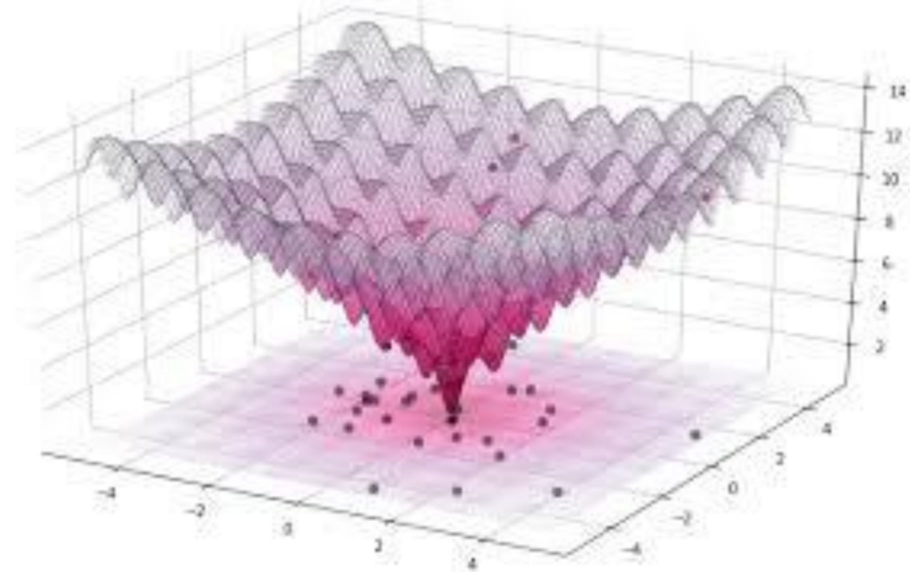
University of Ljubljana, Faculty of Computer and Information Science

Differential evolution and its variants



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Analysis of Algorithms and Heuristic Problem Solving
Version 2024

Idea of differential evolution

- Storn and Price, 1997
- Metaheuristic
- Optimization in R^a
- No need for gradient vector
- Combines ideas from evolutionary computation

Some slides taken from Hossein Talebi and Hassan Nikoo.

Template of evolutionary program

```
generate a population of agents (objects, data structures)
do {
    compute fitness (quality) of the agents
    select candidates for the reproduction using fitness
    create new agents by combining the candidates
    replace old agents with new ones
} while (not satisfied)
```

- immensely general -> many variants

Crossover

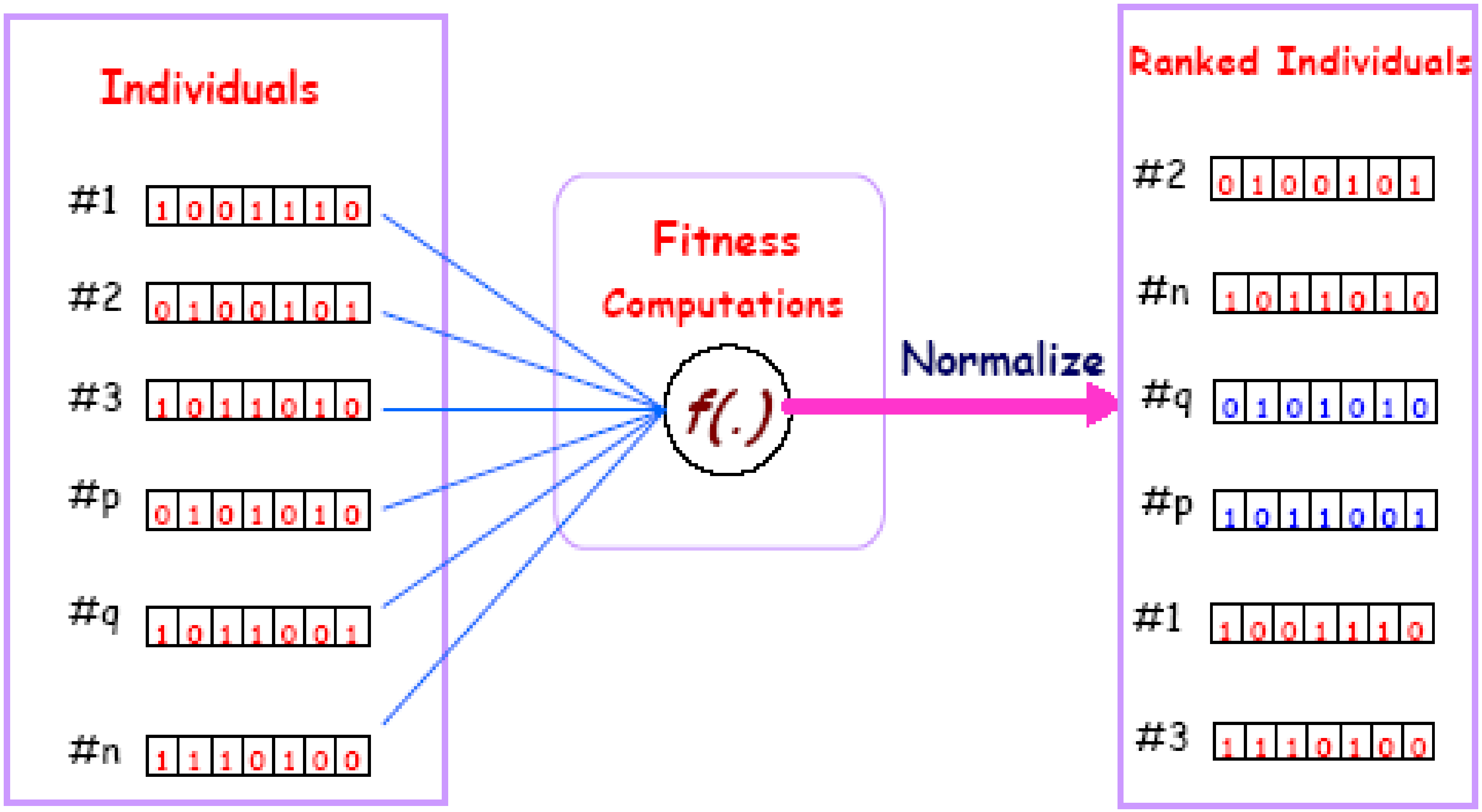
- Single point/multipoint
- Shall preserve individual objects

Crossover: bit representation

Parents: 1101011100 0111000101

Children: 1101010101 0111001100

A fitness function



Crossover: vector representation

Simplest form

Parents: (6.13, 4.89, 17.6, 8.2) (5.3, 22.9, 28.0, 3.9)

Children: (6.13 , 22.9, 28.0, 3.9) (5.3, 4.89, 17.6, 8.2)

In reality: linear combination of parents

Linear crossover

- The linear crossover simply takes a linear combination of the two individuals.
- Let $x = (x_1, \ldots x_N)$ and $y = (y_1, \ldots y_N)$
- Select α in $(0, 1)$
- The results of the crossover is $\alpha x + (1 - \alpha) y$.
- Possible variation: choose a different α for each position.

Mutation

- Adding new information
- Random search?
- Binary representation:
  0111001100 --> 0011001100
- Single point/multipoint
- Lamarckian (searching for locally best mutation)

Gaussian mutation

- When mutating one gene, selecting the new value by choosing uniformly among all the possible values is not the best choice (empirically).
- The mutation selects a position i in the vector of floats and mutates it by adding a Gaussian error: a value extracted according to a normal distribution with mean 0 and variance depending on the problem.

DE introduction

- The original DE was developed for continuous value problems

- Individuals are vectors $x_i, i \in [1..n_s]$ of dimension n_s

- Distance and direction information from current population is used to guide the search process

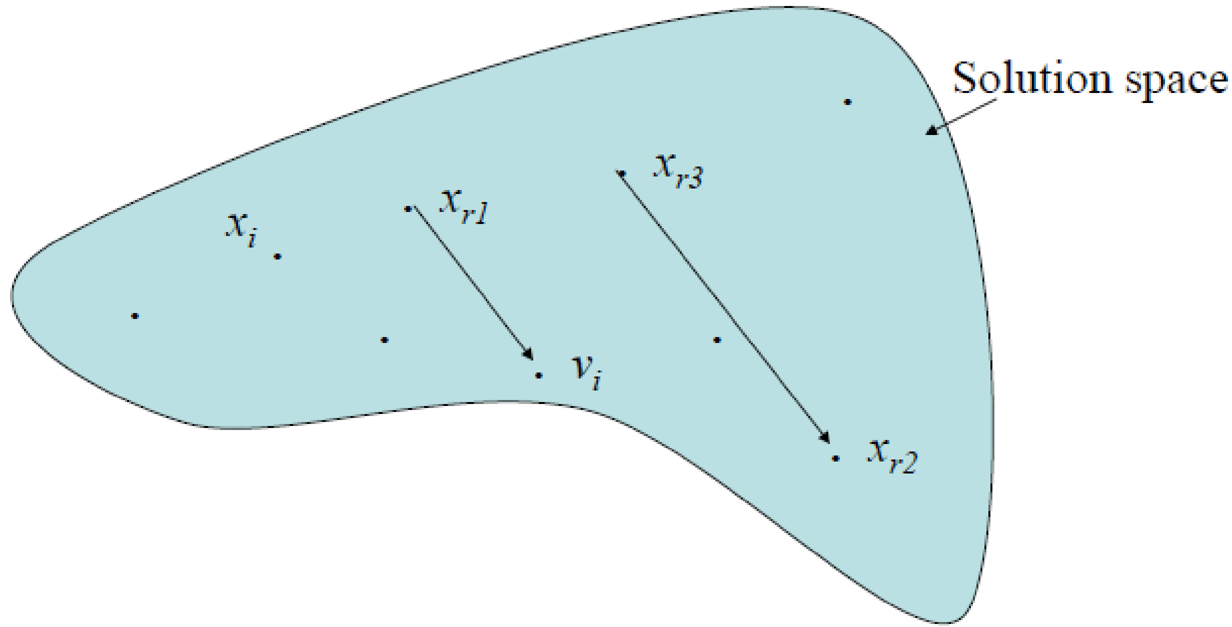
DE background

- DE/rand/1
- Emphasizes mutation but still uses cross-over
- Generate trial vectors (u, mutant, donor) using the following formula:

$$u_i = x_{r1} + \beta\ (x_{r2}\ - x_{r3})$$

- Self-organizing ability

Illustration



Difference of DE with other EAs

1. Mutation is applied first to generate trial vectors, then cross-over is applied to produce offspring

2. Mutation step size is not sampled from prior known PDF (probability density function), it is influenced by difference between individuals of the current population

Difference Vector

- Positions of individuals provide valuable information about fitness landscape.
- At first, individuals are distributed over the search space, and over the time they converge to the same solution
- Differences are large in the beginning of evolution; therefore, we have bigger step size (exploring)
- Differences are smaller at the end of search process; therefore we have smaller step size (exploiting)

DE mutation

- Mutation produces a trial vector for each individual
- This trial vector is then used by the crossover operator to produce offspring
- For each parent $x_i(t)$, we make a trial vector $u_i(t)$

Target vector

$$\mathbf{u}_i(t) = \mathbf{x}_{i_1}(t) + \beta(\mathbf{x}_{i_2}(t) - \mathbf{x}_{i_3}(t))$$

Weighted Differential

$$i_2, i_3 \sim U(1, n_s)$$

$$\beta \in (0, \infty)$$

$$i \neq i_1 \neq i_2 \neq i_3$$

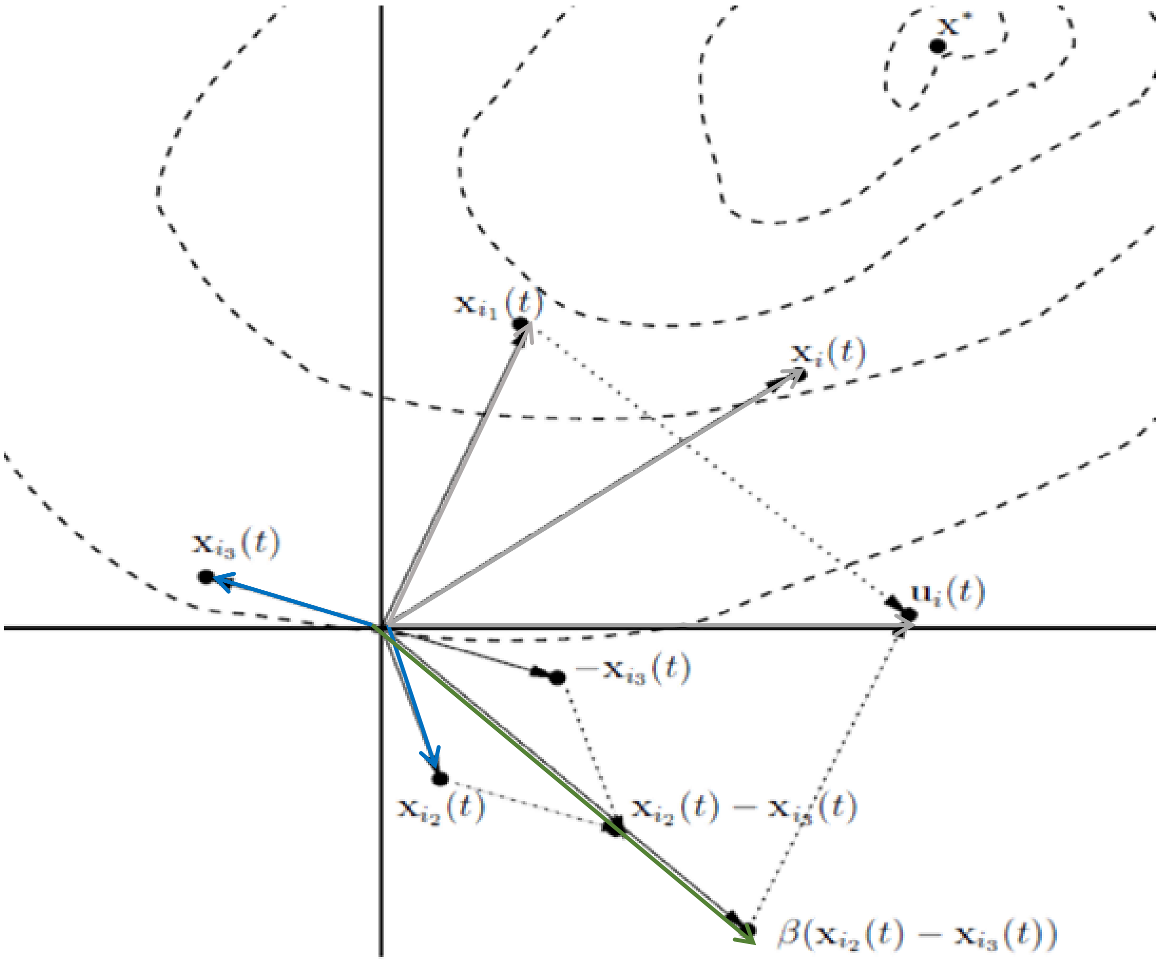
General DE Algorithm

Set the generation counter, $t = 0$;
Initialize the control parameters, β and p_r;
Create and initialize the population, $\mathcal{C}(0)$, of n_s individuals;
while *stopping condition(s) not true* **do**
  for *each individual*, $\mathbf{x}_i(t) \in \mathcal{C}(t)$ **do**
    Evaluate the fitness, $f(\mathbf{x}_i(t))$;
    Create the trial vector, $\mathbf{u}_i(t)$ by applying the mutation operator;
    Create an offspring, $\mathbf{x}_i'(t)$, by applying the crossover operator;
    if $f(\mathbf{x}_i'(t))$ *is better than* $f(\mathbf{x}_i(t))$ **then**
      Add $\mathbf{x}_i'(t)$ to $\mathcal{C}(t+1)$;
    end
    else
      Add $\mathbf{x}_i(t)$ to $\mathcal{C}(t+1)$;
    end
  end
end
Return the individual with the best fitness as the solution;

$$\mathbf{u}_i(t) = \mathbf{x}_{i_1}(t) + \beta(\mathbf{x}_{i_2}(t) - \mathbf{x}_{i_3}(t))$$

$$x_{ij}'(t) = \begin{cases} u_{ij}(t) & \text{if } j \in \mathcal{J} \\ x_{ij}(t) & \text{otherwise} \end{cases}$$

Geometrical Illustration (mutation)



$$\mathbf{u}_i(t) = \mathbf{x}_{i_1}(t) + \beta(\mathbf{x}_{i_2}(t) - \mathbf{x}_{i_3}(t))$$

Crossover

- DE crossover is a recombination of trial vector $u_i(t)$ and parent vector $x_i(t)$ to produce offspring $x_i'(t)$

$$x'_{ij}(t) = \begin{cases} u_{ij}(t) & \text{if } j \in \mathcal{J} \\ x_{ij}(t) & \text{otherwise} \end{cases}$$

Methods to determine $\mathcal{J}$

- Binomial crossover:
- we add at least one, each dimension is independent from others

Problem dimension (n_x)

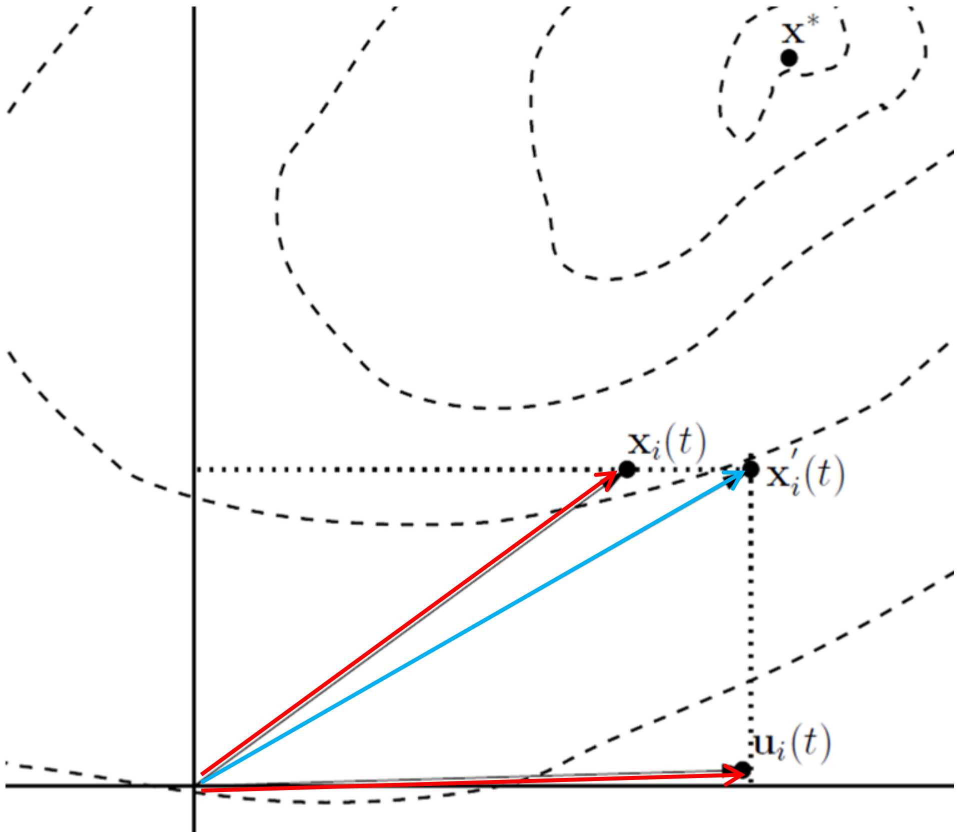
$$
\begin{aligned}
&j^* \sim U(1, n_x);\\
&\mathcal{J} \leftarrow \mathcal{J} \cup \{j^*\};\\
&\textbf{for } each\ j \in \{1, \ldots, n_x\} \textbf{ do}\\
&\quad \textbf{if } U(0,1) < p_r\ and\ j \neq j^* \textbf{ then}\\
&\quad\quad \mathcal{J} \leftarrow \mathcal{J} \cup \{j\};\\
&\quad \textbf{end}\\
&\textbf{end}
\end{aligned}
$$

Methods to determine $\mathcal{J}$

- Exponential crossover:
- we add a connected sequence of dimensions (good for e.g., permutations)

$$
\begin{aligned}
&\mathcal{J} \leftarrow \{\};\\
&j \sim U(0, n_x - 1);\\
&\textbf{repeat}\\
&\quad \mathcal{J} \leftarrow \mathcal{J} \cup \{j+1\};\\
&\quad j = (j+1) \bmod n_x;\\
&\textbf{until } U(0,1) \geq p_r \;\; or \; |\mathcal{J}| = n_x;
\end{aligned}
$$

Geometrical Illustration (crossover)



$$x_{ij}^{'}(t) = \begin{cases} u_{ij}(t) & \text{if } j \in \mathcal{J} \\ x_{ij}(t) & \text{otherwise} \end{cases}$$

Selection

- For mutation to make the trial vector, it selects
  - A random individual
  - A target vector
  - The best individual
  - One of the best individuals
- Selection between a parent and offspring for the next generation
  - The better survives

Control Parameters

Scaling factor β also called F $\beta \in (0, \infty)$

$$\mathbf{u}_i(t) = \mathbf{x}_{i_1}(t) + \beta(\mathbf{x}_{i_2}(t) - \mathbf{x}_{i_3}(t))$$

- The smaller the value of β the smaller the step size
- Shall be small enough to allow differentials to exploit tight valleys, and large enough to maintain diversity.
- Empirical results suggest that β=0.5 generally provides good performance

Control Parameters

Recombination probability p_r also called P_{CR} (crossover probability)

- The higher p_r the more variation is introduced in the new population
- Increasing p_r often results in faster convergence, while decreasing p_r increases search robustness

Notation DE/x/y/z

- x - the vector to be mutated
  - rand (randomly choosen from population)
  - best (from current population)
  - current-to-best (linear combination of current and best)
  - pbest (one of the best, randomly selected
- y - the number of difference vectors used, i.e. 1 or 2, or more
- z – the crossover scheme:
  - bin – binomial (nearly binomial distribution of selected components from donors in random selection from U(0,1) < P_{CR})
  - exp – exponential (selection of components from donor following the random dimension from 1..a, and additional number of components which is a random number from 1..a (circular); useful when nearby components are related)
  - arithmetic recombination $u_i = x_i + k_i\,(v_i - x_i)$, k_i being the same for all components (line recombination) or different for each component

- We previously discussed: DE/rand/1/bin
- population size: typically between 5d and 10d, some variants use dynamic reduction of population size

$\mathbf{DE/best/1/}z$

- Target vector is the best individual in current population $\widehat{x(t)}$,
- One differential vector is used.
- Any of the crossover methods.

$$\mathbf{u}_i(t) = \hat{\mathbf{x}}(t) + \beta(\mathbf{x}_{i_2}(t) - \mathbf{x}_{i_3}(t))$$

$\mathbf{DE}/x/n_v/z$

- Any method for the target vector selection
- More than one difference vector
- Any of the crossover methods

$$\mathbf{u}_i(t) = \mathbf{x}_{i_1}(t) + \beta \sum_{k=1}^{n_v} (\mathbf{x}_{i_2,k}(t) - \mathbf{x}_{i_3,k}(t))$$

- The larger the value of n_v, the more directions can be explored per generation.

DE/rand-to-best/n_v/z

- $\boldsymbol{x}_{i_1}(t)$ is randomly selected
- The closer γ is to 1, the more greedy the search process
- Value of γ close to 0 favors exploration.

$$\mathbf{u}_i(t) = \gamma\hat{\mathbf{x}}(t) + (1-\gamma)\mathbf{x}_{i_1}(t) + \beta\sum_{k=1}^{n_v}(\mathbf{x}_{i_2,k}(t) - \mathbf{x}_{i_3,k}(t))$$

DE/current-to-best/$1+n_v$/z

- At list two difference vectors.

1. Calculated from the best vector and the parent vector
2. While the rest of the difference vectors are calculated using randomly selected vectors

$$\mathbf{u}_i(t) = \mathbf{x}_i(t) + \beta(\hat{\mathbf{x}}(t) - \mathbf{x}_i(t)) + \beta \sum_{k=1}^{n_v} (\mathbf{x}_{i_1,k}(t) - \mathbf{x}_{i_2,k}(t))$$

- Empirical studies have shown **DE/current-to-best/2/bin** shows **good convergence characteristics**

Popular mutation strategies

- DE/rand/1

$$u_i = x_{r1} + \beta\,(x_{r2} - x_{r3})$$

- DE/best/1

$$u_i = x_{best} + \beta\,(x_{r1} - x_{r2})$$

- DE/current-to-best/1

$$u_i = x_i + \beta(x_{best} - x_i) + \beta(x_{r1} - x_{r2}), \beta < 1$$

- DE/best/2

$$u_i = x_{best} + \beta(x_{r1} - x_{r2}) + \beta(x_{r3} - x_{r4})$$

- DE/rand/2

$$u_i = x_{r1} + \beta(x_{r2} - x_{r3}) + \beta(x_{r4} - x_{r5})$$

Hybridization of DE

- Combinations with Particle Swarm Optimization (PSO):
  - Mixtures of populations
  - Mixtures of PSO and DE runs
- Combinations with Genetic Algorithms (GA):
  - Applying GA mutation or Gaussian noise
  - Applying DE mutation and/or crossover in GA
  - Rank based selection in DE
  - Etc.
- Dynamic parameter tuning: dynamic decrease, dependence on fitness, etc.

Many application

- Multiprocessor synthesis
- Neural network learning
- Synthesis of modulators
- Heat transfer parameter estimation
- Radio network design
- …

DE for discrete problems

- For integers: round continuous values
- For binary discrete problems (bit vectors)
  - Limit continuous values to [0, 1] and treat them as probabilities
  - Use angle modulation
- For constraints: use penalization in objective function

Angle modulation DE 1/2

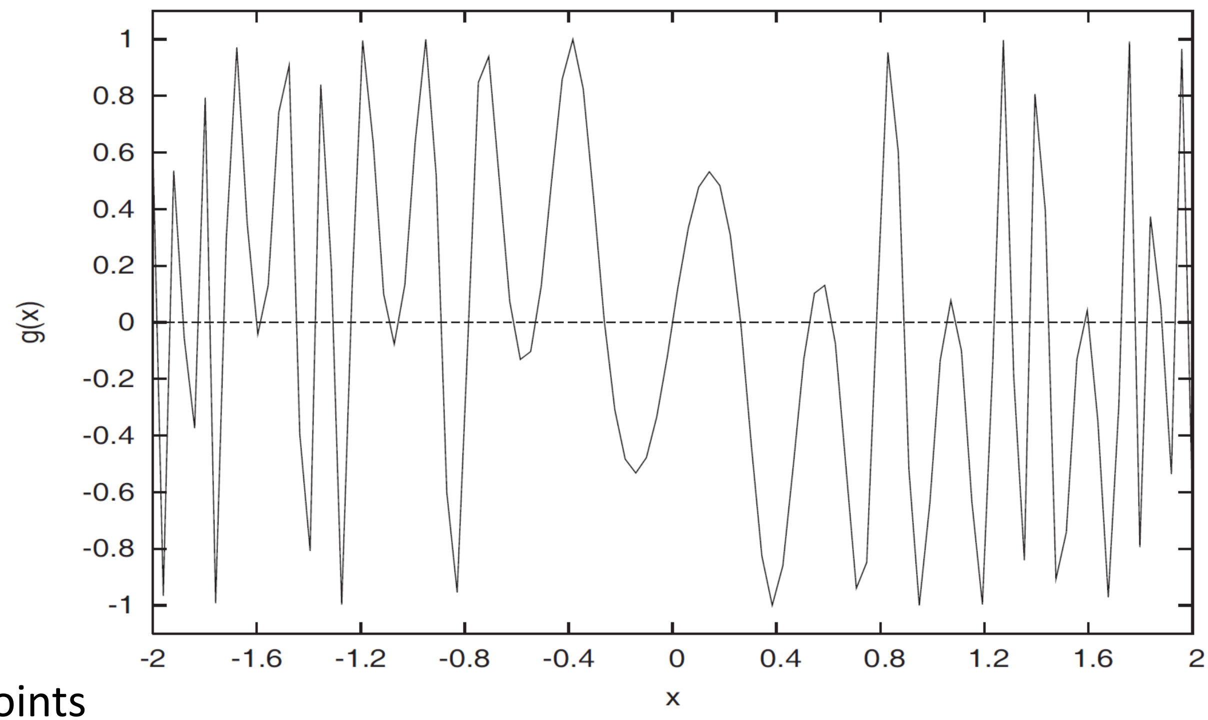
- Bit generator function, example

$$g(x) = \sin(2\pi(x-a) \times b \times \cos(2\pi(x-a) \times c)) + d$$

a = horizontal shift
b = maximum frequency of sin
c=maximum frequency of cos
d=verical shift

a=0, b=1, c=1, d=0

x=[-2, 2]
sample at equal width points
if value > 0, set bit to 1, otherwise to 0



Angle modulation DE 2/2

- use DE to learn good a, b, c, and d

Generate a population of 4-dimensional individuals;
repeat
    Apply any DE strategy for one iteration;
    for *each individual* **do**
        Substitute evolved values for coefficients a, b, c and d into equation
        Produce n_x bit-values to form a bit-vector solution;
        Calculate the fitness of the bit-vector solution in the original bit-valued space;
    end
until *a convergence criterion is satisfied*;

Modern DE variants

- Idea: record history of successful parameters (β, p_r, and n_s) and sample from it for future generations
- SHADE (success-history based adaptive differential evolution)
- Uses DE/current-to-pbest/1/bin DE-strategy, archive A, and an adaptation of control parameters β, p_r,
- DE/current-to-pbest/1

$$u_i = x_i + \beta\left(x_{pbest} - x_i\right) + \beta\,(x_{r1} - x_{r2}), \beta < 1$$

- Where point x_{pbest} is randomly chosen from p*100% of best points
- Archive A is initialized as an empty set
- Each point x_i, which is replaced by its better trial point u_i, is included into archive A during the search process.
- The archive A is adjusted after each generation to have maximal size of n_s, where members removed from A are chosen randomly
- x_{pbest} is chosen from population P, x_{r1} and x_{r2} are chosen from the union of P and A
- L-SHADE (success-history based adaptive differential evolution with linear reduction of population size)

L-SHADE pseudocode

- M_{CR} and M_F are memories of successful P_{CR} and F (i.e. β) parameters
- S_{CR} and S_F are temporal memories of P_{CR} and F parameters
- H is history size

$g \leftarrow 1$, Archive $\mathbf{A} \leftarrow \emptyset$

Initialize population $\mathbf{P}_g = (\vec{x}_{i,g}, \ldots, \vec{x}_{NP,g})$ randomly

Set all values in M_{CR}, M_F to 0.5;

$k \leftarrow 1$ // *index counter*

while the termination criatera are not meet **do**

    $S_{CR} \leftarrow \emptyset, S_F \leftarrow \emptyset$

    for $i = 1$ **to** NP **do**

        $r_i \leftarrow$ select from $[1, H]$ randomly // $H = 6$

        if $M_{CR,r_i} = \perp$ ***then***

            $CR_{i,g} \leftarrow 0$

        else

            $CR_{i,g} \leftarrow \mathcal{N}_i(M_{CR,r_i}, 0.1)$ // *Normal distribution*

        end if

        $F_{i,g} \leftarrow \mathcal{C}_i(M_{F,r_i}, 0.1)$ // *Cauchy distribution*

        $\vec{u}_{i,g} \leftarrow$ *current-to-pBest/1/bin*

    end for

    for $i = 1$ **to** NP **do**

        if $f(\vec{u}_{i,g}) \leq f(\vec{x}_{i,g})$ **then**

            $\vec{x}_{i,g+1} \leftarrow \vec{u}_{i,g}$

        else

            $\vec{x}_{i,g+1} \leftarrow \vec{x}_{i,g}$

        end if

        if $f(\vec{u}_{i,g}) < f(\vec{x}_{i,g})$ **then**

            $\vec{x}_{i,g} \rightarrow \mathbf{A}$, $CR_{i,g} \rightarrow S_{CR}$, $F_{i,g} \rightarrow S_F$

        end if

        Shrink $\mathbf{A}$, if necessary

        Update M_{CR} and M_F (Algorithm 2)

        Apply LPSR strategy // *linear population size reduction*

    end for

    $g \leftarrow g + 1$

end while

Memory update in L-SHADE

if $S_{CR} \neq \emptyset$ **and** $S_F \neq \emptyset$ **then**
    if $M_{CR,k,g} = \perp$ **or** $max(S_{CR}) = 0$ **then**
        $M_{CR,k,g} \leftarrow \perp$
    else
        $M_{CR,k,g+1} \leftarrow mean_{WL}(S_{CR})$
    end if
    $M_{F,k,g+1} \leftarrow mean_{WL}(S_F)$
    $k \leftarrow k + 1$
    if $k > H$ **then**
        $k \leftarrow 1$
    end if
else
    $M_{CR,k,g+1} \leftarrow M_{CR,k,g}$
    $M_{F,k,g+1} \leftarrow M_{F,k,g}$
end if

mean_{WL} is weighted Lehmer mean

$$\text{mean}_{WL}(S) = \frac{\sum_{k=1}^{|S|} w_k \cdot S_k^2}{\sum_{k=1}^{|S|} w_k \cdot S_k}$$

$$w_k = \frac{\Delta f_k}{\sum_{l=1}^{|S_{CR}|} \Delta f_l}$$

$$\Delta f_k = |f(\boldsymbol{u}_{k,G}) - f(\boldsymbol{x}_{k,G})|$$

J. Brest et al (2016). iL-SHADE: Improved L-SHADE Algorithm for Single Objective Real-Parameter Optimization, 2016 IEEE Congress on Evolutionary Computation (CEC)

Lehmer mean

In mathematics, the **Lehmer mean** of a tuple x of positive real numbers, named after Derrick Henry Lehmer,[1] is defined as:

$$L_p(\mathbf{x}) = \frac{\sum_{k=1}^{n} x_k^p}{\sum_{k=1}^{n} x_k^{p-1}}.$$

The **weighted Lehmer mean** with respect to a tuple w of positive weights is defined as:

$$L_{p,w}(\mathbf{x}) = \frac{\sum_{k=1}^{n} w_k \cdot x_k^p}{\sum_{k=1}^{n} w_k \cdot x_k^{p-1}}.$$

The Lehmer mean is an alternative to power means for interpolating between minimum and maximum via arithmetic mean and harmonic mean.

Population in L-SHADE

- Linear population size reduction

$$NP_{G+1} = round\left[NP^{init} - \frac{FES}{MaxFES}\left(NP^{init} - NP^{min}\right)\right]$$

- NP_{G+1} = population size in generation G+1
- Np^{init} – initial population size
- Np^{min}– minimal population size
- FES – current number of fitness evaluations
- MaxFES – maximally allowed number of fitness evaluations