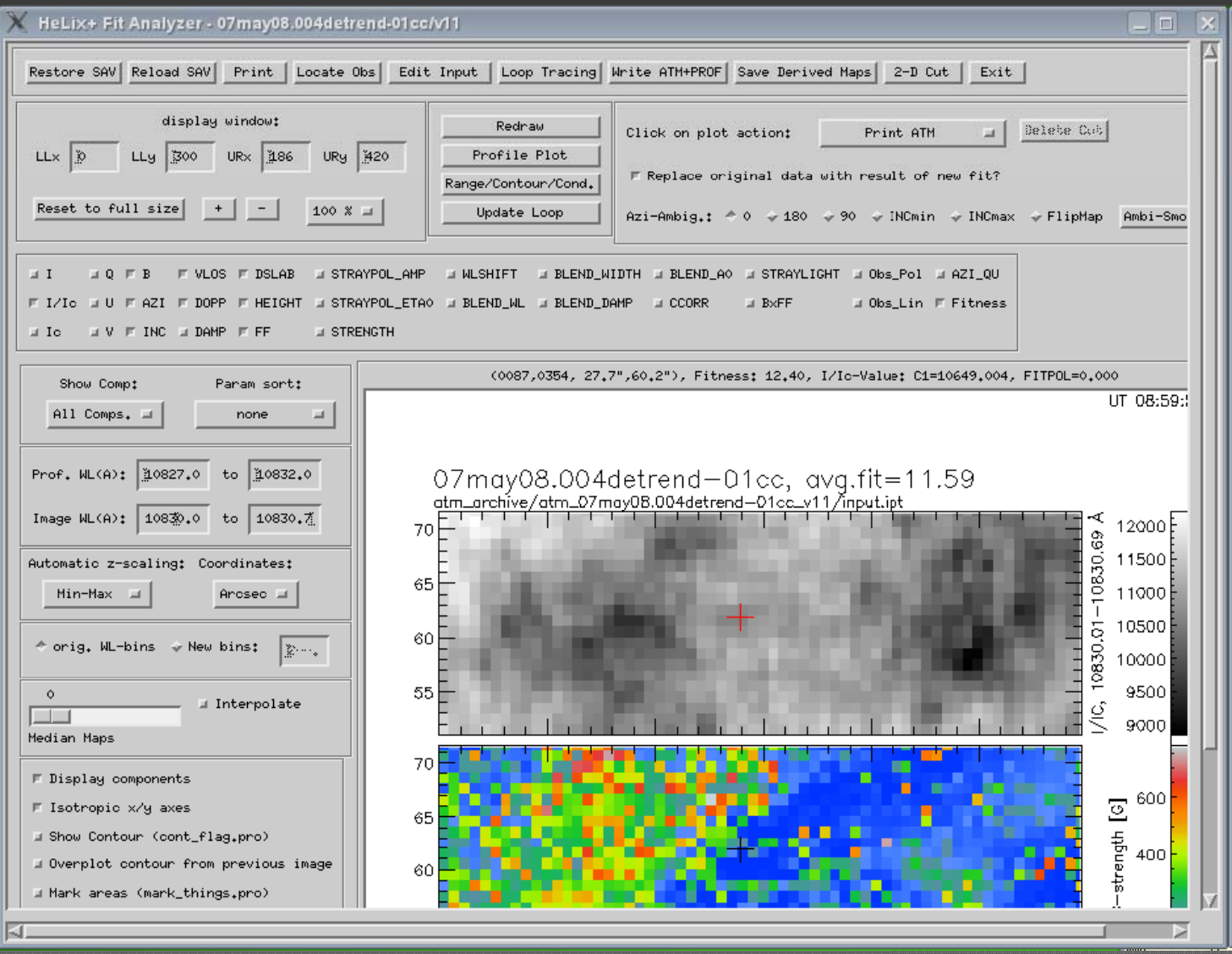
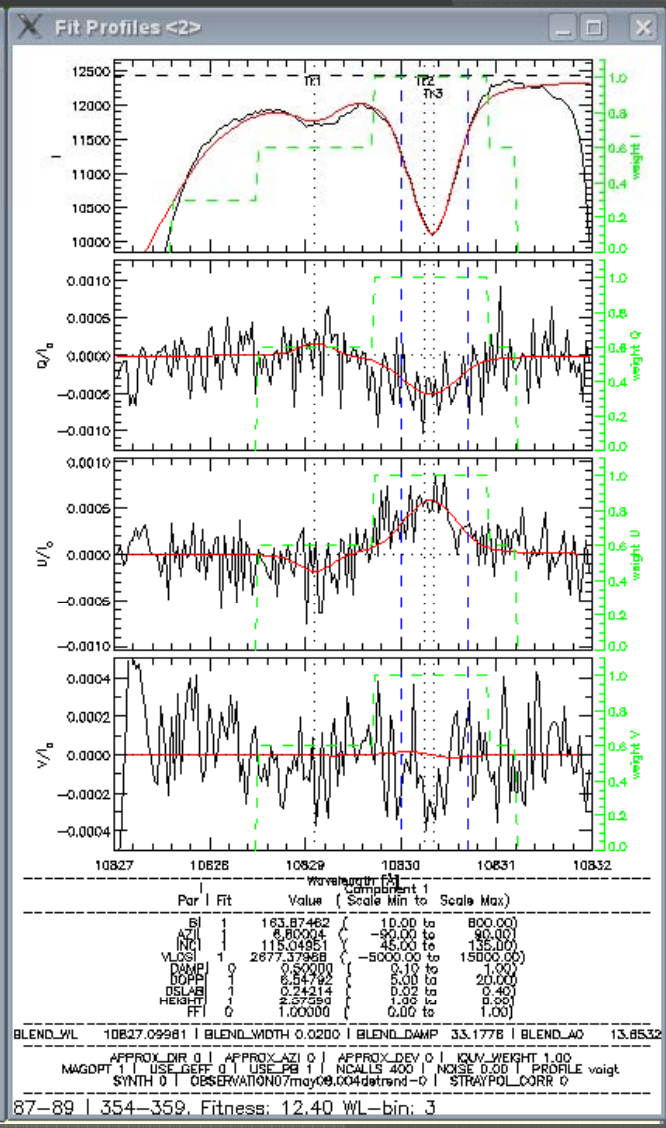
The HeLIx+ inversion code
Genetic algorithms





Inversion of the RTE

Once solution of RTE is known:

- comparison between Stokes spectra of synthetic and observed spectrum
- trial-and-error changes of the initial parameters of the atmosphere („human inversions“)
- until observed and synthetic (fitted) profile matches

Inversions:

Nothing else but an optimization of the trial-and-error part

Problem:

Inversions always find a solution within the given model atmosphere. Solution is seldomly unique (might even be completely wrong).

Goal of this lecture:

Principles of genetic algorithms

Learn the usage of the HeLIx$^+$ inversion code, develop a feeling on the reliability of inversion results.

The merit function

- The quality of the model atmosphere must be evaluated
- Stokes profiles represent discrete sampled functions
- widely used: chisqr definition

$$\chi^2(\mathbf{x}) = \frac{1}{N_{free}} \sum_{s=0}^{3} \sum_{i=1}^{q} \left[\mathbf{I}_s^{obs}(\lambda_i) - \mathbf{I}_s^{syn}(\lambda_i; \mathbf{x}) \right]^2 w_{s,i}^2$$

number of free parameters

sum over Stokes

sum over WL-pixels

weight (also WL-dep)

- RTE gives the Stokes spectrum $\mathbf{I}_s^{syn}$
- The unknowns of the system are the (height dependent) model parameters:

$$\mathbf{x} = (B, \Theta, \phi, v_{LOS}, \ldots)$$

HeLIx+ overview of features

- includes Zeeman, Paschen-Back, Hanle effect (He 10830)
- atomic polarization for He 10830 (He D3)
- magneto-optical effects
- fitting / removing telluric lines
- fitting unknown parameters of spectral lines
- various methods for continuum correction / fitting
- convolution with instrument filter profiles
- user-defined weighting scheme
- direct read access to SOT/SP, VTT-TIP2, SST-CRISP, ...
- flexible atomic data configuration
- extensive IDL based display routines
- MPI support (to invert maps)

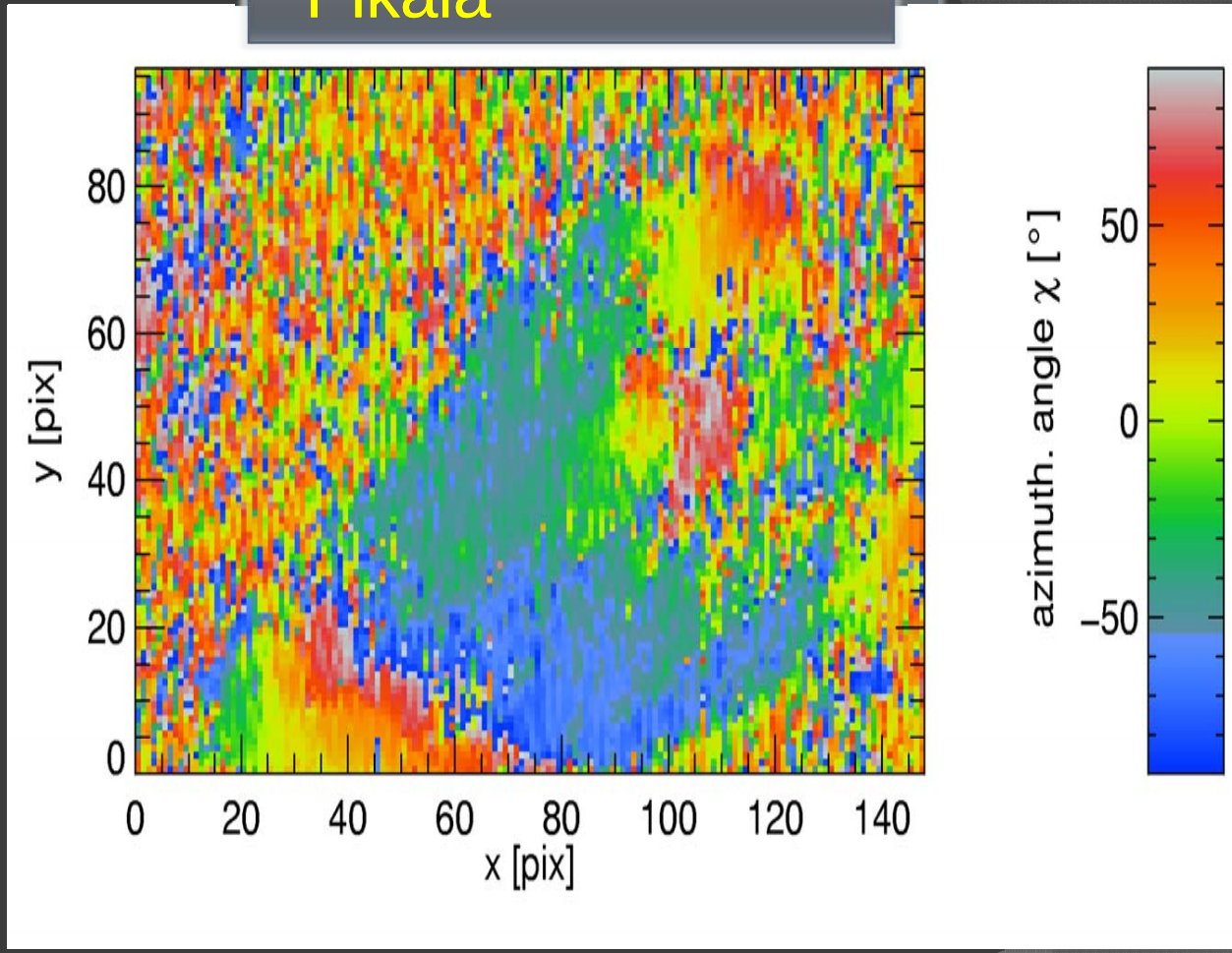
Download from http://www.mps.mpg.de/homes/lagg
GBSO download-section → helix
use *invert* and *IR$soft*

The inversion technique: reliability

Two minimizations implemented:

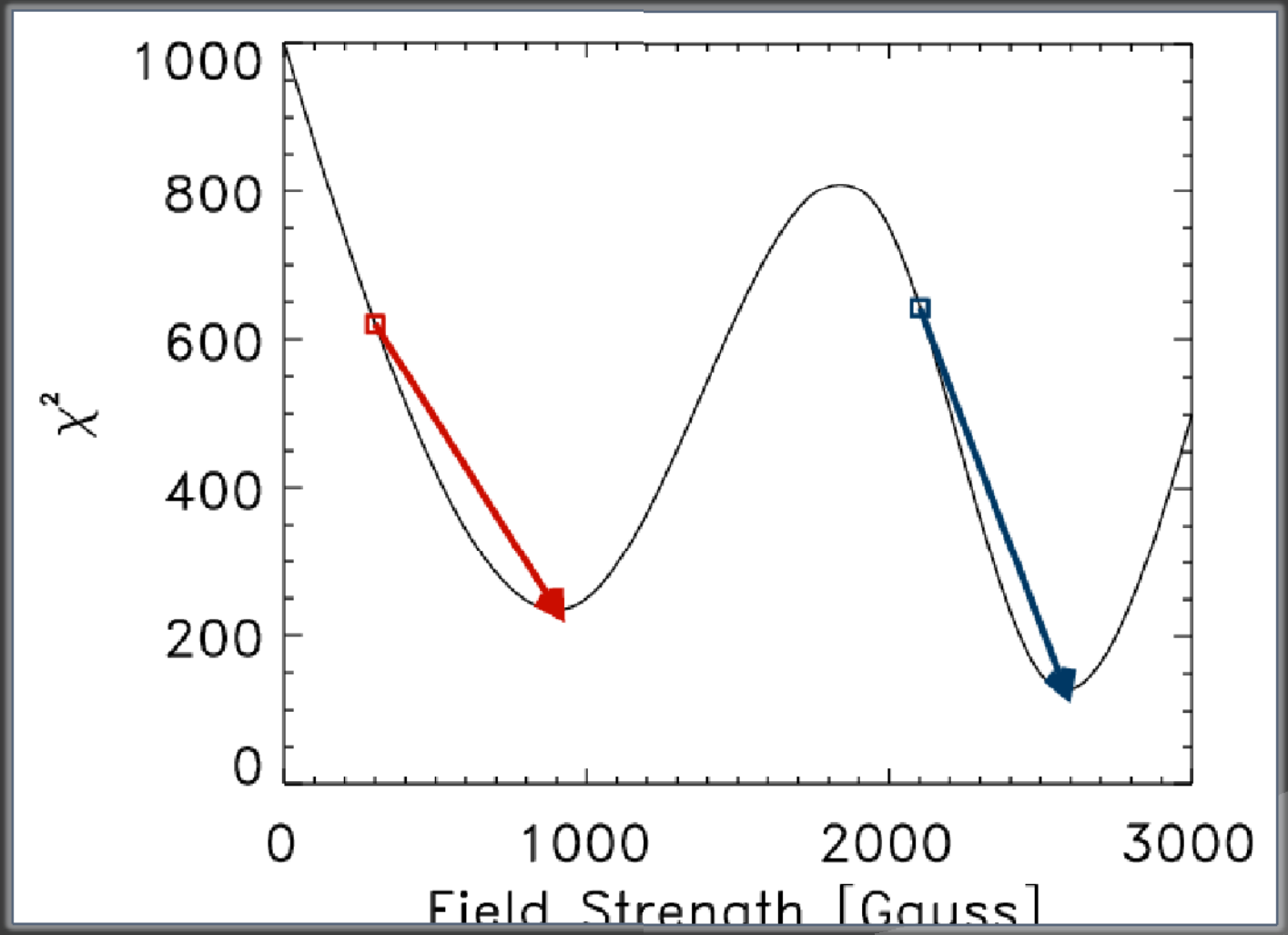
- Levenberg-Marquardt:
  → requires good initial guess
- PIKAIA (genetic algorithm, Charbonneau 1995):
  → no initial guess needed
- planned: DIRECT algorithm (good compromise between global min and speed)

Pikaia



Initial guess problem

Having a good initial guess for the iteration process improves both the speed and the convergence of the inversion.



Initial guess optimizations

Weak field initialization

$$B_L = C_1 V$$
$$B_T = C_2 \sqrt{Q^2 + U^2}$$
$$B = \sqrt{B_L^2 + B_T^2}$$
$$\gamma = \cos^{-1}\left(\frac{B_L}{B_T}\right)$$
$$\phi = \tan^{-1}\left(\frac{Q}{U}\right)$$

Auer77 initialization

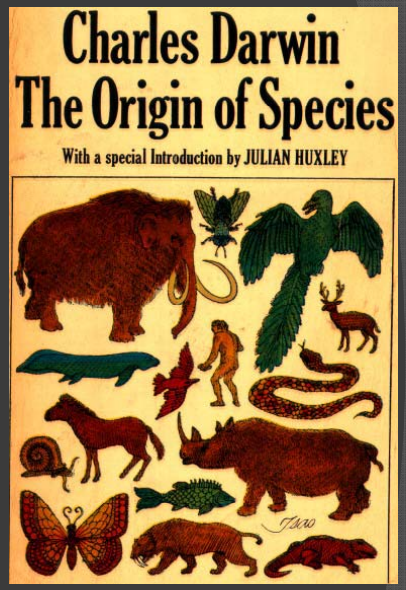
$$R = \frac{2V}{\sqrt{Q^2 + U^2}}$$
$$\gamma = \cos^{-1}\left\{\frac{1}{2}(\sqrt{R^4 + 4} - R)\right\}$$
$$\phi = \frac{1}{4}\tan^{-1}\left\{\frac{\sum_\lambda QU}{\sum_\lambda (Q^2 - U^2)}\right\}$$

Other methods:

- Artificial Neural Networks (ANN)
- MDI / magnetograph formulae
- use a minimization technique which does not rely on initial guess values

Genetic algorithms

- Genetic algorithms (GA's) are a technique to solve problems which need optimization
- GA's are a subclass of Evolutionary Computing
- GA's are based on Darwin's theory of evolution
- History of GA's:
  - Evolutionary computing evolved in the 1960's.
  - GA's were created by John Holland in the mid-70's.



Advantages / drawbacks

- No derivatives of the goodness of fit function with respect to model parameters need be computed; it matters little whether the relationship between the model and its parameters is linear or nonlinear.
- Nothing in the procedure outlined above depends critically on using a least-squares statistical estimator; any other robust estimator can be substituted, with little or no changes to the overall procedure.

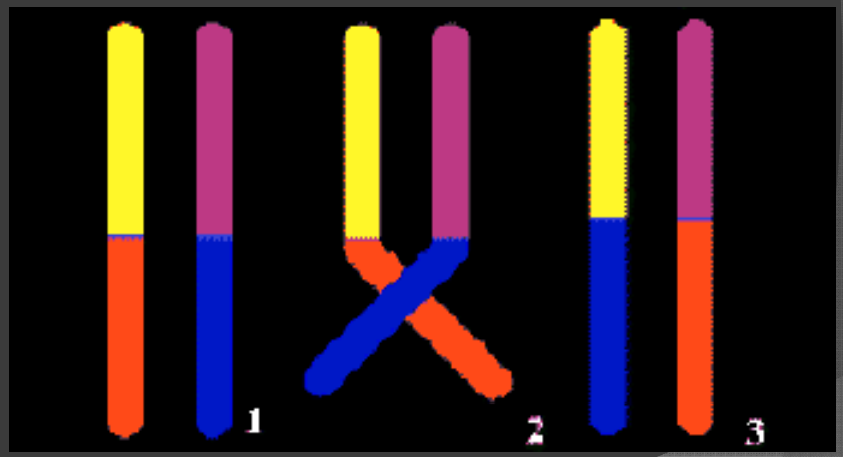
- In most real applications, the model will need to be evaluated (i.e., given a parameter set, compute a synthetic dataset and its associated goodness of fit) a great many times; if this evaluation is computationally expensive, the forward modeling approach can become impractical.

Evolution in biology

- Each cell of a living thing contains chromosomes - strings of DNA
- Each chromosome contains a set of genes - blocks of DNA
- Each gene determines some aspect of the organism (like eye colour)
  - A collection of genes is sometimes called a genotype
  - A collection of aspects (like eye colour) is sometimes called a phenotype
- Reproduction involves recombination of genes from parents and then small amounts of mutation (errors) in copying
- The fitness of an organism is how much it can reproduce before it dies
- Evolution based on “survival of the fittest”

Biological reproducion

- During reproduction “errors” occur
- Due to these “errors” genetic variation exists
- Most important “errors” are:
  - Recombination (cross-over)
  - Mutation



Natural selection

- The origin of species: “Preservation of favourable variations and rejection of unfavourable variations.”
- There are more individuals born than can survive, so there is a continuous struggle for life.
- Individuals with an advantage have a greater chance for survive: survival of the fittest.
- Important aspects in natural selection are:
  - adaptation to the environment
  - isolation of populations in different groups which cannot mutually mate
- If small changes in the genotypes of individuals are expressed easily, especially in small populations, we speak of genetic drift
- “success in life”: mathematically expressed as fitness

How to apply to RTE?

- GA's often encode solutions as fixed length "bitstrings" (e.g. 101110, 111111, 000101)
- Each bit represents some aspect of the proposed solution to the problem
- For GA's to work, we need to be able to "test" any string and get a "score" indicating how "good" that solution is
- definition of "fitness function" required: convenient to use chisqr merit function

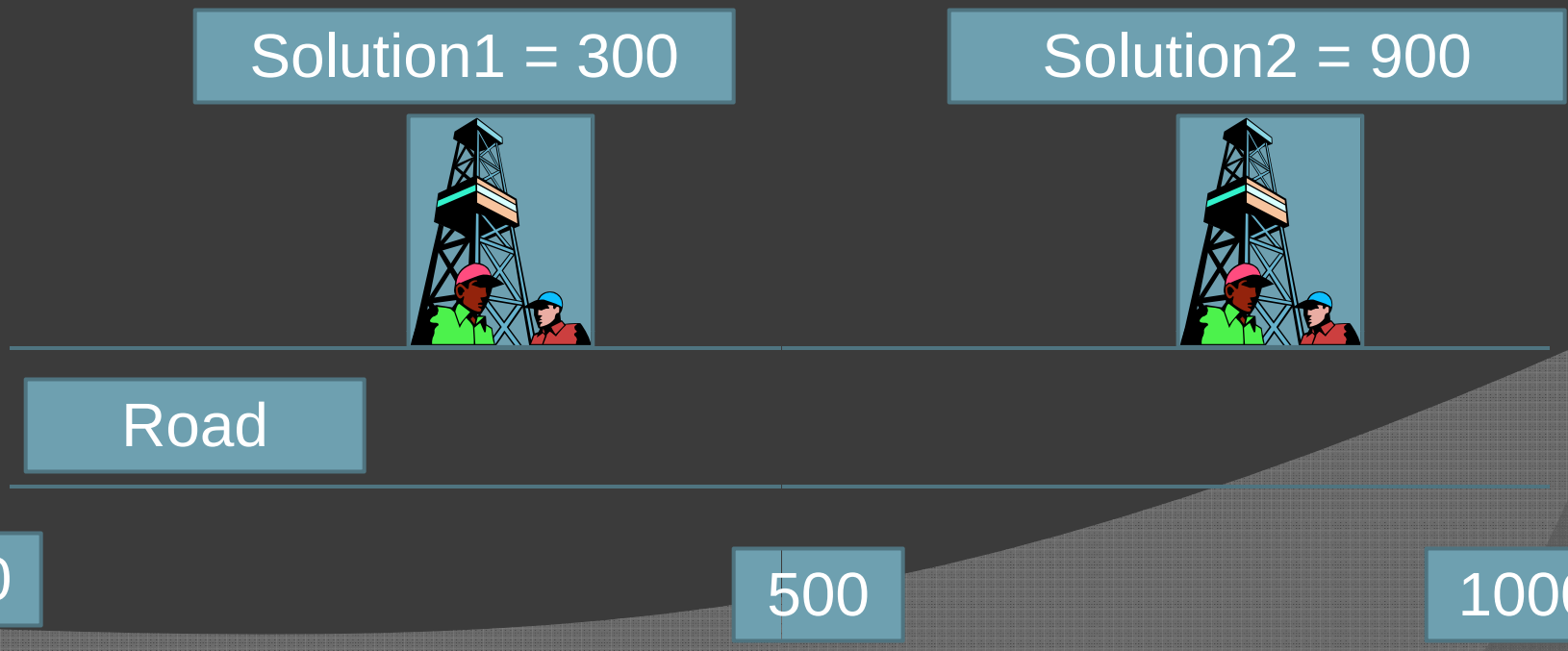
$$F(\mathbf{x}) = \frac{1}{\chi^2(\mathbf{x})}$$

GA's improve the fitness – maximization technique

Example – Drilling for oil

David Hales (www.davidhales.com)

- Imagine you had to drill for oil somewhere along a single 1km desert road
- Problem: choose the best place on the road that produces the most oil per day
- We could represent each solution as a position on the road
- Say, a whole number between [0..1000]



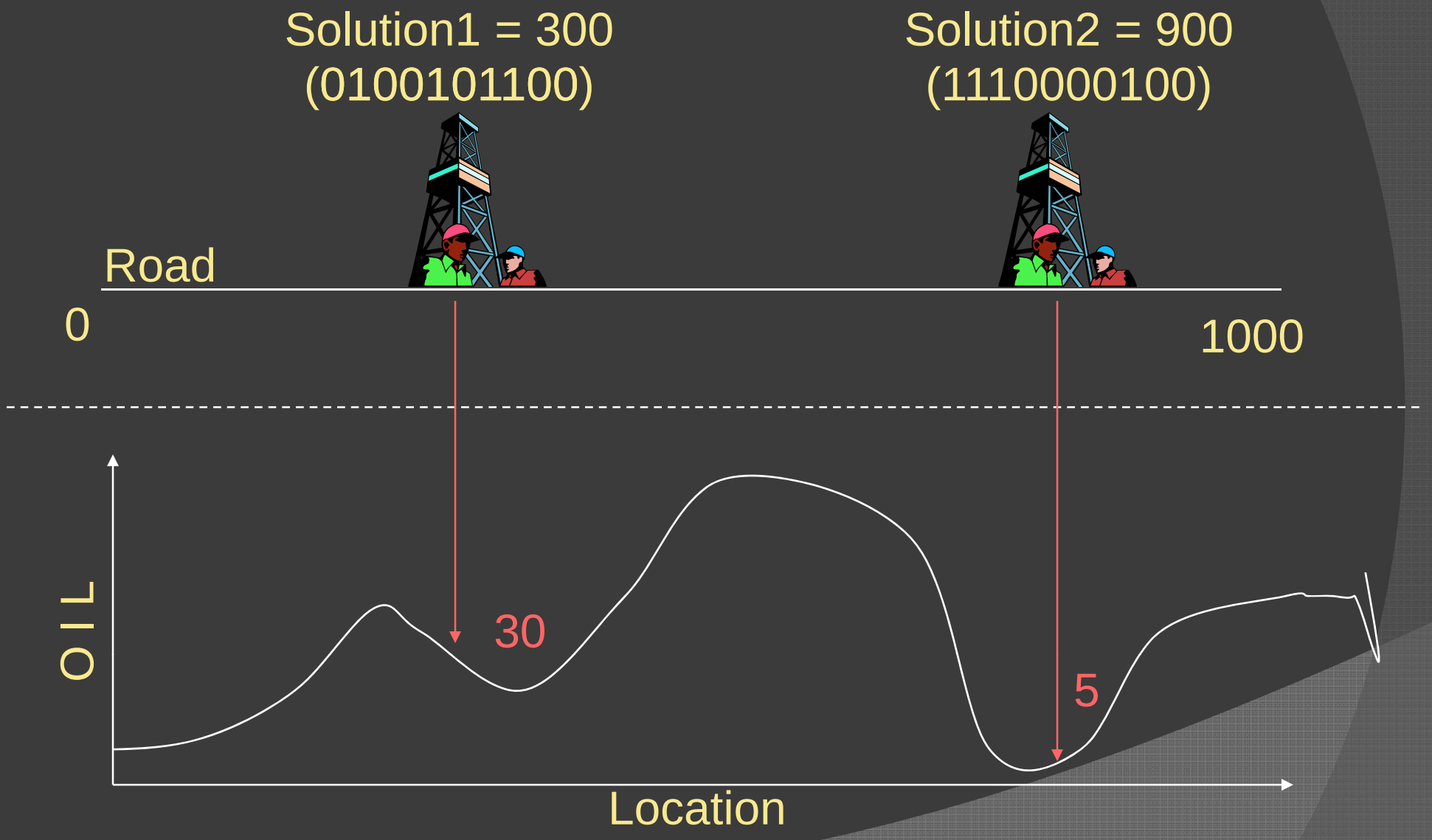
Encoding problem

- The set of all possible solutions [0..1000] is called the search space or state space
- In this case it's just one number but it could be many numbers or symbols
- Often GA's code numbers in binary producing a bitstring representing a solution
- In our example we choose 10 bits which is enough to represent 0..1000

	512	256	128	64	32	16	8	4	2	1
900	**1**	**1**	**1**	**0**	**0**	**0**	**0**	**1**	**0**	**0**
300	**0**	**1**	**0**	**0**	**1**	**0**	**1**	**1**	**0**	**0**
1023	1	1	1	1	1	1	1	1	1	1

In GA's these encoded strings are sometimes called *"genotypes"* or *"chromosomes"* and the individual bits are sometimes called *"genes"*

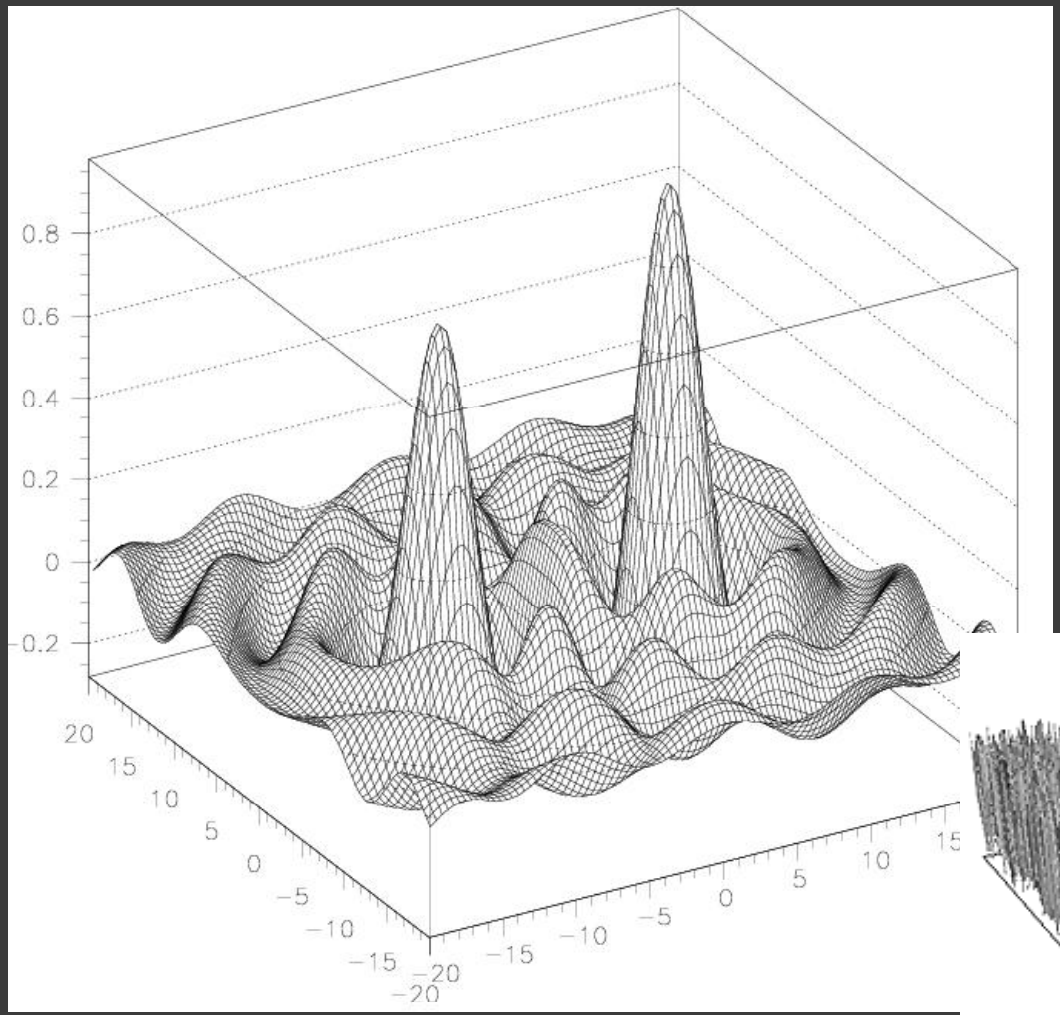
Fitness of oil function

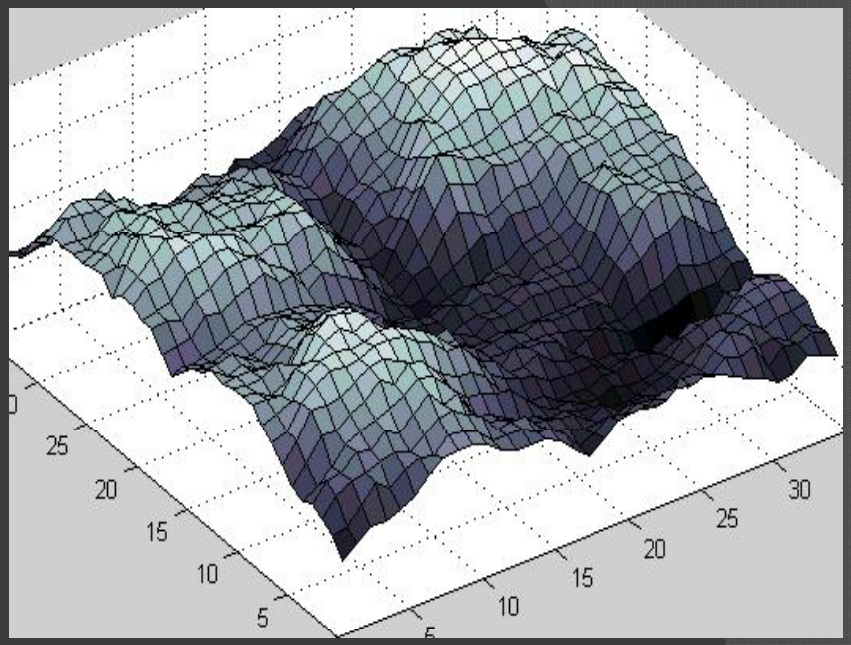


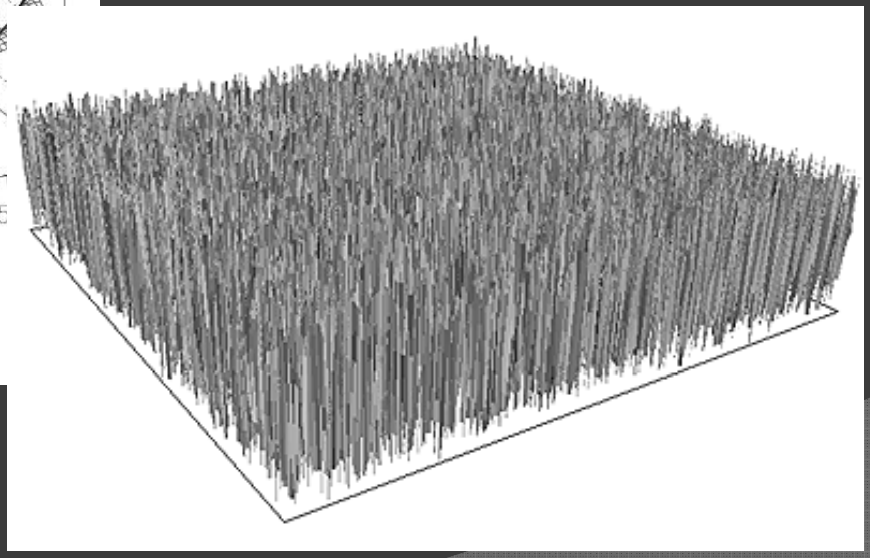
Search space

- Oil example: search space is one dimensional (and stupid: how to define a fitness function?).
- RTE: encoding several values into the chromosome many dimensions can be searched
- Search space an be visualised as a surface or fitness landscape in which fitness dictates height (fitness / chisqr hypersurface)
- Each possible genotype is a point in the space
- A GA tries to move the points to better places (higher fitness) in the space

Fitness landscapes (2-D)







Search space

- Obviously, the nature of the search space dictates how a GA will perform
- A completely random space would be bad for a GA
- Also GA's can, in practice, get stuck in local maxima if search spaces contain lots of these
- Generally, spaces in which small improvements get closer to the global optimum are good

The algorithm

- Generate a set of random solutions
- Repeat
  - Test each solution in the set (rank them)
  - Remove some bad solutions from set
  - Duplicate some good solutions
  - make small changes to some of them
- Until best solution is good enough

How to duplicate good solutions?

Adding Sex

- Two high scoring “parent” bit strings (chromosomes) are selected and with some probability (crossover rate) combined
- Producing two new offsprings (bit strings)
- Each offspring may then be changed randomly (mutation)
- Selecting parents: many schemes possible, example:
  Roulette Wheel
  - Add up the fitness's of all chromosomes
  - Generate a random number R in that range
  - Select the first chromosome in the population that - when all previous fitness’s are added - gives you at least the value R

sex

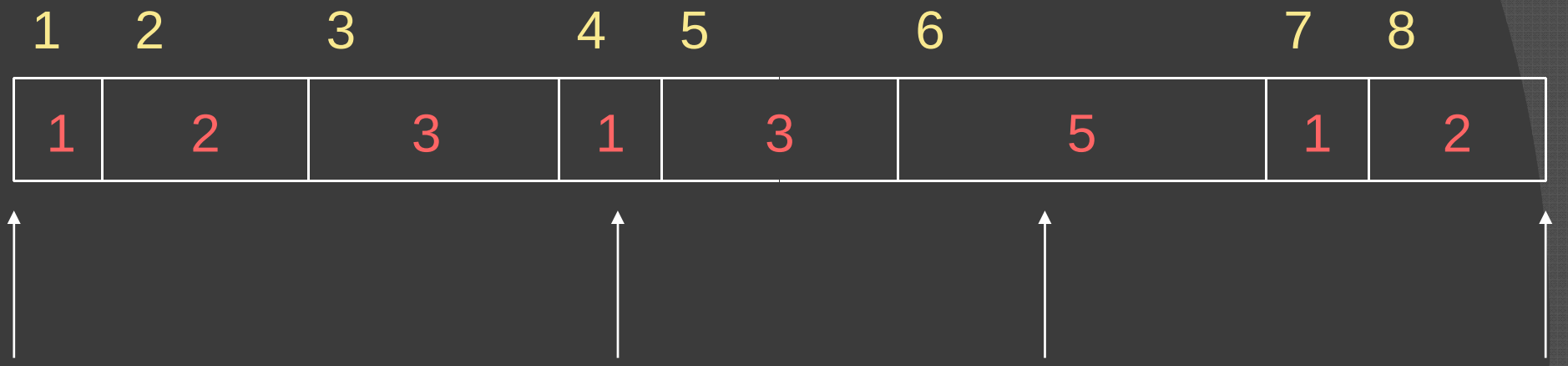
result of sex

parents are seldom happy with the result

Example population

No.	Chromosome	Fitness
1	1010011010	1
2	1111100001	2
3	1011001100	3
4	1010000000	1
5	0000010000	3
6	1001011111	5
7	0101010101	1
8	1011100111	2
		sum: 18

Roulette Wheel Selection



0

Rnd[0..18] = 7

Chromosome4

Parent1

Rnd[0..18] = 12

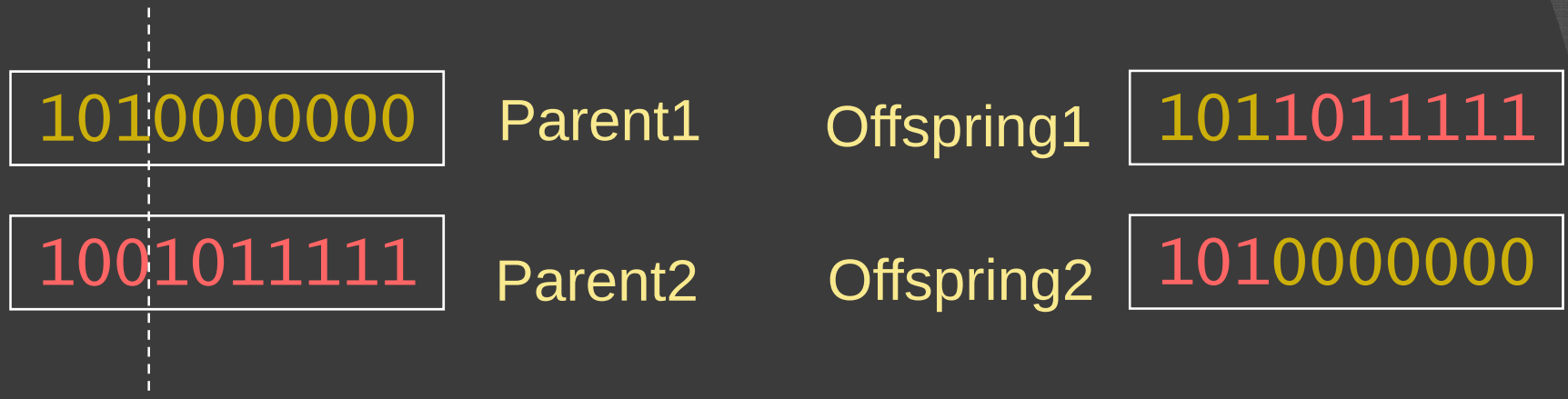
Chromosome6

Parent2

18

Higher chance of picking a fit chromosome!

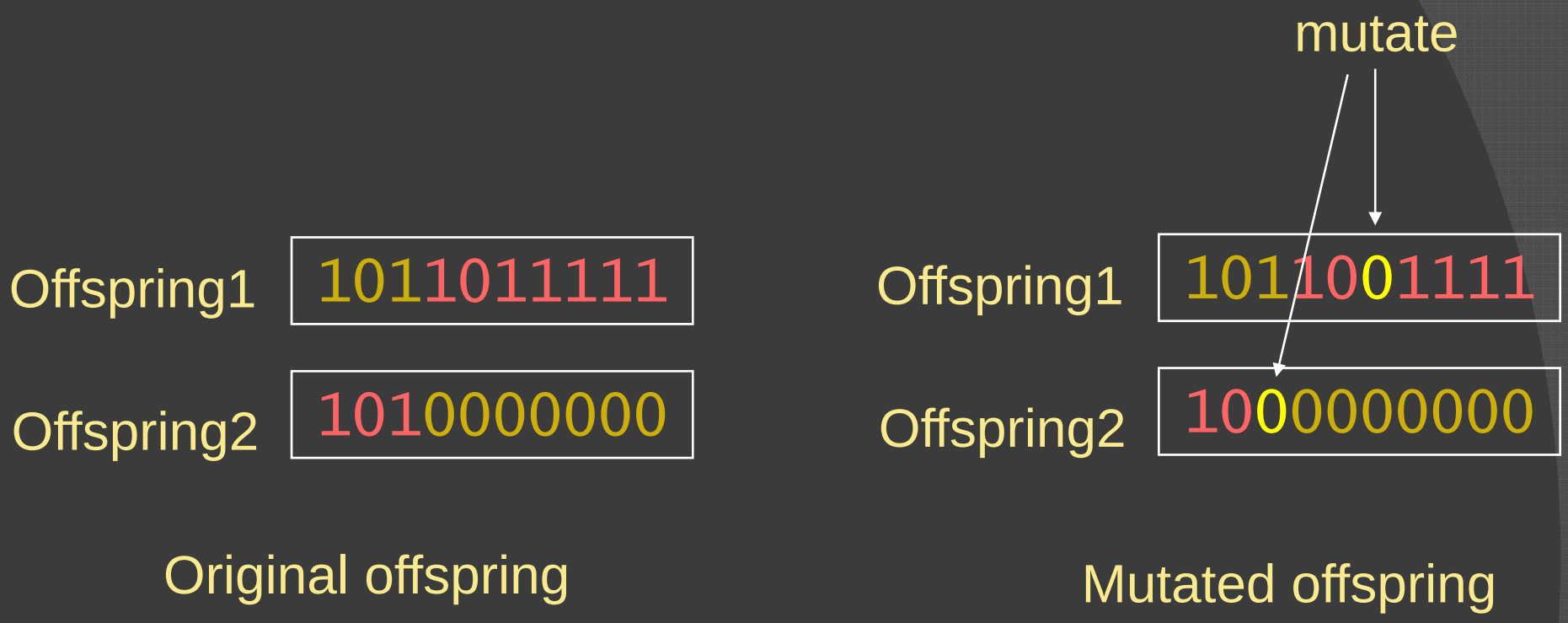
Crossover - Recombination



Crossover single point - random

With some high probability (*crossover rate*) apply crossover to the parents. (*typical values are 0.8 to 0.95*)

Mutation



With some small probability (the *mutation rate*) flip each bit in the offspring (*typical values between 0.1 and 0.001*)

Improved algorithm

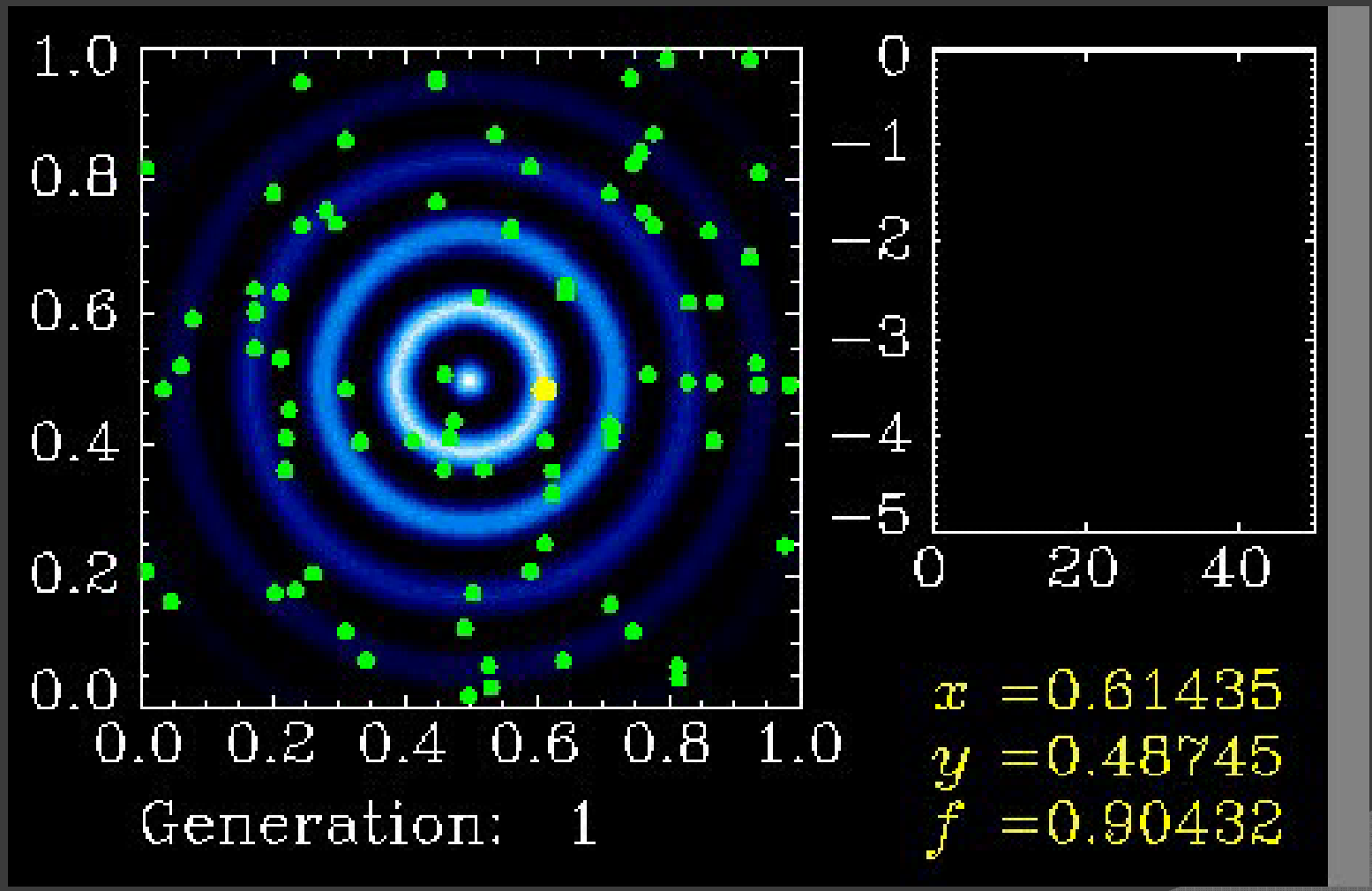
- Generate a *population* of random chromosomes
- Repeat (each generation)
  - Calculate fitness of each chromosome
  - Repeat
    - Use roulette selection to select pairs of parents
    - Generate offspring with crossover and mutation
  - Until a new population has been produced
- Until best solution is good enough

Many Variants of GA

- Different kinds of selection (not roulette):
  Tournament, Elitism, etc.
- Different recombination:
  one-point crossover, multi-point crossover, 3 way crossover etc.
- Different kinds of encoding other than bitstring
  Integer values, Ordered set of symbols
- Different kinds of mutation
  variable mutation rate
- Different reduction plans
  controls how newly bred offsprings are inserted into the population

PIKAIA (Charbonneau, 1995)

How PIKAIA works…



List of ME Codes (incomplete)

- HeLIx+
  A. Lagg, most flexible code (multi-comp, multi line), He 10830 Hanle slab model implemented. Genetic algorithm Pikaia. Fully parallel.
- VFISV
  J.M.Borrero, for SDO HMI. Fastest ME code available. F90, fully parallel. Levenberg-Marquardt with some optimizations.
- MERLIN
  Written by Jose Garcia at HAO in C, C++ and some other routines in Fortran. (Lites et al. 2007 in Il Nouvo Cimento)
- MELANIE
  Hector Socas at HAO. In F90, not parallel. Numerical derivatives.
- HAZEL
  Artoro Lopez Ariste et al. (2008). Optimized for He 10830, He D3, Hanle-slab model.
- MILOS
  Orozco Suarez et al. (2007), IDL, some papers published with it

Installation & Usage of HeLIX+

Follow instructions on user's manual:

He-Line Information Extractor+ HELIX+

Andreas Lagg · Max-Planck-Institut für Sonnensystemforschung · Katlenburg-Lindau, Germany

Basic usage:

- 1-component model, create & invert synthetic spectrum
- discuss problems:
  - parameter crosstalk
  - uniqueness of solution
  - stability & reliability
  - influence of noise

Download from http://www.mps.mpg.de/homes/lagg
GBSO download-section → helix
use *invert* and *IR$soft*

Exercise II:
HeLIx$^+$ installation and basic usage

- install and run IDL interface of HeLIx$^+$
- the first input file: synthesis of Fe I 6302.5
  - change atmospheric parameters (B, INC, …)
  - change line parameters (quantum numbers, g_{eff})
  - display Zeeman pattern
- add noise
- 1st inversion
- play with noise level / initial values / parameter range
- weighting scheme

Synthesis

- add complexity to atmospheric model (stray-light, multi-component)
- add 2nd spectral line (Fe 6301.5)

blind tests:

- take synthetic profile from someone else and invert it

- Which parameters are robust?
- How can robustness be improved?

Download first input file: abisko_1c.ipt
http://www.mps.mpg.de/homes/lagg/