Forward-time simulations using simuPOP, a tutorial

Bo Peng, Ph.D.

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

simuPOP is ...

A forward-time population genetics simulation environment

simuPOP is ...

A forward-time population genetics simulation environment

- A population genetics simulation program

simuPOP is ...

A forward-time population genetics simulation environment

- A population genetics simulation program
- Not coalescent-based

simuPOP is ...

A forward-time population genetics simulation environment

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

What simuPOP does

simuPOP provides

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

What simuPOP does

simuPOP provides

- a large number of functions to manipulate populations, copy, split, merge, modify genotype, modify individuals, 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 ...

This is fun, but is it useful?

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 phenomina

This is fun, but is it useful?

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 phenomina
- study the impact of genetic and demographic forces on the evolution of a population

This is fun, but is it useful?

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

This is fun, but is it useful?

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 phenomina
- 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

This is fun, but is it useful?

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

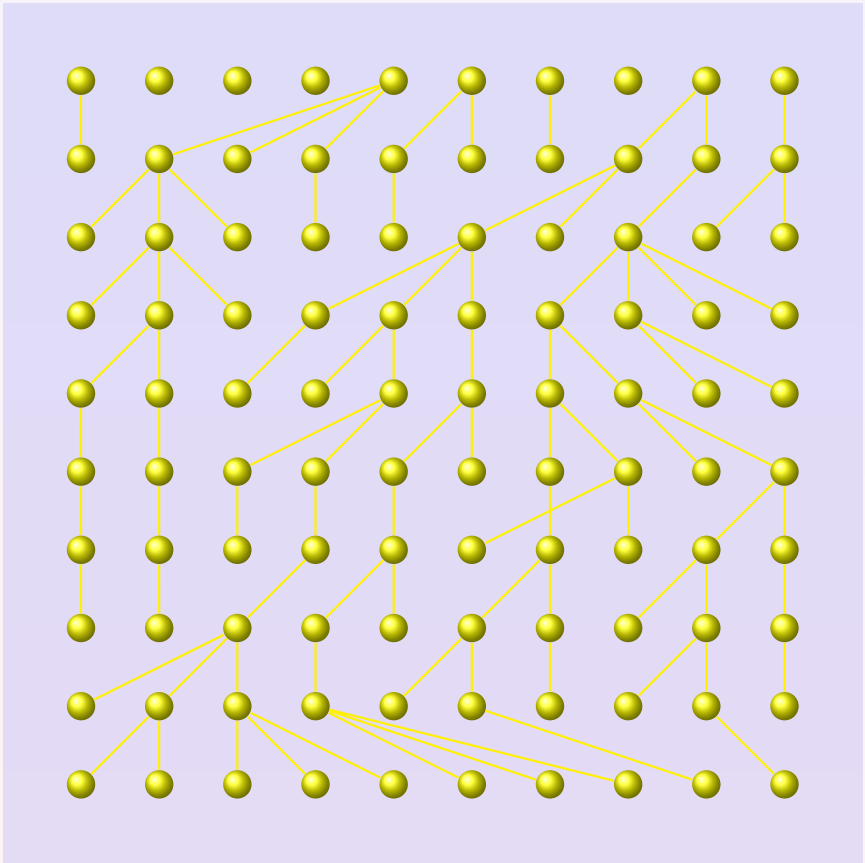
- demonstrate population genetics phenomina
- study the impact of genetic and demographic forces on the evolution of a population
- study the evolution of (complex) genetic diseases
- simulate samples to validate gene-mapping methods
- study ascertainment methods in simulated populations

This is fun, but is it useful?

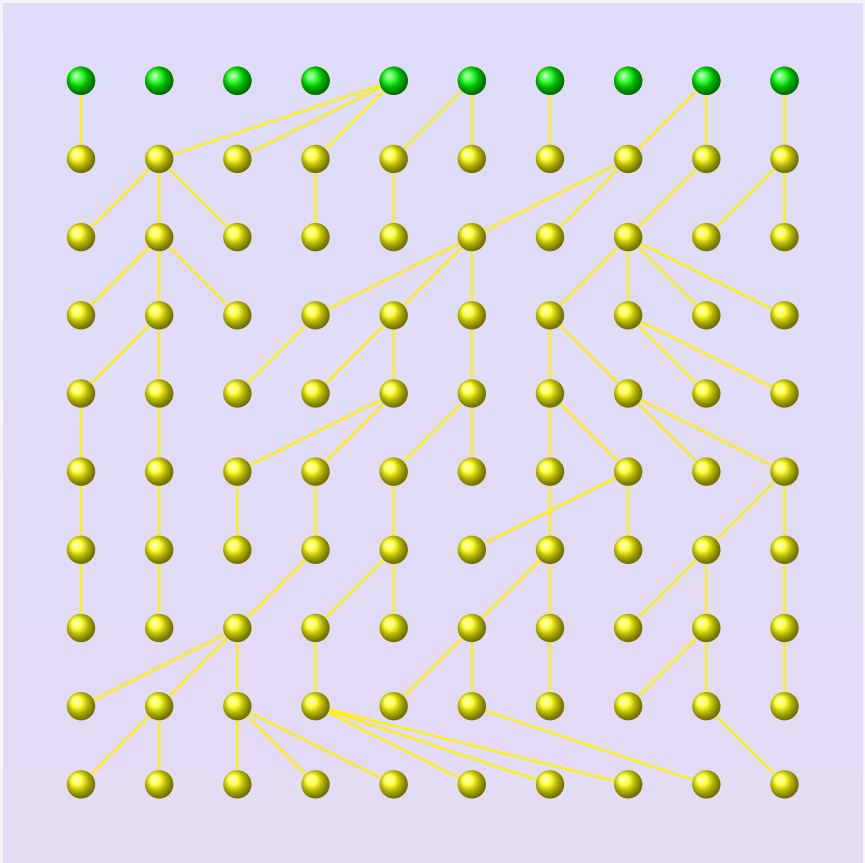
simuPOP can simulate the change of the genetic composition of a population in a complicated evolutionary process. It can be used to

- demonstrate population genetics phenomina
- 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
- ...

Forward-time simulation

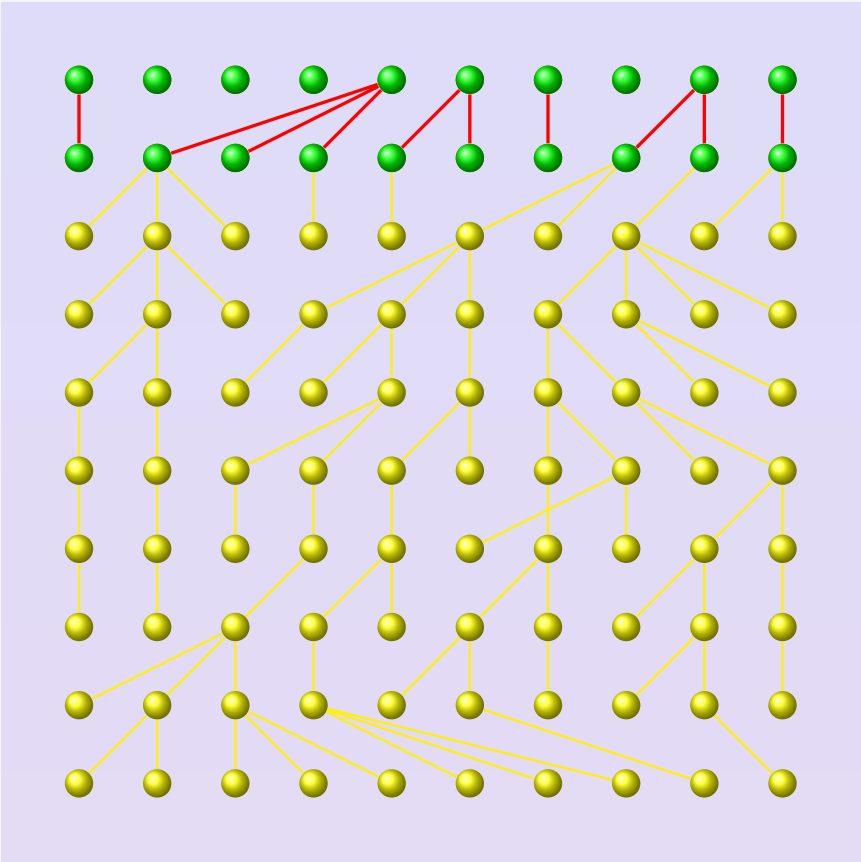


Forward-time simulation



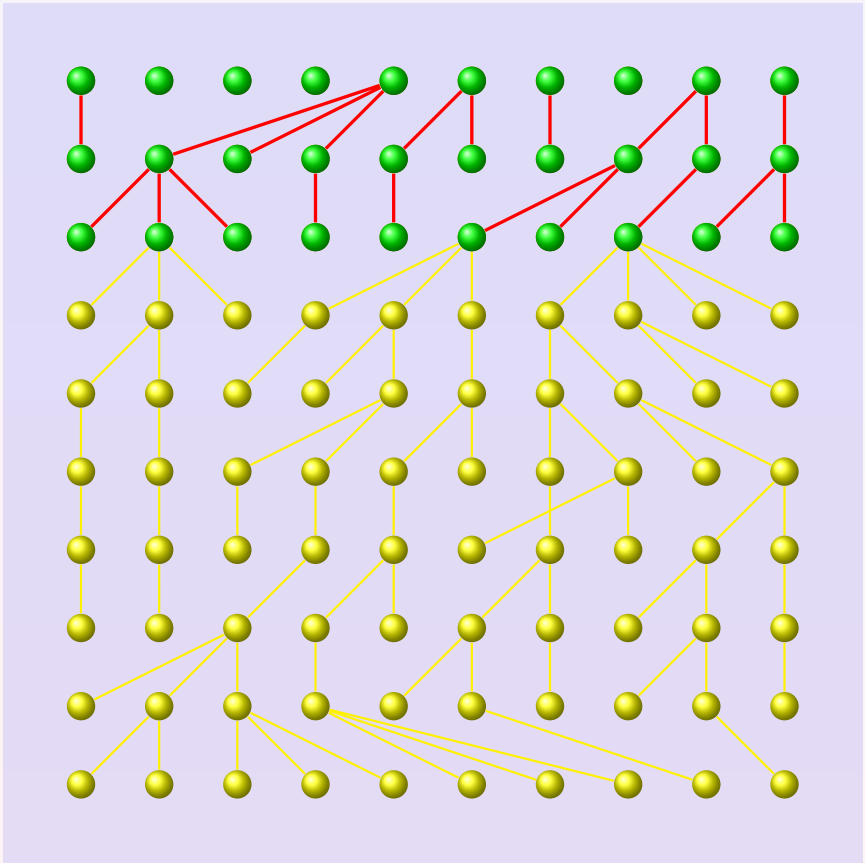
- Start from an initial population

Forward-time simulation



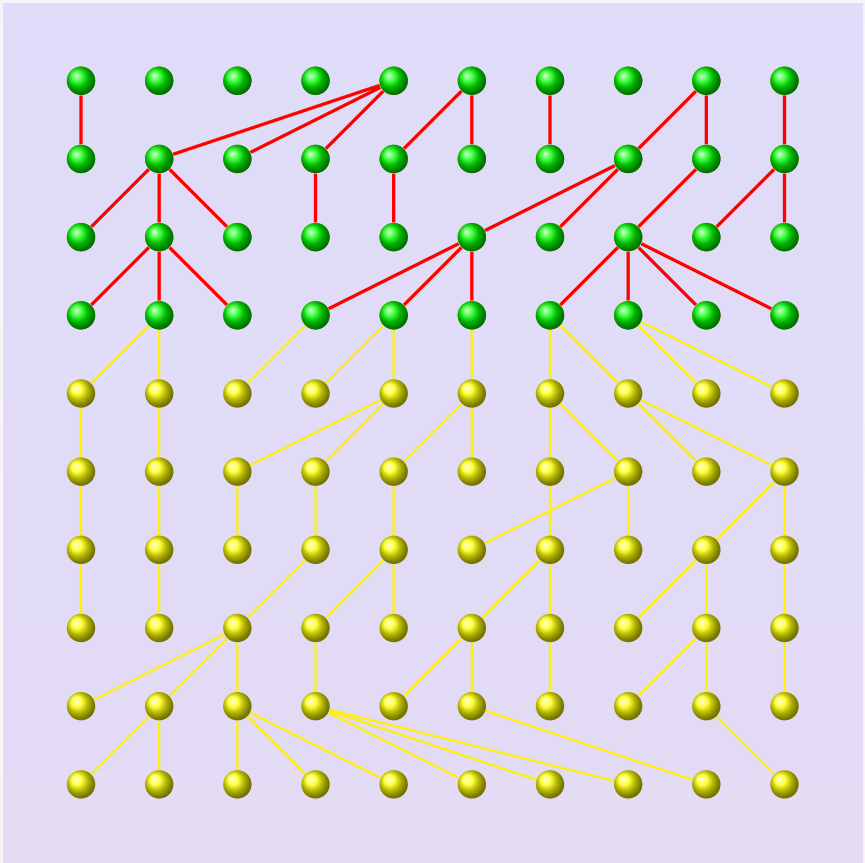
- Start from an initial population
- Evolve forward in time, generation by generation, subject to certain number of genetic and/or demographic effects

Forward-time simulation



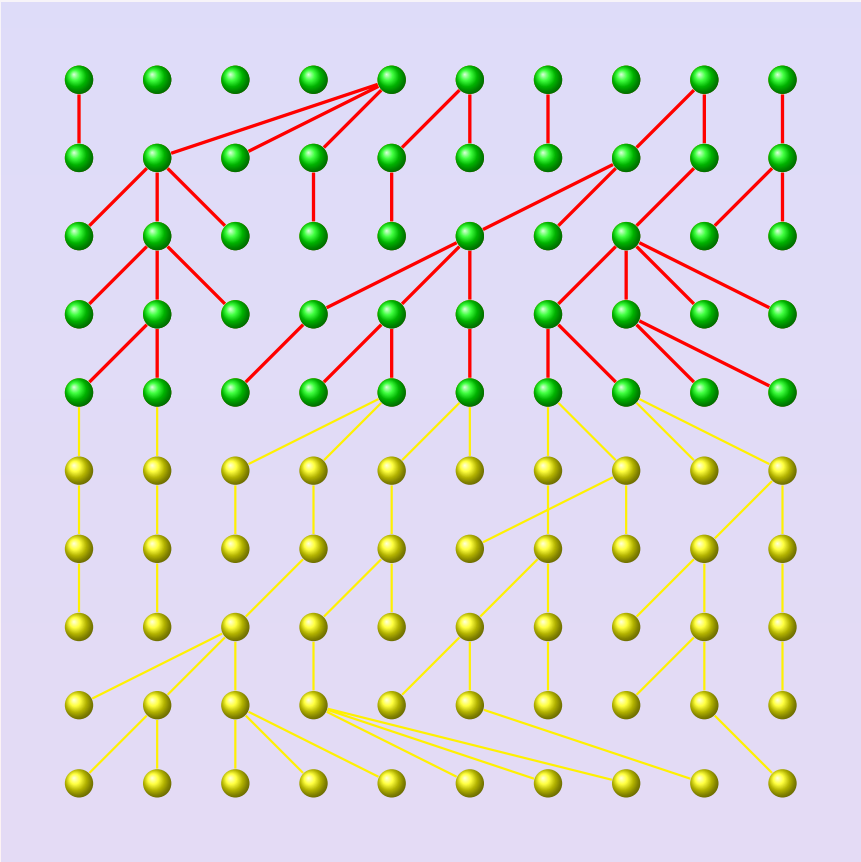
- Start from an initial population
- Evolve forward in time, generation by generation, subject to certain number of genetic and/or demographic effects

Forward-time simulation



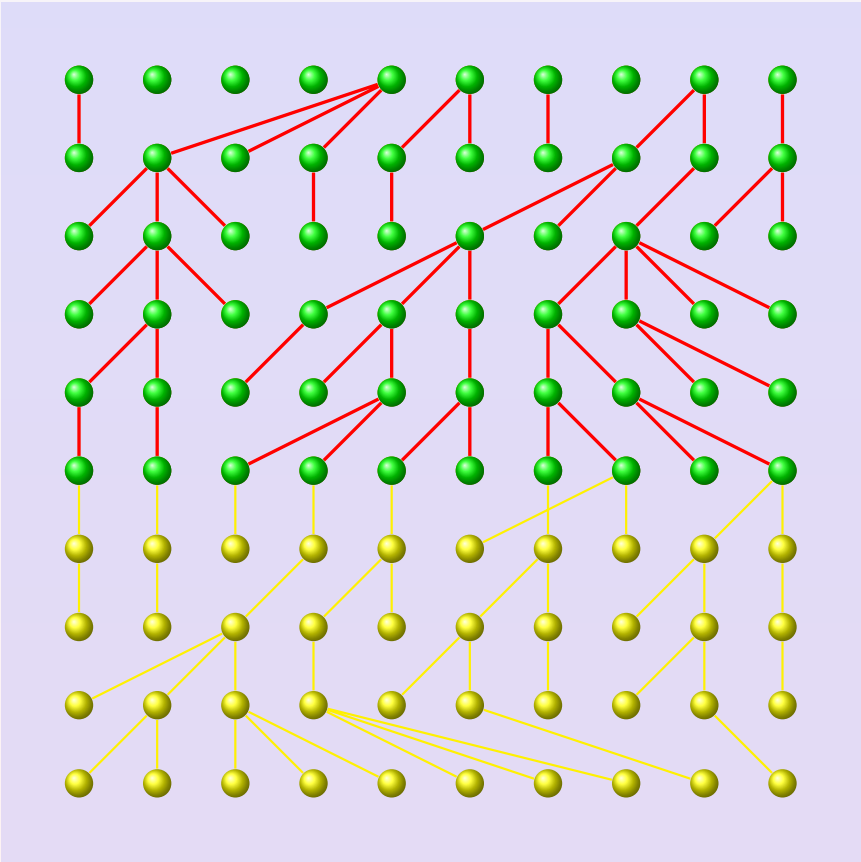
- Start from an initial population
- Evolve forward in time, generation by generation, subject to certain number of genetic and/or demographic effects

Forward-time simulation



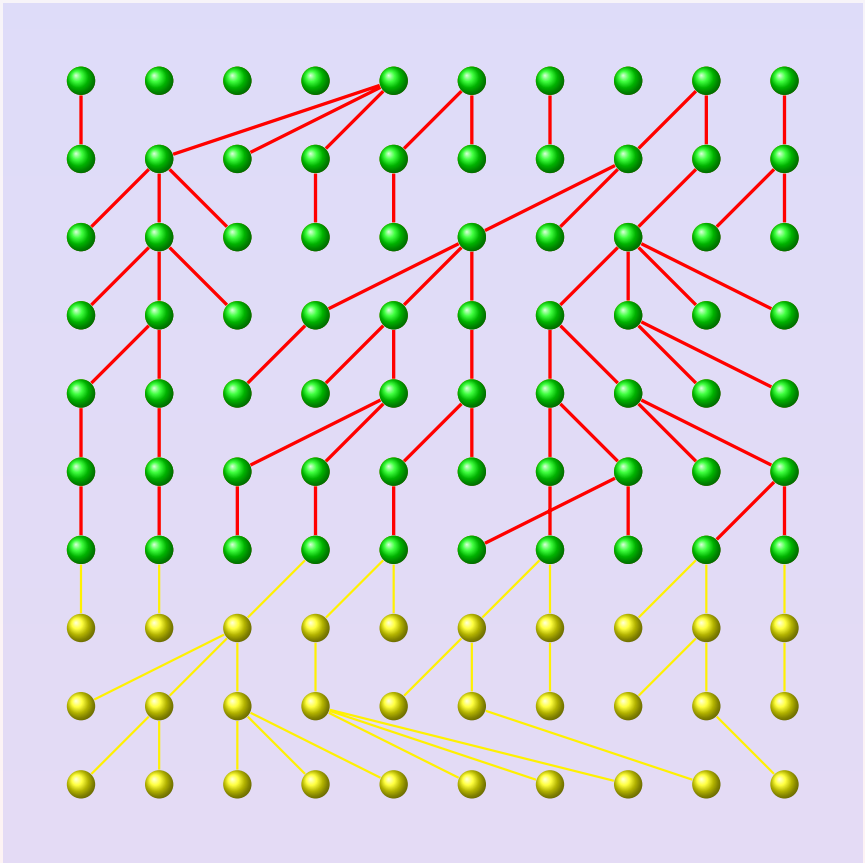
- Start from an initial population
- Evolve forward in time, generation by generation, subject to certain number of genetic and/or demographic effects

Forward-time simulation



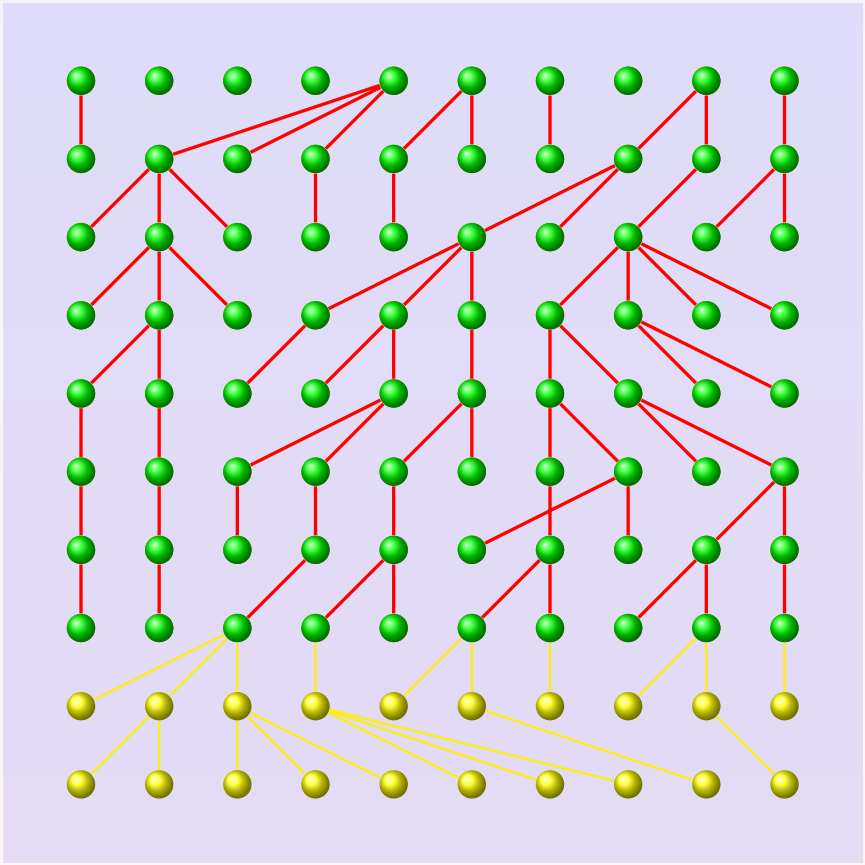
- Start from an initial population
- Evolve forward in time, generation by generation, subject to certain number of genetic and/or demographic effects

Forward-time simulation



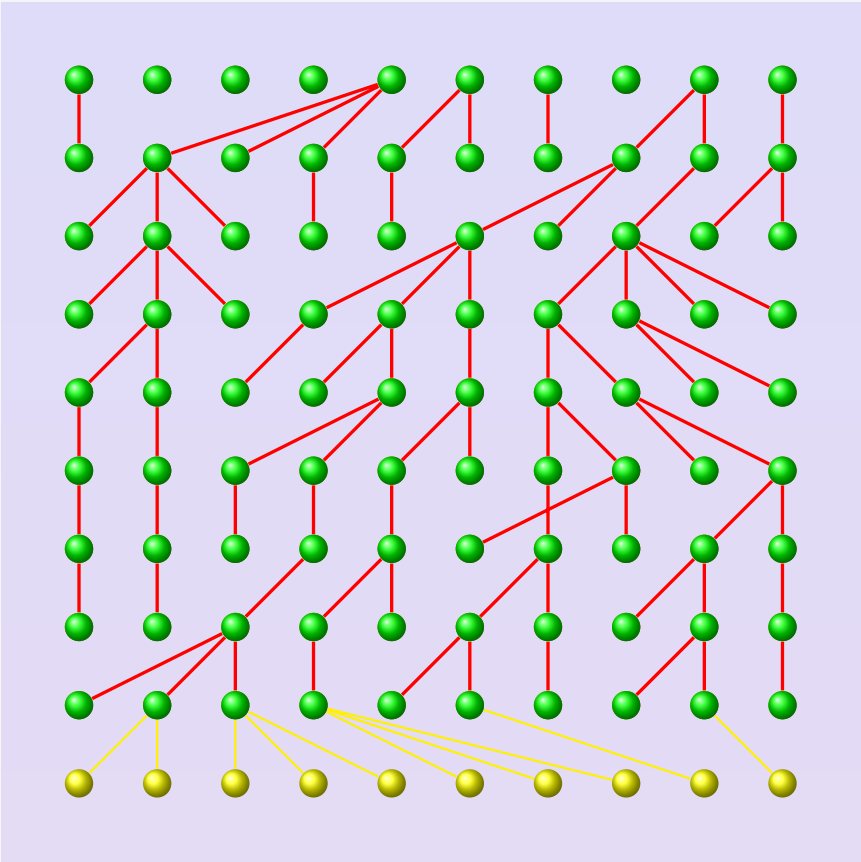
- Start from an initial population
- Evolve forward in time, generation by generation, subject to certain number of genetic and/or demographic effects

Forward-time simulation



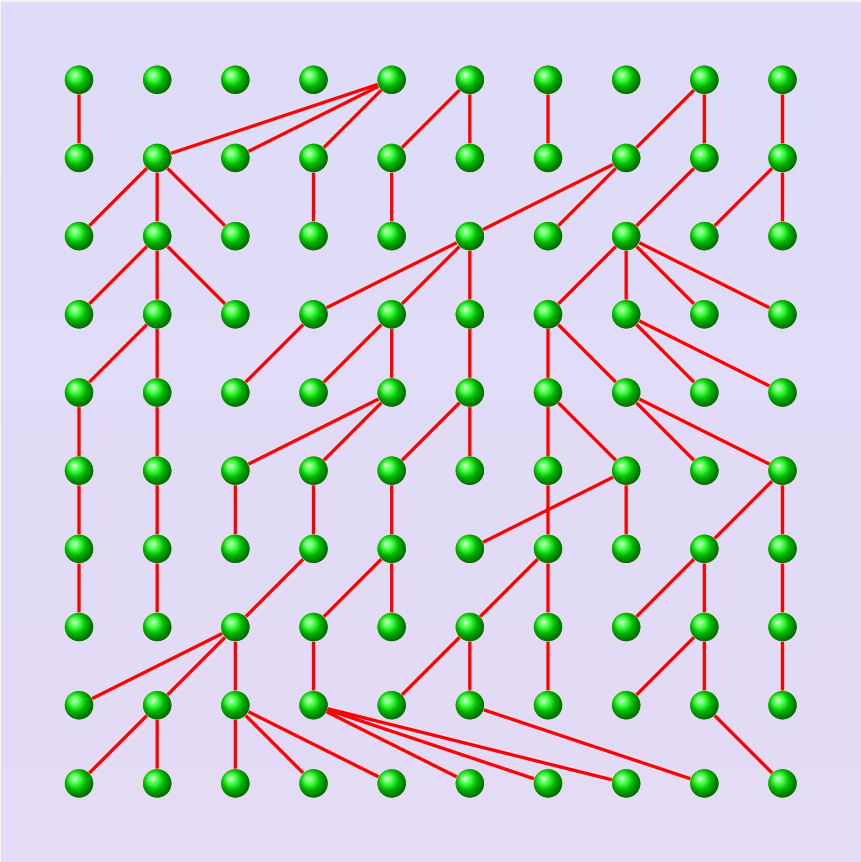
- Start from an initial population
- Evolve forward in time, generation by generation, subject to certain number of genetic and/or demographic effects

Forward-time simulation



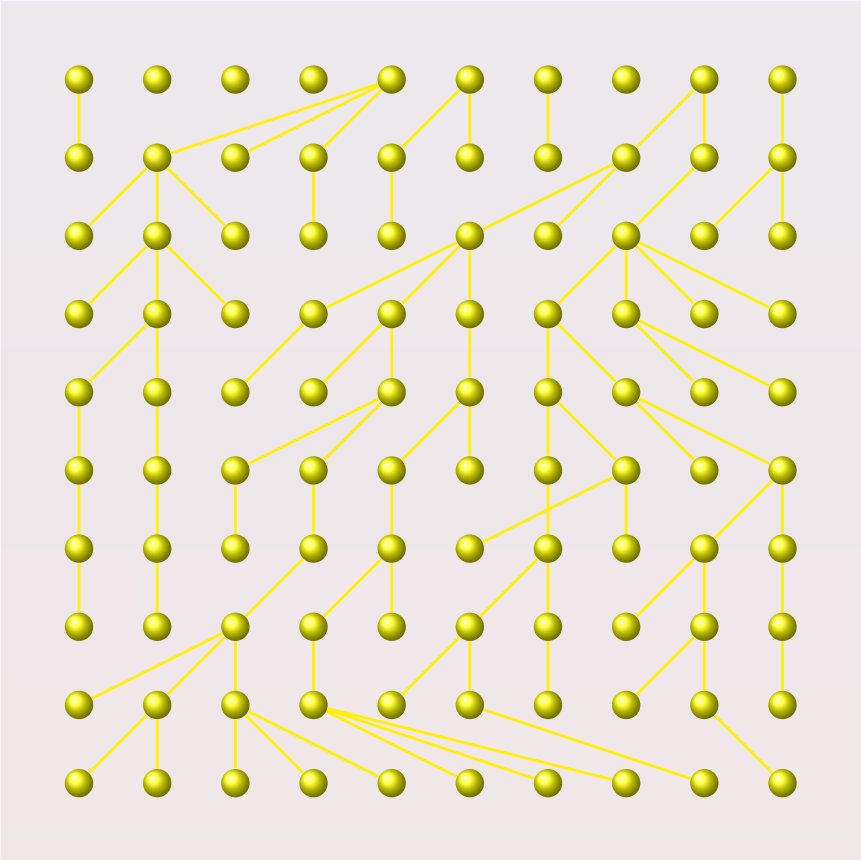
- Start from an initial population
- Evolve forward in time, generation by generation, subject to certain number of genetic and/or demographic effects

Forward-time simulation



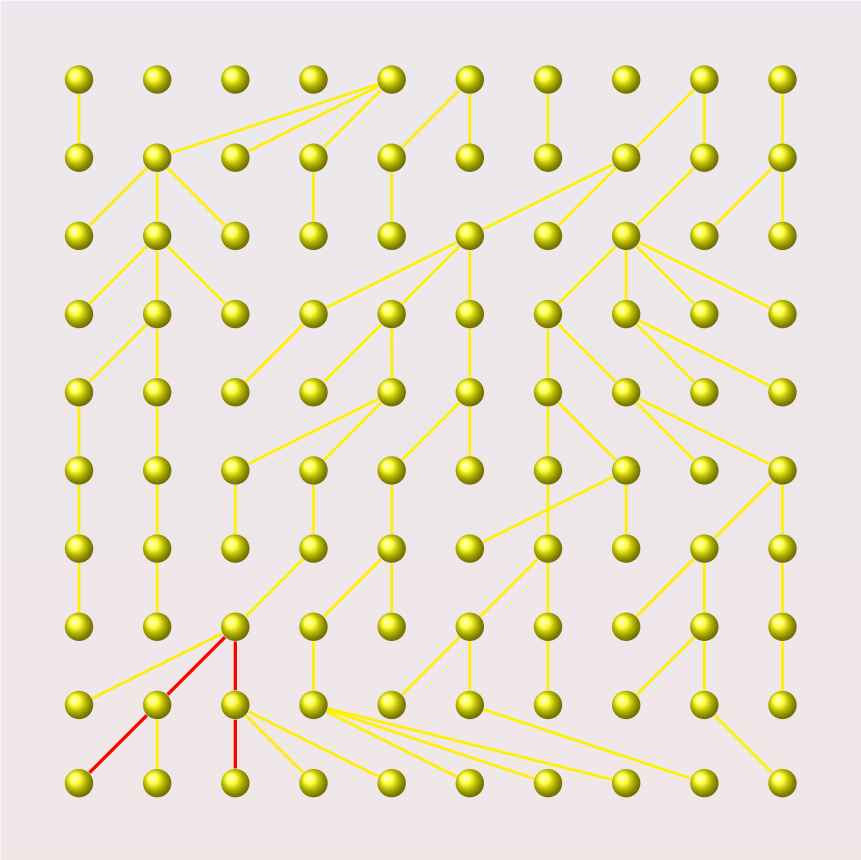
- Start from an initial population
- Evolve forward in time, generation by generation, subject to certain number of genetic and/or demographic effects
- Samples are collected from the last several generations

Backward-time simulation



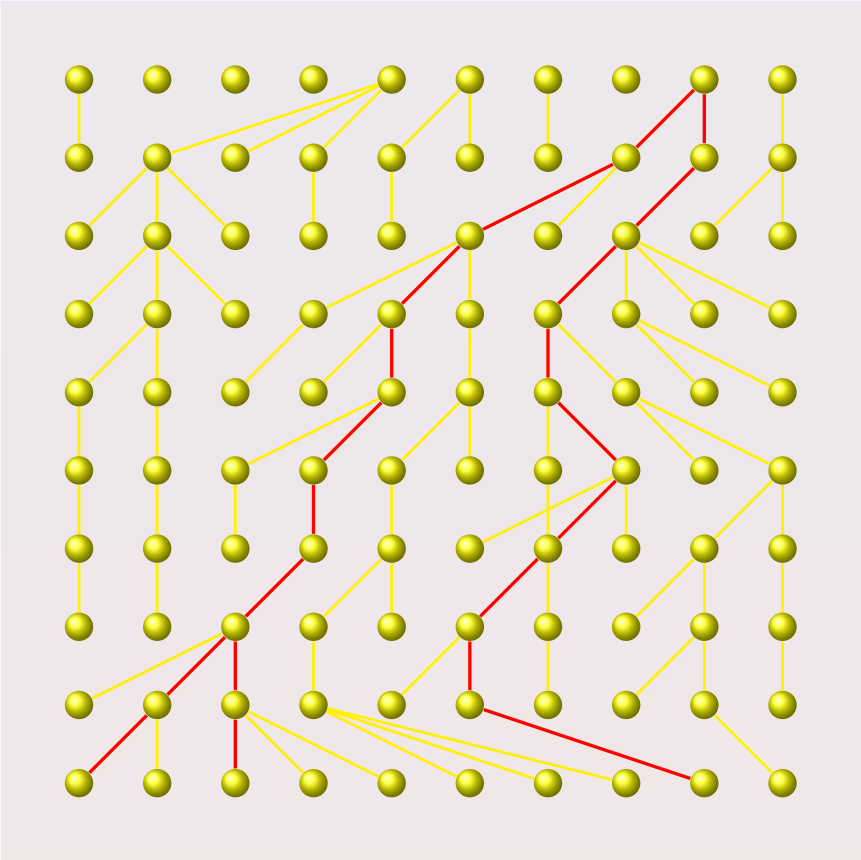
- Start from a sample with unknown genotype
- Coalesce individuals until the most recent common ancestor of all individuals is found
- Starting from the MRCA, proceed forward in time and fill the genotype of each individual

Backward-time simulation



- 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

Backward-time simulation



- 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

Backward-time

- Sample based, efficient.

Forward-time

- Population based, inefficient.

Forward vs. backward-time simulations

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

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

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 area

On the simulations of complex human diseases

Backward-time

- Haploid simulation only

Forward-time

- No limit on ploidy

On the simulations of complex human diseases

Backward-time

- Haploid simulation only
- Additive selection and penetrance models

Forward-time

- No limit on ploidy
- Arbitrary selection and penetrance models

On the simulations of complex human diseases

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

On the simulations of complex human diseases

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
- Simulate populations, which allows more flexible sampling

I like it, but, oohm, Python??

- For efficiency, the core of simuPOP is written in C++
- Python is used to
  - wrap simuPOP core (the glue language)
  - write simuPOP extensions (GUI etc)
  - pass parameters and more

Availability

- 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*

A simple example


```
>>> 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

```
  0    0.198036    0.200709    0.197748
 10    0.064744    0.063100    0.078473
 20    0.013233    0.019795    0.041057
 30    0.002985    0.004931    0.000649
 40    0.023492    0.002948    0.004462
 50    0.006016    0.014262    0.013900
 60    0.011310    0.008717    0.013715
 70    0.016652    0.014545    0.014426
 80    0.007250    0.002506    0.014372
 90    0.016994    0.014455    0.004147
100    0.000425    0.016570    0.008704
```

simuPOP modules


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

Import the default simuPOP module

population

```
>>> 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


```
>>> 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!

```
>>> 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!


```
>>> 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!

```
>>> 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

Operators!

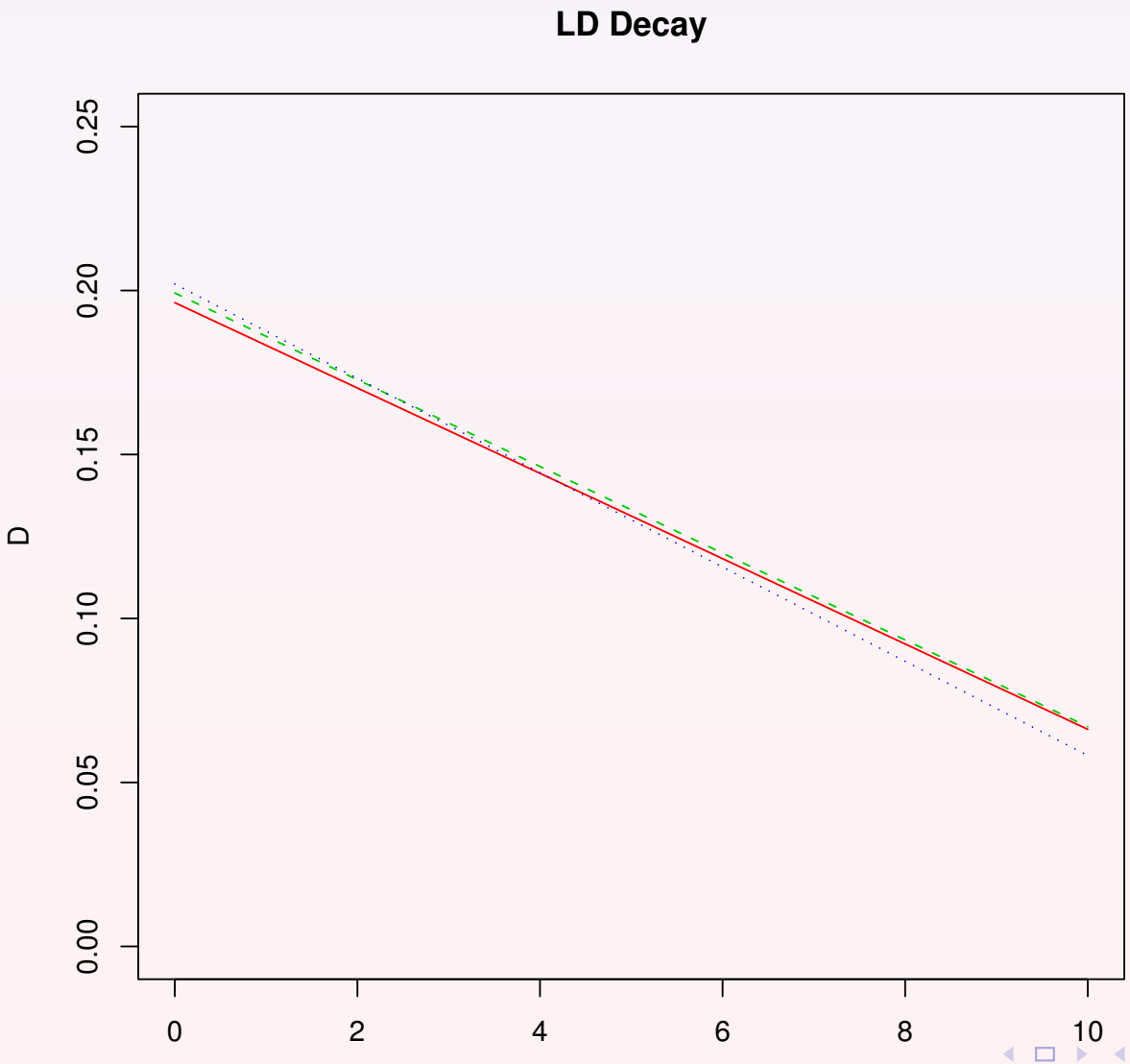
```
>>> from simuPOP import *
>>> simu = simulator(
...     population(size=1000, ploidy=2, loci=[2]),
...     randomMating(),
...     rep = 3)
>>> simu.evolve(
...     preOps = [initByValue([1,2,2,1])],
...     ops = [
...         recombinator(rate=0.1),
...         stat(LD=[0,1]),
...         pyEval(r"'%3d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

Use R to plot

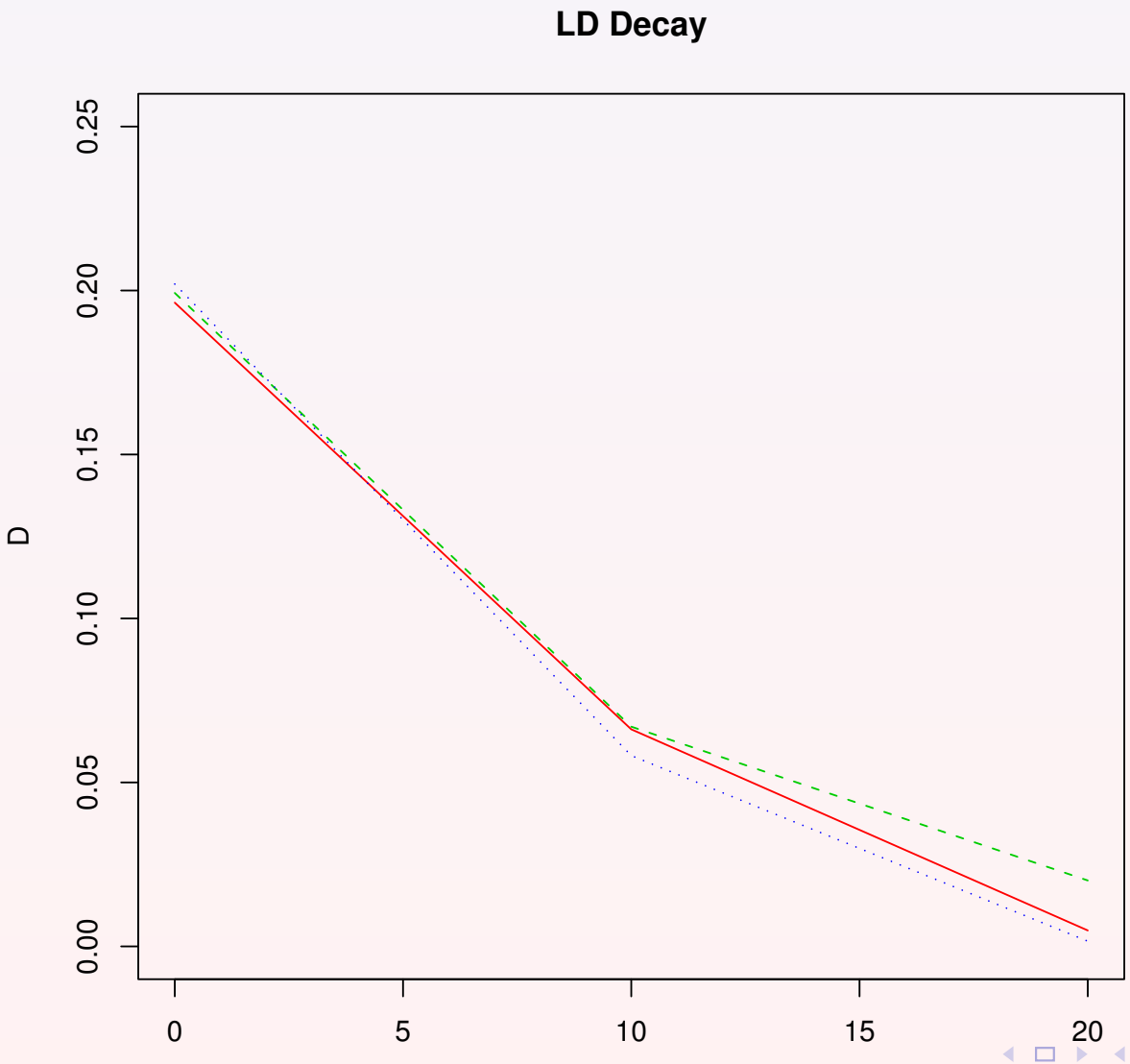
```
>>> from simuPOP import *
>>> from simuRPy import *
>>> simu = simulator(
...     population(size=1000, ploidy=2, loci=[2]),
...     randomMating(),
...     rep = 3)
>>> simu.evolve(
...     preOps = [initByValue([1,2,2,1])],
...     ops = [
...         recombinator(rate=0.1),
...         stat(LD=[0,1]),
...         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!



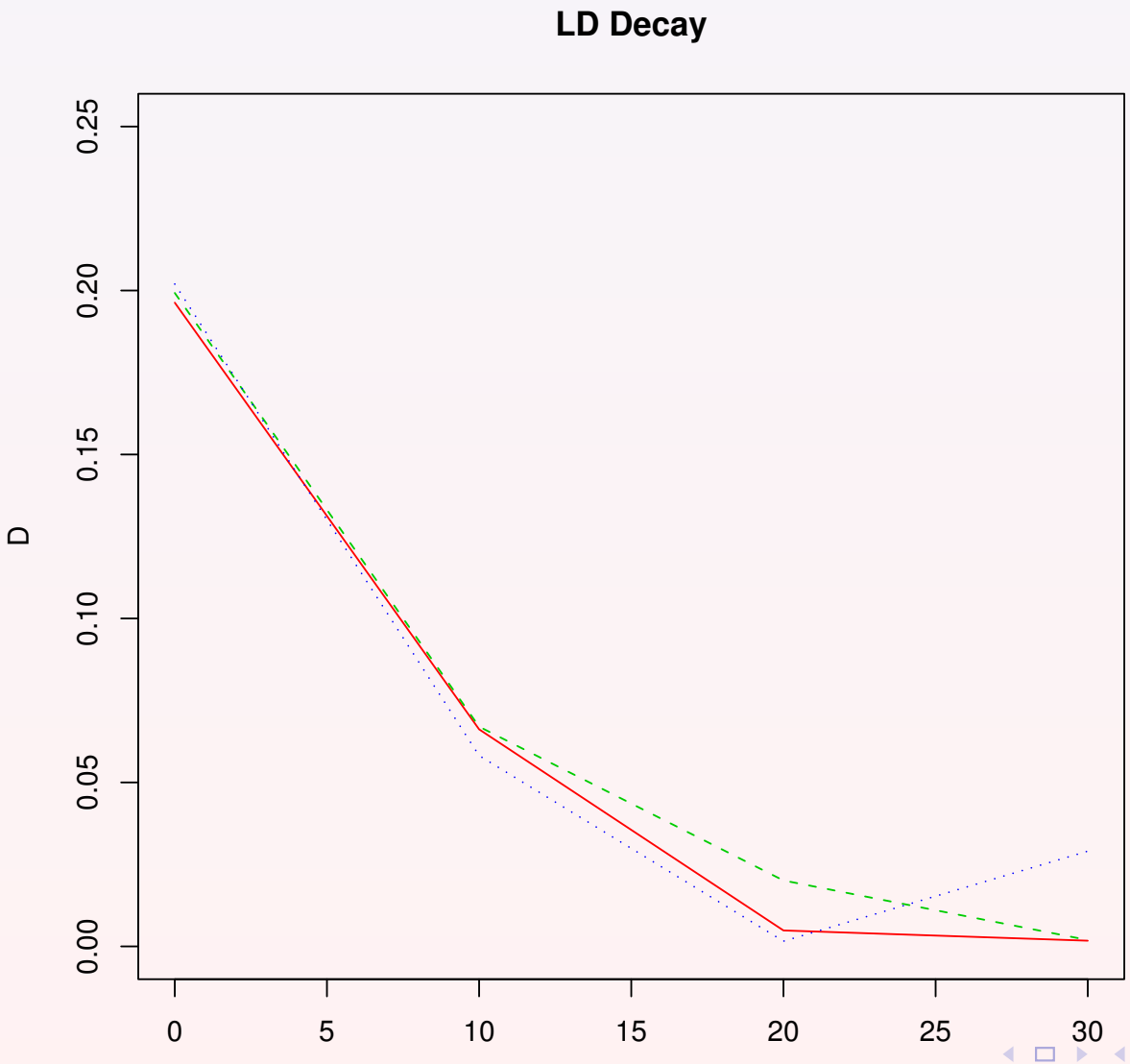
- Update at every 10 generations
- LD=0.25 before generation 0
- LD calculated at the end of each generation

Evolve!



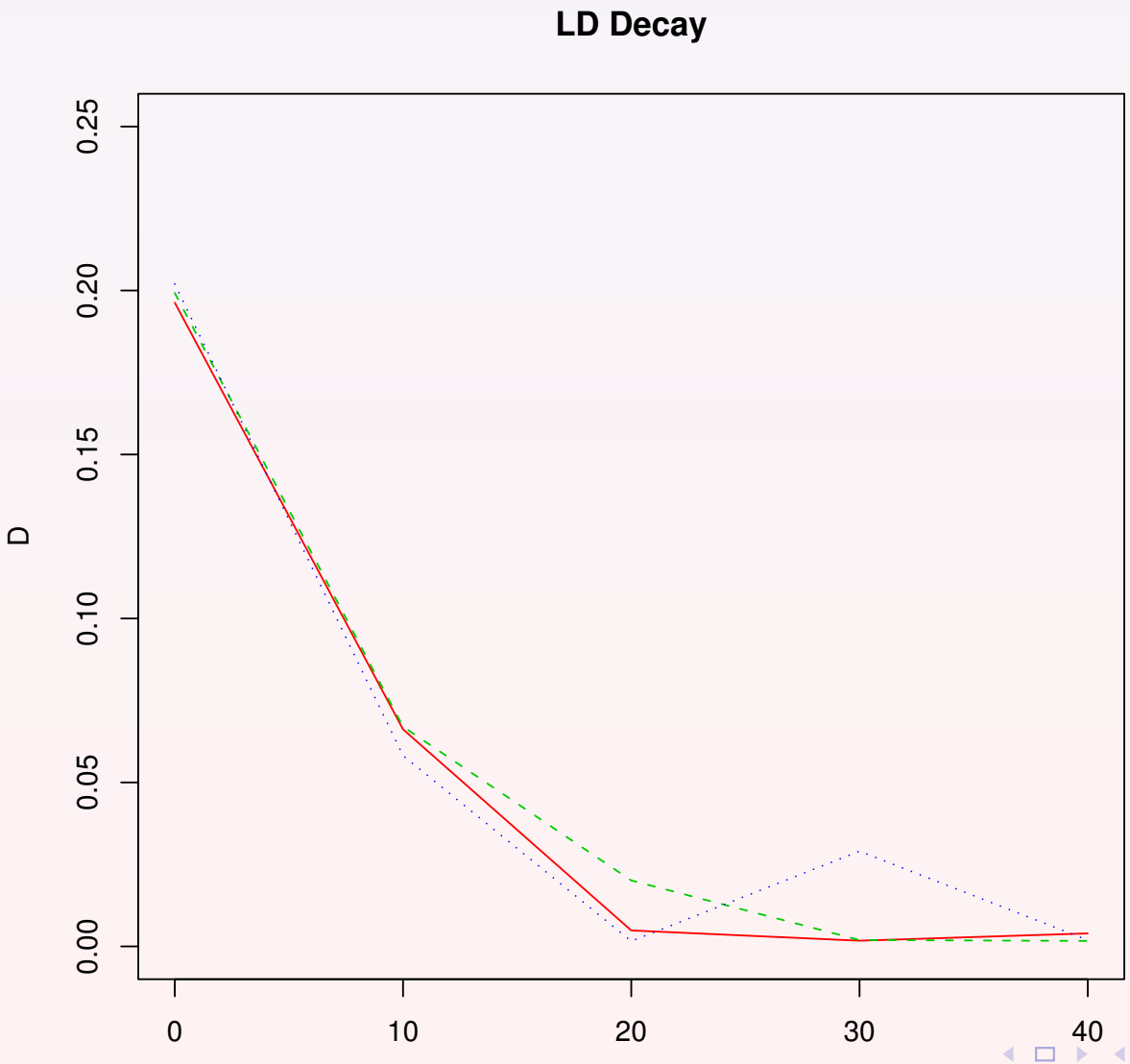
- Update at every 10 generations
- LD=0.25 before generation 0
- LD calculated at the end of each generation

Evolve!



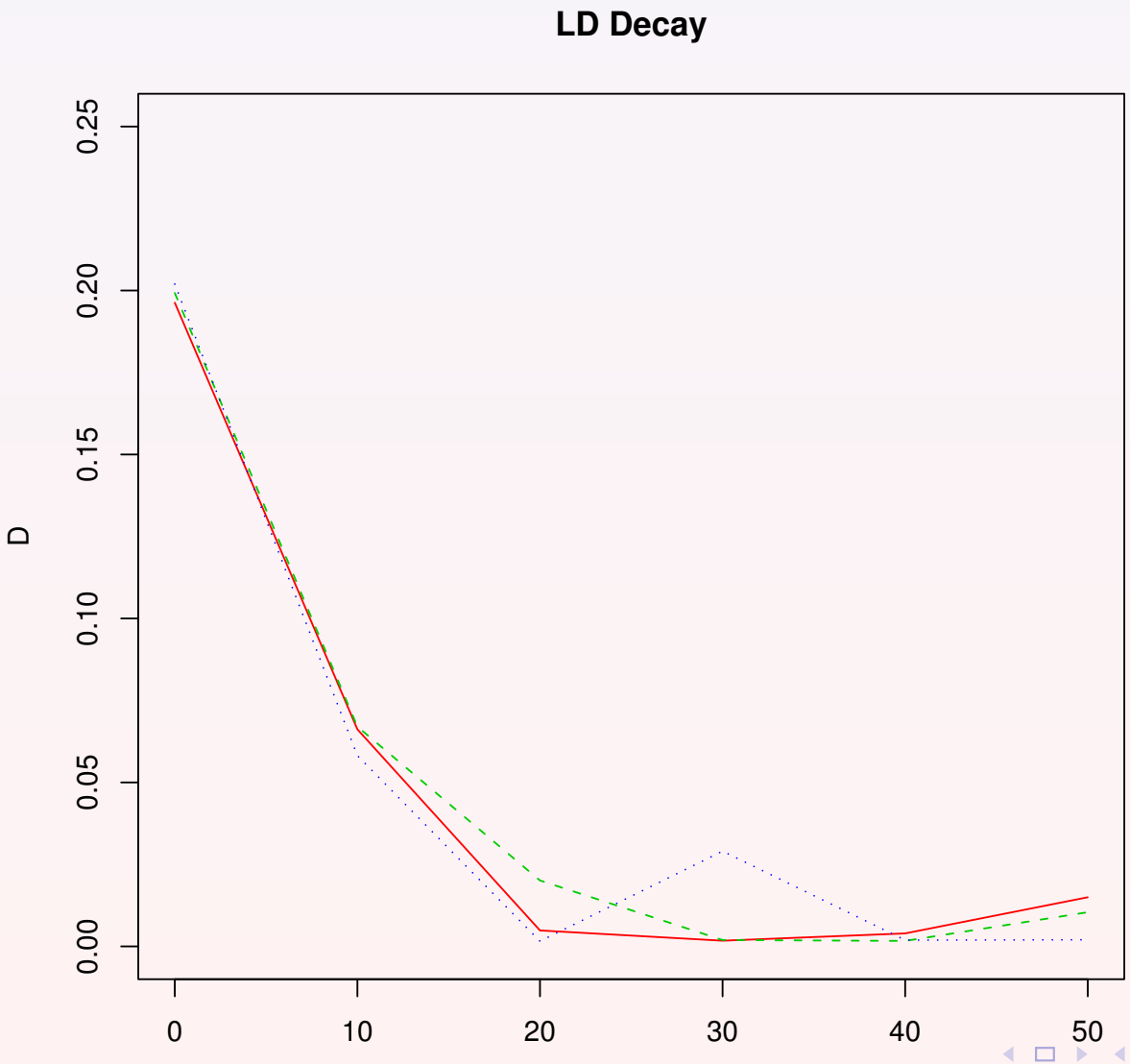
- Update at every 10 generations
- LD=0.25 before generation 0
- LD calculated at the end of each generation

Evolve!



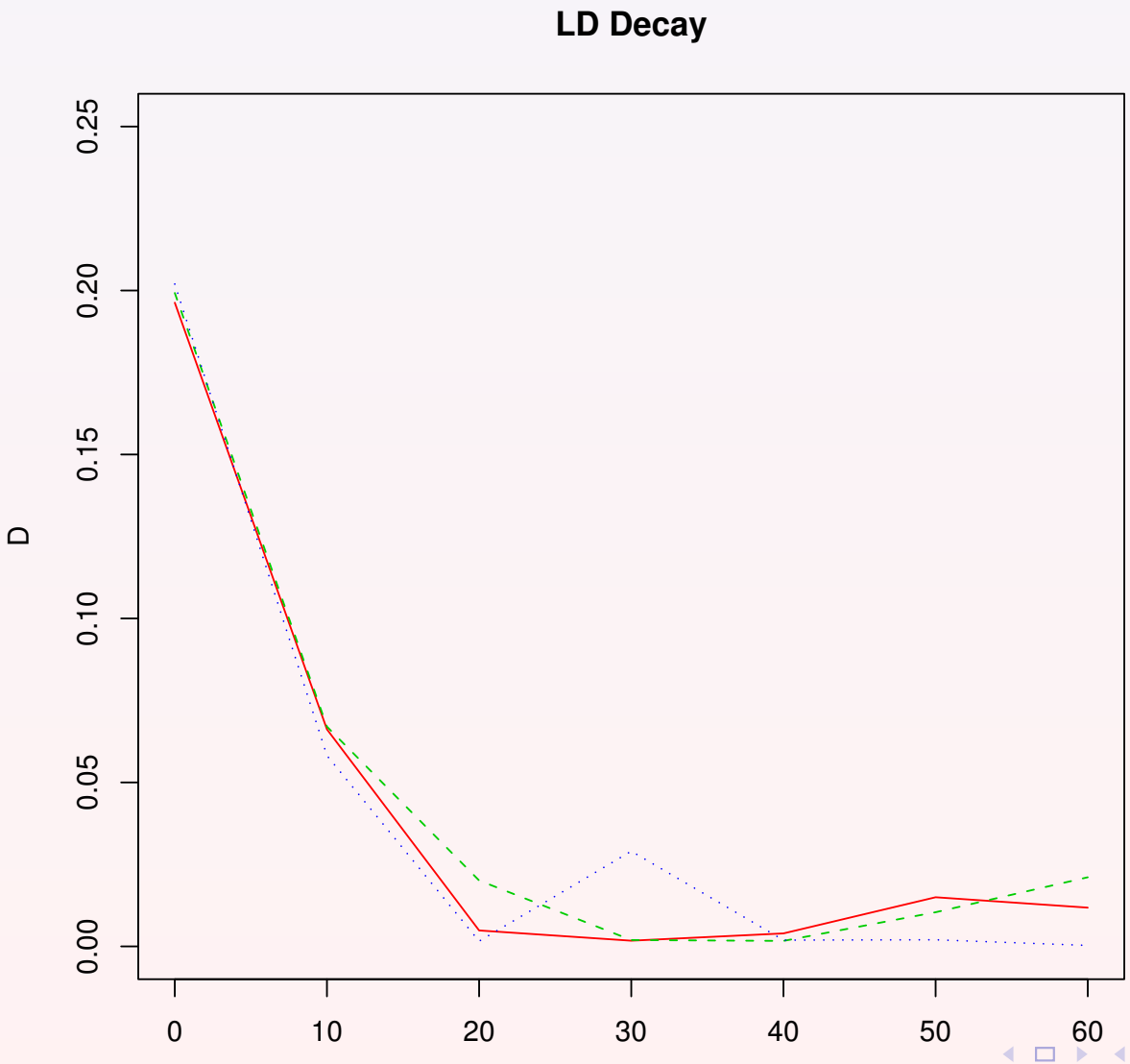
- Update at every 10 generations
- LD=0.25 before generation 0
- LD calculated at the end of each generation

Evolve!



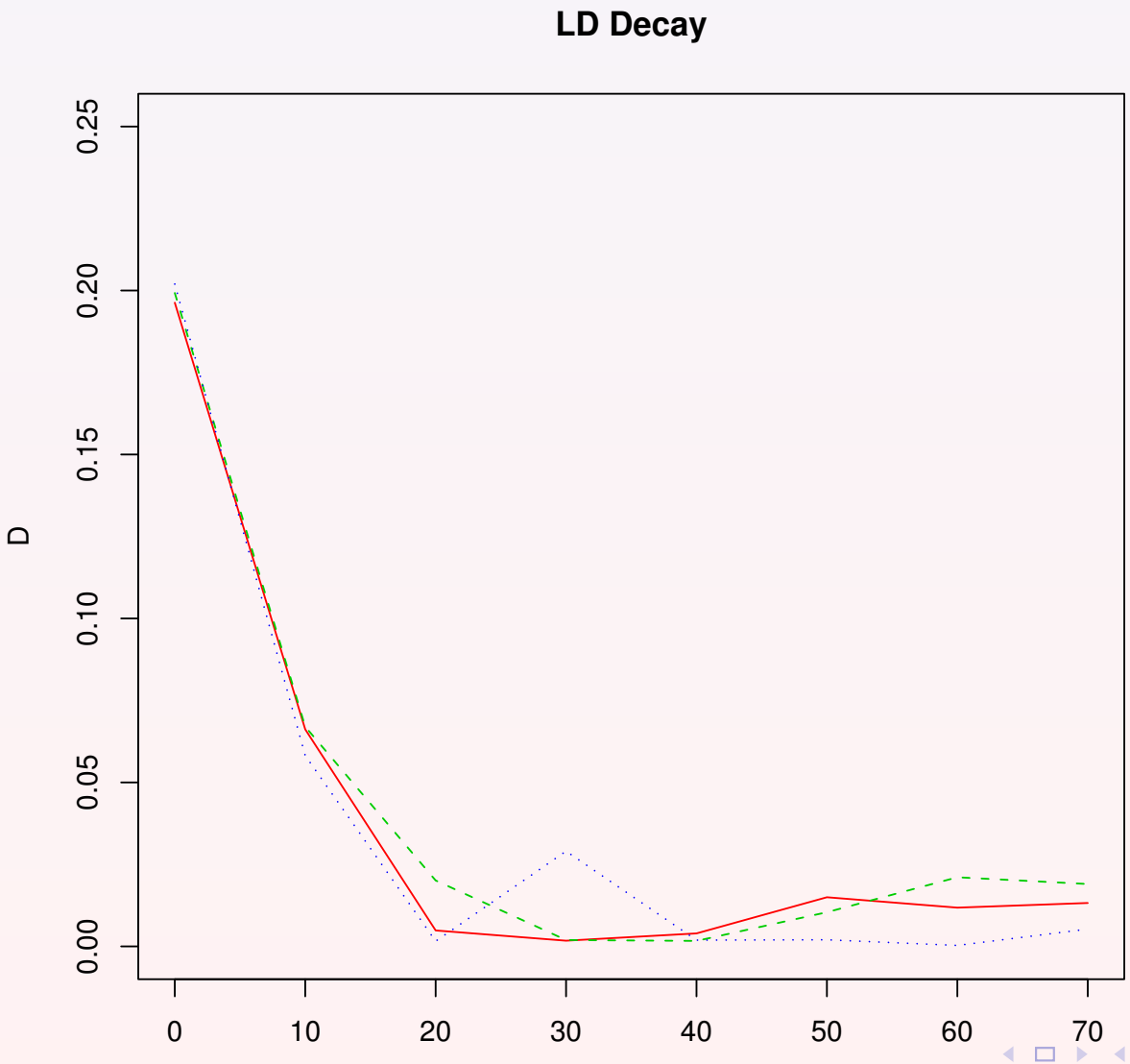
- Update at every 10 generations
- LD=0.25 before generation 0
- LD calculated at the end of each generation

Evolve!



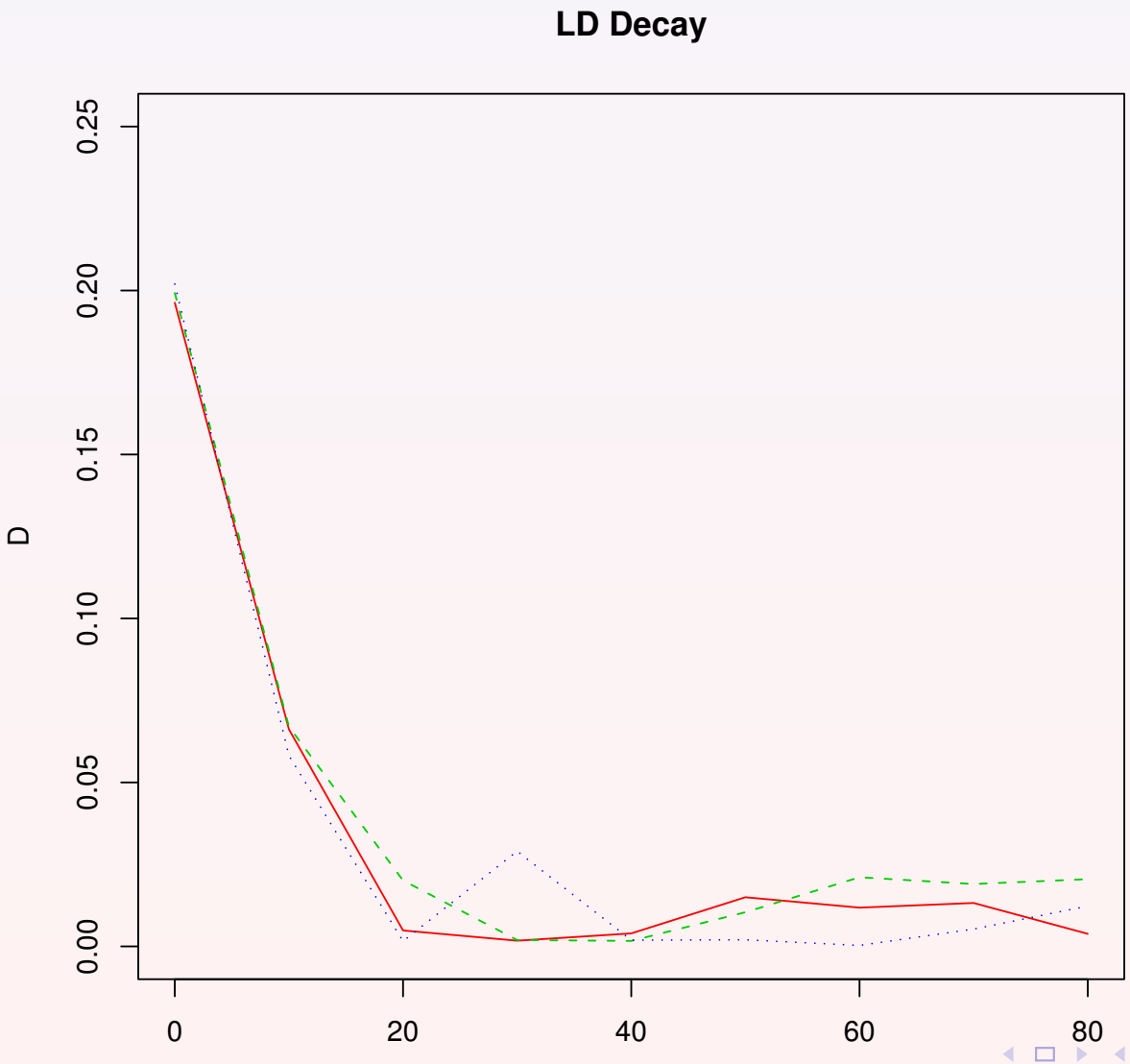
- Update at every 10 generations
- LD=0.25 before generation 0
- LD calculated at the end of each generation

Evolve!



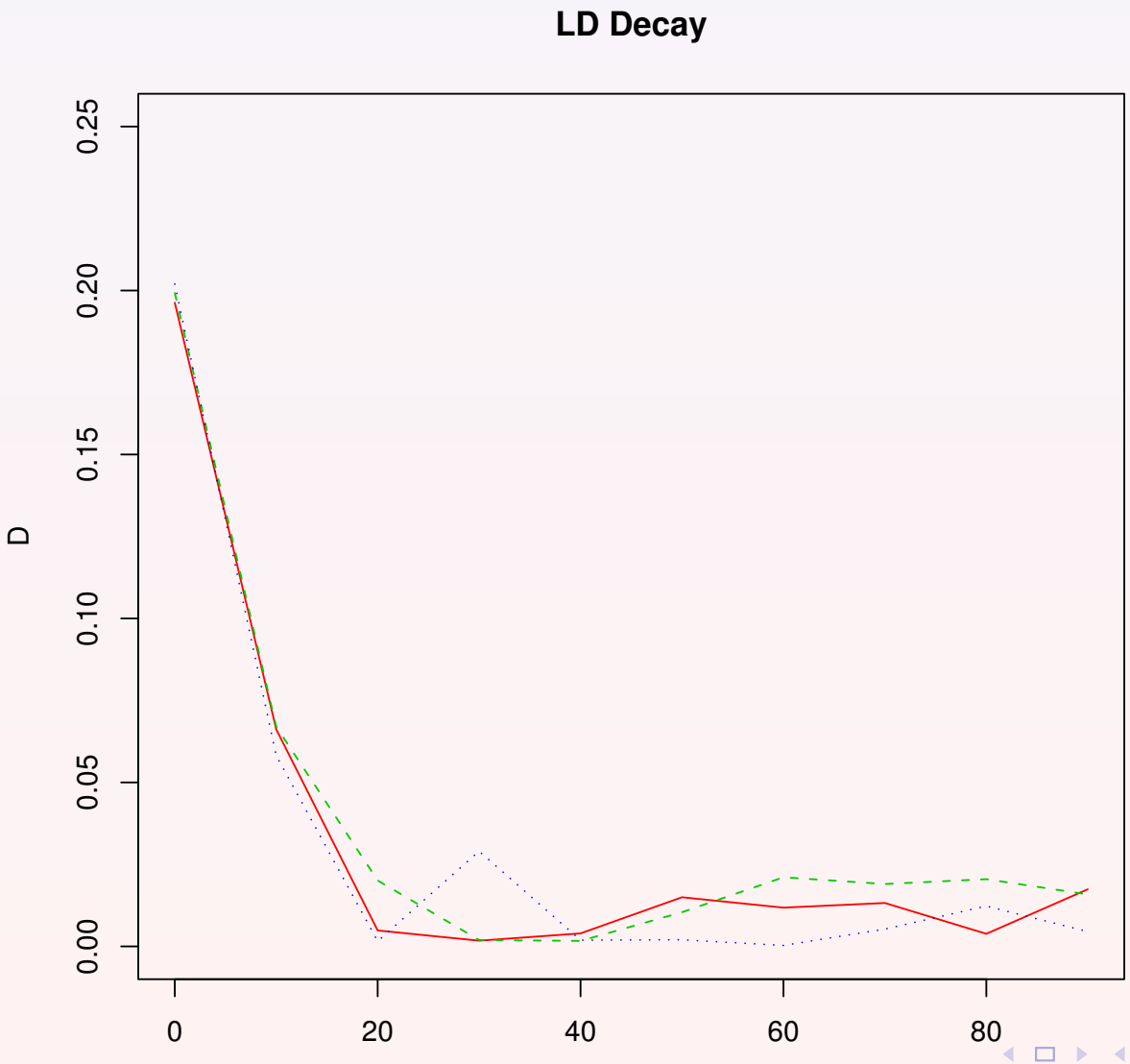
- Update at every 10 generations
- LD=0.25 before generation 0
- LD calculated at the end of each generation

Evolve!



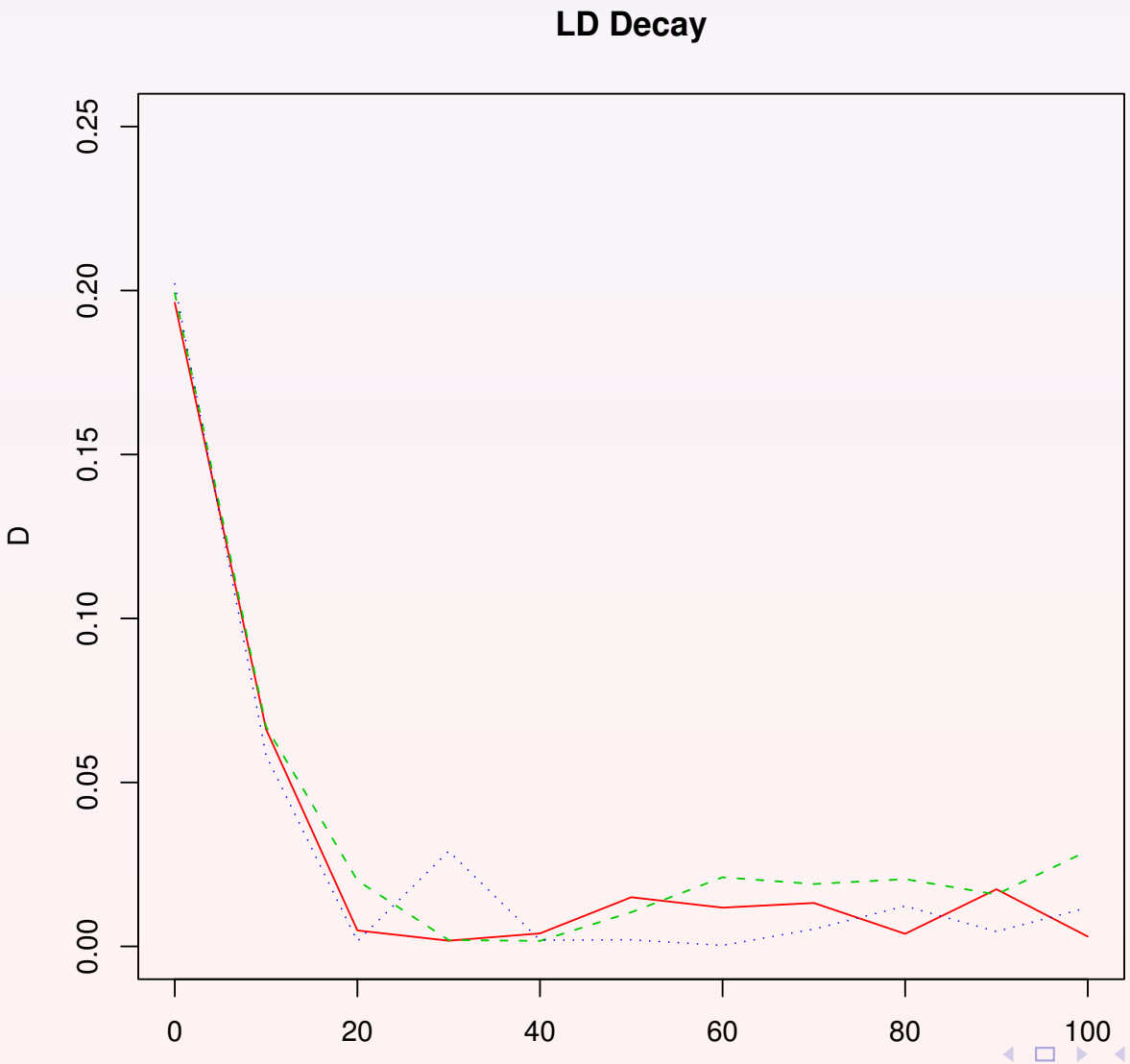
- Update at every 10 generations
- LD=0.25 before generation 0
- LD calculated at the end of each generation

Evolve!



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

Evolve!



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

Exercise time

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

```
pop.ploidyName()
```

- run `tutorial_example1.py`

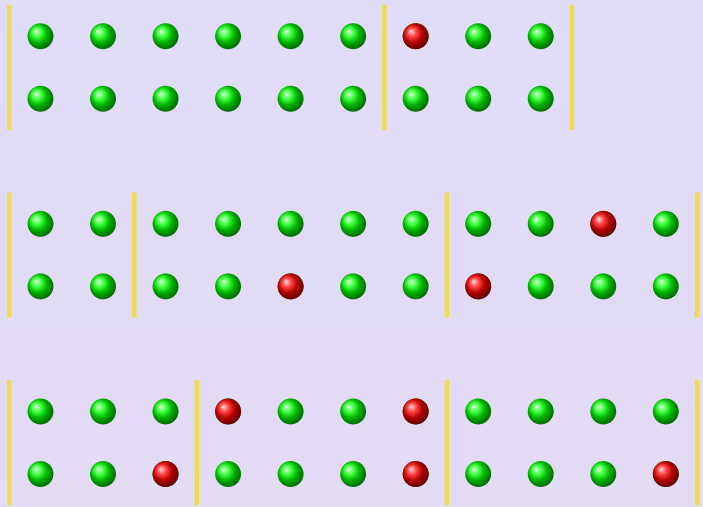
Outline

3 simuPOP components

- Population
- Individual
- Operator
- Mating scheme
- Simulator

Structure of a population

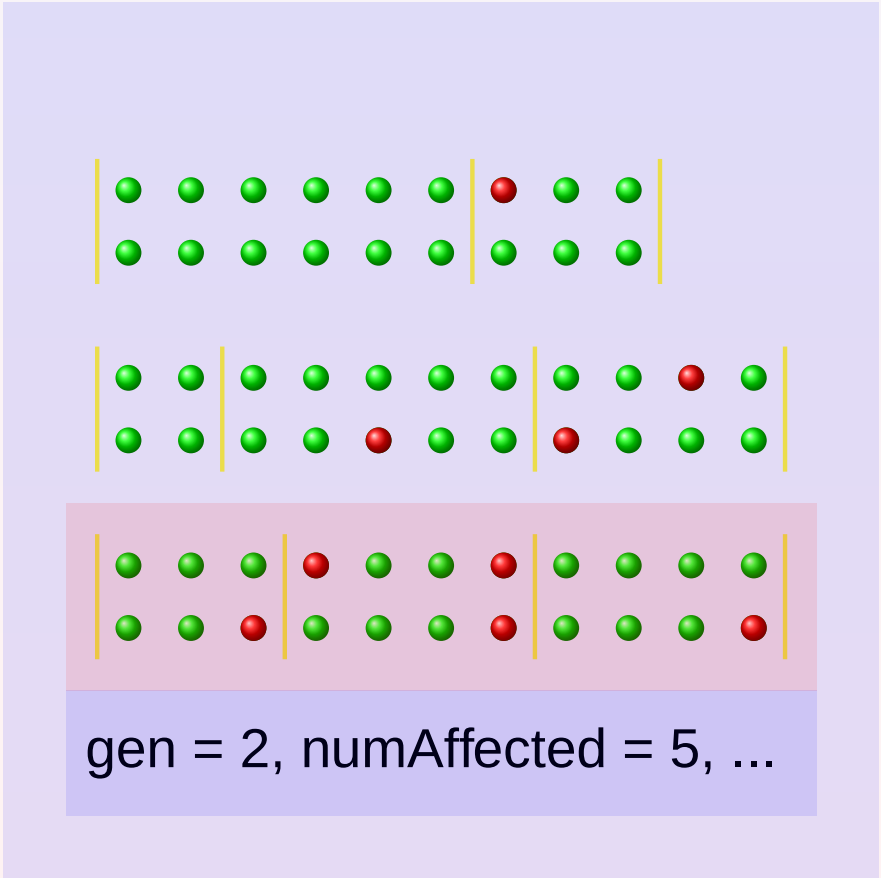
- Unaffected
- Affected



gen = 2, numAffected = 5, ...

Structure of a population

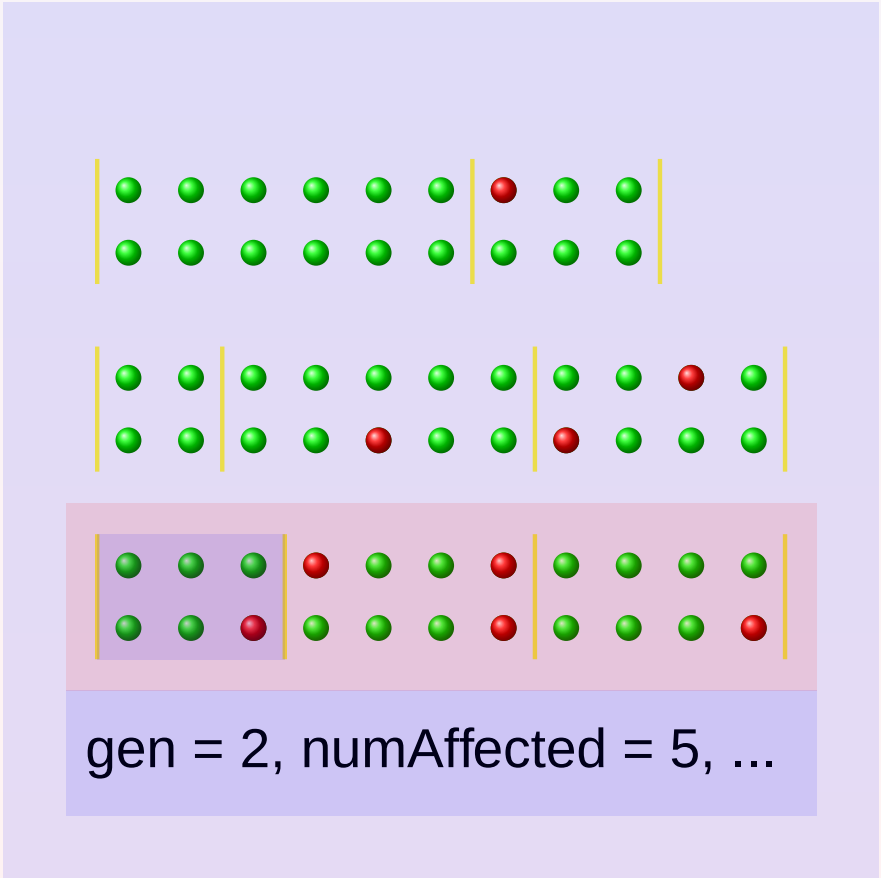
- Unaffected
- Affected



Current generation

Structure of a population

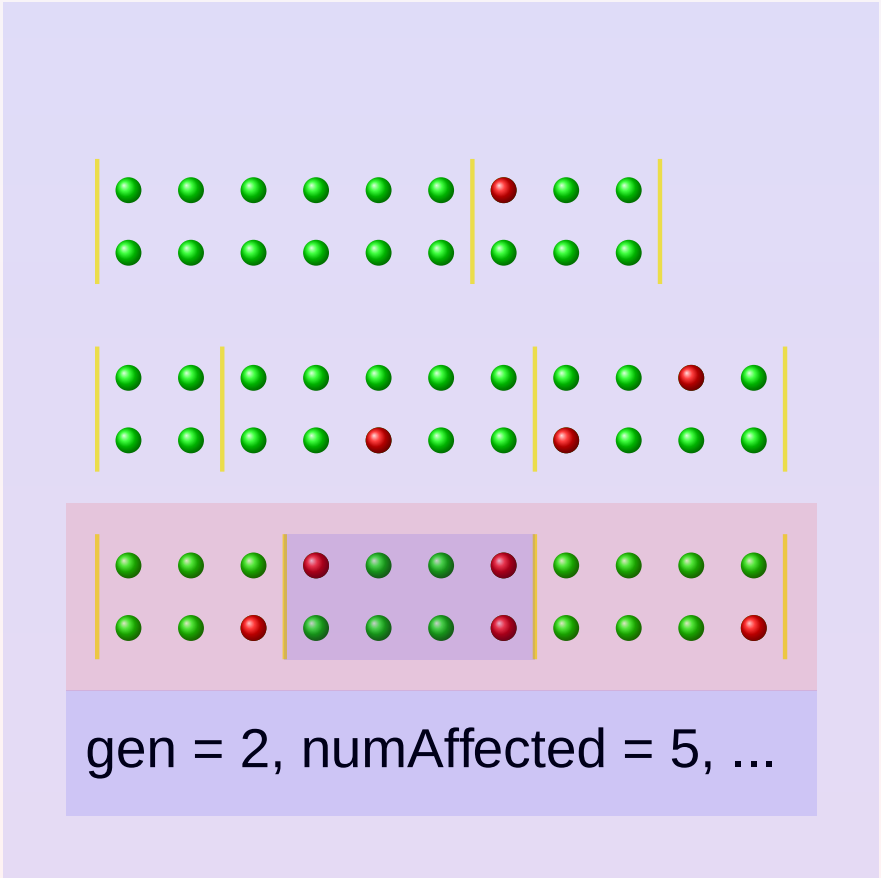
- Unaffected
- Affected



Current generation

Structure of a population

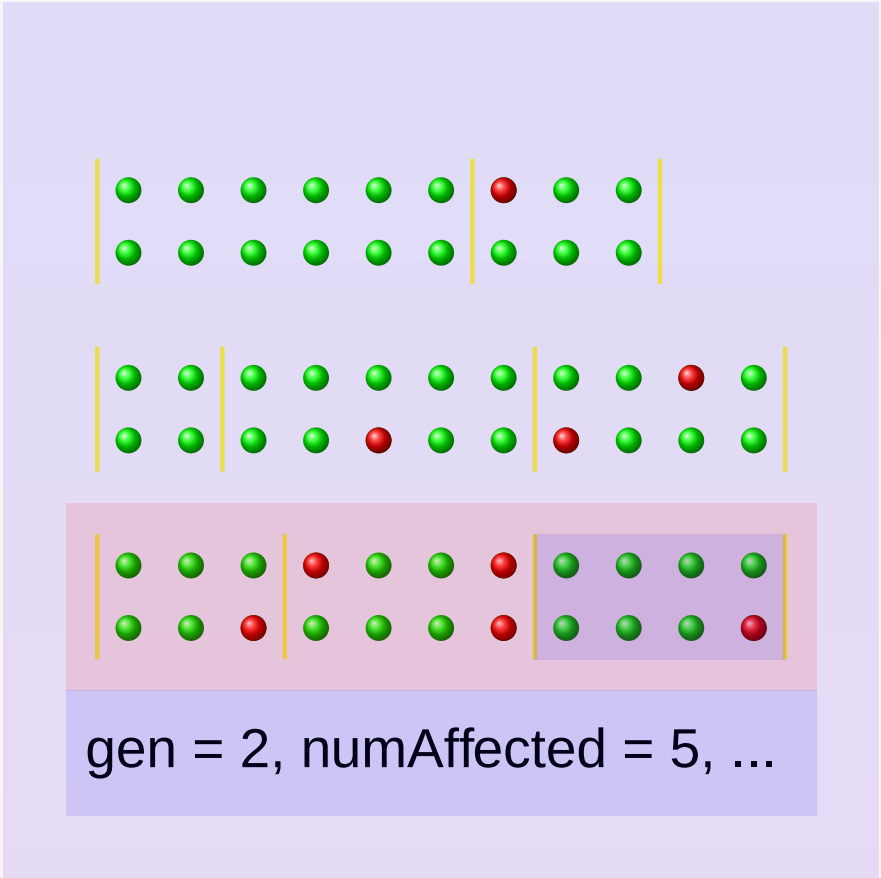
- Unaffected
- Affected



Current generation

Structure of a population

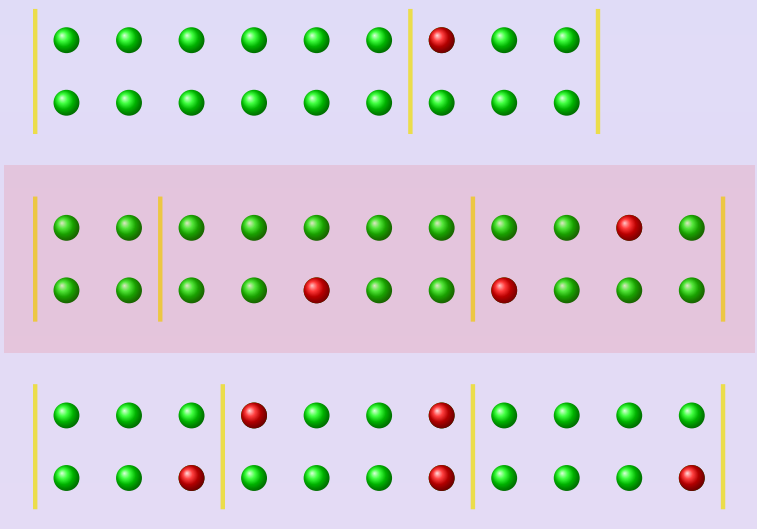
- Unaffected
- Affected



Current generation

Structure of a population

- Unaffected
- Affected

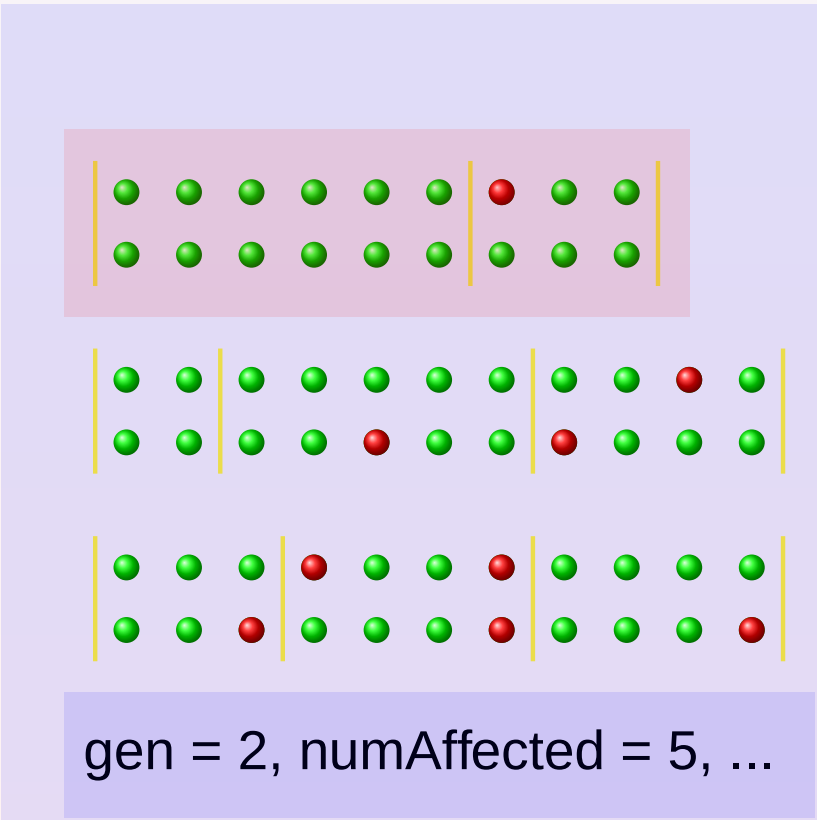


Ancestral generation 1

Current generation

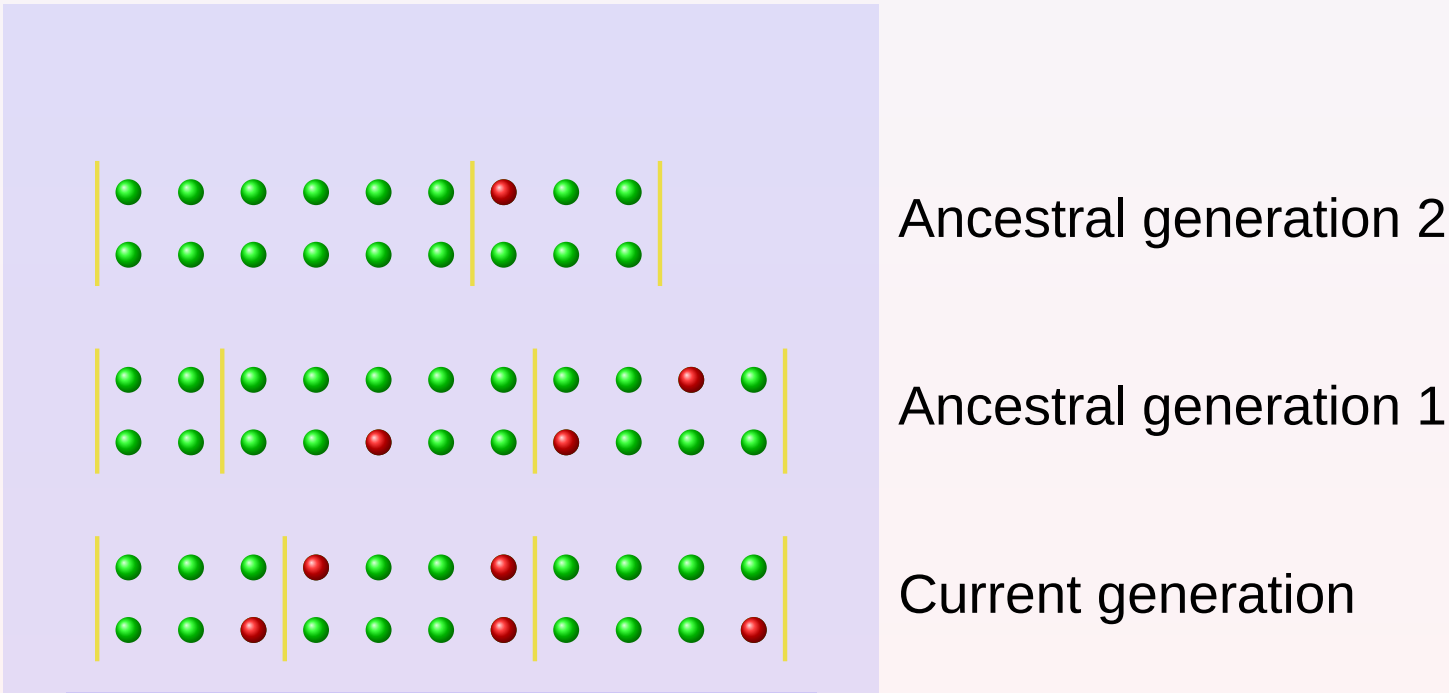
Structure of a population

- Unaffected
- Affected



Structure of a population

- Unaffected
- Affected



Create and manipulate populations


```
>>> 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


```
>>> 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


```
>>> # 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
[[0.8066666666666664, 0.1933333333333333], [0.7960000000000000
>>> # 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.)


```
>>> # 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.)


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

>>>
```

Population variables


```
>>> pop = population(subPop=[5, 10], loci=[5])
>>> InitByFreq(pop, [.6, .3, .1])
>>> Stat(pop, alleleFreq=[1], genoFreq=[2])
>>> print pop.dvars().alleleFreq[1][0]
0.7
>>> from simuUtil import ListVars
>>> ListVars(pop.dvars(), useWxPython=False)
 grp :  -1
 rep :  -1
 alleleNum :
   [1]
     [0]        21
     [1]        7
     [2]        2
 genoFreq :
   [2]
     [0]
       0 :      0.2
       1 :      0.666666666667
       2 :      0.0666666666667
     [1]
       1 :      0.0666666666667
 genoNum :
   [2]
     [0]
       0 :      3.0
       1 :      10.0
       2 :      1.0
     [1]
       1 :      1.0
 alleleFreq :
```

Population variables (cont.)


```
subPop
  [0]
    alleleNum :
      [1]
        [0]    8
        [1]    1
        [2]    1
    genoNum :
      [2]
        [0]
          0 :  2.0
          1 :  2.0
        [1]
          1 :  1.0
    genoFreq :
      [2]
        [0]
          0 :  0.4
          1 :  0.4
        [1]
          1 :  0.2
    alleleFreq :
      [1]
        [0]    0.8
        [1]    0.1
        [2]    0.1
```

Outline

3 simuPOP components

- Population
- Individual
- Operator
- Mating scheme
- Simulator

Structure of Individuals

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

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

Chromosome 0

Male

- Affected

fitness	father_id	···

Structure of Individuals

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	···

Structure of Individuals

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	···

Structure of Individuals

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	...

Structure of Individuals

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


```
>>> 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 inviduals 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: 0.500 Geno: 1 1
Aff: 0 Fit: 0.200 Geno: 2 0
Aff: 0 Fit: 0.050 Geno: 0 0
Aff: 0 Fit: 0.050 Geno: 0 0
Aff: 0 Fit: 0.050 Geno: 0 0
Aff: 1 Fit: 0.200 Geno: 2 0
Aff: 0 Fit: 0.200 Geno: 0 1
Aff: 0 Fit: 0.050 Geno: 0 0
>>>
```

Information fields

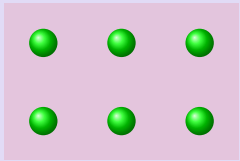

```
>>> pop = population(100, infoFields=['father_idx', 'mother_idx'
>>> simu = simulator(pop, randomMating(numOffspring=2))
>>> simu.evolve(ops=[parentsTagger()], end=5)
True
>>> ind = simu.population(0).individual(0)
>>> ind1 = simu.population(0).individual(1)
>>> print ind.info('father_idx'), ind.info('mother_idx')
56.0 46.0
>>> print ind1.info('father_idx'), ind1.info('mother_idx')
56.0 46.0
>>>
>>>
```

Outline

3 simuPOP components

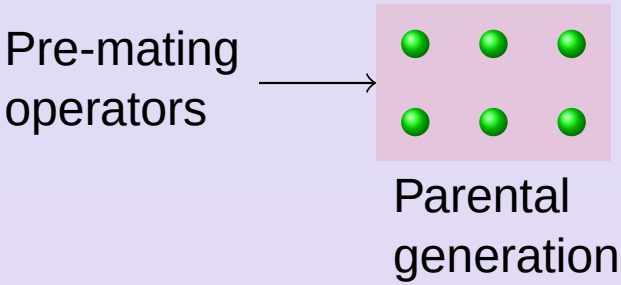
- Population
- Individual
- Operator
- Mating scheme
- Simulator

Life cycle of a generation

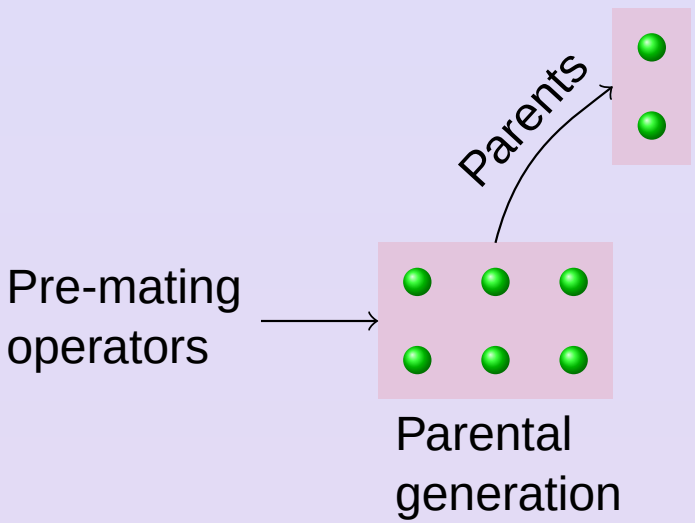


Parental generation

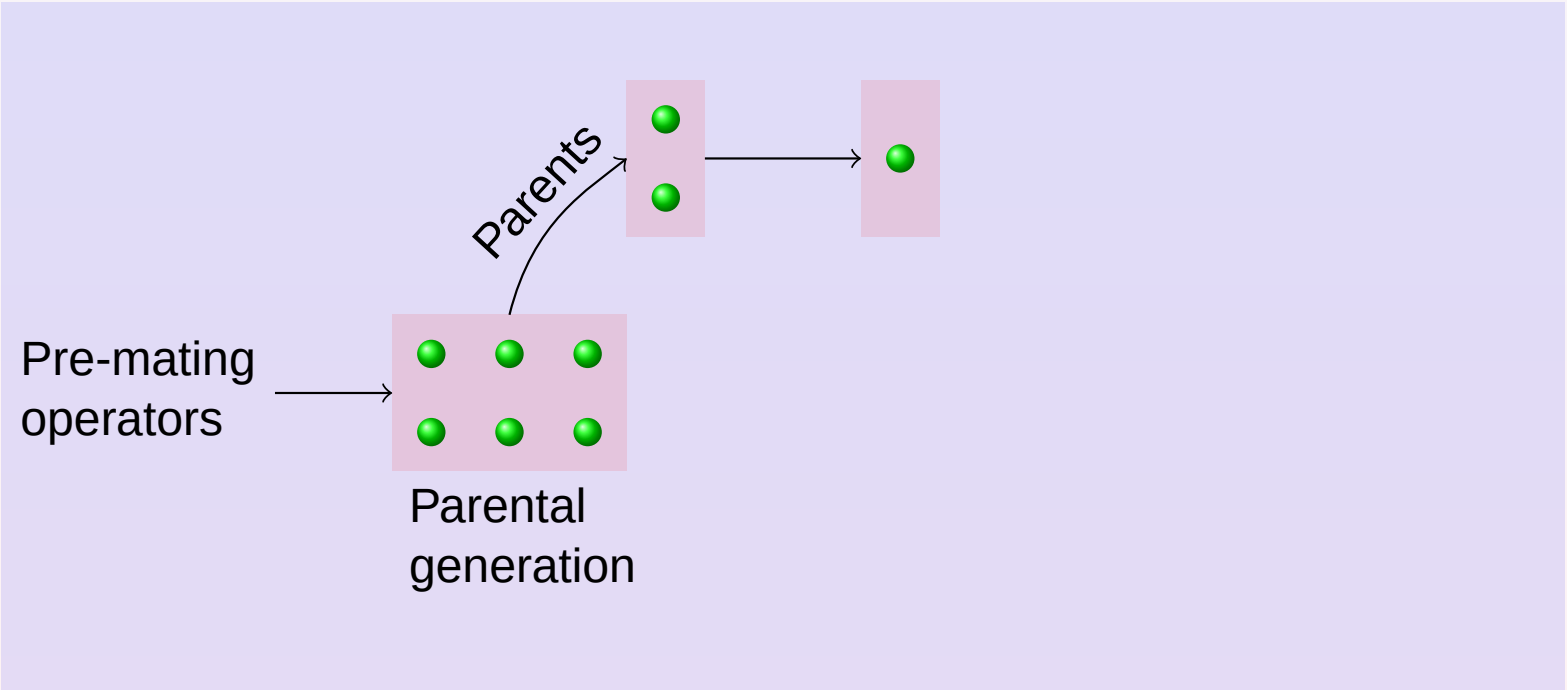
Life cycle of a generation



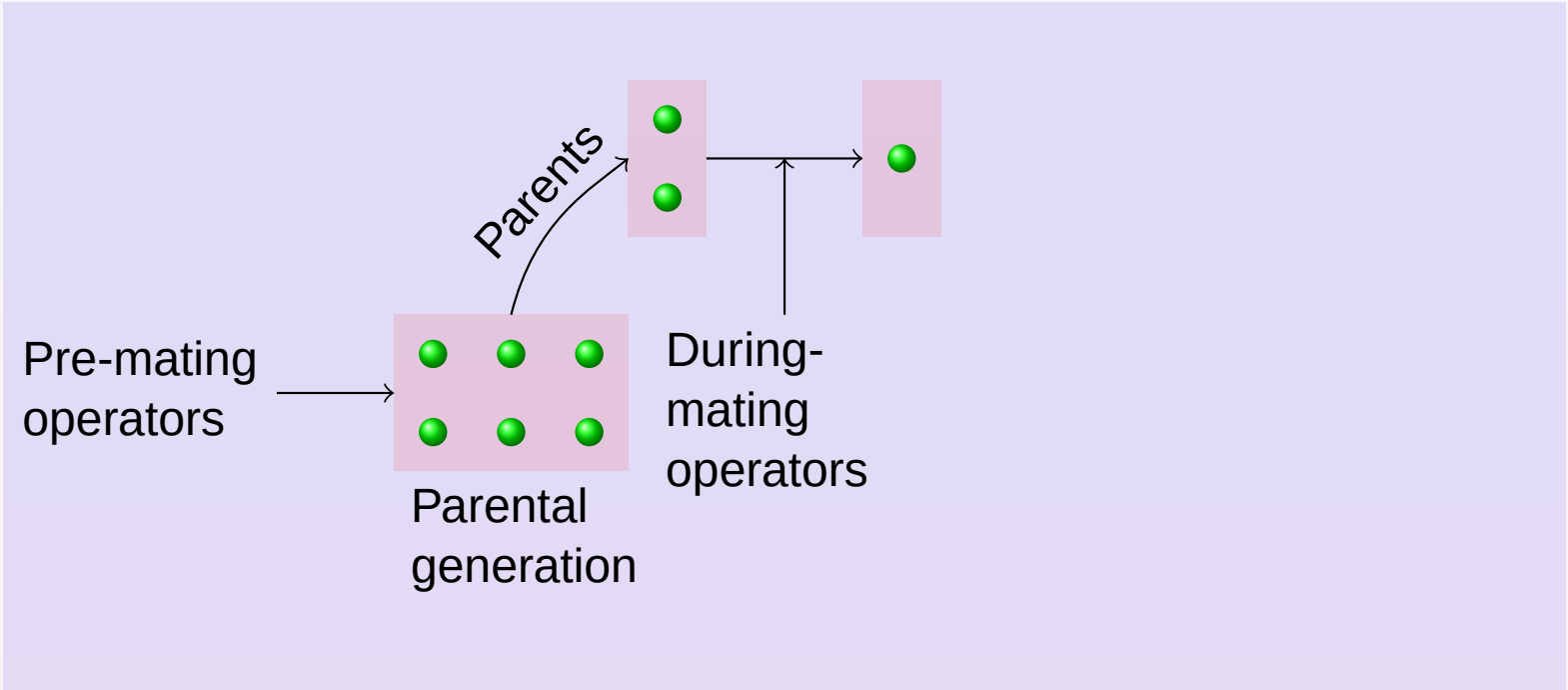
Life cycle of a generation



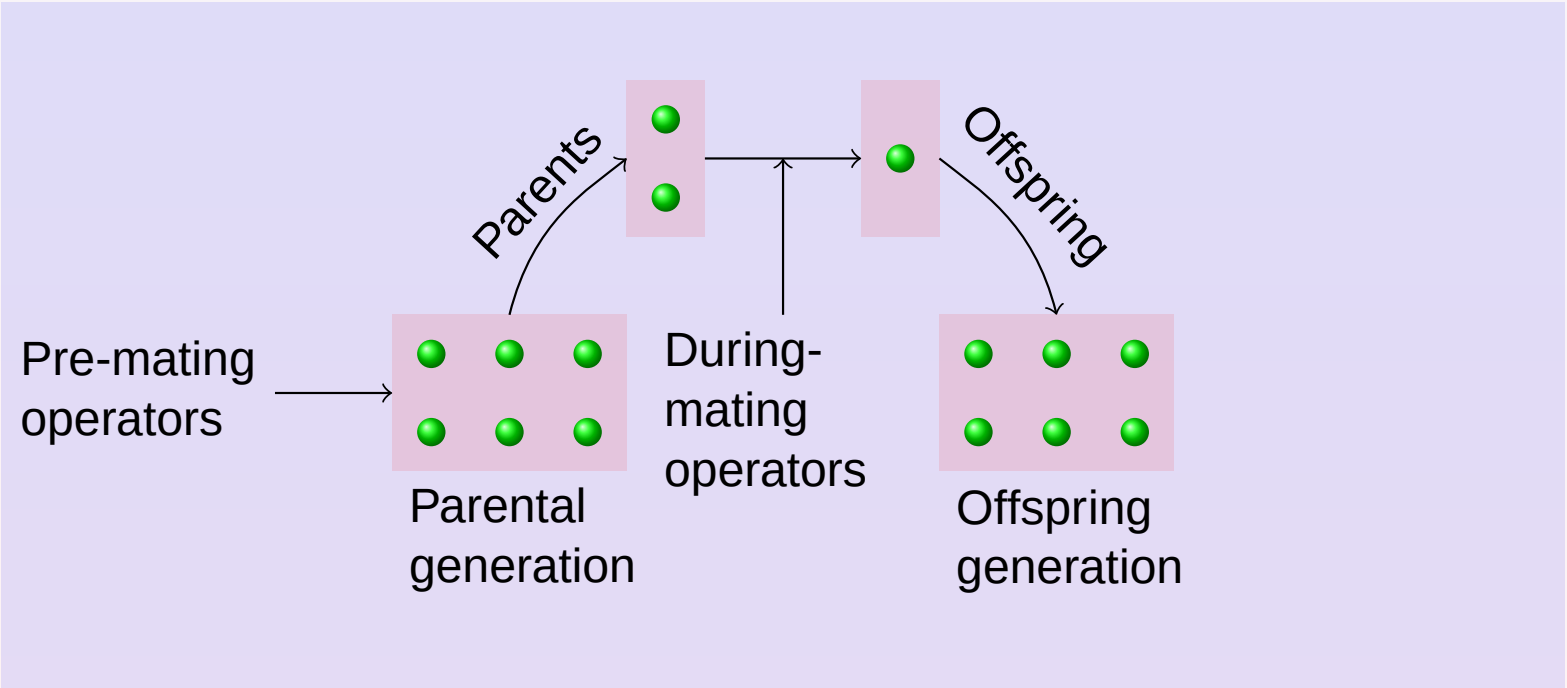
Life cycle of a generation



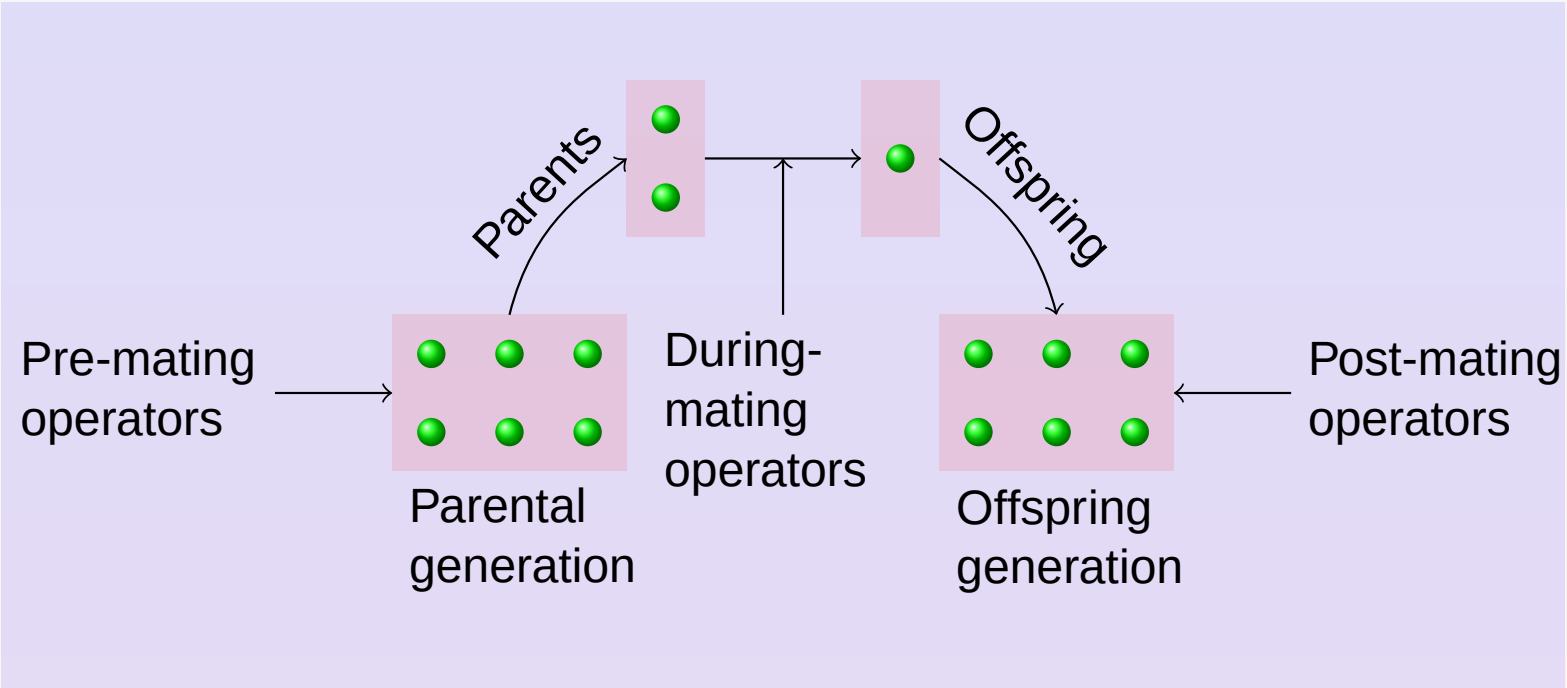
Life cycle of a generation



Life cycle of a generation



Life cycle of a generation



Stages

Stages, an example

Output

Table-like output

Outline

3 simuPOP components

- Population
- Individual
- Operator
- Mating scheme
- Simulator

Mating schemes

Outline

3 simuPOP components

- Population
- Individual
- Operator
- Mating scheme
- Simulator

Simulator