## Constraints

- Examples:
- "A string of numbers should represent a permutation" $(1,2,3)$ is valid; $(1,1,3)$ is not
- "The sum of numbers should not be lower than a threshold"
- Possibility 1: fitness function modification
- setting fitness of unfeasible solutions to zero (search may be very inefficient due to unfeasible solutions)
- penalty function (negative terms for violated constraints)
- barrier function (already penalty if "close to" violation)


## Constraints

- Possibility 2 (preferred method): special encoding
- GA searches always through allowed solutions
- smaller search space
- ad hoc method, may be difficult to find
- Example: permutations (see AI course)


## Mutations for Permutations

- Insert mutation:
- Pick two allele values at random
- Move the second to follow the first, shifting the rest along to accommodate
- Note: this preserves most of the order and adjacency information; changes the position of numbers a lot


Removed Adjancency:
Added Adjacency:
Removed orders:
Added orders:
Changed positions:
$(2,3),(4,5),(5,6)$
$(2,5),(4,6),(5,3)$
3->5, 4->5
5->3, $5->4$
$3,4,5$

## Mutations for Permutations

- Swap mutation:
- Pick two alleles at random and swap their positions
- Disrupts adjacency information and order more; preserves positions
$12314567819 \longrightarrow 15314267189$

Removed Adjancency:
Added Adjacency:
Removed order:
Added order:
Changed positions:
$(1,2),(2,3),(4,5),(5,6)$
$(1,5),(2,6),(4,2),(5,3)$
2->3, 2->4, 2->5, 3->5, 4->5
$5->3,5->4,3->2,4->2,5->2$
2, 5

## Mutations for Permutations

- Inversion mutation:
- Pick two alleles at random and then invert the substring between them.
- Preserves most adjacency information (only breaks two links) but disruptive for order information




## Mutations for Permutations

- Scramble mutation:
- Pick a subset of genes at random (not necessarily consecutive)
- Randomly rearrange the alleles in those positions

$$
\begin{array}{|l|l|l|l|l|l|l|l|l|}
\hline 1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 & 9 \\
\hline
\end{array}
$$

## Crossover for Permutations

- Order one crossover:
- Choose an arbitrary part from the first parent, copy this part to the first child



\section*{| 9 | 3 | 7 | 8 | 2 | 6 | 5 | 1 |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- |}

- Copy the numbers that are not in the first part, to the first child:
- starting right from cut point of the copied part,
- using the order of the second parent and wrapping around at the end

| 1 | 2 | 3 | 4 | 5 | 6 | 7 |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- |

$\longrightarrow \quad 3 / 8 / 2|4| 5|6| 7|1| 9$

| 9 | 3 | 7 | 8 | 2 | 6 | 5 | 1 |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- |

- Analogous for the second child, with parent roles reversed


## Crossover for Permutations

- Partially Mapped Crossover (PMX):
- Choose random segment and copy it from Pı

| Step 1 | $\mathbf{1}$ | 2 | 3 | 4 | 5 | 6 | 7 |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- |
|  |  | 8 | 9 |  |  |  |  |
|  |  |  |  |  |  |  |  |



| 9 | 3 | 7 | 8 | 2 | 6 | 5 | 1 |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- | $\mathbf{4}$

- Starting from the first crossover point look for elements in that segment of $\mathrm{P}_{2}$ that have not been copied
- For each of these i look in the offspring to see what element $j$ has been copied in its place from Pr
- Place i into the position occupied $j$ in $\mathrm{P}_{2}$, since we know that we will not be putting j there (as is already in offspring)
- If the place occupied by j in $\mathrm{P}_{2}$ has already been filled in the offspring k , put i in the position occupied by k in $\mathrm{P}_{2}$

Step 2


|  | 2 | 4 | 5 | 6 | 7 |
| :--- | :--- | :--- | :--- | :--- | :--- |

## Crossover for Permutations

- Partially Mapped Crossover (PMX):
- Having dealt with the elements from the crossover segment, the rest of the offspring can be filled from P2.

| Step 3 |  |  |  |  |  |  |  |  |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- |
| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 |

$$
\begin{array}{|l|l|l|l|l|l|l|l|}
\hline 9 & 3 & 2 & 4 & 5 & 6 & 7 & 1
\end{array} \mathbf{8} .
$$

| 9 | 3 | 7 | 8 | 2 | 6 | 5 | 1 |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- |$|$

- Idea: maintain position


## Order vs Position in

 Permutations- Order, but not position of numbers is important in problems such as the traveling salesman problem (visiting all cities in a certain order)
- Position, but not order of numbers is important in problems such as allocating visitors in hotels to rooms (visitors have to be allocated once to one room, but the order of the allocation does not matter)


## Evolutionary Strategies

- Numerical optimization problems:
- Given a function $f$ from real numbers to a real number
- Find coordinates at which $f$ is maximized



## Evolutionary Strategies

- Main idea: individuals consist of vectors of real numbers (not binary)
- Redefinitions of
- selection
- crossover
- mutation
- Operations executed in the order crossover $\rightarrow$ mutation $\rightarrow$ selection


## ES: Selection

- Not performed before mutation and crossover, but after these operations
- It is assumed mutation (\& crossover) generate $\lambda>\mu$ individuals (where $\mu$ is population size) (typically $\lambda \approx 7 \mu$ )
- Deterministically eliminate worst individuals from
$\bullet$ children only: $(\mu, \lambda)$ - $\mathrm{FS} \rightarrow$ escapes from local optima more easily
(Notational convention)
$\bullet$ parents and children: $(\mu+\lambda)$-ES $\rightarrow$ doesn't forget good solutions ("elitist selection")


## ES: Basic Mutation

- An individual is a vector $\vec{h}=\left(x_{1}, \ldots, x_{n}\right)$
- Mutate each $x_{i}$ by sampling a change from a normal distribution:

$$
x_{i} \leftarrow x_{i}+\Delta x_{i} \text { where } \Delta x_{i} \underset{\sim}{\sim} N(0, \sigma)
$$



Simple modification: mutation rate for each $x_{i}$

Major question:
How to set $\sigma$ or $\sigma_{i}$ ?

## MAIN IDEA: make search more efficient by increasing mutation rate if this seems safe

## ES: Basic Mutation

- An algorithm for setting global $\sigma$ :
- Count the number $G_{s}$ of successful mutations
- Compute the ratio of successful mutations
$p_{s}=G_{s} / G$
- Update strategy parameters according to

$$
\sigma=\left\{\begin{array}{lll}
\sigma_{i} / c & \text { if } & p_{s}>0.2 \\
\sigma . c & \text { if } & n<0.2
\end{array} \quad c \in[0.8,1.0]\right.
$$

## Basic (1+1) ES

- Common use of the $1 / 5$ rule

```
\(t:=0\);
initialize \(P(0):=\{\vec{x}(0)\} \in I, I=\operatorname{IR}^{n}, \vec{x}=\left(x_{1}, \ldots, x_{n}\right)\);
evaluate \(P(0):\{f(\vec{x}(0))\}\)
while not terminate \((P(t))\) do
    mutate: \(\vec{x}^{\prime}(t):=m(\vec{x}(t))\)
        where \(x_{i}^{\prime}:=x_{i}+\sigma(t) \cdot N_{i}(0,1) \forall i \in\{1, \ldots, n\}\)
    evaluate: \(P^{\prime}(t):=\left\{\vec{x}^{\prime}(t)\right\}:\left\{f\left(\vec{x}^{\prime}(t)\right)\right\}\)
    select: \(P(t+1):=s_{(1+1)}\left(P(t) \cup P^{\prime}(t)\right)\);
    \(t:=t+1\);
    if \((t \bmod n=0)\) then
        \(\sigma(t):= \begin{cases}\sigma(t-n) / c & , \text { if } p_{s}>1 / 5 \\ \sigma(t-n) \cdot c & , \text { if } p_{s}<1 / 5 \\ \sigma(t-n) & , \text { if } p_{s}=1 / 5\end{cases}\)
        where \(p_{s}\) is the relative frequency of successful
                mutations, measured over intervals of,
                say, \(10 \cdot n\) trials;
            and \(0.817 \leq c \leq 1\);
    else
        \(\sigma(t):=\sigma(t-1) ;\)
    fi
od
```


## ES Mutation:

## Strategy Parameters

- An individual is a vector $\vec{h}=\left(x_{1}, \ldots, x_{n}, \sigma\right)$ or $\vec{h}=\left(x_{1}, \ldots, x_{n}, \sigma_{1}, \ldots, \sigma_{n}\right)$ where the $\sigma_{i}$ are the standard deviations
- Mutate strategy parameter(s) first Order is important!
- If the resulting child has high fitness, it is assumed that:
- quality of phenotype is good
- quality of strategy parameters that led to this phenotype is good


## ES Mutation:

## Strategy Parameters

- Mutation of one strategy parameter


Here the new $\sigma^{\text {c }}$ is used!

## ES Mutation:

## Strategy Parameters

- Here $\tau_{0}$ is the mutation rate
- $\tau_{0}$ bigger: faster but more imprecise
- $\tau_{0}$ smaller: slower but more imprecise
- Recommendation for setting $\tau_{0}$ :

$$
\tau_{0}=\frac{1}{\sqrt{n}}
$$

*H.-P. Schwefel: Evolution and Optimum Seeking, Wiley, NY, 1995.

## ES Mutation:

## Strategy Parameters

$\bigoplus$ equal probability to place an offspring


- One parameter for each individual
- 2 dimensional genotype $\vec{h}=\left(x_{1}, x_{2}, \sigma\right)$
- 5 individuals


## ES Mutation:

## Strategy Parameters

$\bigoplus$ equal probability to place an offspring


- One parameter for each dimension
- 2 dimensional genotype
$\vec{h}=\left(x_{1}, x_{2}, \sigma_{1}, \sigma_{2}\right)$
- 5 individuals


## ES Mutation:

## Strategy Parameters

- Mutation of all strategy parameters

$$
\begin{aligned}
\sigma_{i}^{\prime} & =\sigma_{i} \cdot \exp \left(\tau^{\prime} \cdot N(0,1)+\tau \cdot N_{i}(0,1)\right) \\
x_{i}^{\prime} & =x_{i}+\sigma_{i}^{\prime} \cdot N_{i}(0,1)
\end{aligned}
$$

Sample from normal distribution, the same for all parameters

Update for this specific parameter

## ES Mutation:

## Strategy Parameters

$\bigoplus \quad$ equal probability to place an offspring


- An individual is a vector
$\vec{h}=\left(x_{1}, \ldots, x_{n}, \sigma_{1}, \ldots, \sigma_{n}, \alpha_{1}, \ldots, \alpha_{m}\right)$
$\alpha_{i}$
encode angles
- Also here mutation can be defined
- Mathematical details skipped

