

# Package ‘xegaGaGene’

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**Title** Binary Gene Operations for Genetic Algorithms

**Version** 1.0.0.1

**Description** Representation-dependent gene level operations of a genetic algorithm with binary coded genes:  
Initialization of random binary genes, several gene maps for binary genes, several mutation operators, several crossover operators with 1 and 2 kids, replication pipelines for 1 and 2 kids, and, last but not least, function factories for configuration.  
See Goldberg, D. E. (1989, ISBN:0-201-15767-5).  
For crossover operators, see Syswerda, G. (1989, ISBN:1-55860-066-3), Spears, W. and De Jong, K. (1991, ISBN:1-55860-208-9).  
For mutation operators, see Stanhope, S. A. and Daida, J. M. (1996, ISBN:0-18-201-031-7).

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**URL** <<https://github.com/ageyerschulz/xegaGaGene>>

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**Author** Andreas Geyer-Schulz [aut, cre]  
(<<https://orcid.org/0009-0000-5237-3579>>)

**Maintainer** Andreas Geyer-Schulz <[Andreas.Geyer-Schulz@kit.edu](mailto:Andreas.Geyer-Schulz@kit.edu)>

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Gray2Bin	<i>Map Gray code to binary.</i>
----------	---------------------------------

---

## Description

Map Gray code to binary.

## Usage

Gray2Bin(x)

## Arguments

x                    Gray code (boolean vector).

## Details

Start with the highest order bit, and  $r[k-i] \leftarrow \text{xor}(n[k], n[k-1])$ .

## Value

Binary code (boolean vector).

## References

Gray, Frank (1953): Pulse Code Communication. US Patent 2 632 058.

## Examples

```
Gray2Bin(c(1, 0, 0, 0))
Gray2Bin(c(1, 1, 1, 1))
```

---

IFxegaGaGene

*The local function list IFxegaGaGene.*

---

## Description

We enhance the configurability of our code by introducing a function factory. The function factory contains all the functions that are needed for defining local functions in genetic operators. The local function list keeps the signatures of functions (e.g. mutation functions) uniform and small. At the same time, variants of functions can use different local functions.

## Usage

```
IFxegaGaGene
```

## Format

An object of class `list` of length 28.

## Details

We use the local function list for

1. replacing all constants by constant functions.  
Rationale: We need one formal argument (the local function list `IF`) and we can dispatch multiple functions. E.g. `IF$verbose()`
2. dynamically binding a local function with a definition from a proper function factory. E.g., the selection methods `lf$SelectGene` and `SelectMate`.
3. gene representations which require special functions to handle them: `lf$InitGene`, `lf$DecodeGene`, `lf$EvalGene` `lf$ReplicateGene`, ...

## See Also

Other Configuration: [xegaGacrossoverFactory\(\)](#), [xegaGageneMapFactory\(\)](#), [xegaGamuTationFactory\(\)](#), [xegaGareplicationFactory\(\)](#)

---

without *Returns elements of vector x without elements in y.*

---

### Description

Returns elements of vector x without elements in y.

### Usage

```
without(x, y)
```

### Arguments

x	A vector.
y	A vector.

### Value

A vector.

### Examples

```
a<-sample(1:15,15, replace=FALSE)
b<-c(1, 3, 5)
without(a, b)
```

---

xegaGACross2Gene *One point crossover of 2 genes.*

---

### Description

xegaGACross2Gene randomly determines a cut point. It combines the bits before the cut point of the first gene with the bits after the cut point from the second gene (kid 1). It combines the bits before the cut point of the second gene with the bits after the cut point from the first gene (kid 2). It returns 2 genes.

### Usage

```
xegaGACross2Gene(gg1, gg2, lF)
```

### Arguments

gg1	A binary gene.
gg2	A binary gene.
lF	The local configuration of the genetic algorithm.

**Value**

A list of 2 binary genes.

**See Also**

Other Crossover (2): [xegaGauCross2Gene\(\)](#), [xegaGaUPCross2Gene\(\)](#)

**Examples**

```
gene1<-xegaGaiNitGene(1FxegaGaGene)
gene2<-xegaGaiNitGene(1FxegaGaGene)
xegaGaDecodeGene(gene1, 1FxegaGaGene)
xegaGaDecodeGene(gene2, 1FxegaGaGene)
newgenes<-xegaGACross2Gene(gene1, gene2, 1FxegaGaGene)
xegaGaDecodeGene(newgenes[[1]], 1FxegaGaGene)
xegaGaDecodeGene(newgenes[[2]], 1FxegaGaGene)
```

---

xegaGACrossGene	<i>One point crossover of 2 genes.</i>
-----------------	--

---

**Description**

xegaGACrossGene randomly determines a cut point. It combines the bits before the cut point of the first gene with the bits after the cut point from the second gene (kid 1). It combines the bits before the cut point of the second gene with the bits after the cut point from the first gene (kid 2).

**Usage**

```
xegaGACrossGene(gg1, gg2, 1F)
```

**Arguments**

gg1	A binary gene.
gg2	A binary gene.
1F	The local configuration of the genetic algorithm.

**Value**

A list of one binary gene.

**See Also**

Other Crossover (1): [xegaGauCrossGene\(\)](#), [xegaGaUPCrossGene\(\)](#)

## Examples

```
gene1<-xegaGacrossGene(1FxegaGacrossGene)
gene2<-xegaGacrossGene(1FxegaGacrossGene)
xegaGacrossGene(gene1, 1FxegaGacrossGene)
xegaGacrossGene(gene2, 1FxegaGacrossGene)
gene3<-xegaGacrossGene(gene1, gene2, 1FxegaGacrossGene)
xegaGacrossGene(gene3[[1]], 1FxegaGacrossGene)
```

---

xegaGacrossGeneFactory

*Configure the crossover function of a genetic algorithm.*

---

## Description

xegaGacrossGeneFactory implements the selection of one of the crossover functions in this package by specifying a text string. The selection fails ungracefully (produces a runtime error) if the label does not match. The functions are specified locally.

Current support:

1. Crossover functions with two kids:
  - (a) "Cross2Gene" returns xegaGacross2Gene.
  - (b) "UCross2Gene" returns xegaGacrossUCross2Gene.
  - (c) "PUCross2Gene" returns xegaGacrossUPCross2Gene.
2. Crossover functions with one kid:
  - (a) "CrossGene" returns xegaGacrossGene.
  - (b) "UCrossGene" returns xegaGacrossUCrossGene.
  - (c) "PUCrossGene" returns xegaGacrossUPCrossGene.

## Usage

```
xegaGacrossGeneFactory(method = "Cross2Gene")
```

## Arguments

method            A string specifying the crossover function.

## Value

A crossover function for genes.

## See Also

Other Configuration: [1FxegaGacrossGene](#), [xegaGacrossGeneMapFactory\(\)](#), [xegaGacrossMutationFactory\(\)](#), [xegaGacrossReplicationFactory\(\)](#)

## Examples

```
XGene<-xegaGacrossoverFactory("Cross2Gene")
gene1<-xegaGainitGene(1FxegaGaGene)
gene2<-xegaGainitGene(1FxegaGaGene)
XGene(gene1, gene2, 1FxegaGaGene)
```

---

xegaGaDecodeGene	<i>Decode a gene.</i>
------------------	-----------------------

---

## Description

xegaGaDecodeGene decodes a binary gene.

## Usage

```
xegaGaDecodeGene(gene, 1F)
```

## Arguments

gene	A binary gene (the genotype).
1F	The local configuration of the genetic algorithm.

## Value

The decoded gene (the phenotype).

## See Also

Other Decoder: [xegaGaGeneMapGray\(\)](#), [xegaGaGeneMapIdentity\(\)](#), [xegaGaGeneMapPerm\(\)](#), [xegaGaGeneMap\(\)](#)

## Examples

```
gene<-xegaGainitGene(1FxegaGaGene)
xegaGaDecodeGene(gene, 1FxegaGaGene)
```

---

xegaGaGene

*Package xegaGaGene.*


---

## Description

Genetic operations for binary coded genetic algorithms.

## Details

For an introduction to this class of algorithms, see Goldberg, D. (1989).

For binary-coded genes, the xegaGaGene package provides

- Gene initialization.
- Decoding of parameters as well as a function factory for configuration.
- Mutation functions as well as a function factory for configuration.
- Crossover functions as well as a function factory for configuration. We provide two families of crossover functions:
  1. Crossover functions with two kids: Crossover preserves the genetic information in the gene pool.
  2. Crossover functions with one kid: These functions allow the construction of gene evaluation pipelines. One advantage of this is a simple control structure at the population level.
  3. Gene replication functions as well as a function factory for configuration. The replication functions implement control flows for sequences of gene operations. For `xegaReplicateGene`, an acceptance step has been added. Simulated annealing algorithms can be configured e.g. by configuring uniform random selection combined with a Metropolis Acceptance Rule and a suitable cooling schedule.

## Binary Gene Representation

A binary gene is a named list:

- `$gene1` the gene must be a binary vector.
- `$fit` the fitness value of the gene (for `EvalGeneDet` and `EvalGeneU`) or the mean fitness (for stochastic functions evaluated with `EvalGeneStoch`).
- `$evaluated` has the gene been evaluated?
- `$evalFail` has the evaluation of the gene failed?
- `$var` the cumulative variance of the fitness of all evaluations of a gene. (For stochastic functions)
- `$sigma` the standard deviation of the fitness of all evaluations of a gene. (For stochastic functions)
- `$obs` the number of evaluations of a gene. (For stochastic functions)



### Abstract Interface of Problem Environment

A problem environment `penv` must provide:

- `$f(parameters, gene, lF)`: Function with a real parameter vector as first argument which returns a gene with evaluated fitness.
- `$genelength()`: The number of bits of the binary-coded real parameter vector. Used in `InitGene`.
- `$bitlength()`: A vector specifying the number of bits used for coding each real parameter. If `penv$bitlength()[1]` is 20, then `parameters[1]` is coded by 20 bits. Used in `GeneMap`.
- `$lb()`: The lower bound vector of each parameter. Used in `GeneMap`.
- `$ub()`: The upper bound vector of each parameter. Used in `GeneMap`.

### Abstract Interface of Mutation Functions

Each mutation function has the following function signature:

```
newGene<-Mutate(gene, lF)
```

All local parameters of the mutation function configured are expected in the local function list `lF`.

### Local Constants of Mutation Functions

The local constants of a mutation function determine the behavior of the function.

Constant	Default	Used in
<code>lF\$BitMutationRate1</code>	0.005	<code>MutateGene</code> <code>IVAdaptiveMutateGene</code>
<code>lF\$BitMutationRate2</code>	0.01	<code>IVAdaptiveMutateGene</code>
<code>lF\$CutoffFit</code>	0.5	<code>IVAdaptiveMutateGene</code>

### Abstract Interface of Crossover Functions

The signatures of the abstract interface to the 2 families of crossover functions are:

```
ListOfTwoGenes<-Crossover2(gene1, gene2, lF)
```

```
ListOfOneGene<-Crossover(gene1, gene2, lF)
```

All local parameters of the crossover function configured are expected in the local function list `lF`.

### Local Constants of Crossover Functions

The local constants of a crossover function determine the the behavior of the function.

Constant	Default	Used in
<code>lF\$UCrossSwap</code>	0.2	<code>UPCross2Gene</code> <code>UPCrossGene</code>

### Abstract Interface of Gene Replication Functions

The signatures of the abstract interface to the 2 gene replication functions are:

ListOfTwoGenes<-Replicate2Gene(gene1, gene2, IF)

ListOfOneGene<-ReplicateGene(gene1, gene2, IF)

### Configuration and Constants of Replication Functions

#### Configuration for ReplicateGene (1 Kid, Default).

Function	Default	Configured By
IF\$SelectGene	SelectSUS	SelectGeneFactory
IF\$SelectMate	SelectSUS	SelectGeneFactory
IF\$CrossGene	CrossGene	xegaGacrossoverFactory
IF\$MutateGene	MutateGene	xegaGaMutationFactory
IF\$Accept	AcceptNewGene	AcceptFactory

#### Configuration for Replicate2Gene (2 Kids).

Function	Default	Configured By
IF\$SelectGene	SelectSUS	SelectGeneFactory
IF\$SelectMate	SelectSUS	SelectGeneFactory
IF\$CrossGene	CrossGene	xegaGacrossoverFactory
IF\$MutateGene	MutateGene	xegaGaMutationFactory

### Global Constants.

Global constants specify the probability that a mutation or crossover operator is applied to a gene. In the xega-architecture, these rates can be configured to be adaptive.

Constant	Default	Used in
IF\$MutationRate	1.0 (static)	xegaGaReplicateGene xegaGaReplicate2Gene
IF\$CrossRate	0.2 (static)	xegaGaReplicateGene xegaGaReplicate2Gene

### Local Constants.

Constant	Default	Used in
IF\$BitMutationRate1	0.005	MutateGene IVAdaptiveMutateGene
IF\$BitMutationRate2	0.01	IVAdaptiveMutateGene
IF\$CutoffFit	0.5	IVAdaptiveMutateGene
IF\$UCrossSwap	0.2	UPCross2Gene UPCrossGene

In the xega-architecture, these rates can be configured to be adaptive.

### The Architecture of the xegaX-Packages

The xegaX-packages are a family of R-packages which implement eXtended Evolutionary and Genetic Algorithms (xega). The architecture has 3 layers, namely the user interface layer, the population layer, and the gene layer:

- The user interface layer (package xega) provides a function call interface and configuration support for several algorithms: genetic algorithms (sga), permutation-based genetic algorithms (sgPerm), derivation-free algorithms as e.g. differential evolution (sgde), grammar-based genetic programming (sgp) and grammatical evolution (sge).
- The population layer (package xegaPopulation) contains population-related functionality as well as support for population statistics dependent adaptive mechanisms and parallelization.
- The gene layer is split into a representation-independent and a representation-dependent part:
  1. The representation independent part (package xegaSelectGene) is responsible for variants of selection operators, evaluation strategies for genes, as well as profiling and timing capabilities.
  2. The representation dependent part consists of the following packages:
    - xegaGaGene for binary coded genetic algorithms.
    - xegaPermGene for permutation-based genetic algorithms.
    - xegaDfGene for derivation-free algorithms as e.g. differential evolution.
    - xegaGpGene for grammar-based genetic algorithms.
    - xegaGeGene for grammatical evolution algorithms.

The packages xegaDerivationTrees and xegaBNF support the last two packages: xegaBNF essentially provides a grammar compiler, and xegaDerivationTrees is an abstract data type for derivation trees.

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### URL

<<https://github.com/ageyerschulz/xegaGaGene>>

### Installation

From CRAN by `install.packages('xegaGaGene')`

### Author(s)

Andreas Geyer-Schulz

## References

Goldberg, David E. (1989) Genetic Algorithms in Search, Optimization and Machine Learning. Addison-Wesley, Reading. (ISBN:0-201-15767-5)

---

xegaGaGeneMap	<i>Map the bit strings of a binary gene to parameters in an interval.</i>
---------------	---

---

## Description

xegaGaGenemap maps the bit strings of a binary string to parameters in an interval. Bit vectors are mapped into equispaced numbers in the interval. Examples: Optimization of problems with real-valued parameter vectors.

## Usage

```
xegaGaGeneMap(gene, penv)
```

## Arguments

gene	A binary gene (the genotype).
penv	A problem environment.

## Value

The decoded gene (the phenotype).

## See Also

Other Decoder: [xegaGaDecodeGene\(\)](#), [xegaGaGeneMapGray\(\)](#), [xegaGaGeneMapIdentity\(\)](#), [xegaGaGeneMapPerm\(\)](#)

## Examples

```
gene<-xegaGaInitGene(1FxegaGaGene)
xegaGaGeneMap(gene$gene1, 1FxegaGaGene$penv)
```

---

xegaGaGeneMapFactory *Configure the gene map function of a genetic algorithm.*

---

## Description

xegaGaGeneMapFactory implements the selection of one of the GeneMap functions in this package by specifying a text string. The selection fails ungracefully (produces a runtime error) if the label does not match. The functions are specified locally.

Current support:

1. "Bin2Dec" returns GeneMap. (Default).
2. "Gray2Dec" returns GeneMapGray.
3. "Identity" returns GeneMapIdentity.
4. "Permutation" returns GeneMapPerm.

## Usage

```
xegaGaGeneMapFactory(method = "Bin2Dec")
```

## Arguments

method            A string specifying the GeneMap function.

## Value

A gene map function for genes.

## See Also

Other Configuration: [lFxegaGaGene](#), [xegaGacrossoverFactory\(\)](#), [xegaGamuTationFactory\(\)](#), [xegaGaReplIcationFactory\(\)](#)

## Examples

```
XGene<-xegaGaGeneMapFactory("Identity")
gene1<-xegaGaInitGene(lFxegaGaGene)
XGene(gene1, lFxegaGaGene$penv)
```

---

`xegaGaGeneMapGray`      *Map the bit strings of a gray-coded gene to parameters in an interval.*

---

### Description

`xegaGaGeneMapGray` maps the bit strings of a binary string interpreted as Gray codes to parameters in an interval. Bit vectors are mapped into equispaced numbers in the interval. Examples: Optimization of problems with real-valued parameter vectors.

### Usage

```
xegaGaGeneMapGray(gene, penv)
```

### Arguments

`gene`                    A binary gene (the genotype).  
`penv`                    A problem environment.

### Value

The decoded gene (the phenotype).

### See Also

Other Decoder: [xegaGaDecodeGene\(\)](#), [xegaGaGeneMapIdentity\(\)](#), [xegaGaGeneMapPerm\(\)](#), [xegaGaGeneMap\(\)](#)

### Examples

```
gene<-xegaGaInitGene(1FxegaGaGene)
xegaGaGeneMapGray(gene$gene1, 1FxegaGaGene$penv)
```

---

`xegaGaGeneMapIdentity`      *Map the bit strings of a binary gene to an identical bit vector.*

---

### Description

`xegaGaGeneMapIdentity` maps the bit strings of a binary vector to an identical binary vector. Faster for all problems with single-bit coding. Examples: Knapsack, Number Partitioning into 2 partitions.

### Usage

```
xegaGaGeneMapIdentity(gene, penv)
```

**Arguments**

gene            A binary gene (the genotype).  
 penv            A problem environment.

**Value**

The decoded gene (the phenotype).

**See Also**

Other Decoder: [xegaGaDecodeGene\(\)](#), [xegaGaGeneMapGray\(\)](#), [xegaGaGeneMapPerm\(\)](#), [xegaGaGeneMap\(\)](#)

**Examples**

```
gene<-xegaGaInitGene(1FxegaGaGene)
xegaGaGeneMapIdentity(gene$gene1, 1FxegaGaGene$penv)
```

---

xegaGaGeneMapPerm        *Map the bit strings of a binary gene to a permutation.*

---

**Description**

xegaGaGeneMapPerm maps the bit strings of a binary string to a permutation of integers. Example: Traveling Salesman Problem (TSP).

**Usage**

```
xegaGaGeneMapPerm(gene, penv)
```

**Arguments**

gene            A binary gene (the genotype).  
 penv            A problem environment.

**Value**

A permutation (the decoded gene (the phenotype))

**See Also**

Other Decoder: [xegaGaDecodeGene\(\)](#), [xegaGaGeneMapGray\(\)](#), [xegaGaGeneMapIdentity\(\)](#), [xegaGaGeneMap\(\)](#)

**Examples**

```
gene<-xegaGaInitGene(1FxegaGaGene)
xegaGaGeneMapPerm(gene$gene1, 1FxegaGaGene$penv)
```

---

xegaGaInitGene            *Generate a random binary gene.*

---

### Description

xegaGaInitGene generates a random binary gene with a given length.

### Usage

```
xegaGaInitGene(1F)
```

### Arguments

1F                        The local configuration of the genetic algorithm.

### Value

A binary gene (a named list):

- \$evaluated: FALSE. See package xegaEvalGene
- \$evalFail: FALSE. Set by the error handler(s) in package xegaEvalGene in the case of failure.
- \$fit: the fitness
- \$gene1: a binary gene

### Examples

```
xegaGaInitGene(1FxegaGaGene)
```

---

xegaGaIVAdaptiveMutateGene  
*Individually variable adaptive mutation of a gene.*

---

### Description

xegaGaIVAdaptiveMutateGene mutates a binary gene. Two mutation rates (1F\$MutationRate() and 1F\$MutationRate2() which is higher than the first) are used depending on the relative fitness of the gene. 1F\$CutoffFit and 1F\$CBestFitness are used to determine the relative fitness of the gene. The rationale is that mutating genes having a low fitness with a higher probability rate improves the performance of a genetic algorithm, because the gene gets a higher chance to improve.

### Usage

```
xegaGaIVAdaptiveMutateGene(gene, 1F)
```



**Arguments**

gene            A binary gene.  
 lF              The local configuration of the genetic algorithm.

**Details**

This principle is a candidate for a more abstract implementation, because it applies to all variants of evolutionary algorithms.

The goal is to separate the threshold code and the representation-dependent part and to combine them in the factory properly.

**Value**

A binary gene

**References**

Stanhope, Stephen A. and Daida, Jason M. (1996) An Individually Variable Mutation-rate Strategy for Genetic Algorithms. In: Koza, John (Ed.) Late Breaking Papers at the Genetic Programming 1996 Conference. Stanford University Bookstore, Stanford, pp. 177-185. (ISBN:0-18-201-031-7)

**See Also**

Other Mutation: [xegaGaMutateGene\(\)](#)

**Examples**

```
parm<-function(x) {function() {return(x)}}
lFxegaGaGene$BitMutationRate1<-parm(1.0)
lFxegaGaGene$BitMutationRate2<-parm(0.5)
gene1<-xegaGaInitGene(lFxegaGaGene)
xegaGaDecodeGene(gene1, lFxegaGaGene)
gene<-xegaGaIVAdaptiveMutateGene(gene1, lFxegaGaGene)
xegaGaDecodeGene(gene, lFxegaGaGene)
```

---

xegaGaMutateGene            *Mutate a gene.*

---

**Description**

xegaGaMutateGene mutates a binary gene. The per-bit mutation rate is given by MutationRate().

**Usage**

```
xegaGaMutateGene(gene, lF)
```

**Arguments**

gene            A binary gene.  
 lF              The local configuration of the genetic algorithm

**Value**

A binary gene.

**See Also**

Other Mutation: [xegaGaIVAdaptiveMutateGene\(\)](#)

**Examples**

```

parm<-function(x) {function() {return(x)}}
lFxegaGaGene$BitMutationRate1<-parm(1.0)
gene1<-xegaGaInitGene(lFxegaGaGene)
xegaGaDecodeGene(gene1, lFxegaGaGene)
lFxegaGaGene$BitMutationRate1()
gene<-xegaGaMutateGene(gene1, lFxegaGaGene)
xegaGaDecodeGene(gene, lFxegaGaGene)

```

---

xegaGaMutationFactory *Configure the mutation function of a genetic algorithm.*

---

**Description**

xegaGaMutationFactory implements the selection of one of the mutation functions in this package by specifying a text string. The selection fails ungracefully (produces a runtime error) if the label does not match. The functions are specified locally.

Current support:

1. "MutateGene" returns xegaGaMutateGene.
2. "IVMGene" returns xegaGaIVAdaptiveMutateGene.

**Usage**

```
xegaGaMutationFactory(method = "MutateGene")
```

**Arguments**

method            A string specifying the mutation function.

**Value**

A mutation function for genes.

**See Also**

Other Configuration: [lFxegaGaGene](#), [xegaGacrossoverFactory\(\)](#), [xegaGaGeneMapFactory\(\)](#), [xegaGaReplicationFactory\(\)](#)

**Examples**

```

parm<-function(x) {function() {return(x)}}
lFxegaGaGene$BitMutationRate1<-parm(1.0)
Mutate<-xegaGaMutationFactory("MutateGene")
gene1<-xegaGaInitGene(lFxegaGaGene)
gene1
Mutate(gene1, lFxegaGaGene)

```

---

xegaGaReplicate2Gene    *Replicates a gene.*

---

**Description**

xegaGaReplicate2Gene replicates a gene by applying a gene reproduction pipeline which uses crossover and mutation. The control flow is as follows:

- A gene is selected from the population. Check if the crossover operation should be applied. (The check is TRUE with a probability of crossrate). If the check is TRUE:
  - Select a mating gene from the population.
  - Perform the crossover operation.
  - Apply mutation with a probability of mutrate.
  - Return a list with both genes.
- Apply mutation with a probability of mutrate.
- Return a list with a single gene.

**Usage**

```
xegaGaReplicate2Gene(pop, fit, lF)
```

**Arguments**

pop	A population of binary genes.
fit	Fitness vector.
lF	The local configuration of the genetic algorithm.

**Value**

A list of either 1 or 2 binary genes.

**See Also**

Other Replication: [xegaGaReplicateGene\(\)](#)

**Examples**

```

lFxegaGaGene$CrossGene<-xegaGaCross2Gene
lFxegaGaGene$MutationRate<-function(fit, lF) {0.001}
names(lFxegaGaGene)
pop10<-lapply(rep(0,10), function(x) xegaGaInitGene(lFxegaGaGene))
epop10<-lapply(pop10, lFxegaGaGene$EvalGene, lF=lFxegaGaGene)
fit10<-unlist(lapply(epop10, function(x) {x$fit}))
newgenes<-xegaGaReplicate2Gene(pop10, fit10, lFxegaGaGene)

```

---

xegaGaReplicateGene    *Replicates a gene.*

---

**Description**

xegaGaReplicateGene replicates a gene by applying a gene reproduction pipeline which uses crossover and mutation. The control flow may have the following steps:

- A gene is selected from the population. Check if the crossover operation should be applied. (The check is TRUE with a probability of crossrate). If the check is TRUE:
  - Select a mating gene from the population.
  - Perform the crossover operation.
  - Apply mutation with a probability of mutrate.
  - Return a list one gene.
- Apply mutation with a probability of mutrate.
- Accept gene. For genetic algorithms: Identity.
- Return a list with a single gene.

**Usage**

```
xegaGaReplicateGene(pop, fit, lF)
```

**Arguments**

pop	Population of binary genes.
fit	Fitness vector.
lF	Local configuration of the genetic algorithm.

**Details**

xegaGaReplicateGene implements the control flow by a dynamic definition of the operator pipeline depending on the random choices for mutation and crossover:

1. A gene  $g$  is selected and the boolean variables  $mut$  and  $cross$  are set to  $runif(1)<rate$ .
2. The local function for the operator pipeline  $OPpip(g, lF)$  is defined by the truth values of  $cross$  and  $mut$ :

- (a) (cross==FALSE) & (mut==FALSE): Identity function.
  - (b) (cross==TRUE) & (mut==TRUE): Mate selection, crossover, mutation.
  - (c) (cross==TRUE) & (mut==FALSE): Mate selection, crossover.
  - (d) (cross==FALSE) & (mut==TRUE): Mutation.
3. Perform the operator pipeline and accept the result.

**Value**

A list of one gene.

**See Also**

Other Replication: [xegaGaReplicate2Gene\(\)](#)

**Examples**

```
lFxegaGaGene$CrossGene<-xegaGaCrossGene
lFxegaGaGene$MutationRate<-function(fit, lF) {0.001}
lFxegaGaGene$Accept<-function(OperatorPipeline, gene, lF) {gene}
pop10<-lapply(rep(0,10), function(x) xegaGaInitGene(lFxegaGaGene))
epop10<-lapply(pop10, lFxegaGaGene$EvalGene, lF=lFxegaGaGene)
fit10<-unlist(lapply(epop10, function(x) {x$fit}))
newgenes<-xegaGaReplicateGene(pop10, fit10, lFxegaGaGene)
```

---

xegaGaReplicationFactory

*Configure the replication function of a genetic algorithm.*

---

**Description**

ReplicationFactory implements the selection of a replication method.

Current support:

1. "Kid1" returns ReplicateGene.
2. "Kid2" returns Replicate2Gene.

**Usage**

```
xegaGaReplicationFactory(method = "Kid1")
```

**Arguments**

method            A string specifying the replication function.

**Value**

A replication function for genes.

**See Also**

Other Configuration: [lFxegaGaGene](#), [xegaGacrossoverFactory\(\)](#), [xegaGaGeneMapFactory\(\)](#), [xegaGaMutationFactory\(\)](#)

**Examples**

```
lFxegaGaGene$CrossGene<-xegaGacrossGene
lFxegaGaGene$MutationRate<-function(fit, lF) {0.001}
lFxegaGaGene$Accept<-function(OperatorPipeline, gene, lF) {gene}
Replicate<-xegaGaReplicationFactory("Kid1")
pop10<-lapply(rep(0,10), function(x) xegaGaInitGene(lFxegaGaGene))
epop10<-lapply(pop10, lFxegaGaGene$EvalGene, lF=lFxegaGaGene)
fit10<-unlist(lapply(epop10, function(x) {x$fit}))
newgenes1<-Replicate(pop10, fit10, lFxegaGaGene)
lFxegaGaGene$CrossGene<-xegaGacross2Gene
Replicate<-xegaGaReplicationFactory("Kid2")
newgenes2<-Replicate(pop10, fit10, lFxegaGaGene)
```

---

xegaGaUCross2Gene      *Uniform crossover of 2 genes.*

---

**Description**

xegaGaUCross2Gene swaps alleles of both genes with a probability of 0.5. It generates a random mask which is used to build the new genes. It returns 2 genes.

**Usage**

```
xegaGaUCross2Gene(gg1, gg2, lF)
```

**Arguments**

gg1	A binary gene.
gg2	A binary gene.
lF	The local configuration of the genetic algorithm.

**Value**

A list of 2 binary genes.

**References**

Syswerda, Gilbert (1989): Uniform Crossover in Genetic Algorithms. In: Schaffer, J. David (Ed.) Proceedings of the Third International Conference on Genetic Algorithms, Morgan Kaufmann Publishers, Los Altos, California, pp. 2-9. (ISBN:1-55860-066-3)

**See Also**

Other Crossover (2): [xegaGacross2Gene\(\)](#), [xegaGauPCross2Gene\(\)](#)

**Examples**

```
gene1<-xegaGauInitGene(1FxegaGauGene)
gene2<-xegaGauInitGene(1FxegaGauGene)
xegaGauDecodeGene(gene1, 1FxegaGauGene)
xegaGauDecodeGene(gene2, 1FxegaGauGene)
newgenes<-xegaGauCross2Gene(gene1, gene2, 1FxegaGauGene)
xegaGauDecodeGene(newgenes[[1]], 1FxegaGauGene)
xegaGauDecodeGene(newgenes[[2]], 1FxegaGauGene)
```

---

xegaGauCrossGene	<i>Uniform crossover of 2 genes.</i>
------------------	--------------------------------------

---

**Description**

xegaGauCrossGene swaps alleles of both genes with a probability of 0.5. It generates a random mask which is used to build the new gene.

**Usage**

```
xegaGauCrossGene(gg1, gg2, 1F)
```

**Arguments**

gg1	A binary gene.
gg2	A binary gene.
1F	The local configuration of the genetic algorithm.

**Value**

A list of one binary gene.

**References**

Syswerda, Gilbert (1989): Uniform Crossover in Genetic Algorithms. In: Schaffer, J. David (Ed.) Proceedings of the Third International Conference on Genetic Algorithms, Morgan Kaufmann Publishers, Los Altos, California, pp. 2-9. (ISBN:1-55860-066-3)

**See Also**

Other Crossover (1): [xegaGacrossGene\(\)](#), [xegaGauPCrossGene\(\)](#)

**Examples**

```

gene1<-xegaGaInitGene(1FxegaGaGene)
gene2<-xegaGaInitGene(1FxegaGaGene)
xegaGaDecodeGene(gene1, 1FxegaGaGene)
xegaGaDecodeGene(gene2, 1FxegaGaGene)
gene3<-xegaGaUCrossGene(gene1, gene2, 1FxegaGaGene)
xegaGaDecodeGene(gene3[[1]], 1FxegaGaGene)

```

---

xegaGaUPCross2Gene      *Parameterized uniform crossover of 2 genes.*

---

**Description**

xegaGaUP2CrossGene swaps alleles of both genes with a probability of 1F\$UCrossSwap. It generates a random mask which is used to build the new gene. It returns 2 genes.

**Usage**

```
xegaGaUPCross2Gene(gg1, gg2, 1F)
```

**Arguments**

gg1	A binary gene.
gg2	A binary gene.
1F	The local configuration of the genetic algorithm.

**Value**

A list of 2 binary genes.

**References**

Spears William and De Jong, Kenneth (1991): On the Virtues of Parametrized Uniform Crossover. In: Belew, Richar K. and Booker, Lashon B. (Ed.) Proceedings of the Fourth International Conference on Genetic Algorithms, Morgan Kaufmann Publishers, Los Altos, California, pp. 230-236. (ISBN:1-55860-208-9)

**See Also**

Other Crossover (2): [xegaGaCross2Gene\(\)](#), [xegaGaUCross2Gene\(\)](#)



**Examples**

```

gene1<-xegaGaInitGene(1FxegaGaGene)
gene2<-xegaGaInitGene(1FxegaGaGene)
xegaGaDecodeGene(gene1, 1FxegaGaGene)
xegaGaDecodeGene(gene2, 1FxegaGaGene)
newgenes<-xegaGaUPCross2Gene(gene1, gene2, 1FxegaGaGene)
xegaGaDecodeGene(newgenes[[1]], 1FxegaGaGene)
xegaGaDecodeGene(newgenes[[2]], 1FxegaGaGene)

```

---

xegaGaUPCrossGene	<i>Parameterized uniform crossover of 2 genes.</i>
-------------------	--

---

**Description**

xegaGaUPCrossGene swaps alleles of both genes with a probability of 1F\$UCrossSwap. It generates a random mask which is used to build the new gene.

**Usage**

```
xegaGaUPCrossGene(gg1, gg2, 1F)
```

**Arguments**

gg1	A binary gene.
gg2	A binary gene.
1F	The local configuration of the genetic algorithm.

**Value**

A list of one binary gene.

**References**

Spears William and De Jong, Kenneth (1991): On the Virtues of Parametrized Uniform Crossover. In: Belew, Richar K. and Booker, Lashon B. (Ed.) Proceedings of the Fourth International Conference on Genetic Algorithms, Morgan Kaufmann Publishers, Los Altos, California, pp. 230-236. (ISBN:1-55860-208-9)

**See Also**

Other Crossover (1): [xegaGaCrossGene\(\)](#), [xegaGaUCrossGene\(\)](#)

**Examples**

```
gene1<-xegaGaInitGene(1FxegaGaGene)
gene2<-xegaGaInitGene(1FxegaGaGene)
xegaGaDecodeGene(gene1, 1FxegaGaGene)
xegaGaDecodeGene(gene2, 1FxegaGaGene)
gene3<-xegaGaUPCrossGene(gene1, gene2, 1FxegaGaGene)
xegaGaDecodeGene(gene3[[1]], 1FxegaGaGene)
```

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