Paetkau et al., 1998b North America
##
## 2 Exploration of variation in genetic diversity across the range North American brown bears
##      NP LocUsed LocCommon
## 2 11      8      8
```

Aim

Table 1: Table of brown bear diversity data from a number of studies around the world.

	Population	N	Study	A	SEA	He	SEHe
1	Carpathians - Romania (1)	16	5	7.78	0.81	0.81	0.01
2	Carpathians - Romania (2)	109	10	8.46	0.57	0.80	0.01
3	Alaska Range, Alaska	28	1			0.78	
4	Kluane, Yukon	50	2	7.38	0.56	0.76	0.02
5	Richardson Mountains, NWT	119	2	7.50	0.63	0.76	0.03
6	Brooks Range, Alaska	148	2	7.63	0.50	0.75	0.02
7	Croatia (Dinara-Pindos NW)	156	9	7.58	0.54	0.74	0.03
8	Slovenia (NW Dinaric Mountains)	513	0	6.68	0.41	0.73	0.02
9	Greece(Dinara-Pindos SE)	49	8	6.33	0.42	0.76	0.02
10	Carpathians - Northern Slovakia	71	10	6.08	0.29	0.71	0.02
11	Scandinavia - NN	29	3	5.59	0.40	0.69	0.02
12	Flathead River, BC/MT	40	2	6.50	0.71	0.69	0.03
13	Carpathians - Central Slovakia	96	10	6.00	0.25	0.70	0.03
14	Scandinavia - NS	108	3	6.18	0.35	0.69	0.03
15	West Slope, Alberta	41	2	6.38	0.56	0.68	0.04
16	Kuskokwim Range, Alaska	55	2	6.13	0.44	0.68	0.03
17	Scandinavia - M	88	3	5.94	0.40	0.68	0.02
18	Scandinavia - S	155	3	5.47	0.33	0.68	0.02
19	East Slope, Alberta	45	2	7.00	0.82	0.67	0.06
20	Carpathians - Eastern Slovakia	16	10	5.23	0.22	0.65	0.03
21	Paulatuk Alaska	58	2	5.75	0.88	0.65	0.65
22	Admiralty Island, Alaska	30	1			0.63	
23	Coppermine, NWT	36	2	5.75	1.03	0.61	0.07
24	Pakistan	28	4	3.92	0.38	0.58	0.04
25	Yellowstone, MT/WY	57	2	4.38	0.60	0.55	0.08
26	Cantabrian (Spain) - W	39	7	3.44	0.30	0.48	0.05
27	Baranof and Chicagof Is, Alaska	35	1			0.49	
28	Apennines	17	5	2.44	0.24	0.44	0.07
29	Gobi (Mongolia)	8	6	2.00		0.29	
30	Cantabrian (Spain) - E	8	7	1.75	0.17	0.28	0.06
31	Kodiak Island, Alaska	34	2	2.13	0.35	0.27	0.10

Looking at the original paper by Paetkau et al., the common markers between both populations are G10B, G10C, G10D, G10L, G10M, G10P, G10X, G1A. We look at the markers in the reference genotypes:

```
locNames(dinaric.genotypes)
```

##	L01	L02	L03	L04	L05	L06	L07
##	"Cxx20"	"G10B"	"G10C"	"G10D"	"G10J"	"G10L"	"G10M"
##	L08	L09	L10	L11	L12	L13	L14
##	"G10P"	"G10X"	"G1A"	"Mu05"	"Mu09"	"Mu10"	"Mu11"
##	L15	L16	L17	L18	L19	L20	
##	"Mu15"	"Mu23"	"Mu50"	"Mu51"	"Mu59"	"Mu61"	

Genetic diversity study of this population included samples of 50 individuals. We need to subset the locus panel using generic names of loci:

```
loci_na <- c("L02", "L03", "L04", "L06", "L07", "L08",
            "L09", "L10")
```

We will resample Dinaric genotypes multiple times to the same sample size that was used the Kluane population study (50 samples) using the same panel of loci to get comparable genetic diversity indices. This will take a while and produce a lot of relatively useless output from each subsample (omitted here)

```
resampled.ar <- subsample.gen(genotypes = dinaric.genotypes,
                             nboots = 1000,
                             nsamps = 50,
                             loci = loci_na)
```

Look at the results:

```
resampled.ar
##      A   SEA   He   SEHe   Ho   SEHo
## 1 6.119 0.7024 0.7311 0.02566 0.7415 0.03067
```

Now we can calculate diversity ratios between the Dinaric bear population and Kluane bears.

```
calcDivRat(ref = 6.12, SEref = 0.7, obs = 7.38,
            SEobs = 0.56, type = "A") #allelic richness ratio

##      Ar   SEAr
## 1 1.206 0.1655

calcDivRat(ref = 0.73, SEref = 0.026, obs = 0.76,
            SEobs = 0.025, type = "He") #heterozygosity ratio

##      Her   SEHer
## 1 1.041 0.05048
```

We can see that allelic richness is 21% higher in Kluane than in Dinaric Mountains, and heterozygosity 4%.

We can now batch-run the corrections for the entire set of North American populations studied by Paetkau et al. using the same locus set:

```
na.pops <- bear.diversity[bear.diversity$Study == 1 | bear.diversity$Study == 2,
                          ]
```

The batch run will TAKE A LONG TIME and produce a lot of useless output on screen. I reduced the number of resamples (`nboots`) to 100 to keep the computation time reasonable. In a real study, you would want `nboots` to be at least 1000.

```
adjusted_na <- runall(N = na.pops$N,
                     genotypes = dinaric.genotypes,
                     loci = loci_na,
                     nboots = 100)
```

Results are presented below.

```
# these are resampled value for the reference population,
# hence prefix 'ref'.
names(adjusted_na) <- paste("ref", names(adjusted_na),
                             sep = "")
pops.adjusted_na <- cbind(na.pops, adjusted_na)
pops.adjusted_na
```

Table 2: North American populations of brown bears studied by Paetkau et al.

	Population	N	Study	A	SEA	He	SEHe
3	Alaska Range, Alaska	28	1			0.78	
4	Kluane, Yukon	50	2	7.38	0.56	0.76	0.02
5	Richardson Mountains, NWT	119	2	7.50	0.63	0.76	0.03
6	Brooks Range, Alaska	148	2	7.63	0.50	0.75	0.02
12	Flathead River, BC/MT	40	2	6.50	0.71	0.69	0.03
15	West Slope, Alberta	41	2	6.38	0.56	0.68	0.04
16	Kuskoskwim Range, Alaska	55	2	6.13	0.44	0.68	0.03
19	East Slope, Alberta	45	2	7.00	0.82	0.67	0.06
21	Paulatuk Alaska	58	2	5.75	0.88	0.65	0.65
22	Admiralty Island, Alaska	30	1			0.63	
23	Coppermine, NWT	36	2	5.75	1.03	0.61	0.07
25	Yellowstone, MT/WY	57	2	4.38	0.60	0.55	0.08
27	Baranof and Chicagof Is, Alaska	35	1			0.49	
31	Kodiak Island, Alaska	34	2	2.13	0.35	0.27	0.10

```

##              Population  N Study  A  SEA
## 3      Alaska Range, Alaska 28    1  NA  NA
## 4      Kluane, Yukon      50    2  7.38 0.56
## 5      Richardson Mountains, NWT 119  2  7.50 0.63
## 6      Brooks Range, Alaska 148    2  7.63 0.50
## 12     Flathead River, BC/MT 40    2  6.50 0.71
## 15     West Slope, Alberta 41    2  6.38 0.56
## 16     Kuskoskwim Range, Alaska 55    2  6.13 0.44
## 19     East Slope, Alberta 45    2  7.00 0.82
## 21     Paulatuk Alaska 58    2  5.75 0.88
## 22     Admiralty Island, Alaska 30    1  NA  NA
## 23     Coppermine, NWT 36    2  5.75 1.03
## 25     Yellowstone, MT/WY 57    2  4.38 0.60
## 27 Baranof and Chicagof Is, Alaska 35    1  NA  NA
## 31     Kodiak Island, Alaska 34    2  2.13 0.35
##      He  SEHe      refPopulation refN
## 3  0.78  NA      Alaska Range, Alaska 28
## 4  0.76 0.025      Kluane, Yukon      50
## 5  0.76 0.030      Richardson Mountains, NWT 119
## 6  0.75 0.019      Brooks Range, Alaska 148
## 12 0.69 0.027      Flathead River, BC/MT 40
## 15 0.68 0.036      West Slope, Alberta 41
## 16 0.68 0.026      Kuskoskwim Range, Alaska 55
## 19 0.67 0.062      East Slope, Alberta 45
## 21 0.65 0.650      Paulatuk Alaska 58
## 22 0.63  NA      Admiralty Island, Alaska 30
## 23 0.61 0.073      Coppermine, NWT 36
## 25 0.55 0.081      Yellowstone, MT/WY 57
## 27 0.49  NA Baranof and Chicagof Is, Alaska 35
## 31 0.27 0.098      Kodiak Island, Alaska 34
##      refStudy refA refSEA refHe refSEHe
## 3      1  NA  NA 0.78  NA
## 4      2  7.38 0.56 0.76 0.025
## 5      2  7.50 0.63 0.76 0.030
## 6      2  7.63 0.50 0.75 0.019
## 12     2  6.50 0.71 0.69 0.027
## 15     2  6.38 0.56 0.68 0.036

```

```

## 16      2 6.13   0.44  0.68   0.026
## 19      2 7.00   0.82  0.67   0.062
## 21      2 5.75   0.88  0.65   0.650
## 22      1  NA    NA   0.63    NA
## 23      2 5.75   1.03  0.61   0.073
## 25      2 4.38   0.60  0.55   0.081
## 27      1  NA    NA   0.49    NA
## 31      2 2.13   0.35  0.27   0.098
##          refrefPopulation refrefN refrefStudy
## 3          Alaska Range, Alaska      28          1
## 4              Kluane, Yukon          50          2
## 5      Richardson Mountains, NWT     119          2
## 6          Brooks Range, Alaska     148          2
## 12         Flathead River, BC/MT      40          2
## 15         West Slope, Alberta        41          2
## 16      Kuskoskwim Range, Alaska      55          2
## 19         East Slope, Alberta        45          2
## 21         Paulatuk Alaska           58          2
## 22      Admiralty Island, Alaska      30          1
## 23         Coppermine, NWT           36          2
## 25         Yellowstone, MT/WY        57          2
## 27 Baranof and Chicagof Is, Alaska    35          1
## 31         Kodiak Island, Alaska      34          2
##          refrefA refrefSEA refrefHe refrefSEHe refrefV1 refrefA
## 3          NA      NA      0.78      NA      28   5.836
## 4      7.38      0.56      0.76      0.025      50   6.156
## 5      7.50      0.63      0.76      0.030     119   6.491
## 6      7.63      0.50      0.75      0.019     148   6.585
## 12     6.50      0.71      0.69      0.027      40   6.041
## 15     6.38      0.56      0.68      0.036      41   6.051
## 16     6.13      0.44      0.68      0.026      55   6.141
## 19     7.00      0.82      0.67      0.062      45   6.074
## 21     5.75      0.88      0.65      0.650      58   6.183
## 22      NA      NA      0.63      NA      30   5.895
## 23     5.75      1.03      0.61      0.073      36   5.963
## 25     4.38      0.60      0.55      0.081      57   6.129
## 27      NA      NA      0.49      NA      35   5.944
## 31     2.13      0.35      0.27      0.098      34   5.923
##          refrefSEA refrefHe refrefSEHe refrefHo refrefSEHo refAr
## 3      0.6606  0.7254  0.0268  0.7395  0.03776  NA
## 4      0.7025  0.7315  0.02547  0.7423  0.0309  1
## 5      0.7163  0.7345  0.0255  0.7407  0.02679  1
## 6      0.7272  0.7361  0.02489  0.7411  0.02526  1
## 12     0.6935  0.7288  0.0257  0.7397  0.03299  1
## 15     0.7008  0.7296  0.02618  0.743  0.03064  1
## 16     0.7001  0.7313  0.02531  0.7423  0.03061  1
## 19     0.6863  0.729  0.02563  0.7387  0.03089  1
## 21     0.7092  0.7314  0.02595  0.7407  0.03156  1
## 22     0.6915  0.7264  0.02634  0.7386  0.03598  NA
## 23     0.6872  0.7269  0.02613  0.7341  0.03278  1
## 25     0.7122  0.7307  0.0257  0.74  0.03031  1
## 27     0.6874  0.7259  0.02605  0.739  0.03328  NA
## 31     0.677  0.726  0.02591  0.7411  0.03369  1
##          refSEAr refHer refSEHer
## 3          NA      1      NA
## 4  0.10731      1  0.04652
## 5  0.11879      1  0.05582
## 6  0.09267      1  0.03583
## 12 0.15448      1  0.05534
## 15 0.12413      1  0.07487
## 16 0.10151      1  0.05407
## 19 0.16567      1  0.13087

```

```
## 21 0.21644      1  1.41421
## 22      NA      1      NA
## 23 0.25333      1  0.16924
## 25 0.19373      1  0.20828
## 27      NA      1      NA
## 31 0.23238      1  0.51331
```

We can now calculate diversity ratios:

```
Ar.na <- with(pops.adjusted_na,
              calcDivRat(ref = refA, SEref = refSEA, obs = A,
                        SEobs = SEA, type = "A"))
Her.na <- with(pops.adjusted_na,
              calcDivRat(ref = refHe, SEref = refSEHe, obs = He,
                        SEobs = SEHe, type = "He"))
pops.adjusted_na <- cbind(adjusted_na, Ar.na, Her.na)
pops.adjusted_na[, c("Population", "Ar", "SEAr", "Her", "SEHer")]

## Error: undefined columns selected
```

To compare Cantabrian bears to the populations in North America, we also calculate reference-population calibrated ratios for this population, and we have comparable genetic diversity indices even if different locus panels and different sample sizes were used. Result is presented in table ??.

```
cant.pops <- bear.diversity[bear.diversity$Study == 7, ]
loci_cant <- c("L02", "L03", "L04", "L05", "L06", "L08", "L09",
              "L10", "L11", "L12", "L13", "L18", "L19", "L20")
adjusted_cant <- runall(N = cant.pops$N,
                      genotypes = dinaric.genotypes,
                      loci = loci_cant,
                      nboots = 100)
names(adjusted_cant) <- paste("ref", names(adjusted_cant), sep = "_")
pops.adjusted_cant <- cbind(cant.pops, adjusted_cant)

Ar.cant <- with(pops.adjusted_cant,
              calcDivRat(ref = refA, SEref = refSEA, obs = A,
                        SEobs = SEA, type = "A"))
Her.cant <- with(pops.adjusted_cant,
              calcDivRat(ref = refHe, SEref = refSEHe, obs = He,
                        SEobs = SEHe, type = "He"))
pops.adjusted_cant <- cbind(adjusted_cant, Ar.cant, Her.cant)

pops.comparison <- rbind(
  pops.adjusted_na,
  pops.adjusted_cant)

pops.comparison[, c("Population", "Ar", "SEAr", "Her", "SEHer")]
```

Look at the population comparison with comparable diversity indices:

```
## Error: object 'pops.comparison' not found
```

Results from the paper

Only resampling reference population corrections are done. You can calculate Ar and Her on your own as an exercise (see the example in previous section).

North America^[2, 3]

Nsamples_usa is a vector of the number of samples.

```
loci_usa <- c("L02", "L03", "L04", "L06",  
             "L07", "L08", "L09", "L10")  
Nsamples_usa <- c(28, 50, 119, 148, 40, 41, 55, 45,  
                 58, 30, 36, 57, 35, 34)  
adjusted_usa <- runall(N = Nsamples_usa,  
                      genotypes = dinaric.genotypes,  
                      loci = loci_usa, nboots = 1000)
```

```
adjusted_usa  
  
##           A      SEA    He      SEHe    Ho      SEHo  
## [1,] 28  5.839 0.6745 0.7242 0.02686 0.7396 0.03621  
## [2,] 50  6.102 0.7021 0.7305 0.02586 0.7404 0.03094  
## [3,] 119 6.479 0.7203 0.7348 0.02512 0.7413 0.02617  
## [4,] 148 6.559 0.7225 0.7352 0.02501 0.7405 0.02579  
## [5,] 40  6.023 0.6929 0.7286 0.02588 0.7412 0.03247  
## [6,] 41  6.036 0.6954 0.7282 0.02596 0.7408 0.03187  
## [7,] 55  6.172 0.7042 0.7317 0.0257  0.7414 0.03029  
## [8,] 45  6.064 0.6957 0.7302 0.02577 0.7407 0.03144  
## [9,] 58  6.175 0.707  0.7315 0.02556 0.7403 0.03009  
## [10,] 30 5.882 0.6795 0.7257 0.0265  0.7411 0.03511  
## [11,] 36 5.967 0.6872 0.7278 0.0261  0.7406 0.03304  
## [12,] 57 6.168 0.7079 0.7317 0.02559 0.7414 0.03007  
## [13,] 35 5.95  0.6897 0.7278 0.02607 0.7413 0.03332  
## [14,] 34 5.935 0.6896 0.7271 0.02621 0.74  0.03393
```

Scandinavia^[4]

```
loci_skandinavia <- c("L02", "L03", "L04", "L05", "L06", "L07",  
                     "L08", "L09", "L10", "L11", "L13", "L15",  
                     "L17", "L18", "L19", "L20")  
Nsamples_skand <- c(108, 29, 155, 88)  
adjusted_skand <- runall(N = Nsamples_skand,  
                        genotypes = dinaric.genotypes,  
                        loci = loci_skandinavia,  
                        nboots = 1000)
```

```
adjusted_skand  
  
##           A      SEA    He      SEHe    Ho      SEHo  
## [1,] 108 6.101 0.44  0.7289 0.01916 0.7288 0.02319  
## [2,] 29  5.599 0.4173 0.7196 0.01993 0.7292 0.02863  
## [3,] 155 6.225 0.4436 0.7301 0.01911 0.7296 0.0224  
## [4,] 88  6.039 0.4369 0.7282 0.01915 0.7291 0.02357
```


Romania and Ital^[5]

```
loci_RO_I <- c("L02", "L03", "L04", "L06", "L08",  
              "L10", "L15", "L18", "L19")  
Nsamples_ROI <- c(16, 17)  
adjusted_ROI <- runall(N = Nsamples_ROI,  
                       genotypes = dinaric.genotypes,  
                       loci = loci_RO_I,  
                       nboots = 1000)
```

```
adjusted_ROI  
  
##           A      SEA    He      SEHe    Ho      SEHo  
## [1,] 16 5.156 0.5557 0.7017 0.02995 0.7291 0.04586  
## [2,] 17 5.193 0.561 0.7025 0.02993 0.7303 0.04628
```

Cantabria^[6]

```
loci_Cantabria <- c("L02", "L03", "L04", "L05", "L06", "L08",  
                   "L09", "L10", "L11", "L12", "L13", "L18",  
                   "L19", "L20")  
Nsamples_Cant <- c(8, 39)  
adjusted_Cant <- runall(N = Nsamples_Cant,  
                        genotypes = dinaric.genotypes,  
                        loci = loci_Cantabria,  
                        nboots = 1000)
```

```
adjusted_Cant  
  
##           A      SEA    He      SEHe    Ho      SEHo  
## [1,] 8 4.574 0.3791 0.6774 0.02534 0.7155 0.04667  
## [2,] 39 5.739 0.4838 0.7135 0.02169 0.7162 0.02909
```

Pakistan^[7]

```
loci_Pakistan <- c("L02", "L03", "L04", "L05", "L06", "L09",  
                  "L10", "L13", "L15", "L17", "L18", "L19")  
Nsamples_Pak <- 28  
adjusted_pak <- runall(N = Nsamples_Pak,  
                       genotypes = dinaric.genotypes,  
                       loci = loci_Pakistan,  
                       nboots = 1000)
```

```
adjusted_pak  
  
##           A      SEA    He      SEHe    Ho      SEHo  
## [1,] 28 5.451 0.5292 0.7151 0.02467 0.7285 0.03457
```

Greece^[8]

```

loci_Greece <- c("L03", "L04", "L05", "L08", "L17", "L19")
Nsamples_Greece <- 49
adjusted_Greece <- runall(N = Nsamples_Greece,
                          genotypes = dinaric.genotypes,
                          loci = loci_Greece,
                          nboots = 1000)

```

```

adjusted_Greece

##           A      SEA    He    SEHe    Ho    SEHo
## [1,] 49 6.542 0.5168 0.766 0.02353 0.7751 0.03569

```

Croatia^[9]

```

loci_Croatia <- c("L02", "L03", "L04", "L05", "L06", "L08",
                  "L09", "L13", "L17", "L18", "L19")
Nsamples_Croatia <- 156
adjusted_Croatia <- runall(N = Nsamples_Croatia,
                          genotypes = dinaric.genotypes,
                          loci = loci_Croatia,
                          nboots = 1000)

```

```

adjusted_Croatia

##           A      SEA    He    SEHe    Ho    SEHo
## [1,] 156 6.467 0.6018 0.7346 0.02525 0.7348 0.0292

```

Slovakia and Romania^[10]

```

loci_SkRo <- c("L02", "L03", "L04", "L05", "L06", "L07",
               "L08", "L09", "L13", "L17", "L18", "L19")
Nsamples_SkRo <- c(71,96,16,109)
adjusted_SkRo <- runall(N = Nsamples_SkRo,
                      genotypes = dinaric.genotypes,
                      loci = loci_SkRo,
                      nboots = 1000)

```

```

adjusted_SkRo

##           A      SEA    He    SEHe    Ho    SEHo
## [1,] 71 6.2 0.5352 0.7332 0.02346 0.7357 0.02891
## [2,] 96 6.293 0.5426 0.7348 0.02329 0.7367 0.02806
## [3,] 16 5.47 0.4896 0.7154 0.02486 0.7366 0.03938
## [4,] 109 6.332 0.5446 0.7351 0.02318 0.736 0.02761

```

Gobi^[11]

```

loci_gobi <- c("L02", "L03", "L04", "L06", "L09", "L10")
Nsamples_gobi <- 8
adjusted_gobi <- runall(N = Nsamples_gobi,
                      genotypes = dinaric.genotypes,
                      loci = loci_gobi,
                      nboots = 1000)

```

```
adjusted_gobi
```

```
##          A      SEA    He      SEHe    Ho      SEHo
## [1,] 8 4.606 0.6216 0.6836 0.03814 0.7344 0.06758
```

References

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- [11] McCarthy TM, Waits LP, Mijiddorj B (2009). Status of the Gobi bear in Mongolia as determined by noninvasive genetic methods. *Ursus* 20(1): 30-38.

```

sessionInfo()

## R version 2.15.1 (2012-06-22)
## Platform: x86_64-pc-mingw32/x64 (64-bit)
##
## locale:
## [1] LC_COLLATE=Slovenian_Slovenia.1250
## [2] LC_CTYPE=Slovenian_Slovenia.1250
## [3] LC_MONETARY=Slovenian_Slovenia.1250
## [4] LC_NUMERIC=C
## [5] LC_TIME=Slovenian_Slovenia.1250
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets
## [6] methods   base
##
## other attached packages:
## [1] adegenet_1.3-4 ade4_1.5-0      MASS_7.3-18
## [4] xtable_1.7-0   knitr_0.6.3
##
## loaded via a namespace (and not attached):
## [1] codetools_0.2-8 digest_0.5.2   evaluate_0.4.2
## [4] formatR_0.4     highlight_0.3.1 parser_0.0-14
## [7] plyr_1.7.1      Rcpp_0.9.10   stringr_0.6
## [10] tools_2.15.1

```