Undaria pinnatifida

Uwai et al. - 2006 - Phycologia

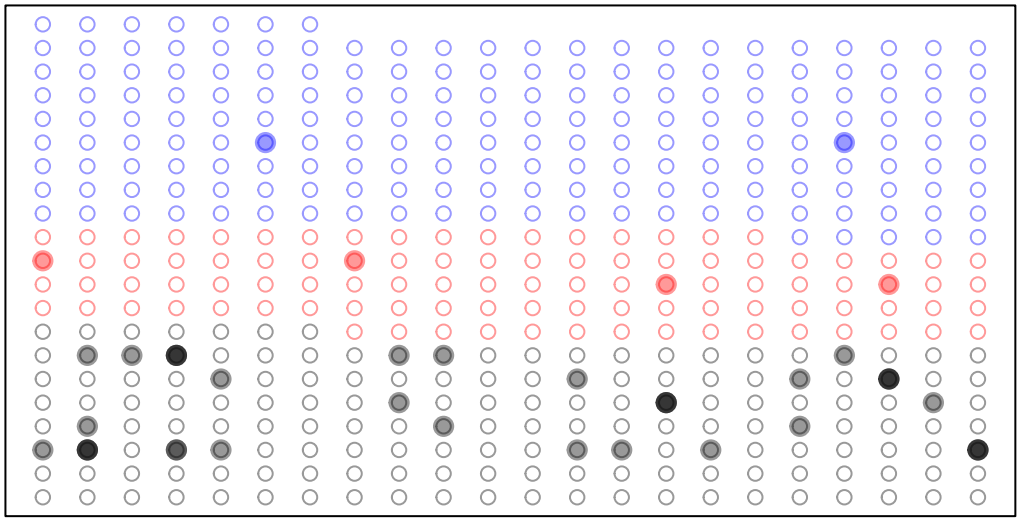
Using Korea and Japan (native), wNA and Eur only

nloci = 2 concatenated mtDNA sequences

nind = 141 ind (Native, wNA, Eur only)

```
## spatstat.geom 2.4-0

## spatstat.random 2.2-0

## spatstat.core 2.4-4

## spatstat.linnet 2.3-2

##
## spatstat 2.3-4       (nickname: 'Watch this space')
## For an introduction to spatstat, type 'beginner'
```

Asia (black); wNA (red); Europe (blue)

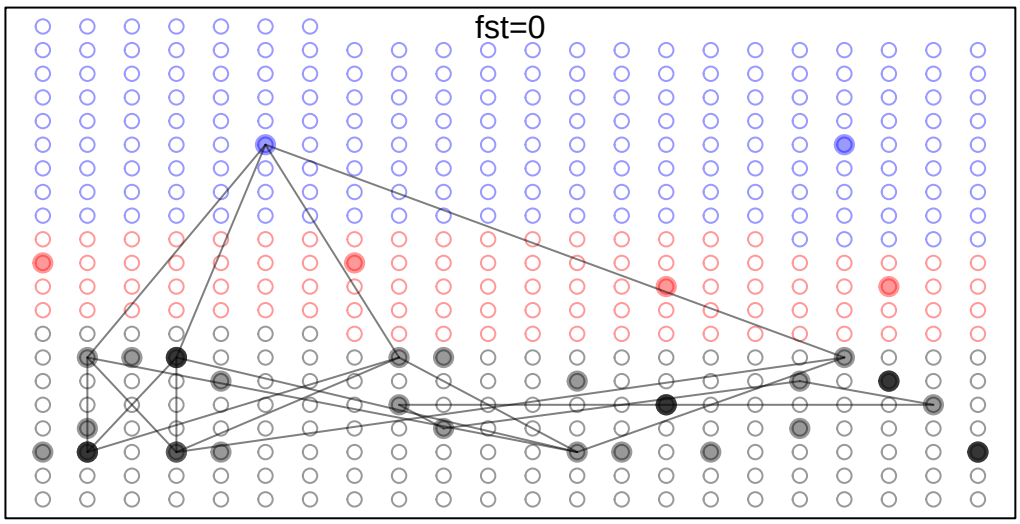


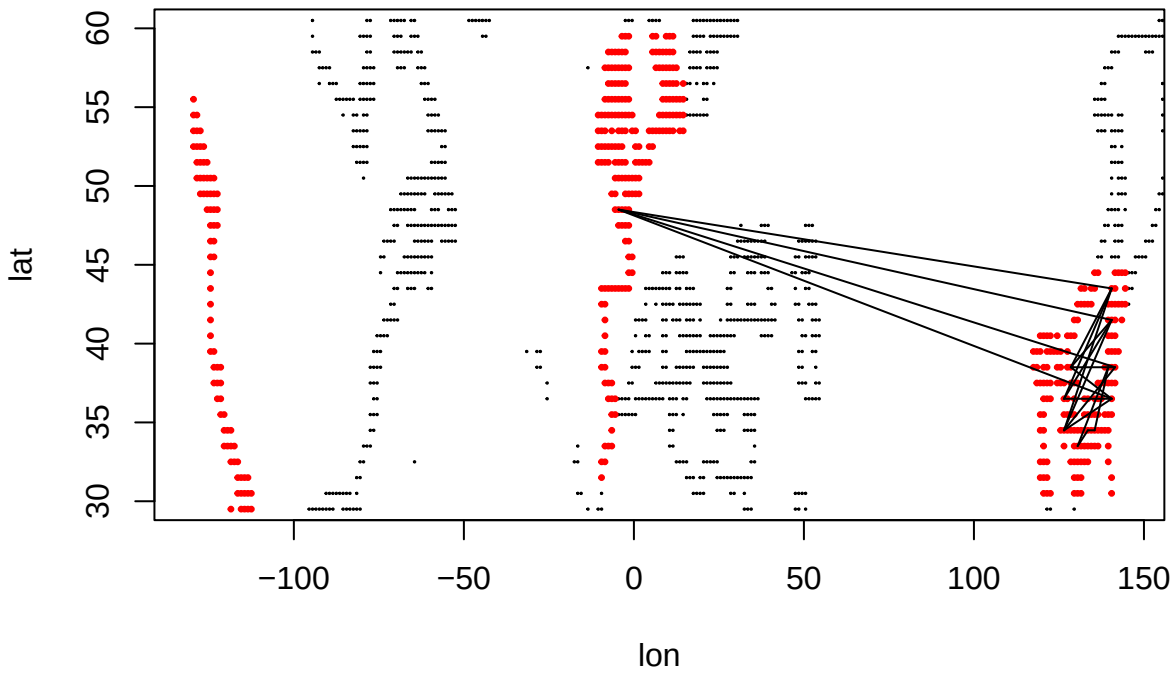
combine pops in that are within the same 1x1º block

Phist

```
##                    label gridID.1 gridID.2 n.1 n.2 CHIsq CHIsq_p.val Fst
## 1  1039 (4) v. 1291 (2)     1039     1291   4   2     6           1   0
## 2  1039 (4) v. 1417 (5)     1039     1417   4   5     9           1   0
## 3 1039 (4) v. 15652 (2)     1039    15652   4   2     6           1   0
## 4 1039 (4) v. 15777 (2)     1039    15777   4   2     6           1   0
## 5  1039 (4) v. 1669 (5)     1039     1669   4   5     9           1   0
## 6 1039 (4) v. 31566 (7)     1039    31566   4   7    11           1   0
##   Fst_p.val PHIst PHIst_p.val
## 1         1    NA          NA
## 2         1    NA          NA
## 3         1     1   0.6666667
## 4         1     1   0.6666667
## 5         1     1   0.6666667
## 6         1     1   0.6666667
```

Asia (black); wNA (red); Europe (blue)




lat
30
35
40
45
50
55
60
−100
−50
0
50
100
150
lon

overall Fst

```
##          estimate     p.val
## CHIsq 3536.000000 1.0000000
## Fst      0.000000 1.0000000
## PHIst    0.639247 0.6666667
```

3 region Fst

```
##                        label gridID.1 gridID.2 n.1 n.2 CHIsq CHIsq_p.val Fst
## 1 1_Asia (116) v. 2_wNA (16)   1_Asia    2_wNA 116  16   132           1   0
## 2  1_Asia (116) v. 3_Eur (4)   1_Asia    3_Eur 116   4   120           1   0
## 3    2_wNA (16) v. 3_Eur (4)    2_wNA    3_Eur  16   4    20           1   0
##   Fst_p.val      PHIst PHIst_p.val
## 1         1 0.17948995   0.6666667
## 2         1 0.06937589   0.6666667
## 3         1 0.59183612   0.6666667
```

native vs non-native Fst

```
##                           label gridID.1  gridID.2 n.1 n.2 CHIsq CHIsq_p.val
## 1 native (116) v. nonnative (20)   native nonnative 116  20   136           1
##   Fst Fst_p.val    PHIst PHIst_p.val
## 1   0         1 0.112597   0.6666667
```

within pop nucleotide divergence (also saved between pop divergence)

```
##     locus stratum         mean q.0      q.0.025        q.0.5     q.0.975
## 1  gene.1    1039 0.0000000000   0 0.000000e+00 0.0000000000 0.000000000
## 2  gene.1    1291 0.0000000000   0 0.000000e+00 0.0000000000 0.000000000
## 3  gene.1    1417 0.0000000000   0 0.000000e+00 0.0000000000 0.000000000
## 4  gene.1   15652 0.0000000000   0 0.000000e+00 0.0000000000 0.000000000
## 5  gene.1   15777 0.0000000000   0 0.000000e+00 0.0000000000 0.000000000
## 6  gene.1    1669 0.0000000000   0 0.000000e+00 0.0000000000 0.000000000
## 7  gene.1   31566 0.0000000000   0 0.000000e+00 0.0000000000 0.000000000
## 8  gene.1   32039 0.0000000000   0 0.000000e+00 0.0000000000 0.000000000
## 9  gene.1   32041 0.0000000000   0 0.000000e+00 0.0000000000 0.000000000
## 10 gene.1   32287 0.0000000000   0 0.000000e+00 0.0000000000 0.000000000
## 11 gene.1   32415 0.0007550019   0 5.662514e-05 0.0011325028 0.001132503
## 12 gene.1   32542 0.0013590034   0 2.548131e-04 0.0011325028 0.002265006
## 13 gene.1   32668 0.0000000000   0 0.000000e+00 0.0000000000 0.000000000
## 14 gene.1   32916 0.0000000000   0 0.000000e+00 0.0000000000 0.000000000
## 15 gene.1   33041 0.0060980922   0 0.000000e+00 0.0090600227 0.011325028
## 16 gene.1   33166 0.0031710079   0 0.000000e+00 0.0000000000 0.007927520
## 17 gene.1   33291 0.0000000000   0 0.000000e+00 0.0000000000 0.000000000
## 18 gene.1   33541 0.0007550019   0 5.662514e-05 0.0011325028 0.001132503
## 19 gene.1   33662 0.0000000000   0 0.000000e+00 0.0000000000 0.000000000
## 20 gene.1   33665 0.0000000000   0 0.000000e+00 0.0000000000 0.000000000
## 21 gene.1   33782 0.0005662514   0 0.000000e+00 0.0005662514 0.001132503
## 22 gene.1   33783 0.0000000000   0 0.000000e+00 0.0000000000 0.000000000
## 23 gene.1   33784 0.0038436460   0 0.000000e+00 0.0011325028 0.009060023
## 24 gene.1   33789 0.0007550019   0 5.662514e-05 0.0011325028 0.001132503
## 25 gene.1   33790 0.0000000000   0 0.000000e+00 0.0000000000 0.000000000
## 26 gene.1   33905 0.0000000000   0 0.000000e+00 0.0000000000 0.000000000
## 27 gene.1   33912 0.0006066979   0 0.000000e+00 0.0011325028 0.001132503
##            q.1
## 1  0.000000000
## 2  0.000000000
## 3  0.000000000
## 4  0.000000000
## 5  0.000000000
## 6  0.000000000
## 7  0.000000000
## 8  0.000000000
## 9  0.000000000
## 10 0.000000000
## 11 0.001132503
## 12 0.002265006
## 13 0.000000000
## 14 0.000000000
## 15 0.011325028
## 16 0.007927520
## 17 0.000000000
## 18 0.001132503
## 19 0.000000000
## 20 0.000000000
## 21 0.001132503
## 22 0.000000000
## 23 0.009060023
```

```
## 24 0.001132503
## 25 0.000000000
## 26 0.000000000
## 27 0.001132503
```

Asia (black); wNA (red); Europe (blue)