

# Understanding the most Massive Stars in the Universe using Genetic Algorithms

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- 7

- $L$

- $\Lambda$

- $\alpha$

$M_{\odot}/\text{yr}$

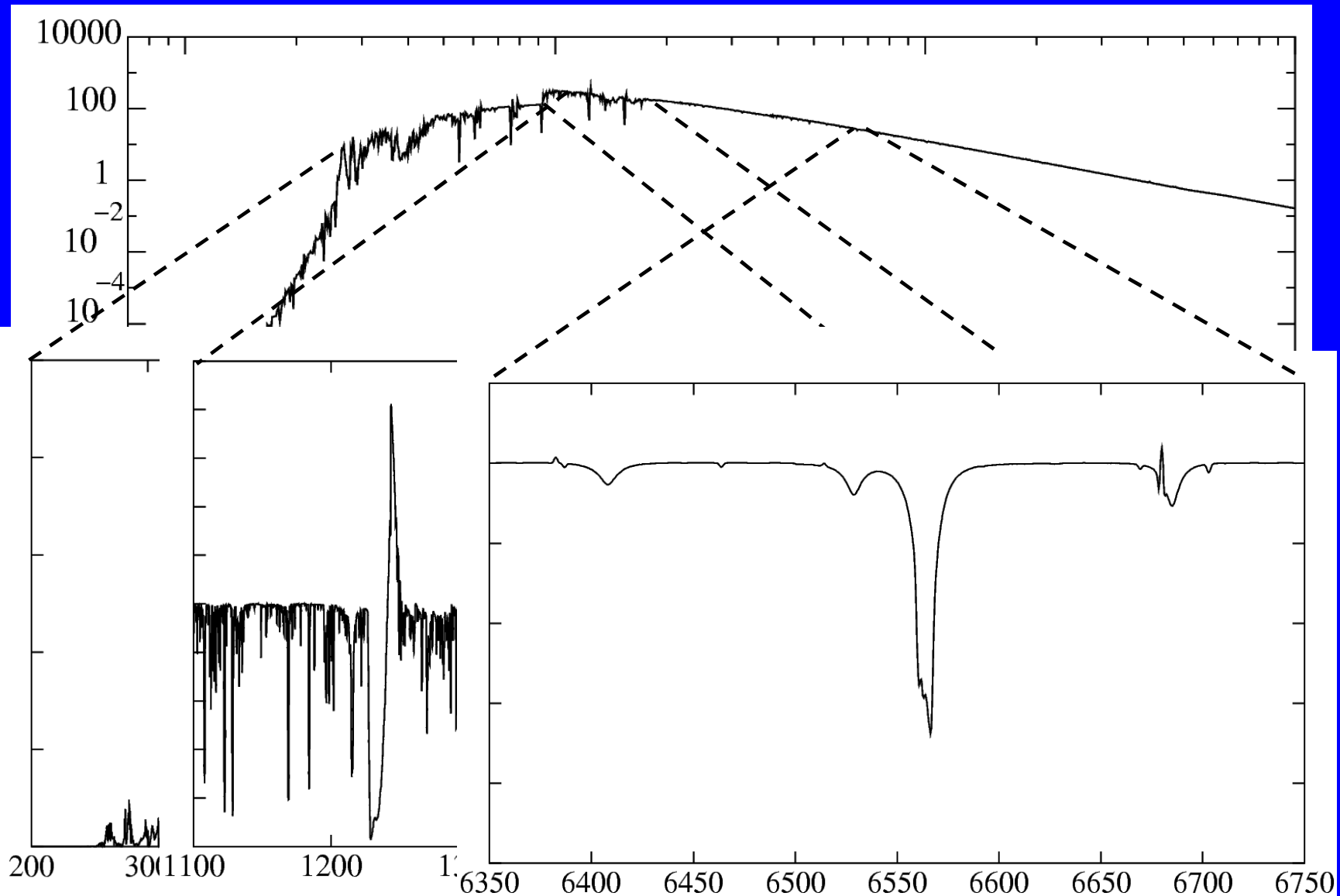


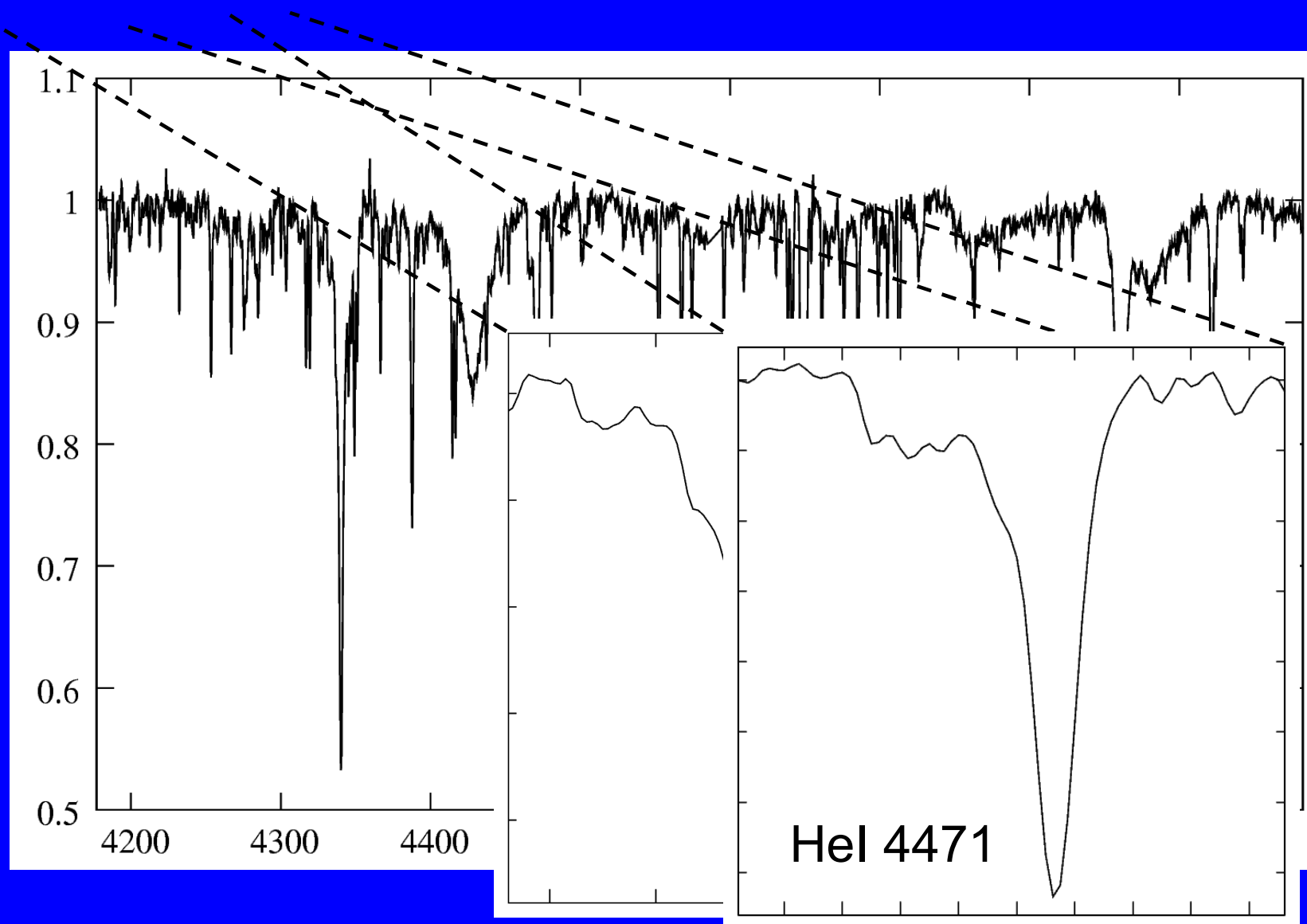
# Importance of massive stars

- Evolution of Galaxies
- Super Novae
- Gamma-ray bursts
- Neutron Stars & Black Holes
- Re-ionization of early universe

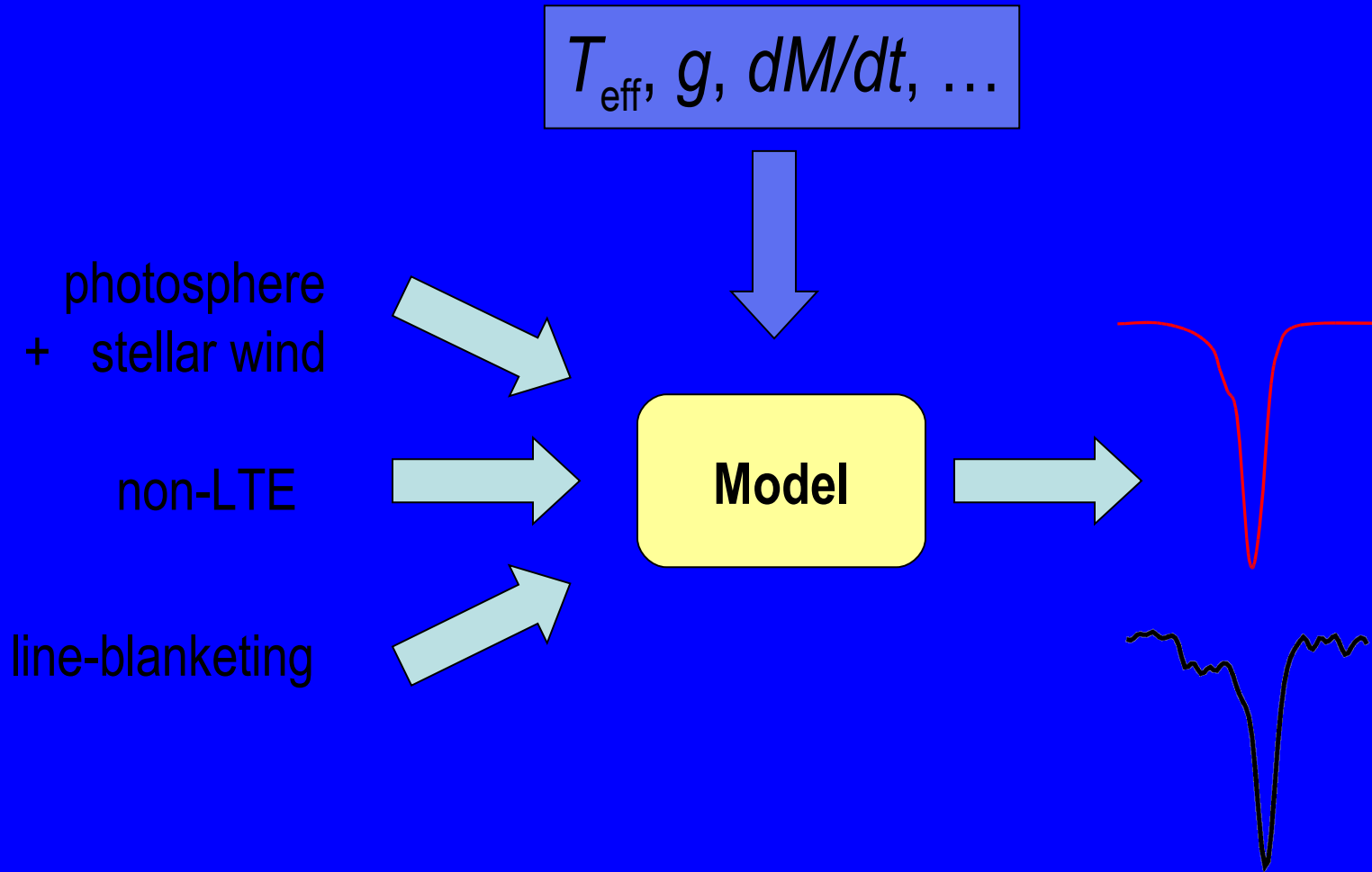
# Large sample analysis

- ~100 analyzed until now
- Flames Survey
  - ~100 hours VLT time
  - Galactic, SMC and LMC fields
  - will double total number of analyzed stars
  - calibration of fundamental parameters
- Quantitative spectroscopy





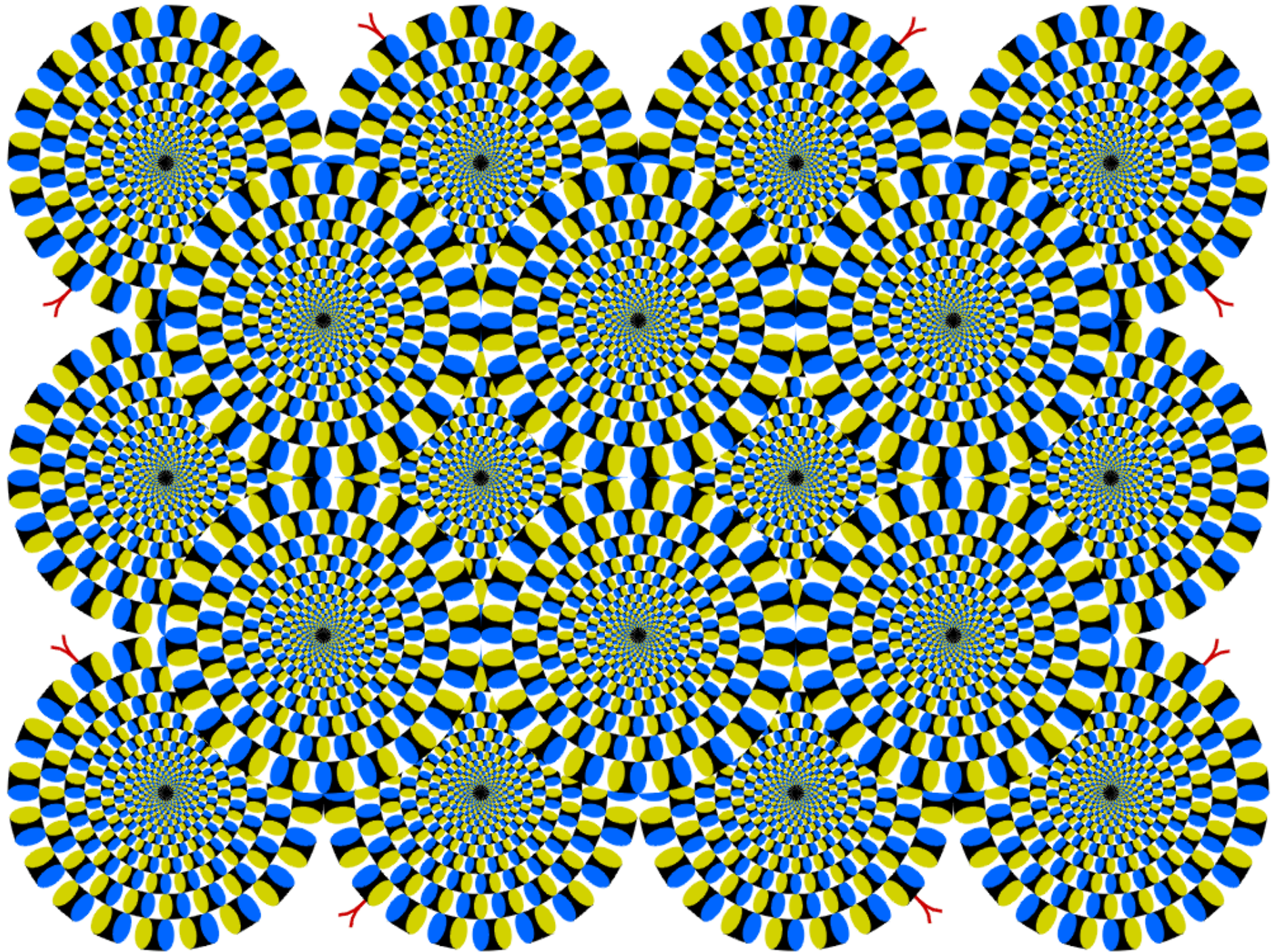
# Quantitative spectroscopy



“by eye”

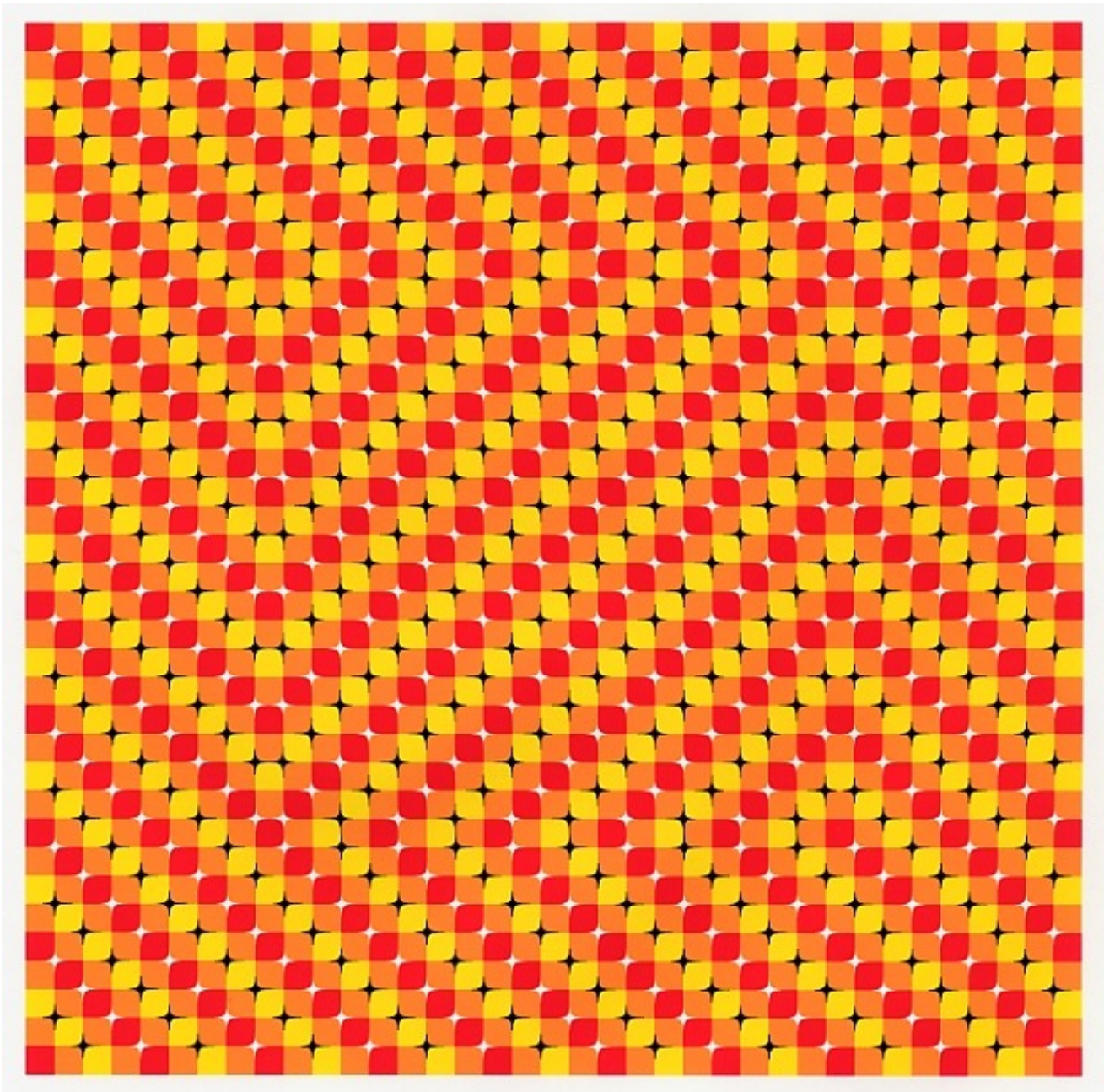
- The conventional method
- However, ...





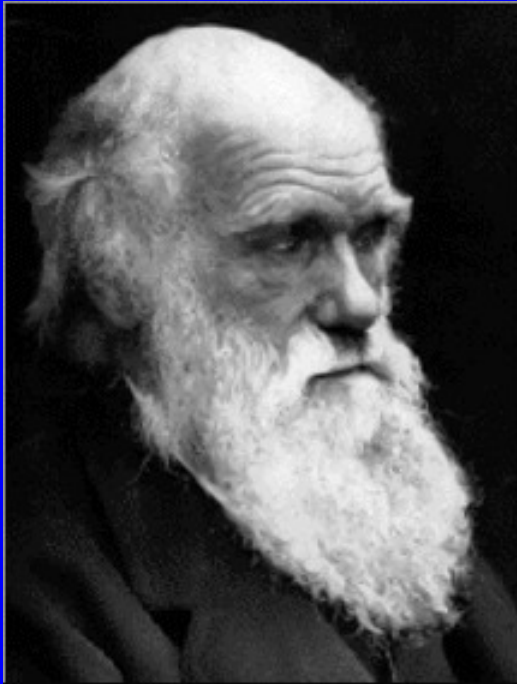
# Drawbacks of fitting “by eye”

- Laborious
- Limited number of physical parameters
- Not reproducible
  - biases
  - best fit?
- No large sample, and ...



It gives you a headache

# Natural selection



Charles Darwin  
1809 -1882

“I have called this principle, by which each slight variation, if useful, is preserved, by the term Natural Selection.”

# Genetic Algorithms

Adaptative heuristic search method using Darwinian principles

## **Applications:**

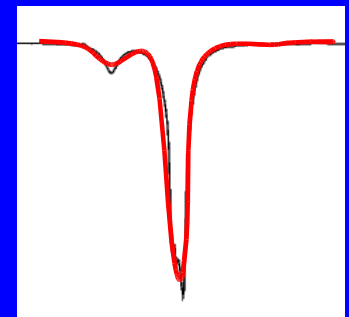
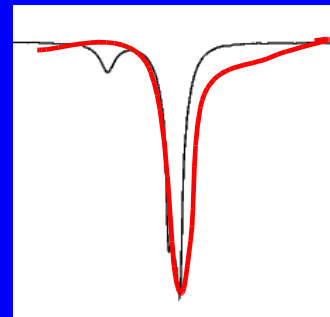
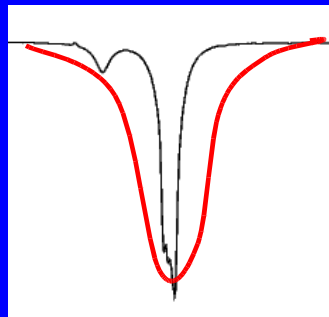
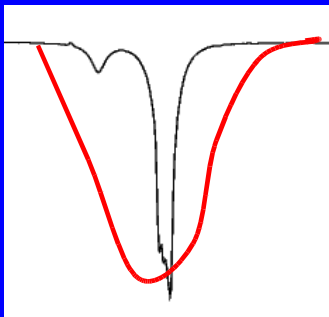
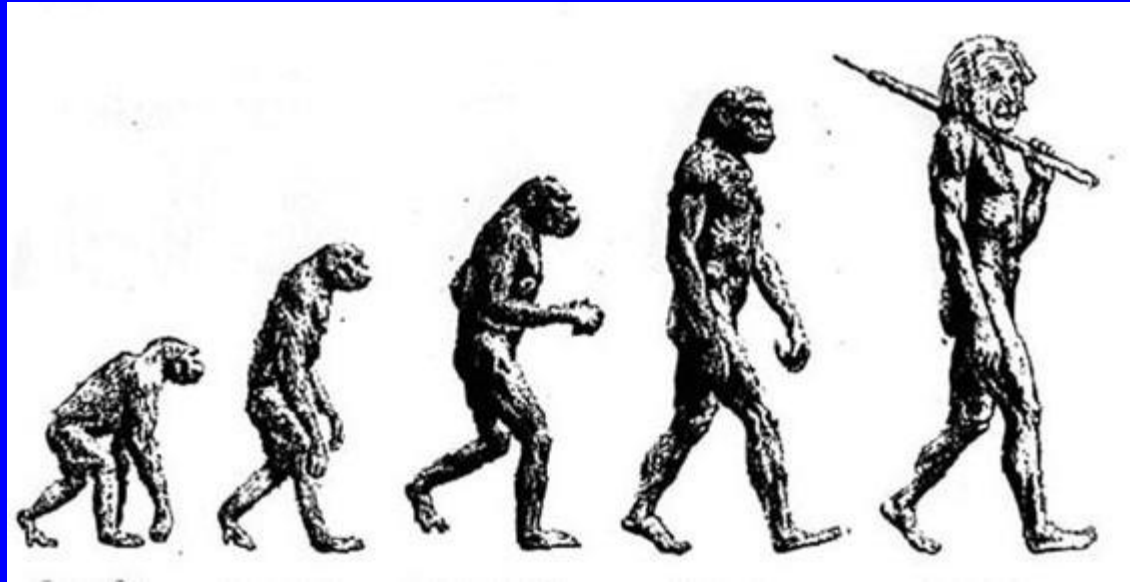
Scheduling, Data fitting, Trend spotting, Budgeting, ...

Any search for which all solutions cannot be tested.

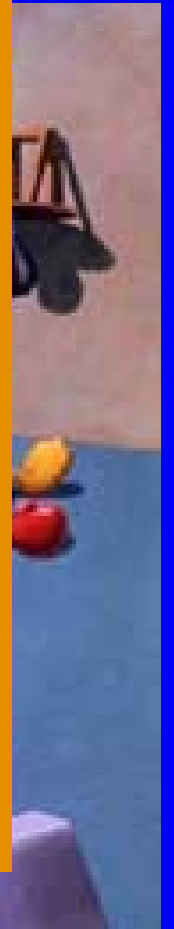
## **Scheme:**

1. Initialization: compute solutions for random parameters
2. Selection: retain successful solutions
3. Reproduction: deduce potentially better model parameters
4. Evaluation: compute and evaluate solutions
5. Termination: the best solution is satisfactory

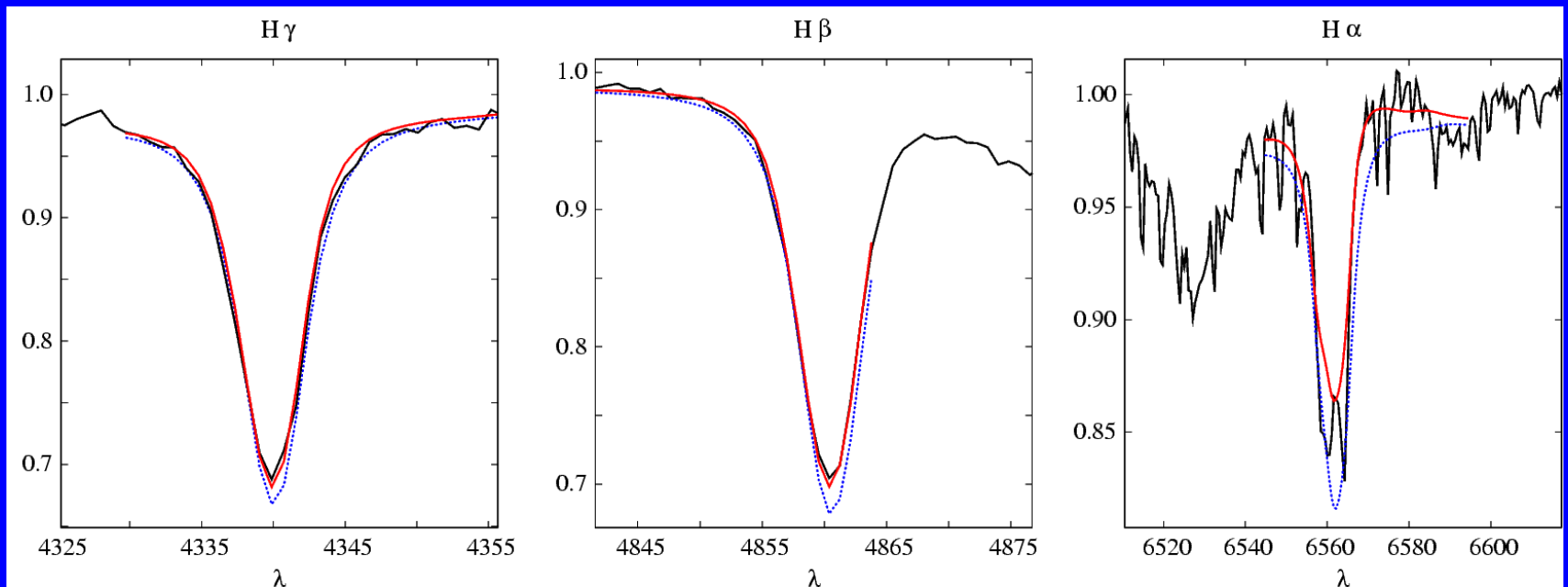
# Optimization technique



# Basic genetic algorithm

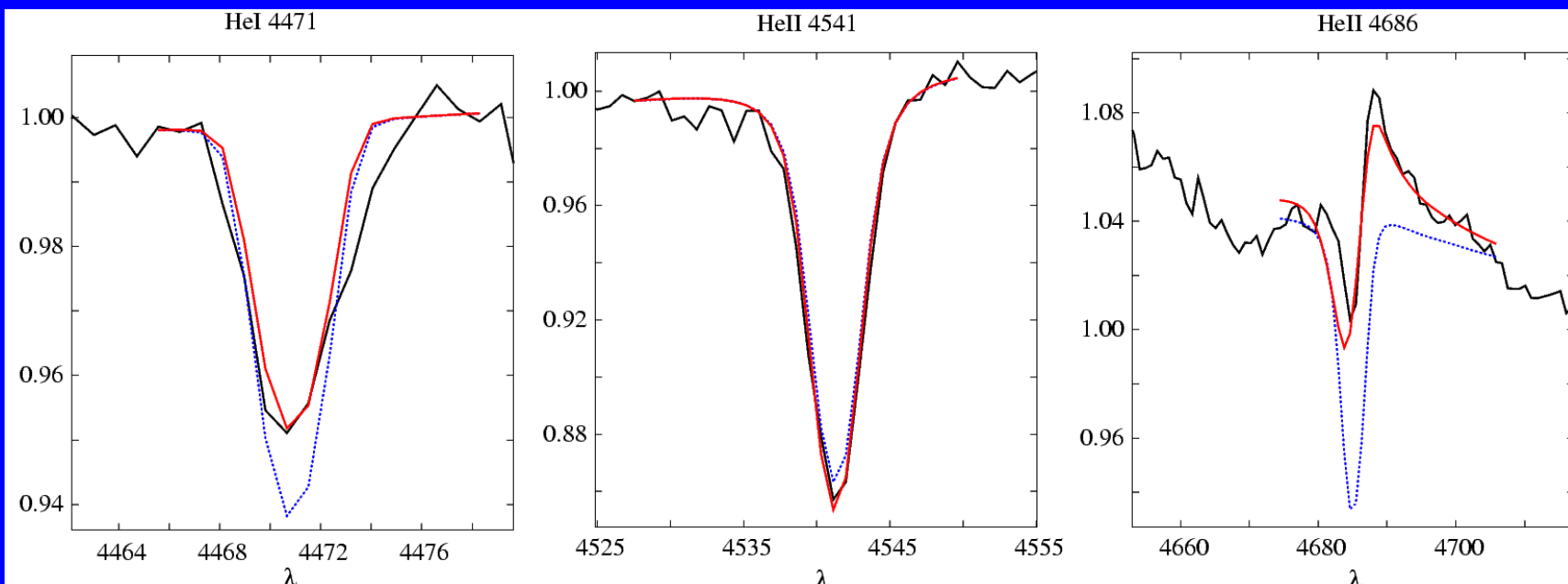


# Cyg OB2 8C O5 If Hydrogen lines





# Helium lines



# Encoding: from parameters to gene

**Bounds of parameters search domain:**

$$P_{imin} < P_i < P_{imax}$$

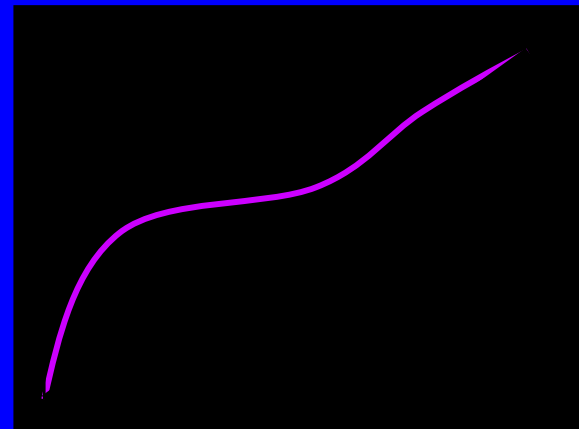
**Coding Function:**

$$F(P_i) = ph_i$$

$$F(31000K) = 0.274396$$

**Precision required:**

$$ph_i = 0.27 \text{ (2 digits)}$$



**Choice of gene base:**

2 (computers), 4 (life), 10 (physics)...

$$g_i = 27$$

**PARAMETERS TO GENE**  
**(31000K, 3.65, 10E-8, 0.8)  $\approx$  27421809**

# Reproduction

## Cross parents:

1, 2 or more cross points

Include complementary kid (base 2)

P1(7395725439)

P2(9243872374)

K1(7393872339)

K2(9245725474)

## Mutate kids:

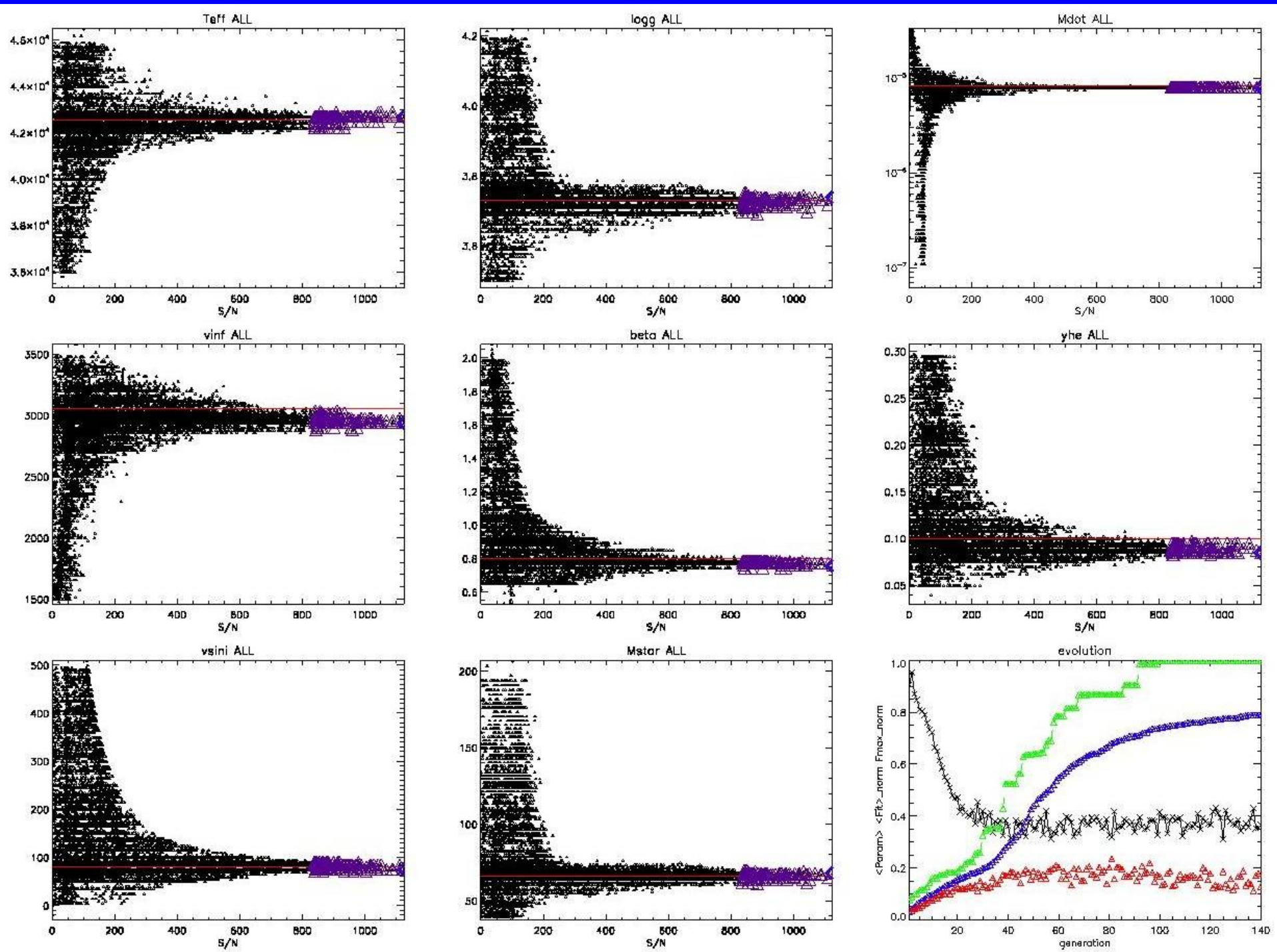
Normal mutation, creep mutation or both

Constant or varying mutation rate

Same or different for each gene locus

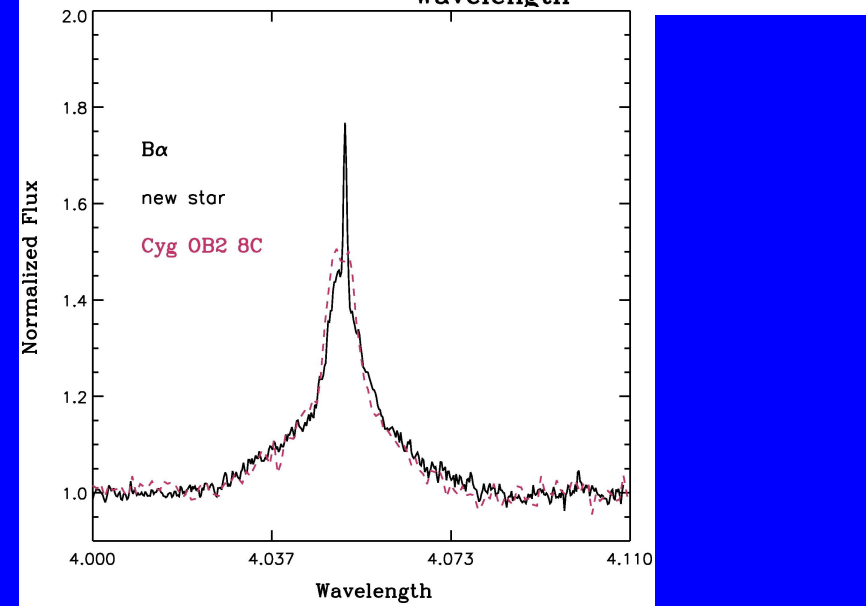
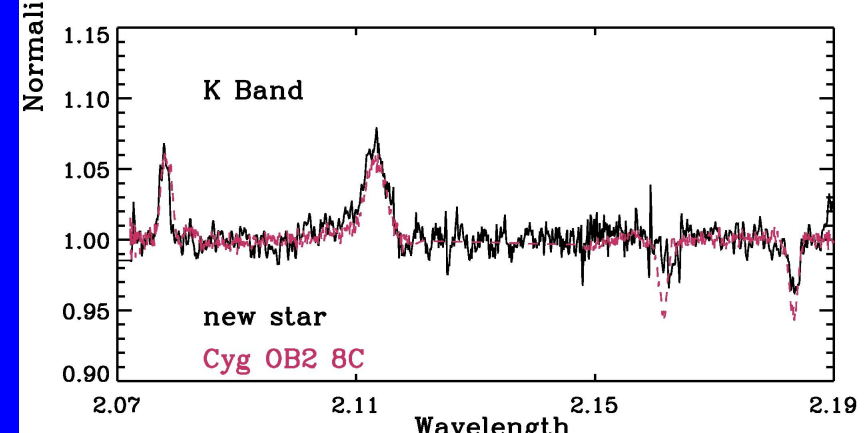
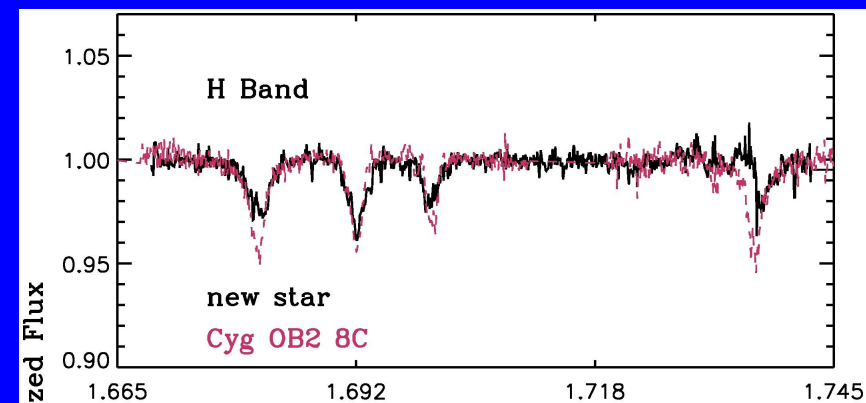
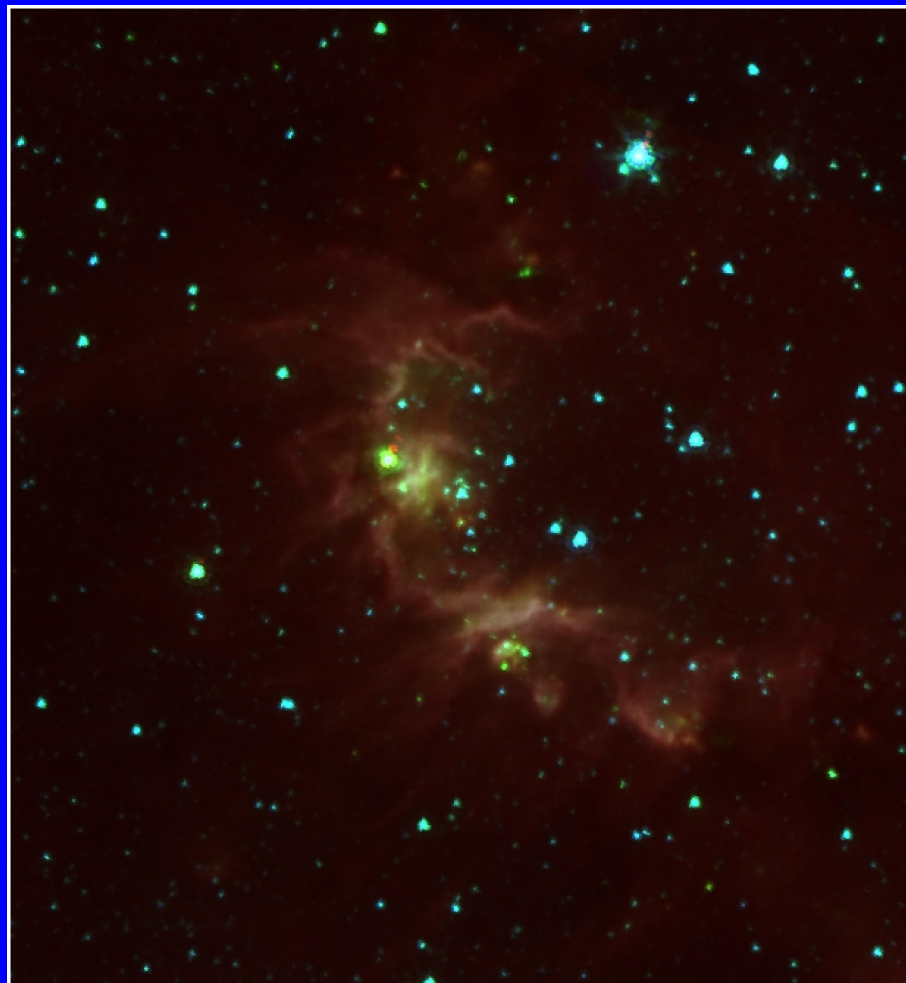
K1(7393972340)

K2(9145725874)



# CESGA PROJECT: New Obscured clusters in the Milky Way

Lenorzer et al 2008



# OUR CASE

About 10 parameters coded on 2 digits each: gene length  $\approx 20$   
Model running in 30 min, 50 processors: population size  $\approx 100$

Random search would take  $\langle 1.E8 \text{ generations} \rangle$  for 1 digit accuracy  
Need a high selection pressure to be “fast”

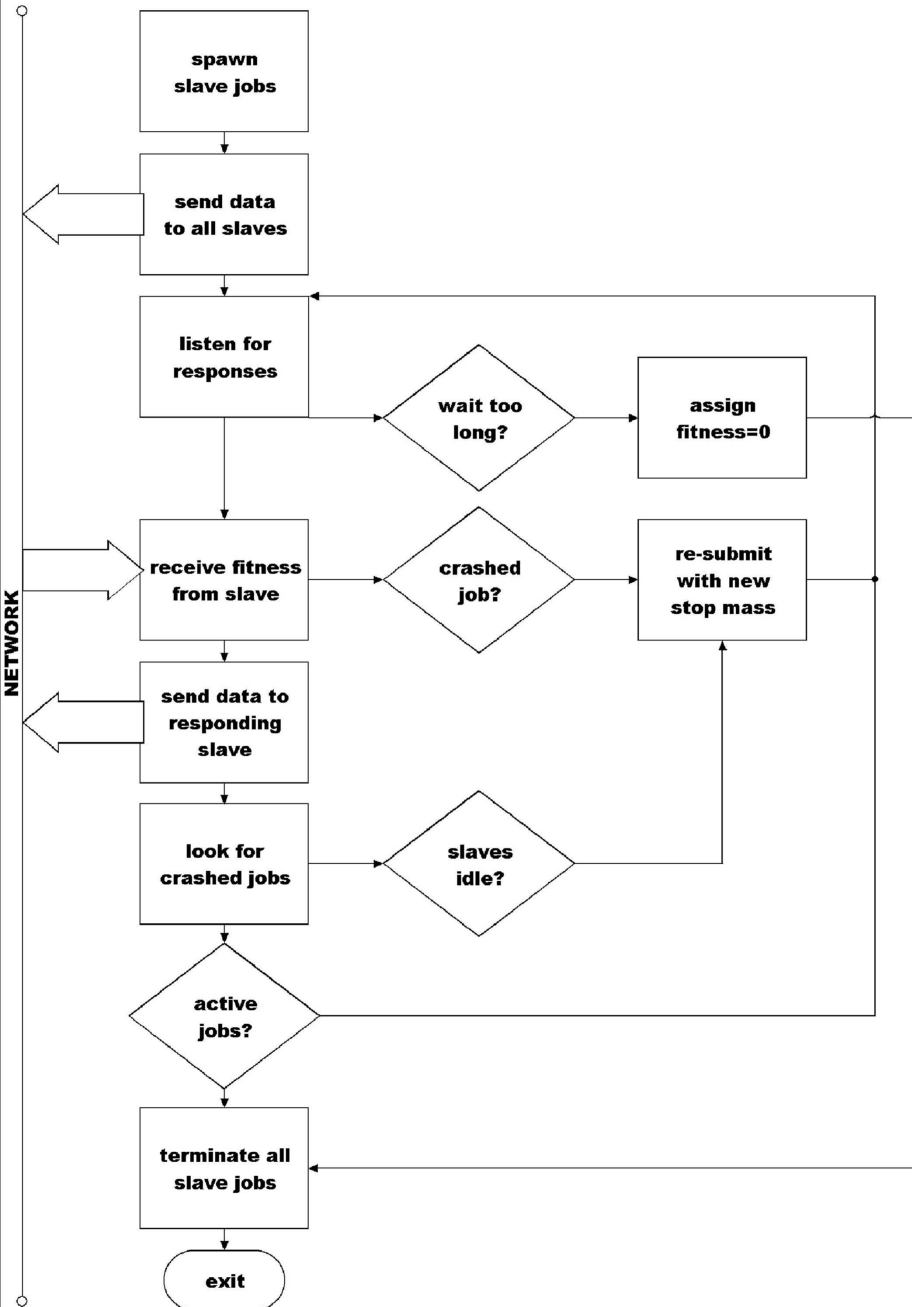
Initial population: each gene value present  $\langle \text{pop}/\text{base} = 10 \text{ times} \rangle$   
Without mutation all genes are the same after  $\approx 50$  generations

Mutation needs to be high enough to keep gene diversity  
Mutation rate needs to be low enough to allow gene convergence  
Uniform mutation  $\Rightarrow$  genetic based adaptive mutation

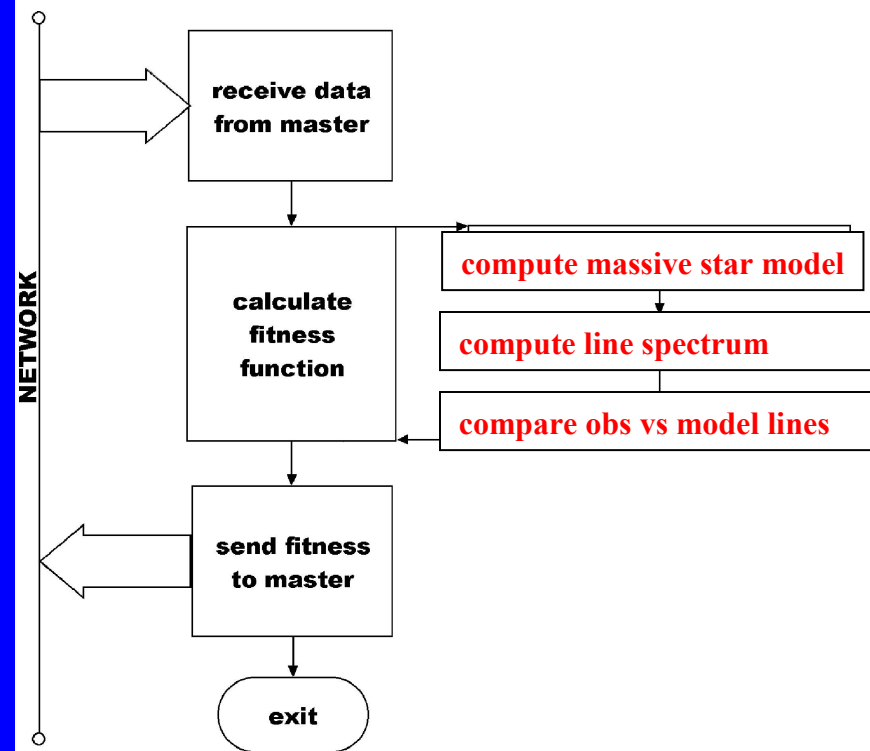
Mutation rate needs to be low enough to maintain evolution  
Full generation replacement  $\Rightarrow$  Steady state replace worst

$$F_{gn} = F_{gn-1} \times P_{sel} \times (1 - P_{mut}) + P_{mut} \times \text{pop}/\text{base}$$

# PVM\_FITNESS.F



# FF\_SLAVE.F



# Scalability on parallel computers

