The search for spinning black hole binaries using a genetic algorithm

Antoine Petiteau, Yu Shang and Stanislav Babak

Max-Planck-Institut fuer Gravitationsphysik, Albert-Einstein-Institut,
Am Muchlenberg 1, D- 14476 Golm bei Potsdam, Germany

E-mail: Antoine.Petiteau@aei.mpg.de

Abstract. We use a genetic algorithm to analyze the data from the third round of the mock LISA data challenge. These data consist of gaussian stationary instrumental noise, a Galactic background and four to six signals from the inspiralling spinning BHs in quasi-circular orbits. We present a particular implementation of the genetic algorithm which uses properties of the signal and the response function. We discuss the results of a preliminary search for a single signal in the instrumental noise.

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1. Introduction

Coalescence of two massive Black Holes (MBH) in the galactic nuclei is the strongest and most promising source of gravitational waves (GW) for LISA. This source is so powerful that the merger will be detected throughout the Universe. The observed event rate and parameters of the binary systems will allow us to trace the history of MBH formation [1]. Gravitational wave observations should enable us to measure masses and spins of MBHs in the binary with unprecedented accuracy [7]. We expect that almost all MBHs are spinning, and the value of spin might vary according to the channel of MBH formation. For example, if significant mass of MBH was acquired through an accretion disk then we could expect MBH to have spin close to the maximum.

The search for two inspiralling binaries in LIGO-VIRGO data usually utilizes the templates for the non-spinning compact objects. The reason behind it is that the non-spinning templates can achieve a reasonable match which is sufficient for the detection. The follow up analysis should reveal whether the compact objects have spins. LISA data analysis is usually not about detection but rather about a very accurate estimation of the parameters. And, as it was shown in [2, 7], including the spins should significantly improve the estimation of parameters due to de-correlation of the parameters entering the expression for the GW phase.

Previously, several algorithms for detecting the non-spinning MBH binaries in the simulated LISA data were demonstrated [16, 3]. In this paper we describe a particular adaptation of a genetic algorithm for searching the GW signal from the inspirall of two spinning MBHs. The genetic algorithm (GA) is one of the methods for optimization (finding extremum). A waveform template here is associated with an organism, and parameters play the role of the set of genes defining that organism. The logarithm of likelihood obtained with a given template defines the quality of the organism. Then we need to adopt the way of evolving the set of organisms to improve the quality: "weak dies, strong lives". In other words, we are searching for maxima of the likelihood.

The structure of the paper is as follows. We describe the model of the GW signal in the Section 2. Then we give the basic principles of a standard GA in the Section 3. In the Section 4 we consider modification and improvements of GA intrinsic to the search for spinning MBH binaries. We give some preliminary results in the Section 5, and we conclude with the summary Section 6.

2. Template and quality estimation

2.1. Model of the signal

The waveform is described by fifteen parameters: the two masses m_1 and m_2, the initial direction of the orbital angular momentum, polar angle θ_L and azimuthal angle ϕ_L, the initial direction of the spins, polar angles θ_{S_1} and θ_{S_2} and azimuthal angles ϕ_{S_1} and ϕ_{S_2}, the dimensionless spin parameters, χ_1 and χ_2, the time at coalescence t_c, the phase at coalescence Φ_c, ecliptic coordinates of the source latitude β and longitude λ, and the

luminosity distance D_L.

The spin-orbit and the spin-spin interactions induce a precession of each binary member's spin vector and of the orbital angular momentum. The precession equations are given in [5] and the waveform used in the mock data is described in details in [6].

We have used two orthogonal (with uncorrelated noise) TDI (time delay interferometry) channels A and E in the phase domain (strain). TDIs are the time delayed combinations of the measurements which significantly reduces the laser noise [8, 9]. In our template, we consider a long wavelength approximation of these signals [11, 12]. This approximation ($L\omega \ll 1$, where L is LISA' armlength and ω is an instantaneous frequency of GW) works pretty well below approximately 5 mHz. We also have assumed rigid LISA with equal arms. Then the waveform takes the following form [11, 12]

$$\begin{aligned} h_I(t) \simeq 2L\ \sin\Delta\phi_{2L}(t_k)\,\{&-h_{S0+}(t_k)\,[\cos\left(2\psi(t_k)\right)F_{+I}(t_k)- \\ &\sin\left(2\psi(t_k)\right)F_{\times I}(t_k)]\sin\phi'(t_k) + h_{S0\times}(t_k)\,[\sin\left(2\psi(t_k)\right)F_{+I}(t_k)+ \\ &\cos\left(2\psi(t_k)\right)F_{\times I}(t_k)]\cos\phi'(t_k)\}\,, \end{aligned} \tag{1}$$

where $I = \{A, E\}$, t_k is the time in LISA frame, ψ is the polarization angle, h_{S0+} and $h_{S0\times}$ are the polarization amplitudes of the GW in the source reference frame, $\Delta\phi_{2L}(t) = (\phi(t_k) - \phi(t_k - 2L))/2$, $\phi'(t) = (\phi(t_k) + \phi(t_k - 2L))/2$ with $\phi(t)$ being the phase of GW. The antenna pattern function F_{+I} and $F_{\times I}$ has the following expression:

$$\begin{aligned} F_+(\theta_d, \lambda_d; t, \Omega) = \frac{1}{32}\,&[6\sin(2\theta_d)\,(3\sin\left(\Phi_T(t) + \lambda_d + \Omega\right) - \sin\left(3\Phi_T(t) - \lambda_d + \Omega\right)) \\ &-18\sqrt{3}\sin^2\theta_d\sin\left(2\Phi_T(t) + \Omega\right) - \sqrt{3}\left(1 + \cos^2\theta_d\right)\times \\ &(\sin\left(4\Phi_T(t) - 2\lambda_d + \Omega\right) + 9\sin\left(2\lambda_d + \Omega\right))] \end{aligned} \tag{2}$$

$$\begin{aligned} F_\times(\theta_d, \lambda_d; t, \Omega) = \frac{1}{16}\,&\Big[\sqrt{3}\cos\theta_d(\cos(4\Phi_T(t) - 2\lambda_d + \Omega) - \\ &9\cos(2\lambda_d + \Omega)) + 6\sin\theta_d(\cos(3\Phi_T(t) - \lambda_d + \Omega) + \end{aligned} \tag{3}$$

$$3\cos(\Phi_T(t) + \lambda_d + \Omega))] \tag{4}$$

with $\theta_d = \beta + \pi/2$, $\lambda_d = \lambda + \pi$, $\Phi_T(t) = 2\pi t/Year$ and $\Omega = 0$ for A and $\Omega = \pi/4$ for E.

2.2. Quality estimation

As we have mentioned before we associate the quality of the organism with logarithm of the likelihood. For a template $h(\widehat{\theta})$ the likelihood is given by

$$\mathcal{L}(\widehat{\theta}) = Ce^{-\langle s - h(\widehat{\theta}) | s - h(\widehat{\theta})\rangle/2} \tag{5}$$

where s is the signal and $\langle h \mid s\rangle$ is the inner product defined as

$$\langle h \mid s\rangle = 2\int_0^\infty df\ \frac{\widetilde{h}(f)\,\widetilde{s}^*(f) + \widetilde{h}^*(f)\,\widetilde{s}(f)}{S_n(f)} \tag{6}$$

The tilde denotes the Fourier transform and $S_n(f)$ corresponds to the power spectral density of LISA' instrumental noise plus Galactic background approximated as described in [10]. The set of parameters $\widehat{\theta}$ maximizing the likelihood is called maximum likelihood estimator [13, 15, 14], and that is what we are searching for.

Before using any numerical maximization methods, it is possible to maximize over the luminocity distance and the phase at coalescence analytically. This is the usual procedure routinely used in the ground-based GW data analysis (see for example [18]).

We also efficiently maximize the likelihood over the time at coalescence by sliding the template across the data (we use correlation instead of the inner products). This procedure is described in [16, 17].

3. Genetic algorithm

3.1. Basic principle

We start with a brief introduction to the genetic algorithm and then give a detailed implementation and describe specific modifications to solve the problems at hand.

The GA is based on the natural selection principle which is the evolution theory established by C. Darwin. In the nature the organisms adapt themselves to their environment: the smartest/strongest/healthiest organism has more chances to survive and participates in the breeding to produce the offsprings. These two processes, selection and breeding, are used in genetic algorithm for making a new generation. Since the best organisms are more likely to participate in breeding, the new generation should be better than the previous one (at least no worse). In order to increase the exploration of the possible organisms, the third process, called mutation, has been introduced. One needs to associate some measure of "goodness" with each organism, in our case it is logarithm of the likelihood ($\log \mathcal{L}$), which we want to "improve" through the evolution of the organisms.

Each template described by a set of parameters $\widehat{\theta}$ is associated with an organism, and parameters play the role of genes. For describing genes we use a binary representation of each parameter. The allowed resolution for each parameter depends on the number of bits used for describing it. If the parameter x_k has a prior range between $x_{k,min}$ and $x_{k,max}$, its resolution is $\Delta x_k = (x_{k,max} - x_{k,min})/2^{N_k}$, where N_k is the number of bits.

We keep the number of organisms in each generation fixed and we allow only one active generation (one generation at the time) ; it means that after the breeding process all the parents are replaced by the children. Next we describe in details the three main processes : selection, breeding and mutation.

3.2. Selection

The selection process chooses the parents for breeding. The probability of selecting one organism is related to its quality in the following way. First the quality Q_i, i.e. the

maximized log-likelihood, of all organisms is computed (index i refers to the organism). The organisms are sorted by decreasing quality Q_i. The selection is made by the roulette selection method : we choose randomly one organism with the probability $Q_i / \sum_j^N Q_j$. With this method the "good" organisms are chosen more often than the "bad" ones.

3.3. Breeding

The second process in GA is the breeding. Two selected parents produce one child. The genes of the child are constructed by mixing the corresponding genes of each parent. We take one part from the first parent and the other part from the second parent. Depending on which parts are chosen, there are several types of breeding. We use two different types : cross-over one point (mid-point) and cross-over two points. For the cross-over one point, each gene of the child is combined out of the first $N/2$ bits of the first parent and from last $N/2$ bits of the second parent (see the left panel of the Figure 1). It is similar for cross-over two points: the gene of the child is build from three equal parental parts (see the right panel of the Figure 1).

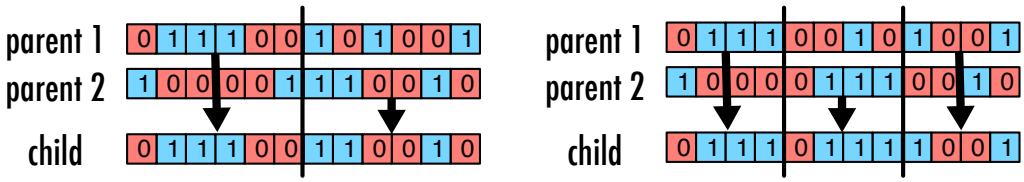

Figure 1. Examples of breeding: cross-over one point on the left and cross-over two points on the right panels

Starting with an initial randomly chosen generation, we increase the quality of our organisms using selection and breeding. But, if we use only those two processes, the range of resulting genes is quite restricted: it is just a combination of the parts from the initial generation. Therefore the exploration of parameter space is rather poor.

3.4. Mutation

In order to increase the exploration of the parameter space, we need to introduce mutation. It works in a way similar to the mutation in the nature. Mutation is a random change of a few alleles in a gene; in our algorithm it corresponds to changing a few bits in a gene of an organism. The probability of mutation is described by a number from 0 to 1 and it is called the probability mutation rate (PMR). We mutate each gene independently and there are several types of mutation. We have used only two possibilities: (i) we always mutate the gene and for each bit we draw a random number from 0 to 1 and flip the bit if the number is lower than PMR (ii) we mutate the gene if the random number is below PMR. Here there are also different ways to mutate a gene: (i) we flip N randomly chosen bits (ii) we flip N adjacent bits. Different types of

mutation together with the value of PMR define the exploration area of the parameter space.

4. Accelerations of genetic algorithm

We have introduced above three fundamental processes of any GA. However, one might need to evolve a very large number of generations before finding the best organisms. To reduce the required number of generations and to give more stability to the algorithm, we introduced several accelerators described below.

4.1. Standard accelerators

In this part, we describe the standard accelerators used in GA.

4.1.1. Elitism The elitism (or cloning) implies that we keep the best organism through the generations. It is possible to clone one or several best organisms into the new generation. The elitism stabilizes the GA because the best point in the parameter space is always preserved and it guarantees the convergence of the algorithm.

4.1.2. Simulated annealing The simulated annealing was already employed in LISA data analysis [16] and proven to be very useful. The smoothness of the quality surface is controlled by the introduced temperature. If it is hot, the quality surface is very smooth and nearly all the organisms ("good" and "bad") can be selected for breeding with a similar probability. If it is cold, the quality surface is very peaked around the mixima and only the best organisms can be selected. Usually, we use a high temperature at the beginning of the search to increase the exploration area and cool it down as we approach the solution.

4.1.3. Evolution of PMR As we said above, the PMR controls the exploration of parameter space. Therefore we can control the search area by changing the PMR during the evolution. Usually we start with a large value for the PMR (about 0.2), then slowly decrease it and give more importance to the breeding. Note that we can control the exploration area using both simulated annealing and PMR, and we use them both as they perform somewhat differently (simulated annealing uses combination of the initial genes without adding new) and the best result is usually achieved if we combine them together.

4.2. Others accelerations

In this part, we describe non-standard acceleration processes introduced by us and which utilizes the properties of the signal and/or of the antenna beam pattern.

4.2.1. Brother We introduced what we call "the brother" system. With each clone we associate one organism (brother) created using specific rules. In our application of the GA for spinning black hole binaries, the brother is used for searching around the mirrored (antipodal) sky position of each clone (we keep all parameters of the clone but flip the sky location).

4.2.2. Local mutation The binary representation creates boundaries in the parameter space. For example, the separation between the gene value 011111 and 100000 is equal to the resolution Δx (i.e. minimal distance) but, as one can see, it is necessary to flip all the bits for making this small step. This problem can be solved by introducing the local mutation. It corresponds to a small random change in the parameter value after mutation.

4.2.3. Fixing bits To find the traces of the signal in the data, we want to explore a large parameter space at the beginning of the search. But after few hundred generations, some of the parameters are already quite well estimated so the exploration of the large range in those parameters starts to slow down the search. At this stage we fix (freeze) the most significant bits of those parameters which reduces the allowed dynamical range.

4.2.4. Specific breeding and mutation As mentioned above, different types of breeding and mutation have different properties (main difference is in the exploration area around the best organism). The genes (i.e. parameters) have not the same evolution during the search. For example, time at coalescence and chirp mass converge to the answer quicker than other parameters. We can customize our algorithm so that each gene has its own type of breeding and mutation and which can also evolve together with the swarm of organisms.

4.2.5. Change of environment A change of the environment corresponds to a change in the quality distribution in the parameter space. The main idea here is that the "good" organism remains "good" in the different environment. Here, we change the maximum allowed frequency of our template (terminate the inspiral at earlier times). The quality distribution for the shortened waveform has not the same local maxima as the quality obtained with the full waveform, but the same global maximum. Therefore, alternating the use of full and chopped waveform helps to move the search away from the local maxima where it has tendency to get stack.

5. First results

We use the GA described above to search GW from inspiralling MBH binaries in Mock LISA Data Challenge 3 [6] and to estimate their parameters. The mock data consist of the gaussian stationary instrumental noise, a Galactic cyclo-stationary background and four to six signals from the inspiralling spinning BHs in the quasi-circular orbits.

To speed up our search and to explore the numerous options which GA provides, we have started with a simplified data set: single GW signal in the instrumental noise. We believe that the algorithm can be easily extended later for more complicated data described above.

To start with, we have done even further simplifications: we have fixed all parameters to their true values besides masses, sky location and time of coalescence. Effectively we started with considering the non-spinning binaries. The spin terms come in GW phase at 1.5 post-Newtonian (spin-orbital coupling) and at 2nd post-Newtonian (spin-spin) orders, so they bring rather small corrections to the phase. This is the idea behind the use of non-spinning templates in LIGO-VIRGO data analysis. Indeed, including the spins in the analysis should only improve accuracy of estimation those parameters. We want to make sure that we can find other parameters before hunting the small corrections. We do not exclude the possibility that including all 15 parameters in the search will create more local maxima in the likelihood and will require extension of our algorithm. However the tuning of GA performed here will work also in the full problem, and preliminary results of all 15-parameters search show that it is true.

The sources can be separated in two types : the sources with a coalescence within the observational time and the ones with a coalescence outside the observational time. We have investigated those two cases separately and present our results below.

5.1. Coalescence within the observational time

We have analyzed one year of simulated LISA data with the signal with following parameters: signal-to-noise ratio SNR = 1250, $\{\ \beta = -0.38896\ rad$, $\lambda = 3.28992\ rad$, $t_c = 19706568.3273\ sec$, $M_c = 1589213.34\ M_\odot$, $\eta = 0.236469\ \}$. We have run GA fifty times with different random initial states for 2000 generations each. Figure 2 shows the best organism obtained from each evolution. For 48 out of 50 runs, the absolute error in the sky position is less than 3 degrees, the fractional error in the chirp mass is less than 0.25 % , in η is less than 0.085 % and in time at coalescence the error is smaller than 0.0005 %.

5.2. Coalescence outside the observational time

Similarly we have considered one year of simulated LISA data with a source coalescing outside the time of observation. The SNR of that signal was 47, and other parameters are $\{\ \beta = -0.90706300796\ rad$, $\lambda = 2.85511464611\ rad$, $t_c = 34603008.0\ sec$, $M_c = 1608239.35302\ M_{solar}$, $\eta = 0.221285791958\ \}$. Figure 3 shows 50 best organisms from each run of GA. The results are sligtly worse, mainly, because of the lower SNR: for 22 out the 50 jobs, the absolute error on the sky is less than 4 degrees, the relative error on chirp mass is less than 0.56 % , η determined with an error smaller than 0.68 % and the error in the time at coalescence less than 0.0012 %. Other 22 best organisms have found the opposite sky position (it is a very strong degeneracy for this (low frequency) source) with similar error in the chirp mass, η and the time at coalescence.

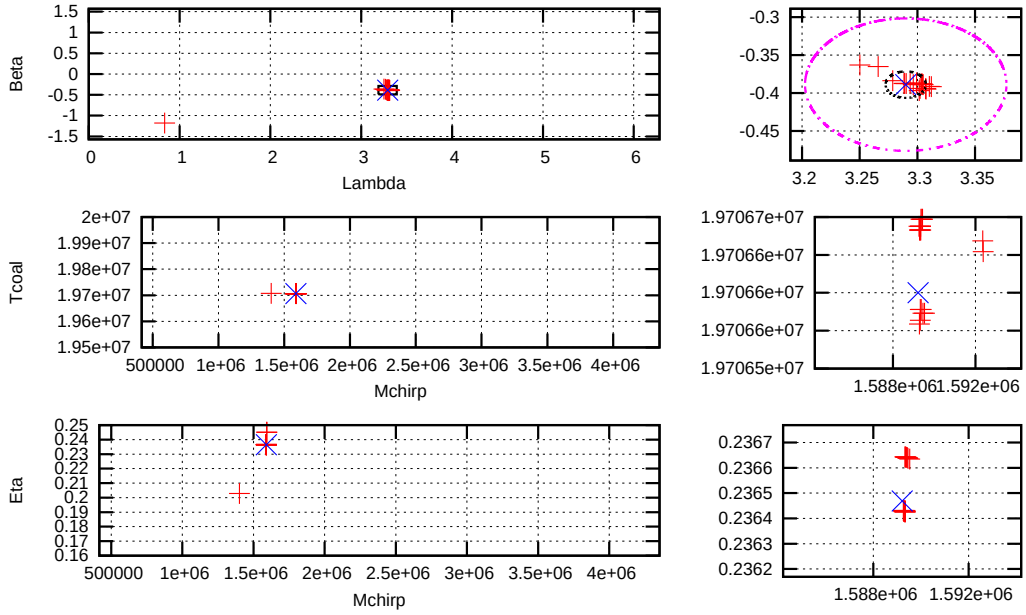

Figure 2. Distribution of 50 best organisms from 50 runs of GA. The source coalesces within the observational time. The pluses '+' correspond to the best organism of each run after 2000 generations. The cross 'x' corresponds to the true value of the parameters. On the left side, graphs show the full prior range of parameters. On the right side, we zoom onto the area around the true value. On the top-right graph, the big circle corresponds to the error of 5 degrees and the small one is 1 degree error area.

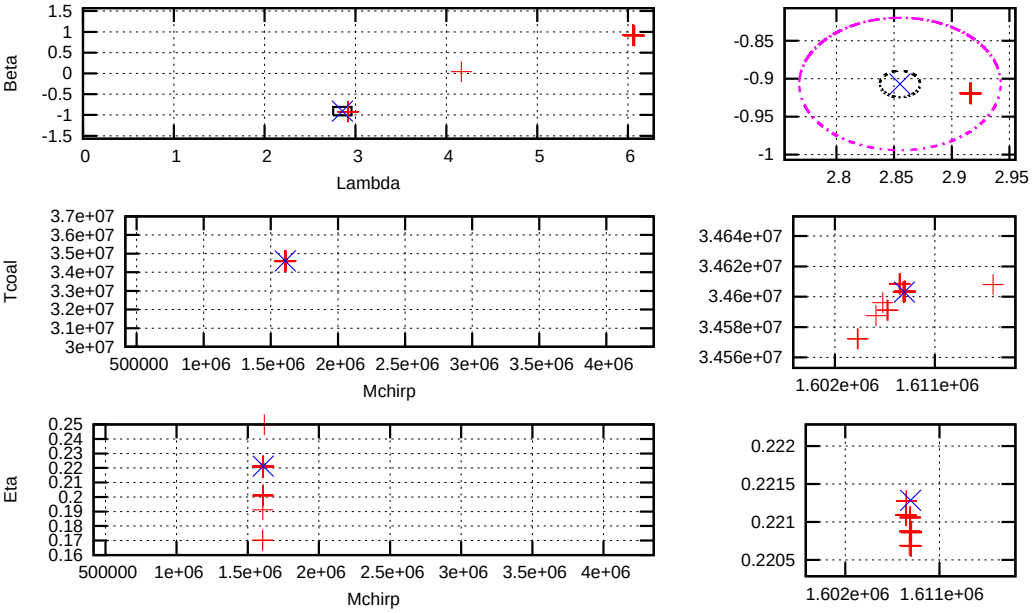

Figure 3. Results of 50 runs of GA for the source with coalescence beyond the end of the observational time. The pluses '+' correspond to the best organisms of each run after 2000 generations. The cross 'x' corresponds to the true value of the parameters. On the left side, graphs show the full prior range of the parameters. On the right side, we zoom around the true value. On the top-right plot, the big circle corresponds to the 5-degrees error circle and the small one is for 1 degree error region.

The GA shows an excellent performance in both cases.

6. Conclusion

We have presented an extended version of the GA to search for spinning BHs in the simulated LISA data. We devised several acceleration procedures for GA which are based on the properties of the signal and of the detector antenna pattern. The algorithm shows remarkable performance for a single signal in the simulated instrumental noise assuming the precession-related parameters are known. We have also recently tried this algorithm in full, 15 parameters, search and we have already got first very promising results. We see that algorithm needs some more tuning, and we should extend it to search for muti-modal (and multiple signals) solutions, this will be the topic of a separate publication.

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