

# Searching for spinning black hole binaries in mock LISA data using a genetic

**Antoine Petiteau**

**in collaboration with Shang Yu, Stanislav Babak  
(Albert Einstein Institute - Potsdam)**

**Video seminar Golm - Hannover**

**5<sup>th</sup> May 2009**





# Likelihood maximization for spinning Black Hole Binary

## 15 parameters :

Ecliptic latitude  $\beta$ , ecliptic longitude  $\lambda$ , chirp mass  $M_c$ , mass ratio  $\eta$ , time of coalescence  $t_c$ , luminosity distance  $D_L$ , phase at coalescence  $\phi_c$ , direction of orbital angular momentum  $\theta_L$  &  $\phi_L$ , spin amplitude  $\chi_1$  &  $\chi_2$  and direction  $\theta_1, \theta_2, \phi_1$  &  $\phi_2$ .

## Model :

Numerical integration of the two spins and the angular momentum using differential equations from **Apostolatos, Cutler, Sussman & Thorne, PRD 49 12 (1994)**

Computation of  $h_+$  and  $h_x$  in barycentric frame and then in LISA frame : phase up to 2PN and amplitude up to 0 PN (**gr-qc08062110: MLDC 1b to 3**).

**TDI** : We use A & E in low frequency approximation

Maximization of likelihood  $\mathcal{L}$  over two extrinsic parameters :  $D_L$  and  $\phi_c$

➔ Reduce the number of parameters to 13.

Maximization over time of coalescence using sliding template.

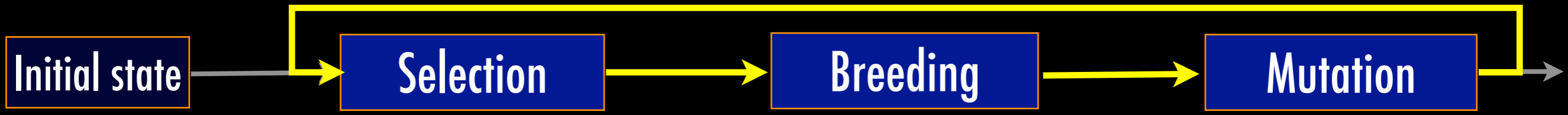




# Genetic Algorithm : Principe

Description : gene ↔ parameter : binary representation :  
 parameter value ↔ 0 1 1 1 0 0 1 0 1 0 0 1

Evolution : organism ↔ template described by a set of genes



**Selection :** Selection of parents for the breeding

Probability of selecting one organism depend on Quality.

1. Quality  $Q_i = \text{Maximized Likelihood}$ ,
2. Sort organisms by decreasing normalized quality
3. Roulette selection : Select one organism with probability equal to  $Q_{Ni} / \sum_j^N Q_{Nj}$

**Breeding :** Making 1 child from the 2 selected parents

Mixing parts of corresponding parental genes. Several types of breeding :

- Crossover one point :
 

	0	1	1	1	0	0	1	0	1	0	0	1
	1	0	0	0	0	1	1	1	0	0	1	0
crossover 1pt midpoint	↓											
	0	1	1	1	0	0	1	1	0	0	1	0
- Crossover two point :
 

	0	1	1	1	0	0	1	0	1	0	0	1
	1	0	0	0	0	1	1	1	0	0	1	0
crossover 2pts	↓				↓							
	0	1	1	1	0	1	1	1	1	0	0	1
- Others ...

**Mutation :** Change few bits in gene

Probability of change described by the 'Probability Mutation Rate' (PMR)  $\in [0,1]$ .

Several types of mutation :

- Mutate bits independently : for each bit compare PMR to a random value  $\alpha$ . If  $\alpha < PMR$ , flip bit (0  $\rightarrow$  1 or 1  $\rightarrow$  0).
- Mutate all the gene : If a random value  $\alpha < PMR$ , mutate the gene. Several types :
  - Choose randomly N bits and flip them.
  - Complete random value

# Acceleration processes

Elitism (cloning): Keep the best organism through the generations.

→ **Stability**: The algorithm always converges.

Simulated annealing: Temperature evolution

→ **Control of smoothness of likelihood space.**

Evolution of PMR of each gene

→ **Control exploration of parameters' space.**

Brother: Construct new organism from the best organism using specific rules.

→ **Look at the opposite sky position of the clone, ...**

Local mutation: small random change of gene value.

→ **Remove boundary of bit zone.**

Fix bits: When the true solution is approaching, fix the most significant bits for reducing the search space

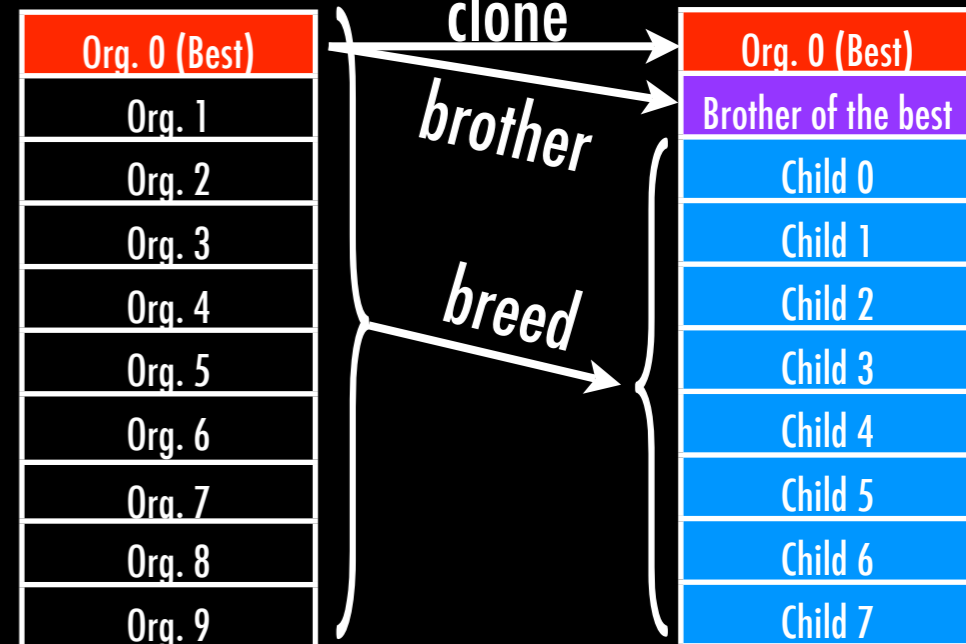
→ **Controls size of parameter space.**

Evolution of specific breeding type and mutation type for each gene.

→ **Customizes the algorithm.**

Change organisms' environment: Frequency cut-off of the waveform

→ **Helps us for finding the global maxima.**





# Multimodal search

[ Large number of modes : multimodal distribution of log-likelihood due to degeneracies in the parameter space, and multiple local maxima.

[ Multiple signals in the data stream

[ For exploring these modes, we put cluster of organisms on each mode

— One clone for each mode,

— Modes are separated using diagonal terms of covariance matrix (inverse of Fisher matrix) and a threshold on SNR.

## A-statistic

[ In our last development, we use as quality function a new function called Astatistic.

[ A-statistic is a geometrical mean of the log-likelihood for the whole duration template and the low-frequency template (shortened).

[ It enhances from the low-frequency part (where our template works the best) and reduces local maxima (in size and in number).



# Preliminary results

(from MLDC 3.2 training & blind test extrapolation)

Find 5 sources in training (true number) and 5 in the blind test.

	$t_c < T_{obs}$ (SNR ~ 100 to 2000)	$t_c > T_{obs}$ (SNR ~ 10 - 20)
Sky position	$\Delta sky \leq 4^\circ$ + opposite sky position	$\Delta sky \leq 6-10^\circ$ + opposite sky position
Time at coalescence	$\Delta t_c \leq 1000$ s + mode corresponding to one cycle shift	$\Delta t_c \leq 10^5$ s - $10^6$ s
Masses	$\Delta M_c \leq 1000 M_S \sim 0.1\%$ ; $\Delta \eta \leq 0.01 \sim 4\%$ (several modes)	$\Delta M_c \leq 2000-5000 M_S \sim 0.2-0.6\%$ ; $\Delta \eta \leq 0.02 \sim 10\%$ (several modes)
Orbital angular momentum	Large number of modes	Large number of possibilities but one part can be excluded
Spin amplitude	$\Delta \chi \leq 0.2$	Very large number of possibilities with similar SNR
Spin direction	Large number of modes	

Works in progress :

- Improve multi-mode system, automatic update of algorithm following parameters and quality evolution,
- Comparison with others methods (first overview of MLDC : SNR obtained with GA similar to the one obtained with MLDC), ...



Thank you

