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.

Should you have problem installing the package, do not hesitate to contact the author.

```
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)

## Length  Class   Mode
##      1 genind     S4

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
```

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	Carphatians - 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	Kuskoskwim 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 Chicgagof 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

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
##                                                                              Aim
## 2 Exploration of variation in genetic diversity across the range North American brown bears
##    NP LocUsed LocCommon
## 2 11       8         8
```

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 28 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 sampe 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, and heterozgosity 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. Result can be found in table 2.

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

Table 2: Diversity ratios between Dinaric bear population and Kluane bears.

	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 Chicgagof Is, Alaska	35	1			0.49	
31	Kodiak Island, Alaska	34	2	2.13	0.35	0.27	0.10

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 = "")
adjusted_na <- cbind(na.pops, adjusted_na)
adjusted_na
```

```
##                            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 Chicgagof 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 Chicgagof 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 Chicgagof 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:

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

##                          Population Ar    SEAr Her    SEHer
## 3              Alaska Range, Alaska NA      NA   1       NA
## 4                     Kluane, Yukon  1 0.10731   1  0.04652
## 5         Richardson Mountains, NWT  1 0.11879   1  0.05582
## 6              Brooks Range, Alaska  1 0.09267   1  0.03583
## 12            Flathead River, BC/MT  1 0.15448   1  0.05534
## 15              West Slope, Alberta  1 0.12413   1  0.07487
```

```
## 16          Kuskoskwim Range, Alaska  1 0.10151   1 0.05407
## 19             East Slope, Alberta  1 0.16567   1 0.13087
## 21               Paulatuk Alaska  1 0.21644   1 1.41421
## 22         Admiralty Island, Alaska NA      NA   1      NA
## 23               Coppermine, NWT  1 0.25333   1 0.16924
## 25             Yellowstone, MT/WY  1 0.19373   1 0.20828
## 27 Baranof and Chicgagof Is, Alaska NA      NA   1      NA
## 31              Kodiak Island, Alaska  1 0.23238   1 0.51331
```

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 ??.

```r
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 = "")
adjusted_cant <- cbind(cant.pops, adjusted_cant)

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

adjusted_na_out <- adjusted_na[, c("Population", "Ar", "SEAr",
                                   "Her", "SEHer")]
names(adjusted_na_out) <- c("Population", "A", "SEA",
                            "He", "SEHe")
pops.comparison <- rbind(
        adjusted_na_out,
        adjusted_cant[, c("Population", "A", "SEA",
                          "He", "SEHe")])

pops.comparison
```

Look at the population comparison with comparable diversity indices:

```
## Error: error in evaluating the argument 'x' in selecting a
## method for function 'print': Error in
## xtable(pops.comparison, caption = "reference-population
## calibrated ratios for this population", : object
## 'pops.comparison' not found
```

Results from the paper

North America[2, 3]

`Nsamples_usa` is a vector of the number of samples.

```r
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]

```r
loci_skandinavija <- 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_skandinavija,
                         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
```

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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 2.15.0 (2012-03-30)
## 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] splines   tools     stats     graphics  grDevices
## [6] utils     datasets  methods   base
##
## other attached packages:
##  [1] adegenet_1.3-4   ade4_1.5-0       MASS_7.3-17
##  [4] xtable_1.7-0     rms_3.5-0        Hmisc_3.9-3
##  [7] survival_2.36-12 highlight_0.3.1  parser_0.0-14
## [10] Rcpp_0.9.10      codetools_0.2-8  gmodels_2.15.3
## [13] Matrix_1.0-6     lattice_0.20-6   knitr_0.6.3
## [16] nlme_3.1-103     ggplot2_0.9.1
##
## loaded via a namespace (and not attached):
##  [1] car_2.0-12        cluster_1.14.2
##  [3] colorspace_1.1-1  dichromat_1.2-4
##  [5] digest_0.5.2      evaluate_0.4.2
##  [7] formatR_0.4       gdata_2.11.0
##  [9] grid_2.15.0       gtools_2.7.0
## [11] labeling_0.1      memoise_0.1
## [13] munsell_0.3       plyr_1.7.1
## [15] proto_0.3-9.2     RColorBrewer_1.0-5
## [17] reshape2_1.2.1    scales_0.2.1
## [19] stringr_0.6
```