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Writing forward-time simulations, an in-depth course

6th June 2007

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simuPOP modules

```
>>> from simuOpt import setOptions
>>> setOptions(alleleType='long', optimized=False)
>>> from simuPOP import *
simuPOP : Copyright (c) 2004-2006 Bo Peng
Version 9.9.9 (Revision 9999, May 21 2007) for Python 2.3.4
[GCC 3.4.6 20060404 (Red Hat 3.4.6-3)]
Random Number Generator is set to mtl9937 with random seed 0x70103f076358dc0
This is the standard long allele version with 65536 maximum allelic states.
For more information, please visit http://simupop.sourceforge.net,
or email simupop-list@lists.sourceforge.net (subscription required).
>>>
```

- Allele type: short, long, binary
- · Standard and Optimized
- MPI (parallel) version, not ready

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Common properties of all individuals

All individuals have the same genotypic structure, which refers to

- Ploidy (diploid, haploid, triploid, ...)
- Number of chromosomes
- Number of loci on each chromosome
- Name and position of loci
- Name of information fields

And less importantly

- Allele names
- Existence of sex chromosome

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Chromosome structure

```
>>> pop = population(size=10, loci=[2, 4, 5])
>>> print pop.numLoci()
(2, 4, 5)
>>> # index starts at zero!
>>> print pop.numLoci(1)
4
>>> print pop.ploidy()
2
>>> print pop.ploidyName()
diploid
>>> print pop.chromBegin(1)
>>> print pop.locusPos(3)
2.0
>>> print pop.locusName(4)
1002-3
>>>
```

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Loci position and names

```
>>> pop = population(size=10, loci=[2, 4], maxAllele=3,
... lociPos=[[1.5, 2.5], [1, 2, 5, 10]],
... lociNames=['loc%x' % x for x in range(6)],
... alleleNames=['A', 'T', 'C', 'G'])
>>> print pop.locusPos(3)
2.0
>>> print pop.locusName(4)
loc4
>>> print pop.alleleName(1)
T
>>>
```

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Have a look at the population

(Dump)

```
>>> Dump(pop)
Ploidy:
Number of chrom:
Number of loci:
Maximum allele state:
Loci positions:
               1.5 2.5
               1 2 5 10
Loci names:
               loc0 loc1
               loc2 loc3 loc4 loc5
population size:
                       10
Number of subPop:
Subpop sizes:
Number of ancestral populations:
individual info:
sub population 0:
  0: MU AA AAAA | AA AAAA
  1: MU AA AAAA | AA AAAA
  2: MU AA AAAA | AA AAAA
  3: MU AA AAAA | AA AAAA
  4: MU AA AAAA | AA AAAA
  5: MIJ AA AAAA | AA AAAA
  6: MU AA AAAA | AA AAAA
  7: MU AA AAAA | AA AAAA
  8: MU AA AAAA | AA AAAA
  9: MU AA AAAA | AA AAAA
                                       mad as indicident insta
```

Have a look at the population

(Dump)

```
>>> InitByFreg(pop, alleleFreg=[0.3, 0.7])
>>> Dump(pop)
Ploidy:
Number of chrom:
Number of loci:
Maximum allele state:
Loci positions:
               1.5 2.5
               1 2 5 10
Loci names:
               loc0 loc1
               loc2 loc3 loc4 loc5
population size:
                       10
Number of subPop:
Subpop sizes:
                       1.0
Number of ancestral populations:
individual info:
sub population 0:
  0: MU TT ATTT
                 TT AATT
  1: FU TT TTTT | TA TATT
  2: FU TT TTAA |
                 AT AAAT
  3: FU TT TTTA
                  TT TTTA
  4: MIJ TA TTTT |
                  TT AATT
  5: MU TT AAAT |
                  TA TTAT
  6: MU TT TTTT
                  TA TATT
     FU TA TATT
                  TT ATAT
  8: FU TT TTTT
                  TT TTAT
```

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Population structure

Create a population with subpopulations

```
>>> pop = population(subPop=[2, 5, 6], loci=[2])
>>> print pop.popSize()
13
>>> print pop.subPopSizes()
(2, 5, 6)
>>> print pop.subPopSize(1)
5
>>> Dump(pop)
Ploidy:
Number of chrom:
Number of loci:
Maximum allele state: 65535
Loci positions:
               1 2
Loci names:
               loc1-1 loc1-2
population size:
Number of subPop:
Subpop sizes:
                      2 5 6
Number of ancestral populations:
individual info:
sub population 0:
  0: MU 0 0 0 0 0 0 1: MU 0 0 0 0 0 0
sub population 1:
   2: MU 0 0 |
   3: MU 0 0 |
                                       4 - MTT 0 0 0 0
```

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Mating is within subpopulation only

```
>>> pop = population(subPop=[5, 6], loci=[2])
>>> simu = simulator(pop, randomMating())
>>> simu.evolve(
        preOps = [
            initByFreq(alleleFreq=[0.2, 0.8], subPop=[0]),
            initByFreg([0, 0, 0, 0.5, 0.5], subPop=[1])
             ],
        ops = [
            dumper(alleleOnly=True, indRange=[[0, 3], [5, 7]]),
. . .
            recombinator(rate=0.1) ],
        end = 1
. . .
. . . )
```

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Mating is within subpopulation only – continue

No ancenstral population recorded. individual info:

sub population 0: 0: MU 1 1

1: FU 1 0 | 1 1

2: FU 1 1 1 1 1

sub population 1:

5: MU 4 4 | 3 4 6: MU 3 4 | 4 3

End of individual info.

No ancenstral population recorded.

True



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Subpopulation manipulations

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Information fields

Pieces of information that can be attached to each individual, e.g.

- fitness: fitness of each individual, calculated by selectors
- father_idx, mother_idx: index of parents in the parental generation
- old_index: index of an individual in the population where it is sampled

Or, self-defined

- birthday
- · geographic location
- ...

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The most flexible operators that can perform any operation, but are less efficient.

The idea: user provide a function with specified input and output, simuPOP calls this function during evolution.

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Python operator

func(pop [, param])

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Python Individual operator

func(ind [, genotype] [, param]), return True/False or an array

- ind: individual
- genotype: if parameter loci is given, genotype at these loci are passed to the function
- param: if parameter param is given, param passed from simuPOP
- return: if parameter infoFields is given, assign return values to these information fields

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Specialized Python operators: pyPenetrance

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evolve!

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Exercise time!

simuLDDecay.py

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Table-like output

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