# ms - a program for generating samples under neutral models

Hudson (2002) Bioinformatics 18:337-8

http://home.uchicago.edu/~rhudson1/source/mksamples.html

### ms

- Generates samples under a variety of assumptions about migration, recombination rate and population size
- Samples are generated using the standard coalescent approach:

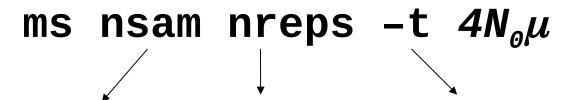
1<sup>st</sup> Generate the genealogy

2<sup>nd</sup> Add mutations to the genealogical tree

- Assumes the small sample approximations of the coalescent (n << N)
- Assumes infinite sites model for mutations
  - BUT, when used in conjunction with other programs, other mutation models can be used

## The ms command line

For a constant population size, with random mating, no recombination and infinite site mutation model the command is:



Number of gene Number of copies sampled repetitions (simulations)

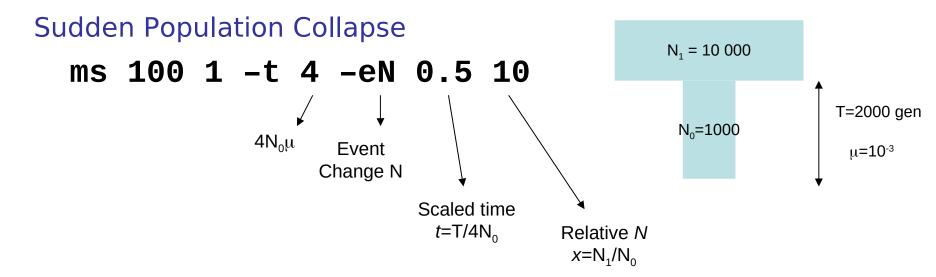
Scaled mutation parameter:  $N_0$  diploid population size  $\mu$  mutation rate for the entire locus

## The ms output

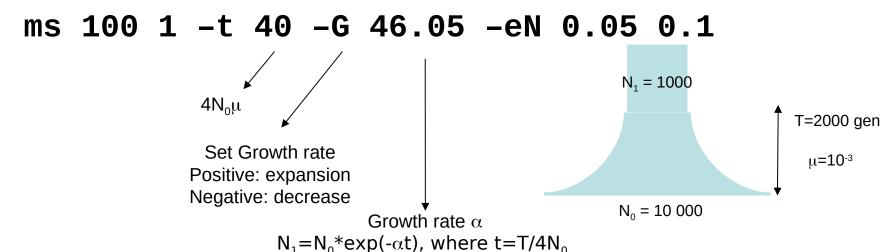
For instance, for the following command line Population with effective size ms 10 1 - t 4 > ms.out1000 and mutation rate 0.001The output is stored in the file ms.out Command line ms 10 1 -t 4 Random number generator seeds 60711 7473 11225 // number segregating sites segsites: 17 positions: 0.1690 0.2248 0.3120 0.3346 0.3662 0.3935 0.4243 0.4814 0.5587 0.5735 0.5753 0.6957 0.7958 0.8226 0.8943 0.9272 0.9404 01010111000010000 **Position of segregating sites** 01010111001010000 01011111010010000 Sample for 10 gene copies and 17 segregating sites 01010111000010000 110101111000010000 0 indicates ancestral state 01010111000110000 1 indicates derived state 01010111000010000 01010111000110000 01010111000010000 10 gene copies (5 diploids) 00100000100001111

17 seg sites

## Population Expansion or Collapse

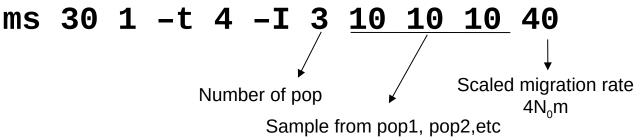


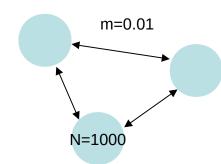
#### Exponentially growing population



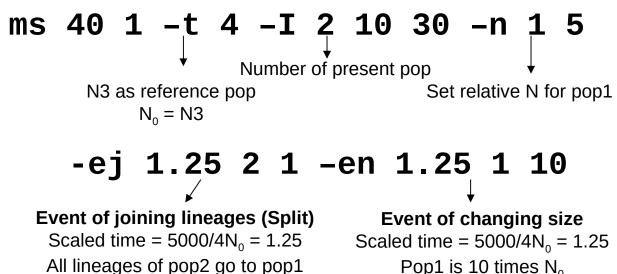
### Population Structure

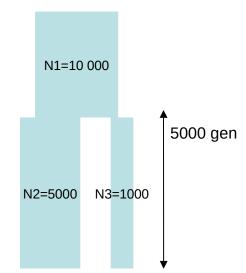
#### Island Model





#### **Population Split**



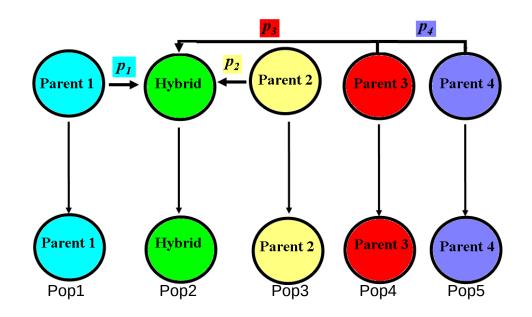


## Remember

•  $N_0$  is the reference effective size, and it can be chosen arbitrarily

 Mutation rate, migration rate and time of the events are scaled by the chosen effective size N₀

### One example of complex ms command



N1=100 N2=100 Nh=100 N3=100 N4=100

Nanc=100

Mutation rate=0.0001

Tadm=100 Tsplit=10000

p1=0.2 p2=0.3 p3=0.1 p4=0.4

Nsam1=20 Nsam2=20 Nsam3=20 Nsam4=20 Nsam5=20

Number of simulations=20

## One example of ms command

ms 100 20 -t 0.04 -l 5 20 20 20 20 20 -n 1 1 -n 2 1 -n 3 1 -n 4 1 -n 5 1 -es 0.25 2 0.2 -ej 0.25 2 1 -es 0.25 6 0.375 -ej 0.25 6 3 -es 0.25 7 0.2 -ej 0.25 7 4 -ej 0.25 8 5 -en 25 1 1 -ej 25 3 1 -ej 25 4 1 -ej 25 5 1 | microsat > ms\_result\_msat.txt JOIN <mark>100 N</mark> =100 N3=100 N4 100 **a**nc=100 SPI Mutation rate=0.0001 Pop 1 Tad**n=10**0 Tsplit=10000 p1=0.2 p2=0.3 p3=0.1 p4=0.4 Nsam1=20 Nsam2=20 Nsam4=20 Nsam5=20 Number of simulations=20

#### Some issues:

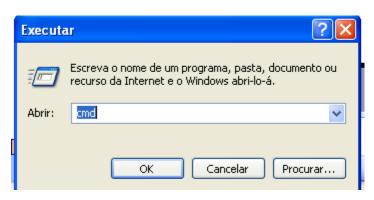
- Population sizes and time are scaled
- long commands for complex models

## Example

- Simulate a sample of 50 gene copies with 5000 nucleotides, from a constant population with effective size 10 000 and mutation rate 10<sup>-8</sup> per nucleotide per generation
- Open the command line. If you are on Windows do: START>Run>cmd
- Go to the folder with ms.exe
- Compute  $4N_0\mu = 4*10000*5000*10^{-8}$ =20

ms 50 1 -t 20 > ms\_stable.out

Have a look at the file ms\_stable.out with a text editor (TextPad, WordPad, NotePad, etc)



```
C:\WINDOWS\system32\cmd.exe

Microsoft Windows XP [Versão 5.1.2600]
(C) Copyright 1985-2001 Microsoft Corp.

C:\Documents and Settings\Proprietário\cd c:\ms

C:\ms\cd msdir

C:\ms\msdir\ms 50 1 -t 20 \rangle ms_stable.out

C:\ms\msdir\
```