

# R&D Europe (Germany) Future Technology Research

MOO-EALib (Part 2): Functions

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# Chapter 1

# Abstract

Most of optimization problems in the real world are Multiobjective Optimization (MOO) problems. Thus, these problems are very popular now and many researchers are developing several methods for MOO.

In order to try them, we needed the platform for MOO research. Thus, we developed MOO-EALib for multiobjective evolution strategies. This MOO-EALib is a C++ Class library. The original EALib was developed by Ruhr University Bochum in 1995. But, EALib was designed for Single Objective Optimization. Thus, we developed the extended version of EALib for MOO which we are calling MOO-EALib.

In the first report "MOO-EALib (Part 1): Structure", we explained the concept of MOO-EALib and the structure of MOO-EALib [1]. In this report, we explain the functions in MOO-EALib.

In Chapter 2, we explain  $Class\ Individual MOO$  which corresponds to  $Class\ Individual$  in the original EALib. In Chapter 3,  $Class\ Population MOO$ , which corresponds to  $Class\ Population$ , is explained .

If you compare MOO-EALib with the original EALib, you can recognize that many functions are the same. However, they were re-designed for MOO problems. Thus, we explained them in this report again.

# Chapter 2

# **IndividualMOO**

In this chapter, to clarify the explanation, the following words will be used:

*Individual*: individual which is for single objective optimization. This is generated by class *Individual*.

*IndividualMOO*: individual which is for multi objective optimization. This is generated by class *IndividualMOO*.

### 2.1 Internal variable

In class Individual MOO, the following variables are defined.

**MOOFitness:** The vector to store the fitness variables. The type of this variable is *vector*< *double* >.

MOORank: The number of a rank. The type of this variable is unsigned.

**MOOShare:** The value of sharing. The type of this variable is *double*. Some times we can use this variable as a niche count.

### 2.2 Constructors

In the constructors, interval variables are initialized:

$$MOOFitness[i] = 0.0$$
 (2.1)

$$MOOFitness.size() = 0 (2.2)$$

$$MOORank = 0$$
 (2.3)

$$MOOShare = 0.0$$
 (2.4)

MOOFitness.size() means the number of objective functions.

IndividualMOO( );

Generate an empty Individual MOO.

Parameters: None.
Return Value: None.
Caveats: None.

No. TO-IM-002

Individual MOO( unsigned n );

Generate a new Individual MOO and reserves memory for n chromosomes.

**Parameters:** n - The number of chromosomes.

Return Value: None. Caveats: None.

No. TO-IM-003

IndividualMOO( unsigned n,

const Chromosome & chrom );

Generate an Individual MOO that consists of n clones of the chromosome chrom.

**Parameters:** n - The number of chromosomes.

chrom - Chromosome to be cloned.

Return Value: None.

Caveats: None.

No. TO-IM-004

IndividuaMOO( const Chromosome& chrom0 );

Generates an *Individual MOO* that consists of the chromosome *chrom0*.

**Parameters:** chrom0 - Chromosome to be cloned.

IndividualMOO( const Chromosome& chrom0,

const Chromosome& chrom1 );

Generates an Individual MOO that consists of the chromosomes chrom0 and chrom1.

Parameters: chrom0 - First chromosome, which is part of the new Individ-

ual MOO.

chrom1 - Second chromosome, which is part of the new Individ-

ual MOO.

Return Value: None.

Caveats: None.

No. TO-IM-006

IndividualMOO( const Chromosome& chrom0 .. chrom2 );

Generates an Individual MOO that consists of the chromosomes chrom0 to chrom2.

 $\textbf{Parameters:} \qquad \textit{chrom0} \ \dots \ \textit{chrom2} \ \text{-} \quad \text{Chromosomes that make up the new } \textit{Indi-}$ 

vidual MOO.

Return Value: None.

Caveats: None.

No. TO-IM-007

 ${\bf Individual MOO}(\quad \ {\rm const} \ \, {\rm Chromosome} \& \ \, {\it chrom0} \ \, ... \ \, {\it chrom3} \quad );$ 

Generates an Individual MOO that consists of the chromosomes chrom0 to chrom3.

Parameters: chrom0 .. chrom3 - Chromosomes, that make up the new Indi-

vidual MOO.

Return Value: None. Caveats: None.

No. TO-IM-008

IndividualMOO( const Chromosome& chrom0 .. chrom4 );

Generates an Individual MOO that consists of the chromosomes chrom0 to chrom4.

Parameters: chrom0 .. chrom4 - Chromosomes, that make up the new Indi-

vidual MOO.

IndividualMOO( const Chromosome& chrom0 .. chrom5 );

Generates an Individual MOO that consist of the chromosomes chrom0 to chrom5.

Parameters: chrom0 .. chrom5 - Chromosomes, that make up the new Indi-

vidual MOO.

Return Value: None.

Caveats: None.

### No. TO-IM-010

IndividualMOO( const Chromosome& chrom0 .. chrom6 );

Generates an Individual MOO that consist of the chromosomes  $chrom\theta$  to  $chrom\theta$ .

Parameters:  $chrom\theta$  ..  $chrom\theta$  - Chromosomes, that make up the new Indi-

vidual MOO.

Return Value: None.

Caveats: None.

### No. TO-IM-011

**IndividualMOO**( const Chromosome& chrom0 .. chrom7 );

Generates an Individual MOO that consist of the chromosomes chrom0 to chrom7.

 $\textbf{Parameters:} \qquad \textit{chrom0} \ \dots \ \textit{chrom7} \ \text{-} \quad \text{Chromosomes, that make up the new} \ \textit{Indi-}$ 

vidual MOO.

Return Value: None.

Caveats: None.

### No. TO-IM-012

IndividualMOO( const vector < Chromosome\* > & chrom1 );

Generates an Individual MOO that consists of the chromosomes stored in vector chrom 1.

**Parameters:** *chrom1* - The vector of chromosomes.

IndividualMOO( const Individual& indiv1 );

Generates an *IndividualMOO* that is a copy of *Individual indiv* including the internal class variables. Before copying, *Individual indiv* will be converted into *IndividualMOO*.

Parameters: indiv1 - Individual.

Return Value: None.
Caveats: None.

No. TO-IM-014

IndividualMOO( const IndividualMOO& indmoo );

Generates an Individual MOO that is a copy of Individual MOO ind moo including the internal class variables.

 $\textbf{Parameters:} \qquad ind moo \ - \ Individual MOO.$ 

Return Value: None.
Caveats: None.

### 2.3 Destructor

### No. TO-IM-015

 $\sim$  IndividualMOO( );

Removes all chromosomes, that are contatined in the *IndividualMOO this* and then destroys *this* itself.

Parameters: None.
Return Value: None.
Caveats: None.

### 2.4 Operators

### 2.4.1 Assignment Operators

No. TO-IM-102

```
IndividualMOO& operator = ( const IndividualMOO& indmoo );
```

Assigns the *Individual MOO ind moo* (i.e. the chromosomes that are contained in *ind moo* and the values of the internal class variables) to *this*.

Parameters: indmoo - IndividualMOO that will be assigned to this.

Return Value: The Individual MOO this with its new values.

Caveats: None.

No. TO-IM-104

```
Individual MOO\& operator = (const Individual \& ind);
```

Assigns the *Individual ind* (i.e. the chromosomes that are contained in *ind* and the values of the internal class variables) to *this*. Before assigning, *Individual ind* will be converted into *Individual MOO*.

**Parameters:** ind - Individual that will be assigned to this. **Return Value:** The Individual MOO this with its new values.

Caveats: None.

### 2.4.2 Comparison Operators

No. TO-IM-103

```
bool operator == ( const Individual MOO \& indmoo ) const;
```

Checks whether the current *IndividualMOO* this and the *IndividualMOO* indmoo are equal. The *IndividualMOO*s are equal, if they contain the same number of chromosomes, if any chromosome of this is equal to its corresponding chromosome in ind and if all values of the internal class variables are equal.

Parameters: indmoo - IndividualMOO that will be compared with this.

Return Value: true - The IndividualMOOs are equal,

false - The Individual MOOs are not equal.

### 2.4.3 Operators for Extracting a Single Chromosome

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IN ()		1_1	/I _ I	1 11

Chromosome& **operator** [] ( unsigned i );

Returns the chromosome with index i in the Individual MOO this.

**Parameters:** i - Index of the chromosome in *this*, to be returned. i must be less than the number of chromosomes in *this*, otherwise the

method will be aborted with an error message.

**Return Value:** Chromosome with index i.

Caveats: None.

No. TO-IM-101

const Chromosome& operator[] ( unsigned i ) const;

Returns the chromosome with index i in the Individual MOO this.

**Parameters:** i - Index of the chromosome in *this*, to be returned. i must be

less than the number of chromosomes in  $\it this$ , otherwise the

method will be aborted with an error message.

**Return Value:** Chromosome with index i.

Caveats: None.

### 2.5 Information about the structure

No. TO-IM-020

 $unsigned \ \mathbf{size}( \hspace{0.5cm} ) \ const;$ 

Returns the number of chromosome in this.

Parameters: None.

Return Value: Number of chromosomes in this.

Caveats: None.

No. TO-IM-021

unsigned totalSize( ) const;

Returns the number of all alleles of the chromosomes in this.

Parameters: None.

Return Value: The whole number of alleles in this.

### 2.6 Methods for internal variables

### 2.6.1 Internal variable fitness

No. TO-IM-030

void  $\mathbf{setFitness}($  double fit );

Sets the fitness and scaled fitness of this to the new value fit.

Parameters: fit - New value for the normal and scaled fitness.

Return Value: None.

Caveats: None.

No. TO-IM-031

double **fitnessValue**( ) const;

Returns the fitness value of the current Individual MOO this.

Parameters: None.

Return Value: Fitness value of this.

Caveats: None.

No. TO-IM-032

double **getFitness**( ) const;

Returns the fitness value of the current Individual MOO this.

Parameters: None.

Return Value: Fitness value of this.

Caveats: None.

### 2.6.2 Internal variable scaledFitness

No. TO-IM-033

void **setScaledFitness**( double *scalef* )

Sets the scaled fitness of this to the new value scalef.

**Parameters:** scalef - New value for the scaled fitness.

double **getScaledFitness**( ) const;

Returns the scaled fitness value of the current Individual MOO this.

Parameters: None.

Return Value: Scaled fitness value of this.

Caveats: None.

### 2.6.3 Internal variable age

### No. TO-IM-035

```
void \mathbf{setAge}( unsigned age );
```

Sets the age of this to the new value age.

Parameters: age - New age of this. The default is 0.

Return Value: None. Caveats: None.

### No. TO-IM-036

```
{\rm void} \ \ \mathbf{incAge}( \hspace{0.5cm} );
```

Increments the age of this by 1.

Parameters: None.
Return Value: None.
Caveats: None.

### No. TO-IM-037

```
unsigned getAge( ) const;
```

Returns the age of this, i.e. the generation.

Parameters: None.

Return Value: Age of this.

Caveats: None.

### 2.6.4 Internal variable selProb

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void setSelectionProbability( double prob );

Sets the selection probability of this to the new value prob.

**Parameters:** prob - New selection probability for this.

Return Value: None.
Caveats: None.

No. TO-IM-039

void  $\mathbf{setSelProb}($  double prob );

Sets the selection probability of this to the new value prob.

**Parameters:** prob - New selection probability for this.

Return Value: None.

Caveats: None.

No. TO-IM-040

double **selectionProbability**( ) const;

Returns the selection probability of this.

Parameters: None.

Return Value: The selection probability of this.

Caveats: None.

No. TO-IM-041

double **getSelProb**( ) const;

Returns the selection probability of this.

Parameters: None.

Return Value: The selection probability of this.

### 2.6.5 Internal variable numCopies

### No. TO-IM-042

void **setNumCopies**( unsigned *num* );

Sets the number of copies of this to the new value num.

**Parameters:** num - New value for the number of copies.

Return Value: None.

Caveats: None.

### No. TO-IM-043

unsigned numberOfCopies( ) const;

Returns the number of reproductions of this that occured during the last selection.

Parameters: None.

Return Value: Number of reproductions of this.

Caveats: None.

### No. TO-IM-044

unsigned **getNumCopies**( ) const;

Returns the number of reproductions of this that occured during the last selection.

Parameters: None.

Return Value: Number of reproductions of this.

Caveats: None.

### 2.6.6 Internal variable evalFlg

### No. TO-IM-045

void **setEvaluationFlag**( );

Sets evalFlg to "true".

Parameters: None.

Return Value: None.

void **clearEvaluationFlag**( );

Sets evalFlg to "false".

Parameters: None.
Return Value: None.
Caveats: None.

No. TO-IM-047

void setEvalFlg( bool flg );

Sets the flag of evaluation of this to the new value flg.

**Parameters:** flg - New value for the flag of evaluation.

Return Value: None. Caveats: None.

No. TO-IM-048

bool **needEvaluation**( ) const;

Returns the status of the evalFlg, i.e. whether the IndividualMOO must be evaluated.

Parameters: None.

Return Value: Status of evalFlg:

true - An evaluation of this is necessary,

false - The Individual MOO needs no evaluation.

Caveats: None.

No. TO-IM-049

bool **getEvalFlg**( ) const;

Returns the status of the evalFlg, i.e. whether the IndividualMOO must be evaluated.

Parameters: None.

Return Value: Status of evalFlg:

true - An evaluation of this is necessary,

false - The Individual MOO needs no evaluation.

### 2.6.7 Internal variable feasible

No. TO-IM-050

 ${\tt void} \ \ \mathbf{setFeasible}( \quad \ \mathsf{bool} \ \mathit{fea} \quad \ );$ 

Sets the feasible flag to the new value fea.

**Parameters:** fea - New value for the feasible flag:

true - The Individual MOO is a possible solution for the

current optimization problem,

false - The Individual MOO does not represent a feasible

solution.

Return Value: None.
Caveats: None.

No. TO-IM-051

bool isFeasible( ) const;

Returns whether this is a possible solution for the current optimization problem.

Parameters: None.

Return Value: Status of the feasible-flag:

true - The Individual MOO is a possible solution, false - The Individual MOO cannot used as solution.

Caveats: None.

No. TO-IM-052

bool **getFeasible**( ) const;

Returns whether this is a possible solution for the current optimization problem.

Parameters: None.

Return Value: Status of the feasible-flag:

true - The IndividualMOO is a possible solution, false - The IndividualMOO cannot used as solution.

### 2.6.8 Internal variable elitist

### No. TO-IM-053

```
void setElitist( bool eli );
```

Sets the *elitist* flag to the new value *eli*.

Parameters: eli - New value for the elitist flag:

true - The IndividualMOO is a elitist, false - The IndividualMOO is not a elitist.

Return Value: None.

Caveats: None.

### No. TO-IM-054

bool **isElitist**( ) const;

Returns the status of the elitist-flag, i.e. whether this was chosen as elite IndividualMOO during the last selection.

Parameters: None.

Return Value: Status of the *elitist*-flag:

true - The IndividualMOO was chosen as elitist, false - The IndividualMOO was not chosen.

Caveats: None.

### No. TO-IM-055

bool **getElitist**( ) const;

Returns the status of the *elitist*-flag, i.e. whether *this* was chosen as elite *IndividualMOO* during the last selection.

Parameters: None.

Return Value: Status of the *elitist*-flag:

true - The Individual MOO was chosen as elitist,

false - The Individual MOO was not chosen.

# 2.7 Methods for internal variables ( Individual-MOO )

### 2.7.1 The number of objective functions

No. TO-IM-060

void setNoOfObj( unsigned n );

Sets the number of objective functions to the new value n.

**Parameters:** n - New value for the number of objective functions.

Return Value: None.
Caveats: None.

No. TO-IM-061

unsigned **getNoOfObj**( );

Returns the number of objective functions.

Parameters: None.

Return Value: The number of objective functions.

Caveats: None.

### 2.7.2 Internal variable MOORank

No. TO-IM-062

void setMOORank( unsigned n );

Sets the rank to the new value n.

**Parameters:** n - New value for the rank.

Return Value: None.

Caveats: None.

No. TO-IM-063

unsigned **getMOORank**( );

Returns the rank of this.

Parameters: None.

Return Value: The rank of this.

### 2.7.3 Internal variable MOOShare

### No. TO-IM-064

```
void setMOOShare( double n );
```

Sets the sharing value to the new value n.

**Parameters:** n - New value for the sharing (or the niche count).

Return Value: None.

Caveats: None.

### No. TO-IM-065

```
unsigned getMOOShare( );
```

Returns the value of sharing (or the niche count) of this.

Parameters: None.

Return Value: The value of sharing ( or the niche count ) of this.

Caveats: None.

### 2.7.4 Internal variable MOOFitness

### No. TO-IM-066

```
void setMOOFitness( unsigned nof, double fit );
```

Sets the nof th fitness value to the new value fit.

**Parameters:** nof - The index of the fitness value which you want to change.

fit - New value for the fitness value.

Return Value: None.

Caveats: None.

### No. TO-IM-067

```
double getMOOFitness( unsigned nof );
```

Gets the fitness value of the *nof* th objective function.

**Parameters:** nof - The index of the fitness value which you want to know.

Return Value: The fitness value of the nof th objective function.

void setMOOFitnessValues( double  $f\theta$  );

Sets the fitness value of the  $\theta$  th objective function to the new value  $f\theta$ .

**Parameters:**  $f\theta$  - New fitness value for the  $\theta$  th objective function.

Return Value: None.

Caveats: None.

No. TO-IM-069

void setMOOFitnessValues( double f0, double f1 );

Sets the fitness values of the objective functions to the new values  $f0 \dots f1$ .

**Parameters:**  $f\theta$  - New fitness value for the  $\theta$  th objective function.

f1 - New fitness value for the 1 st objective function.

Return Value: None. Caveats: None.

No. TO-IM-070

void **setMOOFitnessValues**( double f0 .. f2 );

Sets the fitness values of the objective functions to the new values  $f\theta$  .. f2.

**Parameters:**  $f0 \dots f2$  - New fitness values for the objective functions.

Return Value: None.

Caveats: None.

No. TO-IM-071

void setMOOFitnessValues( double  $f\theta ... f3$  );

Sets the fitness values of the objective functions to the new values f0 .. f3.

**Parameters:** for ... for ... for ... for ... for ... for the objective functions.

void **setMOOFitnessValues**( double f0 .. f4 );

Sets the fitness values of the objective functions to the new values  $f0 \dots f4$ .

**Parameters:** f0 ... f4 - New fitness values for the objective functions.

Return Value: None. Caveats: None.

No. TO-IM-073

void **setMOOFitnessValues**( double f0 .. f5 );

Sets the fitness values of the objective functions to the new values f0 .. f5.

**Parameters:** f0 ... f5 - New fitness values for the objective functions.

Return Value: None.
Caveats: None.

No. TO-IM-074

void **setMOOFitnessValues**( double f0 .. f6 );

Sets the fitness values of the objective functions to the new values  $f0 \dots f6$ .

**Parameters:**  $f\theta$  ..  $f\theta$  - New fitness values for the objective functions.

Return Value: None.
Caveats: None.

No. TO-IM-075

void setMOOFitnessValues( double  $f\theta ... f7$  );

Sets the fitness values of the objective functions to the new values  $f\theta$  .. f7.

**Parameters:**  $f0 \dots f7$  - New fitness values for the objective functions.

```
void setMOOFitnessValues( vector< double >& fit );
```

Sets the fitness values of the objective functions to the new values in the vector fit.

 $\textbf{Parameters:} \hspace{0.5cm} \textit{fit} \hspace{0.1cm} \textbf{-} \hspace{0.1cm} \textbf{The vector which stores new fitness values for the objective}$ 

functions.

Return Value: None.

Caveats: None.

### No. TO-IM-077

```
vector < double > \& getMOOFitnessValues( );
```

Returns the fitness values.

Parameters: None.

Return Value: The fitness values.

Caveats: None.

### No. TO-IM-078

```
void initializeMOOFitness( double x );
```

Sets the fitness values of all objective functions to the new value x.

**Parameters:** x - New value for all fitness values.

Return Value: None.
Caveats: None.

### 2.8 Change the structure

### No. TO-IM-110

```
\begin{array}{ccc} \text{void} & \textbf{replace}( & \text{unsigned} & i, \\ & \text{const Chromosome}\& \ \textit{chrom} & ); \end{array}
```

Replaces chromosome number i with the content of chromosome chrom.

**Parameters:** i - Index of the chromosome of this, to be replaced. i must

be less than the number of chromosomes in *this*, otherwise the method will be aborted with an error message.

chrom - Chromosome that replaces the old chromosome in this.

Inserts chromosome chrom at position i into this.

Parameters: i - Insertion-position in  $\it{this}$ . The maximum value for  $\it{i}$ 

shall be equal to the number of chromosomes in  $\it this,$  otherwise the method will be aborted with an error mes-

sage.

chrom - Chromosome to be inserted into this.

Return Value: None. Caveats: None.

No. TO-IM-112

void **append**( const Chromosome& chrom );

Appends the chromosome *chrom* at the end of *this*.

**Parameters:** chrom - Chromosome to be appended at the end of this.

Return Value: None.
Caveats: None.

No. TO-IM-113

void **remove**( unsigned i );

Removes the chromosome with index i from this.

Parameters: i - Index of the chromosome to be removed from this. i must be

less than the number of chromosomes in  $\it this, otherwise$  the

method will be aborted with an error message.

 $\begin{array}{ccc} \hline \text{void} & \mathbf{remove}( & \text{unsigned } i, \\ & \text{unsigned } j & ); \end{array}$ 

Removes all chromosomes with indices in the range [i, j].

Parameters:

- i Index of the first chromosome to be removed. i must be less than the number of chromosomes in this and not greater as j or the method will be aborted with an error message.
- j Index of the last chromosome to be removed. j must be less than the number of chromosomes in this and not smaller as i or the method will be aborted with an error message.

Return Value: None. Caveats: None.

### 2.9 Aggregation Methods

### No. TO-IM-200

double aggregation( const vector < double > & weight );

Calculate the weighted sum of fitness values:  $\sum_{i=0}^{n-1} w_i f_i$ .

 $\textbf{Parameters:} \qquad \textit{weight} \ \ \text{-} \quad \text{The vector which stores the values of weight for an}$ 

 ${\it aggregation} \ {\it method}.$ 

Return Value: The weighted sum of fitness values.

Caveats: None.

### No. TO-IM-201

double **simplesum**( ) const;

Calculate the sum of fitness values:  $\sum_{i=0}^{n-1} f_i$ .

Parameters: None

Return Value: The sum of fitness values.

# 2.10 Output data

### No. TO-IM-500

void **printIM**( ) const;

Outputs the data of the individual this.

Parameters: None.
Return Value: None.
Caveats: None.

# Chapter 3

# **PopulationMOO**

In this chapter, to clarify the explanation, the following words will be used:

*Individual*: individual which is for single objective optimization. This is generated by Class *Individual*.

*Individual MOO*: individual which is for multi objective optimization. This is generated by Class *Individual MOO*.

**Population:** population which is for single objective optimization and stores *Individuals*. This is generated by Class *Population*.

**PopulationMOO**: population which is for multi objective optimization and stores *IndividualMOO*s. This is generated by Class *PopulationMOO*.

### 3.1 Constructors

# No. TO-PM-001 PopulationMOO( ); Generates a new PopulationMOO. Parameters: None. Return Value: None. Caveats: None. No. TO-PM-002 PopulationMOO( unsigned n );

Generates a new Population MOO and reserves space for n Individual MOOs of undefined type.

**Parameters:** n - Number of Individual MOOs in the new Population MOO.

**PopulationMOO**( const IndividualMOO& indmoo );

Generates a new PopulationMOO that consists of the IndividualMOO indmoo.

**Parameters:** indmoo - Individual MOO that makes up the new Population-MOO.

Return Value: None.

Caveats: None.

### No. TO-PM-004

**PopulationMOO**( unsigned n,

const IndividualMOO& indmoo );

Generates a new Population MOO consisting of n copies of the Individual MOO individual MOO individual n

Parameters: n - Number of copies of the  $Individual MOO\ ind moo\$ to

form the new PopulationMOO.

indmoo - IndividualMOO that makes up the new Population-

MOO.

Return Value: None.

Caveats: None.

### No. TO-PM-005

**PopulationMOO**( unsigned n,

const Chromosome&  $chrom\theta$ );

Generates a new Population MOO consisting of n Individual MOOs that are formed by cloning chromosome chrom0.

**Parameters:** n - Number of IndividualMOOs that make up the new

Population MOO.

 $chrom\theta$  - Chromosome.

const Chromosome& chrom0 .. chrom1

Generates a new Population MOO that consists of n Individual MOOs formed by cloning the chromosomes chrom0 and chrom1.

Parameters: n - Number of Individual MOOs that make up the new Population MOO.

chrom0 .. chrom1 - Chromosomes to be cloned.

Return Value: None.

Caveats: None.

### No. TO-PM-007

PopulationMOO( unsigned n, const Chromosome&  $chrom\theta$  .. chrom2);

Generates a new Population MOO that consists of n Individual MOOs formed by cloning the chromosomes chrom0 to chrom2.

Parameters: n - Number of Individual MOOs that make up the new Population MOO.

chrom0 .. chrom2 - Chromosomes to be cloned.

Return Value: None.
Caveats: None.

### No. TO-PM-008

Generates a new Population MOO that consists of n Individual MOOs formed by cloning the chromosomes chrom0 to chrom3.

Parameters: n - Number of Individual MOOs that make up the new Population MOO.

chrom0 .. chrom3 - Chromosomes to be cloned.

## ${\bf Population MOO} (\qquad {\rm unsigned} \qquad \qquad n,$

const Chromosome& chrom0 .. chrom4 )

Generates a new Population MOO that consists of n Individual MOOs formed by cloning the chromosomes chrom0 to chrom4.

Parameters: n - Number of Individual MOOs that make up the new Population MOO.

chrom0 .. chrom4 - Chromosomes to be cloned.

Return Value: None.

Caveats: None.

### No. TO-PM-010

**PopulationMOO**( unsigned n, const Chromosome&  $chrom\theta$  .. chrom5);

Generates a new Population MOO that consists of n Individual MOOs formed by cloning the chromosomes chrom0 to chrom5.

Parameters: n - Number of Individual MOOs that make up the new Population MOO.

chrom0 .. chrom5 - Chromosomes to be cloned.

Return Value: None.
Caveats: None.

### No. TO-PM-011

Generates a new Population MOO that consists of n Individual MOOs formed by cloning the chromosomes chrom0 to chrom6.

Parameters: n - Number of Individual MOOs that make up

the new Population MOO.

chrom0 .. chrom6 - Chromosomes to be cloned.

### PopulationMOO(

unsigned

const Chromosome& chrom0 .. chrom7 );

Generates a new Population MOO that consists of n Individual MOOs formed by cloning the chromosomes chrom0 to chrom7.

Parameters:

- Number of *IndividualMOO*s that make up the new *PopulationMOO*.

chrom0 .. chrom7 - Chromosomes to be cloned.

Return Value: None.

Caveats: None.

### No. TO-PM-013

PopulationMOO(

unsigned

n

);

const vector < Chromosome \*> & chrom

Generates a new Population MOO that consists of n Individual MOOs formed by cloning the chromosomes that are stored in vector chrom.

Parameters:

Number of IndividualMOOs that make up the new PopulationMOO.

chrom - Vector with chromosomes to be cloned.

Return Value: None. Caveats: None.

### No. TO-PM-014

PopulationMOO(

const PopulationMOO& popmoo

Generates a new Population MOO that consists of a copy of the Population MOO popmoo including the values for the flags ascending, spinOnce, subPop and index.

Parameters: popmoo - PopulationMOO whose copy will form the new Popu-

lation MOO.

**PopulationMOO**( const Population& pop );

Generates a new *PopulationMOO* that consists of a copy of the *Population pop* including the values for the flags *ascending*, *spinOnce*, *subPop* and *index*. Before generating a new *PopulationMOO*, *Population pop* will be converted into *PopulationMOO*.

**Parameters:** pop - Population whose copy will form the new PopulationMOO.

Return Value: None.

Caveats: None.

### 3.2 Destructor

### No. TO-PM-016

```
\sim Population MOO( );
```

If the destructor is called by a subpopulation nothing happens, else all *IndividualMOO*s in the *PopulationMOO* are removed and the *PopulationMOO* itself is destroyed.

Parameters: None.
Return Value: None.

Caveats: The destructor is virtual. The destructor should not be called

directly.

### 3.3 Operators

### 3.3.1 Assignment Operators

No. TO-PM-042

```
\label{eq:populationMOO\& operator} PopulationMOO\& \ \ \textbf{operator} = ( \quad \  \text{const IndividualMOO\& } \textit{indmoo} \quad );
```

The values of the *IndividualMOO* indmoo will be assigned to all *IndividualMOO*s of this.

**Parameters:** indmoo - Individual MOO.

Return Value: The PopulationMOO with its new IndividualMOOs.

```
PopulationMOO& operator = ( const Individual& ind );
```

The values of the *Individual ind* will be assigned to all *IndividualMOO*s of *this*. Before assignment, *Individual ind* will be converted into *IndividualMOO*.

Parameters: ind - Individual.

Return Value: The PopulationMOO with its new IndividualMOOs.

Caveats: None.

### No. TO-PM-044

```
PopulationMOO& operator = ( const PopulationMOO& popmoo );
```

Assigns all *IndividualMOOs* of *popmoo* to *this*. This method will only work if both *PopulationMOOs* consist of the same number of *IndividualMOOs* or if *this* is no subpopulation, otherwise the method will be aborted with an error message.

Parameters: popmoo - PopulationMOO.

Return Value: The PopulationMOO with its new IndividualMOOs.

Caveats: None.

### No. TO-PM-045

```
PopulationMOO& operator = ( const Population& pop );
```

Assigns all *Individuals* of *pop* to *this*. Before assignment, all *Individuals* in *Population pop* will be converted into *IndividualMOO*s. This method will only work if both *PopulationMOO* and *Population* consist of the same number of individuals ( *IndividualMOO* or *Individual*) or if *this* is no subpopulation, otherwise the method will be aborted with an error message.

Parameters: pop - Population.

Return Value: The PopulationMOO with its new IndividualMOOs.

### 3.3.2 Comparison Operators

### No. TO-PM-046

bool **operator** = =( const PopulationMOO& popmoo ) const;

Tests whether the *PopulationMOO* this and *popmoo* are equal. this and *popmoo* are equal, if they contain the same number of *IndividualMOO*s, all *IndividualMOO*s of *this* are equal to the corresponding *IndividualMOO*s of *popmoo* and the values of all internal variables of *this* and *popmoo* are the same.

Parameters: popmoo - PopulationMOO that shall be compared with this.

Return Value: true - this and popmoo are equal,

false - this and popmoo are different.

Caveats: None.

### 3.3.3 Operators for Extracting a Single Individual MOO

### No. TO-PM-040

Individual MOO & **operator** [ ]( unsigned i );

Returns Individual MOO number i out of this.

**Parameters:** i - Index of the IndividualMOO to be returned. i must be less

than the number of Individual MOOs in this, otherwise the

method will be aborted with an error message.

Return Value: The Individual MOO numbered i.

Caveats: None.

No. TO-PM-041

const Individual MOO & **operator** []( unsigned i ) const;

Returns Individual MOO number i out of this.

Parameters: i - Index of the IndividualMOO to be returned. i must be less

than the number of Individual MOOs in this, otherwise the

method will be aborted with an error message.

Return Value: The Individual MOO numbered i.

## 3.4 Information about Class PopulationMOO

No. TO-PM-030

unsigned **size**( ) const;

Returns the number of Individual MOOs in this.

Parameters: None.

Return Value: Number of Individual MOOs in this.

Caveats: None.

No. TO-PM-031

Individual\*\* begin( );

Returns the first data of the vector in this.

Parameters: None.

Return Value: The first data of the vector in this.

Caveats: None.

No. TO-PM-032

Individual\*\* end( );

Returns the last data of the vector in this.

Parameters: None.

Return Value: The last data of the vector in this.

Caveats: None.

## 3.5 Methods for internal variables

## 3.5.1 Internal variable ascending

No. TO-PM-050

void **setMaximize**( );

Sets the value of the ascending-flag to "false", so all Individual MOOs will be sorted by descending fitness values fitness.

#### No. TO-PM-051

void  $\mathbf{setMinimize}()$ ;

Sets the value of the *ascending*-flag to "true", so all *IndividualMOO*s will be sorted by ascending fitness values *fitness*.

Parameters: None.
Return Value: None.
Caveats: None.

No. TO-PM-052

void setAscending( bool strategy );

Sets the ascending-flag to the new value strategy.

Parameters: strategy - New value for the ascending-flag.

true - Minimize. The Individual MOOs are sorted by

ascending fitness values fitness.

false - Maximize. The Individual MOOs are sorted by

descending fitness values fitness.

Return Value: None.
Caveats: None.

No. TO-PM-053

bool **ascendingFitness**( ) const;

Returns whether the *IndividualMOO*s inside *this* are sorted by ascending or descending fitness values *fitness*.

Parameters: None.

Return Value: Value of the ascending-flag:

true - The Individual MOOs are sorted by ascending fitness values

fitness

false - The Individual MOOs are sorted by descending fitness val-

ues fitness.

bool **getAscending**( ) const;

Returns whether the Individual MOOs inside this are sorted by ascending or descending fitness values fitness.

Parameters: None.

Return Value: Value of the ascending-flag:

true - The Individual MOOs are sorted by ascending fitness values

fitness,

false - The Individual MOOs are sorted by descending fitness val-

ues fitness.

Caveats: None.

## 3.5.2 Internal variable spinOnce

No. TO-PM-055

 $\ \ \, \mathbf{void} \ \, \mathbf{spinWheelOneTime}( \hspace{0.5cm} );$ 

Sets the value of the spinOnce-flag to "true", so the roulette wheel will be spinned only one time during the next selectRouletteWheel-method call.

Parameters: None.
Return Value: None.
Caveats: None.

No. TO-PM-056

void spinWheelMultipleTimes( );

Sets the value of the *spinOnce*-flag to "false", so the roulette wheel will be spinned several times during the next *selectRouletteWheel*-method call.

#### No. TO-PM-057

void **setSpinOnce**( bool *spin* );

Sets spinOnce-flag to the new value spin.

**Parameters:** spin - New value for spinOnce-flag.

true - the roulette wheel will be spinned only one time. false - the roulette wheel will be spinned several times.

Return Value: None.
Caveats: None.

No. TO-PM-058

bool getSpinOnce( ) const;

Returns spinOnce-flag.

true - the roulette wheel will be spinned only one time. false - the roulette wheel will be spinned several times.

Parameters: None.

Return Value: The value of spinOnce-flag.

Caveats: None.

#### 3.5.3 Internal variable index

No. TO-PM-059

void  $\mathbf{setIndex}($  unsigned i )

Sets index to the new value i.

**Parameters:** i - New value for index of this.

Return Value: None.
Caveats: None.

No. TO-PM-060

unsigned **getIndex**( ) const;

Returns the value of *index*.

Parameters: None.

Return Value: The value of index.

## 3.5.4 Internal variable subPop

#### No. TO-PM-061

void  $\mathbf{setSubPop}(\quad bool \ sub \quad );$ 

Sets subPop to the new value sub.

**Parameters:** sub - New value for subPop of this.

true - This PopulationMOO is a sub PopulationMOO. false - This PopulationMOO is not a sub PopulationMOO.

Return Value: None.

Caveats: None.

No. TO-PM-062

bool **getSubPop**( ) const;

Returns the value of subPop.

true - This PopulationMOO is a sub PopulationMOO.

false - This PopulationMOO is not a sub PopulationMOO.

Parameters: None.

Return Value: The value of subPop.

Caveats: None.

## 3.5.5 Internal variable age in the class Individual

#### No. TO-PM-124

void  $\mathbf{setAge}($  unsigned a );

Sets the age of all IndividualMOOs in this to the new value a.

**Parameters:** a - New age of the IndividualMOOs. The default value is 0.

Return Value: None.

Caveats: None.

No. TO-PM-125

void incAge( );

Increases the age of all Individual MOOs inside this by 1.

# 3.6 Methods for internal variables ( Individual-MOO )

## 3.6.1 The number of objective functions

No. TO-IM-200

void **setNoOfObj**( unsigned *NOO* );

Sets the number of objective functions inside all  $\mathit{IndividualMOO}$ s to the new value NOO.

Parameters: NOO - New value for the number of objective functions.

Return Value: None.
Caveats: None.

## 3.6.2 Internal variable MOOFitness

No. TO-IM-201

void setMOOFitness( double obj );

Sets all *MOOFitness* in *this* to the new value *obj*.

 $\textbf{Parameters:} \hspace{0.5cm} \textit{obj} \hspace{0.1cm} \textbf{-} \hspace{0.1cm} \text{New value for the fitness values of all objective functions}$ 

inside all IndividualMOOs.

Return Value: None. Caveats: None.

## 3.6.3 Internal variable MOORank

No. TO-IM-202

void  $\mathbf{set}\mathbf{MOORank}($  unsigned MOOR );

Sets all MOORank in all Individual MOOs to the new value MOOR.

**Parameters:** MOOR - New value for MOORank of all IndividualMOOs.

## 3.6.4 Internal variable MOOShare

No. TO-IM-203

```
void setMOOShare( double MOOS );
```

Sets all MOOShare in all Individual MOOs to the new value MOOS.

Parameters: MOOS - New value for MOOShare of all IndividualMOOs.

Return Value: None. Caveats: None.

## 3.7 Change the structure

#### 3.7.1 The number of *IndividualMOO*s

No. TO-PM-033

```
void resize( unsigned n );
```

Changes the size of the Population MOO to the new value n. If n is less than the old size m of this, then all m - n Individual MOOs at the end of this will be removed, if n is greater than m, then n - m new empty Individual MOOs will be appended at the end of this. All other Individual MOOs will remain unchanged.

**Parameters:** n - New size of the Population MOO.

Return Value: None.

Caveats: None.

## 3.7.2 Replace IndividualMOOs

No. TO-PM-070

```
void \mathbf{replace}( unsigned i, const Individual \&ind );
```

Replaces IndividualMOO number i by the Individual ind.

 $\begin{array}{lll} \textbf{Parameters:} & i & - \text{ Index of the } \textit{IndividualMOO} \text{ inside of } \textit{this} \text{ to be replaced.} \\ & i \text{ must be less than the number of } \textit{IndividualMOOs} \text{ in } \textit{this}, \\ & \text{otherwise the method will be aborted with an error mes-} \\ \end{aligned}$ 

sage.

ind - Individual to replace the old one. First, Individual ind will

be converted into an *Individual MOO*.

 $\begin{array}{cccc} \hline \text{void} & \textbf{replace}( & \text{unsigned} & i, \\ & \text{const IndividualMOO\&} & indmoo & ); \\ \hline \end{array}$ 

Replaces Individual MOO number i by the Individual MOO ind moo.

Parameters: i - Index of the IndividualMOO inside of this to be replaced. i must be less than the number of Individual-MOOs in this, otherwise the method will be aborted

with an error message.

indmoo - IndividualMOO to replace the old one.

Return Value: None.
Caveats: None.

#### No. TO-PM-072

```
\begin{array}{ccc} \text{void} & \mathbf{replace}( & \text{unsigned} & i, \\ & \text{const Population} \& \ pop & ); \end{array}
```

Replaces all IndividualMOOs inside of this, begining with the one at position number i, by the IndividualMOOs which are converted from Individuals of the Population pop. If the number of Individuals inside of pop is greater than the number of Individuals of this begining at position t, then the method will be aborted with an error message.

**Parameters:** i - Index of the first *IndividualMOO* inside of *this* to be replaced.

pop - Population to replace the old Individual MOOs.

Return Value: None.
Caveats: None.

#### No. TO-PM-073

```
\begin{array}{ccc} \text{void} & \textbf{replace}( & \text{unsigned} & i, \\ & \text{const PopulationMOO} \& \ popmoo & ); \end{array}
```

Replaces all Individual MOOs inside of this, beginning with the one at position number i, by the Individual MOOs in the Population MOO popmoo. If the number of Individual MOOs inside of popmoo is greater than the number of Individual MOOs in this beginning at position i, then the method will be aborted with an error message.

**Parameters:** i - Index of the first *IndividualMOO* inside of *this* to be replaced.

popmoo - PopulationMOO to replace the old IndividualMOOs.

#### 3.7.3 Insert Individual MOOs

#### No. TO-PM-074

 $\begin{array}{c} \text{void} \ \ \textbf{insert}( \quad \text{unsigned} \qquad \quad i, \\ \text{const Individual} \& \ ind \quad ); \end{array}$ 

Inserts the *Individual ind* at index *i* inside the *PopulationMOO this*. Before insertion, *Individual ind* will be converted into *IndividualMOO*.

Parameters:

- Index at which *ind* is inserted in *this*. *i* must be at most as great as the number of *IndividualMOO*s in *this*, otherwise the method will be aborted with an error message.
- ind Individual to be inserted.

Return Value: None.

Caveats: None.

#### No. TO-PM-075

Inserts the  $Individual MOO\ ind moo\ at\ index\ i$  inside the  $Population MOO\ this.$ 

Parameters:

- Index at which *indmoo* is inserted in *this*. *i* must be at most as great as the number of *IndividualMOO*s in *this*, otherwise the method will be aborted with an error message.
- indmoo IndividualMOO to be inserted.

Return Value: None.

Caveats: None.

#### No. TO-PM-076

 $\begin{array}{ccc} \text{void} & \textbf{insert}( & \text{unsigned} & i, \\ & \text{const Population\& } pop & ); \end{array}$ 

Inserts all *Individuals* of *pop* into *this*, beginning at position *i*. Before insertion, all *Individuals* will be converted into *IndividualMOO*s.

Parameters:

- Index of *this* where the first *Individual* of *pop* is inserted. *i* must be at most as great as the number of *Individual MOO*s in *this*, otherwise the method will be aborted with an error message.
- pop Population with the Individuals that will be inserted into this.

void insert( unsigned i,

const PopulationMOO& popmoo );

Inserts all Individual MOOs of popmoo into this, beginning at position i.

 $\textbf{Parameters:} \hspace{0.5cm} i \hspace{1.5cm} - \hspace{0.5cm} \textbf{Index of } \textit{this} \textbf{ where the first } \textit{IndividualMOO} \textbf{ of } \textit{popmoo}$ 

is inserted. i must be at most as great as the number of IndividualMOOs in this, otherwise the method will

be aborted with an error message.

popmoo - PopulationMOO with the IndividualMOOs that will

be inserted into this.

Return Value: None.

Caveats: None.

## 3.7.4 Append IndividualMOOs

#### No. TO-PM-078

void append( const Individual & ind );

Appends Individual ind at the end of this. Before appending, Individual ind will be converted into Individual MOO.

**Parameters:** ind - The Individual to be appended to this.

Return Value: None.
Caveats: None.

No. TO-PM-079

void append( const IndividualMOO& indmoo );

Appends Individual MOO indmoo at the end of this.

Parameters: indmoo - The Individual MOO to be appended to this.

Return Value: None.
Caveats: None.

No. TO-PM-080

void **append**( const Population& pop );

Appends all *Individuals* of *Population pop* at the end of *PopulationMOO this*. Before appending, all *Individuals* of *Population pop* will be converted into *IndividualMOOs*.

**Parameters:** pop - Population to be appended to this.

void append( const PopulationMOO& popmoo );

Appends all Individual MOOs of Population MOO popula at the end of Population MOO this.

**Parameters:** popmoo - PopulationMOO to be appended to this.

Return Value: None.

Caveats: None.

## 3.7.5 Remove Individual MOOs

#### No. TO-PM-082

```
void remove( unsigned i );
```

Removes Individual MOO number i from this.

 $\textbf{Parameters:} \hspace{5mm} i \hspace{3mm} \text{-- Index of the } \textit{Individual MOO} \text{ that is to be removed from } \textit{this}.$ 

i must be less than the number of *IndividualMOO*s in *this*, otherwise the method will be aborted with an error message.

Return Value: None.
Caveats: None.

No. TO-PM-083

```
void \mathbf{remove}( unsigned i, unsigned k );
```

Removes all IndividualMOOs in the range [i, k] from the PopulationMOO this.

Parameters:

- i Index of the first IndividualMOO of this to be removed. i
  must be less than the number of IndividualMOOs in this,
  otherwise the method will be aborted with an error message. Additionally, i must be at most as great as k or no
  IndividualMOO will be removed from this.
- k Index of the last IndividualMOO to be removed from this. k must be less than the number of IndividualMOOs in this, otherwise the method will be aborted with an error message.

## 3.7.6 Exchange all Individual MOOs

No. TO-PM-098

void **exchange**( PopulationMOO& popmoo );

Swaps all *IndividualMOO*s of *popmoo* with the *IndividualMOO*s of *this*. The *PopulationMOO*s must contain the same number of *IndividualMOO*s, otherwise the method will be aborted with an error message.

Parameters: popmoo - PopulationMOO to be exchanged.

Return Value: None.

Caveats: None.

## 3.8 Change the order of *IndividualMOO*s

#### No. TO-PM-090

```
void \mathbf{swap}( unsigned i, unsigned j );
```

Swaps Individual MOOs number i and j. The method also works properly, when i is greater than j.

Parameters:

- i Index of the first Individual MOO. i must be less than the number of Individual MOOs in this, otherwise the method will be aborted with an error message.
- j Index of the second IndividualMOO. j must be less than the number of IndividualMOOs in this, otherwise the method will be aborted with an error message.

Return Value: None.

Caveats: None.

No. TO-PM-093

```
void sortIndividuals( vector< Individual *> & indvec );
```

Sorts all *Individuals* or *IndividualMOOs* in *indvec* according to *ascending*-flag. If the flag is set to "true", then all *Individuals* or *IndividualMOOs* are sorted by ascending fitness *fitness*, otherwise by descending fitness *fitness*.

Parameters: indvec - Vector with Individuals or IndividualMOOs to be sorted.

void sort( );

Sorts all *Individuals* or *IndividualMOO*s inside of *this* according to the setting of the ascending-flag. If the flag is set to "true", then the *Individuals* or *IndividualMOO*s will be sorted by ascending fitness values *fitness*, if it is set to "false", they will be sorted by descending fitness values *fitness*.

Parameters: None.
Return Value: None.
Caveats: None.

No. TO-PM-095

void **shuffle**( );

Randomly changes the positions of the Individuals or IndividualMOOs inside of this.

Parameters: None.
Return Value: None.
Caveats: None.

## 3.9 Compare IndividualMOOs

No. TO-PM-091

bool lessFitness( IndividualMOO\*const& i1,

Individual MOO \* i2 )

Returns whether the fitness of  $IndividualMOO\ i1$  is less than the fitness of  $IndividualMOO\ i2$ .

**Parameters:** i1 - The first Individual MOO to be compared.

i2 - The second Individual MOO to be compared.

Return Value: Status of the fitness comparison:

true - The fitness of Individual MOO i1 is less than the fitness of

Individual MOO i2,

false - The fitness of Individual MOO i1 is greater than or equal

to the fitness of Individual MOO i2.

bool greaterFitness( IndividualMOO\*const& i1, IndividualMOO\*const& i2 );

Returns whether the fitness of Individual MOO i1 is greater than the fitness of Individual MOO i2.

**Parameters:** i1 - The first Individual MOO to be compared.

i2 - The second Individual MOO to be compared.

Return Value: Status of the fitness comparison:

true - The fitness of Individual MOO i1 is greater than the fitness

of IndividualMOO i2,

false - The fitness of Individual MOO i1 is less than or equal to

the fitness of Individual MOO i2.

Caveats: None.

#### No. TO-PM-096

```
bool greaterScoreAscending( IndividualMOO* const& i1, IndividualMOO* const& i2 );
```

Auxiliary method for *selectEPTournament*. Checks whether the scaled fitness of *IndividualMOO i1* is greater or whether the normal fitness is less than the corresponding values of *IndividualMOO i2*.

**Parameters:** i1 - The first Individual MOO to be compared.

*i2* - The second *IndividualMOO* to be compared.

Return Value: true - The scaled fitness of Individual MOO i1 is greater than the

scaled fitness of IndividualMOO i2 or the normal fitness of IndividualMOO i1 is less than the normal fitness of IndividualMOO

i2.

false - The scaled fitness of Individual MOO i1 is less than the scaled fitness of Individual MOO i2 or the normal fitness of Individual MOO i1 is greater than the normal fitness of Individual MOO

i2.

bool **greaterScoreDescending**( IndividualMOO\*const& i1, IndividualMOO\*const& i2 );

Auxiliary method for *selectEPTournament*. Checks whether the scaled or normal fitness of *IndividualMOO i1* is greater than the corresponding values of *Individual-MOO i2*.

Parameters: i1 - The first Individual MOO to be compared.

i2 - The second Individual MOO to be compared.

Return Value: true - The scaled fitness of Individual MOO i1 is less than the

scaled fitness of IndividualMOO i2 or the normal fitness of IndividualMOO i1 is greater than the normal fitness of Individual-

MOO i2.

false - The scaled fitness of IndividualMOO i1 is greater than the scaled fitness of IndividualMOO i2 or the normal fitness of IndividualMOO i1 is less than the normal fitness of IndividualMOO

i2.

Caveats: None.

No. TO-PM-110

IndividualMOO& best (IndividualMOO& i1,

IndividualMOO& i2 ) const;

Returns the Individual MOO with the better fitness values.

 $\textbf{Parameters:} \hspace{0.5cm} \textit{i1 -} \hspace{0.5cm} \textbf{The first } \textit{IndividualMOO} \text{ to be compared.} \\$ 

i2 - The second Individual MOO to be compared.

Return Value: The Individual MOO with the "better" fitness according to

ascending-flag. If the flag sets to "true", then the *Individual-MOO* with the smaller fitness value will be returned, if the flag sets to "false", the *IndividualMOO* with the greater fitness value

is returned.

Returns the Individual MOO with the better fitness values.

**Parameters:** i - The index of the first IndividualMOO to be compared.

j - The index of the second Individual MOO to be compared.

Return Value: The Individual MOO with the "better" fitness according to

ascending-flag. If the flag sets to "true", then the Individual-MOO with the smaller fitness value will be returned, if the flag sets to "false", the IndividualMOO with the greater fitness value

is returned.

Caveats: None.

#### No. TO-PM-112

Returns the Individual MOO with the worst fitness values.

Parameters: i1 - The first Individual MOO to be compared.

*i2* - The second *IndividualMOO* to be compared.

Return Value: The Individual MOO with the "worst" fitness value according to

ascending-flag. If the flag sets to "true", then the IndividualMOO with the greater fitness value will be returned, if the flag sets to "false", the IndividualMOO with the smaller fitness value is

returned.

Caveats: None.

#### No. TO-PM-113

Returns the *Individual MOO* with the worst fitness values.

**Parameters:** i - The index of the first Individual MOO to be compared.

j - The index of the second *Individual MOO* to be compared.

Return Value: The Individual MOO with the "worst" fitness according to

ascending-flag. If the flag sets to "true", then the Individual-MOO with the greater fitness value will be returned, if the flag sets to "false", the IndividualMOO with the smaller fitness value

is returned.

## 3.10 Information about *IndividualMOO*s

#### No. TO-PM-120

double minFitness( ) const;

Returns the minimum fitness value inside *this*. This value is selected from all fitness values *fitness*, not MOO fitness values *MOOFitness*.

Parameters: None.

Return Value: Minimum fitness value of the PopulationMOO or 0.0, if the Pop-

ulation MOO is empty.

Caveats: None.

#### No. TO-PM-121

double maxFitness( ) const;

Returns the maximum fitness value inside *this*. This value is selected from all fitness values *fitness*, not MOO fitness values *MOOFitness*.

Parameters: None.

Return Value: Maximum fitness value of the PopulationMOO or 0.0, if the Pop-

ulation MOO is empty.

Caveats: None.

#### No. TO-PM-122

double **meanFitness**( ) const;

Returns the mean fitness value of all *IndividualMOO*s in the *PopulationMOO*.

Parameters: None

Return Value: The mean fitness value of the PopulationMOO or 0.0 if the Pop-

ulation MOO is empty.

Caveats: None.

#### No. TO-PM-123

double **stdDevFitness**( ) const;

Returns the standard deviation of all fitness values of the Population MOO computed as  $\sigma = \frac{1}{n} \sum_{i=0}^{n-1} \left[ f(this_i) - \overline{f(this_i)} \right]^2$  with n = |this|. f is the function that evaluates the fitness of an Individual MOO.

Parameters: None.

Return Value: Standard deviation of all fitness values or 0.0, if the Population-

MOO is empty.

## 3.11 Select one IndividualMOO

## 3.11.1 The best IndividualMOO

No. TO-PM-100

unsigned bestIndex( ) const;

Returns the index of the *IndividualMOO* with the best fitness value. The best fitness value depends on the value of the *ascending*-flag. If *ascending* is set to "true", the minimum fitness value is the best, if *ascending* is set to "false", the maximum fitness value is the winner. The *PopulationMOO* must contain at least one *IndividualMOO*, otherwise the method will be aborted with an error message. This method also works properly, when the *IndividualMOO*s are not already sorted.

Parameters: None.

Return Value: Index of the *Individual MOO* with the best fitness value.

Caveats: None.

No. TO-PM-104

IndividualMOO& best( );

Same as above (method bestIndex), but here not only the index of the best IndividualMOO, but the IndividualMOO itself is returned.

Parameters: None.

Return Value: Individual MOO with the best fitness value.

Caveats: None.

No. TO-PM-105

const IndividualMOO& best( ) const;

Same as above (method bestIndex), but here not only the index of the best IndividualMOO, but the IndividualMOO itself is returned.

Parameters: None.

Return Value: Individual MOO with the best fitness value.

IndividualMOO& oneOfBest();

Return one of Individual MOOs with the best fitness value. A random is used to select one of them.

Parameters: None.

Return Value: Randomly selected Individual MOO from the Individual MOOs

with the best fitness value.

Caveats: None.

No. TO-PM-103

const IndividualMOO& oneOfBest( ) const;

Return one of Individual MOOs with the best fitness value. A random is used to select one of them.

Parameters: None.

Return Value: Randomly selected Individual MOO from the Individual MOOs

with the best fitness value.

Caveats: None.

#### 3.11.2 The worst IndividualMOO

No. TO-PM-101

unsigned worstIndex( ) const;

Returns the index of the IndividualMOO with the worst fitness value. The worst fitness value depends on the value of the ascending-flag. If ascending is set to "true", the maximum fitness value is the worst, if ascending is set to "false", the minimum fitness value is the looser. The PopulationMOO must contain at least one IndividualMOO, otherwise the method will be aborted with an error message. This method also works properly, when the IndividualMOOs are not already sorted.

Parameters: None.

**Return Value:** Index of the *Individual MOO* with the worst fitness value.

#### No. TO-PM-106

IndividualMOO& worst();

Same as above (method worstIndex), but here not only the index of the worst IndividualMOO, but the IndividualMOO itself is returned.

Parameters: None.

Return Value: Individual MOO with the worst fitness value.

Caveats: None.

#### No. TO-PM-107

const IndividualMOO& worst( ) const;

Same as above (method worstIndex), but here not only the index of the worst IndividualMOO, but the IndividualMOO itself is returned.

Parameters: None.

Return Value: Individual MOO with the worst fitness value.

Caveats: None.

## 3.11.3 The randomly chosen Individual MOO

No. TO-PM-108

IndividualMOO& random( );

Returns a randomly chosen Individual MOO of this.

Parameters: None.

Return Value: An Individual MOO of this.

Caveats: None.

No. TO-PM-109

const IndividualMOO& random( ) const;

Returns a randomly chosen Individual MOO of this.

Parameters: None.

Return Value: An Individual MOO of this.

## 3.12 Selection for SOO

## 3.12.1 Preparation for Selection

#### Initialization

No. TO-PM-400
void selectInit( );

Initializes the internal variables of all Individual MOOs of the Population MOO for a following selection method.

Parameters: None.
Return Value: None.
Caveats: None.

#### Select Elitists

No. TO-PM-401

void selectElitists( PopulationMOO& offspring, unsigned numElitists );

Looks for *numElitists Individuals* with the best fitness values and copies them to the beginning of the *PopulationMOO this*. The selection probability of the elitists and the reminders of *IndividualMOO*s will be adapted.

Parameters: offspring - The mutated PopulationMOO.

numElitists - Number of elitists. If numElitists is greater than the number of IndividualMOOs in this, then only as many elitists are sought as this contains IndividualMOOs.

#### Roulette Wheel

No. TO-PM-402

void selectRouletteWheel( PopulationMOO& popmoo, unsigned numElitists );

Selects the reminders of *Individuals* after selecting elitists with a roulette wheel. The basic idea behind this selection method is a spinning roulette wheel. Depending on the value of the *spinOnce*-flag, the wheel can be spinned several times (flag = "false") which is similar to a stochastic selection or only one time (flag = "true") which is similar to a non-stochastic selection. For more information cf. [5] and [6].

Parameters: popmoo - PopulationMOO from which the reminders are

chosen after selecting elitists.

numElitists - Number of elitists to be selected.

Return Value: None. Caveats: None.

## **3.12.2** $(\mu, \lambda), (\mu + \lambda)$ Selection

No. TO-PM-410

void **selectMuLambda**( PopulationMOO& offspring, unsigned numElitists );

Selects IndividualMOOs from the mutated PopulationMOO offspring and/or from the current PopulationMOO this for reproduction. numElitists elite IndividualMOOs will be taken over from offspring and this. If numElitists is set to zero, then all current IndividualMOOs will be dismissed; this is equal to a  $(\mu, \lambda)$ -selection. If numElitists greater than zero, then this number of elitists will be taken over from both PopulationMOOs; this is equal to a  $(\mu + \lambda)$ -selection. For more information cf. [7].

**Parameters:** offspring - The mutated PopulationMOO.

numElitists - Number of elitists to be taken over from both PopulationMOOs, e.g. a parent and an offspring. The

default value is 0.

#### 3.12.3Proportional Selection

#### No. TO-PM-405

void linearDynamicScaling( vector < double > & window, unsigned long );

Scales the fitness values of all Individual MOOs of this using the scaling window window at time t. For more information about scaling methods cf. [8].

Parameters: window - Window that is used for the scaling.

> Time (that means position inside the window) at which is scaled.

Return Value: None. None.

#### No. TO-PM-412

Caveats:

void **selectProportional**( PopulationMOO& popmoo, unsigned numElitists);

Selects Individuals from the mutated PopulationMOO popmoo and the current Population MOO this for reproduction using the proportional selection, i.e. all fitness values will be adapted in a way that they are proportional to the scaled fitness values. After that, the Individual MOOs are chosen for reproduction by calling the method selectRouletteWheel.

For more information cf. [2].

Parameters: - The mutated *PopulationMOO* to be selected. popmoo

> numElitists -Number of elitists to be taken over. If numElitists is zero, then a proportional selection takes place. If the value is greater than zero, numElitists elitists will be taken over from both Population-*MOO*s and the rest will be selected from *popmoo*.

Return Value: None.

Caveats: The fitness values of all *IndividualMOO*s of the population must

be positive.

No. TO-PM-413

IndividualMOO& selectOneIndividual( );

Selects an Individual MOO for reproduction by using proportional selection, i.e. the selection probability of all *Individual MOO*s will be adapted to scaled fitness values. After that, an Individual MOO will be chosen by calling the method select Roulette-Wheel.

For more information cf. [2].

Parameters: None.

Return Value: The selected Individual MOO.

Caveats: The fitness values of all *IndividualMOO*s must be positive.

#### 3.12.4Ranking Selection

#### Linear Ranking

No. TO-PM-418

void selectLinearRanking( PopulationMOO& offspring, double etaMax, numElitistsunsigned );

Selects Individual MOOs from the Population MOO offspring for reproduction by using the method of Linear Ranking, i.e. each Individual MOO receives a selection probability based upon its "ranking" inside the PopulationMOO. The ranking is determined by the order of the Individual MOOs referring to descending fitness values. After evaluating the probabilities, the *IndividualMOO*s are selected using the method selectRoulette Wheel. Additionally numElitists elitists can be taken over from the current *PopulationMOO* and the mutated *PopulationMOO*.

For more information cf. [10] and [12].

Parameters: offspring- The mutated *PopulationMOO*.

> etaMaxMaximum reproduction rate, the default value is

numElitists -Number of elitists to be taken over from both Pop-

ulation MOOs. The default is set to 0.

Return Value: None. Caveats: None.

## Whitlye's Linear Ranking

No. TO-PM-419

void **selectLinearRankingWhitley**( PopulationMOO& offspring, double unsigned numElitists

Same as above, but here the evaluation of the selection probability differs. For more information cf. [14].

Parameters: offspring The mutated *PopulationMOO*.

Maximum reproduction rate, the default value is

set to 1.1.

numElitists -Number of elititst to be taken over from both Pop-

ulationMOOs. The default is 0.

## **Uniform Ranking**

No. TO-PM-416

void selectUniformRanking( PopulationMOO& offspring, unsigned numElitists );

Selects Individual MOOs from the Population MOO offspring for reproduction using the method of select Uniform Ranking, i.e. each Individual MOO receives the same selection probability and the method  $select Roulette\ Wheel$  is used for selection. Additionally numElitists elitits can be taken over from the current Population MOO this and the mutated Population MOO offspring. For more information cf. [2].

Parameters: offspring - The mutated PopulationMOO from which elititsts

can be taken over.

numElitists - Number of elititsts. The default value is 0.

Return Value: None.

Caveats: None.

No. TO-PM-417

void reproduce( PopulationMOO& offspring,

unsigned numElitists);

Same as method selectUniformRanking.

Parameters: offspring - See above.

numElitists - See above.

#### 3.12.5 Tournament Selection

#### No. TO-PM-414

void selectTournament(	PopulationMOO& offspring,		
	unsigned	q,	
	unsigned	num Elitists	);

Selects the best IndividualMOO out of a randomly chosen group of q Individual-MOOs from the mutated PopulationMOO offspring and takes it over to the new PopulationMOO this. This selection is repeated as long as there are free slots in the new PopulationMOO. Additionally numElitists elitists can be taken over from offspring and this. No correction of the selection probabilities for elitists will take place.

For more information cf. [8].

**Parameters:** offspring - The mutated PopulationMOO.

q - Number of tournament opponents, the default

number is 2.

numElitists - Number of elitists to be taken over from both Pop-

ulation MOOs, the default value is 0.

Return Value: None. Caveats: None.

## 3.12.6 EP-Style Tournament Selection

#### No. TO-PM-415

void selectEPTournament(	PopulationMOO& offspring,		
	unsigned	q	);

Selects IndividualMOOs from the mutated PopulationMOO offspring and the PopulationMOO this by using the EP-style Tournament Selection by D. B. Fogel. Each IndividualMOO of both PopulationMOOs has to compete against q randomly chosen individuals of the PopulationMOOs this and offspring. An IndividualMOO wins a round, when it has collected more wins during the last round, i.e. when its fitness value was better than the value of its opponent. If two IndividualMOOs have the same number of wins, then the IndividualMOO with the better fitness value wins. For more information cf. [15].

**Parameters:** offspring - The mutated PopulationMOO.

q - Number of opponents for each Individual MOO.

#### 3.12.7 Other Selections

#### No. TO-PM-411

PopulationMOO& offspring,		
unsigned	lifespan,	
unsigned	adolescence  );	

Selects some IndividualMOOs from the PopulationMOO this and its mutated PopulationMOO offspring for reproduction. The "youngest" IndividualMOOs will be chosen first, i.e. those IndividualMOOs, whose age is less than the value of adolescence. Second, those IndividualMOOs will be selected, which do not belong to the set of "youngest", but whose lifespan has not reached the value lifespan yet. Older IndividualMOOs will be dismissed.

**Parameters:** offspring - The mutated PopulationMOO.

 ${\it lifespan} \qquad {\it -} \quad {\rm Maximum\ lifespan\ of\ an}\ {\it Individual MOO}, \ {\rm the\ de-}$ 

fault value is 1.

adolescence - An Individual MOO must have fallen short of this

age to be in the set of "youngest" Individual-

MOOs. The default value is 0.

## 3.13 Ranking

## 3.13.1 Domination

#### No. TO-PM-210

```
int Dominate( unsigned i1, unsigned i2 );
```

Checks the relationship between  $Individual MOOs\ i1$  and i2 according to the value ascending.

Parameters: i1 - The index of Individual MOO which is compared.

i2 - The index of Individual MOO which is compared.

Return Value: the following value which shows the relationship between Individ-

 $ualMOOs\ i1$  and i2.

3: i1 dominates i2 strongly. 2: i1 dominates i2 weakly.

1: i1 equals i2.

0: The error occured in the calculation.

-1: There is a trade-off relationship between i1 and i2.

-2: *i2* dominates *i1* weakly. -3: *i2* dominates *i1* strongly.

Caveats: None.

#### 3.13.2 MOGA

## Goldberg

```
No. TO-PM-212
```

```
{\bf void} \ \ {\bf MOGAGoldbergRank} ( \hspace{0.5cm} );
```

Calculates the rank of *IndividualMOO*s according to the value *ascending* by Goldberg's method and sets these values to *MOORank*.

## Fonseca & Flemming

No. TO-PM-211

```
void MOGAFonsecaRank( );
```

Calculates the rank of Individual MOOs according to the value ascending by Fonseca & Flemming's method and sets these values to MOORank.

Parameters: None.
Return Value: None.
Caveats: None.

## 3.13.3 NSGA II

No. TO-PM-213

```
void NSGAIIRank( );
```

Calculates the rank of Individual MOOs according to the value ascending by NSGA II method and sets these values to MOORank. The complexity of this calculation is  $o(N^2)$ .

## 3.14 Transfer MOO to SOO

#### 3.14.1 Rank

No. TO-PM-250

void MOORankToFitness( );

Transfers the data of rank MOORank to the variable fitness.

In the minimization problem, the original values of MOORank are copied to fitness. In the maximization problem, the values R in the following equation are copied to fitness.

 $R_i = max(MOORank_j, j \in PopulationMOO) - MOORank_i + 1.$ 

Parameters: None.
Return Value: None.
Caveats: None.

## 3.14.2 Aggregation

No. TO-PM-251

void Aggregation( const vector< double >& weight );

Calculates the weighted sum of MOOFitness and sets it to fitness.

**Parameters:** weight - The vector which stores the weight.

Return Value: None. Caveats: None.

No. TO-PM-252

void SimpleSum( );

Calculates the sum of MOOFitness and sets it to fitness.

## 3.14.3 One of MOOFitness

## No. TO-PM-253

void SimpleTransferFitness( unsigned i );

Picks up one of MOOFitness and sets it to fitness.

 $\textbf{Parameters:} \hspace{5mm} i \hspace{3mm} \text{-} \hspace{3mm} \text{The index of objective function which you want to use as} \\$ 

single objective function.

## 3.15 Selection Probability

## 3.15.1 Preparation

No. TO-PM-450

void NormalizeSelectProb( );

Normailzes selection probability of all Individual MOOs in this.

Parameters: None.
Return Value: None.
Caveats: None.

## 3.15.2 Michalewicz

No. TO-PM-451

void SelectProbMichalewicz( double c );

Calculates the selection probability of all *IndividualMOO*s in *this*.

**Parameters:** c - The constant c in the following equation.

 $p = c \times (1.0 - c)^{r-1}$ 

Here r shows the rank. The default value is 0.075.

#### 3.16 Distance on Phenotypic Fitness Space

In MOO-EALib, I prepared the following distances.

$$N_1 = \sum_{i}^{n} |x_i - y_i| \tag{3.1}$$

$$N_{1} = \sum_{i}^{n} |x_{i} - y_{i}|$$

$$N_{2} = \sqrt{\sum_{i}^{n} (x_{i} - y_{i})^{2}}$$
(3.1)

$$N_{\infty} = \max(|x_i - y_i|, i = 1, ..., n)$$
(3.3)

#### No. TO-PM-600

double PhenoFitDisN1( unsigned i1, unsigned i2);

Calculates the  $N_1$  distance between Individual MOOs i1 and i2.

i1 - The index of Individual MOO. Parameters:

i2 - The index of Individual MOO.

**Return Value:** The  $N_1$  distance between Individual MOOs i1 and i2.

Caveats: None.

No. TO-PM-601

double PhenoFitDisN2( unsigned i1, unsigned i2);

Calculates the  $N_2$  distance between Individual MOOs i1 and i2.

i1 - The index of Individual MOO. Parameters:

i2 - The index of Individual MOO.

**Return Value:** The  $N_2$  distance between IndividualMOOs i1 and i2.

Caveats: None.

No. TO-PM-602

double PhenoFitDisNM( unsigned i1, unsigned i2);

Calculates the  $N_{\infty}$  distance between *IndividualMOOs* i1 and i2.

i1 - The index of Individual MOO. Parameters:

i2 - The index of Individual MOO.

**Return Value:** The  $N_{\infty}$  distance between *IndividualMOOs* i1 and i2.

## 3.17 Sharing

#### 3.17.1 Niche Count

#### No. TO-PM-700

```
unsigned NicheCountPFN1( unsigned i1, double sr);
```

Calculates Niche count with sharing radius sr. The return value means the number of IndividualMOOs within sharing radius sr. The distance is calculated by  $N_1$ .

**Parameters:** i1 - The index of Individual MOO.

sr - Sharing radius.

**Return Value:** Niche count with sharing radius sr. The distance is calculated by

 $N_1$ .

Caveats: None.

#### No. TO-PM-701

```
unsigned NicheCountPFN2( unsigned i1, double sr );
```

Calculates Niche count with sharing radius sr. The return value means the number of IndividualMOOs within sharing radius sr. The distance is calculated by  $N_2$ .

**Parameters:** i1 - The index of Individual MOO.

sr - Sharing radius.

**Return Value:** Niche count with sharing radius sr. The distance is calculated by

 $N_2$ .

Caveats: None.

#### No. TO-PM-702

```
unsigned NicheCountPFNM( unsigned i1, double sr );
```

Calculates Niche count with sharing radius sr. The return value means the number of IndividualMOOs within sharing radius sr. The distance is calculated by  $N_{\infty}$ .

**Parameters:** i1 - The index of Individual MOO.

sr - Sharing radius.

**Return Value:** Niche count with sharing radius sr. The distance is calculated by

 $N_{\infty}$ .

#### No. TO-PM-703

```
void NicheCountPFN1( double sr );
```

Calculates Niche counts with sharing radius sr for all Individual MOOs and sets them to MOOShares. The distance is calculated by  $N_1$ .

**Parameters:** sr - Sharing radius.

Return Value: None. Caveats: None.

No. TO-PM-704

```
void NicheCountPFN2( double sr );
```

Calculates Niche counts with sharing radius sr for all Individual MOOs and sets them to MOOShares. The distance is calculated by  $N_2$ .

**Parameters:** sr - Sharing radius.

Return Value: None.

Caveats: None.

No. TO-PM-705

```
void NicheCountPFNM( double sr );
```

Calculates Niche counts with sharing radius sr for all IndividualMOOs and sets them to MOOShares. The distance is calculated by  $N_{\infty}$ .

**Parameters:** sr - Sharing radius.

## 3.17.2 Sharing Function ( $s = 1.0 - \frac{d}{\sigma_{share}}$ )

#### No. TO-PM-710

```
double SharingTriPFN1( unsigned i1, double sr);
```

Calculates sharing value by  $1.0 - \frac{N_1}{sr}$ . Here  $N_1$  and sr are a distance and a sharing radius, respectively.

**Parameters:** i1 - The index of Individual MOO.

sr - Sharing radius.

**Return Value:** Sharing value by  $1.0 - \frac{N_1}{sr}$ .

Caveats: None.

## No. TO-PM-711

```
double SharingTriPFN2( unsigned i1, double sr);
```

Calculates sharing value by  $1.0 - \frac{N_2}{sr}$ . Here  $N_2$  and sr are a distance and a sharing radius, respectively.

**Parameters:** i1 - The index of Individual MOO.

sr - Sharing radius.

**Return Value:** Sharing value by  $1.0 - \frac{N_2}{sr}$ .

Caveats: None.

#### No. TO-PM-712

```
double SharingTriPFNM( unsigned i1, double sr);
```

Calculates sharing value by  $1.0-\frac{N_{\infty}}{sr}$ . Here  $N_{\infty}$  and sr are a distance and a sharing radius, respectively.

**Parameters:** i1 - The index of *IndividualMOO*.

sr - Sharing radius.

**Return Value:** Sharing value by  $1.0 - \frac{N_{\infty}}{sr}$ .

#### void **SharingTriPFN1**( double sr );

Calculates sharing values by  $1.0-\frac{N_1}{sr}$  for all Individual MOOs and sets them to MOOS hares. Here  $N_1$  and sr are a distance and a sharing radius, respectively.

**Parameters:** sr - Sharing radius.

Return Value: None.
Caveats: None.

#### No. TO-PM-714

```
void SharingTriPFN2( double sr );
```

Calculates sharing values by  $1.0 - \frac{N_2}{sr}$  for all Individual MOOs and sets them to MOOS hares. Here  $N_2$  and sr are a distance and a sharing radius, respectively.

**Parameters:** sr - Sharing radius.

Return Value: None. Caveats: None.

#### No. TO-PM-715

```
void SharingTriPFNM( double sr );
```

Calculates sharing values by  $1.0-\frac{N_{\infty}}{sr}$  for all Individual MOOs and sets them to MOOShares. Here  $N_{\infty}$  and sr are a distance and a sharing radius, respectively.

**Parameters:** sr - Sharing radius.

Return Value: None.
Caveats: None.

### 3.17.3 Sharing Function ( $s = 1.0 - (\frac{d}{\sigma_{share}})^p$ )

#### No. TO-PM-720

```
double SharingPowPFN1( unsigned i1, double sr, double pw);
```

Calculates sharing value by  $1.0 - (\frac{N_1}{sr})^{pw}$ . Here  $N_1$ , sr and pw are a distance, a sharing radius and an exponent, respectively.

**Parameters:** i1 - The index of *IndividualMOO*.

sr - Sharing radius. pw - The exponent.

**Return Value:** Sharing value by  $1.0 - (\frac{N_1}{sr})^{pw}$ .

Caveats: None

#### No. TO-PM-721

```
double SharingPowPFN2( unsigned i1, double sr, double pw);
```

Calculates sharing value by  $1.0 - (\frac{N_2}{sr})^{pw}$ . Here  $N_2$ , sr and pw are a distance, a sharing radius and an exponent, respectively.

**Parameters:** i1 - The index of Individual MOO.

sr - Sharing radius. pw - The exponent.

**Return Value:** Sharing value by  $1.0 - (\frac{N_2}{sr})^{pw}$ .

Caveats: None.

#### No. TO-PM-722

Calculates sharing value by  $1.0 - (\frac{N_{\infty}}{sr})^{pw}$ . Here  $N_{\infty}$ , sr and pw are a distance, a sharing radius and an exponent, respectively.

**Parameters:** i1 - The index of Individual MOO.

sr - Sharing radius. pw - The exponent.

**Return Value:** Sharing value by  $1.0 - (\frac{N_{\infty}}{sr})^{pw}$ .

Caveats: None.

```
void SharingPowPFN1( double sr, double pw );
```

Calculates sharing values by  $1.0 - (\frac{N_1}{sr})^{pw}$  for all Individual MOOs and sets them to MOOShares. Here  $N_1$ , sr and pw are a distance, a sharing radius and an exponent, respectively.

**Parameters:** sr - Sharing radius.

pw - The exponent.

Return Value: None.

Caveats: None.

#### No. TO-PM-724

```
void SharingPowPFN2( double sr, double pw );
```

Calculates sharing values by  $1.0 - (\frac{N_2}{sr})^{pw}$  for all Individual MOOs and sets them to MOOShares. Here  $N_2$ , sr and pw are a distance, a sharing radius and an exponent, respectively.

**Parameters:** sr - Sharing radius.

pw - The exponent.

Return Value: None.

Caveats: None.

#### No. TO-PM-725

```
\begin{array}{ccc} \text{void} & \textbf{SharingPowPFNM}( & \text{double } \textit{sr}, \\ & \text{double } \textit{pw} & ); \end{array}
```

Calculates sharing values by  $1.0 - (\frac{N_{\infty}}{sr})^{pw}$  for all Individual MOOs and sets them to MOOS hares. Here  $N_{\infty}$ , sr and pw are a distance, a sharing radius and an exponent, respectively.

**Parameters:** sr - Sharing radius.

pw - The exponent.

Return Value: None.
Caveats: None.

#### 3.17.4 Share values

#### No. TO-PM-790

```
void SharingSelProb( );
```

Shares a selection probability. The calculation will be done by  $p_{share} = \frac{p}{s}$ . Here  $p_{share}$ , p and s are a shared selection probability, an original selection probability and a sharing value ( or Niche count ). After this calculation, normalization of selection probability should be done.

Parameters: None.
Return Value: None.
Caveats: None.

#### No. TO-PM-791

```
void SharingFitness( );
```

Shares a fitness value for SOO. The calculation will be done by  $f_{share} = \frac{f}{s}$ . Here  $f_{share}$ , f and s are a shared fitness value, an original fitness value and a sharing value ( or Niche count ).

Parameters: None.
Return Value: None.
Caveats: None.

#### No. TO-PM-792

```
void SharingMOOFitness( );
```

Shares fitness values for MOO. The calculation will be done by  $f_{share} = \frac{f}{s}$ . Here  $f_{share}$ , f and s are a shared fitness value, an original fitness value and a sharing value ( or Niche count ).

Parameters: None.
Return Value: None.
Caveats: None.

#### 3.18 Selection for MOO

#### 3.18.1 Preparation

No. TO-PM-800

void **SelectByRoulette**( PopulationMOO& offsprings, unsigned elit );

Selects Individual MOOs after selecting elit elitists with a roulette wheel.

**Parameters:** offsprings - The mutated PopulationMOO.

elit - The number of elitists which have been selected al-

ready.

Return Value: None. Caveats: None.

#### 3.18.2 Tournament Selection

No. TO-PM-801

void SelectTournamentNCPFN1( PopulationMOO& offsprings, double share, unsigned elit );

Selects IndividualMOOs after selecting elit elitsits with Tournament selection. Two IndividualMOOs are selected randomly. If one IndividualMOO dominates the other, then this IndividualMOO is selected. If the trade-off relationship among IndividualMOOs exists, the IndividualMOO with small niche count is selected. If niche counts are the same, IndividualMOO is selected randomly.  $N_1$  distance is used on Phenotypic Fitness space to calculate the distance.

**Parameters:** offsprings - The mutated PopulationMOO.

share - The sharing radius.

elit - The number of elitists which have been selected al-

ready.

Return Value: None.

Caveats: NCPFN1 means "Niche Count", "Phenotypic Fitness space" and

" $N_1$  distance".

void **SelectTournamentNCPFN2**( PopulationMOO& offsprings, double share, unsigned elit );

See the function whose number is "TO-PM-801".  $N_2$  distance is used on Phenotypic Fitness space to calculate the distance.

**Parameters:** offsprings - The mutated PopulationMOO.

share - The sharing radius.

elit - The number of elitists which have been selected al-

ready.

Return Value: None.

Caveats: NCPFN2 means "Niche Count", "Phenotypic Fitness space" and

" $N_2$  distance".

No. TO-PM-803

See the function whose number is "TO-PM-801".  $N_{\infty}$  distance is used on Phenotypic Fitness space to calculate the distance.

**Parameters:** offsprings - The mutated PopulationMOO.

share - The sharing radius.

elit - The number of elitists which have been selected al-

ready.

Return Value: None.

Caveats: NCPFNM means "Niche Count", "Phenotypic Fitness space" and

" $N_{\infty}$  distance".

## void SelectTournamentSTPFN1( PopulationMOO& offsprings, double double share, unsigned elit );

Selects IndividualMOOs after selecting elit elitsits with Tournament selection. Two IndividualMOOs are selected randomly. If one IndividualMOO dominates the other, then this IndividualMOO is selected. If the trade-off relationship among IndividualMOOs exists, the IndividualMOO with small sharing value is selected. If sharing values are the same, IndividualMOO is selected randomly. The sharing function  $s=1.0-\frac{d}{\sigma_{share}}$  and  $N_1$  distance are used on Phenotypic Fitness space to calculate the distance.

 $\textbf{Parameters:} \qquad \textit{offsprings} \ \ \text{-} \quad \text{The mutated } \textit{PopulationMOO}.$ 

share - The sharing radius.

elit - The number of elitists which have been selected al-

ready.

Return Value: None.

Caveats: STPFN1 means "Sharing function  $s = 1.0 - \frac{d}{\sigma_{share}}$ ", "Phenotypic

Fitness space" and " $N_1$  distance".

No. TO-PM-805

void SelectTournamentSTPFN2(	PopulationMOO& offsprings,		
	double	share,	
	unsigned	elit	);

See the function whose number is "TO-PM-804". The sharing function  $s=1.0-\frac{d}{\sigma_{share}}$  and  $N_2$  distance are used on Phenotypic Fitness space to calculate the distance.

**Parameters:** offsprings - The mutated PopulationMOO.

share - The sharing radius.

elit - The number of elitists which have been selected al-

ready.

Return Value: None.

Caveats: STPFN2 means "Sharing function  $s = 1.0 - \frac{d}{\sigma_{share}}$ ", "Phenotypic

Fitness space" and " $N_2$  distance".

# void **SelectTournamentSTPFNM**( PopulationMOO& offsprings, double share, unsigned elit );

See the function whose number is "TO-PM-804". The sharing function  $s=1.0-\frac{d}{\sigma_{share}}$  and  $N_{\infty}$  distance are used on Phenotypic Fitness space to calculate the distance.

**Parameters:** offsprings - The mutated PopulationMOO.

share - The sharing radius.

elit - The number of elitists which have been selected al-

ready.

Return Value: None.

Caveats: STPFNM means "Sharing function  $s = 1.0 - \frac{d}{\sigma_{share}}$ ", "Phenotypic

Fitness space" and " $N_{\infty}$  distance".

No. TO-PM-807

PopulationMOC	0& offspring	$\overline{s}$ ,
double	share,	
double	pow,	
${ m unsigned}$	elit	);
	double double	double $pow$ ,

Selects IndividualMOOs after selecting elit elitsits with Tournament selection. Two IndividualMOOs are selected randomly. If one IndividualMOO dominates the other, then this IndividualMOO is selected. If the trade-off relationship among IndividualMOOs exists, the IndividualMOO with small sharing value is selected. If sharing values are the same, IndividualMOO is selected randomly. The sharing function  $s=1.0-(\frac{d}{\sigma_{share}})^p$  and  $N_1$  distance are used on Phenotypic Fitness space to calculate the distance.

 $\textbf{Parameters:} \qquad \textit{offsprings} \; \text{--} \quad \text{The mutated } \textit{PopulationMOO}.$ 

share - The sharing radius.

pow - The exponent in the sharing function.

elit - The number of elitists which have been selected al-

ready.

Return Value: None.

Caveats: SPPFN1 means "Sharing function  $s = 1.0 - (\frac{d}{\sigma_{share}})^p$ ", "Pheno-

typic Fitness space" and " $N_1$  distance".

#### void SelectTournamentSPPFN2( PopulationMOO& offsprings, double share, double pow,unsigned elit);

See the function whose number is "TO-PM-807". The sharing function s=1.0 $(\frac{d}{\sigma_{share}})^p$  and  $N_2$  distance are used on Phenotypic Fitness space to calculate the distance.

Parameters: offsprings - The mutated PopulationMOO.

> shareThe sharing radius.

The exponent in the sharing function. pow

The number of elitists which have been selected alelit

ready.

Return Value: None.

SPPFN2 means "Sharing function  $s=1.0-(\frac{d}{\sigma_{share}})^p$ ", "Phenotypic Fitness space" and " $N_2$  distance". Caveats:

No. TO-PM-809

$\overline{\text{void } \mathbf{SelectTournamentSPPFNM}(}$	( PopulationMOO& offsprings,		$\eta s,$
	double	share,	
	double	pow,	
	unsigned	elit	);

See the function whose number is "TO-PM-807". The sharing function s=1.0 $(\frac{d}{\sigma_{share}})^p$  and  $N_{\infty}$  distance are used on Phenotypic Fitness space to calculate the distance.

Parameters: The mutated Population MOO. offsprings -

> The sharing radius. share

powThe exponent in the sharing function.

elitThe number of elitists which have been selected al-

ready.

Return Value: None.

SPPFNM means "Sharing function  $s=1.0-(\frac{d}{\sigma_{share}})^p$ ", "Phenotypic Fitness space" and " $N_{\infty}$  distance". Caveats:

#### 3.18.3 Tournament Selection with a comparison set

#### No. TO-PM-810

${\bf void} \ \ {\bf SelectComparisonNCPFN1} ($	PopulationMOO&	off springs,	
	unsigned	nc,	
	double	share,	
	unsigned	elit	);

Selects IndividualMOOs after selecting elit elitsits. Two IndividualMOOs are selected randomly and also nc IndividualMOOs are selected randomly as a comparison set. If one IndividualMOO dominates all IndividualMOOs in the comparison set and the other doesn't, then this IndividualMOO is selected. In the other cases, the IndividualMOO with small niche count is selected. If niche counts are the same, IndividualMOO is selected randomly.  $N_1$  distance is used on Phenotypic Fitness space to calculate the distance.

 $\textbf{Parameters:} \qquad \textit{offsprings} \; - \; \; \text{The mutated} \; \textit{PopulationMOO}.$ 

nc - The number of Individual MOOs in the comparison

set.

share - The sharing radius.

elit - The number of elitists which have been selected al-

ready.

Return Value: None.

Caveats: NCPFN1 means "Niche Count", "Phenotypic Fitness space" and

" $N_1$  distance".

#### No. TO-PM-811

void SelectComparisonNCPFN2(	PopulationMOO&	offsprings,	
	unsigned	nc,	
	double	share,	
	unsigned	elit	);

See the function whose number is "TO-PM-810".  $N_2$  distance is used on Phenotypic Fitness space to calculate the distance.

**Parameters:** offsprings - The mutated PopulationMOO.

nc - The number of Individual MOOs in the comparison

set.

share - The sharing radius.

elit - The number of elitists which have been selected al-

ready.

Return Value: None.

Caveats: NCPFN2 means "Niche Count", "Phenotypic Fitness space" and

" $N_2$  distance".

#### 

See the function whose number is "TO-PM-810".  $N_{\infty}$  distance is used on Phenotypic Fitness space to calculate the distance.

**Parameters:** offsprings - The mutated PopulationMOO.

nc - The number of Individual MOOs in the comparison

 $\operatorname{set}.$ 

share - The sharing radius.

elit - The number of elitists which have been selected al-

ready

Return Value: None.

Caveats: NCPFNM means "Niche Count", "Phenotypic Fitness space" and

" $N_{\infty}$  distance".

#### No. TO-PM-813

void	${\bf Select Comparison STPFN1} ($	Population MOO&	$of\! f\! springs,$	
		unsigned	nc,	
		double	share,	
		unsigned	elit	);

Selects IndividualMOOs after selecting elit elitsits. Two IndividualMOOs are selected randomly and also nc IndividualMOOs are selected randomly as a comparison set. If one IndividualMOO dominates all IndividualMOOs in the comparison set and the other doesn't, then this IndividualMOO is selected. In the other cases, the IndividualMOO with small sharing value is selected. If sharing values are the same, IndividualMOO is selected randomly. The sharing function  $s=1.0-\frac{d}{\sigma_{share}}$  and  $N_1$  distance is used on Phenotypic Fitness space to calculate the distance.

**Parameters:** offsprings - The mutated PopulationMOO.

nc - The number of Individual MOOs in the comparison

set.

share - The sharing radius.

elit - The number of elitists which have been selected al-

ready.

Return Value: None.

Caveats: STPFN1 means "Sharing function  $s = 1.0 - \frac{d}{\sigma_{share}}$ ", "Phenotypic

Fitness space" and " $N_1$  distance".

void **SelectComparisonSTPFN2**( PopulationMOO& offsprings,

nc, double share, unsigned elit

);

See the function whose number is "TO-PM-813". The sharing function  $s=1.0-\frac{d}{\sigma_{share}}$  and  $N_2$  distance is used on Phenotypic Fitness space to calculate the distance.

Parameters: offsprings - The mutated PopulationMOO.

nc - The number of Individual MOOs in the comparison

 $\operatorname{set}.$ 

share - The sharing radius.

elit - The number of elitists which have been selected al-

ready.

Return Value: None.

Caveats: STPFN2 means "Sharing function  $s = 1.0 - \frac{d}{\sigma_{share}}$ ", "Phenotypic

Fitness space" and " $N_2$  distance".

No. TO-PM-815

 ${\tt void} \ \ \textbf{SelectComparisonSTPFNM} ( \ \ \ \ Population MOO\& \ \textit{offsprings},$ 

 $\begin{array}{ccc} & & & & & \\ & & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ &$ 

See the function whose number is "TO-PM-813". The sharing function  $s=1.0-\frac{d}{\sigma_{share}}$  and  $N_{\infty}$  distance is used on Phenotypic Fitness space to calculate the distance.

**Parameters:** offsprings - The mutated PopulationMOO.

nc - The number of Individual MOOs in the comparison

 $\operatorname{set}$ .

share - The sharing radius.

elit - The number of elitists which have been selected al-

ready.

Return Value: None.

Caveats: STPFNM means "Sharing function  $s=1.0-\frac{d}{\sigma_{share}}$ ", "Phenotypic

Fitness space" and " $N_{\infty}$  distance".

$\overline{\text{void } \mathbf{SelectComparisonSPPFN1}(}$	PopulationMOO& offsprings,		
	unsigned	nc,	
	double	share,	
	double	pow,	
	unsigned	elit	);

Selects Individual MOOs after selecting elit elitsits. Two Individual MOOs are selected randomly and also nc Individual MOOs are selected randomly as a comparison set. If one Individual MOO dominates all Individual MOOs in the comparison set and the other doesn't, then this Individual MOO is selected. In the other cases, the Individual MOO with small sharing value is selected. If sharing values are the same, Individual MOO is selected randomly. The sharing function  $s=1.0-(\frac{d}{\sigma_{share}})^p$  and  $N_1$  distance is used on Phenotypic Fitness space to calculate the distance.

 $offsprings \ - \ \ {\rm The \ mutated} \ Population MOO.$ Parameters:

The number of *Individual MOO*s in the comparison

set.

shareThe sharing radius.

- The exponent in the sharing function. pow

The number of elitists which have been selected alelit

ready.

Return Value: None.

SPPFN1 means "Sharing function  $s=1.0-(\frac{d}{\sigma_{share}})^p$ ", "Phenotypic Fitness space" and " $N_1$  distance". Caveats:

# voidSelectComparisonSPPFN2(PopulationMOO& offsprings,<br/>unsigned<br/>double<br/>offsprings,<br/>unsigned<br/>offsprings,<br/>double<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,<br/>offsprings,

See the function whose number is "TO-PM-816". The sharing function  $s=1.0-(\frac{d}{\sigma_{share}})^p$  and  $N_2$  distance is used on Phenotypic Fitness space to calculate the distance.

**Parameters:** offsprings - The mutated PopulationMOO.

nc - The number of Individual MOOs in the comparison

 $\operatorname{set}.$ 

share - The sharing radius.

pow - The exponent in the sharing function.

elit - The number of elitists which have been selected al-

ready.

Return Value: None.

Caveats: SPPFN2 means "Sharing function  $s = 1.0 - (\frac{d}{\sigma_{share}})^p$ ", "Pheno-

typic Fitness space" and " $N_2$  distance".

No. TO-PM-818

voidSelectComparisonSPPFNM(PopulationMOO& offsprings,<br/>unsignednc,<br/>doubledoubleshare,<br/>doublepow,<br/>unsignedunsignedelit);

See the function whose number is "TO-PM-816". The sharing function  $s=1.0-(\frac{d}{\sigma_{share}})^p$  and  $N_{\infty}$  distance is used on Phenotypic Fitness space to calculate the distance.

**Parameters:** offsprings - The mutated PopulationMOO.

nc - The number of Individual MOOs in the comparison

set.

share - The sharing radius.

pow - The exponent in the sharing function.

elit - The number of elitists which have been selected al-

ready.

Return Value: None.

Caveats: SPPFNM means "Sharing function  $s = 1.0 - (\frac{d}{\sigma_{share}})^p$ ", "Pheno-

typic Fitness space" and " $N_{\infty}$  distance".

#### 3.18.4 Elitists for MOO

In MOO-EALib, I used the following words:

elitist: The Individual MOO with Rank 1 and niche count (sharing value) 1.

sub-elitist: The Individual MOO with Rank 1.

It is clear that the set of *sub-elitists* includes the whole set of *elitists*.

#### No. TO-PM-850

```
bool EvaluationMOOElitists( unsigned i1 );
```

Evaluates i1th Individual MOO. If this individual MOO is an elitist, "True" will be returned. If not, "False" will be returned.

**Parameters:** i1 - The index of *IndividualMOO* which is evaluated.

Return Value: True: This Individual MOO is an elitist.

False: This Individual MOO is not an elitist.

Caveats: None.

#### No. TO-PM-851

```
unsigned getNoOfRankOne( );
```

Gets the number of Individual MOOs with Rank 1.

Parameters: None.

Return Value: The number of Individual MOOs with Rank 1.

Caveats: None.

unsigned SelectMOOElitists(	PopulationMOO&	z offsprings,
	unsigned	MOR,
	unsigned	MOS,
	double	SR,
	double	POW );

Selects elitists and gets the number of *IndividualMOO*s which are selected as elitists.

Parameters: offsprings - The mutated PopulationMOO.

MOR - The function number ( 211 - 213 ) for Rank. MOS - The function number ( 703 - 725 ) for sharing.

SR - The sharing radius.

POW - The exponent in the sharing function. If powed

sharing function is used, this value is valid.

Return Value: The number of Individual MOOs which are selected as elitists.

Caveats: None.

#### No. TO-PM-853

${\it unsigned} \ \ {\bf SelectMOOElitistsSub} ($	PopulationMOO&	z offsprings,	
	unsigned	MOR,	
	unsigned	MOS,	
	double	SR,	
	double	POW	);

Selects sub-elitists and gets the number of Individual MOOs which are selected as sub-elitists.

**Parameters:** offsprings - The mutated PopulationMOO.

MOR - The function number ( 211 - 213 ) for Rank. MOS - The function number ( 703 - 725 ) for sharing.

SR - The sharing radius.

POW - The exponent in the sharing function. If powed

sharing function is used, this value is valid.

Return Value: The number of Individual MOOs which are selected as sub-elitists.

Caveats: None.

## Chapter 4

## Conclusion

In this report, we explained the functions in MOO-EALib. Chapter 2 and 3 can be used as the manual of MOO-EALib.

Now, we are concluding this report. But, the development of MOO-EALib is ongoing. Every day, some functions are added in MOO-EALib and some functions are updated. Of course, if some functions have bugs, then they will be corrected. Thus, this report is on our way to our final goal. Probably, some additional reports are necessary in the near future to support new functions. In that time, we will write some additional reports.

We will promise them !!!

## Acknowledgement

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