INF FAKULTÄT FÜR INFORMATIK

Evolutionary Algorithms

Encoding, Fitness, Selection

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Outline

Desirable properties of an encoding

now: deeper investigation of the different elements of an EA

At first: **encoding of a solution candidate**

- encoding has to be chosen problem-specific
- no general „recipe“ to find a good encoding
- but: some principes which should be taken into consideration

Desirable properties of an encoding:

- Representation of similar phenotypes by similar genotype
- Similar fitness on similar candidates
- Closure on Ω under the used evolutionary operators

Encoding: first desirable trait

Similar phenotypes should be represented by similar genotypes

- mutations of certain genes result in similar genotypes (particular changes of allels $\rightarrow$ small change of the chromosome)
- if trait is not satisfied, obvious changes cannot be generated in some cases
- consequence: huge change of the genotype to end up in a similar (and perhaps better) phenotype

Demonstration example:

- Optimization of a real function $y = f(x_1, \ldots, x_n)$
- Representation of the (real) arguments by binary codes
- Problem: binary representation leads to „Hamming-Cliffs“

Some neighbors in real space have very different binary representations: 1000 is next to 0111, but all bits flip.

Binary coding of real numbers

given: real interval $[a, b]$ and coding precision ε

desired: coding rule for $x \in [a, b]$ as binary number z
so that devation of z and x is lower than ε

Idea: divide $[a, b]$ in equidistant sections of length $\leq \varepsilon$

$\Rightarrow$ 2^k sections with $k = \left\lceil \log_2 \frac{b-a}{\varepsilon} \right\rceil$
coded by $0, \ldots, 2^k - 1$

We normally do this with IEEE 754, but that will make the Hamming cliffs worse.

Remember, 754 divides the bit string into a sign, the exponent, and the mantissa.

Binary coding of real numbers

Sections: $k = \left\lceil \log_2 \frac{b-a}{\varepsilon} \right\rceil$ or $k = \left\lceil \log_2 \frac{b-a}{2\varepsilon} \right\rceil$

Coding: $z = \left\lfloor \frac{x-a}{b-a}(2^k - 1) \right\rfloor$ or $z = \left\lfloor \frac{x-a}{b-a}(2^k - 1) + \frac{1}{2} \right\rfloor$

Decoding: $x = a + z \cdot \frac{b-a}{2^k - 1}$

Example: intervall $[-1, 2]$, precision $\varepsilon = 10^{-6}$, $x = 0.637197$

$$k = \left\lceil \log_2 \frac{2-(-1)}{10^{-6}} \right\rceil = \left\lceil \log_2 3 \cdot 10^6 \right\rceil = 22$$

$$z = \left\lfloor \frac{0.637197-(-1)}{2-(-1)}(2^{22} - 1) \right\rfloor = 2288966_{10}$$

$$= 1000101110110101000110_2$$

Hamming-Cliffs

Problem:

- adjacent numbers can be coded very differently
- encodings have big Hamming-distance (# different Bits)
- Mutations/Crossover overcome „Hamming-Cliffs“ poorly

Example:

- Representation of the numbers from 0 til 1 by 4-Bit-Numbers
- also mapping $\frac{k}{15} \rightarrow k$

$\Rightarrow$ $\frac{7}{15}$ (0111) and $\frac{8}{15}$ (1000) have the same Hamming-distance 4

Gray-Codes: Avoidance of Hamming-Cliffs

Solution: Gray-Codes
Hamming-distance of adjacent numbers = 1 Bit

binär	Gray
0000	0000
0001	0001
0010	0011
0011	0010

binär	Gray
0100	0110
0101	0111
0110	0101
0111	0100

binär	Gray
1000	1100
1001	1101
1010	1111
1011	1110

binär	Gray
1100	1010
1101	1011
1110	1001
1111	1000

Gray-Codes: Computation

- **Gray-Codes are not unique**
- each code where encodings of adjacent numbers differ in only 1 Bit is called Gray-Code
- Computation of Gray-Codes is usually started from binray number enconding

Most frequent form:

$$\textit{Encoding:} \quad g = z \oplus \left\lfloor \frac{z}{2} \right\rfloor$$

$$\textit{Decoding:} \quad z = \bigoplus_{i=0}^{k-1} \left\lfloor \frac{g}{2^i} \right\rfloor$$

$\oplus$: Exclusive-Or of the binary representation

Gray-Codes: Computation

Example: interval $[-1, 2]$, precision $\varepsilon = 10^{-6}$, $x = 0.637197$

$$z = \left\lfloor \frac{0.637197 - (-1)}{2 - (-1)} (2^{22} - 1) \right\rfloor = 2288966_{10}$$
$$= 1000101110110101000110_2$$

$$g = 1000101110110101000110_2$$
$$\oplus \quad 1000101110110101000011_2$$
$$= 1100111001101111100101_2$$

Gray-Codes: Implementation

```
unsigned int num2gray (unsigned int x)
{                                   /* --- convert number to Gray code */
  return x ^ (x >> 1);              /* exclusive or with shifted input */
}  /* num2gray() */
```

```
unsigned int gray2num (unsigned int x)
{                                   /* --- convert Gray code to number */
  unsigned int y = x;               /* copy the input number and */
  while (x >>= 1) y ^= x;           /* do an exclusive or with all */
  return y;                         /* shift downs of the input */
}  /* gray2num() */                 /* and return the result */
```

```
unsigned int gray2num (unsigned int x)
{                                   /* --- convert Gray code to number */
  x ^= x >> 16; x ^= x >> 8;        /* do an exclusive or with all */
  x ^= x >>  4; x ^= x >> 2;        /* shift downs of the input */
  return x ^ (x >> 1);              /* and return the result */
}  /* gray2num() */                 /* (32 bit integers only) */
```

Encoding: second desirable trait

Similarly encoded candidate solutions should have a similar fitness

Problem of the epistasis:

- *in biology:* one allele of a (so-called epistatic) gene suppresses the effect of all possible alleles of another gene
- *in evolutionary algorithms:*
  interaction between genes of a chromosome,
  Changes of the fitness by modifying one gene strongly depends on the value(s) of (an)other gene(s)

Example: The Traveling Salesman Problem

Find a round trip of n cities with respect to minimal costs

two different encodings of the round trip:

1. Permutation of the cities
   - visit city at the k-th position in the k-th step
   - *low epistasis:* z.B. swapping two cities alters fitness(costs) by comparable amounts (only local changes)

2. Specification of a list of numbers that state the position of the next city to be visited in a (sorted) list from which all already visited cities have been deleted
   - *high epistasis:* Modifying a single gene (esp. the closer to the top) may alter the complete round trip (global tour-change)

   $\Rightarrow$ leads mostly to large changes of the fitness

Second encoding: Effect of a Mutation

Mutation	Chromosome	Remaining cities	Round trip
before	5 3 3 2 2 1	1, 2, 3, 4, **5**, 6 1, 2, **3**, 4, 6 1, 2, **4**, 6 1, **2**, 6 1, **6** **1**	5 3 4 2 6 1
after	1 3 3 2 2 1	**1**, 2, 3, 4, 5, 6 2, 3, **4**, 5, 6 2, 3, **5**, 6 2, **3**, 6 2, **6** **2**	1 4 5 3 6 2

Epistasis: summary

- high epistatic encoding: no regularities

$\Rightarrow$ Mutation/Crossover leads to almost random fitness changes

$\Rightarrow$ optimization problem is very hard to solve by EAs

- very low epistatic encoding: other methods often more successful

- [Davidor, 1990] tried to classify optimization problems as *easy or hard to solve by an EA* based on the notion of epistasis$\Rightarrow$ failure
- since: epistasis = property of the encoding, **not** of the problem itself
- $\exists$ encodings of a problem with higher and lower epistasis
- $\exists$ problems with low epistatic encoding: too hard to solve by an EA

Encoding: 3^{rd} desirable trait

If possible, the search space Ω should be closed under the used genetic operators.

In general: **Space is left**, if

- new chromosome cannot be meaningfully interpreted or decoded
- a candidate solution does not fulfill certain basic requirements
- a candidate solution is evaluated incorrectly by the fitness function

Problem of **coordination** of encoding and EA-operators:

- choose or design encoding-specific genetic operators
- use mechanisms to „repair“ chromosomes
- introduce a penalty term that reduces the fitness of such individuals $\notin \Omega$

Leaving the space: example

n-Queens-Problem

Two different encodings: chromosome of length n

1. File positions of queens per rank (alleles $0, \ldots, n-1$)
   Operators: One-point Crossover, standard mutation
   generates always valid vectors of file position
   $\Rightarrow$ search space is not left

2. Numbers of the field (alleles $0, \ldots, n^2-1$) of the queens
   Operators: One-point crossover, standard mutation
   generates chromosomes with more than one queen per field
   $\Rightarrow$ search space is left

Leaving the space: solving approachs

n-Queens-Problem

- **Use other encoding:** first encoding avoids problem and Ω is considerably smaller (if feasible, best method!)
- **Encoding-specific evolutionary operators:**
  - *Mutation:* Excluding of already existing alleles on random
  - *Crossover:* look at first for field numbers of each chromosome which are not contained in other chromosomes and apply one-point crossover on shortened chromosomes
- **Repair mechanisms:** find und replace multiple occuring field numbers until all field numbers are distinct
- **Penalty term:** reduce fitness by amount of multiple allocations of fields multiplied with weight if necessary

One more: any child that leaves search space is a fatality; continue reproduction until you have the target # of survivors.

Leaving space using the example of TSP

- Representation of the round trip by permutation of the cities (city at k-th position is visited in the k-th step.)
- one-point crossover can exceed the space of permutations

3	5	2	8	1	7	6	4
1	2	3	4	5	6	7	8

3	5	2	4	5	6	7	8
1	2	3	8	1	7	6	4

- **Encoding-specific evolutionary operators:**
  - *Mutation:* e.g. pair swaps, shift/cyclic permutation, inversion
  - *Crossover:* edge recombination (will be discussed later)
- **Repair mechanisms:** remove twice occuring cities and append the missing cities at the end:

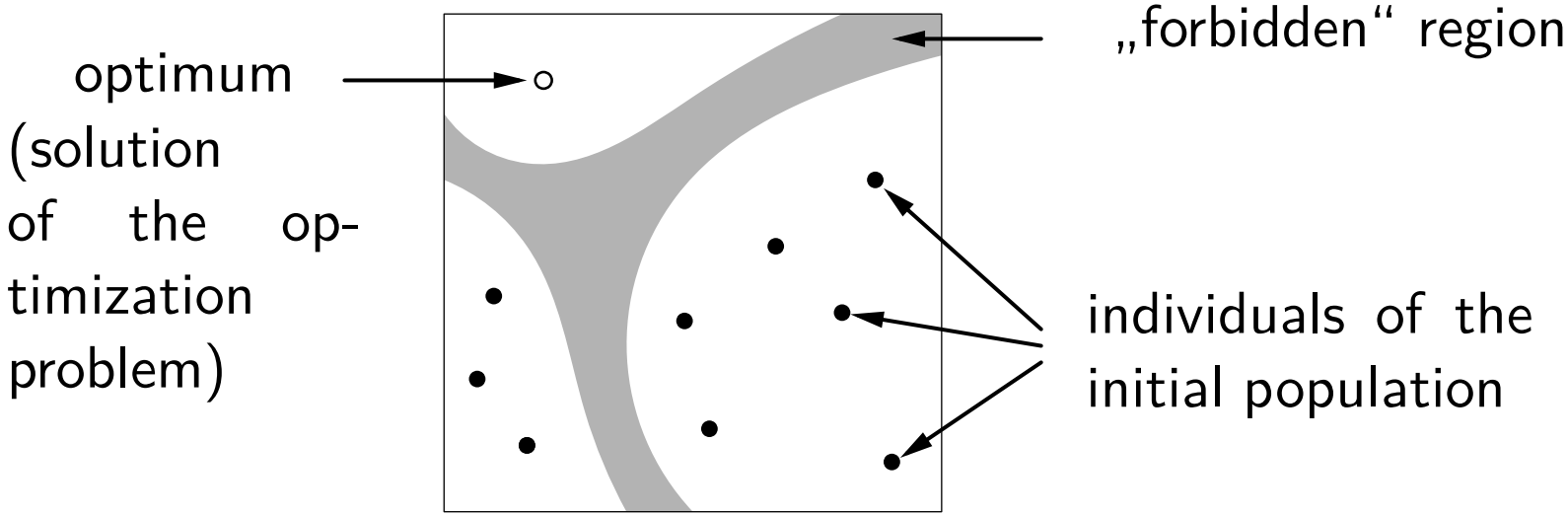
3	5	2	4	~~5~~	6	7	8	1

- **Penalty term:** reduce fitness by value c for each missing city

Weakness of fatality approach: what fraction of possible crossovers/mutations yields a surviving chromosome?

Leaving the space

- if Ω is *not connected*, *repair mech.* can complicate the search
- immediately restoring of „forbidden“ $x \in \Omega$ in permitted regions



- in such cases: introduce **penalty term**
- $x \in \Omega$ in „forbidden“ region is penalized but not removed
- penalty term should be increased on time: suppresses $x \in \Omega$ in „forbidden“ regions in following generations

Outline

Principe of selection

- better individuals (better fitness) should have better chances to create offspring(differential reproduction)
- **Selective pressure:** Strength of preferencing good individuals
- Choice of selective pressure: Contrast of
  Exploration of the space:
  - deviation of the individuals over Ω as wide as possible
  - preferably big chances to find global optimum

  $\Rightarrow$ smaller selective pressure is desired

  Exploitation (of good individuals):
  - Strive for (perhaps local) optimum in the vicinity of good individuals
  - Convergence to optimum

  $\Rightarrow$ higher selective pressure is preferred

Choice of the selective pressure

- **best strategy:** time-dependent selective pressure
  low selective pressure in prior generations
  higher selective pressure in later generations

$\Rightarrow$ at first good exploration of the space, then exploitation of the promising region

- regulation of the selective pressure by adapting the fitness function or by the parameter of selection method

- important **selection methods:**
  Roulette-wheel Selection, Rank-based Selection, Tournament Selection
- important **adaption methods:**
  Adaption of the variation of the fitness, linear dynamical scaling, σ-scaling

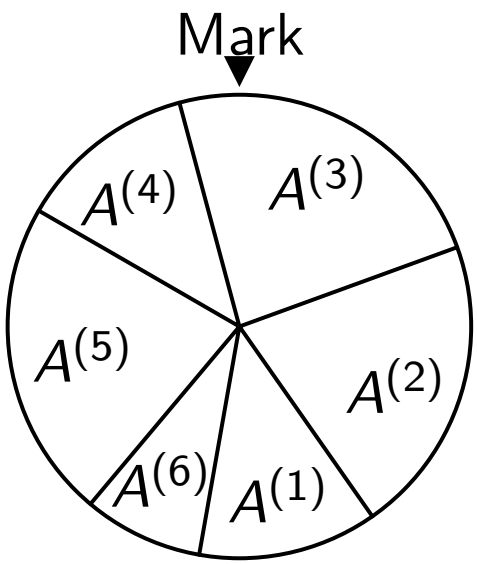
Roulette wheel selection (dt. Glücksradauswahl)

- best known selection method
- compute the relative fitness of the individuals $A^{(i)}$, $1 \leq i \leq |P|$

$$f_{\text{rel}}\left(A^{(i)}\right) = \frac{A^{(i)}.F}{\sum_{j=1}^{|P|} A^{(j)}.F}$$

  and interprete $f_{\text{rel}}\left(A^{(i)}\right)$ as a probability to be selected
  (so called **fitness-proportionate Selection**)
- **Please note:** absolute fitness $A.F$ may not be negative
- **Attention:** fitness has to be maximized
  (otherwise: selection of bad individuals with high probability)
- **Demonstration:** Roulette-wheel with 1 sector per individuual $A^{(i)}$,
  sector size = relative fitness values $f_{\text{rel}}\left(A^{(i)}\right)$

Roulette-wheel selection: Demonstration



Selection of an individual:

1. set the roulette-wheel into motion
2. choose the ind. of the corresponding sector

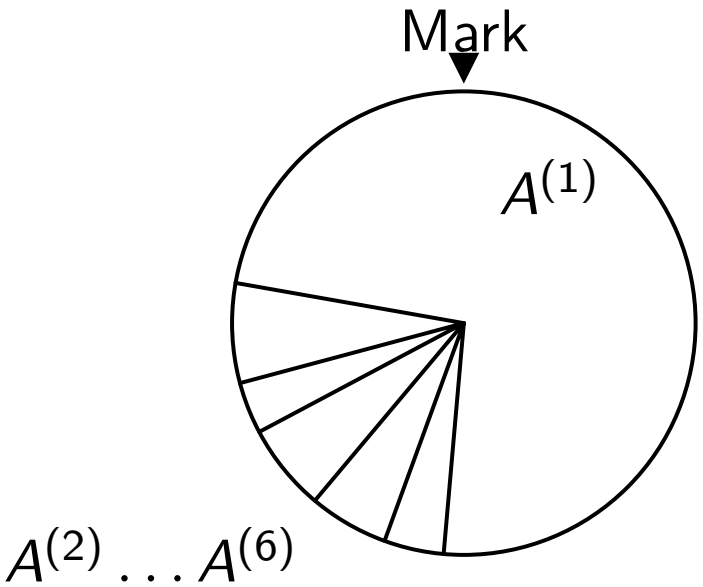
Selection of the next population:

- repeat selection # individuals-times

Disadvantage: Calculation of the relative fitness by summing up all fitness values (normalization factor)

- constant initial population during the selection
- aggravated parallelization of the implementation

Roulette-wheel selection: Dominance Problem



- individual with a very high fitness may **dominate** the selection
- Due to many copies/very similar individuals: dominance may become even stronger in subsequent generations

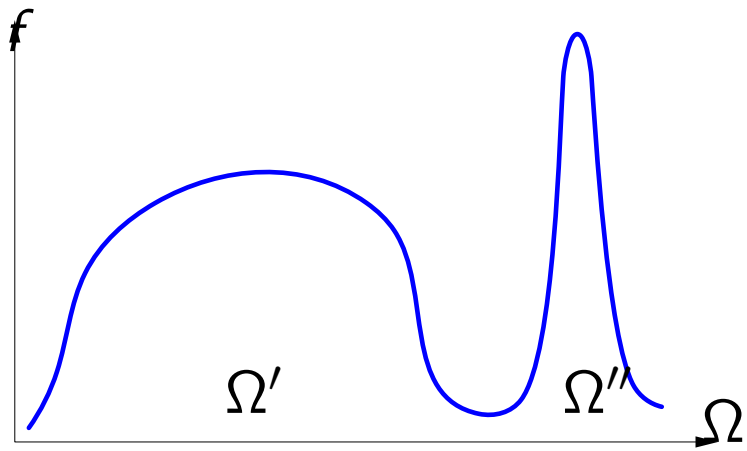
$\Rightarrow$ **Crowding:** population of very similar/identical individuals

- results in a very fast find of the (local) optimum
- **Disadvantage:** diversity of the population vanishs
  - Exploitation of worse individuals
  - No exploration of the space but local optimization (preferred in later generations, undesirable at the beginning)

Fitness function: Premature convergence

Dominance problem illustrates the strong influence of the fitness function on the effect of the fitness-proportionate selection

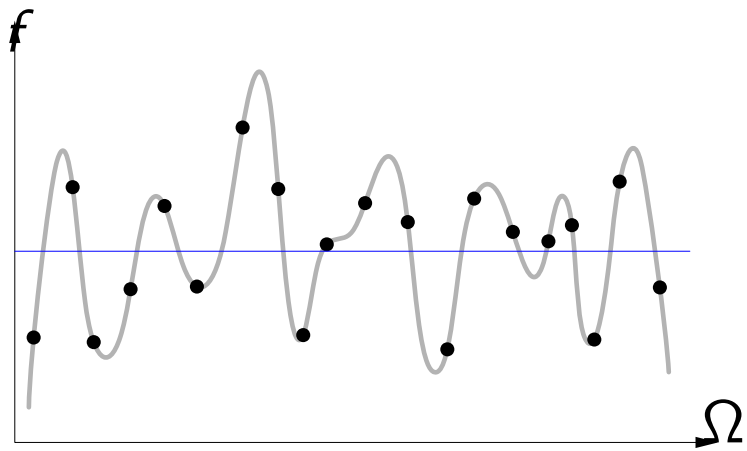
- Problem of **premature convergence:**
  If (value) range of the maximizing function is very huge
- Example: no chromosome at the beginning in the section $\Omega'' \rightarrow$ population remains by selection in the vicinity of the local maximum in the section Ω'



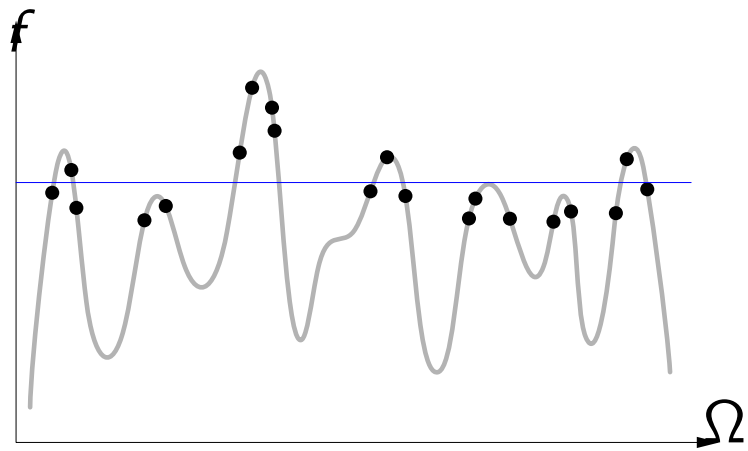
Individuals which converge to the section between Ω' and Ω'' have worse chances to create offspring

Vanishing selective pressure

- Problem is perhaps grounded on the EA itself
- it increases tendentially the (average) fitness of the individuals
- higher selective pressure at the beginning due to random fitness values
- later: smaller selective pressure (inverse way is preferred)
- Example: points illustrate individuals of the generation



early generation



later generation

Adapting of the fitness function

Approach: **Scaling of the fitness**

linear dynamical scaling:

$$f_{\text{lds}}(A) = \alpha \cdot A.F - \min\left\{A^{(i)}.F \mid P(t) = \left\{A^{(1)}, \ldots, A^{(r)}\right\}\right\}, \quad \alpha > 0$$

- instead minimum of $P(t)$, minimum of the last k generations can be used
- usually $\alpha > 1$

σ-**Scaling:**

$$f_\sigma(A) = A.F - (\mu_f(t) - \beta \cdot \sigma_f(t)), \quad \beta > 0$$

- Problem: Choice of the parameter α and β

Adaption of the fitness function: dependence on time

- determine f_{rel} not directly from $f(x)$ but $g(x) \equiv (f(x))^{k(t)}$
- time-dependent exponent $k(t)$ regulates selective pressure
- **Method to determine** $k(t)$ [Michalewicz, 1996]
  (should limit selection intensity I_{sel} in the vicinity of $I^*_{\text{sel}} \approx 0.1$)

$$k(t) = \left(\frac{I^*_{\text{sel}}}{I_{\text{sel}}}\right)^{\beta_1} \left(\tan\left(\frac{t}{T+1} \cdot \frac{\pi}{2}\right)\right)^{\beta_2 \left(\frac{I_{\text{sel}}}{I^*_{\text{sel}}}\right)^{\alpha}}$$

I^*_{sel}, β_1, β_2, α: parameter of the method

I_{sel}: coefficient of variation (e.g. estimated from $P(t=0)$)

T: max. number of remaining generations to be computed

t: current time step (number of generation)

- Recommended: $I^*_{\text{sel}} = 0.1,\ \beta_1 = 0.05,\ \beta_2 = 0.1,\ \alpha = 0.1$

Adaption of the fitness function: Boltzmann-Selection

- determine relative fitness not directly from $f(x)$ but from $g(x) \equiv \exp\left(\frac{f(x)}{kT}\right)$
- time-dependent **temperature** T controls selective pressure
- k is normalizing constant
- Temperature decreases e.g. linearly to the predefined maximum number of generations

Outline

Roulette-wheel Selection: vaiance problem

- Selection of individuals is indeed proportional to the fitness, but random
- no guarantee that „fitter“ individuals are taken to the next generation, not even for the best individual
- gen.: high deviation (**high variance**) of the offspring of an individual
- Computation of the mean value: see the exercise sheet
- very simple but not implicitly a recommendable solution: **Discretization of the fitness range**
  - compute $\mu_f(t)$ and $\sigma_f(t)$ of P
  - if $\mu_f(t) - \sigma_f(t) > f(x)$: 0 offspring
  - if $\mu_f(t) - \sigma_f(t) \leq f(x) \leq \mu_f(t) + \sigma_f(t)$: 1 offspring
  - if $f(x) > \mu_f(t) + \sigma_f(t)$: 2 offsprings

Rank-based Selection

1. Sort individuals decendingly according to their fitness:
   Rank is assigned to each individual in population
   (from statistics: distribution-free techniques, z.B. rank correlation)
2. Define prob. distribution over Rank scale:
   the lower the rank the lower the probability
3. Roulette-wheel selection based on the distribution

Adavantage:

- Avoidance of dominance problem: decoupling of fitness value and selection probability
- regulation of the selective pressure by prob. distribution on rank scale

Disadvantage: Sort of individuals (complexity: $|P| \cdot \log |P|$)

Tournament selection

1. Draw k individuals ($2 \leq k < |P|$) randomnly from $P(t)$ (draw can be reclined or not, selection *without* regarding the fitness, let k be the **tournament size**).
2. Individuals carry out the tournament and best indivual wins: Tournament winner receives a descendant in the next population
3. *All* participants (even the winner) of the tournament are returned to $P(t)$

Advantage:

- Avoidance of the dominance problem: decoupling of fitness value and selection probability
- regulation of the selective pressure by tournament size with limitations

Modification: f_{rel} of the participants determine winning probability (Roulette-wheel selection of an individual in tournament)

Elitism

- only the expected value model (and some of its variants) ensures that the best individual enters the next generation
- if best individual in next population: no protection from modifications by genetic operators
  (even in the expected value model)

$\Rightarrow$ fitness of the best individual can decrease from one generation to the next (= undesired)

Solution: Elitism

- *unchanged* transfer of the best individual (or the k, $1 \leq k < |P|$ best individuals) into the next generation
- *elite* of a population never gets lost, hence *elitism*
- **Attention:** elite is *not* exclued from normal selection: genetic operator can improve them

Elitism

- many times: offspring (Mutation-/Crossover products) replace their parents
- **„local“ elitism** (Elitism between parents and offspring)
  - *Mutation:* mutated individual replaces its parents $\leftrightarrow$ it has at least the same fitness
  - *Crossover:* sort the four involved individuals (2 parents, 2 descendants) according to the fitness, both best individuals $\rightarrow$ next generation
- **Adavantage:** better convergence as the local optimum is intended more consequently
- **Disadvantage:** pretty high risk of getting stuck in local optima as no local degradation is possible