

simuPOP
tutorial

Bo Peng,
Ph.D.

What is
simuPOP

An example

simuPOP
components

Population
manipulation

Forward-time simulations using simuPOP, a tutorial

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Department of Epidemiology
U.T. M.D. Anderson Cancer Center
Houston, TX

June. 6, 2007
Programmers' Cross Training
U.T. M.D. Anderson Cancer Center

outline

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- 4 Population manipulation

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A forward-time population genetics simulation environment

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A forward-time population genetics **simulation** environment

- A population genetics simulation program

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A **forward-time** population genetics simulation environment

- A population genetics simulation program
- Not coalescent-based

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A forward-time population genetics simulation **environment**

- A population genetics simulation program
- Not coalescent-based
- Based on an object-oriented scripting language (Python)

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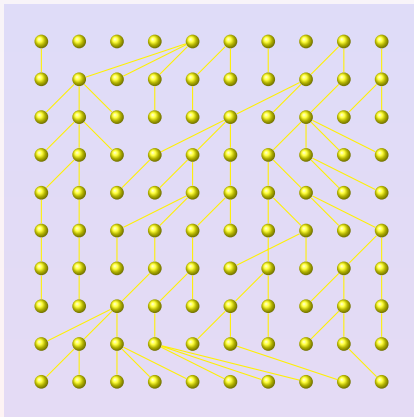
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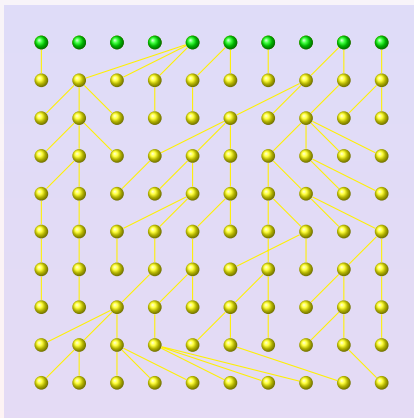
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- Start from an initial population



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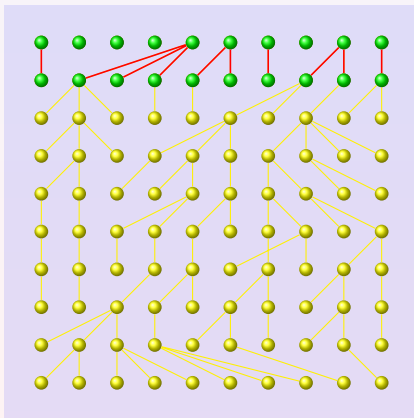
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- Start from an initial population
- Evolve forward in time, generation by generation, subject to certain number of genetic and/or demographic effects

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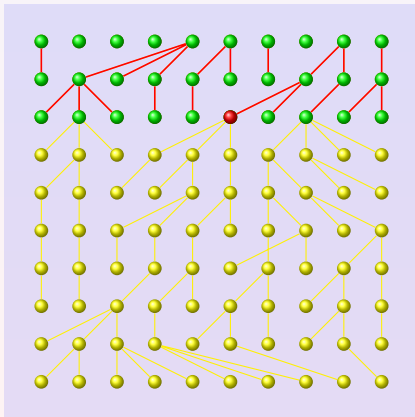
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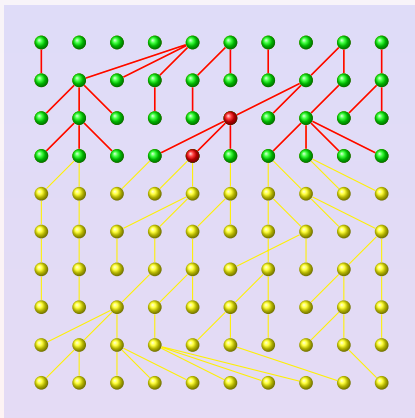
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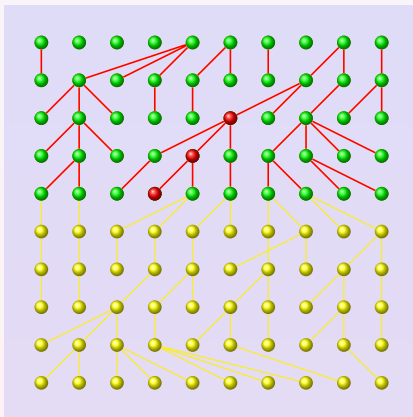
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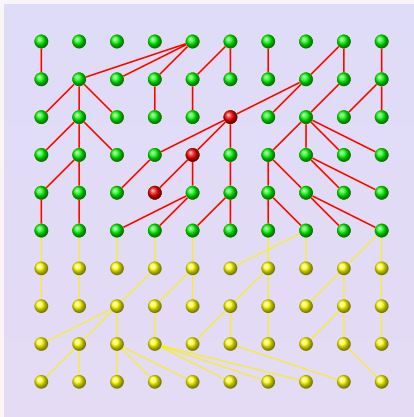
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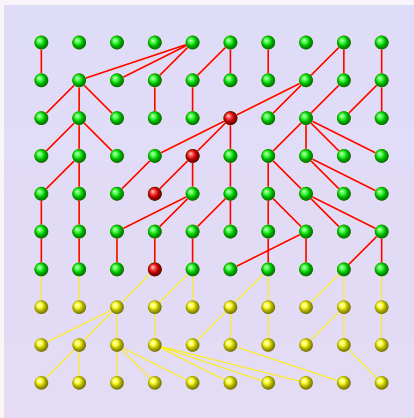
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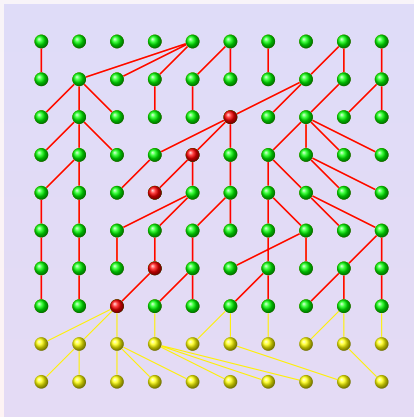
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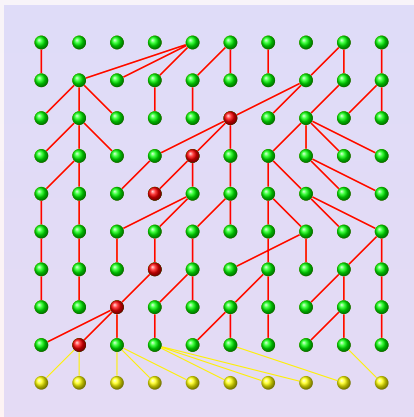
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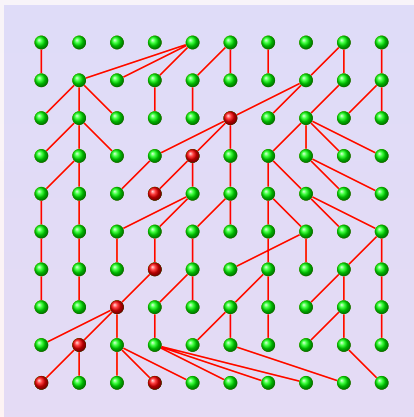
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- Start from an initial population
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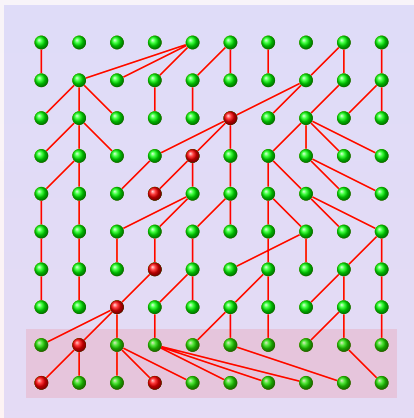
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- Start from an initial population
- Evolve forward in time, generation by generation, subject to certain number of genetic and/or demographic effects
- Samples are collected from the last several generations

Backward-time simulation

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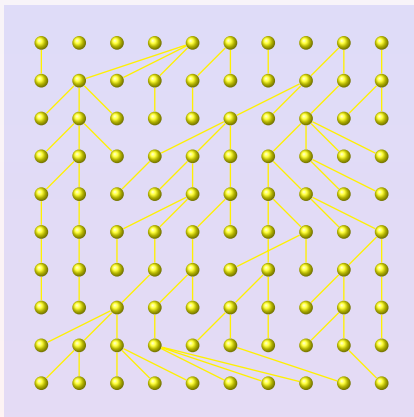
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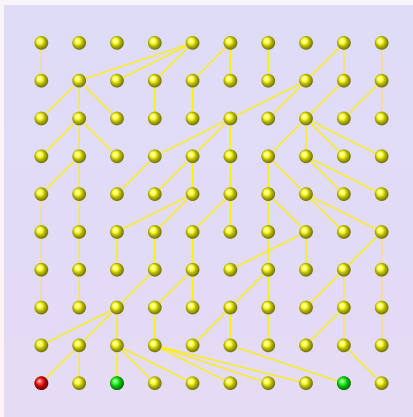
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Population manipulation

- Start from a sample with unknown genotype



Backward-time simulation

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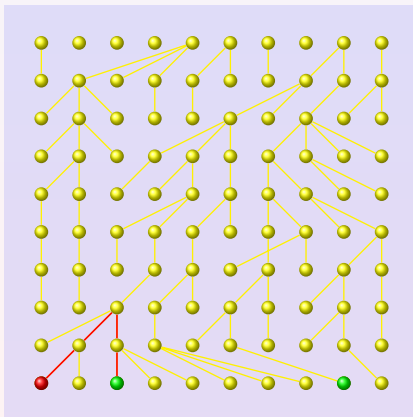
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Population
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- Start from a sample with unknown genotype
- Coalesce individuals until the most recent common ancestor of all individuals is found

Backward-time simulation

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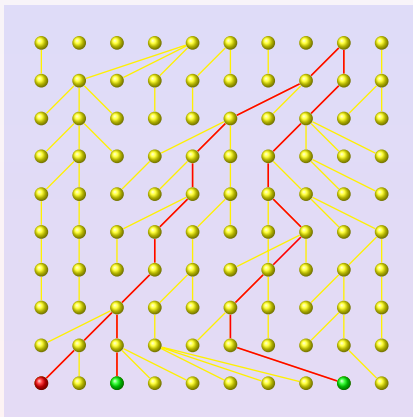
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- Start from a sample with unknown genotype
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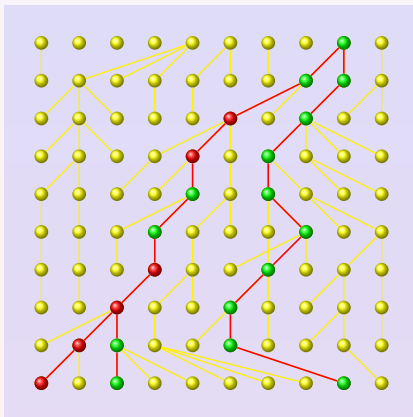
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Population manipulation



- Start from a sample with unknown genotype
- Coalesce individuals until the most recent common ancestor of all individuals is found
- Starting from the MRCA, proceed forward in time and fill the genotype of each individual

Forward vs. backward-time simulations

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Population manipulation

Backward-time

- Sample based,
efficient

Forward-time

- Population based,
inefficient

Forward vs. backward-time simulations

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Population manipulation

Backward-time

- Sample based, efficient
- Limited selection, recombination models and mating schemes

Forward-time

- Population based, inefficient
- Can simulate almost arbitrary evolutionary scenarios

Forward vs. backward-time simulations

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Backward-time

- Sample based, efficient
- Limited selection, recombination models and mating schemes
- Can not study population properties, or properties of ancestral generations

Forward-time

- Population based, inefficient
- Can simulate almost arbitrary evolutionary scenarios
- Can study population properties and ancestral generations

Forward vs. backward-time simulations

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Population
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Backward-time

- Sample based, efficient
- Limited selection, recombination models and mating schemes
- Can not study population properties, or properties of ancestral generations
- Used mostly for sample generation

Forward-time

- Population based, inefficient
- Can simulate almost arbitrary evolutionary scenarios
- Can study population properties and ancestral generations
- Wider application areas

Forward-time simulation programs

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Population manipulation

For specific applications

- Easy to write simple simulations
- Difficult to write complicated simulations
- A few programs are available (EasyPOP, FPG, Nemo, ...), easy to use if they happen to fit your need

Forward-time simulation programs

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For specific applications

- Easy to write simple simulations
- Difficult to write complicated simulations
- A few programs are available (EasyPOP, FPG, Nemo, ...), easy to use if they happen to fit your need

For general purposes

- Difficult to write
- Easy to set up complicated simulations
- simuPOP fits in this category

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Population manipulation

simuPOP provides

- a large number of functions to manipulate populations
copy, split, merge, manipulate individual genotypes,
determine affection status, save to and load from
various formats, generate sample, ...

What simuPOP does

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Population manipulation

simuPOP provides

- a large number of functions to manipulate populations copy, split, merge, manipulate individual genotypes, determine affection status, save to and load from various formats, generate sample, ...
- and a mechanism to evolve populations forward in time subject to arbitrary demographic and genetic forces such as population size changes, mutation, migration, recombination, selection, ...

What distinguishes simuPOP from others

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Population manipulation

scripting simuPOP is provided as a set of Python modules, and is therefore backed by a full-blown object-oriented programming language.

flexibility simuPOP does not impose any limit on the size of genome, population, demographic model, etc. Using a large number of standard and hybrid (Python-assisted) operators, users can simulate almost arbitrarily complex evolutionary processes.

integration Owing to the 'glue language' nature of Python, it is easy to integrate simuPOP with other languages and programs.

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Population manipulation

simuPOP can simulate the change of the genetic composition of a population in a complicated evolutionary process. It can be used to

- Demonstrate population genetics phenomena

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simuPOP can simulate the change of the genetic composition of a population in a complicated evolutionary process. It can be used to

- Demonstrate population genetics phenomena
- Study the impact of genetic and demographic forces on the evolution of a population

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- Study the impact of genetic and demographic forces on the evolution of a population
- Study the evolution of (complex) genetic diseases

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- Study the impact of genetic and demographic forces on the evolution of a population
- Study the evolution of (complex) genetic diseases
- Simulate samples to validate gene-mapping methods

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- Study the impact of genetic and demographic forces on the evolution of a population
- Study the evolution of (complex) genetic diseases
- Simulate samples to validate gene-mapping methods
- Study ascertainment methods in simulated populations

This is fun, but is it useful?

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simuPOP can simulate the change of the genetic composition of a population in a complicated evolutionary process. It can be used to

- Demonstrate population genetics phenomena
- Study the impact of genetic and demographic forces on the evolution of a population
- Study the evolution of (complex) genetic diseases
- Simulate samples to validate gene-mapping methods
- Study ascertainment methods in simulated populations
- ...

Simulations of complex human diseases

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Population manipulation

Backward-time

- Haploid simulation only

Forward-time

- No limit on ploidy

Simulations of complex human diseases

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Population manipulation

Backward-time

- Haploid simulation only
- Additive selection and penetrance models

Forward-time

- No limit on ploidy
- Arbitrary selection and penetrance models

Simulations of complex human diseases

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Backward-time

- Haploid simulation only
- Additive selection and penetrance models
- One disease susceptibility locus

Forward-time

- No limit on ploidy
- Arbitrary selection and penetrance models
- Multiple DSL with interaction

Simulations of complex human diseases

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Backward-time

- Haploid simulation only
- Additive selection and penetrance models
- One disease susceptibility locus
- Generate independent samples

Forward-time

- No limit on ploidy
- Arbitrary selection and penetrance models
- Multiple DSL with interaction
- Generate multi-generation populations

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I like it, but, oohm, why Python??

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Population manipulation

- The core of simuPOP is written in C++ for efficiency
- Python is the glue language, a wrapper of the core
- Python is used to write simuPOP extensions (user interface etc)
- The core sometimes calls Python (Python operators) for maximum flexibility

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- simuPOP website:
`http://simupop.sourceforge.net`
- Mailing list:
`simupop-list@lists.sourceforge.net`
- License: GPL 2.0
- Platforms: all OS on which Python is available
- Monthly release, currently at 0.7.10
- Documentation: *simuPOP User's Guide* and *simuPOP Reference Manual*

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Visualization with R

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A simple example

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```
>>> from simuPOP import *
>>> simu = simulator(
...     population(size=1000, ploidy=2, loci=[2]),
...     randomMating(),
...     rep = 3)
>>> simu.evolve(
...     preOps = [initByValue([1,2,2,1])],
...     ops = [
...         recombinator(rate=0.1),
...         stat(LD=[0,1]),
...         pyEval(r"'%3d    ' % gen", rep=0, step=10),
...         pyEval(r"'%f    ' % LD[0][1]", step=10),
...         pyEval(r"'\n'", rep=REP_LAST, step=10)
...     ],
...     end=100
... )
```

Output of the example

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Visualization with R

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0	0.196745	0.200253	0.202646
10	0.070055	0.069072	0.053272
20	0.011108	0.024689	0.025818
30	0.001009	0.008473	0.012216
40	0.000663	0.004254	0.010879
50	0.025414	0.004853	0.002686
60	0.027291	0.000917	0.003569
70	0.022889	0.009723	0.001386
80	0.001847	0.004545	0.006552
90	0.011127	0.034419	0.000716
100	0.001537	0.000542	0.010050

simuPOP modules

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What is simuPOP

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Population manipulation

```
>>> from simuPOP import *  
>>> simu = simulator(  
...     population(size=1000, ploidy=2, loci=[2]),  
...     randomMating(),  
...     rep = 3)
```

Import the default simuPOP module

population

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```
>>> from simuPOP import *
>>> simu = simulator(
...     population(size=1000, ploidy=2, loci=[2]),
...     randomMating(),
...     rep = 3)
```

Create a **population** of 1000 **diploid** individuals, each having two **loci** on the first chromosome

simulator and mating scheme

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```
>>> from simuPOP import *
>>> simu = simulator(
...     population(size=1000, ploidy=2, loci=[2]),
...     randomMating(),
...     rep = 3)
```

Create a **simulator** that has one replicate of this population, and a random mating scheme

Operators!

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Population manipulation

```
>>> from simuPOP import *
>>> simu = simulator(
...     population(size=1000, ploidy=2, loci=[2]),
...     randomMating(),
...     rep = 3)
>>> simu.evolve(
...     preOps = [initByValue([1,2,2,1])],
...     ops = [
...         recombinator(rate=0.1),
...         stat(LD=[0,1]),
...         pyEval(r"'%3d    ' % gen", rep=0, step=10),
...         pyEval(r"'%f    ' % LD[0][1]", step=10),
...         pyEval(r"'\\n'", rep=REP_LAST, step=10)
...     ],
...     end=100
... )
```

`initByValue` is applied before evolution

Operators!

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```
>>> from simuPOP import *
>>> simu = simulator(
...     population(size=1000, ploidy=2, loci=[2]),
...     randomMating(),
...     rep = 3)
>>> simu.evolve(
...     preOps = [initByValue([1,2,2,1])],
...     ops = [
...         recombinator(rate=0.1),
...         stat(LD=[0,1]),
...         pyEval(r"%3d    ' % gen", rep=0, step=10),
...         pyEval(r"%f    ' % LD[0][1]", step=10),
...         pyEval(r"\n", rep=REP_LAST, step=10)
...     ],
...     end=100
... )
```

recombinator is applied at every generation when an offspring is produced

Operators!

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```
>>> from simuPOP import *
>>> simu = simulator(
...     population(size=1000, ploidy=2, loci=[2]),
...     randomMating(),
...     rep = 3)
>>> simu.evolve(
...     preOps = [initByValue([1,2,2,1])],
...     ops = [
...         recombinator(rate=0.1),
...         stat(LD=[0,1]),
...         pyEval(r"%3d    ' % gen", rep=0, step=10),
...         pyEval(r"%f    ' % LD[0][1]", step=10),
...         pyEval(r"\n", rep=REP_LAST, step=10)
...     ],
...     end=100
... )
```

stat is applied to the offspring generation at every generation

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```
>>> from simuPOP import *
>>> simu = simulator(
...     population(size=1000, ploidy=2, loci=[2]),
...     randomMating(),
...     rep = 3)
>>> simu.evolve(
...     preOps = [initByValue([1,2,2,1])],
...     ops = [
...         recombinator(rate=0.1),
...         stat(LD=[0,1]),
...         pyEval(r"'%3d    ' % gen", rep=0, step=10),
...         pyEval(r"'%f    ' % LD[0][1]", step=10),
...         pyEval(r"'\\n'", rep=REP_LAST, step=10)
...     ],
...     end=100
... )
```

pyEval is applied every 10 generations

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Use R to plot

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```
>>> from simuPOP import *
>>> from simuRPy import *
>>> simu = simulator(
...     population(size=1000, ploidy=2, loci=[2]),
...     randomMating(),
...     rep = 3)
>>> simu.evolve(
...     preOps = [initByValue([1,2,2,1])],
...     ops = [
...         recombinator(rate=0.1),
...         stat(LD=[0,1]),
...         varPlotter('LD[0][1]', numRep=3, step=10,
...             saveAs='ld', ylim=[0,.25],
...             lty=range(1, 4), col=range(2, 5),
...             xlab='generation', ylab='D',
...             title='LD Decay'),
...     ],
...     end=100
... )
True
>>>
```

Evolve!

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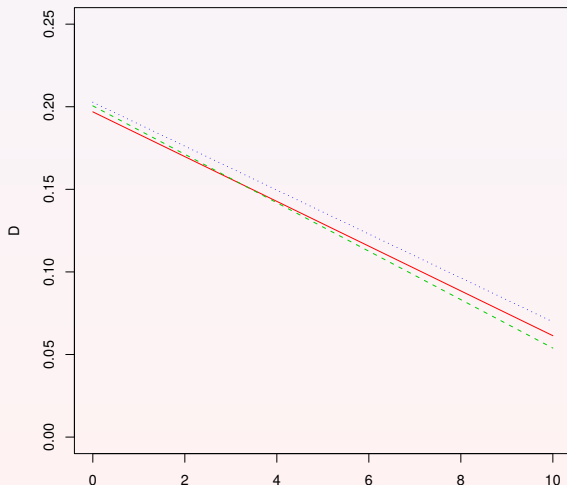
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LD Decay



- Update at every 10 generations
- $LD=0.25$ before generation 0
- LD is calculated at the end of each generation

Evolve!

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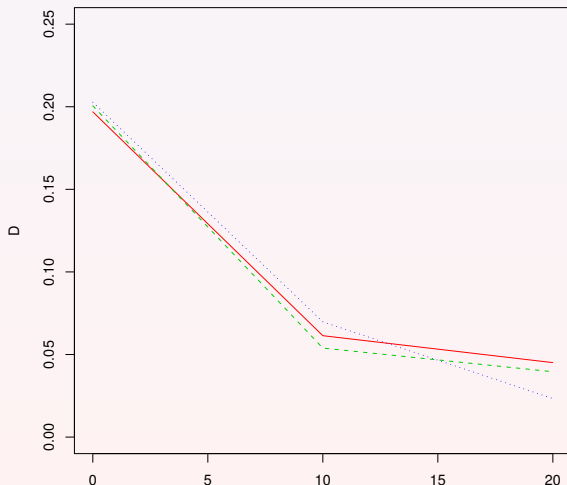
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- Update at every 10 generations
- LD=0.25 before generation 0
- LD is calculated at the end of each generation

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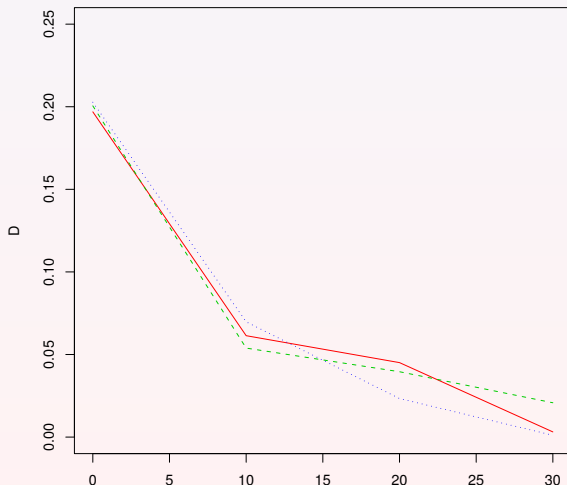
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- Update at every 10 generations
- $LD=0.25$ before generation 0
- LD is calculated at the end of each generation

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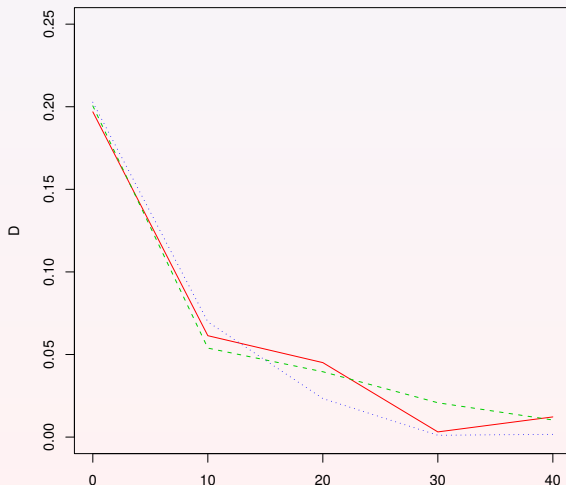
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- LD is calculated at the end of each generation

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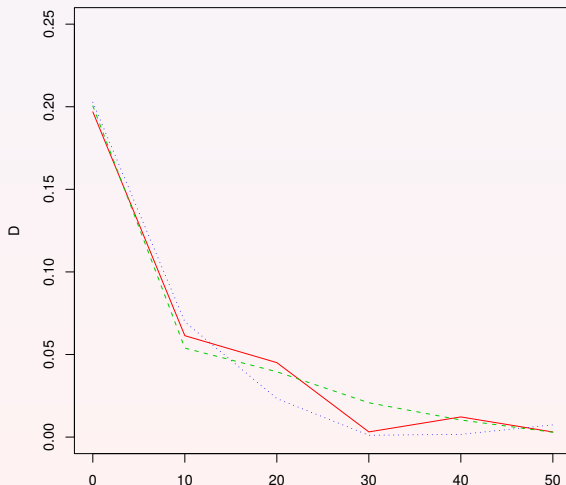
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- LD=0.25 before generation 0
- LD is calculated at the end of each generation

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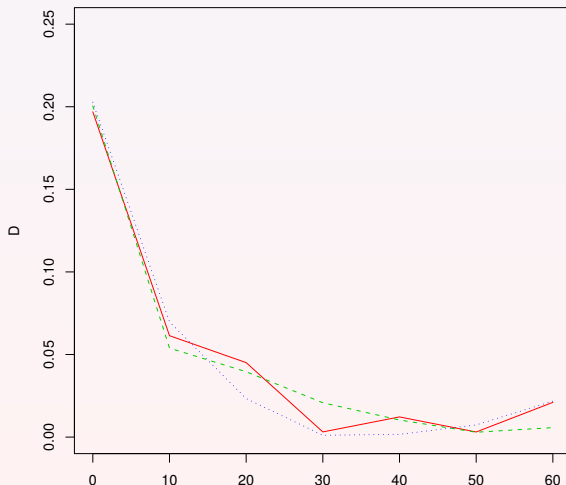
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- Update at every 10 generations
- LD=0.25 before generation 0
- LD is calculated at the end of each generation

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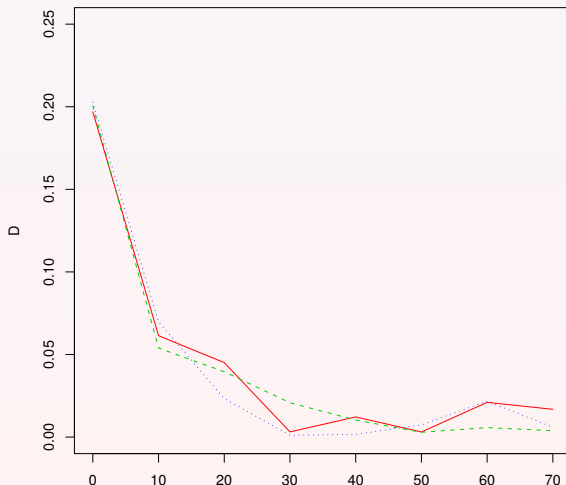
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- Update at every 10 generations
- LD=0.25 before generation 0
- LD is calculated at the end of each generation

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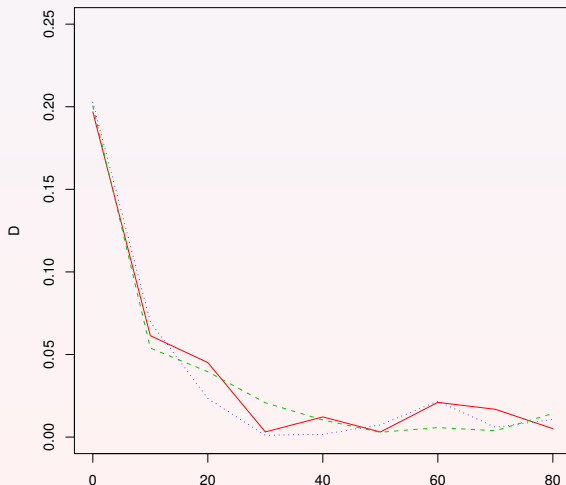
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- Update at every 10 generations
- $LD=0.25$ before generation 0
- LD is calculated at the end of each generation

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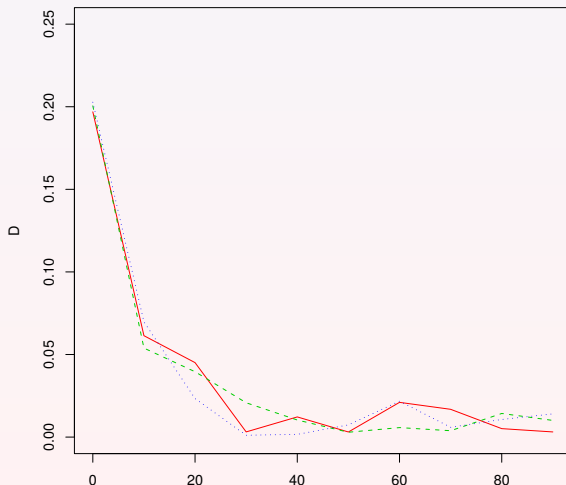
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- $LD=0.25$ before generation 0
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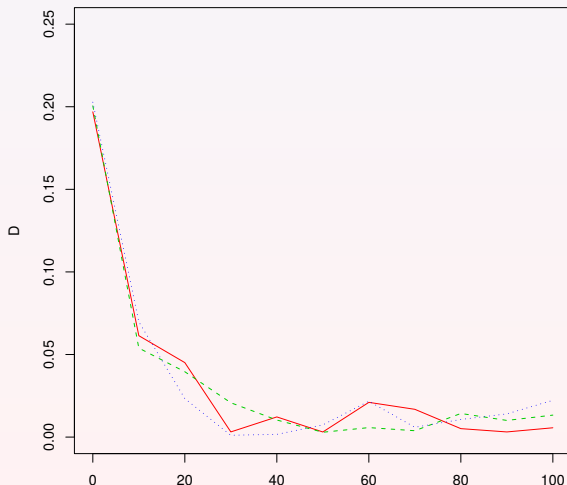
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- Update at every 10 generations
- $LD=0.25$ before generation 0
- LD is calculated at the end of each generation

Exercise time

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Population manipulation

- Start python
- Load simuPOP
- Create a population and run

```
pop.ploidyName( )
```

- run tutorial_example1.py

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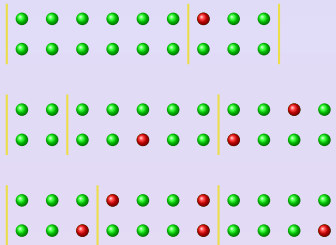
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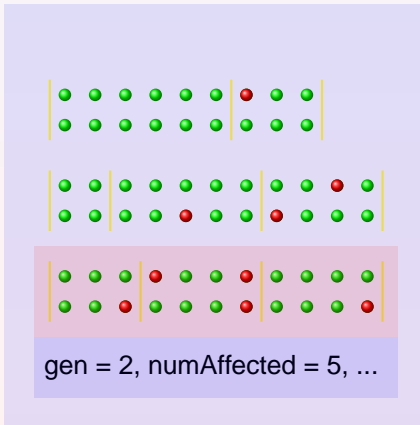
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- Unaffected
- Affected



Current generation

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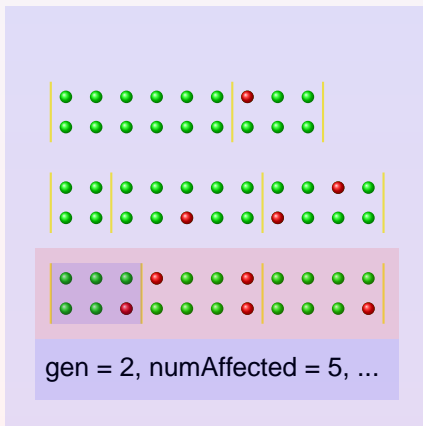
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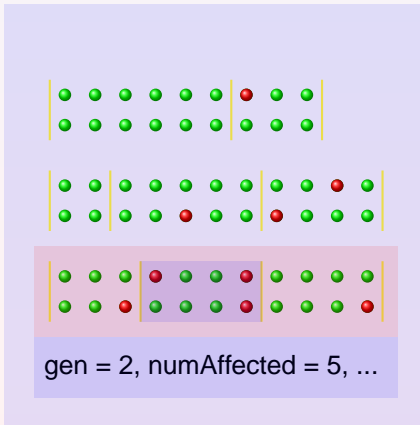
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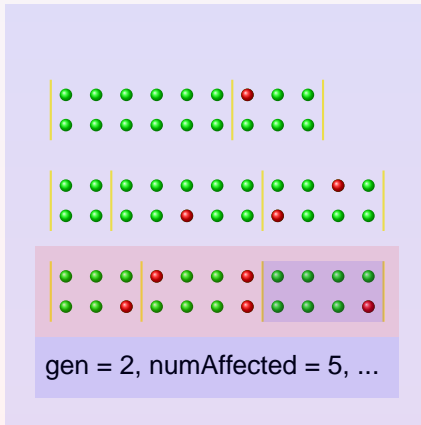
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- Unaffected
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Current generation

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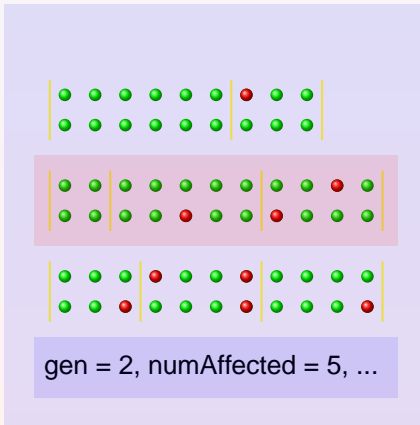
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Ancestral generation 1

Current generation

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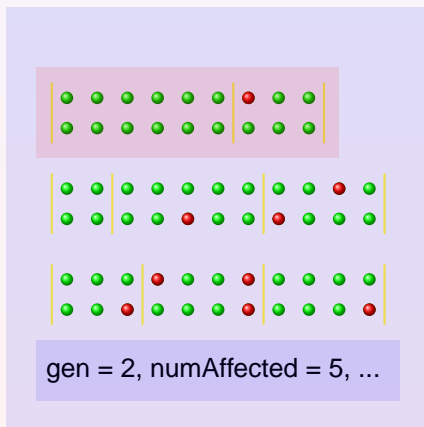
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Ancestral generation 2

Ancestral generation 1

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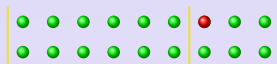
Mating scheme

Simulator

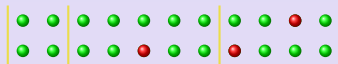
Other utilities

Population manipulation

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Ancestral generation 2



Ancestral generation 1



Current generation

gen = 2, numAffected = 5, ...

Population variables

Create and manipulate populations

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Population manipulation

```
>>> pop = population(size=10, loci=[2, 3])
```

```
>>> Dump(pop)
```

```
Ploidy:                2
Number of chrom:       2
Number of loci:        2 3
Maximum allele state:  255
Loci positions:
```

```
    1 2
    1 2 3
```

```
Loci names:
```

```
    loc1-1 loc1-2
    loc2-1 loc2-2 loc2-3
```

```
population size:      10
Number of subPop:     1
Subpop sizes:         10
Number of ancestral populations: 0
individual info:
sub population 0:
```

```
    0: MU    0  0    0  0  0 |    0  0    0  0  0
    1: MU    0  0    0  0  0 |    0  0    0  0  0
    2: MU    0  0    0  0  0 |    0  0    0  0  0
    3: MU    0  0    0  0  0 |    0  0    0  0  0
```

Genotypic structure

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Population manipulation

```
>>> pop = population(subPop=[200, 300], loci=[3, 2],
...                   maxAllele=3, ploidy=3,
...                   lociPos=[[1, 3, 5], [2.5, 4]],
...                   alleleNames=['A', 'C', 'T', 'G'])
>>> pop.numLoci(0)
3
>>> pop.totNumLoci()
5
>>> pop.locusPos(4)
4.0
>>> pop.subPopSize(1)
300
>>> pop.popSize()
500
>>> pop.ploidyName()
'triploid'
>>> pop.individual(1).allele(1, 2)
0
>>>
```

Population manipulation

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Population manipulation

```
>>> # make a copy of pop
>>> pop1 = pop.clone()
>>> # remove loci 2, 3, 4
>>> pop.removeLoci(keep=[0, 1])
>>> # pop2 will have 3 chromosomes, with loci 2, 3, 2
>>> pop2 = MergePopulationsByLoci(pops=[pop, pop1])
>>> # randomly assign alleles using given allele frequencies
>>> InitByFreq(pop2, [0.8, .2])
>>> # calculate population allele frequency
>>> Stat(pop2, alleleFreq=range(pop2.totNumLoci()))
>>> # print allele frequency
>>> print pop2.dvars().alleleFreq
[[0.794666666666666663, 0.205333333333333334], [0.814666666666666666, 0.185333333333333333]]
>>> # assign affection status using a penetrance model
>>> MapPenetrance(pop2, locus=1,
...               penetrance={'0-0': 0.05, '0-1': 0.2, '1-1': 0.8})
>>> # draw case control sample
>>> (sample,) = CaseControlSample(pop2, cases=5, controls=5)
>>> # save sample in Merlin QTDT format
>>> from simuUtil import SaveQTDT
>>> SaveQTDT(sample, output='sample', affectionCode=['U', 'A'],
...          fields=['affection'])
```

Population manipulation (cont.)

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```
>>> # have a look at the sample in Merlin-QTDT Format
>>> print open('sample.map').read()
CHROMOSOME MARKER POSITION
1      loc1-1  1.000000
1      loc1-2  3.000000
2      loc1-1_1      1.000000
2      loc1-2_1      3.000000
2      loc1-3  5.000000
3      loc2-1  2.500000
3      loc2-2  4.000000

>>> print open('sample.dat').read()
A      affection
M      loc1-1
M      loc1-2
M      loc1-1_1
M      loc1-2_1
M      loc1-3
M      loc2-1
M      loc2-2
```

Population manipulation (cont.)

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```
>>> print open('sample.ped').read()
1 1 0 0 2 A 1 1 1 1 1 2 1 1 2 1 2 1 1 2
2 1 0 0 2 A 1 1 2 1 1 2 1 1 1 1 1 1 1 1
3 1 0 0 2 A 1 1 1 2 1 1 1 1 1 1 1 1 1 2
4 1 0 0 1 A 2 1 2 2 1 2 2 1 1 1 1 2 1 2
5 1 0 0 1 A 1 2 1 1 1 2 1 1 1 1 1 1 2 1
6 1 0 0 1 U 1 2 1 1 1 2 2 1 1 1 1 1 1 1
7 1 0 0 2 U 1 1 1 1 1 1 2 1 1 2 1 1 1 1
8 1 0 0 2 U 1 1 1 1 1 2 1 1 2 1 1 1 1 1
9 1 0 0 1 U 1 1 1 1 1 2 1 1 1 1 1 2 2 1
10 1 0 0 2 U 1 1 1 1 1 1 2 2 1 1 1 1 2 2

>>>
```

Population variables

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```
>>> pop = population(subPop=[5, 10], loci=[5])
>>> InitByFreq(pop, [.6, .3, .1])
>>> Stat(pop, alleleFreq=[1], genoFreq=[2])
>>> print pop.dvars().alleleFreq[1][0]
0.666666666666667
>>> from simuUtil import ListVars
>>> ListVars(pop.dvars(), useWxPython=False)
grp : -1
rep : -1
alleleNum :
  [1]
    [0]      20
    [1]       7
    [2]       3
genoFreq :
  [2]
    [0]
      0 :      0.266666666666667
      1 :      0.266666666666667
      2 :      0.333333333333333
    [1]
      1 :      0.066666666666667
      2 :      0.066666666666667
genoNum :
  [2]
    [0]
      0 :      4.0
      1 :      4.0
      2 :      5.0
    [1]
      1 :      1.0
```

Population variables (cont.)

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```
[1]          0.233333333333333
[2]          0.1
subPop
[0]
  alleleNum :
    [1]
      [0]    7
      [1]    2
      [2]    1
  genoNum :
    [2]
      [0]
        0 : 2.0
        1 : 2.0
        2 : 1.0
  genoFreq :
    [2]
      [0]
        0 : 0.4
        1 : 0.4
        2 : 0.2
  alleleFreq :
    [1]
      [0]    0.7
      [1]    0.2
      [2]    0.1
```

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Assume ploidy = 2, maxAllele = 1

0	1	2	3	4	5	6
0	1	1	1	0	0	1
0	0	1	1	1	0	1

0	1	2	3	4	5
0	1	0	0	0	1
1	0	1	1	0	0

Male

● Affected

fitness	father_id	...
---------	-----------	-----

Structure of Individuals

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Assume ploidy = 2, maxAllele = 1

0	1	2	3	4	5	6
0	1	1	1	0	0	1
0	0	1	1	1	0	1

Chromosome 0

0	1	2	3	4	5
0	1	0	0	0	1
1	0	1	1	0	0

Male

● Affected

fitness	father_id	...
---------	-----------	-----

Structure of Individuals

simuPOP tutorial

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Ph.D.

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Assume ploidy = 2, maxAllele = 1

0	1	2	3	4	5	6
0	1	1	1	0	0	1
0	0	1	1	1	0	1

Chromosome 0

0	1	2	3	4	5
0	1	0	0	0	1
1	0	1	1	0	0

Chromosome 1

Male

● Affected

fitness	father_id	...
---------	-----------	-----

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Assume ploidy = 2, maxAllele = 1

0	1	2	3	4	5	6
0	1	1	1	0	0	1
0	0	1	1	1	0	1

Chromosome 0

0	1	2	3	4	5
0	1	0	0	0	1
1	0	1	1	0	0

Chromosome 1

Male

Sex

● Affected

fitness	father_id	...
---------	-----------	-----

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Assume ploidy = 2, maxAllele = 1

0	1	2	3	4	5	6
0	1	1	1	0	0	1
0	0	1	1	1	0	1

Chromosome 0

0	1	2	3	4	5
0	1	0	0	0	1
1	0	1	1	0	0

Chromosome 1

Male

Sex

● Affected

Affection status

fitness	father_id	...
---------	-----------	-----

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Assume ploidy = 2, maxAllele = 1

0	1	2	3	4	5	6
0	1	1	1	0	0	1
0	0	1	1	1	0	1

Chromosome 0

0	1	2	3	4	5
0	1	0	0	0	1
1	0	1	1	0	0

Chromosome 1

Male

Sex

● Affected

Affection status

fitness | father_id | ...

Information
fields

Individuals

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Population manipulation

```
>>> pop = population(subPop=[5, 8], loci=[5],
...                   infoFields=['penetrance'])
>>> InitByFreq(pop, [.6, .3, .1])
>>> MaPenetrance(pop, locus=2, penetrance=[0.05, 0.2, 0.5],
...              wildtype=[0], infoFields=['penetrance'])
>>> # iterate through all individuals in subPop 1
>>> for ind in pop.individuals(1):
...     print 'Aff: %d Fit: %.3f Geno: %d %d' % \
...           (ind.affected(), ind.info('penetrance'), \
...            ind.allele(2, 0), ind.allele(2, 1))
...
Aff: 0 Fit: 0.200 Geno: 0 2
Aff: 0 Fit: 0.050 Geno: 0 0
Aff: 0 Fit: 0.200 Geno: 0 2
Aff: 0 Fit: 0.200 Geno: 0 1
Aff: 0 Fit: 0.200 Geno: 0 1
Aff: 1 Fit: 0.200 Geno: 1 0
Aff: 0 Fit: 0.050 Geno: 0 0
Aff: 0 Fit: 0.050 Geno: 0 0
>>>
```

Information fields

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Population manipulation

```
>>> pop = population(100, loci=[5, 8],  
...     infoFields=['father_idx', 'mother_idx'])  
>>> simu = simulator(pop, randomMating(numOffspring=2))  
>>> simu.evolve(ops=[parentsTagger()], end=5)  
True  
>>> ind = simu.population(0).individual(0)  
>>> ind1 = simu.population(0).individual(1)  
>>> print ind.info('father_idx'), ind.info('mother_idx')  
56.0 88.0  
>>> print ind1.info('father_idx'), ind1.info('mother_idx')  
56.0 88.0  
>>>  
>>>
```


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Life cycle of a generation

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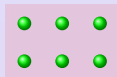
Operator

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Parental
generation

Every operator has a default stage, and a **stage** parameter to change it.

Life cycle of a generation

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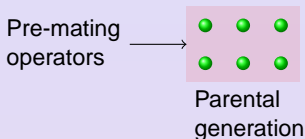
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Every operator has a default stage, and a **stage** parameter to change it.

Life cycle of a generation

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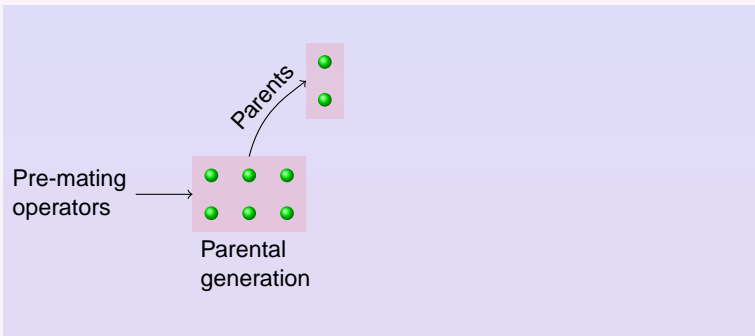
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Every operator has a default stage, and a **stage** parameter to change it.

Life cycle of a generation

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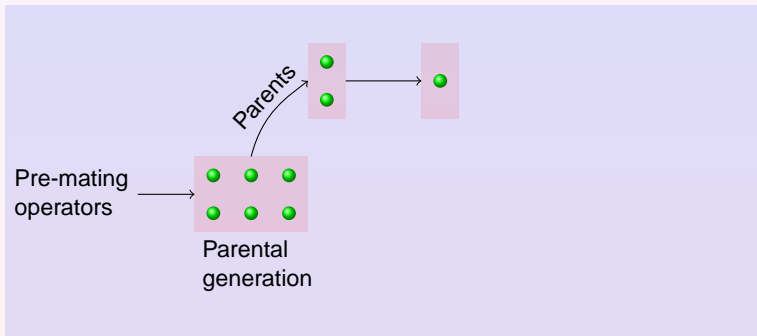
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Every operator has a default stage, and a **stage** parameter to change it.

Life cycle of a generation

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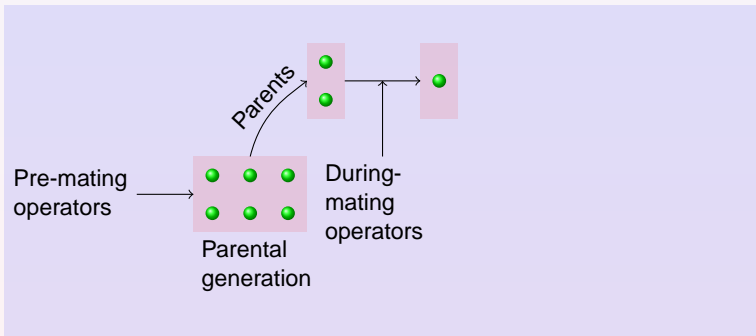
Operator

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Every operator has a default stage, and a **stage** parameter to change it.

Life cycle of a generation

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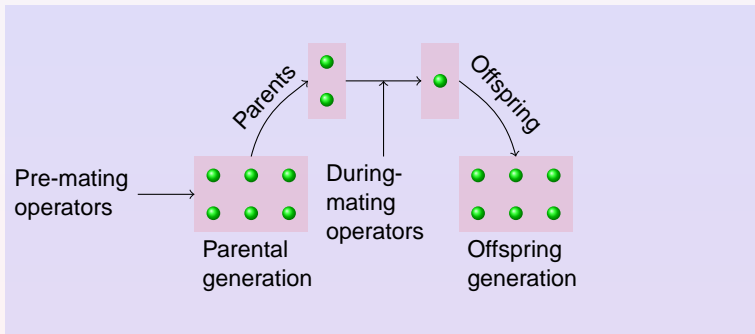
Operator

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Every operator has a default stage, and a **stage** parameter to change it.

Life cycle of a generation

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What is simuPOP

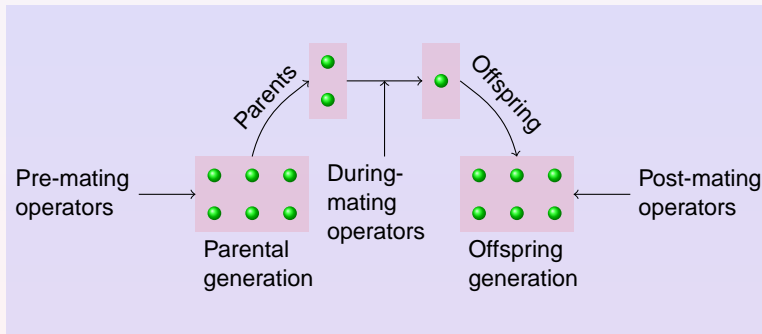
An example

simuPOP components

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Every operator has a default stage, and a **stage** parameter to change it.

Pre-, During- and PostMating operators

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simuPOP components

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Population manipulation

```
>>> simu = simulator(
...     population(subPop=[20, 80], loci=[3]),
...     randomMating())
>>> simu.evolve(
...     preOps = [initByFreq([0.2, 0.8])],
...     ops = [
...         kamMutator(maxAllele=10, rate=0.00005, atLoci=[0,2]),
...         recombinator(rate=0.001),
...         dumper(stage=PrePostMating),
...         stat(alleleFreq=[1]),
...     ],
...     dryrun=True
... )
```

Dryrun mode: display calling sequence

Apply pre-evolution operators

Replicate 0

- <simuPOP::initByFreq> end at 1

Start evolution

Replicate 0

Pre-mating operators

- <simuPOP::dumper> at all generations

Start mating

- <simuPOP::recombination> at all generations

Apply post-mating operators

- <simuPOP::k-allele model mutator K=10> at all generations

- <simuPOP::dumper> at all generations

- <simuPOP::statistics> at all generations

True

>>>

Applicable generations

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Population manipulation

```
>>> simu = simulator(
...     population(10000, loci=[3]),
...     randomMating())
>>> eval1 = r"'Gen: %3d Freq: %f\n' % (gen, alleleFreq[1][0])"
>>> eval2 = r"'Last Gen: %3d Freq: %s\n' % (gen, alleleFreq[1])"
>>> simu.evolve(
...     preOps = [initByFreq([0.3, 0.7])],
...     ops = [
...         recombinator(rate=0.01, begin=10, end=30),
...         stat(alleleFreq=[1], step=10),
...         pyEval(eval1, step=10),
...         pyEval(eval2, at=[-1])
...     ],
...     end = 50
... )
Gen: 0 Freq: 0.298050
Gen: 10 Freq: 0.298300
Gen: 20 Freq: 0.298150
Gen: 30 Freq: 0.295000
Gen: 40 Freq: 0.295350
Gen: 50 Freq: 0.299200
Last Gen: 50 Freq: [0.29920000000000002, 0.70079999999999998]
True
>>>
```

Applicable replicates

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Population manipulation

```
>>> simu = simulator(
...     population(100, loci=[3]),
...     randomMating(),
...     rep=5, grp=[1,1,2,2,2])
>>> simu.evolve(
...     preOps = [initByFreq([0.5, 0.5])],
...     ops = [
...         stat(alleleFreq=[1]),
...         recombinator(rate=0.01, grp=1),
...         recombinator(rate=0.01, grp=2),
...         pyEval(r"'%.2f ' % alleleFreq[1][0]", grp=1),
...         pyEval(r"'\n'", rep=REP_LAST),
...     ],
...     end=5
... )
0.43 0.43
0.48 0.41
0.47 0.47
0.48 0.46
0.47 0.45
0.45 0.41
True
>>>
```

Output

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```
>>> simu = simulator(
...     population(100, loci=[3]),
...     randomMating(),
...     rep=5, grp=[1,1,2,2,2])
>>> simu.evolve(
...     preOps = [initByFreq([0.5, 0.5])],
...     ops = [
...         stat(alleleFreq=[1]),
...         pyEval(r"'%.2f ' % alleleFreq[1][0]",
...             output='>>out'),
...         pyEval(r"\n", rep=REP_LAST, output='>>out'),
...         pyEval(r"'%.2f ' % alleleFreq[1][0]",
...             outputExpr=">>out%d' % grp"),
...     ],
...     end=2
... )
True
>>> print open('out').read()
0.41 0.53 0.41 0.54 0.52
0.40 0.55 0.43 0.52 0.52
0.40 0.56 0.46 0.51 0.55

>>> print open('out1').read()
0.41 0.53 0.40 0.55 0.40 0.56
>>> print open('out2').read()
0.41 0.54 0.52 0.43 0.52 0.52 0.46 0.51 0.55
>>>
```

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Mating schemes

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Mating schemes

- Population offspring subpopulation from corresponding parental subpopulation
- Can change subpopulation size
- Select parents according to their `fitness` value (information field)
- Can produce more than one offspring

Demographic model

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Population manipulation

```
>>> def lin_inc(gen, oldsize=[]):  
...     return [10+gen]*5  
...  
>>> simu = simulator(  
...     population(subPop=lin_inc(1), loci=[1]),  
...     randomMating(newSubPopSizeFunc=lin_inc)  
... )  
>>> simu.evolve(  
...     ops = [  
...         stat(popSize=True),  
...         pyEval(r'"%d %d\n"%(gen, subPop[0]["popSize"])'),  
...     ],  
...     end=5  
... )  
0 10  
1 11  
2 12  
3 13  
4 14  
5 15  
True  
>>>
```

Number of offspring

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Population manipulation

```
>>> simu = simulator(  
...     population(size=10000, loci=[1]),  
...     randomMating(),  
... )  
>>> simu.evolve(  
...     preOps = [initByFreq([0.1, 0.9])],  
...     ops = [ ], end=100  
... )  
True  
>>> simu.setMatingScheme(randomMating(numOffspring=2))  
>>> simu.addInfoFields(['father_idx', 'mother_idx'])  
>>> simu.setAncestralDepth(1)  
>>> simu.step(ops=[parentsTagger()])  
True  
>>> pop = simu.getPopulation(0)  
>>> MaPenetrance(pop, locus=0, penetrance=[0.05, 0.1, 0.5])  
>>> AffectedSibpairSample(pop, size=100)  
[<simuPOP::population of size 200>]  
>>>
```


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A simulator manages

- Replicates of a population
- A mating scheme
- Many operators

and evolve the populations.

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simuCDCV.py demonstrate the evolution of allelic spectrum

loadHapMap.py

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```
from simuOpt import setOptions
setOptions(optimized=True, alleleType='binary')
from simuPOP import *
```

loadHapMap.py

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```
def load_population(pop, ch, type):
    '''Load population from file, with type (subpopulation type)

    # For the CEU and YRI the haplotypes are arranged as follows:
    # row 1 - trio 1 parent 1 transmitted haplotype
    # row 2 - trio 1 parent 1 untransmitted haplotype
    # row 3 - trio 1 parent 2 transmitted haplotype
    # row 4 - trio 1 parent 2 untransmitted haplotype
    # row 5 - trio 2 parent 1 transmitted haplotype
    # row 6 - trio 2 parent 1 untransmitted haplotype
    # row 7 - trio 2 parent 2 transmitted haplotype
    # row 8 - trio 2 parent 2 untransmitted haplotype
    # .
    # For the JPT+CHB the haplotypes are arranged as
    # row 1 - individual 1 haplotype 1
    # row 2 - individual 1 haplotype 2
    # row 3 - individual 2 haplotype 1
    # row 4 - individual 2 haplotype 2
    # row 5 - individual 3 haplotype 1
    # row 6 - individual 3 haplotype 2
    # .
    # We are loading row by row, so actually only load the parents c
    # populations.

    subPop = { 'CEU':0, 'YRI':1, 'JPT+CHB':2}[type]
```

loadHapMap.py

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```
if __name__ == '__main__':
    ps = [0,0,0]
    for ch in range(1, 23):
        popFile = "hapmap_%d.bin" % ch
        print "Processing chromosome %d..." % ch
        (lociPos, lociName) = getLoci(ch)
        print "    Number of loci", len(lociPos)
        print "    Getting population size and verifying data file"
        popSize = getPopSize(len(lociPos), ch)
        print "    Population size %s (CEU and YRI only counts p"
        if ps[0] == 0:
            ps = popSize
        else:
            if ps[0] != popSize[0] or ps[1] != popSize[1] or ps[2] != popSize[2]:
                print "Population size does not match across chr"
                sys.exit(1)
        print "    Creating population"
        pop = population(subPop=popSize, ploidy=2, loci=[len(lociPos)],
                        lociPos=lociPos, lociNames=lociName)
        print "    Loading CEU population...",
        load_population(pop, ch, type='CEU')
        print "    Loading YRI population...",
        load_population(pop, ch, type='YRI')
```

loadHapMap.py

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Population manipulation

```
from simuOpt import setOptions
setOptions(optimized=True, alleleType='binary')
from simuPOP import *
```