

SUPPORTING INFORMATION for

H. T. Vy and Y. Kim, A composite likelihood method for detecting incomplete selective sweep from population genomic data, submitted to Genetics

File S1

Scripts to generate simulated data sets:

1. For testing power of CL, iHS, nSL:

- $R = 4Nr = 2000$
 - Neutral model:
/msms 20 10000 -N 100000 -s 3000 -r 2000 100000
 - Selective sweep model:
/msms 20 10000 -N 100000 -s 2999 -r 2000 100000 -SAA 1000 -SaA 500 -SF 0 0.5 -Sp 0.5 –
Smark
/msms 20 10000 -N 100000 -s 2999 -r 2000 100000 -SAA 2000 -SaA 1000 -SF 0 0.5 -Sp 0.5 –
Smark
/msms 20 10000 -N 100000 -s 2999 -r 2000 100000 -SAA 4000 -SaA 2000 -SF 0 0.5 -Sp 0.5 –
Smark
- $R = 4 = 4000$
 - Neutral model:
/msms 20 10000 -N 100000 -s 3000 -r 4000 100000
 - Selective sweep model:
/msms 20 10000 -N 100000 -s 2999 -r 4000 100000 -SAA 1000 -SaA 500 -SF 0 0.5 -Sp 0.5 –
Smark
/msms 20 10000 -N 100000 -s 2999 -r 4000 100000 -SAA 2000 -SaA 1000 -SF 0 0.5 -Sp 0.5 –
Smark
/msms 20 10000 -N 100000 -s 2999 -r 4000 100000 -SAA 4000 -SaA 2000 -SF 0 0.5 -Sp 0.5 –
Smark

2. For generating neutral data matching the sample size, mean recombination rate, and the mean density of polymorphic sites to those of Drosophila genome data (to calculate T_1 when apply composite likelihood test to Drosophila genomes):

```
/ms 22 20 -t 35000 -r 60000 5000000
```

3. To simulate data under different demographic assumptions:

- Population bottleneck:
 - With different severities:
/ms 20 1000 -s 3000 -r 4000 100000 -eN 0.05 0.2 -eN 0.1 1.0

```
/ms 20 1000 -s 3000 -r 4000 100000 -eN 0.05 0.1 -eN 0.1 1.0
/ms 20 1000 -s 3000 -r 4000 100000 -eN 0.05 0.05 -eN 0.1 1.0
```

➤ With different recombination rates:

```
/ms 20 1000 -s 3000 -r 4000 100000 -eN 0.05 0.05 -eN 0.1 1.0
/ms 20 1000 -s 3000 -r 6000 100000 -eN 0.05 0.05 -eN 0.1 1.0
/ms 20 1000 -s 3000 -r 8000 100000 -eN 0.05 0.05 -eN 0.1 1.0
/ms 20 1000 -s 3000 -r 10000 100000 -eN 0.05 0.05 -eN 0.1 1.0
/ms 20 1000 -s 3000 -r 12000 100000 -eN 0.05 0.05 -eN 0.1 1.0
```

• Exponential population growth:

➤ With different growth rates:

```
/ms 20 1000 -s 3000 -r 4000 100000 -G 500 -eG 0.0032 0.0
/ms 20 1000 -s 3000 -r 4000 100000 -G 100 -eG 0.016 0.0
/ms 20 1000 -s 3000 -r 4000 100000 -G 10 -eG 0.016 0.0
```

➤ With different recombination rates:

```
/ms 20 1000 -s 3000 -r 4000 100000 -G 100 -eG 0.016 0.0
/ms 20 1000 -s 3000 -r 6000 100000 -G 100 -eG 0.016 0.0
/ms 20 1000 -s 3000 -r 8000 100000 -G 100 -eG 0.016 0.0
/ms 20 1000 -s 3000 -r 10000 100000 -G 100 -eG 0.016 0.0
```

• Population subdivision:

➤ With different migration rates:

```
/ms 20 1000 -s 3000 -r 4000 100000 -I 2 20 0 0.1
/ms 20 1000 -s 3000 -r 4000 100000 -I 2 20 0 1.0
/ms 20 1000 -s 3000 -r 4000 100000 -I 2 20 0 10
```

➤ With different recombination rates:

```
/ms 20 1000 -s 3000 -r 1000 100000 -I 2 20 0 0.1
/ms 20 1000 -s 3000 -r 2000 100000 -I 2 20 0 0.1
/ms 20 1000 -s 3000 -r 4000 100000 -I 2 20 0 0.1
/ms 20 1000 -s 3000 -r 6000 100000 -I 2 20 0 0.1
```