

Battillaria attramentaria

Miura et al 2006 PNAS

Using Japan (native) vs wNA

nloci = 1 mtDNA sequences

nind = 180 ind

```
## spatstat.geom 2.4-0
```

```
## spatstat.random 2.2-0
```

```
## spatstat.core 2.4-4
```

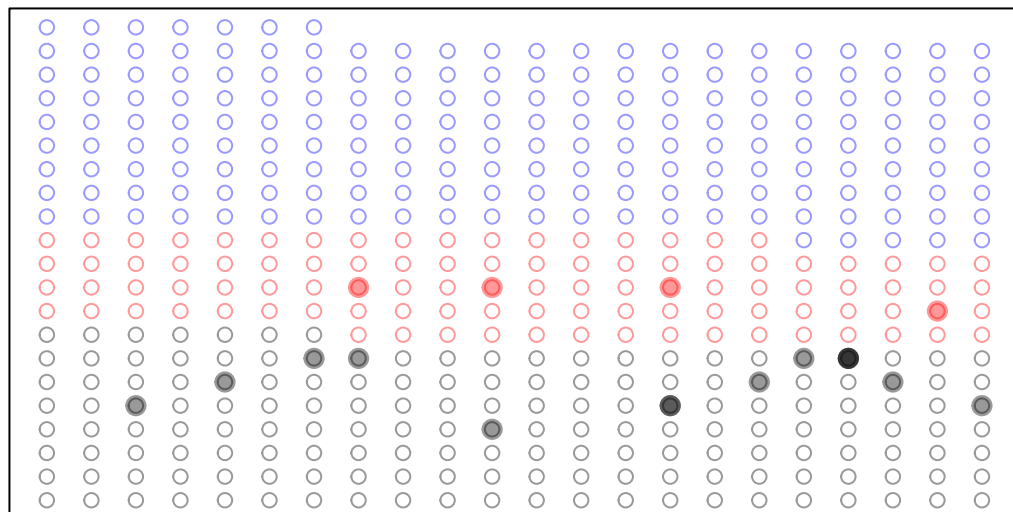
```
## spatstat.linnet 2.3-2
```

```
##
```

```
## spatstat 2.3-4      (nickname: 'Watch this space')
```

```
## For an introduction to spatstat, type 'beginner'
```

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

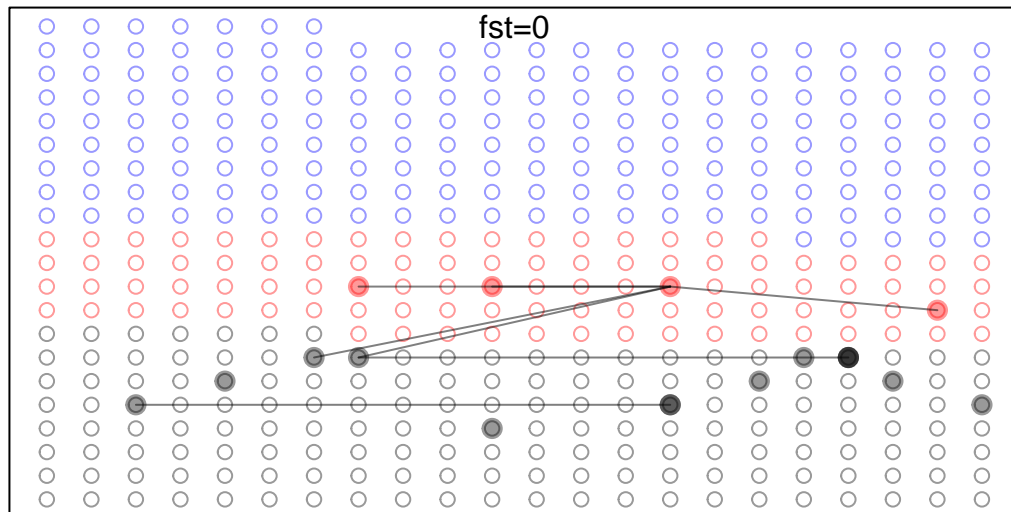


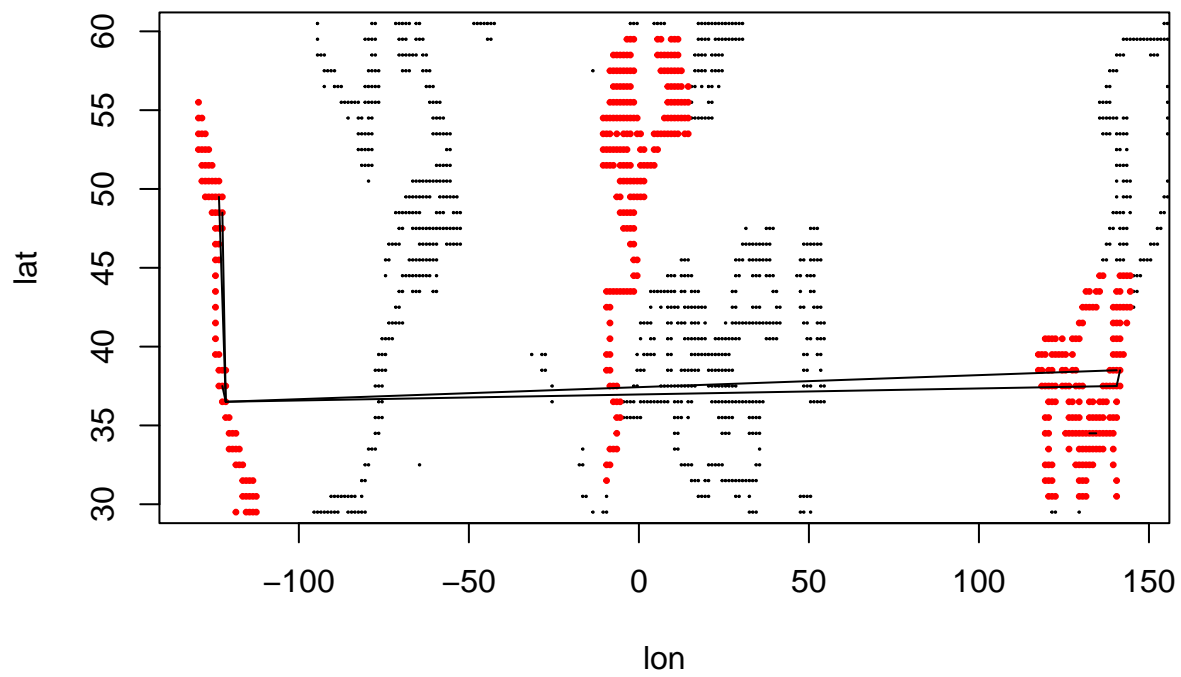
combine pops in that are within the same $1 \times 1^\circ$ block

Phist

```
##          label gridID.1 gridID.2 n.1 n.2 CHIsq CHIsq_p.val Fst
## 1 1039 (10) v. 32543 (10) 1039 32543 10 10 20 1 0
## 2 1039 (10) v. 32791 (10) 1039 32791 10 10 20 1 0
## 3 1039 (10) v. 33041 (20) 1039 33041 10 20 30 1 0
## 4 1039 (10) v. 33167 (10) 1039 33167 10 10 20 1 0
## 5 1039 (10) v. 33291 (10) 1039 33291 10 10 20 1 0
## 6 1039 (10) v. 33661 (10) 1039 33661 10 10 20 1 0
## Fst_p.val PHist PHist_p.val
## 1 1 0.7448023 0.6666667
## 2 1 0.8941836 0.6666667
## 3 1 0.9276992 0.6666667
## 4 1 0.9238045 0.6666667
## 5 1 0.8830943 0.6666667
## 6 1 0.9854243 0.6666667
```

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





overall Fst

```
##          estimate      p.val
## CHIsq 2520.000000 1.0000000
## Fst      0.000000 1.0000000
## PHIs     0.786847 0.6666667
```

3 region Fst

```
##          label gridID.1 gridID.2 n.1 n.2 CHIsq CHIsq_p.val Fst
## 1 1_Asia (140) v. 2_wNA (40) 1_Asia 2_wNA 140 40 180      1 0
## Fst_p.val PHIs PHIs_p.val
## 1      1 0.167125 0.6666667
```

native vs non-native Fst

```
##          label gridID.1 gridID.2 n.1 n.2 CHIsq CHIsq_p.val
## 1 native (140) v. nonnative (40) native nonnative 140 40 180      1
## Fst Fst_p.val PHIs PHIs_p.val
## 1 0      1 0.167125 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	q.1
## 1	gene.1	1039	0.0011668611	0	0	0.000000000	0.004667445	0.005834306
## 2	gene.1	32543	0.0070530274	0	0	0.007001167	0.015169195	0.015169195
## 3	gene.1	32791	0.0000000000	0	0	0.000000000	0.000000000	0.000000000
## 4	gene.1	33041	0.0001166861	0	0	0.000000000	0.001166861	0.001166861
## 5	gene.1	33167	0.0004667445	0	0	0.000000000	0.001166861	0.002333722
## 6	gene.1	33291	0.0002333722	0	0	0.000000000	0.001166861	0.001166861
## 7	gene.1	33661	0.0000000000	0	0	0.000000000	0.000000000	0.000000000
## 8	gene.1	33665	0.0023596525	0	0	0.001166861	0.006884481	0.007001167
## 9	gene.1	33787	0.0000000000	0	0	0.000000000	0.000000000	0.000000000
## 10	gene.1	33788	0.0033709322	0	0	0.000000000	0.012835473	0.012835473
## 11	gene.1	33911	0.0004667445	0	0	0.000000000	0.001166861	0.002333722
## 12	gene.1	33912	0.0042972679	0	0	0.001166861	0.017502917	0.018669778
## 13	gene.1	776	0.0000000000	0	0	0.000000000	0.000000000	0.000000000
## 14	gene.1	902	0.0000000000	0	0	0.000000000	0.000000000	0.000000000
## 15	gene.1	913	0.0000000000	0	0	0.000000000	0.000000000	0.000000000

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

