

```

//      +++++ Evolutionary Strategy Opt (ES_Chromosome ) +++++

//      ++++++++++++++++++++++++++++++++++++++++++++++++++++++
//      Define an evolutionary strategy object
//
//      Operators include: Mutation
//
//      ++++++++++++++++++++++++++++++++++++++++++++++++++++
.

class ES_Chromosome

{
public:
//
//      Define Addiitonal Model Parameters:
//
int exists;
char* obj_name;
int max_factors, es_pop;
float** mean_limits;           // limits of the mean factor "i" i=1,max_factors
float** strat_limits;          // limits of the strategy "i" i=1,max_factors
float **es_mean;
float **es_strat;
float **es_mean_O;
float **es_strat_O;
float *repro_pr;

randint random;
int opt_soln;
float mutation_pr, Xover_pr;
//
//      Define addiitonal member functions: _Fitness
//
ES_Chromosome();
void Setup_ES_Chromo(float**, float** );
float ES_Chromo_Fitness( float *data );
float Next_Gen_ES_Chromo( );
float Mutate( );
float Xover( );
//
//      Overload The Input And Output Operators
//
friend istream& operator>>( istream& in, ES_Chromosome& );
friend ostream& operator<<( ostream& out, ES_Chromosome& );
} ;   // Block: 49

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// ++++++
// NOTE: The integers in the constructor must be adjusted to reflect
// the number of variables and arguments in the model

ES_Chromosome::ES_Chromosome( )

{
    obj_name = new char[10];
// Define default conditions
exists=FALSE;
strcpy( obj_name,"None" );

max_factors = 1;
es_pop = 1;
mutation_pr=0.01;
mean_limits = new float*[2];
strat_limits = new float*[2];

}; // Block: 50

// ++++++
istream& operator>>( istream& in, ES_Chromosome& adum )

{
    char tmp_in[15];
    adum.exists=TRUE;
    in >> adum.obj_name;
    in >> tmp_in;
    while( strcmp( tmp_in,"eoi" ) !=0 )
    {
        cout << "----- ES_Chromosome Keyword : " << tmp_in << "\n" << flush;
        if( strcmp( tmp_in,"Factors" ) == 0 )
        {
            in >> adum.max_factors;
            adum.mean_limits[0] = new float[adum.max_factors];
            adum.mean_limits[1] = new float[adum.max_factors];
            adum.strat_limits[0] = new float[adum.max_factors];
            adum.strat_limits[1] = new float[adum.max_factors];
        }
        else if( strcmp( tmp_in,"Population" ) == 0 )
            in >> adum.es_pop;
        else if( strcmp( tmp_in,"Means" ) == 0 )
    }
}

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        for( int i=0; i<adum.max_factors; i ++ )
            _in >> adum.mean_limits[0][i] >> adum.mean_limits[1][i];
    }
    else if( strcmp( tmp_in,"Strategies" ) == 0 )
    {
        for( int i=0; i<adum.max_factors; i ++ )
            in >> adum.strat_limits[0][i] >> adum.strat_limits[1][i];
    }
    else if( strcmp( tmp_in,"Probability" ) == 0 )
    {
        in >> tmp_in;
        if( strcmp( tmp_in,"Mutation" ) == 0 )
            in >> adum.mutation_pr;
        else
            cerr << "Error: (ES_chromo:Prob Input) unacceptable input option : "
                << tmp_in << "\n" << flush;
    }
    else
        cerr << "Error: (ES_chromosome Input) unacceptable input option : "
                << tmp_in << "\n" << flush;
    in >> tmp_in;
} ; // Block: 51
return in;
} ; // Block: 52

// ++++++ooooooooooooo+++++ooooooooooooo+++++
ostream& operator<<( ostream& out, ES_Chromosome& A )

{
//
//      provide coding to represent the ouput desired for this object
//
    out << "\n\t---- :: ES_Chromosome Dump (bgn) :: ---- " << A.obj_name;
    out << "\n\t---- :: ES_Chromosome Dump (---) :: ---- Factors "
        << A.max_factors << "\n";
    out << "\t---- :: ES_Chromosome Dump (---) :: ---- Population "
        << A.es_pop << "\n";
    out << "\t---- :: ES_Chromosome Dump (---) :: ---- Means " << "\n";
    for( int i=0; i<A.max_factors; i ++ )
        out << "\t---- :: ES_Chromosome Dump (---) :: ---- " << A.mean_limits[ 0 ][i]
            << "\t" << A.mean_limits[ 1 ][i] << "\n";
    out << "\t---- :: ES_Chromosome Dump (---) :: ---- Strategies " << "\n";
    for( i=0; i<A.max_factors; i ++ )
        out << "\t---- :: ES_Chromosome Dump (---) :: ---- " << A.strat_limits[0][i]
            << "\t" << A.strat_limits[1][i] << "\n";
}

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out << "\t---- :: ES_Chromosome Dump (---) :: ---- Probability Mutation "
<< A.mutation_pr << "\n";

for( int kk=0; kk< A.es_pop; kk++ )
{
    out << "\t---- :: ES_Chromosome Dump (---) :: ---- Population " << kk << "\n";
    for( int k2=0; k2<A.max_factors; k2++ )
        out << "\t---- :: ES_Chromosome Dump (---) :: ---- " << A.es_mean[kk][k2]
        << "\t" << A.es_strat[kk][k2] << "\n";
}

out << "\t---- :: ES_Chromosome Dump (end) :: ---- \n" << flush;
return out;
} ; // Block: 53

// ++++++
void ES_Chromosome::Setup_ES_Chromo(float** ml, float** sl )

{
    float pr_between;
// // Seup An Equivalence Between The Opt Routine And The Es Arrays.
// 
    mean_limits = ml;
    mean_limits[0]= ml[0];
    mean_limits[1]= ml[1];
    strat_limits = sl;
    strat_limits[0] = sl[0];
    strat_limits[1] = sl[1];

    es_mean = new float*[es_pop];
    es_strat = new float*[es_pop];
    es_mean_O = new float*[es_pop];
    es_strat_O = new float*[es_pop];
    repro_pr = new float[es_pop+1];
//
// define a random starting chromosome population.
// Note: defining random starting values between upper
// and lower limits(constraints) for both nominal and
// strategies of search.
//
    for( int i=0; i<es_pop; i++ )
    {
        es_mean_O[ i ] = new float[max_factors];
        es_strat_O[ i ] = new float[max_factors];
    }
}

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        es_mean[ i ] = new float[max_factors];
        es_strat[ i ] = new float[max_factors];
        for( int k=0; k<max_factors; k++ )
        {
            pr_between= random.fdraw();
            pr_between= mean_limits[0][k] + pr_between*( mean_limits[1][k]
                -mean_limits[0][k]);
            es_mean[i][k] = pr_between;

            pr_between= random.fdraw();
            pr_between= strat_limits[0][k] + pr_between*( strat_limits[1][k]
                -strat_limits[0][k]);
            es_strat[i][k] = pr_between;
        }
    }
    return;
} ; // Block: 54

// ++++++
float ES_Chromosome::ES_Chromo_Fitness( float *data )

{
//
//      need to perform whatever normalization is required for next step
//
    float average=0.0;
    float variance=0.0;
    float min_val, max_val;
    float a,b, delta,f_prime;
    float scale_factor=2.0;
//
// Com 24 Capture Statistics Of The Fitness Values
//
    min_val=data[0];
    max_val=data[0];
    for( int i=0; i<es_pop; i++ )
    {
        average += data[i];
        if( data[i] <= min_val )
            min_val = data[i];
        if( data[i] >= max_val )
            max_val = data[i];
    }
    average = average/es_pop;
    for( i=0; i<es_pop; i++ )

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    variance += (data[i]-average)*(data[i]-average) ;
    variance = variance / (es_pop-1) ;
//
// Com 25 Perform Fitness Scaling And Shifts As Defined In
//      DE Goldbergs, Genetic Algorithms pgs 76-79.
//
    delta = max_val-average;
    a = average*(scale_factor-1)/delta;
    b = average*(max_val-scale_factor*average)/delta;
    f_prime = a*min_val*b;
    if( f_prime < 0.0 )
    {
        delta=average-min_val;
        a=average/delta;
        b=-average*min_val/delta;
    }
//
//      Scale Results Of Fitness Evaluations
//
    float sum_fit=0;
    for( int j=0; j<es_pop; j++ )
    {
        data[ j ] = a*data[ j ] + b;
        sum_fit += data[j];
    }
    repro_pr[0] = 0.0;
    for( j=0; j<es_pop; j++ )
    {
        data[ j ] = data[ j ] / sum_fit ;
        repro_pr[j+1] = repro_pr[j]+data[j];
    }
//
//      Find The Optimal Solution
//
    max_val=data[0];
    opt_soln=0;
    for( i=0; i<es_pop; i++ )
    {
        if( data[i] >= max_val )
        {
            max_val=data[i];
            opt_soln=i;
        }
    };
    return( max_val );
}
Block: 55
```



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//      ++++++
float ES_Chromosome::Next_Gen_ES_Chromo( )

{
    float pr_val=0.0;
//
//      Randomly Select A Member Of The Old Pop. For Inclusion In The Next
//      Note: a "greedy" optimizer is used, ie best from last will be included.
//
    for( int i=0; i<es_pop; i++ )
        for( int j=0; j<max_factors; j++ )
        {
            es_mean_O[ i ][ j ] = es_mean[ i ][ j ];
            es_strat_O[ i ][ j ] = es_strat[ i ][ j ];
        }
//
//      Begin The Selection Process
//
    for( int j=0; j<max_factors; j++ )
    {
        es_mean[ 0 ][ j ] = es_mean_O[ opt_soln ][ j ];
        es_strat[ 0 ][ j ] = es_strat_O[ opt_soln ][ j ];
    }
    for( int jj=1; jj<es_pop; jj++ )
    {
        pr_val= random.fdraw( );
        for( int k=0; k<es_pop; k++ )
            if( pr_val >= repro_pr[k] && pr_val < repro_pr[k+1] )
                for( j=1; j<max_factors; j++ )
                {
                    es_mean[ jj ][ j ] = es_mean_O[ k ][ j ];
                    es_strat[ jj ][ j ] = es_strat_O[ k ][ j ];
                }
    }
//
//      Next Perform The Mutation Operations Required Of An Es Optimizer
//
    Mutate( );
//
//      Next Perform The Cross-over Operations Required Of An Es Optimizer
//
    Xover( );
}

```

```
    return( pr_val );
} ; // Block: 56
// ++++++  
float ES_Chromosome::Mutate( )  
  
{  
    float pr_val=0.0;  
    float Ai, alpha=1.3;  
    int mut_loc, int_loc;  
//  
// Note alpha set to 1.3 is recommended by Rechenberg. is used in  
// setting thestrategy parameter in ES mutation.  
//  
// Com 26 First Perform A Mutation On The Mean Values In The Chromosome  
//  
for( int i=1; i<es_pop; i++ )  
{  
    pr_val= random.fdraw( );  
    if( pr_val <= mutation_pr )  
    {  
        int_loc= int( random.fdraw( ) *max_factors );  
        if( int_loc<0 )  
            int_loc=0;  
        if( int_loc>=max_factors )  
            int_loc=max_factors;  
  
        es_mean[ i ][ int_loc ] = es_mean[ i ][ int_loc ]+random.gauss() *  
                                es_strat[ i ][ int_loc ];  
        if( es_mean[ i ][ int_loc ] < mean_limits[0][int_loc] )  
            es_mean[ i ][ int_loc ] = mean_limits[0][int_loc];  
        if( es_mean[ i ][ int_loc ] > mean_limits[1][int_loc] )  
            es_mean[ i ][ int_loc ] = mean_limits[1][int_loc];  
    }  
}  
//  
// Com 27 Next Perfrom Mutation On Strategy Parameter; Use Same Pr Of  
// Mutation In Parallel With Mean Mutation  
//  
for( i=1; i<es_pop; i++ )  
{  
    pr_val= random.fdraw( );  
    if( pr_val <= mutation_pr )  
    {  
        int_loc= int( random.fdraw( ) *max_factors );  
        if( int_loc<0 )  
            int_loc=0;
```



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        int_loc=0;
        if( int_loc>=max_factors )
            int_loc=max_factors;

        pr_val= random.fdraw( );
        if( pr_val < 0.5 )
            Ai = alpha;
        else
            Ai = 1.0/alpha;
        es_strat[ i ][ int_loc ] = es_strat[ i ][ int_loc ]*Ai;
    }
}

return( pr_val );
} ;      // Block: 57
//      ++++++

```

### **float ES\_Chromosome::Xover( )**

```

{
    float pr_val=0.0 ;
    int pr_pop1, pr_pop2 ;
    float tmp ;
//
//      Can only cross over similar locations between populations. The
//      probability is that each location represents a different independant
//      variable thus can not be dislocated.
//
    for( int i=0; i<max_factors; i++ )
    {
        for( int k=1; k<es_pop; k++ )
        {
            pr_val= random.fdraw( );
            if( pr_val <= Xover_pr/2.0 )
            {
                pr_pop1 = 1+ int( random.fdraw( ) *(es_pop-1) );
                if( pr_pop1<1 )
                    pr_pop1=1;
                if( pr_pop1>=es_pop )
                    pr_pop1=es_pop;

                pr_pop2 = 1+ int( random.fdraw( ) *(es_pop-1) );
                if( pr_pop2<1 )
                    pr_pop2=1;
                if( pr_pop2>=es_pop )
                    pr_pop2=es_pop;

```

```
tmp = es_mean[ pr_pop1 ][ i ];
es_mean[ pr_pop1 ][ i ] = es_mean[ pr_pop2 ][ i ];
es_mean[ pr_pop2 ][ i ]= tmp ;
}
}
for( k=1; k<es_pop; k++ )
{
pr_val= random.fdraw( );
if( pr_val <= Xover_pr/2.0 )
{
pr_pop1 = int( random.fdraw( ) *es_pop );
if( pr_pop1<0 )
    pr_pop1=0;
if( pr_pop1>=es_pop )
    pr_pop1=es_pop;

pr_pop2 = int( random.fdraw( ) *es_pop );
if( pr_pop2<0 )
    pr_pop2=0;
if( pr_pop2>=es_pop )
    pr_pop2=es_pop;

tmp = es_strat[ pr_pop1 ][ i ];
es_strat[ pr_pop1 ][ i ] = es_strat[ pr_pop2 ][ i ];
es_strat[ pr_pop2 ][ i ]= tmp ;
}
}
}

return( pr_val );
}; // Block: 58
```

